KENYA MEDICAL RESEARCH INSTITUTE

KEMRI

In Search of Better Health

14th KASH CONFERENCE

Theme:

Harnessing Biomedical Research Innovations and Big Data for Health System Resilience, Local Manufacturing and Commercialization

ABSTRACT BOOK

KEMRI Annual Scientific & Health (KASH) Conference

13th - 16th February, 2024

Safari Park Hotel, Nairobi, Kenya

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In Search of Better Health

The 14th KEMRI Annual Scientific & Health (KASH) Conference

13th - 16th February 2024
SAFARI PARK HOTEL,
NAIROBI, KENYA

Theme:
Harnessing Biomedical Research Innovations and Big Data for Health System Resilience, Local Manufacturing and Commercialization

Organized by:
Kenya Medical Research Institute (KEMRI)

P. O. Box 54840-00200
Nairobi, Kenya.
www.kemri.go.ke

ACKNOWLEDGEMENTS

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Design and Layout

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MESSAGE FROM DIRECTOR GENERAL KEMRI

PROF. Elijah Songok

A warm welcome to the 14th KEMRI Annual Scientific and Health Conference, aptly named KASH 14. This year's event is marked by a unique pre-conference session that takes an innovative dive into medical manufacturing, setting the stage for the main discourse during this conference. This groundbreaking approach emphasizes the integral connection between research outputs and the commercialization of health products and technologies, reflecting our commitment to a comprehensive exploration of healthcare advancements.

KEMRI, as a premier biomedical research institution, has consistently played a pivotal role in advancing disease diagnosis, treatment, and management. Through our relentless dedication to product development, innovative technologies, clinical trials, and service provision, we have contributed immensely to the improvement of healthcare outcomes.

This year, KEMRI is taking a bold step towards fostering a collaborative environment for the development, nurturing, and evaluation of public value. Together with our parent Ministry of Health, we have joined hands with the local manufacturers, various health research institutions, and the private sector to create an ecosystem that promotes Health Products and Technologies (HPT) economic growth. Our shared vision is to drive innovation, inclusivity, and sustainability in the healthcare sector in Kenya.

I am excited to announce a key highlight of this year’s KASH conference—an exhibition and dialogue on the local manufacture of HPT. This initiative is our humble contribution towards instilling confidence in locally manufactured HPT while leveraging on KEMRI's expertise to generate solutions geared to revamp the local manufacturing landscape. By actively shaping and co-creating markets, is a clear demonstration of the government's political will in the advancement of the Universal Health Coverage (UHC) agenda through locally manufactured HPT.

In conclusion, let me express our collective excitement for the opportunities that lie ahead during KASH 14. May this conference be a melting pot of ideas, a catalyst for collaboration and groundbreaking advancements in biomedical research.

On behalf of the KEMRI Board of Directors and the Management, I would like to take a moment to express our heartfelt gratitude to our dedicated staff for the immense hard work they have put in. Their unwavering commitment has been instrumental in achieving the milestones we have been able to, to date. Each member of our team has played a crucial role in advancing the Institute’s mission and contributing to the noteworthy successes we celebrate today.

To all the participants who submitted their abstracts, thank you for contributing to the academic richness of this conference. Your research, findings, and experiences that shall be shared during the next four days will undoubtedly contribute to advancing the collective understanding of crucial issues in health and biomedical research. Your active participation is the cornerstone of the success of KASH 14.

I thank you all for your participation and support.

Prof. Elijah Songok
Ag. Director General
KENYA MEDICAL RESEARCH INSTITUTE

CONFERENCE OVERVIEW BY KASH CHAIR

DR. CECILIA MBAE

A warm welcome to each and every one of you to the prestigious 14th KEMRI Annual Scientific and Health Conference (KASH14) being held from February 13th, to 16th, 2024. This year's theme, "Harnessing Biomedical Research Innovations and Big Data for Health System Resilience, Local Manufacturing, and Commercialization," underscores our commitment to advancing healthcare through cutting-edge research and the utilization of transformative technologies.

The KASH conference stands as a cornerstone in KEMRI's annual calendar of events, aiming to convene researchers,collaborators (both local and international), policymakers, and various stakeholders in the field of medical research. This year, the conference takes a different shape in that it is preceded by a pre-conference event with the theme "Market Shaping For Local Innovations and Manufacturing of Health Products and Technologies Towards Attainment of UHC In Kenya: The Role of Research & Development". A dialogue seeking to promote confidence in locally manufactured Health Products and Technology (HPT) and showcase government commitment to advancing the Universal Health Coverage (UHC) through locally made products.

The upcoming conference promises an extensive array of scientific content, featuring 10 plenary talks and nine symposia dedicated to exploring topical issues in health research. Notably, we are delighted to announce the reception of a total of 364 abstract submissions, an increase from 253 abstracts submitted last year. We will have 243 abstracts presented in 27 parallel oral sessions and 77 poster presentations. It is worth mentioning that the abstracts hail from various countries, including the United States, Netherlands, Germany, Ghana, Tanzania, and more, solidifying KASH's status as an international conference.

In recognition of the significance of nurturing young talent, we have dedicated a session to young investigators, receiving 40 submissions. The winners of this session will be duly acknowledged. Additionally, attendees will have ample opportunities to network, establish new connections, and foster long-term partnerships, both through in-person interactions and the dynamic virtual platform.

The conference boasts distinguished keynote and plenary speakers—world-class scientists possessing profound insights and a wealth of knowledge not only on disease burdens but also on practical health interventions. The Opening Keynote Address will be delivered by Mr. Rajni Vora, delving into the topic of "Translating Research Outputs into Health Security through Commercialization of Health Products and Technologies – Learning for Targeted Investment." The plenary sessions will feature nine speakers addressing a spectrum of topics, including partnerships in digital health, universal health coverage, research innovation, forensic science, issues of triple threat, and various other biomedical research themes.

Ladies and gentlemen, I would like to express our heartfelt appreciation to our sponsors for their indispensable support in bringing the 14th KEMRI Annual Scientific and Health Conference to fruition. Special appreciation to KCB Bank and F&S Scientific in the Platinum category, Carramore International Limited, Anatech Africa, and TNO Innovation and Development Program in the Gold category, the Center for Health Solutions Kenya, PS Kenya Limited, Inqaba Biotec Limited, Geminia Insurance Company Limited, in the Silver category, and over 20 exhibitors who took up the booths. Your partnership has been truly uplifting, and we are grateful for your pivotal role in making this event a success. Thank you for your commitment to advancing scientific and health initiatives. Your support has created a collaborative platform that significantly contributes to our shared goals.

As the local organizing committee, we are delighted in devoting ourselves to provide leadership, information, and capacity leading to the enhancement of human health, and quality of life through dissemination of research findings, innovations and service delivery. I encourage all participants to actively engage in the interesting explorations over the next three days and wish you a successful, fruitful, and a memorable conference.

Cecilia Mbae, PhD
Chair, KASH Organizing Committee

PROGRAM AT A GLANCE

DAY ONE, TUESDAY 13TH FEBRUARY 2024	
TIME	**MARKET SHAPING FOR LOCAL INNOVATIONS AND MANUFACTURING OF HEALTH PRODUCTS AND TECHNOLOGIES TOWARDS ATTAINMENT OF UHC IN KENYA: THE ROLE OF RESEARCH & DEVELOPMENT**
0800-0830hrs	**Arrival & Registration**
0830-1000hrs	**KASH Official Opening Ceremony**
0830 - 0920hrs	Remarks • Remarks • Chair KASH • DRD, KEMRI • Director General, KEMRI • Chair BoD, KEMRI • Director HPT, MoH • Director General, MoH
	Official Address and Opening by the Chief Guest: – Cabinet Secretary, Ministry of Health, Nakhumicha S. Wafula.
0920 - 0950hrs	**Keynote Address** Empowering Kenya through Local Manufacturing of Innovative Health Products and Technologies for Universal Health Coverage (UHC). **Mr. Rajni Vora,** MD, Revital Healthcare (EPZ) Limited **Session Chair: Dr Steve Wandiga** **Co-Chair: Lilian Mayieka**
0950-1030hrs	**Diagnostics** **KEMRI Case Study:** Translating Research Outputs into Health Security through Commercialization of Health Products and Technologies – Learning for Targeted Investment. **Dr. James Kimotho, Prof. Samson Muuo, NAPREDA/CTMDR**
1030-1100hrs	**TEA BREAK & EXHIBITIONS**
11-00-1130hrs	**Launch of KEMRI Documentary** **KEMRI Corporate Communications**
11-30-1250hrs	**Biopharmaceuticals** Building a Regional Biopharmaceutical Innovation & Production Ecosystem [10 min presentation by each panelist followed by 30 min panel discussion] • **MoH, Health Products and Technology –** Dr. Tom Menge (Pharma innovation/manufacturing policy) • **KEMRI** – Dr. Bernards Ogutu (Drug discovery) • **Villgro Africa** – Dr. Robert Karanja (Biologicals discovery) • **DNDi** - Prof. Sam Kariuki (Clinical validation) • **BIOVAX** – Dr. Michel Lusiola – Pharma industry (Vaccine manufacturing) • **AMREF** – Innovations Landscape **Session Chair: Dr. Lucas Nyabero** **Co-Chair: Dr. James Kimotho**
12-50-1310hrs	KHF/USAID
1310-1410hrs	**LUNCH BREAK & EXHIBITIONS**

1410-1530hrs	**Medical Devices & Equipment** **Building a Regional Medtech Innovation & Production Ecosystem** [10 min presentation by each panellist followed by 30 min panel discussion] • Kenyatta University – Dr. June Madete • HewaTele – Dr. Bernard Olayo/Dr. Wali Zulfiqar • Villgro Africa – Eng. Wambui Gachiengo-Nyabero • Drop Access – Eng. Norah Magero • DeKUT – Prof. Eng. Ndirangu Kioni/Rice University **Session Chair: Dr. Robert Karanja** **Co-Chair: Dr. Veronica Manduku**
1530-1540hrs	**Recap and recommendations,** Dr. Damaris Matoke-Muhia
1540-1600hrs	**Launch of Research Management Administration, KEMRI** Director Cooperate Services, KEMRI
1600-1700hrs	**Launch of KEMRI Human Genetics and Forensics Society. Chair:** Ms. Eva Aluvaala
1700-1705hrs	**Vote of Thanks – Chair KASH**, Dr. Cecilia Mbae
1705-1730hrs	**TEA BREAK & DEPARTURE**
DAY TWO, 14TH FEBRUARY 2024	
0730-0830hrs	Arrival & Registration
0830-0900hrs	Plenary Session 1: **Dr. Sam Akech** “Sustainable Partnership to Strengthen Data Availability and Surveillance Capacity to Effectively Prevent, Detect, and Respond to Known and Emerging Threats”
0900-0925hrs	Plenary Session 2: **Dr. Joyce Wamicwe** “Digital Health and Universal Health Coverage- Unpacking the Vision for Implementation.”
0925hrs-0950hrs	Plenary Session 3: **Prof Ben Ngoye** “Capacity Building for the Achievement of UHC in Kenya: Current Problems and Future Challenges."
0950- 1015hrs	Plenary Session 4: **Dr. Robert Karanja** “Research innovation and Commercialization: Bridging the Know-Do Gap to Transform Research Outputs to Impact”
Session Chair:	**Dr Steve Wandiga**
Rapporteur:	**Lilian Mayieka**
1015HRS-1045HRS: TEA BREAK	

SCIENTIFIC SESSION 1 – 6 PARALLEL SESSIONS					
1045hrs-1245hrs	**1045hrs-1245hrs**	**1045hrs-1245hrs**	**1045hrs-1245hrs**	**1045hrs-1245hrs**	**1045hrs-1245hrs**
Scientific Session 1: Rising Star Award-1 **VENUE:** AMBOSELI	**Scientific Session 2:** Natural Products **VENUE:** TSAVO	**Scientific Session 3:** MCH -1 **VENUE:** SAMBURU	**Scientific Session 4:** Malaria-1 **VENUE:** BOGORIA	**Scientific Session 5:** Health Systems -1 **VENUE:** MT. KENYA C	**Scientific Session 6:** Mental Health **VENUE:** MT. KENYA D
Session Chair : Dr Joseph Mwangangi/ Dr. Doris Njomo **Rapporteur :** Dr Limbaso Konongoi//Francis Kimani/Jane Ikapesi/Maureen Ekisa	**Session Chair:** Dr. Beatrice Irungu **Rapporteur:** Dr. Sospeter Njeru	**Session Chair :** Dr. Benson Singa **Rapporteur :** Schiller Mbuka	**Session Chair:** Dr. Jeremiah Gathirwa **Rapporteur:** Brian Seda	**Session Chair:** Bridget Kimani **Rapporteur:** Mariam Macharia	**Session Chair:** Dr. Mary Bitta **Rapporteur:** Dr. Lucy Chite
1245hrs-1345hrs LUNCH BREAK					

1345-1430HRS POSTER SESSION					
Poster Session: **Screen 1-** Public Health **VENUE:**	**Poster Session 2:** **Screen 2:** Health Systems **VENUE:**	**Poster Session 3:** **Screen 3-** Virology **VENUE:**	**Poster Session 4:** **Screen 4-** Malaria **VENUE:**	**Poster Session:** **Screen 5:** Vector Biology **VENUE:**	**Poster Session:** **Screen 6-** TB **VENUE:**
Judges: Dr. Sophie Uyoga Bridget Kimani	**Judges:** Kariuki Ngumo Susan Kavai	**Judges:** Dr. Konongoi Limbaso Dr. Samoel Khamadi	**Judges:** Dr. Sospeter Njeru Francis Kimani	**Judges:** Dr. Damaris Matoke-Muhia Seline Omondi	**Judges:** Dr. Jane Ong'ang'o Asiko Ong'ayo
SYMPOSIUM 1-6					
1430 – 1700hrs	**1430 – 1700hrs**	**1430 – 1700hrs**	**1430 – 1700hrs**	**1430 – 1700hrs**	**1430 – 1700hrs**
Symposium 1: Genomics without tears **VENUE:** AMBOSELI	**Symposium 2:** Advancing Evidence for the Global Implementation of Spatial Repellents (AEGIS) **VENUE:** TSAVO	**Symposium 3:** Knowledge Management **VENUE:** SAMBURU	**Symposium 4:** KEMRI Programs and Clusters Flagship Projects **VENUE:** BOGORIA	**Symposium 5:** Broad One Health Endoctocide-base Malaria Intervention in Africa (BOHEMIA) **VENUE:** MT. KENYA C	**Symposium 6:** Harnessing Big Data for Population Health, Clinical Decision Making and Health System Resilience **VENUE:** MT. KENYA D
Session Chair: Dr. John Waitumbi **Rapporteur :** Dr. Beth Mutai & Ruth Cheruto	**Session Chair:** Dr. Steve Harvey **Rapporteur:** Dr. Bernard Abongo & Sheila Mbaabu	**Session Chair:** Lillian Mayieka **Rapporteur:** Wambui Njonge & Mercy Tuluso	**Session Chair:** Dr. Steve Wandiga **Rapporteur:** Jennifer Ngetich & Bridget Kimani	**Session Chair:** Dr. Joseph Mwangangi **Rapporteur:** Ruth Shambi &Tabitha Wambui	**Session Chair:** Prof. Wallace Bulimo **Rapporteur:** Belinda Azzam & Asiko Ong'ayo
TEA BREAK AND DEPARTURE					
END OF DAY 2					

DAY THREE, THURSDAY 15TH FEBRUARY 2024	
0730-0830hrs	**Arrival & Registration**
	PLENARY SESSION
0830- 0855hrs	Plenary Session 4: **Prof. Rosemary Rochford** "Uncovering the Etiology of Burkitt Lymphoma: Results from a 20-Year Odyssey in Kenya."
0855 - 0920hrs	Plenary Session 5: **Dr. John Kimani** "Forensic Biology Trend In Kenya (Past, Present and Future)"
0920hrs-0950hrs	Plenary Session 6: **Dr. Oduor Johanssen** "Shakahola Cases; Human Remains Identification Process; Case Presentation."
Session Chair	**Dr. Eric Ochomo**
Rapporteur	**Ibrahim Mwangi**

PARALLEL SCIENTIFIC SESSION 7 – 12

1005-1105hrs	1005-1105hrs	1005-1105hrs	1005-1105hrs	1005-1105hrs	1005-1105hrs
Scientific Session 7: TB **VENUE:** AMBOSELI	**Scientific Session 8:** Health Systems-2 **VENUE:** TSAVO	**Scientific Session 9:** Malaria-2 **VENUE:** SAMBURU	**Scientific Session 10:** Public Health-1 **VENUE:** BOGORIA	**Scientific Session 11:** Vector Biology-1 **VENUE:** MT. KENYA C	**Scientific Session 12:** MCH -2 **VENUE:** MT. KENYA D
Session Chair: Dr Jane Ong'ang'o **Rapporteur:** Barbra Miheso	**Session Chair:** Enock Kebenei **Rapporteur:** Timothy Kipkosgei	**Session Chair :** Dr. Sophie Uyoga **Rapporteur :** Mercy Tuluso	**Session Chair:** Dr. Richard Omore **Rapporteur:** Steven Onteri	**Session Chair:** Ernest Wandera **Rapporteur:** Dr. Edith Chepkorir	**Session Chair:** Dr Elizabeth Echoka **Rapporteur:** Schiller Mbuka

1105-1130hrs: TEA BREAK

PARALLEL SCIENTIFIC SESSION 13-18

1130-1300hrs	1130-1300hrs	1130-1300hrs	1130-1300hrs	1130-1300hrs	1130-1300hrs
Scientific Session 13: Health Systems -3 **VENUE:** AMBOSELI	**Scientific Session 14:** Rising Star Award-2 **VENUE:** TSAVO	**Scientific Session 15:** Public Health-2 **VENUE:** SAMBURU	**Scientific Session 16:** Vector Biology - 2 **VENUE:** BOGORIA	**Scientific Session 17:** MCH -3 **VENUE:** MT. KENYA C	**Scientific Session 18:** NCDs **VENUE:** MT. KENYA D
Session Chair : Dr. Richard Mutisya **Rapporteur :** Ishmael Ahamed	**Session Chair** Dr Joseph Mwangangi/ Dr. Doris Njomo **Rapporteur:** Dr Limbaso Konongoi//Francis Kimani/Jane Ikapesi/Maureen Ekisa	**Session Chair :** Dr. Rose Bosire **Rapporteur:** Dr. Beatrice Ongadi	**Session Chair:** Dr. Damaris Matoke-Muhia **Rapporteur:** Seline Omondi	**Session Chair:** Dr. Phelgona Otieno **Rapporteur:** Olga Mashedi	**Session Chair:** Dr. Vera Manduku **Rapporteur:** Ibrahim Mwangi

1400-1430hrs: LUNCH BREAK

1400-1430hrs: POSTER SESSION

Poster Session: Screen 1- NCDs **VENUE:**	**Poster Session 2: Screen 2-** NTDs **VENUE:**	**Poster Session 3: Screen 3-** MCH **VENUE:**	**Poster Session 4: Screen 4-** HIV **VENUE:**	**Poster Session: Screen 5-** AMR **VENUE:**	
Judges: Dr. Vera Manduku Dr. Linet Ongeri	**Judges:** Dr. Erastus Mulinge Henry Kanyi	**Judges:** Dr. Benson Singa Dr. Lucy Chite	**Judges:** Dr. Samuel Khamadi Dr. Edith Chepkorir	**Judges:** Dr. John Mwaniki Susan Kavai	

SYPOSIUM 7-10 & PARALLEL SCIENTIFIC SESSION 19, 20, 21

1430 – 1700hrs	1430 – 1700hrs	1430 – 1700hrs	1430 – 1700hrs	1430 – 1700hrs	1430 – 1700hrs
Symposium 7: Human Genomics and Forensics **VENUE:** AMBOSELI	**Symposium 8:** Management and control of invasive Anopheles stephensi in Kenya **VENUE:** TSAVO	**Symposium 9:** KEMRI Programs and Clusters Flagship Projects **VENUE:** SAMBURU	**Scientific Session 19:** Public Health- 3 **VENUE:** BOGORIA	**Scientific Session 20:** Health Systems -4 **VENUE:** MT. KENYA C	**Scientific Session 21:** HIV **VENUE:** MT. KENYA D

Session Chair Eva Aluvaala **Rapporteur:** Belinda Azzam & Tiffany Wandera	**Session Chair** Dr. Elijah Juma **Rapporteur:** Benyl Ondeto & Tabitha Wambui	**Session Chair** Dr. Linnet Ongeri **Rapporteur:** Julie Mkawuda & Lydia Matoke	**Session Chair :** Dr. Joan Olale **Rapporteur :** Viola Chuchu	**Session Chair :** Susan Kavai **Rapporteur :** Kelvin Kering	**Session Chair:** Dr. Samoel Khamadi **Rapporteur:** Asiko Ong'ayo

TEA BREAK AND DEPARTURE

END OF DAY 3

DAY FOUR, FRIDAY 16TH FEBRUARY 2024

0700-0830hrs	**ARRIVAL & REGISTRATION**

PLENARY SESSION

0830- 0855hrs	Plenary Session 7**: Dr. Ruth Masha** "Whole Government Approach Towards Ending Adolescent Triple Threat (New HIV Infections, Adolescent Pregnancies and Sexual and Gender-based Violence in Kenya)"
0855 - 0920hrs	Plenary Session 8: **Dr. Pauline Mwinzi** "The Remarkable Progress in Eliminating Neglected Tropical Diseases in Africa"
0920hrs-0950hrs	Plenary Session 9: **Prof Digby Warner** "Re-imag(in)ing Tuberculosis through a Different Lens"
Session Chair:	**Dr. Doris Njomo**
Rapporteur:	**Susan Kavai**

PANEL DISCUSSION

0950-1030hrs	Complementary Feeding: The Role of different Sectors Organized by Academia and Research -Academic Research Networks- Scaling up Nutrition Movement (SUN)
Session Moderator:	Dr. Zipporah Bukania
Rapporteur:	Kariuki Ngumo

1030 - 11000hrs TEA BREAK

1100-1300hrs	**1100-1300hrs**	**1100-1300hrs**	**1100-1300hrs**	**1100-1300hrs**	**1100-1300hrs**
Scientific Session 22: Public Health-4 **VENUE:** AMBOSELI	**Scientific Session 23:** Virology **VENUE:** TSAVO	**Scientific Session 24:** AMR **VENUE:** SAMBURU	**Scientific Session 25:** NTDs and One Health **VENUE:** BOGORIA	**Scientific Session 26:** Vector Biology-3 **VENUE:** MT. KENYA C	**Scientific Session 27:** Health Systems -5 **VENUE:** MT. KENYA D
Session Chair: Dr. Elizabeth Echoka **Rapporteur:** Schiller Mbuka	**Session Chair :** Dr Fred Eyase **Rapporteur :** Kelvin Kering	**Session Chair :** Dr. John Mwaniki **Rapporteur :** Susan Kiiru	**Session Chair:** Dr. Erastus Mulinge **Rapporteur:** Olga Mashedi	**Session Chair:** Dr. Damaris Matoke-Muhia **Rapporteur:** Tiffany Wandera	**Session Chair:** Bridgit Kimani **Rapporteur:** Ruth Cheruto

1300-1400HRS: LUNCH BREAK

CLOSING CEREMONY

1400-1630hrs	Master Of Ceremony: **Dr. Sophie Uyoga**
	Conference Outcomes & Resolutions Chief Rapporteur: **Dr. Steve Wandiga**
	Awarding Ceremony: **Dr. Vera Manduku**
	Sponsors and Exhibitors: **Dr Linus Ndegwa**
	Official Closing remarks: KASH Chair: **Dr. Cecilia Mbae** Ag. Director Research and Development: **Prof. Nelly Mugo** Ag. Director General & CEO, KEMRI: **Prof. Elijah Songok** Chair KEMRI Board of Directors: **Dr. Abdullahi Ali Ibrahim, CBS**
	Vote of thanks: **Dr. Damaris Matoke-Muhia**

KEYNOTE SPEAKER

Mr Rajnikant Chandulal Vora

Bio

Chairman to Revital Healthcare, Mr Rajni holds extensive experience after holding a business position for over 40 years. Mr Rajni began his entrepreneurial journey at the age of 16 by trading various small commodities in Mombasa.
This led to the eventual development of the family business, D.C.K Chandulal Vora and Companies LTD. The company held distribution rights for multinational organisations such as Reckitt Benckiser, Unilever, Beta Healthcare, Colgate Palmolive, Nestle foods, and Kapa Oil to assist these companies' expansion across the East African territory. Over his journey, the Chairman has held experience with the Agriculture, Accounting, Import/Export Trading, and Confectionary sectors while establishing industries of Toothpaste in Uganda and confectionary manufacturing in Tanzania.
His vision led to the establishment of Revital Healthcare [EPZ] Ltd. In 2008.
Under his stewardship and supervision at Revital, the following milestones have been achieved:

- Over the past 15 years in operation, Revital has grown to become the largest manufacturer of medical devices in Africa, manufacturing over 50+ essential health commodities, and a network across 28 countries globally.
- Achieved 8 WHO-PQ Certifications for Re-Use Prevention Syringes (only manufacturer in Africa to achieve this status).
- Stand out as a global manufacturer with international accreditations such as ISO 13485, CE mark for Europe, and USFDA.
- Guided the company to achieve a patent for Africa's first ever early activation syringe, and 1 out of 4 companies globally.
- Collaborated with the team to work alongside the Gates Foundation to develop the above patent.
- Advised the team on the partnership with various organizations including UNICEF, PFSCM, AMSP and others for the procurement of medical devices for global supply.

Title Talk

Empowering Kenya through Local Manufacturing of Innovative Health Products and Technologies for Universal Health Coverage (UHC)

PLENARY SPEAKERS

Dr. Pauline NM Mwinzi, PhD

Technical Officer
Expanded Special Project for Elimination of NTDs (ESPEN)
WHO Regional Office for Africa

Bio

Dr Pauline Mwinzi is the WHO regional advisor for Schistosomiasis (SCH), also known as Bilharzia, and soil-transmitted helminthiasis (STH), including neglected zoonotic diseases in the Africa region. Her current role includes technical support to Member States to implement the WHO NTD Roadmap 2030 and tracking progress towards elimination for SCH/STH in the Africa region. Before joining the WHO, She was the Chief Research Scientist and Head of NTD Unit, as well as the PI, KEMRI-CDC at the Center for Global Health Research (CGHR), Kenya Medical Research Institute (KEMRI), Kisumu, Kenya. Her specialization is in Parasitology and Immunology (PhD, 2005). She trained at the Universiteit Utrecht Medical School, The Netherlands on a post graduate research fellowship, CDC Atlanta on an ISID scholarship and at Kenyatta University on a WHO/TDR PhD scholarship. She was a Wellcome Trust Fellow between 2008-2010. While at KEMRI, she served as Principal Investigator for multi-country collaborative projects with SCORE (www.uga.edu/score) and EFINTD (EFINTD.org) among others. She was among a cohort of 6 fellows whom WHO/TDR recruited for Research Leadership in 2010 in Geneva. Between 2004-2005, She trained in Bioethics at the University of Cape Town, and on Research Leadership at the University of Amsterdam in 2012. She was the Founding Chair for the ARNTD.org from 2012-2016. She also founded and convened the KEMRI Annual NTD Conference, which had held over 12 annual conferences by 2019, before merging with INCO-NTD an initiative of the ARNTD. From 2014-2016, She served as Chair of the KEMRI Annual Scientific Health Conference (KASH). During this time, she introduced the "American society for Tropical Medicine & Hygiene (ASTMH) in Kenya" convened alongside KASH. Between 2004 and 2017, she taught graduate school Bioethics and Immunology/ Parasitology in Kenyan Universities. She has experience in leading large research teams, programme management, capacity building, fundraising and public health policy & advocacy. She has published over 90 peer reviewed scientific papers and serves in several international scientific advisory committees for research networks on tropical diseases. During her free time, Dr Mwinzi mobilizes professionals for community development in her home country, Kenya.

Talk Title:

Unleashing Hope: The Remarkable Progress in Eliminating Neglected Tropical Diseases in Africa

Abstract

The World Health Organization (WHO) oversees a portfolio of 20 Neglected Tropical Diseases and c(NTDs), which contribute to approximately 14.5 million disability-adjusted life years (DALYs). NTDs historically affect marginalized populations, perpetuating poverty cycles. Over the past decade, global progress against NTDs has been remarkable, with a 25% reduction in demand for interventions, representing an 80 million-person decrease between 2020 and 2021. The calculated burden of disease in disability-adjusted life years has consistently declined. By January 2024, at least 50 countries globally have eliminated at least one NTD, marking significant progress toward the 100-country target for 2030. Despite these achievements, challenges persist, particularly in the African Region, where 584 million individuals, 35.3% of global demand, require annual treatments.

This presentation will delve into the transformative impact of NTD elimination, emphasizing restored hope, dignity, and improved quality of life in affected communities. It will highlight the collective efforts of governments, NGOs, and global health initiatives, covering topics such as mass drug administration, research advancements, community-based interventions, and multi-stakeholder partnerships. The talk aims to inspire sustained commitment, encourage knowledge-sharing, and explore further advancements in the global initiative to eliminate NTDs in Africa.

Robert M. Karanja, PhD

Co-Founder and Chief Innovation Officer, Villgro Africa

Bio

Robert is a biomedical scientist and development entrepreneur with over 20 years of experience in STEM and development sectors. He holds a PhD in Parasitology and Entomology from the Jomo Kenyatta University of Agriculture & Technology (JKUAT).
Starting his career as a scientist at the Kenya Medical Research Institute (KEMRI), Robert was actively involved in the establishment of the intellectual property (IP) and technology transfer office (TTO). This nurtured his passion for transforming Africa's development challenges into market opportunities through innovation in the life sciences. He contributed to intrapreneurial ventures at KEMRI such as developing diagnostics, nutraceuticals & phytomedicines products. Building on this experience, he launched a bio-entrepreneurship bootcamp at Strathmore University Business School for research commercialization in health and agriculture sectors. This paved the way for his entrepreneurial career as the Founding CEO at Villgro Africa, a position he held until 2020, to focus on building the health and life sciences innovation ecosystem in the role of Chief Innovation Officer. In addition, Robert provides strategic leadership in developing Africa's knowledge economy in various capacities including as Chairman - ISAAA Africenter; Director & Chairman, Technical Committee – KeNIA; Chairman - Association of Startup & SME Enablers of Kenya (ASSEK), and Chairman, Steering Committee – Coaliton for Health Research & Development (CHReaD).
Contacts: Email *Robertkaranja@villgroafrica.org* ; Mobile +254 722 915838

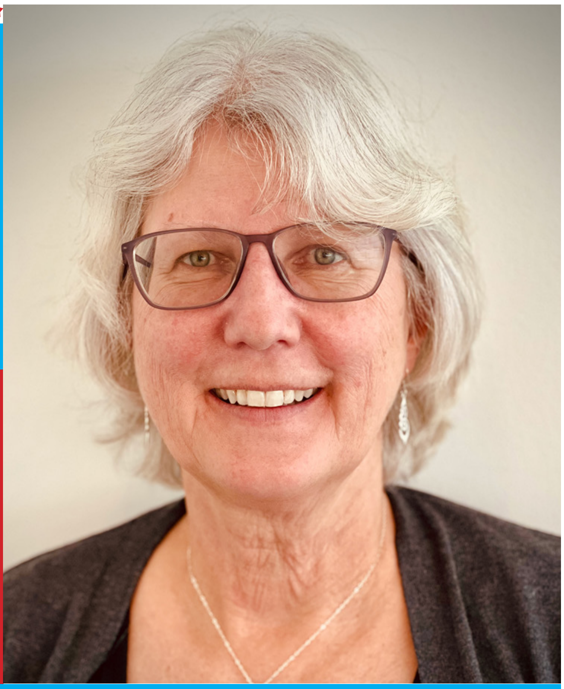
Talk Title:

Research innovation and Commercialization: Bridging the Know-Do Gap to Transform Research Outputs to Impact.

Abstract

Problem statement: Africa contributes 7.6% of publications to the world of science and one-third of all international publications in tropical medicine. This denotes a robust and mature health R&D ecosystem with significant infrastructure, critical mass of human resource and strategic linkages with global collaborators. However, this investment has failed to translate into Africa's health security with the recent COVID19 pandemic revealing the soft underbelly of the continent's dependence on imported health technologies.

Bridging the know-do gap: The last 10 years have seen a significant change in the health R&D landscape with the emergence of a nascent health and life sciences bioeconomy in Kenya and the region. Villgro Africa has been at the vanguard of this transformation as the first sector-specific early-stage investor and business incubator that is investing in the development of research outputs into health products and their commercialization in Africa and abroad. This has catalyzed the growth of a health innovation ecosystem that provides new services and resources that were previously not available to entrepreneurial scientists that have a desire to translate their scientific output into tangible health solutions that impact patients' lives. Here, we highlight these new opportunities to inform academia on how to take advantage of the ecosystem's offerings to explore an impactful and fulfilling career as an entrepreneurial scientist.



Prof. Rosemary Rochford

Bio

Dr. Rosemary Rochford is a Professor Emeritus at the University of Colorado. Dr. Rosemary Rochford earned her PhD in 1989 from the University of California, Irvine. She went on to a post-doctoral fellowship in Immunology at The Scripps Research Institute in La Jolla California. Dr. Rochford has held faculty positions at the University of Michigan, SUNY Upstate Medical University and University of Colorado. Dr. Rochford served in several academic leadership roles including Chair of Microbiology and Immunology, SUNY Upstate Medical University and co-Director of the Climate and Health Program at the University of Colorado. Throughout her career, her research interests have been on persistent viruses and how they emerge to cause disease. Her research on the etiology of Burkitt lymphoma has been funded through the US National Institutes of Health since 2004.

Talk Title:

Uncovering the etiology of Burkitt lymphoma: results from a 20 year odyssey in Kenya

Abstract

Burkitt lymphoma is a cancer that is common in children in sub-Saharan Africa. Clues to the etiology of this cancer came within the first decade after the description of the cancer by Denis Burkitt in 1958. The tumor was found to be infected with Epstein-Barr virus (EBV) and the cancer occurred where there were repeated infections with *P. falciparum* malaria. But the question remained, how did these two pathogens interact to drive development of a malignant B cell? For 20 years, the research team at the Center for Global Health Research in Kisumu Kenya has been working to answer that question. The results of those studies have revealed a complex multi-step interaction that starts early in life, disrupts stable persistence of EBV and drives oncogenic transformation

Dr. Digby Warner

Bio

Digby Warner is the Professorial Director of the Institute of Infectious Disease and Molecular Medicine at the University of Cape Town, South Africa. His research focuses on fundamental aspects of *Mycobacterium tuberculosis* metabolism, and the intersection of host, environmental, and mycobacterial factors driving tuberculosis (TB) transmission. In recent years, he has a developed a strong interest in the utilization of advanced microscopy in infectious disease research, and in making imaging technologies accessible in low-resource settings. Examples include his involvement in the *Africa Microscopy Initiative*, a pioneering project which aims to increase the awareness and utilization of bioimaging across the continent, and *openScopes Africa*. He also serves as co-founding Director of Eh!woza, a community engagement platform with a focus on TB and its social impacts in high-burden communities.

Talk Title:

Re-imag(in)ing tuberculosis through a different lens

Abstract

Understanding *Mycobacterium tuberculosis* physiology and evolution is critical to the development of novel interventions (including new antibiotics) for tuberculosis (TB), a leading cause of mortality owing to a single infectious agent and a major contributor to antimicrobial resistant deaths. This presentation will highlight some of our recent work combining molecular tools and microscopy to investigate cellular and genetic function in mycobacteria. I will also touch on the development of technologies to investigate *M. tuberculosis* aerobiology given the importance of airborne transmission as a still very poorly understood stage in the TB disease cycle. Through these examples, I hope to highlight the utility of image-based analyses in elucidating cellular and genetic function in mycobacteria, and to amplify the call for continued development of novel tools to understand the biology – and potential vulnerabilities – of a pathogen exquisitely adapted to its obligate human host.

Dr. Ben Ngoye

Bio

Dr Ben Ngoye MBChB, MPH, PhD is a Senior Lecturer in Strategy, Change and Performance Management primarily in the Health and Public Sectors at Strathmore University/Strathmore Business School. He is also a Visiting Lecturer in Strategy at the Lagos Business School, a reviewer for several international journals (IPMR, PMR, CRJ and Queios), and has been a PhD-level external examiner for University of Witwatersrand, South Africa. He has also served as a member of the National Healthcare Human Resource Technical Working Group (GOK, MOH) and the Review Team for the National Guidelines for the Development and Review of Curriculum for Professional Medical Education, 2013-2014. Dr Ngoye is currently the Principal Investigator for a Bill and Melinda Gates Foundation Funded Project that is aimed at enhancing Leadership, Management and Governance Competencies for NMCP, MOH and their Partners, toward the control and elimination of Malaria in 10 African Countries. He is also a co-PI for another Foundation-Funded Project aimed at supporting the advancement of women in leadership roles in healthcare institutions

Talk Title:

Capacity Building for the Achievement of UHC in Kenya: Current Problems and Future Challenges.

Abstract

UHC as a concept refers to the possibility of all people and communities receiving the quality health services they need, and are protected from health threats, without suffering financial hardship. Though adopted as a term by the World Health Assembly in 2005, it is not a new concept as evidenced by article 25.1 of the 1948 Universal Declaration of Human Rights, the 1966 International Convention on Economic, Social and Cultural Rights that recognized the right of every individual to the enjoyment of the highest attainable standard of health, the Alma Ata Declaration of 1978 and the vision of Health for All; and even earlier by the German 1883 Health Insurance Bill that made nationwide health insurance mandatory, and the UK enactments of the National Insurance Act (1911) and National Health Service (1948). Connected to SDG3 and Target 3.8, it has however remained aspirational and elusive for most countries, Kenya included. Whereas a lot of literature and discussion has homed in on how health financing reforms can accelerate progress towards UHC - so much so that UHC is equivalenced in many jurisdictions with raising and pooling financial resources and purchasing health services to ensure optimal use of such resource – there is much more to it given the complexities of health systems, ergo the focus in this plenary discussion, on capacity building. Our guiding questions for this discussion are therefore (1) what are the current and anticipated problems and challenges with the plans toward the achievement of UHC in Kenya? and (2) how can we build capacity to better address the triple aims of extension of the population covered, expansion of the range of services, and establishment of financial risk protection mechanisms? Or put differently, how can we build capacity to overcome existing and potential challenges in delivering high-quality, people-centered, and integrated interventions as the Kenya UHC Policy 2020-2030 aspires to? Our rapid assessment revealed that the challenges identified during the drafting of the said policy, that cut across the pillars of health leadership and governance, health financing, the organization of service delivery, HRH, access to priority health products and technologies, HIS, health infrastructure, and weak links between policy, research, and implementation, persist. To this list we add changing social expectations and beliefs about health and healthcare, new ways of perceiving health and illness, and an ever-increasing number of new technologies. Addressing these challenges and future-proofing the journey toward UHC with capacity building as the linchpin will require going beyond individual and institutional capacity building to addressing the system parts and the whole. Consequently, to give structure to the discussion we make use of a novel composite health system framework and draw on lessons from other jurisdictions to present proposals regarding how capacity building can help advance the UHC agenda. It is anticipated that academics and practitioners will benefit from the exposition of this novel organizing framework, while policy makers and practitioners will further benefit from a wider appreciation of the factors that may contribute to lackluster UHC goal achievement and get to know which and how capacity building levers could be adjusted to unlock value to better assure progress in UHC.

Key words: Universal Health Coverage, Capacity Building

Dr. John Kimani Mungai

Bio

John Kimani Mungai holds a Bachelor of Science degree in Biochemistry and Chemistry from the University of Nairobi, Kenya, and a Master of Science degree in Forensic Science from London South Bank University, Britain. He has thirty-four years of experience working at various forensic science laboratories of the Government Chemists Department, Kenya. He was the head of the Forensic Science Division of the Departments headquartered in Nairobi, with branches in Kisumu and Mombasa, and is now retired. He provided evidence in numerous cases in various courts of law in Forensics in Kenya.

He attended and presented at local and international conferences, seminars, and workshops. He is a pioneer of the Forensic DNA laboratories in Kenya and within the East African region. He conducted training sessions for healthcare providers, scene of crime officers, investigators, and prosecutors both locally and internationally in forensic evidence management to protect and maintain quality evidence and the chain of custody in the crime scene to court pathway.

He handled evidential material on human identification during disaster human identifications (DVI) and in succession cases. He was a member of the Task force that foresaw the implementation of the Sexual Offences Act (SOA, 2006) and also a member of a task force that foresaw the implementation of non-custody sentencing for petty offenders to decongest Kenyan prisons.

He was tasked with initiating a Forensic DNA laboratory for the Kenya Defense Forces (KDF) for storing DNA profiles for soldiers before deployment to war zones or peacekeeping missions. The laboratory is fully operational now. He is a member of the African Society of Forensic Medicine and was awarded the best presenter during the 7th annual conference in South Africa. In March 2023, he equally received the best presenter award during the 10th African Society of Forensic Medicine and Science conference held in Kigali, Rwanda. In 2022, he won the award for "My Voice for Justice" in recognition of his outstanding contribution to promoting justice and human rights in Africa.

Currently, he is engaged in private consultancy. He consulted for The International Institute for Justice and the Rule of Law (IIJ) based in Malta, on developing a curriculum for Forensic evidence management in counter-terrorism cases. Additionally, he is a consultant with the International Criminal Investigative Training Assistant Program (ICITAP) in aiding the Government Chemists Department and the Forensic laboratory at the Directorate of Criminal Investigation (DCI) to achieve ISO 17025.

Talk Title:

Forensic biology trend in kenya (Past, Present and Future)

Abstract

Forensic science is providing crime investigators with a powerful tool in fighting modern crimes.

Forensic DNA profiling is one of the most valuable tools available for forensic work for the criminal justice system including the development of terrorism and counterterrorism measures globally.

In Kenya several incidences of mass fatalities resulting from terrorism have been witnessed over several decades. The resulting problem of human identification resulting from mutilation of human parts from the action of explosives and environmental action has caused a major challenge in human identification process, In this regard, over a period of time, the Forensic biology in Kenya has undergone various trends in Human identification process.

Developing countries would be best advised to invest in the DNA technology which is relatively affordable even for low-income countries

Dr. Joyce Wamicwe

Bio

Medical doctor with post-graduate training in field epidemiology, a FELTP alumnus. Currently based at the MoH, Directorate of Digital Health, Informatics, Policy & Research where she is the team lead at the Policy and Research Division and deputy to the Director. Eighteen years' experience working at clinical, programme and policy levels within the healthcare system. Data driven, pro-technology and innovation to improve experiences of various stakeholders (patients, clients, healthcare workers, researchers, innovators, policy makers) within the healthcare system. Believes that many if not all of the solutions to the various challenges within the healthcare system lie within data driven conversations and community led interventions.

Talk Title:

Abstract

Many Kenyans in the recent past can acknowledge having been involved in some sort of fundraising to offset medical related bills either for themselves or for a family member or a friend. Further there is evidence of sub-optimal health services including actual availability of health products and technologies in many of our health facilities especially in the public sector. On the other hand, the Constitution of Kenya provides that every Kenyan has the right to quality health care. This contrast is what forms the basis for the many conversations related to delivery of Universal Health Coverage (UHC), a key aspiration for Government for the last decade or so. The Ministry of Health is set on delivering it right this time round and ensuring that all Kenyans access quality health care services without incurring catastrophic health expenditure. The time to deliver UHC is now!

The Ministry of Health is implementing universal health coverage on a foundation of primary health care based on primary care networks. These networks have as their base the community level that are then connected to the hub, a sub-county level hospital through dispensaries and health centres. This foundation is then supported by four key pillars namely human resources for health, health products and technology, health information system through optimal use of technology and health care financing. Implementation will take on a paradigm shift from a predominantly curative – based health system to one that is more promotive and preventive.

Delivery of quality health care is dependent on availability of real-time quality data within the health ecosystem at the right time and to the right person for decision making at all levels. There is evidence that correct and ethical use of technology can enable this, and therefore we must take full advantage to harness the benefits. Digital health is therefore a critical enabler for the attainment of UHC. The Government through the Bottom-up Economic Transformative Agenda (BETA) is fully cognizant of this and hence the reason why key commitments include delivering a fully robust dynamic digital economy that will serve all sectors, health being one of them.

Digital health in Kenya has been in some form or another for the last three decades. It is the aspiration of the Ministry of Health to ensure that deployment of digital health implementations is done in a holistic manner within the health ecosystem. From a legal perspective, The Digital Health Act, 2023 was recently enacted and this is a win for Kenyans in that we now have a legal framework that provides a solid foundation to the digitization of the health ecosystem. We must never lose sight of why the Government and its partners is heavily investing in all this – the data therein is what must be our goal – its security, its quality, its capability, and its potential! Going forward, meaningful, thought-provoking partnerships and collaborations will be key in delivery of this.

Digitization of the health ecosystem will bring about increased efficiencies, cost savings and empowered communities.

Dr. Ruth Laibon Masha

Bio

Dr. Ruth Laibon-Masha, PhD, is an expert in Public Health with more than 22 years of work experience serving in Government, United Nations, and Civil Society Organisations. She is currently the Chief Executive Officer at National Syndemic Diseases Control Council (NSDCC) formerly recognized as the National AIDS Control Council in Kenya since September 2020. In this position, she bears the significant responsibility of overseeing the comprehensive initiatives to address the multifaceted challenges posed by HIV and other related epidemics in Kenya. She plays a vital role in leading multiple stakeholders' efforts towards policy development, resource mobilization, partnership cultivation, the provision of technical guidance and monitoring and evaluation.

At the global level, Dr. Masha extends her leadership influence where she serves as a member of the UNAIDS Global Council on Inequality, AIDS, and Pandemics, and a representative of Kenya on the UNAIDS Programme Coordinating Board. She is the Chairperson of the HIV Multisectoral Leadership forum of Director Generals of National AIDS Coordinating Agencies from 35 Countries, facilitating international collaboration and knowledge sharing in the field of HIV prevention under the umbrella of Global HIV Prevention Coalition. As part of this effort, she hosts multiple countries under the global south to south learning initiative on HIV prevention and engages in live lectures, including with the University of Washington's "Principles of STI and HIV Research and Public Health Practice Course."

Dr. Masha's career trajectory spans a diverse spectrum, encompassing impactful contributions at both international and regional levels, as well as within the national and grassroots spheres. Prior to her current role, she served as the Advisor for Global HIV Prevention Coalition and Adolescent Health in Geneva, Switzerland, as well as in the capacities of Partnership Adviser and Community Mobilisation and Networking Adviser in Kenya, all under the auspices of the United Nations Programme for HIV and AIDS.

Her professional journey also includes pivotal roles at esteemed organizations such as ActionAid International, Engender Health, and Family Health Options Kenya. Dr. Masha earned a doctoral degree in Public Health from Jomo Kenyatta University of Agriculture and Technology in Kenya, complemented by a Master's degree in the same field.

Talk Title:

Whole Government Approach Towards Ending Adolescent Triple Threat (New HIV Infections, Adolescent Pregnancies and Sexual and Gender-based Violence in Kenya)

Abstract

Kenya is committed to ending AIDS as a public health threat by the year 2030. Tremendous progress has been made in the HIV response in Kenya since the first case was officially documented in 1984. The country has registered remarkable progress in the HIV response evidenced by the significant reduction in new HIV infections from a high of 101,448 in 2013 to 22,154 in 2022, translating to a 78.2% reduction over the last decade.

However, a closer look at existing data shows that the curve of new HIV infections is not flattening fast enough to end the HIV epidemic as a public health threat in Kenya by the year 2030.

New HIV Infections: Adolescents and young people aged 15-24 years are disproportionately affected by HIV with 41% of the adult new HIV infections attributed to this age group (Kenya HIV Estimates 2023).

Adolescent Pregnancies: 55% of the 1,499,514 pregnancies that occurred in Kenya in 2023, were among Adolescents and Young Women aged 10-24 years, whereas 17% (254,753) were among adolescent girls aged 10-19 years, translating to 696 adolescent pregnancies in a day.

Sexual and Gender Based Violence: In addition to acquiring HIV and getting pregnant, adolescents also experienced gender-based violence (GBV), an infringement on basic human rights. A total of 53,765 cases of Sexual and Gender Based Violence (SGBV) were reported at health facilities/rescue centres in 2023 out of which 37% (20,053) were among adolescent girls aged 10-17 years. Only 42% of all SGBV cases and 40% of SGBV cases among adolescents were reported within 72 hours, minimising chances of success of post-exposure prophylaxis further increasing chances of HIV transmission.

These overlapping challenge of new HIV infections, unintended pregnancies, and sexual and gender-based violence among adolescent girls and young people known herein as “Triple Threat” present a malignant triad of sexual risk and vulnerabilities which must be addressed if progress is to be maintained in addressing HIV as a public health challenge.

This presentation will highlight on the whole of Kenya Government approach towards ending the Triple Threat by Leveraging on the national community, health, and social systems to combat the triple threat of new HIV infections, pregnancies, and sexual and gender-based violence among adolescents aged 10-19, as spearheaded by the National Syndemic Diseases and Control Council (NSDCC).

Dr. Johanssen Oduor

Personal details

Name: Dr. Johansen Oduor Nyayal Married with 3 children
Education:

- MBCHB University of Nairobi, 2000
- Mmed Pathology, University of Nairobi 2007 LLB. University of Nairobi 2021
- Diploma in Forensic Medicine, College of Medicine, South Africa, 2008 Diploma in Law (advocate training program) ongoing
- Other trainings
- Diploma in leadership, Strathmore Business School, Nairobi, Kenya, 2014, Trainings in human rights investigations, management of the dead during catastrophes, scene processing management and Disaster victim identification, among others in various institutions

Work

1. Ministry of Health Nairobi Kenya, as the Chief Government Pathologist
2. Acting Coroner General, Department of Justice, State Law Office, Kenya
3. Honorary lecture, University of Nairobi Kenya; Jomo Kenyatta University of Technology Kenya
4. Independent Medico Legal Services, a human right organisation: consulting for them
5. Homicide division, Directorate of criminal Investigations, National Police services- consulting for them
6. Involved in routine post mortem services
7. Expert witness in court of law
8. Analysis of medicolegal reports and giving independent opinions

Membership of professional bodies

1. Kenya Association of Clinical Pathologists
2. African Society of Forensic Medicine (ASFM) (president emeritus)
3. Association of Pathologists East Central and Southern Africa (APECSA)
4. Member, Kenya Medical Association (KMA).
5. Registered with the Kenya Medical and Dentists Practitioners Board
6. Alumni of Strathmore Business School and University of Nairobi

Notable works involved in

1. Founder member of African Society of forensic medicine after which I was president for 2 terms
2. Investigations of various high-profile cases of death in Kenya
3. Part of DVI African team
4. Lead in management of fatality disasters including the following;
   - Nakumatt Supermarket fire: fire broke out I a supermarket known as Nakumatt within downtown, Nairobi City on 28th January 2009. 29 people died
   - Westgate mall terrorist attack, Nairobi in 21st September 2013. 68killed.
   - Mpeketoni, a region in Lamu, Kenya, terrorist attack, 16th June 2014, 48killed
   - Garissa: terrorist attack to university in 2nd April 2015. 148 students were killed. Done was DVI and autopsy.
   - Dusit D2, A business complex in Nairobi, Kenya. Terrorist attack on 16th January 2019. 22killed plus all the 5 terrorists
   - Shakahola: ongoing, a case of religious extremist in which followers were urged to starve to death after which they were buried in an expansive land in a place called Shakahola within Kilifi County in Kenya. So far we have exhumed and performed autopsy on a total of 429 bodies.

Talk Title:

Shakahola cases; human remains identification process Case Presentation

Abstract

On 22nd March 2023, we (The Office of the Chief Government Pathologist) received a letter from the Directorate from the Directorate of Criminal Investigations (DCI) requesting for help in form of exhumation of bodies of two children who had died and thereafter buried in a shallow grave within Chakama Ranch in Kilifi County. It was believed that they died due to religious extreme practices, involving starving of the congregants.

Upon reaching the burial site, we discovered that we were dealing with mass graves. A larger team had to be constituted before commencing the exhumation process. The process of exhumation involved identification of graves by use of informants, securing the grave by sealing off the grave site, marking the grave, mapping the area, photography and subsequent exhumation. The bodies were than given unique identifiers, bagged and transported to Malindi subcounty hospital mortuary where they were received and were given an admission number. They were then stored in refrigerators, ready for autopsy. So far, the number of bodies we have dealt with are 429, with the exercise still ongoing.

Our objective is to ensure that the relatives are reunited with their loved ones and help in building up the prosecution case.

The autopsies were performed in phases. Three autopsy tables were set, each made of teams comprising of pathologists, crime scene officers, investigating officers, analysis from the government chemist, morticians and observers from human right organisations.

Each body first underwent craniofacial X-ray. The body were then placed on an autopsy table while still in body bag and photographs were taken. The body bag was then opened, photographs were again taken and evidence collected. Clothes were then noted, recorded and the body was then undress. External features were then recorded after which dissection was performed, using the standard Y incision and anatomical findings were then recorded.

Under guidance of analysts from the government chemist, samples were collected for DNA analysis. These included fingernails, molar and premolar teeth, shaft of long bones, one whole clavicle, cartilages (costochondral) and buccal smears (for fresh bodies)

The samples were then placed in collection containers provided by the Government Chemist, sealed, and labelled. Chain of custody documents were then filled and signed.

By the time of writing this abstract, a total of 429 autopsies were performed. We are still waiting for the results of DNA analysis from the government analyst. We were faced with a number of challenges; including; Level of decomposition, overwhelming number of cases, inadequate resources the government chemist depletion of reagents and Small size of the mortuary.

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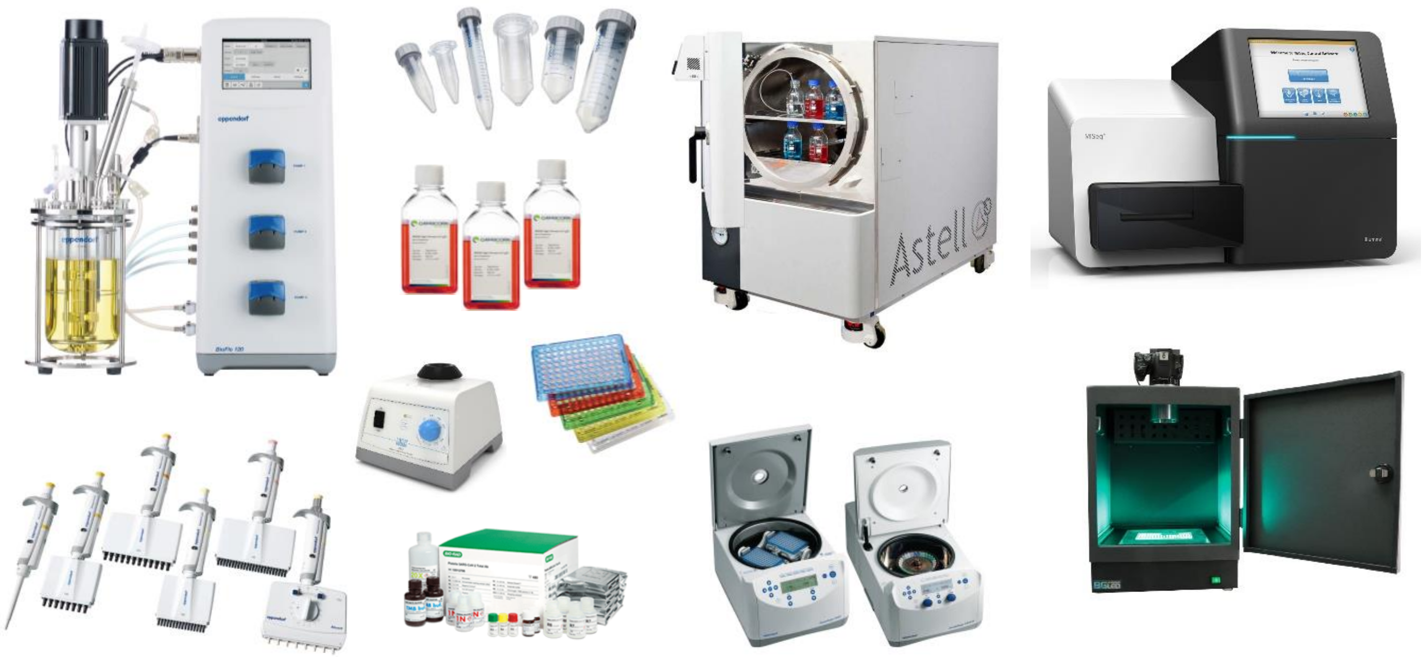

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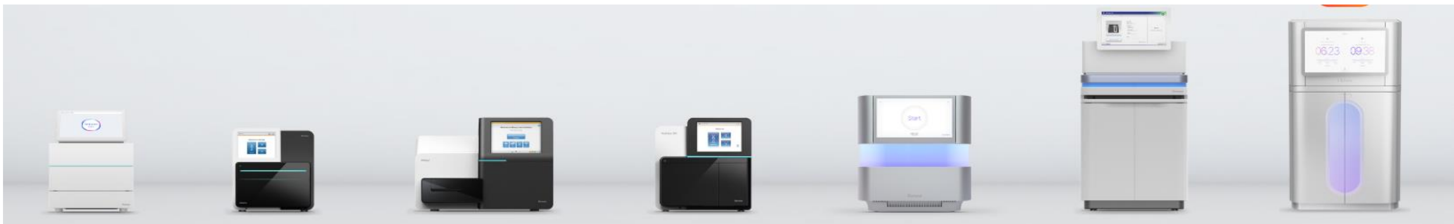

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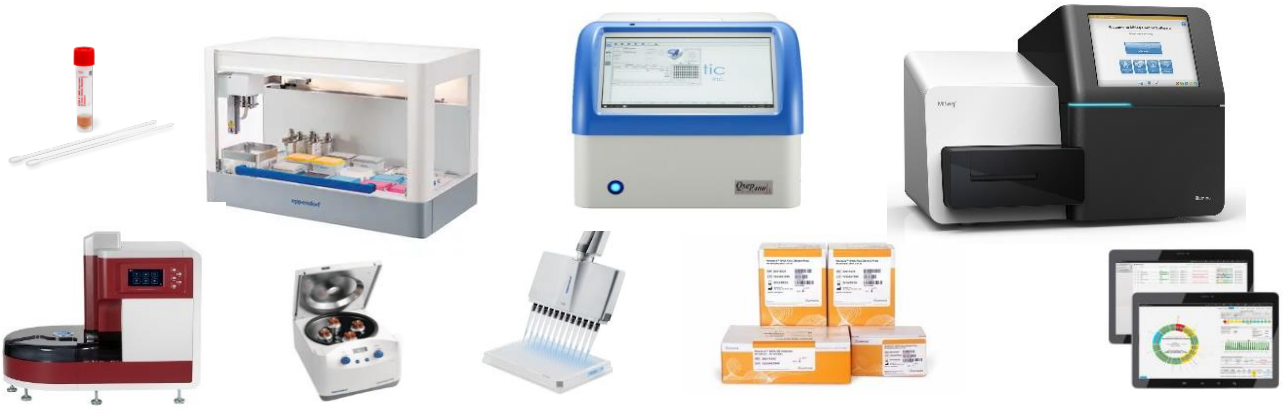

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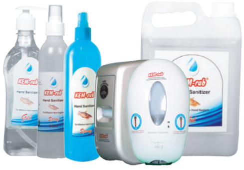

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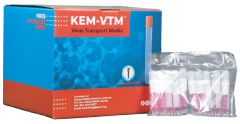

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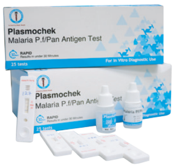

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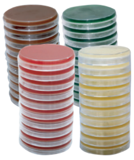

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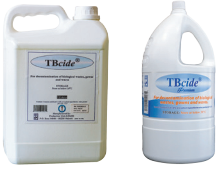
> ISO 9001:2015 and ISO 13485:2016 conditions
> Delivery under strict cold-chain



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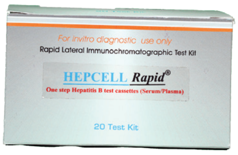
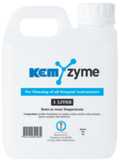


HEPCELL

Hepatitis Rapid Test Kit



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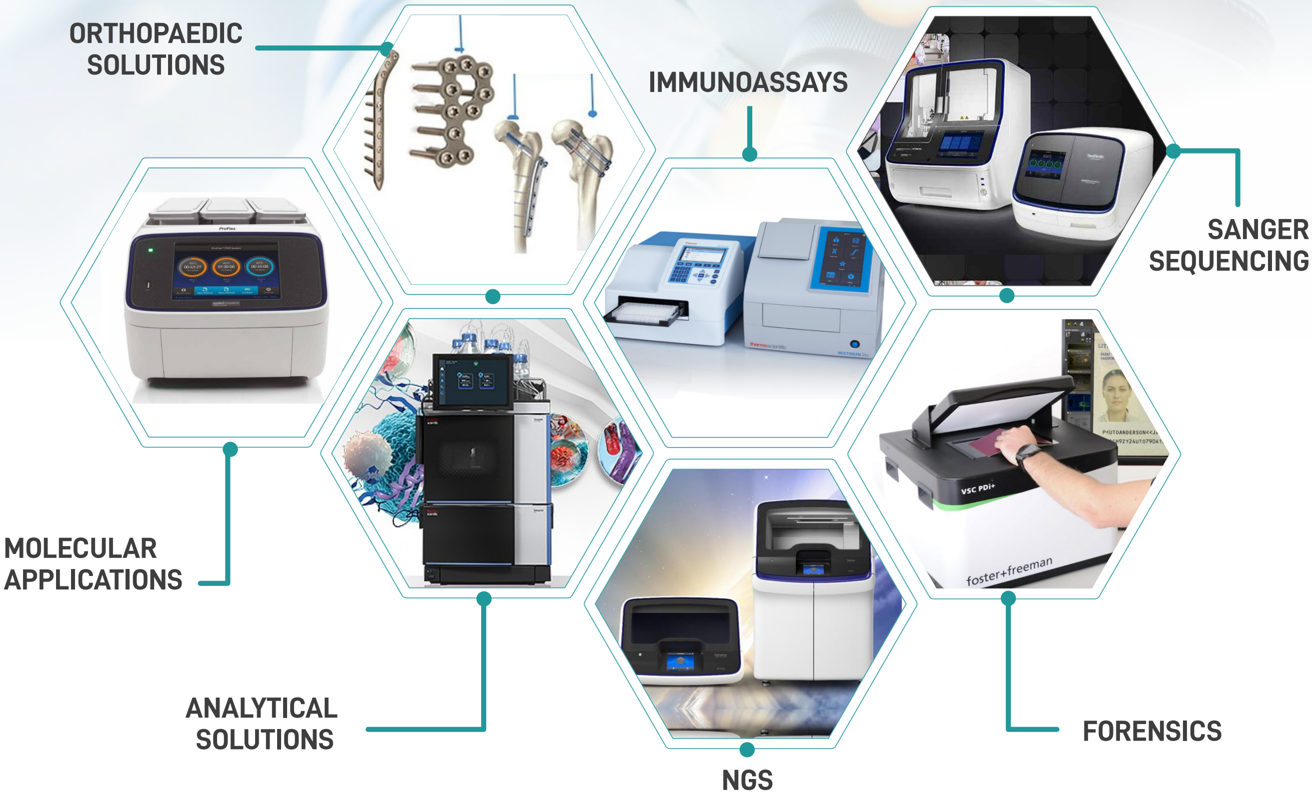

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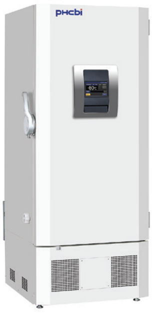
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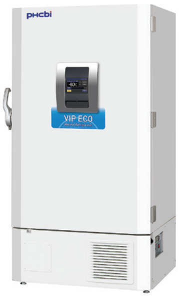
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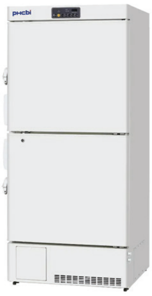
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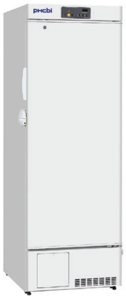
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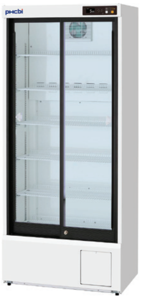
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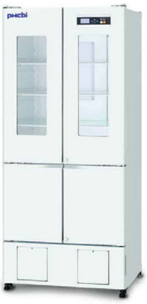
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SCIENTIFIC PROGRAM

DAY TWO, WEDNESDAY, 14th FEBRUARY 2024

TIME	
0700-0900hrs	Arrival and Registration of Delegates
0825-0830hrs	**Opening Remarks: Dr. Cecilia Mbae- Chairperson, KASH**
0830-0900hrs	Plenary Session **1: Dr. Sam Akech** “Sustainable Partnership to Strengthen Data Availability and Surveillance Capacity to Effectively Prevent, Detect, and Respond to Known and Emerging Threats”
0900-0925hrs	Plenary Session **2: Dr. Joyce Wamicwe** “Digital Health and Universal Health Coverage- Unpacking the Vision for Implementation.”
0925-0950hrs	Plenary Session **3: Prof Ben Ngoye** “Capacity Building for the Achievement of UHC in Kenya: Current Problems and Future Challenges.”
0950- 1015hrs	Plenary Session **4: Dr. Robert Karanja** “Research innovation and Commercialization: Bridging the Know-Do Gap to Transform Research Outputs to Impact”
Session Chair	**Dr Steve Wandiga**
Rapporteur	**Lilian Mayieka**

1050 – 1115hrs TEA BREAK

1115-1245hrs SCIENTIFIC SESSION 1-6

Time (EAT) **1115-1245hrs**	**Abstract No**	**Scientific Session 1:** Rising Star Award-1 **VENUE: AMBOSELI** **Session Chair :** Dr Joseph Mwangangi/Dr. Doris Njomo **Rapporteur :** Dr Limbaso Konongoi//Francis Kimani/Jane Ikapesi/Maureen Ekis
	1.	Performance and Comparative Evaluation of a Novel Diagnostic Assay, Novaplex™ Malaria Assay Kit, against Routine Diagnostic Techniques in the detection of different *Plasmodium spp.* in Kenya; **Lewis Mbabu**
	2.	Improving TB case finding and adherence to TB treatment at a go- Kabete Sub County, Kiambu County, Kenya; **Annfreshia Wangari**
	3.	Challenges and Lessons Learnt in implementing cervical cancer screening in HIV positive females in rural and urban settings in Kenya; **Sophia Kongoti**
	4.	Sputum cytokines association with tuberculosis culturable cough aerosols; **Wilfried Bundi**
	5.	Diabetes health care specific services readiness and availability in Kenya: Implications for Universal Health Coverage; **Stephen Onteri**
	6.	Exclusive breastfeeding interruption in a comprehensive support setting in Western Kenya: secondary analysis of Prosynk study data; **Micah June**
	7.	Malaria vector surveillance and phenotypic insecticide resistance in *Anopheline Mosquitoes* in Isiolo County, northeastern, Kenya; **Stanley Kitur**
	8.	Individual-level factors that contribute to delayed diagnosis of cervical cancer, among patients at the Kenyatta National Hospital, Kenya; **Martha Kerubo**
	9.	Multidrug resistant bacterial infections in COVID-19 patients admitted in Kenyatta National Hospital, Kenya; **Jennifer Mutua**
	10.	Hypothermia amongst neonatal admissions in Kenya: A Retrospective Cohort Study Assessing Prevalence, Trends, Associated Factors, and its Relationship with All-Cause Neonatal Mortality; **John Mwangi**
	11.	Anti-proliferation effects of *Rhamnus prinoides* and *Grewia villosa* extracts based on in vitro, network pharmacology and molecular docking approaches against cervical cancer; **Sally Kamau**
	12.	Pathways of Exposure to *Vibrio Cholerae* in an Urban Informal Settlement in Nairobi, Kenya; **Kevin Kering**
	13.	Identification of insecticide resistance markers in *Anopheles arabiensis* and *Anopheles gambiae* from Kenya and Benin using Weighted Gene Correlation Network Analysis; **Cynthia Odhiambo**

	14.	Epidemiology of soil -transmitted helminthiasis infection among school aged children in pastoralist communities of Narok County, Kenya: A cross-sectional study; **Richelle Kihoro**
	15.	Assessment of the Collibri™ ES DNA Library Prep Kit performance in Human mitochondrial genome sequencing for development of a forensic quality reference database; **Belinda Azzam**
	16.	Impact of Time To Transportation on Detection and Isolation of *Mycobacterium tuberculosis* from Sputum Sample; **Joseph Ouma**
	17.	Factors Associated with Pregnancies Among Adolescents Girls Aged (15-19) years in Korogwe District, Tanga Region. A mixed Method study; **Neema Magoti**
	18.	Screening of SARS-CoV-2 from Selected Sewerage Systems in Kenya; **Christine Jobita**
	19.	Anti-infective and cytotoxicity potential of the root bark of *Dalbergia melanoxylon* Guill. & Perr; **Duncan Mutiso**
	20.	Genetic diversity of quinolone efflux pump (qepA) among *E. coli* isolated from children under five years being discharged from hospitals in Kenya; **Kevin Kariuki**
Time (EAT) 1115-1245hrs	**Abstract No**	**Scientific Session 2:** Natural Products **Venue:** TSAVO **Session Chair:** Dr. Beatrice Irungu **Rapporteur:** Dr. Sospeter Njeru
	21.	A study on attitudes and perceptions on the nutritional value and health benefits of raw bitter gourd and bitter gourd related products in the market on general public in Colombo District, Sri Lanka; **Chathura Nilipul**
	22.	Pathogenicity Test, Antifungal Mechanisms, and Secondary Metabolites of Bacillus spp from L. Bogoria as Biocontrol of *Rhizoctonia solani* in *Phaseolus vulgaris* L; **Tofick Barasa**
	23.	From Natures pharmacy to Modern Pharmacy: A Journey through the Landscape of Cancer Drug Discoveries; **Sabina Wachira**
	24.	Network pharmacology, molecular docking, and in vitro study on *Aspilia pluriseta* against prostate cancer; **Innocent Okpako**
	25.	Phytocompounds of Cajanus cajan as Potential Anticancer Agents against Breast Cancer; An Analysis through Network Pharmacology and Molecular Docking; **Douglas Njuguna**
	26.	Challenges mapping of medicinal resources with potential to mitigate COVID-19 and other SARS-like ailments in the K1-7 flora regions of Kenya: Field Experience; **Bakhita Barbara**
	27.	Climate change and its Environmental Impact on Health; **Paul Faluma**
Time (EAT) 1115hrs-1245hrs	**Abstract No**	**Scientific Session 3:** MCH -1 **VENUE:** SAMBURU **Session Chair:** Dr. Benson Singa **Rapporteur:** Schiller Mbuka
	28.	Facilitators of low skilled delivery at Miritini CDF Health Center, Mombasa; **Nasibo Sarbo**
	29.	Adverse Birth Outcomes and Associated Factors among Adolescent Mothers in Nabdam District: A Facility-based Cross-sectional Study; **Farukh Saah**
	30.	Stakeholder engagement in the development of a post discharge breastfeeding support intervention for sick ill malnourished infant under 6months (IBAMI-2); **Fridah Munene**
	31.	Improved adherence to early infant diagnosis algorithm for HIV-exposed infants during implementation of a point-of-care early infant diagnosis project in Homabay County, Kenya; **Everlyne Akinyi**
	32.	Developing a toolkit to optimize nutrition care for children with severe acute malnutrition: human-centered design process with healthcare workers at Migori County Referral Hospital; **Olieng'o Okoth**
	33.	Malaria, Schistosomiasis, and Soil-Transmitted Helminthiasis Co-infections and Their Association with Anaemia in Pregnant Women in Busia County, Western Kenya; **George Imbusi**
	34.	The effects of pro/synbiotics and engagement in a clinical trial on growth during infancy in western Kenya; **Alloys K'Oloo**

Time (EAT) **1115-1245hrs**	**Abstract No**	**Scientific Session 4:** Malaria-1 **VENUE:** BOGORIA **Session Chair:** Dr. Jeremiah Gathirwa **Rapporteur:** Brian Seda
	35.	Prevalence and Predictors of Asymptomatic Malaria Infection in the Boricha District, Sidama Region, Ethiopia: Implications for Elimination Strategies; **Desalegn Dabaro**
	36.	Comparative analysis of peripheral whole blood transcriptome from asymptomatic carriers reveals upregulation of subsets of surface proteins implicated in *Plasmodium falciparum* phenotypic plasticity; **Joseph Gisaina**
	37.	Red blood cell tension protects against severe malaria in the Dantu blood group; **Brian Kabugu**
	38.	Advancing Active Malaria Case Detection via Contact Testing in Nyamira, Kenya: A Strategic Approach; **Wayne Otieno**
	39.	Evidence and Lessons learned from the Malaria Vaccine Implementation Programme (2019-2023); **Jonathan Schultz**
	40.	Pfkelch-13 Sequencing Strategy on Identifying Artemisinin Resistance in Busia County, Kenya; **Mark Makau**
	41.	Specificity and Sensitivity of Microscopy and Malaria Diagnostic Kit (mRDT First Response™) among Pregnant women presenting for Delivery in Busia County, Western Kenya; **Dickson Kipchirchir**
	42.	Evaluation of Malaria Surveillance System in Homa Bay County, Kenya, January—March 2023; **Diana Rose**
Time (EAT) **1115-1245hrs**	**Abstract No**	**Scientific Session 5:** Health Systems -1 **VENUE:** MT. KENYA C **Session Chair:** Bridget Kimani **Rapporteur:** Mariam Macharia
	43.	Influence of Health System Management on occurrence of postpartum hemorrhage among women of reproductive age 15 - 49 years in Homabay County, Kenya; **Ottoman Adel**
	44.	Patterns of Facility and Patient Related Factors to The Orthopedic and Trauma Admissions at The Kenyatta National Hospital: A Qualitative Assessment; **Maxwell Omondi**
	45.	Laboratory samples online remote logging, a key tool for improving turnaround time and monitoring patients care: a case study in Seme sub county Kenya; **Celline Okuta**
	46.	Exploring the viability of community public-private partnerships for chronic illness diagnostic services in East Africa; **James Kariuki**
	47.	Relationship between Strategic Leadership style and the Adoption of Clinical Innovations by Public referral hospitals in Nairobi County, Kenya; **George Kirigi**
	48.	Impact Of Using Web Remote Logging System To Improve Tuberculosis Culture Samples Referral To Kisumu KEMRI CGHR Lab In Western Kenya; **Ben Odhiambo**
	49.	Sociodemographic Factors influencing Health worker utilization of electronic health information system: A case of District Health Information Software (DHIS2) in Burundi; **Innocent Yandemye**
Time (EAT) **1115-1245hrs**	**Abstract No**	**Scientific Session 6:** Mental Health **VENUE:** MT. KENYA D **Session Chair:** Dr. Mary Bitta **Rapporteur:** Dr. Lucy Chite
	50.	A Randomized Trial of Non-Specialist, Psychotherapy or Psychopharmacological Treatment of Major Depression and Posttraumatic Stress Disorder in Kisumu, Kenya; **Linnet Ongeri**
	51.	Mental Health disorders Among Sudanese Medical Students in the Midst of 2023 Conflict: Prevalence, Predictors, and Implications; **Esra Alfadul**
	52.	Characterizing Alcohol and other Substance Use Disorder Among In-Patients at the Portreitz Mental Hospital in Mombasa - Kenya 2021-2022; **Abdalla Mpigabao**
	53.	The Role of Social Support on Mental Health among Parenting Adolescent Girls and Young Women: A nested Cross-sectional Study in south-western Kenya; **Nita Akech**
	54.	Effect of Pregnancy Intendedness on Maternal Attitude, Adjustment and Bonding Post-Pregnancy among Adolescent Girls and Young Women in Southwestern Kenya; **Dennis Kegode**
	55.	Intimate Partner Violence Among Gay, Bisexual, and Other Men who have sex with Men in south-western Kenya: Prevalence and Risk Factors; **Vincent Kipchumba**

1245-1345hrs: LUNCH BREAK

1345-1430hrs POSTER SESSION (001-022)

Time (EAT) **1345-1430hrs**	**Abstract No**	**Poster Session: Screen 1-** Public Health **Judges:** Dr. Sophie Uyoga & Bridget Kimani
	001.	Climate change awareness and its effects on human health among residents in Mavoko sub county in Athi-River; **Sharon Khanguha**
	002.	AFP Surveillance System Evaluation, Kenya, 2020-2021; **Serah Nduta**
	003.	Evaluation of *Meningococcal meningitis* Surveillance System in West Pokot County Kenya, 2017-2021; **Pius Mutuku**
	004.	Mycological and aflatoxin analysis of *Camellia sinensis* from selected counties in Kenya; **Sally Loronyokie**
	005.	Influenza-like-illness and severe acute respiratory illness cases in Kenya: Burden estimates and associated factors 2019 – April 2023; **Mercy Cheptoo**
	006.	Factors associated with Nontyphoidal *Salmonella* infection in children below 5 years in an Urban Informal settlement in Nairobi, Kenya; **Georgina Odityo**
	007.	Development of a specific immune lateral flow assay for cholera detection; **Freek Hoen**
	008.	Evaluation of Acute Flaccid Paralysis Surveillance System in Eight Priority Counties in Kenya, 2020 to 2022; **Lydia Khalayi**
	009.	Surpassing the targets of Oral Cholera Vaccination Campaign "A boon for future outbreaks"- in Kenya, August 2023; **Oscar Adidi**
	010.	Evaluation of Factors Contributing to Low Recency Uptake Based on Online Recency Dashboard Data in Kabondo Sub County Hospital; **Nicholas Odiemo**
	011.	Depression prevalence and associated factors among undergraduate students at Gulu university, Uganda; **Nansubuga Federes**
	012.	Case Report: AMELY Y, DYS576 and DYS570, DYS481 and DYS458 Drop out encountered during routine Paternity testing.; **Ngure Kirosh**
	013.	Exploring the expression profile of genes associated with Salt-Sensitive Hypertension among Kenyan Women diagnosed with Breast Cancer; **John Gitau**
	014.	Acute Febrile Illness Outbreak in Northern Kenya: Emerging *Plasmodium Vivax* spp. Malaria; **Richard Kimenye**
Time (EAT) **1345-1430hrs**	Abstract No	**Poster Session 2: Screen 2:** Health Systems Judges: Kariuki Ngumo & Susan Kavai
	015.	Evaluating the Morphological Traits of Red Blood Cells and Their Relevance in Predicting Patient Prognosis within Hematological Disorders; **Dan Ngugi**
	017.	Use of a digital platform and behavioural insights to empower and motivate adolescents and young people, to access SRH services in selected counties in Kenya; **Hilina Hailemariam**
	018.	An Assessment of Commodity Management System Indicators in Case Management of Tuberculosis in Selected High Tuberculosis Burden Counties January 2020 – March 2023; **Carey Abuya**
	019.	Behavioral change still remains an impediment to ending HIV epidemic in Kenya, Analysis of reasons for Post Exposure Prophylaxis use at Kendu Sub-county hospital, Rachuonyo North Sub County, Homa Bay County, Kenya; **Kevin Mimba**
	020.	A Review of the Development and Utilization of Community-Based Health Information Systems (CBHIS) in Kenya; **Beatrice Kuvuna**
	021.	Uptake of Digital Health Systems in Public Hospitals in Kenya; **Pauline Ombiri**
	022.	Modelling count data for HIV-positive patients on Antiretroviral Treatment (ART) in Kenya; **Muricho Anna**
Time (EAT) **1345-1430hrs**		**Poster Session 3: Screen 3-** Virology Judges: Dr. Limbaso Konongoi & Dr. Samoel Khamadi
	023.	Isolation and Growth Kinetics of Bogoria Virus from Phlebotomine Sand Flies Sampled in Baringo Kenya; **Jane Thiiru**

	024.	Metagenomic analysis of *Aedes aegypti* virome diversity during a dengue outbreak in Kisumu, Kenya; **Tabitha Nganga**
	025.	Seroprevalence of Yellow fever and Dengue viruses among Human population in Nguruman and Kerio Valley in Kenya, 2021–2023; **Mercy Kibathi**
	026.	Entomologic Risk Assessment of Yellow Fever Outbreak in Kenya 2022; **James Mutisya**
	027.	Metagenomic analysis of the bat virome in Coastal and Western Kenya; **George Kisoi**
	028.	Rotavirus diarrhoea outbreak in Kiambu and Mombasa counties, Kenya, April-May 2023; **Carlene Sang**
	029.	Seroprevalence of Ngari Virus in the Human Population Residing in Selected Sites of Baringo and Kajiado Counties; **Titus Kitonyo**
	030.	Analysis of Phytochemical Composition of Antivir-H and IMB Herbal Supplements Used for Management of COVID -19; **Athuman Chiguzo**
	031.	Predicting factors of COVID-19 vaccine uptake among persons aged 18 years and above in Kiambu County, Kenya; **Said Abdulla**
	032.	SARS-CoV2 Beyond the Pandemic Era; **Gathii Kimita**
	033.	Evaluating COVID-19 vaccination uptake in healthcare workers: results from a survey in Kenya; **Abigael Awuor**
Time (EAT) **1345-1430hrs**		**Poster Session 4: Screen 4-** Malaria Judges: Dr. Sospeter Njeru & Francis Kimani
	034.	Trends in Insecticide-Treated Net Indices and Effect on Community Malaria Prevalence - western Kenya, 2015-2020; **Jonathan Schultz**
	035.	*Plasmodium falciparum* histidine rich protein-2 levels in blood but not saliva as a predictor of parasite density and clinical malaria status in patients with acute uncomplicated malaria in Chulaimbo, Western Kenya; **Ruth Awuor**
	036.	Var Acidic Terminal Sequence (varATS) screening for sub-patent malaria in peripheral blood of women attending antenatal care in Lagos, Nigeria; **Aminat Olamide**
	037.	Malaria morbidity in children less than five years following vaccination with RTS,S vaccine at Likindu health centre in Vihiga county; **Diana Omboko**
	038.	Malaria test positivity rates in community surveillance as compared to health facility surveillance in malaria endemic area Rarieda sub-county, western Kenya; **Jonathan Schultz**
	039.	Implementing High Quality Community Case Management & Data Reporting: Lessons from The Field in Siaya, Western Kenya; **Jonathan Schultz**
	040.	Assessment of genetic diversity of *P. falciparum* chondroitin sulfate a ligand; a pregnancy-associated malaria vaccine antigen; **Rotich Alex**
	041.	Assessment of Repeated Malaria Infections in Siaya County, June 2021-May 2022; **Cynthia Musemba**
	042.	Identification of conserved cross-species B-cell linear epitopes in human malaria: A subtractive proteomics and immuno-informatics approach targeting merozoite stage proteins; **Sebastian Musundi**
	043.	Attractive Targeted Sugar Baits for malaria control in western Kenya (ATSB-Kenya): cohort study recruitment; **Alice Kamau**
	044.	Describing Birth Outcome in Women with Malaria in Pregnancy in Matungu Sub- County, January 2019 to December 2021; **Lydia Khalayi**
	045.	Assessment of Antimalarial drug susceptibility patterns in Kisumu and Marigat between 2018 and 2023 based on in vitro testing, genomic analyses and passive monitoring of treatment outcomes; **Doris Njoroge**
	046.	Association between bed net use and malaria prevalence by age group in Rarieda sub-county, Western Kenya (2015-2020); **Jonathan Schultz**
Time (EAT) **1345-1430hrs**		**Poster Session: Screen 5:** Vector Biology Judges: Dr. Damaris Matoke-Muhia & Seline Omondi
	047.	Mosquito species diversity and human bite rates as a measure of risk of disease emergence, Mombasa, Kenya; **Francis Musili**

	048.	Vector competence of *Aedes* (Stegomyia) species for transmission of yellow fever virus in Kerio Valley, Baringo County and Nguruman, Kajiado County, Kenya; **Cynthia Chelangat**
	049.	Detection and characterization of *Negeviruses* isolated from mosquitoes in Kenya; **Janet Majanja**
Time (EAT) **1345-1430hrs**		**Poster Session:** Screen 6- TB Judges: Dr. Jane Ong'ang'o & Asiko Ong'ayo
	050.	Childhood tuberculosis and factors associated with favourable treatment outcomes in Nyeri county, Kenya 2017-2022; **Grace Kaluai**
	051.	Health Care Worker Related Factors Associated with Tuberculosis Treatment Non-Adherence among Patients in Kisumu East Sub-County, Kisumu Kenya; **Marlyn Ochieng**
	052.	Test Result Concordance Rate between Two Diagnostic Tests TB LAM and Gene-expert Using TB Laboratory Information Management Systems in Kabondo Sub County; **Nicholas Odiemo**
SYMPOSIUM 1-6		
Time (EAT) 1430-1700hrs	**Symposium 1: Genomics without tears** **VENUE: AMBOSELI** **Session Chair:** Dr. John Waitumbi **Rapporteur :** Beth Mutai & Ruth Cheruto	
Time (EAT) 1430-1700hrs	**Symposium 2: Advancing Evidence for the Global Implementation of Spatial Repellents (AEGIS)** **VENUE: TSAVO** **Session Chair:** Dr. Steve Harvey **Rapporteur:** Dr. Bernard Abongo & Sheila Mbaabu	
Time (EAT) 1430-1700hrs	**Symposium 3: Knowledge Management** **VENUE: SAMBURU** **Session Chair:** Lillian Mayieka **Rapporteur :** Wambui Njonge & Mercy Tuluso	
Time (EAT) 1430-1700hrs	**Symposium 4: KEMRI Programs and Flagship Projects** **VENUE: BOGORIA** **Session Chair:** Dr. Steve Wandiga **Rapporteur:** Jennifer Ngetich & Bridget Kimani	
Time (EAT) 1430-1700hrs	**Symposium 5: BOHEMIA** **VENUE: MT. KENYA C :** **Session Chair:** Dr. Joseph Mwangangi **Rapporteur:** Rebecca Shambi & Tabitha Wambui	
TEA BREAK AND DEPARTURE		
END OF DAY 2		
DAY THREE, THURSDAY 15TH FEBRUARY 2024		
0700-0830hrs	**Arrival & Registration**	
	PLENARY SESSION	
0830- 0855hrs	Plenary Session 4: **Prof. Rosemary Rochford** "Uncovering the Etiology of Burkitt Lymphoma: Results from a 20-Year Odyssey in Kenya"	
0855- 0920hrs	Plenary Session 5: **Dr. John Kimani** "Forensic Biology Trend In Kenya (Past, Present and Future)"	
0920 -0945hrs	Plenary Session 6: **Dr. Oduor Johanssen** "Shakahola Cases; Human Remains Identification Process; Case Presentation	
Session Chair:	Dr. Eric Ochomo	
Rapporteur:	Ibrahim Mwangi	
Time (EAT) **1005-1105hrs**	Abstract No	**Scientific Session 7: TB** **VENUE: AMBOSELI.** **Session Chair:** Dr Jane Ong'ang'o **Rapporteur:** Barbra Miheso
	56.	High Number of TB Relapse Cases in an MDR surveillance in Western Kenya; **Joseph Orure**
	57.	Effects of Sputum volume and quality on MTB yield and Smear positivity from samples received at KEMRI TB lab Western Kenya; **Ruth Sitati**

	58.	Effectiveness of Anti-tuberculosis Treatment Among Patients Receiving Highly Active Anti-Retroviral Therapy; **Moses Parmeiyan**
	59.	Genetic distribution of *Mycobacterium tuberculosis* complex, drug resistance and transmission among presumptive tuberculosis patients in Western Kenya; **Albert Okumu**
	60.	Scaling uptake of TB preventive therapy amongst Healthcare Workers; **Emelder Auma**
	61.	Leveraging Support Networks: Assessing Support Group Impact on Sustained Treatment Adherence among Tuberculosis Patients in Makueni and Machakos Counties; **Elizabeth Atieno**
	62.	The burden of *Mycobacterium* Intracellular TB among presumptive TB patients in Western Kenya; KEMRI-TB Laboratory based Surveillance; **Caroline Ochola**
	63.	Integrating TB active case finding in index testing services to aid in early tb diagnosis in Arombe dispensary, Migori county; **Loriet Otieno**
	64.	Screening of miners using digital chest X-ray in Masara Suna west Sub county; **Peter Omware**
	65.	Leveraging on community TB activities to scale up TB case finding; **Peter Omware**
	66.	Enhancing Public Health: Comprehensive Strategies for Improved Surveillance in TB Contact Investigation; **Gladys Njaka**
Time (EAT) **1005-1105hrs**	Abstract No	**Scientific Session 8: Health Systems-2** **VENUE: TSAVO** **Session Chair:** Enock Kebenei **Rapporteur:** Timothy Kipkosgei
	67.	Comparison between the Smart Triage model and the Emergency Triage Assessment and Treatment (ETAT) guidelines in triaging children presenting to the emergency departments of two public hospitals in Kenya; **Stephen Kamau**
	68.	Spatial analysis of public health facilities utilization on Tuberculosis patient management in Nairobi County: preliminary analysis of characteristics of Tuberculosis diagnosed patients attending Rhodes chest clinic; **Fred Orina**
	69.	Connected diagnostics for semi-real time epidemiological surveillance of infectious diseases in Africa: Kisumu County malaria case study; **Felix Bahati**
	70.	Costs associated with antimicrobial resistance among pediatric in-patients at the Kenyatta National Hospital; **Teresa Ita**
	71.	Outcomeof implementation of laboratory quality management systems in reducing errors: a case study of Rangwe Sub-county, Homabay county; **Everlyne Akinyi**
	72.	Evaluating Specimen Rejection as a Quality Assessment Tool for Intervention at KEMRI-TB Reference Laboratory; **Elizabeth Awour**
	73.	MiMBa pregnancy exposure registry in Western Kenya: Cohort description, challenges, and opportunities for scalability; **Benard Omondi**
	74.	Provision of Adolescent and Youth-Friendly Services in Public Health Facilities in Migori County, Kenya; **Lillian Nyaga**
	75.	Factors identifying Ideal Scientific Communication Channels at Kenya Medical Research Institute: Viewpoint; **Isaac Joseph**
Time (EAT) **1005-1105hrs**	Abstract No	**Scientific Session 9: Malaria-2** **VENUE: SAMBURU** **Session Chair :** Dr. Sophie Uyoga **Rapporteur :** Mercy Tuluso
	76.	HSP90 as a potential biomarker: Exploring the complex relationship between antimalarial treatment and *Plasmodium falciparum* Heat shock protein 90 expression; **Lewis Mbabu**
	77.	Evidence of *P. vivax* in Northern Kenya, an emerging malaria control threat; An incidence report from the outcome of the mid-2023 epidemic response survey; **Francis Kimani**
	78.	Effectiveness of indoor residual spray on malaria control; a review of the malaria cases among children under five years in Rachuonyo North Sub County, Homa Bay County and Nyakach Sub County Kisumu County, Kenya; **Gabriel Kotewas**
	79.	Detection of twelve *Plasmodium falciparum* Kelch 13 gene mutations in clinicals samples from four sites across Kenya reveals intense genomic events; **Benjamin Opot**

	80.	Utility of Ex vivo malaria SYBR Green I assay in susceptibility profiles of *Plasmodium falciparum* and non-falciparum co-infections in Western Kenya; **Agnes Cheruiyot**
Time (EAT) **1005-1105hrs**	Abstract No	**Scientific Session 10: Public Health-1** **VENUE: BOGORIA** **Session Chair:** Dr Richard Omore **Rapporteur:** Steven Onteri
	81.	Factors Associated with Low Measles-Rubella Vaccination Coverage: An Assessment of Post Outbreak Vaccination Campaign in ASAL Counties, Kenya, 2022; **Serah Nduta**
	82.	Knowledge, Attitudes and Practices and sources of information toward Anthrax among High-Risk occupational Groups in Murang'a and Meru Counties, Kenya; **Juster Mungiria**
	83.	Evaluation of the Influenza Sentinel Surveillance System in Kenya, 2021–2022; **Valentine Kabita**
	84.	Community preferred drug delivery approaches for roll-out of novel pediatric schistosomiasis treatment option in two endemic counties of Kenya; A mixed methods study; **Janet Masaku**
	85.	Community smearing day in prevention and control of Tungiasis, a case of Emanyinya CU in Emuhaya subcounty, Vihiga county; **Fanuel Khaingaa**
	86.	Influence of Radio Programs in Creating Awareness on Covid-19 Pandemic among Residents of Lunga Lunga Sub County, Kwale County, Kenya; **Richard Korir**
Time (EAT) **1005-1105hrs**	Abstract No	**Scientific Session 11: Vector Biology-1** **VENUE: MT. KENYA C** **Session Chair: Dr.** Ernest Wandera **Rapporteur:** Dr Edith Chepkorir
	87.	First report of *Anopheles stephensi* in Southern Ethiopia; **Dawit Hawaria**
	88.	Evaluation of passive cooling options and vector proofing for indoor heat reduction and mosquito control in western Kenya; **Bernard Abong'o**
	89.	Influence of Blood Meal Origins on Reproductive Outcomes in *Anopheles gambiae*: Enhancing Fecundity in a Mass Rearing Environment; **Celestine Wekesa**
	90.	Identification of insecticide resistance markers in *Anopheles arabiensis* and *Anopheles gambiae* from Kenya and Benin using Weighted Gene Correlation Network Analysis; **Cynthia Odhiambo**
	91.	Application of MALDI-TOF MS in parity status prediction of field collected malaria vectors; **Mercy Tuwei**
	92.	Late morning biting behaviour of *Anopheles funestus* is a risk factor for transmission in schools in Siaya, western Kenya; **Seline Omondi**
	93.	Experimental hut and field evaluation of a metofluthrin based spatial repellent against pyrethroid resistant *Anopheles funestus* in Siaya County, western Kenya; **Silas Agumba**
	94.	Addressing Malaria challenge through durability monitoring of long lasting Insecticide Nets: Results for attrition and fabric integrity over 12 months of net use in Kenya; **Paul Gichuki**
Time (EAT) **1005-1105hrs**	Abstract No	**Scientific Session 12: MCH -2** **VENUE: MT. KENYA D** **Session Chair:** Dr Elizabeth Echoka **Rapporteur:** Schiller Mbuka
	95.	An interrelational study on hypertensive disorders in pregnancy and neonatal health outcomes at Thika level five hospital, Kenya; **Jared Ronoh**
	96.	Identification of children with wasting using a family MUAC supported by a two-way SMS platform; **Benson Singa**
	97.	Evaluating the proportion of mortality associated with under-nutrition among under-five year old children hospitalized with hypoxemia in Uganda; **Bernard Ochieng**
	98.	Perceived barriers and facilitators to quality contraceptive decision support for adolescent girls and young women (AGYW) among pharmacy staff: A qualitative study in Western Kenya; **Dismus Congo**
	99.	Malnutrition Associated Deaths Among Children aged 1-59 months in Rural and Urban Western Kenya, for the period May 2017- December 2022: Findings from the Child Health Mortality Prevention Surveillance (CHAMPS) Network; **Sagam Kimutai**
	100.	Incidence and Risk factors Associated with Caesarean Section Deliveries: Findings from a Prospective Cohort Study in Western Kenya, 2020-2022; **Edwin Kiplagat**

	101.	Management outcomes of burns in pediatric patients <13 years at Thika level v hospital, Kiambu county, Kenya; **Alphonce Oyugi**
1105 hrs - 1130 hrs TEA BREAK		
Time (EAT) **1130-1300hrs**	Abstract No	**Scientific Session 13: Health Systems -3** **VENUE: AMBOSELI** **Session Chair :** Dr. Richard Mutisya **Rapporteur :** Ishmael Ahamed
	102.	Quality Assurance in the Kenya Polio Laboratory: Cell Sensitivity Assay, 2022–2023; **Shadrack Barmasai**
	103.	Laboratory and Public Health collaration in prompt management of covid 19 cases through homebased care at Nyahera sub county Hospital, Kisumu county, Kenya; **Duncan Odhiambo**
	104.	What does it take to integrate HIV NCD Services in Primary Health Care? A case study of Nyalkinyi Hospital Homabay County; **Jeff Omondi**
	105.	Understanding the treatment burden of people with chronic conditions in Kenya: A cross-sectional analysis using the Patient Experience with Treatment and Self- Management (PETS) questionnaire; **Hillary Kimutai**
	106.	Barriers and solutions to accessing eye care in Meru County, Kenya: A multi-phased mixed methods study; **Sarah Karanja**
	107.	Feasibility of provider collected and participant self-collected swabs among adolescent girls and young women participating in HPV vaccine trial in southwestern Kenya; **Imelda Wakhungu**
	108.	Assessing Health System Capacities for Maternal and Child Nutrition: A Comprehensive Study of Meru, Tharaka Nithi, Nyeri, Nyandarua, and Kirinyaga Counties; **Christine Nderitu**
	109.	Missed opportunities for data use in health care decision-making in Kenya: Cross sectional digital health landscape assessment; **Mercy Terer**
	110.	Availability and uptake of cervical cancer screening and treatment services at 19 Kenyan Health Facilities; **Catherine Wrexler**
Time (EAT) **1130-1300hrs**	Abstract No	**Scientific Session 14: Rising Star Award-2** **VENUE: TSAVO** **Session Chair:** Dr Joseph Mwangangi/ Dr. Doris Njomo **Rapporteur:** Dr Limbaso Konongoi//Francis Kimani/Jane Ikapesi/Maureen Ekisa
	111.	Socio-behavioral factors influencing scabies infestation among children under 5 years of age in Kwale County, Kenya; **Mariam Macharia**
	112.	Characterization of *Proteus mirabilis* Isolates from Ticks Collected in Isiolo County, Kenya; **Bryson Kimemia**
	113.	Mixed Effects Models in the Analysis of Epstein-Barr virus Serological Responses in Children from Chulaimbo, Western Kenya; **Onditi Ian**
	114.	Genotypic and Phenotypic Profiles of Antimicrobial Resistance in Pathogenic Bacteria isolated from Septicemic Patients in Western Kenya; **Joseph Khamisi**
	115.	Microsporidia mb relationship with associated microbiota in the midgut and ovaries of *Anopheles gambiae* and *Anopheles funestus*; **Mark Kivumbi**
	116.	Design and optimization of a Malaria Pf/Pan Antigen Detection Kit in KEMRI, Kenya; Advancing Healthcare through Local Manufacturing of Medical Devices; **Abdiaziz Gosar**
	117.	Isolation and characterization of environmental lytic bacteriophages against endemic Multidrug-resistant *Enterococcus faecalis* and *Enterococcus faecium* in Kenya; **Oumarou Soro**
	118.	Comparison between Sanger sequencing and Oxford Nanopore sequencing of Polioviruses: The KEMRI Polio laboratory experience; **Mercy Onyango**
	119.	Comparative evaluation of the automated Vitek 2 and Microbroth dilution methods on colistin antibiotic susceptibility test results; **Allan Barasa**
	120.	Case Series of Hemoglobinuria Associated with Malaria in Children Aged 3-13 years at Siaya County Referral Hospital (SCRH); **Getrude Kamuyu**
	121.	Deep learning approaches for functional annotation of hypothetical coding sequences in phages; **James Muturi**

	122.	Immune responses to red blood cell antigens among transfused sickle cell anaemia patients in Kilifi, Kenya; **Michael Musembi**
	123.	Integrated Approaches to improve nutritional status of children under five: Case of Positive Deviance Hearth Model in Konoin Sub-County, Bomet County in Kenya: Preliminary Findings; **Lorraine Ombogo**
	124.	Assessing the risk of Rift Valley Fever and other arbovirus transmission in Nguruman, Kajiado County; **Faith Cherop**
	125.	Extra-occupational predictors of COVID-19 disease among Hospital Health Workers. Findings from a case control study in Kenya; **John Macharia**
	126.	Characterization of fetal versus maternal innate immune responses against placental malaria; **Samuel Chenge**
	127.	Characterization of EBV infection in tonsils of children residing in malaria holoendemic region of western Kenya; **Emily Jepkemboi**
	128.	Malaria morbidity due to Nutrition deficiency in Endemic Zones Western, Kenya; **Redemtah Yeda**
Time (EAT) **1130-1300hrs**	Abstract No	**Scientific Session 15: Public Health-2** **VENUE: SAMBURU** **Session Chair :** Dr. Rose Bosire **Rapporteur :** Dr. Beatrice Ongadi
	129.	Modelling COVID-19 waves in Kenya; **Wandera Ogana**
	130.	Malaria prevalence and determinants of optimal intermittent preventive malaria therapy and insecticide-treated nets among pregnant women in Busia County, Kenya; **Everlyne Chimwani**
	131.	Leveraging advocacy to reduce frequent uptake of ECPs among students of tertiary institutions; **Lordlaro Lidoros**
	132.	The Impact of Home - Based Care on Infectious Respiratory Disease: A Case of COVID-19; **Henry Wanjala**
	133.	The effect of COVID-19 pandemic on healthcare seeking in an urban informal settlement in Nairobi and a rural setting in western Kenya; **George Agogo**
	134.	Health providers' perceptions of the use of long-acting HIV prevention products during pregnancy and lactation in Kenya: A qualitative study; **Cherotich Sharon**
	135.	The Epidemiology of circulating vaccine derived poliovirus type 2 (cVDPV2) in Kenya in, 2023; **Shadrack Barmasai**
	136.	COVID 19 Testing: Positivity Rate in Context to Vaccination Status at Nyahera Sub County Hospital, Kisumu County, Kenya; **Duncan Odhiambo**
	137.	Exploring the Diversity of the Human Mitochondrial Genome Along the Kenyan Coast: Progress Towards Establishing a Forensic Reference Database for Kenya; **Eva Aluvaala**
	138.	Challenges faced during Mass Drug Administration for Trachoma Elimination in a Pastoral Conflict area: Experiences of Program Implementers in Baringo County, Kenya; **Bridget kimani**
Time (EAT) **1130-1300hrs**	Abstract No	**Scientific Session 16: Vector Biology-2** **VENUE: TSAVO** **Session Chair :** Dr Damaris Matoke-Muhia **Rapporteur :** Seline Omondi
	139.	Efficacy of the PermaNet® Dual compared to the Interceptor® G2 and the PermaNet® 3.0 in experimental huts in Siaya County, western Kenya; **Nashon Ogutu**
	140.	Cost comparison analysis of different workflows for entomological surveillance using a decision-tree approach; **Jonathan Kazungu**
	141.	Host-Symbiont Interaction in Microsporidia MB infected ***Anopheles arabiensis*** mosquitoes; **Jacqueline Wahura**
	142.	Microsporidia MB infection rates in *Anopheles gambiae s.s*. and *Anopheles arabiensis* from Busia, a malaria endemic zone of Western Kenya; **Tiffany Wandera**
	143.	Species diversity and abundance of ticks collected from livestock in selected pastoral regions in Kenya; **Hellen Koka**
	144.	Insecticide resistance, resting behavior and sporozoite infection rates in *Anopheles gambia*e and *Anopheles funestus* in Teso Sub-County, Western Kenya; **Sarah Nyasende**

	145.	Entomological Surveillance of Malaria Vectors in Baringo County, Kenya; **Lucy Njeri**
	146.	Climate change associated ecological impacts on vector-borne disease transmission - A contemporary global perspective on disparate climate vulnerability; **James Mutunga**
	147.	Validation using Attractive Sugar Baits (ASBs) containing a fluorescent dye in Siaya county, western Kenya: An evaluation of Anopheles feeding rates; **Jackline Jeruto**
Time (EAT) **1130-1300hrs**	Abstract No	**Scientific Session 17: MCH -3** **VENUE: MT. KENYA C** **Session Chair:** Dr. Phelgona Otieno **Rapporteur:** Olga Mashedi
	148.	Childhood hospital readmission following acute illness in Africa and South Asia: a secondary analysis of CHAIN cohort.; **Moses Ngari**
	149.	Burden, timing, causes and factors associated with stillbirth and neonatal mortalities in a Health and Demographic Surveillance System in rural western Kenya, 2018-2022; **George Otieno**
	150.	Impact of HIV Infection and Malaria Parasitemia on Immunogenicity of Inactivated Influenza Vaccine in Pregnant Women and on Mother-to-Child Vaccine-induced Antibody Transfer; **Michael Otieno**
	151.	Prenatal Exposure to SARS-CoV-2 Infection during Pregnancy and Neurodevelopmental Outcomes among Infants in Western Kenya at 6 months of age; **Paul Otieno**
	152.	Assessment of Social Support Levels and Associated Factors among Women Attending Postnatal Clinic at Gulu Regional Referral Hospital, Uganda; **Nannungi Christine**
	153.	Maternal HIV status and the risk of adverse pregnancy outcomes: a cohort of women participating in IMPROVE 1 and IMPROVE 2 studies; **Everlyne Ondieki**
	154.	Development of a Shigella multivalent bioconjugate vaccine: A phase I/II randomized, controlled and age descending study including dose finding in Kenyan infants; **Jane Adetifa**
	155.	Impact of malnutrition on clinical outcomes among children with severe acute respiratory illness in Kakuma, Kenya: **Joel Machuki**
Time (EAT) **1130-1300hrs**	Abstract No	**Scientific Session 18: NCDs** **VENUE: MT. KENYA D** **Session Chair:** Dr. Vera Manduku **Rapporteur:** Ibrahim Mwangi
	156.	Patterns of orthopedic and trauma admissions to a tertiary teaching and referral health facility in Kenya: Chart review; **Maxwell Omondi**
	157.	Evaluation of bacterial pathogens from selected diabetic foot ulcer patients at Thika level 5 hospital, Kiambu county, Kenya**; Ameyo Daglas**
	158.	Understanding the After Violence Care for Adolescent Girls and Young Women Experiencing Gender Based Violence in Kisumu County; **Omollo Mevis**
	159.	Prevalence of hypertension among diabetes clients: a case study of diabetic clinic, Homabay county referral hospital; **Evans Odoyo**
	160.	Clinical outcomes of patients hospitalized with femoral fractures at Gulu regional referral hospital: a retrospective cohort study; **Yakobo Nsubuga**
	161.	Evaluation of chemicals of concern in selected hair relaxers used by women in Embu county; **Beatrice Irungu**
	162.	Prevalence of overweight and obesity amongst primary school children aged 8 - 11 in Thika West Sub-County, Kenya; **Margaret Mburu**
	163.	Severe Acute Respiratory Illness in Patients with Sickle Cell Disease Hospitalized in Two Western Kenya Referral Hospitals; **Peter Kinuthia**
	164.	Predictors of mortality among patients on maintenance hemodialysis attending Nakuru county referral and teaching hospital; **Zachary Mwambi**
	165.	A transcriptome analysis of breast tumors from Kenyan women; **Francis Makokha**
	166.	Prevalence of minor red blood group antigens among sickle cell anaemia patients in Kilifi, Kenya; **Ephy Akoko**
1300-1400hrs LUNCH BREAK		
1400-1430hrs POSTER SESSION		

1400-1430hrs		**Poster Session: Screen 1- NCDs** **Judges:** Dr. Vera Manduku & Dr. Linnet Ongeri
	055.	Prevalence and Determinants of hypertension among Type 2 Diabetes Mellitus Patients in Mombasa County, Kenya; **Habiba Ramadhan**
	056.	Towards the Development of a Microfluidic Device for Point-of-care Detection of Viable *Cryptococcus neoformans*; **Mary Wachira**
	057.	Male Partner Experiences and Social Support during Cervical Cancer Screening, Treatment and Follow-Up; **Natabhona Mabachi**
	058.	Neoantigen profiling in Kenyan breast cancer patients using whole exome and RNA sequencing; **Francis Makokha**
	059.	Co-occurrence of Hypertension and Type 2 Diabetes: Prevalence and Determinants among Diabetic Patients in Mombasa County, Kenya; **Habiba Ramadhan**
	060.	Willingness to start insulin therapy among insulin-naïve persons with type 2 Diabetes mellitus at Gulu regional referral hospital, Uganda; **Nakitto Brenda**
1400-1430hrs		**Poster Session 2: Screen 2- NTDs** **Judges: Dr. Erastus Mulinge & Henry Kanyi**
	061.	First serological evidence of louse borne relapsing fever in northern Kenya: a retrospective study; **John Njeru**
	062.	Comparison of intestinal Schistosomiasis-related ultrasound detectable morbidities in low and high-risk areas in Western Kenya; **Dollycate Njagi**
	063.	Placental metrics and perinatal outcomes associated with malaria in pregnancy in Busia, western Kenya; **Odhiambo Caleb**
	064.	Prevalence and risk factors associated with geo-helminths and intestinal protozoa infections in school-going children in Nyeri county, Kenya; **Anthony Muthee**
	065.	Molecular characterization of the TPRM-PZQ Resistance gene in *Schistosoma mansoni* parasites isolated from infected participants from Siaya County, Kenya; **Peter Olilah**
1400-1430hrs		**Poster Session 3: Screen 3- Maternal & Child Health (MCH) 1** **Judges:** Dr. Benson Singa & Dr. Lucy Chite
	066.	Men involvement in increased ANC attendance among pregnant mothers, a case of Ekwanda Health Unit, Vihiga county; **Fanuel Khainga**
	067.	Effects of Malaria Exposure During Pregnancy on the Levels of EBV anti-gp350 IgA and anti-gp350 IgG Among Infants in Western Kenya; **Stellah Achumbe**
	068.	Assessment of the performance of malaria diagnostic tools in diagnosing malaria in pregnancy and placental malaria; **Melvin Mbalitsi**
	069.	Empowering Male Engagement in PMTCT: Pioneering Zero Mother-to-Child HIV Transmission; **Wayne Otieno**
1400-1430hrs		**Poster Session 4: Screen 4- HIV** **Judges: Dr. Samoel Khamadi & Dr. Edith Chepkorir**
	070.	Factors associated with Viral non-suppression among Adolescents and Young adults on Anti-retroviral Therapy in Nyandarua County, July 2023; **Lucy Njoki**
	071.	Breaking barriers: Addressing Gender-Based Violence and Improving Treatment Adherence among Sero Positive Women in Discordant Relationships in Kuria East Sub County; **Nancy Mwita**
	072.	Roles of Health Care Providers toward HIV Self-Testing (HIVST) approach to achieve global target to end HIV by 2030; **Andrea James**
	073.	Exploring the role of religion in Addressing HIV viral suppression in three community sites, Homabay Kenya; **Joan Ondigo**
1400-1430hrs		**Poster Session: Screen 5- AMR** **Judges:** Dr. John Mwaniki & Susan Kavai
	074.	Antimicrobial Susceptibility and Genetic Basis of Resistance of *Klebsiella* spp Isolated from Diarrheic and Non-Diarrheic Children at Health Facilities in Mukuru Informal Settlement, Nairobi, Kenya; **Celestine Wairimu**

	075.	Environmental reservoirs of multidrug-resistant pseudomonads in a geographical location with predominantly community-acquired infections in Kenya; **Polly Mubassu**
	076.	Targeting *Mycobacterium tuberculosis* with mycobacteriophage; **Joseph Gitari**
	077.	Isolation and characterization of bacteriophages with lytic activity against drug-resistant non-typhoidal *Salmonella* from Nairobi City County, Kenya; **Michael Mugo**
1430-1700hrs	Abstract No	**Symposium 7: Human Genomics and Forensics** **VENUE: AMBOSELI** **Session Chair :** Eva Aluvaala **Rapporteur:** Belinda Azzam & Tiffany Wandera
1430-1700hrs	Abstract No	**Symposium 8: Management and control of invasive Anopheles stephensi in Kenya** **VENUE: TSAVO** **Session Chair :** Dr. Elijah Juma **Rapporteur:** Benyl Ondeto & Tabitha Wambui
1430-1700hrs	Abstract No	**Symposium 9:** **KEMRI Programs and Flagship Projects** **VENUE: SAMBURU** **Session Chair :** Dr. Linette Ongeri **Rapporteur:** Julie Mkawuda & Lydiah Matoke
1430-1700hrs	Abstract No	**Scientific Session 19: Public Health- 3** **VENUE: BOGORIA** **Session Chair :** Dr. Joan Olale **Rapporteur:** Viola Chuchu
	167.	Qualitative Study Exploring Challenges and Influences on Azithromycin Mass Treatment Uptake in Turkana Pastoral Communities in Kenya, 2023; **Stephen Olubulyera**
	168.	A preliminary scoping review on the etiology and distribution of diarrheal diseases in Kenya; **Latifah Benta**
	169.	Assessment of Coverage of Vitamin A Supplementation, Deworming among Children Aged 6-59 months in Meru, Tharakanithi, Nyeri, Nyandarua, Kirinyaga and Kilifi Counties of Kenya; **Caleb Ombati**
	170.	Concurrent Sexual Relationships and Partner's HIV Status Awareness among Girls and Young Women aged 15-24 Years Old; **George Otieno**
	171.	The Impact of communication and advocacy through storytelling on the Road to Zero Neglected Tropical Diseases (NTDs); **Mercy Mumo**
	172.	Bridging Facilities, Empowering Lives: The Impact of Psychosocial Support Groups in PMTCT (Prevention of Mother-to-Child Transmission) in the Community in Kasipul sub county; **Millicent Achieng**
	173.	Sexual Relationship Power and Safe Sex Practices Among Kenyan Adolescent Girls and Young Women in south-western Kenya; **Teresia Atieno**
	174.	Clinical and serological characteristics of the post-COVID-19 status of healthy volunteers from Kenyatta University; **Martin Theuri**
	175.	Revolutionizing Global Health: Bridging Innovations, Emerging Technologies, and Vaccines for Sustainable Product Development; **John Giteru**
	176.	Modelling heat stress in conjunction with other stressors: identification of vulnerable populations; **Bernice Scholten**
1430-1700hrs	Abstract No	**Scientific Session 20: Health Systems - 4** **VENUE: MT. KENYA C** **Session Chair :** Susan Kavai **Rapporteur :** Kelvin Kering
	177.	Barriers of participation and access to mass drug administration for trachoma elimination among pastoral communities of Baringo County, Kenya; **Tabitha Kanyui**
	178.	Reporting and Methodological Quality of Clinical Practice Guidelines for Management of Malnutrition in the East African Community. A Systematic Review; **Sagam Caleb**
	179.	Mentorship as a pathway to generating high quality cancer data for decision making in Sub-Saharan Africa; **Evans Tanui**
	180.	Transforming data systems to improve pandemic readiness and response 2020-2023; **Peninah Munyua**

	181.	Utilization of sub-national public health emergency operations centers to respond to public health events in Kenya, 2020-2023; **Daniel Wako**
	182.	Health and Demographic Surveillance System (HDSS) profile: A Population-based surveillance platform in an urban informal settlement in Kibera; **Clifford Oduor**
	183.	Quality Healthcare Redefined: National Hospital Insurance Fund (NHIF)'s Influence on Service Standards at Public Hospital in Kenya; **Ndirangu Ngunjiri**
1430-1700hrs	Abstract No	**Scientific Session 21: HIV** **VENUE: MT. KENYA D** **Session Chair:** Dr. Samoel Khamadi **Rapporteur:** Asiko Ong'ayo
	184.	Effect of Status Disclosure on Quality of Life among People Living with HIV/AIDS in Ghana: A Health Facility-based Cross-sectional Study; **Farukh Saah**
	185.	The Burden of overnutrition among Adult PLHIVs on Care at Homabay County and referral Hospital 2023; **Nancy Atieno**
	186.	An assessment of antiretroviral (ART) resistance amongst Patients on Salvage and third line regimens, Homabay County Kenya 2023; **Corneleous Edward**
	187.	ART Experience, VL Suppression and CD4 Status of HIV Patients admitted to Homabay County Hospital Inpatient Department in 2021; **Corneleous Edward**
	188.	Role of Orphans and Vulnerable Community Interventions in Addressing Viral Suppression amongst Children and Adolescents Living with HIV in Rachuonyo North Sub County, Homabay; **Victor Owuor**
	189.	An evaluation of early infant diagnosis of HIV among infants attending selected level 4 and level 5 Health Facilities in Kenya; **Emily Barsito**
	190.	Unraveling the Threads of HIV/AIDS: A Comprehensive Study of Patients at the KEMRI Clinic in Kisumu County, Kenya; **Cindy Nyandiko**
	191.	Empowering Adolescent Girls and Young Women (AGYW): Peer-Led Mobilization for Enhanced HIV Prevention Services in Siaya County, Kenya; **Wayne Otieno**
	192.	Progress towards eMTCT: a comparison of study outcomes from 2014-2015 vs 2020-2023; **Catherine Wrexler**
	193.	In silico genomic recombination analysis reveals HIV-1 and HIV-2 mosaic genomes in circulation; **Edwin Magomere**
	194.	Review of Generational HIV Status Change From HIV Positive Adolescents to HIV Negative Children in Rachuonyo East Sub County Homabay County, Kenya; **Nicholas Odiemo**
TEA BREAK AND DEPARTURE		
END OF DAY 3		
DAY FOUR, FRIDAY 16TH FEBRUARY 2024		
ARRIVAL & REGISTRATION		
PLENARY SESSION		
0830- 0855hrs	**Plenary Session 7: Dr. Ruth Masha** "Whole Government Approach Towards Ending Adolescent Triple Threat (New HIV Infections, Adolescent Pregnancies and Sexual and Gender-based Violence in Kenya) "	
0855 - 0920hrs	**Plenary Session 8: Dr. Pauline Mwinzi** "The Remarkable Progress in Eliminating Neglected Tropical Diseases in Africa."	
0920 - 0950hrs	**Plenary Session 9: Prof Digby Warner** "Re-imag(in)ing Tuberculosis through a Different Lens"	
Session Chair:	Dr. Doris Njomo	
Rapporteur:	Susan Kavai	
PANEL DISCUSSION		
0950-1030hrs	Complementary Feeding: The Role of different Sectors Organized by Academia and Research -Academic Research Networks- Scaling up Nutrition Movement (SUN)	
Session Moderator:	Dr. Zipporah Bukania	
Rapporteur:	Kariuki Ngumo	

1030-1100hrs TEA BREAK

PARALLEL SCIENTIFIC SESSION 22 – 26

1100-1300hrs	Abstract No	**Scientific Session 22: Public Health-4** **VENUE: AMBOSELI** **Session Chair:** Dr. Elizabeth Echoka **Rapporteur:** Schiller Mbuka
	195.	Mathematical Model of COVID-19 with a Double-Dose Vaccine; **Henry Wanjala**
	196.	Enhancing Universal Health Coverage for Malaria through Weekly Household Sweeps by CHVs in Nyamira, Kenya; **Dorah Wafula**
	197.	Epidemiology of case-based lab confirmed measles virus cases in Kenya, 2021-2023; **Diana Wanjiru**
	198.	Community acceptability of Attractive Targeted Sugar Baits in a cluster randomized controlled trial in Western Kenya; **Caroline Ogwang**
	199.	Factors associated with poor treatment outcomes among Tuberculosis patients in Meru County, Kenya, 2022; **Abdiaziz Mahamud**
	200.	Facilitators and Barriers to Implementation of Long-acting HIV Prevention Products among Pregnant and Lactating Women in Kenya: A qualitative study; **Maryeve Gikwa**
	201.	Knowledge and Adherence to the National Malaria Treatment Guidelines for Malaria Diagnosis in Pregnancy among Health-Care Workers in Rangwe Sub County, Homabay County; **Everlyne Akinyi**
	202.	Air quality monitoring based on low-cost sensors and labelled air pollution modelling; Bas Henzing
1100-1300hrs	Abstract No	**Scientific Session 23: Virology** **VENUE: TSAVO** **Session Chair :** Dr. Fred Eyase **Rapporteur :** Kelvin Kering
	203.	Comparative analysis of cell-culture based method and direct detection method in Poliovirus surveillance; **Collins Cheruiyot**
	204.	Characterization of West Nile Virus Koutango Lineage isolated from Phlebotomine Sand flies in Kenya 2021; **Jane Thiiru**
	205.	Closed or Open Canal in Environmental Sampling? Evidence from Retrospective Analysis of SARS-CoV2 and Enteric Virus Isolation; **Stephen Ochieng**
	206.	Trends in acute flaccid paralysis cases from Kenya and Somalia; **Samira Ali**
	207.	Lineage diversity of Rift Valley Fever virus associated with human outbreaks in Kenya; **Konongoi Limbaso**
	208.	Previous Exposure of Camels to MERS-CoV Virus as indicated by sero-positivity in Mandera East; **Guyo Sora**
	209.	Molecular characterization of virulent strains of Newcastle disease virus isolated from dead chickens collected in southern highlands and eastern zone of Tanzania; **Charlie Amoia**
	210.	Illness outcomes of in-and-out patients co-infected with SARS-CoV-2 and Malaria, 2020-2022; **Jorim Ayugi**
	211.	Whole Genome Characterization of G8P[14] Rotavirus Strain Detected in Kenya: Evidence For Artiodactyl -To-Human Interspecies Transmission and Reassortment; **Ernest Wandera**
	212.	Longitudinal Study for SARS-CoV-2 and Neutralizing Antibodies between April 2021 and March 2022 in Kombewa, Western Kenya; **Esther Omuseni**
	213.	Presence of SARS-CoV-2 RNA in wastewater and correlation with reported covid-19 prevalence in the Thika sub-county; **Samuel Nganga**
	214.	Temporal Dynamics of Dengue Virus 1 Mutant Populations during a Dengue Fever Outbreak at the Kenyan Coast; **Josphat Nyataya**
1100-1300hrs	Abstract No	**Scientific Session 24: AMR** **VENUE: SAMBURU** **Session Chair : Dr. John Mwaniki** **Rapporteur : Susan Kiiru**
	215.	Monitoring the battleground: Exploring Antimicrobial Resistance, Antibiofilm Trends, and Virulence Factors in Wound Bacterial Isolates; **Silas Awuor**

	216.	Fungal spore air pollution in various environments in Nairobi Kenya; **Vincent Kiprop**
	217.	Phenotypic and molecular characterization of β-lactamase-producing *Klebsiella species* among children discharged from hospital in Western Kenya; **Doreen Wanjira**
	218.	Environmental Contamination and Seasonal Trends of Non-Typhoidal *Salmonella* in a Disease Endemic setting in Nairobi, Kenya; **Collins Kebenei**
	219.	Antimicrobial resistance in a changing climatic context: an emerging Public Health threat in Africa; **Collins Otieno**
	220.	Antimicrobial resistance and Intestinal shedding of Non-typhoidal *Salmonella* among Children under Five years and carriage in asymptomatic hosts in Kenya; **Kelvin Kering**
	221.	Role of Gallstones in *Salmonella Typhi* Carriage and Fecal Shedding, Antimicrobial Resistance and Biofilm Formation; **Peter Muturi**
	222.	Unveiling the Resilience Mechanisms of *Acinetobacter baumannii* in Nosocomial Settings: Insights from AMR and Virulence Gene Carriage; **Vanessa Onyonyi**
	223.	Genomic characterization of lytic bacteriophages isolated in Kenya identifies candidate phages for treatment of *Pseudomonas aeruginosa* infections; **Collins Kigen**
	224.	Host range determination of lytic *Pseudomonas aeruginosa* phages isolated from Kenyan wastewater identifies six phages with broad activity across endemic strain types; **Martin Omondi**
	225.	Antimicrobial resistance among Shigella Isolates from children aged 6-35months with medically attended diarrhea (MAD) in rural western, Kenya: Findings from the Enterics for Global Health Shigella Surveillance Study (EFGH) 2022-2023; **Alex Awuor**
1100-1300hrs	Abstract No	**Scientific Session 25: NTDs and One Health** **VENUE: BOGORIA** **Session Chair:** Dr. Erastus Mulinge **Rapporteur:** Olga Mashedi
	226.	Prevalence and Economic Impact of Cystic Echinococcosis in Narok County, Kenya; **Tonny Nyandwaro**
	227.	Prevalence and Spectrum of fungal pathogens isolated from inmates with Respiratory and Urinary tract infections in Nairobi, Kenya; **Larry Afundi**
	228.	Preventive chemotherapy with ivermectin, diethylcarbamazine and albendazole triple-drug therapy for the elimination of lymphatic filariasis in Kenya: Programmatic implementation and results of baseline survey and the first impact surveillance; **Sammy Njenga**
	229.	Climate adaptation approaches and proposed Modeling of Climatic Variables to predict VL transmission and Informing Outbreak Prevention and early response in Marigat Sub-County, Baringo County in Kenya; **Bernard Ongondo**
	230.	Investigation of an Acute Febrile Illness Outbreak in Laisamis Sub- County, Marsabit County, May 2023; **Victor Ofula**
	231.	Evaluation of lymphatic filariasis seroprevalence following triple therapy mass treatment with ivermectin, diethylcarbamazine and albendazole in coastal Kenya; **Henry Kanyi**
	232.	Impact of deworming on the prevalence of intestinal parasitic infections in Oloisukut conservancy community, Narok county, Kenya; **Zipporah Njeri**
	233.	Co-infections of *Leishmania donovani* and *Leishmania major* in blood of patients with visceral leishmaniasis from Northern Kenya; **Vane Omwenga**
	234.	Community perception on factors associated with *Schistosoma mansoni* prevalence and intensity in the endemic parts of siaya county; **Austine Okinyo**
	235.	Delay in Leprosy Diagnosis in Kilifi and Kwale Counties in Kenya; **Bakhita Barbra**
	236.	One Health in practice: Anthrax outbreak investigation in Murang'a County, Kenya, May 2023; **Mark Matheka**
	237.	Comparing infection susceptibility between exposed Laboratory inbred lines and third generation from the field on *Biomphalaria sudanica* and *Biomphalaria choanomphala* in Western Kenya: Preliminary results; **George Ogara**
1100-1300hrs	Abstract No	Scientific Session 26: Vector Biology-3 VENUE: MT. KENYA C Session Chair: Dr. Damaris Matoke-Muhia Rapporteur: Tiffany Wandera

	238.	Seasonal dynamics of *Aedes aegypti* and assessment of dengue virus infection prevalence; **David Tchouassi**
	239.	Harnessing mosquito symbionts for malaria transmission blocking; **Jeremy Heren**
	240.	Entomological surveillance of malaria vectors in Turkana County, an arid and Semi-arid region in Kenya; **Lucy Wachira**
	241.	Diversity of Anopheles mosquitoes in very low malaria transmission epidemiological zones in Kenya; **Jacinta muli**
	242.	Species Composition and Insecticide Resistance Profiles of Main Malaria Vectors in Kwale County, Kenya; **Miguel Okoko**
	243.	Prevalence, and seasonality of Microsporidia MB in Anopheles mosquitoes in Kwale, coastal Kenya; **Kelly Ominde**
1100-1300hrs	Abstract No	**Scientific Session 27: Health Systems -5** **VENUE: MT. KENYA D** **Session Chair: Bridgit Kimani** **Rapporteur: Ruth Cheruto**
	244.	Supply-Side Factors Influencing Informal Payments for Healthcare at Public Health Facilities in Kenya; **Evelyn Kagure**
	245.	Profiling of human biological samples exported by KEMRI researchers between 2018 and 2020; **Timothy Kipkosgei**
	246.	Recommendation for Early Preparation Toward the Ageing Society – Suggestion from Health and Demographic Surveillance System (HDSS) data from Kwale County; **Hideki Yamamoto**
	247.	Continuous Quality Improvement, Triple R Approach to Scale Up Case Identification through Social Network Strategy at Arombe Dispensary, Migori County; **Loriet Otieno**
	248.	Quality improvement approach to scale up family planning uptake amongst women and adolescents of reproductive age the case of Suna Ragana Dispensary; **Jairus Onyoni**
	249.	Strengthening the diagnostic capacity and quality testing of rural Laboratories in line with universal health coverage: Lessons from Homa Bay County Inter-Laboratory Comparison program; **Gabriel Kotewas**
	250.	Beyond enemy lines: A strategy to providing HIV Prevention Care and Treatment Services in Migingo Island, Migori County; **Eugene Ariya**
1300-1400HRS: LUNCH BREAK		
1400-1600hrs	**CLOSING CEREMONY**	
	Master Of Ceremony: **Dr. Sophie Uyoga**	
	Conference Outcomes & Resolutions Chief Rapporteur: **Dr. Steve Wandiga**	
	Awarding Ceremony: **Dr. Vera Manduku**	
	Recognition of Sponsors and Exhibitors: **Dr Linus Ndegwa**	
	Official Closing remarks: KASH Chair: **Dr. Cecilia Mbae** Ag. Director Research and Development- **Prof. Nelly Mugo** Ag. Director General & CEO, KEMRI: **Prof. Elijah Songok** Chair KEMRI Board of Directors: **Dr. Abdullahi Ali Ibrahim, CBS**	
	Vote of thanks: **Dr Damaris Matoke-Muhia**	

SCIENTIFIC SESSION 1:

RISING STAR AWARD – 1

ORALS

1.

PERFORMANCE AND COMPARATIVE EVALUATION OF A NOVEL DIAGNOSTIC ASSAY, NOVAPLEX™ MALARIA ASSAY KIT, AGAINST ROUTINE DIAGNOSTIC TECHNIQUES IN THE DETECTION OF DIFFERENT *PLASMODIUM SPP.* IN KENYA

Authors: Lewis k Mbabu (Kenya Medical Research Institute)*; Kelvin Thiongo (Kenya Medical Research Institute); Maureen Otinga (Kenya Medical Research Institute); Mary Ombati (Kenya Medical Research Institute); Lynette Wangechi (Kenya Medical Research Institute); Noah Machuki (Kenya Medical Research Institute); Francis T Kimani (KEMRI)

Background: Accurate and rapid malaria diagnosis is vital for effective treatment and control of this deadly disease. Additionally, species identification is crucial for tailoring treatment strategies toward the specific *Plasmodium* species responsible for the infection. Different species of *Plasmodium* exhibit variations in their pathogenicity and susceptibility to antimalarial drugs. Failure to correctly identify the species could result in inadequate treatment, leading to prolonged illness, parasite resistance, and potentially life-threatening complications. By accurately determining the infecting species, healthcare providers can better assess the potential disease severity and implement appropriate management strategies. This study sought to assess the performance of the Novaplex™ Malaria Assay, a novel malaria diagnostic kit, against established diagnostic methods, including microscopy, rapid diagnostic tests (RDTs), and polymerase chain reaction (PCR), in *Plasmodium* detection.

Methods: Blood samples were collected from 142 suspected malaria cases in Matayos, Kenya. The samples were tested using microscopy, RDTs, Novaplex™ Malaria Assay, and qPCR to determine positivity and identify the *Plasmodium* species. Various diagnostic parameters, such as sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), accuracy, and agreement (Cohen's kappa), were calculated to evaluate the assay's diagnostic performance in comparison to the other techniques.

Results: Novaplex™ Malaria Assay exhibited superior sensitivity, accuracy, and NPV when compared to microscopy and RDTs. Furthermore, the assay showed diagnostic agreement with qPCR, which was considered the "gold standard" for this analysis. In terms of species identification, the Novaplex™ assay demonstrated performance on par with qPCR. Specifically, the assay exhibited a sensitivity of 95.5% and a specificity of 87.5%, while microscopy and RDTs had sensitivities of 63.7% and 61.5%, respectively. The PPV and NPV for the assay were 99.2% and 53.9%, in contrast to microscopy and RDTs, which had low NPVs of 12.5% and 11.9%, respectively. The overall accuracy of the Novaplex™ assay was 95.1%, with a substantial agreement with qPCR (k=0.642). In contrast, microscopy and RDTs had lower accuracy levels (65.5% and 63.4%, respectively) and slight agreement with qPCR (k=0.148 and k=0.136, respectively).

Conclusion: Novaplex™ Malaria Assay outperformed traditional methods such as microscopy and RDTs while showing comparable performance to qPCR in identifying and speciating *Plasmodium spp*. responsible for malaria infections. Its high sensitivity and specificity make it a promising diagnostic tool for malaria.

Keywords: Malaria, Novaplex, Species-specific, qPCR, Sensitivity and Speciicity.

2.

IMPROVING TB CASE FINDING AND ADHERENCE TO TB TREATMENT AT A GO- KABETE SUB COUNTY, KIAMBU COUNTY, KENYA.

Authors: Annfreshia Wangari Maina (Moh)*

Background: Over the years, contact tracing has primarily focused on identifying household contacts for screening and investigating Tuberculosis (TB). However, the yield has not been optimal, especially among men in urban and peri-urban areas. Many of them live alone, with their families residing in villages, posing a challenge in reaching them for TB screening. Additionally, those residing in villages often spend their time with peers in town centers or workplaces. The Mount Kenya region faces a significant challenge of high rates of unmarried men, particularly those with alcohol use disorder. In 2022, retreatment cases accounted for 18% (51/276), with 88% (45/51) among men, and 24% (12/51) identified as alcoholics, emphasizing the need to reach out to social contacts for TB patients, especially men. In 2023, retreatment cases decreased to 14% (36/250), with 86% (31/36) among males and 31% (11/36) being alcoholics. In November 2022, a concerning trend of TB was observed among a group of men associated with a specific club in the Kinoo and Muthure areas in Kabete and Kikuyu Sub-Counties.

Intervention: We implemented a strategy to engage social contacts by educating TB patients about TB transmission modes and risk factors. All TB patients were tasked with bringing at least one social contact for TB screening, after educating them on identifying symptoms in their social contacts. Community sensitization efforts were also conducted. Patients were informed about the risk of reinfection if they failed to recognize TB symptoms in their friends and family. For those uncomfortable talking to their friends, they invited us to their social gathering areas for TB sensitization and screening. By providing information on transmission and risk factors, we aimed to reduce stigma, a significant hindrance to social contact linkage.

Results: The implementation of social contact invitations for TB screening yielded 25 patients since November, with the majority being men with alcohol use disorder. Adherence also improved, as these patients held each other accountable, ensuring treatment completion.

Conclusion: Social contact invitation is an effective strategy to increase TB patient yield and enhance treatment adherence. Proper implementation creates awareness, reduces stigma, and improves TB treatment uptake, thereby reducing community-level transmission. This strategy is also effective for active case finding (ACF), empowering clients with the knowledge to link others in their social network early for TB diagnosis, regardless of their TB status.

Keywords: Innovation, Improved Case finding, and better treatment oucome

3.

CHALLENGES AND LESSONS LEARNT IN IMPLEMENTING CERVICAL CANCER SCREENING IN HIV POSITIVE FEMALES IN RURAL AND URBAN SETTINGS IN KENYA

Authors: Sophia Kongoti (KEMRI) Mary Inziani (KEMRI), Sheila Mbaabu (Kenya Medical Research Institute), Caroline Baliach (Kenya Medical Research Institute, Betty Njoroge (KEMRI) Samoel Khamadi (KEMRI)

Introduction: Research has inadvertently linked HIV and cervical cancer. The increasing trend of cervical cancer among HIV positive females in developing countries has been attributed to suboptimal uptake of screening. Researchers face a myriad of challenges while implementing cervical cancer screening. Such challenges include shortages of trained female personnel, regulatory requirements, cultural and social barriers and loss of follow up during treatment. **Methods:** This was a cross-sectional study of HIV positive women aged between 18-65 years, enrolled in national ART programme. Cervical cancer screening was done in Mbagathi hospital located in Nairobi county and Makueni county hospital located in rural setting. The researchers assessed the willingness of the population to participate in the study and research regulations established by the local authorities. Observations were made on time taken to consent, samples collected from each facility within the same period, turnaround time for approvals and the resources used during the research period. **Results:** A total of 400 samples were collected; 25% from Mbagathi hospital and 75% from Makueni hospital. Nairobi county has rigid research regulations, the approval took two months and a payment of $160 was made. Mbagathi county hospital has put in restrictive measures requiring fresh approval from hospital administration. This is regardless of ethical/County approvals. Participants from Mbagathi county were less willing to participate in the study with consenting period taking at least 15 minutes. In Makueni county the hospital administration was less restrictive, only ethical and county approvals were needed. The Makueni county health committee approved the research within two weeks. With the assistance of local community health workers, most of the participants consented within 10 minutes. **Conclusion and Recommendations**: Implementation of screening services in rural settings is fast, easy and reliable. Administrative and regulatory challenges especially in urban settings negatively affect implementation of research. There is also need to identify reasons, which affect optimal uptake of cervical cancer screening in urban populations. The national commission for science, technology and innovation approval or certificate should be a gateway to research in all counties in Kenya. The counties research teams can be looped in during approvals.

Keywords: Cervical cancer, HIV, rural and urban

4.

SPUTUM CYTOKINES ASSOCIATION WITH TUBERCULOSIS CULTURABLE COUGH AEROSOLS

Authors: Wilfred Bundi Murithi (Kenya Medical Research Institute)*; Max Segnitz (University of washington); Lilian Njagi (Kenya Medical Research Institute); Zipporah Mwongera (Kenya Medical Research Institute); Lenis Njagi (Kenya Medical Research Institute); ROBI CHACHA (KEMRI); Dave Horne (University of washington); Thomas Hawn (University of washington); Videlis Nduba (Kenya Medical Research Institute)

Introduction: Isolation of culturable cough aerosols from active tuberculosis (TB) patients is a better marker for TB infectiousness than sputum microscopy. However, collection of cough aerosols is complex and prone to contamination therefore not feasible for clinical use. There is need for better tools that can identify highly infectious individuals who can be targeted by public interventions to halt transmission. We sought to determine the host immunological factors that may predict TB infectiousness.

Method: Participants who were enrolled were Genexpert MTB/RIF or Ultra (Xpert) positive, cough aerosols were collected using cough aerosol sampling system (CASS) before treatment initiation. Spot sputum samples were processed for cytokine analysis by digestion with 10% sputolysin and supernatants stored after addition of protease inhibitor solution. Concentrations of IL6, IL-1β and CXCL8 were measured in the sputum supernatants using ELISA (R&D systems, Inc. Minneapolis, USA).

Results: We measured sputum IL6, IL-1β and CXCL6 levels in 30 CASS-positive and 82 CASS-negative individuals. The concentration of CXCL8 and IL-1β were significantly higher in CASS positive compared to CASS negative participants (P value = 0.017 and 0.031 respectively). In contrast, IL6 had no difference (p value =0.27). CXCL8, IL-1β and IL6 were associated with higher bacillary load as measured by Xpert Ct. (p value = 0.007, 0.00007, 0.0009 respectively) only IL-1β was associated with cavitary disease (p value =0.0007).

Conclusion: The concentrations of IL6, CXCL8 and IL=1β are variably associated with TB culturable cough aerosols, bacillary load and cavitary lung disease. This demonstrates the potential role of inflammation biomarkers in TB infectiousness and transmission which requires further investigation.

Keywords: Cytokines, Tuberculosis culturable cough aerosol.

5.

DIABETES HEALTH CARE SPECIFIC SERVICES READINESS AND AVAILABILITY IN KENYA: IMPLICATIONS FOR UNIVERSAL HEALTH COVERAGE

Authors: Stephen N Onteri (Kenya Medical Research Institute)*

Diabetes is a major cause of morbidity and mortality. Undetected and untreated diabetes results in serious human suffering and disability which negatively impacts on individual's socioeconomic status threatening economic prosperity. There is scarcity of data on health system diabetes service readiness and availability in Kenya which necessitated an investigation. Using the Kenya service availability and readiness mapping tool and a cross-sectional descriptive design, 598 health facilities were randomly selected in 12 purposively selected counties. Health facilities were classified as defined by Kenya Essential Package of Health into primary and secondary levels before statistical analysis using IBM SPSS version 25. Exploratory data analysis techniques were employed to uncover the distribution structure of continuous study variables. For categorical variables, descriptive statistics in terms of proportions, frequency distributions and percentages were used. Of the 598 facilities visited, 83.3% were classified as primary while 16.6% as secondary. A variation in specific diabetes service availability and readiness was depicted in the 12 counties and between primary and secondary level facilities. Human resources for health reported a low mean availability (46%; 95% CI 44%-48%) with any NCDs specialist and nutritionist the least carder available. Basic equipment and diagnostic capacity reported a fairly high mean readiness (73%; 95% CI 71%-75%) and (64%; 95%CI 60%-68%) respectively. Generally, primary health facilities had low diabetic-specific service availability and readiness compared to secondary facilities: capacity to cope with diabetes increased as the level of care ascended to higher levels. Significant gaps were identified in overall availability and readiness in both primary and secondary levels facilities particularly in terms of human resources for health specifically nutrition and laboratory profession. Being the first care point easily accessible to majority of the population more investment is required at primary level to improve diabetes service readiness and availability.

Keywords: Diabetes, Service availability, Service readiness, Primary level, Secondary level

6.

EXCLUSIVE BREASTFEEDING INTERRUPTION IN A COMPREHENSIVE SUPPORT SETTING IN WESTERN KENYA: SECONDARY ANALYSIS OF PROSYNK STUDY DATA

Authors: Micah June June (KEMRI-LSTM)*; Mary Otiti (KEMRI); Alloys O K'Oloo (KEMRI-CGHR); Angucia Bridget (Uganda Cancer Institute); Fred Amimo (Jaramogi Oginga Odinga University of Science and Technology); Stephen Allen (LSTM); Daniel Onguru (Jaramogi Oginga Odinga University of Science and Technology)

Background: Exclusive breastfeeding (EBF) is defined as feeding babies with only breast milk and not any other foods or liquids, except for medications or vitamin and mineral supplements before the age of 6 months. In a setting with comprehensive support, we evaluated factors associated with interruption of EBF and growth outcomes.

Methods: We conducted a secondary analysis of a random sample of 366 infants enrolled in a trial of pro/synbiotics in Homa Bay County, western Kenya (PROSYNK) where mothers received intensive support for breastfeeding and child health practices. Socio-demographic and anthropometric data and when and why interruption of EBF occurred were abstracted from participant's files. Chi-square and Fisher's exact tests used to compare categorical variables and bivariate and multivariate analysis to investigate further associations.

Results: EBF was interrupted in 165/366 (45.1%) infants. Perception that breast milk was not enough was the major reason for interruption (83; 50.3%). Reasons for EBF interruption differed according to timing, early interruption was mostly due to school resumption (48%, 23/48) while late interruption was mostly due to perception of breastmilk was not enough (53%, 62/117) p=0.002. Interrupted EBF was associated with mothers who were younger (p=0.01), single ($p<0.01$) and with fewer children ($p<0.04$). Mean weight-for-length z score at 6 months among infants with EBF interruption (-0.1, SD=1.2) was lower than infants exclusively breastfed (0.3, SD=1.1; $p < 0.01$).

Conclusion: EBF was uncommon despite comprehensive support. Support for breastfeeding to younger mothers, especially those who are unmarried and still attending school, needs to be prioritized.

Keywords: Infants, interruption of exclusive breastfeeding, comprehensive support, growth

7.

MALARIA VECTOR SURVEILLANCE AND PHENOTYPIC INSECTICIDE RESISTANCE IN ANOPHELINE MOSQUITOES IN ISIOLO COUNTY, NORTHEASTERN, KENYA

Authors: Stanley Kitur (KEMRI)*; Luna Kamau (Kemri); Damaris Matoke (KEMRI); Charles M Mbogo (KEMRI); Lucy Njeri Wachira (KEMRI); SARAH KEMUNTO NYASENDE (KEMRI GRADUATE SCHOOL)

Introduction: Increased malaria transmission in areas with little or no information on the vectors is a major public health concern in controlling the disease. In Kenya, areas with high malaria cases are known, but the emergence of malaria in non-endemic areas is a point that needs more research. Isiolo County is one of those areas that have experienced recent malaria outbreaks, yet information on malaria transmission in the area is scanty; therefore, this study sought to fill the gap.

Methods: Adult mosquitoes were collected indoors using CDC light traps and hand aspirators, while larvae were collected using dippers. Sampling was done from three sub-counties of Isiolo County and two randomly selected villages from each sub-county. The collection was done during the short and long rains between June 2019 and May 2021. Morphological identification was done using Gillies and Coetzee's 1987 keys. Sub-species identification of the complexes was done. Females were analyzed for *Plasmodium falciparum* sporozoite infection and host blood meal source through enzyme-linked immunosorbent assays (ELISA).Insecticide susceptibility tests were done on a 2–5-day-old emerged adult *Anopheles* mosquito following WHO 2013 guidelines.

Results: 1640 *Anopheles gambiae* s.l. were collected from the three sub-counties and 2 villages in each sub-county: Merti at 35.3% (579), Mataarba at 32.6% (536). Tene 12.3% (202), Gubadida 5.5% (91), Ngaremara 8.6% (141), and Eremet 5.5% (91) in northern Kenya 1586 mosquitoes were successfully amplified and identified as: 1.3% were *Anopheles parensis*, and 98.7% were Anopheles arabiensis; 54 samples did not amplify. None of the samples collected were positive for *Plasmodium falciparum* sporozoite. 125 were blood-fed: 76% of mosquitoes fed on humans, 3.2% goat, cat, human/dog, 0.8% cat/dog, and 1.6% bovine, human/cat. The mosquito insecticide susceptibility test was done using Permethrin and Deltamethrin on *Anopheles gambiae*. Permethrin: 81% 60 min and 100% KD; deltamethrin 60 min: 59% and 100% KD after 24 hours.

Discussion and Conclusion: The study found that *Anopheles arabiensis* is the most abundant mosquito in Isiolo County. Also, the study found *Anopheles arabiensis* is susceptible to pyrethroids. During the sampling period, none of the malaria vectors were positive for *Plasmodium*, indicating low malaria transmission in the area for that given period. Malaria vector control tools need to be rolled out to counter any potential malaria outbreaks in the county.

Keywords: vector surveillance and phenotypic insecticide resistance in *Anopheline* Mosquitoes in Isiolo County, northeastern, Kenya

8.

INDIVIDUAL-LEVEL FACTORS THAT CONTRIBUTE TO DELAYED DIAGNOSIS OF CERVICAL CANCER, AMONG PATIENTS AT THE KENYATTA NATIONAL HOSPITAL, KENYA.

Authors: Marthaclaire Kerubo Zammit (Jomo Kenyatta University of Agriculture and Technology)*; Jackline Nyaberi (Jomo Kenyatta University of Agriculture and Technology); Susan Mambo (Jomo Kenyatta University of Agriculture and Technology); Careena Otieno (Great Lakes University of Kisumu)

Background: Cervical Cancer is the 4th leading cancer affecting women globally. In Kenya, it is the second most diagnosed and top cause of cancer-related deaths among women. Early diagnosis (Stages I and II), is associated with a 98% 5-year survival rate, while delayed diagnosis (Stages III and IV), is associated with lower rates (17% 5-year survival rate). Over 80% of Cervical Cancer diagnoses in developing countries are made late. This study focused on determining the individual-level factors that contribute to delayed Cervical Cancer diagnosis.

Methods: An analytical hospital-sited cross-sectional mixed method study was adopted, to collect data on; Soci-demographics, Affordability and use of health insurance, Cervical Cancer and Human Papillomavirus (HPV) screening awareness, Prior HPV screening, Diagnosis circumstances, Time taken to seek medical attention, Fears and social support experiences, from 139 cervical cancer patients systematically sampled at the Kenyatta National Hospital, using a semi-structured questionnaire. Additionally, 8 Key Informants namely; Oncologists, Department nurses, and Social workers were purposively selected, to provide in-depth qualitative information on patient-related factors. The key outcome was Stage at diagnosis, categorized as; Early (stages I and II) or Delayed (III and IV) diagnosis. Quantitative data was analyzed by Stata and Logistic regression was done for bivariate and multivariate analysis. Qualitative data was analyzed using NVIVO 14.

Results: 139 Participants were interviewed in September 2023. The mean age was 51 years and majority (63.31%) were married and educated up to the primary level. more than half 61.15% were not employed. The prevalence of delayed diagnosis was 86(61.9%).

The risk factors for delayed diagnosis were; >60yrs age (OR=11.074, 95% CI=2.538-48.310, p-value=0.001), Unemployment(OR=2.585, 95%CI:1.272-5.252, p-value=0.009), Family member paying for NHIF(OR=2.470,95%CI:1.180-5.171, p-value=0.017), Lack of Cervical Cancer awareness (OR=2.883,95%CI:1.310-6.348, p-value=0.009), Lack of HPV screening awareness(OR= 4.100,95%CI:1.975-8.508, p-value=0.000), Lack of prior HPV screening (OR=3.111,95%CI:1.456-6.650,p-value=0.003) and Seeking medical attention due to a symptomatic trigger (OR=2.781,95%CI:1.095-7.060, p-value=0.031) in the bivariate model. Unemployment(AOR=8.538,95%CI:1.896-38.448, p-value=0.005) and Seeking medical attention due to a symptomatic trigger (AOR=3.188,95%CI:1.079-9.421, p-value=0.036) were statistically significant in the multivariate model. KIIs reported that inability to afford diagnosis, cultural beliefs and myths, and patients seeking medical attention after symptoms worsen, contribute to delayed diagnosis.

Conclusion: Gaps identified in awareness of cervical cancer and HPV screening and affordability of health insurance. More programs should be encouraged to support community-level awareness, provide social support, and encourage more women to embrace NHIF.

Keywords: Individual-level factors that contribute to delayed diagnosis of cervical cancer, among patients at KN

9.

MULTIDRUG RESISTANT BACTERIAL INFECTIONS IN COVID-19 PATIENTS ADMITTED IN KENYATTA NATIONAL HOSPITAL, KENYA

Authors: Jeniffer M. Mutua (Kenyatta National Hospital)*; John Mwaniki (KEMRI); Abednego Musyoki (Kenyatta University)

Bacterial infections are among the crucial determinants of the clinical outcomes in patients hospitalized with COVID-19. At the beginning of pandemic, about 77% of the patients were prescribed antibiotics regardless of disease severity and without lab-based evidence of bacterial infection .AMR is likely to cause 10 million deaths yearly and 100 billion USD loss by 2050, Empirical therapy could negatively impact global and NAP on AMR control programs.

This study aimed to determine the spectrum, antimicrobial susceptibility profiles and molecular characteristics of pathogenic bacteria among hospitalized patients with COVID-19 at Kenyatta National Hospital (KNH), Kenya. An analytical cross-sectional study design was adopted and a total of 120 participants purposively recruited among severely ill COVID-19 patients. Nasopharyngeal and oropharyngeal swabs, tracheal aspirates and blood samples were collected, transported to KNH microbiology lab, and analyzed following the standard bacteriological methods. Bacterial isolation was done on selected culture media, whereas isolates identification and AST were done using MALDI-TOF MS and VITEK® 2 COMPACT system, respectively. The screening for ESBL-production was conducted using the Double-Disc Synergy Tests, and confirmed through Phenotypic Confirmatory Disc Diffusion Test. ESBL-resistant genes were PCR-detected from all ESBL-producers at CMR, KEMRI. An overall prevalence of 44.2% (53/120) bacterial infections was found among the study participants, with a 31.7% (38/120) mortality rate. Isolates of Gram-negative bacteria (GNB) exhibited greater prevalence, (73.1%, 49/67). Majority (69.6%, 32/46) of multidrug resistant (MDR) bacteria were GNB. K. *pneumoniae* (45.5%, 15/33) was the dominant ESBL producer and most of MDR-GNB harboring the TEM (83%, n=10/12) and SHV resistance gene (100%, n=7/7) were resistant to β- lactamase inhibitors including amoxicillin/clavulanate but susceptible to piperacillin/tazobactam (60%, n=6/10). Male patients were more likely to have bacterial infections (aOR = 2.61, 1.2 – 5.65), including those caused by ESBL producing bacteria (aOR=0.21, 0.06 - 0.68). Individuals with pre-existing comorbidities were found to have a five-fold increased likelihood of harboring ESBL-producing bacteria (cOR=5.46, 1.37 - 21.67). Patients: aged 25 to 44 years (aOR = 0.13, 0.02 – 0.6), hospitalized in the IDU ward (aOR=3.27, 1.08–6.89), vaccinated for COVID-19 (aOR = 0.2, 0.05 – 0.83) and hospitalized for short duration (0 -5 days) (aOR=14.28, 3.25 - 62.76) had a positive hospitalization outcome. These results highlight a significant burden of bacterial infections among COVID-19 patients, with males at higher risk. Those: not vaccinated, admitted to CCU, aged over 60 years, and with pre-existing comorbidities had poor outcome. There is urgent need for systematic and continuous AMR surveillance at KNH and beyond to inform prevention interventions in accordance with national and global action plans.

Keywords: AMR, ESBL Resistance, Gram negative bacteria, COVID-19, Multidrug resistance

10.

HYPOTHERMIA AMONGST NEONATAL ADMISSIONS IN KENYA: A RETROSPECTIVE COHORT STUDY ASSESSING PREVALENCE, TRENDS, ASSOCIATED FACTORS, AND ITS RELATIONSHIP WITH ALL-CAUSE NEONATAL MORTALITY

Authors: John Mwangi Wainaina (KEMRI Wellcome Trust Research Programme)*

Background: Globally, neonatal hypothermia, associated with increased morbidity and mortality, prevails widely, ranging from 32% to 85% in hospital settings immediately post-birth. Reports on hypothermia from high-burden countries like Kenya amongst sick newborns often include few centers or relatively small sample sizes. This study endeavored to describe: (i) the burden of hypothermia on admission across 21 newborn units in Kenya, (ii) any trend in prevalence of hypothermia over time, (iii) factors associated with hypothermia at admission, and (iv) hypothermia's association with inpatient neonatal mortality.

Methods: A retrospective cohort study was conducted between January 2020 and March 2023, including all admissions of small and sick newborns across 21 Newborn Units (NBUs) at the designated study sites. Trained Health Records and Information Officers retrospectively abstracted data from patient files upon discharge. The primary and secondary outcome measures were admission hypothermia and mortality during the index admission, respectively. An ordinal logistic regression model was used to estimate the relationship between selected factors and the outcomes cold stress (36.0oC - 36.4oC) and hypothermia (<36.0oC). Factors associated with neonatal mortality, including hypothermia defined as body temperature below 36.0oC, were also explored using logistic regression.

Results: A total of 58,804 newborns from newborn units in 21 study hospitals were included in the analysis. Out of these, 47,999 (82%) had their admission temperature recorded and 8,391 (17.5%) had documented hypothermia. Hypothermia prevalence decreased over the study period while admission temperature documentation increased. Significant associations were found between low birthweight and very low (0-3) APGAR scores with hypothermia at admission. Odds of documented hypothermia reduced as ambient temperature and month of participation in the Clinical Information Network (a collaborative learning health platform for healthcare improvement) increased. Hypothermia at admission was associated with 35% (95% CI 1.22, 1.50) increase in odds of neonatal inpatient death.

Conclusions: A substantial proportion of newborns are admitted with hypothermia, indicating a breakdown in warm chain protocols after birth and intra-hospital transport that increases odds of mortality. Urgent implementation of rigorous warm chain protocols, particularly for low-birth-weight babies, is crucial to protect these vulnerable newborns from the detrimental effects of hypothermia.

Keywords: Newborn; inpatient; hypothermia; mortality; warm chain

11.

ANTI-PROLIFERATION EFFECTS OF *RHAMNUS PRINOIDES* AND GREWIA VILLOSA EXTRACTS BASED ON IN VITRO, NETWORK PHARMACOLOGY AND MOLECULAR DOCKING APPROACHES AGAINST CERVICAL CANCER.

Authors: Sally W Kamau (KEMRI)*; Sospeter N Njeru (KEMRI); Mathew Piero (Kenyatta University); Peter G Mwitari (KEMRI); Mercy Jepkorir (KEMRI)

Background: Cancer is a leading cause of mortality globally. The burden is heaviest in LMICs. It is second as a leading cause of mortality according to the National Cancer Institute of Kenya after infectious diseases and cardiovascular diseases. Cervical cancer is the third most diagnosed cancer however it is the leading cause of mortality. Chemotherapy is the most common treatment, however, the cost of treatment coupled with severe side effects are often associated therein. Medicinal plants offer an alternative that is cost-effective, locally available and fewer side effects. Medicinal plants also serve as a reservoir for the development of more efficacious drugs for the treatment.

Method: *Rhamnus prinoides* and *Grewia villosa* plants were collected, air-dried and ground into a powder. Cold extraction technique was used for the extraction followed by solvent partitioning to obtain four extracts based on the solvent (crude (DCM: MeOH), Ethyl acetate, Hexane and Water). The MTT ((3-[4,5-dimethylthiazol-2-yl]-2,5 diphenyl tetrazolium bromide) assay was used to test for the anti-proliferative activity of the extracts against cervical cancer cells (HeLa) and normal cells (Vero-ccl 81) and the selectivity index determined. Qualitative phytochemical screening was conducted according to standard methods as well as GC/MS. The compounds obtained were run through various databases to determine their putative pharmacokinetic properties (ADMET values) and then based on their results, some were selected for network pharmacology and molecular docking studies and RT-qPCR used to validate them.

Results: Following qualitative phytochemical screening, *Rhamnus prinoides* extracts had glycosides, saponins, tannins and phenols in abundance while the *Grewia villosa* extracts had alkaloids, phenols and tannins in abundance. The IC50 (Inhibitory concentration that kills 50% of cancerous cells) values for the extracts of Rhamnus prinoides were198 µg/ml, 155 µg/ml and 78 µg/ml (ethyl acetate extract) with corresponding CC50 (Cytotoxic concentration that kills 50% of non-cancerous cells) values of 519 µg/ml, 568 µg/ml and 177 µg/ml respectively showing their strong selectivity. The IC50 values for *Grewia villosa* were 380 µg/ml, 205 µg/ml and 107 µg/ml for the crude, hexane and ethyl acetate extracts respectively with 735 µg/ml, 428 µg/ml and 226 µg/ml CC50 values respectively. The top 5 genes identified through network pharmacology analysis were; for *Rhamnus prinoides* (TNF, STAT3, EGFR, IL1B and NFKB1) and for *Grewia villosa* (AKT1, EGFR, STAT3, NFKB1, and PTGS2). Molecular docking analysis was carried out and all the genes had a binding affinity of ≤ 0.0 however only the ones with binding affinities ≤ -7.0 were selected. Scratch assay also showed that the extracts limit migration. The activity of the genes was then validated in vitro through RT-qPCR.

Conclusion: The results confirm the potential of traditional plants in drug development for the treatment of cancer.

Keywords: cervical cancer, molecular docking, anti-proliferative, medicinal plants

12.

PATHWAYS OF EXPOSURE TO *VIBRIO CHOLERAE* IN AN URBAN INFORMAL SETTLEMENT IN NAIROBI, KENYA

Authors: Kelvin Kering (KEMRI)*; Michael M Mugo (KEMRI); Beatrice Ongadi (KEMRI); Georgina A Odityo (Kenya Medical Research Institute); Peter Muturi (KEMRI); Cecilia Mbae (KEMRI); Samuel Kariuki (KENYA MEDICAL RESEARCH INSTITUTE)

Background: Cholera is a diarrheal disease caused by the toxigenic *Vibrio cholerae* (V. cholerae) bacterium. V. *cholerae* can spread to drinking water sources and food through contaminated runoff, especially in overcrowded informal settlements and refugee camps with poor sanitation, where several cholera outbreaks have been reported recently (October 2022- October 2023) in Kenya. This study aimed to identify the environmental transmission routes of V. cholerae within the Mukuru informal settlement of Nairobi County.

Methods: Samples from nine environmental sample types (flood water, surface water, shaved ice, raw produce, soil, and public latrine swabs) were collected weekly for 5 months and (drinking water open drains street food) 12 months respectively. All samples were subjected to culture and qPCR detection of *V. cholerae*, while qPCR-positive samples were quantified using a V. cholerae DNA standard. Behavioural data was used to determine the frequency of contact with the environment for adults and children.

Results: Of the samples collected, 20.4% (164/803) were positive by the qPCR. However, none were positive for V. *cholerae* by the culture method. V. *cholerae* specific genes were present in most environmental water samples 79.3% (119/150), including open drains, flood water, and surface water, but only in small proportions in other sample types. Positive environmental water samples showed higher mean V. *cholerae* concentrations [2490–3469 genome copies (gc) per millilitre (mL)] compared to drinking water samples (25.6 gc/mL). Combined with the behavioural data, the exposure assessment showed that surface water had the highest contribution to the total V.

cholerae exposure among children, while municipal water drinking water, surface water, as well as street food and produce in Mukuru Kwa Reuben, made substantial contributions to the total V. *cholerae* exposure for adults.

Conclusion: The presence of V. *cholerae* in raw produce, street food, and drinking water is concerning because it can lead to cholera outbreaks. The exposure to V. *cholerae* through multiple environmental pathways is a public health concern and highlights the need for improved water and sanitation infrastructure and the rollout of oral cholera vaccination.

Keywords

Vibrio cholerae, Environmental samples, Exposure assessment, Informal settlement, Kenya

13.

IDENTIFICATION OF INSECTICIDE RESISTANCE MARKERS IN *ANOPHELES ARABIENSIS* AND *ANOPHELES GAMBIAE* FROM KENYA AND BENIN USING WEIGHTED GENE CORRELATION NETWORK ANALYSIS

Authors: Cynthia Odhiambo

Background: Indoor Residual Spraying (IRS) and Insecticide-Treated Nets (ITN) are the two main methods used to control mosquito populations for malaria prevention. Currently, efficacy of these strategies is threatened insecticide resistance (IR) which may compromise malaria control efforts. Studies of the genetic evolution leading to insecticide resistance could enable an identification of molecular markers that can be used for IR surveillance and an improved understanding of the molecular mechanisms associated with IR. This study aimed to use a Weighted Gene Co-Expression Network Analysis (WGCNA) algorithm, a systems biology method, to identify genes with similar co-expression patterns and hub genes that can be used as molecular markers for insecticide resistance surveillance in Kenya and Benin.

Methods: *Anopheles arabiensis* and *An. gambiae* from Kenya and Benin, respectively, were phenotyped for resistance to alphacypermethrin, permethrin and deltamethrin insecticides. RNA was extracted from unexposed, susceptible and resistant samples followed by Illumina sequencing. WGCNA was conducted on the resulting sequences to evaluate co-expression patterns of genes to identify modules, hub genes and generate a gene co-expression network.

Results: A total of 20 and 26 gene co-expression modules (sft:20,18) were identified via the average linkage hierarchical clustering from *An. arabiensis* (Kenya) and *An. gambiae* (Benin), respectively. The top modules based on the number of genes in *An. arabiensis* and *An. gambiae* were identified to be salmon (n=3197) and blue (n=3839) modules. The genes with the strongest connection (hub genes) were found in all modules. Serine protease, E3 ubiquitin-protein ligase, cuticular protein RR2 and leucine-rich immune protein were identified as hub genes in both species.

Conclusion: This is the first study to conduct WGCNA based on IR transcriptomic data. Four biologically relevant hub genes shared between the two species were identified as potential markers for insecticide resistance. Functional validation of these genes as IR markers should be conducted through in vitro and in vivo studies.

Keywords: Hub genes, insecticide resistance markers, *Anopheles gambiae*, *Anopheles arabiensis*, Benin, Kenya.

14.

EPIDEMIOLOGY OF SOIL-TRANSMITTED HELMINTHIASIS INFECTION AMONG SCHOOL AGED CHILDREN IN PASTORALIST COMMUNITIES OF NAROK COUNTY, KENYA: A CROSS-SECTIONAL STUDY

Authors: Richelle Kihoro

Background: Soil-transmitted helminthiasis (STH) are a major public health problem in sub-Saharan Africa. In Kenya, the National School Based Deworming Program (NSBDP) was launched in 2012 with a goal of reducing STH prevalence in school-aged children (SAC) to <1%, however monitoring and evaluation results have consistently showed > 20% prevalence in Narok County. We conducted a study to investigate the prevalence, intensity and factors associated with STH infections among SAC in Narok County.

Methods: A cross-sectional study was conducted among 514 SAC from five schools in Trans Mara West sub-county, Narok. The sub-county was selected because it had participating schools within the NSBDP with a high prevalence of STH infection. Participants were selected using systematic random sampling. Stool samples collected from participants were examined for STH eggs using Kato-Katz technique. An open data kit questionnaire was used to collect socio-demographics, household, and STH knowledge information from 139 of the 514 SAC. Descriptive statistics was used to summarize the data, prevalence and mean intensity of infections were calculated, and logistic regression used to determine factors associated with STH infections.

Results: The overall prevalence of any STH infection was 24.6% (95%CI: 21.1-28.6). Trichuris trichiura 14.4% (95%CI: 11.7-17.8), Ascaris lumbricoides 12.5% (95%CI: 9.9-15.7) and hookworm 0%. The mean intensity of any STH infection was 870 epg (95%CI: 520-1454) with species specific intensity of 792 epg (95%CI: 363-1725) for A. lumbricoides and 78 epg (95%CI: 42-145) for T. trichiura. The average household size was 9 (SD 3; range: 3-18) with a majority 104 (74.8%) having 5 to 10 members. Farming was the primary economic activity in 58.9%. Most households (78.4%) used stream/river water for drinking and cooking, with mud being the primary construction material for houses (75.5%). SAC showed good hygiene practices with 88.5% always wearing shoes, 76.9% having access to latrine facilities, and 81.3% having prior knowledge about STH, with stomach ache as the most common reported symptom (65.5%). From multivariable analysis the only factors significantly associated with increased risk of STH infection were, children attending Karda and Nkarano schools with aOR=5.29 (95%CI: 1.45-19.24); p=0.011 and aOR=4.53 (95%CI: 1.29-15.97); p=0.019 respectively. For A. lumbricoides, children attending Nkarano School were associated with a significant risk of infection with aOR= 7.81 (95%CI: 1.81-33.63); p=0.006.

Conclusions: Despite the ongoing work of NSBDP, the STH prevalence is still ≥ 20% in Narok County, among SAC. This underscores the need for continued annual MDA. The study found a correlation between children attending specific schools and STH infection risk, suggesting the importance of health education and improved water, sanitation, and hygiene practices in selected schools in the county to alleviate the burden of STH.

Keywords*:* Soil-transmitted helminthiasis, school aged children, prevalence

15.

ASSESSMENT OF THE COLLIBRI™ ES DNA LIBRARY PREP KIT PERFORMANCE IN HUMAN MITOCHONDRIAL GENOME SEQUENCING FOR DEVELOPMENT OF A FORENSIC QUALITY REFERENCE DATABASE

Authors: Belinda Cherono Azzam (Kenya Medical Research Institute)*; Ngure Kirosh Mwiwawi (KEMRI-HID LAB); Lewis k Mbabu (Kenya Medical Research Institute); Eva K Aluvaala (KEMRI)

Background: Mitochondrial DNA (mtDNA) sequencing has become an essential tool in forensic genetics research, particularly for human identification, ancestry determination and phylogenetic studies. While Sanger-type sequencing (STS) of the mtDNA control region has been routine practice in forensic casework, the coding region of the mitochondrial genome (mitogenome) contains rapidly mutating sites, providing enhanced discriminatory power and the ability to resolve common haplotypes in hypervariable regions evoking the need for a population reference database. Thus the advent of Next Generation Sequencing (NGS) presents an opportunity to acquire mitochondrial genome sequences rapidly and cost-effectively, yielding high-throughput data.

In this study, we aimed to assess the performance of the Collibri™ ES DNA Library Prep Kit in generating high quality data. Previous studies have described the use of Nextera XT and KAPA Hyperplus library preparation kits for sequencing the mitochondrial genome on the Illumina system. To evaluate the kit's performance, the Collibri™ ES DNA Library Prep Kit and Illumina MiSeq™ were utilized to generate forensic quality mitogenome reference haplotypes from 92 anonymized samples representing the Kenyan population.

Methodology: Long range PCR was used to amplify the whole genome as two overlapping fragments. Library preparation was performed using Collibri™ ES DNA Library Prep Kit as per manufacturer's instructions. Normalized libraries were pooled and diluted as described in Illumina® protocol for sequencing on the MiSeq™ instrument. The sequences obtained underwent bioinformatics analysis using CLC genomics v.22 and the AQME (AFDIL-QIAGEN mtDNA Expert) tool to determine haplogroups.

Results : 96 samples were successfully sequenced producing full mitochondrial genomes (16,569 bp). This included 2 positive controls and 2 reagent blanks. The Collibri™ ES DNA Library Prep Kit produced sufficient data (≈ 12G) when all 96 samples were sequenced simultaneously. Over 95% of the samples sequenced had a depth of coverage exceeding 1000x with an average coverage of about 4378x. Low level variant calling at 5% and 2% was observed across the genome.

Conclusion: The high-quality data produced by the The Collibri™ libraries on the Illumina MiSeq™ provides a reliable method for whole mitochondrial genome sequencing. This method gives similar quality of data to routine Sanger-type sequencing methods (STS) while providing a high throughput option. This protocol can be used to generate a population reference database of complete human mitogenome sequences and for use in forensic laboratories for routine mtgenome processing.

Keywords

Mitochondrial genome (mitogenome), Collibri ES DNA prep kit, Illumina Miseq, Haplotypes

16.

IMPACT OF TIME TO TRANSPORTATION ON DETECTION AND ISOLATION OF *MYCOBACTERIUM TUBERCULOSIS* FROM SPUTUM SAMPLE

Authors: JOSEPH OUMA MUGAH (KENYA MEDICAL RESEARCH INSTITUTE)*; Patrice Madara (KEMRI); Fredrick A Ogumbo (Kenya Medical Research Institute); Steve Wandiga (KEMRI); BEN ODHIAMBO OKOTH (KEMRI)

Background: Time to transportation (TTT) is the time elapsed from the moment the sputum sample is collected until it is transported to the laboratory for diagnosis of *Mycobacterium tuberculosis* (MTB). TTT can affect the quality and viability of the sputum sample, and consequently, the accuracy and reliability of the diagnostic test and the treatment outcome. According to the standard operating procedure of the KEMRI-CGHR TB laboratory, sputum samples should be transported and be processed within three to five days of sample collection for optimal detection and isolation of MTB. However, due to logistical technicalities, some samples are brought to the laboratory past the recommended time frame hence affecting the detection outcome.

Objective: The aim of this study was to assess the effect of different TTT on the detection and recovery of MTB from sputum samples using microscopy, and culture methods.

Methodology: This cross-sectional study evaluated sputum specimens received at the KEMRI-CGHR TB laboratory between January 2022 to December 2022 from Health facilities in western Kenya and North Rift for tuberculosis multi-drug resistance surveillance. The sample collection dates, date of processing and results for microscopy, culture, and molecular tests were obtained from the KEMRI TB laboratory data management system and analyzed in Excel.

Results: The total number of samples was 5989. Samples that were received in the laboratory between days one and five after collection were 4083. The positivity rate for these samples was; microscopy 596(14.96%) and culture 453(11.09). For days 6-15, 1719 were received. 194(14.31%), and 180(10.47%) turned positive for microscopy and culture respectively. Between days 16-30, of 187 samples that were received, 27(14.43%) turned out positive for microscopy and 13(6.95%) turned positive for culture. The proportion of the positive results decreased as the TTT increased with the lowest positivity rate observed in samples that were received between days 15 and 30 after sample collection.

Conclusion: The TTT is an important factor that influences the diagnosis and recovery of MTB from sputum samples. The optimal TTT for MTB detection and isolation from sputum samples is within five days of sample collection as it ensures the highest quality and viability of the samples and the best performance of diagnostic methods. Delaying the transportation of sputum samples can lead to false-negative results, delayed diagnosis and poor treatment outcomes. Therefore, it is recommended to transport the sputum samples to the laboratory as soon as possible after collection.

Keywords: *Mycobacterium Tuberculosis*, diagnosis, culture, microscopy, Time to Transportation (TTT), multi-drug resistance surveillance,

17.

FACTORS ASSOCIATED WITH PREGNANCIES AMONG ADOLESCENTS GIRLS AGED (15-19) YEARS IN KOROGWE DISTRICT, TANGA REGION. A MIXED METHOD STUDY

Authors: Neema Magoti Kilimanjaro Christian Medical University) Doris Njomo (KEMRI) Linnet Ongeri

Background: Globally the majority of the population are adolescents aged 10-19 which is about 16%. According to the WHO, 2022 Adolescent Birth Rate has declined from 49/1000 to 44/1000 births. However, the number of Adolescent Birth Rate is still very high in SSH, where 33% percent have started childbearing. In Tanzania, there has been no significant decline in adolescent pregnancies for the past 10 years, although the national goal was to have less than 100/1000 births by 2020. The aim of this study was to assess factors associated with pregnancies among girls aged 15-19 in Korogwe District Council, Tanga region, Tanzania.

Methodology: Community-based, cross-sectional study using a mixed method design, was conducted from 1st – 30th June 2023. For the quantitative arm, face-to-face interviews using questionnaires were conducted with 418 adolescent girls aged (15-19) who were sampled using multistage sampling technique. For the qualitative arm, focus group discussions were conducted with adolescent boys and girls, parents with adolescent girls, teachers, and village leaders and in-depth interviews with the district education officer, and the social welfare officer and pregnant adolescents .All study participants were purposively selected based on their experience with issues related to adolescent pregnancies. Descriptive and Analytical statistics methods were used to analyze quantitative data and a thematic framework was used to analyze qualitative data

Results: In the quantitative part, a total of 418 adolescents were enrolled with mean age of 17 (SD 1.4). The prevalence of adolescence pregnancy was 16%. In logistic regression, higher odds for adolescent pregnancies were age 15-17, ever being in a union, never been to school and low knowledge about family planning (FP) methods. In the qualitative part, majority of the community members had a negative perception of adolescent pregnancies and modern contraceptive use, especially using Contraceptives before giving birth to a first born. Poverty, misconception on FP methods, lack of poor parental guidance, and long distance to school were the main reasons for adolescent pregnancies.

Conclusion: Adolescent pregnancy remains a problem in Korogwe District. Interventions to keep girls at school, prevent child marriages, address contraceptive methods, and improve parent-to-child communication on sexual and reproductive health issues need to be implemented.

Keywords: Factors, Prevalence, Reasons, Perception, Adolescence pregnancy, Community

18.

SCREENING OF *SARS-COV-2* FROM SELECTED SEWERAGE SYSTEMS IN KENYA

Authors: Christine Jobita1, Joseph Wainaina1, Priska Bwana1, Nancy Kagendi1, Gloria Wandera1, Kevin Wafula1, Matilu Mwau1

Corresponding author: christine.jobita@gmail.com

1Kenya Medical Research Institute, KEMRI

Introduction: SARS-CoV-2 was responsible for the 2019 Covid pandemic with over 770 million confirmed cases and 6 million deaths reported globally. In some countries, the virus has been detected in wastewater contaminated with urine and faeces and this approach has been used for public health disease surveillance purposes.

Objective: To detect *SARS-CoV-2* virus in wastewater.

Methods: This was a longitudinal study in which wastewater samples were collected twice a month for a period of 12 months: July 2022 to June 2023 in Nairobi and September 2022 to August 2023 in Busia. In Nairobi, the samples were collected from a single site, an open sewer line in Lindi Ward, Kibra (-1.3186649, 36.7940268) while in Busia, the samples were collected from Busia sewerage treatment plant which had six different sample collection points. Thereafter, the samples were transported at 4°C to the Kenya Medical Research Institute labs in sterile 1L plastic bottles for screening on the day of collection. The samples were screened for *SARS CoV-2* using Abbott Real-time *SARS-Cov-2* assay and later stored at -40◦C. The Abbott sample results were interpreted as *SARS-CoV-2* Detected or Not Detected, recorded and were analyzed using descriptive statistics.

Results: A total of 182 samples was collected. From Kibra, 11 out of 26 (42.31%) samples tested SARS- CoV-2 positive with CT values ranging from 24.40 to 28.32. From Busia, an overall of 12 out of 156 (7.69%) samples tested SARS-CoV-2 positive with CT values ranging from 25.94 to 29.68. Specifically, each of the 6 collection points at the Busia sewerage treatment plant had 26 samples. Of the samples collected at the 1st, 2nd, 3rd and 4th sample collection points, 6 (23.08%), 4 (15.36%), 1 (3.85%) and 1 (3.85%) samples respectively tested SARS-CoV-2 positive while all the samples collected at the 5th and 6th sample collection points tested SARS-CoV-2 negative.

Conclusion: This study revealed that *SARS-CoV-2* was detectable in wastewater. In addition, the samples collected from Kibra, which is an open sewer line, had a higher positivity rate than samples collected from Busia sewerage treatment plant. Of note, the positivity rate of samples collected from Busia sewerage treatment plant decreased across the six sample collection points, showing the effectiveness of the sewerage treatment plant before the treated water is released to the environment.

Recommendation: Wastewater based surveillance can be an effective tool for monitoring the virus's transmission within different areas. The amount of virus is very little based on the CT values, therefore effective methods must be used to detect the virus.

Keywords: *SARS-CoV-2*

19.

ANTI-INFECTIVE AND CYTOTOXICITY POTENTIAL OF THE ROOT BARK OF *DALBERGIA MELANOXYLON GUILL. & PERR*

Authors: Duncan Mutiso Chalo (University of Nairobi)*; Abiy Yenesew (University of nairobi); Esezah kakudidi (Makerere University); Katrin Franke (Leibniz Institute of Plant Biochemistry)

Background: Infectious diseases account for 90% of the disease burden worldwide with developing countries highly affected. Infectious agents have been reported to raise the risk of human cancer. The major contributor to these menace is drug resistance to the available conventional drugs. In search for alternative drug sources, Dalbergia melanoxylon that is ethno medicinally utilized against infectious diseases was investigated for its potential anti-infective agents and its cytotoxicity.

Methods: Chromatographic separation of the CH2Cl2/MeOH (1:1) extracts of the root bark was done and the isolated compounds were elucidated by spectroscopy methods. Antibacterial activity against *Bacillus subtilis* and *Aliivibrio fischeri* was determined in a turbidimetric assay. Pure compounds were further tested against Enterococcus faecalis, Escherichia coli, Mycobacterium vaccae, Staphylococcus aureus, methicillin resistant Staphylococcus aureus and *Pseudomonas aeruginosa* using agar diffusion assay. For antifungal activity, *Phytophthora infestans*, *Botrytis cinerea*, and *Septoria tritici* strains using turbidimetric assay were deployed. Further testing of pure compounds against *Sporoidiobolus salmonicolor*, *Candida albicans* and *Penicillium chrysogenum* using agar diffusion assay was done. Antihelminthic activity using *Caenorhabditis elegans* was tested. Cytotoxicity (CC50) of the crude extracts against the human prostate cancer (PC-3) and colon adenocarcinoma (HT-29) was done using colorimetric cell viability assays. For the most promising active pure compound, methylene blue assay against HeLa cells was performed

Results: Phytochemical investigation yielded six undescribed prenylated isoflavanones (1-6), isoflavanoids (7-10), neoflavones (11-13) and alkyl hydroxycinnamates (14). Significant antibacterial activity against B. *subtilis* was exhibited by the crude extract (50 & 500 µg/mL). The same pathogen alongside A. *fischeri* were also inhibited by compounds (3R)-tomentosanol B (9) and sophoraisoflavanone A (10). Compounds Kenusanone H (7) and (9) further showed superior antibacterial activity against methicillin resistant S. *aureus* and M. *vaccae* compared to reference drug ciprofloxacin with MIC (0.8 and 6.2 µg/mL). Promising antifungal activity was reported by crude extract (125 µg/mL), compounds (10) and (7) at 42 µg/mL. The most active compound (7) exhibited moderate toxicity CC50 against HeLa cells at 1.8 ± 1.4 µg/mL (4.2 µM). No antihelmintic activity was observed. Discussion: The observed biological effects support the traditional use of D. melanoxylon. Rare 3-hydroxisoflavanones and flavonoids with prenylation at B- and C-rings have been described in the genus *Dalbergia*. Prenylation increases lipophilicity and thus affinity to biological membranes hence enhanced antimicrobial activity.

Conclusion: D. melanoxylon is not toxic in general but show selective antibacterial and antifungal activities. The plant possess vast array of unique anti-infective structures.

Keywords: Cytotoxicity; isoflavanones; infectious diseases, antibacterial; antifungal; anti- helminthic; cytotoxic activities,

20.

GENETIC DIVERSITY OF QUINOLONE EFFLUX PUMP (QEPA) AMONG *E. COLI* ISOLATED FROM CHILDREN UNDER FIVE YEARS BEING DISCHARGED FROM HOSPITALS IN KENYA.

Authors: Kevin M Kariuki (Kenya Medical Research Institute)*; Susan Musembi (Kenyatta University); Doreen Wanjira Rwigi (KEMRI-Graduate School); Mareme Diakhate (University of Washington); Stephanie Tornberg-Belanger (Atrium Health Wake Forest Baptist Health); Timothy Mutuma (Kenya Medical Research Institute); Kirk Tickell (UW); Olusegun Soge (University of Washington); Benson Singa (KEMRI); Judd Walson (University of Washington); Patricia Pavlinac (University of Washington); Samuel Kariuki (KENYA MEDICAL RESEARCH INSTITUTE)

Introduction: There is a high risk of carriage of antimicrobial resistance (AMR) in enteric bacteria among children being discharged from health facilities in sub-Saharan Africa (SSA) due to exposure to antibiotics during treatment. The discharged children can be potential sources of transmission in the community upon returning home. The qepA gene is one of the genetic determinants responsible for fluoroquinolone resistance, an important antibiotic given to children to treat enteric infections. The efflux pump-carrying gene mediates reduced susceptibility to fluoroquinolones in qepA-carrying bacteria. There is limited information on the prevalence and epidemiologic characteristics of qepA alleles circulating in Kenya and the sub-Saharan (SSA) region.

Objective: This study aimed to detect, characterize, and determine the strain clustering patterns of qepA variants among ciprofloxacin non-susceptible *Escherichia coli* (E. coli) isolates from children discharged from Kisii and Homa Bay Teaching Referral hospitals.

Methods: A total of 188 ciprofloxacin non-susceptible E. *coli* isolates were recovered from 406 children aged 6-59 months being discharged from hospitals. The E. *coli* isolates were subjected to antimicrobial susceptibility testing (AST) by disc diffusion and Etest methods, genotypic characterization of extended-spectrum beta-lactamase (ESBL), and plasmid-mediated quinolone resistance (PMQR) genes by polymerase chain reaction (PCR). The qepA alleles and mutations were analyzed by Sanger sequencing. Clustering patterns were determined using GTG analysis.

Results: Of the 188 E. *coli* isolates analyzed, 16(8.5%) were found to carry the qepA gene. Among the 16 isolates, 13 (81%) had a high minimum inhibitory concentration (MIC) of 32 µg/mL. All isolates were positive for blaCTX-M, while 13/16 (81%) isolates were also positive for blaTEM; 3/16 (19%) isolates co-carried blaTEM, blaSHV, and blaCTX-M. Five isolates had co-carriage of qepA with other PMQR genes, specifically qnrS and aac(6')-lb-cr. The qepA4 variant was the major qepA allele identified in nine isolates with amino-acid substitutions at F95L and V134I. Mutation D87N 14/16 (88%) was the most common amino-acid substitution, in the gyrA subunit while S80I 14/16 (88%) in the parC subunit. Three isolates had four non-synonymous mutations on gyrA and parC: D87N, S83L, S80I, and E84G. The qepA-positive isolates were clustered into five unique clusters, varying in site, gene co-carriage, and allele types.

Conclusion: We found novel circulating variants of the qepA efflux pump mediating fluoroquinolone resistance among children being discharged from Kisii and Homa Bay Referral hospitals in Kenya. These findings shed light on the genetic context and diversity of the qepA alleles circulating in parts of Kenya and emphasize the need for active genomic surveillance and enhanced antimicrobial stewardship in public health facilities for control and prevention.

Keywords: Antimicrobial resistance, Ciprofloxacin, *Escherichia coli*, post-hospital discharge, quinolone efflux pump,

21.

A STUDY ON ATTITUDES AND PERCEPTIONS ON THE NUTRITIONAL VALUE AND HEALTH BENEFITS OF RAW BITTER GOURD AND BITTER GOURD RELATED PRODUCTS IN THE MARKET ON GENERAL PUBLIC IN COLOMBO DISTRICT, SRI LANKA

Authors: Chathura nilupul L. V perera (University of Northumbria)*

Background and Objectives: This study examines the attitudes and perceptions of the general public in the Colombo District, Sri Lanka, regarding the nutritional value and health benefits of raw bitter gourd and bitter gourd-related products.

Methods: This research combines quantitative data collection techniques. Forum based questioner were given to the consumers and non-consumer individuals to understand their experiences and perception. Additionally, surveys were analyzed using Microsoft Excel.

Results: Despite the potential health benefits, there is a lack of research on bitter gourd preferences and products. The findings reveal that taste preference is the primary reason for non-consumption, with 49% of respondents expressing dislike for the taste. Additionally, 25% of respondents reported a general dislike for the vegetable. However, respondents displayed a level of awareness regarding bitter gourd's health benefits, including blood sugar control, cholesterol reduction, weight loss, and immune system support. Although some respondents were familiar with bitter gourd products such as crackers, biscuits, chips, and juice, there was uncertainty about their availability.

Conclusion: Future research should focus on education initiatives to increase awareness, innovative product development to cater to diverse tastes, exploration of culinary applications, clinical studies to further understand the health benefits, analysis of consumer preferences and market dynamics, promotion of sustainable cultivation practices, and long-term health impact assessment. These findings provide valuable insights for future research, policy formulation, and marketing strategies to promote bitter gourd consumption and leverage its nutritional value and health benefits in Sri Lanka. By addressing taste concerns, enhancing awareness, and diversifying product offerings, bitter gourd could be more widely embraced as a nutritious vegetable with potential health advantages in the Colombo District and beyond.

Keywords: Bitter gourd, Diabetic mellitus, Cholesterol reduction, Health benefits, Increase awareness.

SCIENTIFIC SESSION 2: NATURAL PRODUCTS

22.

ANTIFUNGAL MECHANISMS, AND SECONDARY METABOLITES OF BACILLUS SPP FROM LAKE BOGORIA AS BIOCONTROL AGAINST *RHIZOCTONIA SOLANI* IN *PHASEOLUS VULGARIS.*

Authors: TOFICK BARASA WEKESA (Webuye)*

Background: The common bean (Phaseolus vulgaris L.) is a yearly herbaceous plant grown for its edible dry seeds. Despite that, pests and diseases have contributed to the decline of common bean production in Kenya. Therefore, the study aimed to identify bacteria from Lake Bogoria, screen for effective antifungal agents and determine secondary metabolites produced against Rhizoctonia solani.

Methodology: A serial dilution technique was used to isolate bacteria from the sample. Pure cultures were characterized using standard microbiological and Gram stain techniques. Antifungal mechanisms were assayed using co-culture technique. Molecular identification of bioactive isolates was determined using sanger sequencing by use of universal bacterial primers for the amplification of 27 F (5'-AGAGTTTGATCCTGGCTCAG. 3') and 1492. R (5'-CGGCTACCTTGTTACGACTT-3'). The secondary metabolites production was determined using Gas Chromatography-Mass Spectrometry.

Results: A total of 49 bacteria were isolated, of which 10 isolates had antifungal activity against *Rhizoctonia solani*. The molecular characterization based on 16 S ribosomal RNA confirmed the selected bioactive bacterial strains' identity with a diversity similar to the Bacillus genus. Gas Chromatography-Mass Spectrometry analysis of secondary metabolites showed the antimicrobial compounds produced by *Bacillus subtilis* were; 3-Heptanone, 5-ethyl-4-, Pyrrolo [1,2-a] pyrazine-1,4- dione, hexahydro, 9-Octadecen-1-ol, (Z)-, Cyclononasiloxane, octadecamethyl- and Benzeneacetic acid.

Discussion: Lake Bogoria harbours diversity of microbes with diverse morphological, physiochemical and molecular identity. Majority of the microbes belong to Bacillus genus with antifungal activity against diverse plant pathogen. The antifungal activity is due to the secondary metabolites production having antifungal and antibacterial activity.

Conclusion: Lake Bogoria harbors useful microbes as bio-control agents against *Rhizoctonia solani*. Therefore, the isolates can be assessed further for toxicological and Eco-toxicological studies and registered by Pest Control Products Board (PCPB) as a bio control for management of the most common diseases caused by *Rhizoctonia solani* in beans farming.

Keywords: *Phaseolus vulgaris* L, *Rhizoctonia solani*, biocontrol, Secondary metabolites, Volatile compounds

23.

FROM NATURES PHARMACY TO MODERN PHARMACY: A JOURNEY THROUGH THE LANDSCAPE OF CANCER DRUG DISCOVERIES

Authors: Sabina W. Wachira (KEMRI)*; Mary Sofia Wanjiku Nyangi (Kenya Medical Research Institute); Beatrice N Irungu (Kenya Medical Research Institute).

Background: Nature's pharmacy has long been a constant source of inspiration and exploration in the search for effective treatments across various ailments, including cancer. Within this diverse realm of nature, the discovery of cancer drugs has been particularly remarkable. Natural products derived from plants, animals, and microorganisms have emerged as the foundation for such groundbreaking advancements. Visionary pioneers in this field have revolutionized cancer therapies, shaping the current landscape of treatments we rely on today. The pivotal role of nature's pharmacy in the discovery of cancer drugs cannot be overstated, providing invaluable insights to researchers. This research aimed to understand the significant contribution of nature's pharmacy to the discovery of cancer drugs. Recognizing its invaluable role will enables us to explore its vast potential, fostering strides in cancer treatment discovery and development.

Methods: To understand the impact of nature's pharmacy on cancer drug discovery, extensive research and analysis were conducted. This involved a thorough examination and review of scientific literature, publications, FDA, EMA, NCI drug approval reports, and cancer drug databases to gather relevant.

Results: The findings reveal that out of the 295 cancer drugs that have received licenses from both the FDA and the EMA, 33 of them have been derived from natural products and their structural analogues. This represents approximately 11% of the total number of licensed drugs. These results strongly suggest that nature's pharmacy continues to be a promising and valuable resource for the development of cancer treatments. Additionally, nature's pharmacy has played a crucial role in the establishment of a chemical library that contains a diverse range of chemical structures. This chemical library serves as a valuable foundation for the development of new compounds and the expansion of chemical libraries utilized in drug discovery. The contributions of the natural pharmacy to the development of modern cancer drugs are undeniably significant.

Conclusion: nature's pharmacy has played a crucial role in the development of modern cancer drugs. Natural products and their derivatives have provided crucial leads for the development of licensed anticancer drugs and supportive therapies. To further advance this field, future efforts should focus on establishing a comprehensive database specifically dedicated to African natural products with potential for developing cancer drugs. This database would serve as a valuable resource for researchers, speeding up the discovery of novel and effective treatments from Africa's rich biodiversity for the benefit of our population.

Keywords: Nature's, pharmacy, Cancer, Drug, Discoveries

24.

IN VITRO ANTIPROLIFERATIVE ACTIVITY OF *ASPILIA PLURISETA* AGAINST PROSTATE CANCER

Authors: Innocent Okpako (Pan African University Institute of Basic Sciences, Technology and Innovation)*; Florence Ng'ong'a (Jomo Kenyatta University of Agriculture and Technology); Cleophas Kyama (Jomo Kenyatta University of Agriculture and Technology); Sospeter N Njeru (KEMRI)

Background: Prostate cancer is the second most prevalent cancer among men after the age of 65. Annual incidences are estimated to be 1.41 million and 375,000 deaths worldwide. Current treatments are associated with life-threatening side effects, hence the need to search for effective and safe treatment alternatives. *Aspilia pluriseta* has been demonstrated to have anticancer activity in lung and liver cancer cell lines. This study investigated the antiproliferative effects of A. pluriseta on prostate cancer cells.

Methods: A. *pluriseta* root crude extract was prepared using dichloromethane/methanol (1:1 v/v) and partitioned into hexane, ethyl acetate, and water fractions. The MTT assay was used to screen the fractions for antiproliferative activity on cancerous DU-145 at a single concentration of 200 µg/ml. The active fractions were further tested at 6.25–200 µg/ml on the cancerous cells and non-cancerous Vero E6 cells. Qualitative phytochemical and gas chromatography-mass spectrometry (GC-MS) analyses were done to identify the active chemical compounds in the active fractions. Network pharmacology was then explored to predict the putative molecular targets and mechanisms of action of drug-like compounds. Molecular docking and real-time qPCR were used to validate the predictions.

Results: The active fractions were crude dichloromethane/methanol, hexane, and ethyl acetate fractions. They inhibited the proliferation of DU-145 cells with IC50 values of 16.94, 20.06, and 24.14 µg/ml, respectively. Selectivity indices were 6.04 (crude), 3.62 (hexane), and 6.68 (ethyl acetate). Identified phytochemicals included phenols, terpenoids, flavonoids, tannins, sterols, and saponins. Seventy-nine (79) compounds were identified by GC-MS, and seven (7) of the compounds met the set ideal drug candidate parameters; their top molecular targets included MAPK3, MAPK1, IL6, TP53, ESR1, PTGS2, MMP9, MDM2, AR, and MAP2K1, while deregulation of PI3K/Akt, MAPK, and p53 signalling pathways was indicated as the most probable mechanisms of action. The main compounds were found to be 1-heneicosanol, lanosterol, andrographolide, and retinoic acid. Lanosterol had the strongest binding activities with MAPK21 (-9.7 kcal/mol), ESR1 (-8.9 kcal/mol), and MAPK1 (-8.8 kcal/mol). The mRNA expression of AR was downregulated and p53 was upregulated in DU-145 cells treated with A. pluriseta but not in control cells that were exposed to 0.2% DMSO. Similarly, both CDK1 and BCL-2 were downregulated, while caspase-3 was upregulated.

Conclusions: A. pluriseta inhibited the growth of DU-145 without causing cellular toxicity and has promising potential to be developed as an anti-prostate cancer agent. However, further in vitro and in vivo experiments are recommended.

Keywords: Prostate cancer. Antiproliferative activity. *Aspilia pluriseta*. Network pharmacology. Molecular docking. Gene expression.

25.

PHYTOCOMPOUNDS OF CAJANUS CAJAN AS POTENTIAL ANTICANCER AGENTS AGAINST BREAST CANCER; AN ANALYSIS THROUGH NETWORK PHARMACOLOGY AND MOLECULAR DOCKING.

Authors: Douglas K Njuguna (KEMRI)*; Peter Mwitari (KEMRI)

Introduction: Breast cancer is a leading cause of deaths among women in developing countries, mostly due to unaffordability of chemotherapeutics. As a result, many cancer patients seek complementary and alternative medicines (CAM) which are deemed cheaper and safer. It is therefore critical to enhance research to elucidate the anticancer potential of CAM. Cajanus cajan is a food crop rich in phytocompounds which have various pharmacological effects; cajanol in particular was shown to have activity against MCF7 breast cancer cells, however, the anticancer activity of the other phytocompounds and their mechanisms of action have not been fully elucidated.

Methods: Active compounds of *Cajanus cajan* were retrieved from IMPPAT 2.0 database and from literature and were subjected to filtering conditions of Lipinski Rule, GSK 4/400, Pfizer 3/75 and Drug Likeness score and their target genes predicted using Swiss Target Prediction. GEO, DisGeNet, GeneCards and OMIM databases were used to retrieve breast cancer target genes. The target genes were imported to Venny to obtain drug-disease common target genes. PPI network was constructed using STRING and visualized in Cytoscape. CytoHubba was used to predict the Hub genes. Gene Ontology (GO) enrichment analysis and KEGG Pathway analysis was conducted using DAVID Bioinformatics database. Top 10 enriched Biological Processes (BP), Cellular Components (CC) and Molecular Functions (MF) and top 20 KEGG Pathways were visualized in Bioinformatics.com. Molecular docking was performed using Vina plug-in in PyRx and visualization done in Biovia Discovery Studio.

Results: A total of 76 compounds of *Cajanus cajan* were retrieved and 10 compounds were retrieved after subjection to filtering conditions, these were 2’-Hydroxygenistein, Cajanol, Cajanin, Cajaquinone, Apigenin , Luteolin , Genistein , Naringenine, Quercetin and Isorhamnetin. A total of 257 target genes of the active compounds were obtained, 2510 breast cancer target genes were retrieved from GEO, 115 from DisGeNet, 200 from OMIM and 884 from GeneCards. A total of 113 common target genes were retrieved as the common target genes between active compounds and breast cancer. From the PPI network, a total of 10 Hub genes were identified (SRC, PIK3CA, PIK3R1, PIK3CD, PIK3CB, HSP90AA1, ESR1, AKT1, EGFR and PTK2) and were considered as the potential targets of the 10 active compounds of Cajanus cajan in the treatment of breast cancer. GO enrichment analysis involved 91 BP, 19 CC and 30 MF. KEGG pathway involved 110 pathways. The 10 active compound demonstrated good biding properties at the 10 core targets (binding energy less than -5.0.

Conclusion: The 10 active compounds of *Cajanus cajan* exert anticancer effects by acting on signaling pathways such as VEGF, ErbB, Estrogen and Prolactin through key targets such as SRC, PIK3CA and HSP90AA1 thus providing predictive indicators for further research to verify their mechanisms of action.

Keywords: Network pharmacology, Molecular Docking, breast cancer, gene ontology, KEGG Pathway, complementary and alternative medicines.

26.

CHALLENGES MAPPING OF MEDICINAL RESOURCES WITH POTENTIAL TO MITIGATE COVID-19 AND OTHER SARS-LIKE AILMENTS IN THE K1-7 FLORA REGIONS OF KENYA: FIELD EXPERIENCE

Authors: Bakhita Barbara (KEMRI)*

Introduction: The COVID-19 pandemic prompted a global search for effective treatments and preventive measures. In the absence of a known cure for COVID-19, many turned to the use of alternative medicine which have been used for centuries in various cultures to treat illnesses and boost immunity, Kenya was no exception. This paper presents field experiences while collecting traditional medicine and medicinal products with the potential to mitigate COVID-19.

Methods: Participatory ethno-botanical and ethno-medical surveys were done in the K1-K7 plant distribution regions of Kenya and mapping of medicinal plants, herbal products and food resources used to mitigate COVID-19 and other SARS-like ailments. Local healers, herbalists, and Traditional Health Practitioners (THPs) were engaged in interviews and discussions. Forest transect walks guided by lead practitioners were conducted to identify, quantify, document, and collect medicinal resources known for their medicinal properties believed to possess antiviral or immune-boosting properties.

Results: Samples from 434 medicinal plants mentioned by the THPs to be in use in the management of COVID-19 and related respiratory illnesses were collected. The field experiences were as follows: The THPs and communities were very protective of their resources and only allowed collection of very small quantities of some of the medicinal plants. In some instances there was theft of the medicinal plant samples collected from the forests presumably by the THPs, who are otherwise denied access to the forests. Following a new directive by Chief Conservator of Forests the research team was denied permission to access government forests in Trans Nzoia County hence they resorted to collecting samples in farmers' fields, open grounds and along roadsides. The plant collection took place during the dry season, resulting in difficulties obtaining certain plant parts, such as leaves or, at times, the entire plant. The THPs expressed research fatigue and skepticism, likely stemming from past experiences of exploitation by researchers or quacks. Some of the survey areas like Pokot and Baringo were insecure due to banditry hence could not be accessed.

Conclusion: This paper explored the challenges faced during COVID-19 plant collection, including limited access to medicinal plant resources, regulatory barriers, and cultural factors. The findings underscore the importance of integrating traditional knowledge with scientific approaches to develop effective and culturally appropriate interventions against COVID-19.

Keywords: Leprosy, Delayed diagnosis, Disability

27.

CLIMATE CHANGE AND ITS ENVIROMENTAL IMPACT ON HEALTH

Author: Paul M Faluma (Uzima University)*

Background: Climate change poses significant threats to global environmental stability, leading to various adverse effects on human health. This abstract explores the intricate relationship between climate change and its environmental impact on health. It explores the various direct and indirect pathways through which climate change influences health outcomes, encompassing changes in temperature, extreme weather events, air quality, and vector borne diseases.

Methods: A comprehensive review of peer-reviewed literature and scientific reports was conducted to analyze the diverse impacts of climate change on environmental health. Various case studies and empirical evidence were synthesized to elucidate the connections between environmental shifts and health outcomes.

Results: Rising temperatures contribute to heat-related illnesses, exacerbate air pollution, and escalate the prevalence of vector-borne diseases. The intergovernmental Panel on Climate Change reported that the prevalence of waterborne disease that are responding to changing climate has increased in recent decades and that prevalence of malaria, dengue, Lyme disease, and West Nile Virus infection in particular are expected to further increase if measures are not taken to adapt and strengthen control (Thomson et al.,2022). Additionally, alterations in ecosystems disrupt food and water security, amplifying malnutrition risks and fostering the spread of infectious diseases.

According to Alahmad et al 2023, changes in air quality, driven by shifts in atmospheric conditions, contribute to respiratory and cardiovascular issues. The evidence shows that exposure to short term concentrations of fine particulate matter is associated with increased risks of myocardial infarction, stroke, and death from other cardiovascular diseases.

Climate change has shown to affect mental health as a result of disruption of social and economic structures that populations depend on for good health, including mental health. Globally, climate change has had effects of varying duration on mental health, both directly and indirectly. Some direct impacts of climate change on mental health include trauma suffered due to climate events such as wildfires, hurricanes, earthquakes, and droughts (Merali et al., 2022).

Conclusion: Climate change is an overarching threat that significantly jeopardizes environmental conditions crucial for human well-being. The identified impacts highlight the urgency of implementing robust mitigation and adaptation strategies to safeguard public health against the evolving challenges posed by a changing climate. As the global community strives to address these interconnected challenges. Interdisciplinary collaboration and a holistic approach are essential for fostering resilient communities and promoting a healthier, sustainable feature.

Keywords: Climate change, environmental health, public health, impacts, adaptation, mitigation, ecosystems, human health.

SCIENTIFIC SESSION 3:

MCH -1

28.

FACILITATORS OF LOW SKILLED DELIVERY AT MIRITINI CDF HEALTH CENTER, MOMBASA

Authors: Nasibo Sarbo (DoHs, Mombasa County)*; Nassoro J Mwanyalu (Kenya FELTP)

Introduction: The burden of maternal mortality is higher in Sub Saharan Africa with estimation of 500,000 deaths annually. In Kenya, skilled delivery is below the international target of 90% and maternal mortality ratio is at 362/100,000 live births despite various interventions. There was low number of skilled deliveries in Miritini ward, Mombasa county. We aimed to explore the facilitators contributing to home deliveries in Miritini, Mombasa county.

Methodology: This was an exploratory design conducted in Miritini ward, 2018. Seven villages were purposively selected based on the number of babies receiving BCG injection at Miritini CDF health center. We held Focused Group Discussions(FGD) with women of child bearing age and using an open ended questionnaire. To identify facilitators for home deliveries, we manually categorized the data into Key themes and sub themes. The facilitator took notes during the discussion.

Results: Respondents were aged between 21-37 years (median 28) and most of the women were para 2 and above. Women preferred unskilled delivery services and the key themes facilitating this were Cultural issues, experiences from staffs at facility and facility operating hours. The sub themes identified were services friendly services offered by Traditional Birth Attendants (TBAs) for post-delivery care, unfriendly health workers, deliveries were conducted only during the day, and parity of the women; Staffs were not confident enough to deliver prime-gravida hence referring them out.

Conclusion: We identified cultural issue, unfriendly health care workers, TBA and fear for delivering Prime-gravida as the likely barriers for seeking skilled delivery. We recommend training of healthcare workers, provision of ambulance services, behavior change communication on cultural issues and create a linkage between Healthcare workers and the TBAs.

Interventions: Rewarded 15 TBAs with highest referrals and sensitized 10 Community Health Promoters on Behavior Change Communication and Referrals.

Keywords: Parity, Ambulance, Infant, Pregnancy, Kenya

29.

ADVERSE BIRTH OUTCOMES AND ASSOCIATED FACTORS AMONG ADOLESCENT MOTHERS IN NABDAM DISTRICT OF GHANA: A FACILITY-BASED RETROSPECTIVE STUDY

Authors: Farrukh I Saah (Ministry of Health Rwanda)*; Sylvia Nborah (Zanlerigu Health Centre); Oforiwaa Gifty Gyamera (School of Public Health and Governance, Ghana Institute of Management and Public Administration)

Background: Pregnancy and childbirth for adolescents are at higher risk of adverse outcomes than for older women. They often lack the physiological, psychological, social, and financial capabilities, risking adverse birth outcomes such as preterm birth (PTB), low birth weight (LBW), asphyxia, and stillbirth. This study investigated birth outcomes and associated factors among adolescent mothers in the Nabdam District of Ghana.

Methods: This was a facility-based retrospective study. Birth records of adolescent girls occurring in health facilities in the Nabdam district from January 2021 to December 2022 were extracted. There were 373 records of births among adolescent girls analysed using SPSS v22. Proportion, mean, chi-square, and binary logistic regression tests were done with statistical significance set at $p<0.05$ at a 95% confidence interval (CI).

Results: The study found that 142 (38.1%) of the adolescents had at least one adverse birth outcome. Specifically, 78 (20.9%) had PTB, 56 (15.0%) had newborns with asphyxia, 55 (14.7%) had infants with LBW, and 1 (0.3%) had a stillbirth. Adolescents in the Pelungu subdistrict were 2.95 times (95%CI=1.44-6.05) more likely to have an adverse birth outcome compared to those in the Zanlerigu subdistrict. Lower odds of adverse birth outcome were found among adolescents aged 16–19 years (AOR=0.26, 95%CI=0.08–0.89) and those with 8 or more antenatal care (ANC) visits (AOR=0.30, 95%CI=0.10–0.96) compared to those aged below 16 years and those with less than 8 ANC visits, respectively.

Conclusion: There is a high prevalence of adverse birth outcomes among adolescents in the Nabdam District associated with younger age, residence in the Pelungu subdistrict, and a lower number of antenatal care visits. These findings underscore the need for targeted interventions to improve adolescent maternal health in the district. Strategies could include enhancing access to and utilisation of ANC services, particularly for younger adolescents and those residing in high-risk subdistricts.

Keywords Quality of life; People living with HIV/AIDS; Status disclosure; Social support

30.

STAKEHOLDER ENGAGEMENT IN THE DEVELOPMENT OF A POSTDISCHARGE BREASTFEEDING SUPPORT INTERVENTION FOR SICK ILL MALNOURISHED INFANT UNDER 6MONTHS (IBAMI-2)

Authors: Fridah K Munene (KEMRI-wellcome trust)*; Martha Mwangome (KEMRI-wellcome trust); Caroline Jones (KEMRI-wellcome trust)

Background: Globally, acute malnutrition affects 8.5 million infants under 6 months of age (u6m). The World Health Organization (WHO) has recognized acute malnutrition in infants u6m as a significant problem. The prevalence of suboptimal breastfeeding among infants u6m being treated for acute malnutrition is reported as up to 90%. Underlying factors include poor maternal physical health, social support, and wider household, socio-cultural economic and political structures.

The recommendations on management of malnourished infants u6m are supporting mothers to reestablish breastfeeding while hospitalized and link with community-based follow-up upon discharge. However, in most low- and middle-income settings such support structures to help transition mother-infant pair from hospital to home setting are either non-existent or if present are not linked to the public health system.

Justification: Providing a package of home-based care with breastfeeding support to mothers of infants u6m recovering from acute malnutrition has the potential to improve the retention of exclusive breastfeeding and lead to enhanced infant growth and survival. To date, no such post-discharge package of care is available in Kenya. The study is being implemented in two phases, phase 1 involves intervention development and piloting of the intervention while phase 2 is a randomized control trial. The objective of phase 1 was to engage with national and county level Maternal, Infant and Young Child (MIYCN) stakeholders to develop a structured breastfeeding support intervention (BFSI) for mothers of infants discharged from hospital following admission for an acute serious illness and with a diagnosis of malnutrition.

Methodology: The study entailed the use of qualitative and participatory approaches to develop the intervention including guideline policy and article review, stakeholder mapping and analysis and participatory intervention development workshops. The stakeholders involved were health care professionals, government and non-governmental stakeholders involved in nutrition and child health policy and practice in Kilifi County and at national level in Kenya. These were invited in a series of 5 workshops: three physical meetings with the county stakeholders and two online meetings with the national stakeholders. These meetings facilitated discussions on the content and structure of the intervention which was later piloted among 20 mother-infant pairs.

Conclusion: A breastfeeding support intervention that entails the use of breastfeeding peer supporters to support mothers of infants discharged from KCH following hospitalization has been developed. The package includes an individualized breastfeeding support through providing 3 face-to-face home visits, 3scheduled calls and linkage to available social support post discharge that is being piloted at KCH.

Keywords: Breastfeeding, Malnutrition, Stakeholder Engagement

31.

IMPROVED ADHERENCE TO EARLY INFANT DIAGNOSIS ALGORITHM FOR HIV-EXPOSED INFANTS DURING IMPLEMENTATION OF A POINT-OF-CARE EARLY INFANT DIAGNOSIS PROJECT IN HOMABAY COUNTY, KENYA

Authors: EVERLYNE AKINYI MBOGA (MOH,HOMABAY)*; Mourin ojwang (LVCT)

Background: Early infant diagnosis of HIV (EID) is vital to ensure HIV-infected infants begin lifesaving treatment as soon as possible. A testing algorithm is employed to ensure reliable final diagnosis. . We determine the level of adherence to the confirmatory testing algorithm for HEIs with an initial positive result during implementation point-of-care (POC) EID project which began in August 2017.

Methods: Retrospective conventional EID data were collected from HEI registers at seven high-volume health facilities in Homabay in 2017 prior to implementation of POC EID. Prospective POC EID data were collected from the same facilities from August 2017 to June 2018. We tabulated the total number of HIV-infected infants, number of HIV-infected infants who underwent a confirmatory EID test, and the number of HIV-infected infants who received a baseline viral load test during both time periods at each facility.

Results: Retrospective chart abstraction yielded 59 infants with an initial HIV-positive result. Only 23 (40.0%) had a sample collected for a confirmatory test and 16 (27.1%) had a sample collected for a baseline viral load test. Thirteen infants (22.0%) with an initial positive EID test died or were lost to follow-up. Prospective POC EID data collection yielded 51 infants with 49 (96.1%) having a confirmatory

EID test and 45 (88.2%) with a baseline viral load test. One infant had a baseline viral load test conducted without a confirmatory test while one infant (2.0%) was lost to follow-up.

Conclusion: POC EID testing improved adherence to the EID algorithm and has potential to reduce loss to follow up/deaths.

Keywords: QMS, PRE ACCREDITATION, ACCREDITATION

32.

DEVELOPING A TOOLKIT TO OPTIMIZE NUTRITION CARE FOR CHILDREN WITH SEVERE ACUTE MALNUTRITION: HUMAN-CENTERED DESIGN PROCESS WITH HEALTHCARE WORKERS AT MIGORI COUNTY REFERRAL HOSPITAL.

Authors: Olieng'o Okoth Geoffrey (KEMRI)*; Megan Lewis (University of Washington); Phlona Amam (Kemri/UW); Oduol Chrisantus (Kemri/UW); Catherine A Otieno (KEMRI); Sarah Gimbel (University of Washington); Beth Kolko (University of Washington); Ariana Means (University of Washington); Benson Singa (KEMRI); Megan Coe (University of Washington)

Background: Children with severe acute malnutrition (SAM) are 6 times more likely to die during hospitalization, due to gaps in implementation of existing guidelines. Human-centered design approaches place individuals at the center of the process of developing solutions that are tailored to their settings and needs. In this study, we co-designed the Team Approach to Malnutrition Services (TeAMS) Toolkit to optimize provision of care for children presenting to Migori County Referral Hospital with SAM.

Methods: This was a qualitative study that enrolled healthcare workers (HCWs) providing care to children with SAM. We used purposive sampling to select participants to participate individually in design sessions to provide input and guide tailoring of the toolkit to their needs using key details from the IMAM guideline and Basic Pediatric Protocol, summaries of staff roles, scenarios of tasks and challenges about the care of children with SAM. Three design session cycles were conducted to identify the content and features HCWs preferred, which informed the iterative design and revision of the toolkit. Feedback was summarized and collated to guide tailoring of toolkit formatting and content on teamwork, staff roles, and documentation.

Results: Fourteen HCWs participated individually in 18 design sessions. Three participants participated in two or more design session cycles due to their supervisory roles. Participants identified admission process, feeding prescription, involving caregivers in documentation of night feeds, and flow charts as helpful information to include in the toolkit. About admission process, several participants suggested that displaying the admission workflow would be the most helpful and that the person making first contact with the child should triage. The majority indicated that including feeds prescription and calculation would be helpful to support timely initiation of feeds. There were varied opinion about involving caregivers in documentation given the difference in literacy levels. All participants in design cycle 3 felt that the developed charts were easy to follow with guiding instructions and would feel comfortable prescribing and initiating feeding based on the chart. One meeting was held with participants with supervisory roles to gain consensus on areas where feedback among participants was inconsistent; final revisions were made and the Toolkit presented for piloting.

Conclusion: We successfully developed the TeAMS Toolkit, a resource that consolidates information from Basic Pediatric Protocol and the Integrated Management of Acute Malnutrition guidelines in one place to optimize utilization to improve quality of care. The TeAMS Toolkit development process using the human-centered design approach serves as a technique that can be used to design solutions to challenges faced by HCWs in resource-limited settings. A pilot of the Toolkit has been completed and a feasibility and acceptability evaluation are planned.

Keywords: Severe Acute Malnutrition (SAM), Teams Approach to Malnutrition Services (TeAMS), Human Centered Design

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33.

MALARIA, SCHISTOSOMIASIS, AND SOIL-TRANSMITTED HELMINTHIASIS CO-INFECTIONS AND THEIR ASSOCIATION WITH ANAEMIA IN PREGNANT WOMEN IN BUSIA COUNTY, WESTERN KENYA

Authors: GEORGE N IMBUSI (EGERTON UNIVERSITY)*; Duncan M Wakoli (Department of Biochemistry and Molecular Biology Egerton University, US Army Medical Research Directorate-Africa); SIKUKU DANIEL (EGERTON UNIVERSITY); DICKSON KIPCHIRCHIR (KEMRI-CGHR); Odhiambo Caleb (Egerton University); EVERLYNE CHIMWANI KHALIVINZWA (Jaramogi Oginga Odinga University of Science and Technology); Stellah A Chumbe (Maseno University/KEMRI); RAKEL MAKANDI (EGERTON UNIVERSITY); Michael Ong'echa (KEMRI); Bartholomew Ondigo (Laboratory of Malaria Immunology and Vaccinology, National

Institute of Allergy and Infectious Disease, NIH, Bethesda, Maryland, USA;)

Background: Malaria, schistosomiasis, and soil-transmitted helminthiasis (STH) burden pose the greatest public health challenge in developing countries, especially in sub-Saharan Africa. Despite the geographical distribution of these parasites overlapping, most studies focus on mono-infection and, among school and pre-school children while less is done among the at-risk population of pregnant women. Consequently, there is a paucity of co-infection data on these diseases and their impact on pregnant women's health. This study assessed malaria, schistosomiasis, and helminthiasis co-infections and their association with anaemia among pregnant women presenting for delivery in Southern Busia sub-County hospitals, western Kenya.

Methods: A total of 224 pregnant women aged 18 years and above presenting at Port Victoria and Sio Port Sub County hospitals for delivery between April and September 2023 were enrolled in this cross-sectional study after consenting. About 1 mL of finger prick blood was collected from each participant and analyzed for malaria using mRDT (First Response™) and microscopy. Haemoglobin levels were determined using the Mission Plus® machine. Stool samples were analyzed for *S. mansoni* and soil-transmitted helminthiasis (STH) using the Kato-Katz method.

Results: Out of 224 samples tested, 38 (17%) and 30 (16.4%) were positive for malaria by microscopy and mRDT, respectively. More malaria cases were reported at Sio Port compared to Port Victoria by microscopy: 24 (63.2%) vs. 14 (36.2%) (P = 0.0006). P. falciparum was the most prevalent species detected by microscopy 37/38 (97.4%), followed by *P. malariae* 1/38 (2.6%). Malaria infection intensities were 8 (21.1%), 13 (34.2%), 13 (34.2%), and 4 (10.5%) for very low, low, moderate, and high parasitaemia, respectively. The overall prevalence of *S. mansoni* was 21.6% (95% CI: 58.59-93.60). *Ascaris lumbricoides* was the most prevalent STH 40 (41.2%) followed by Hookworm 22 (22.7%) and Trichuris trichiura 17 (21.6%). Co-infection between malaria and S. *mansoni* and malaria and STH was 3/21 (14.3%) and 16/79 (20.3%), respectively. Additionally, anaemia was significantly reported in this study at a prevalence of 166/202 (57.4%). The median haemoglobin (Hb) and interquartile range of anaemic individuals were 9.85 (9.33-10.40). However, there was no association between anaemia vs. malaria, STH, or *S. mansoni* (P > 0.05).

Conclusion: Our preliminary findings show co-infection of P. *falciparum,* STH, and S. mansoni infections, as well as high anaemia prevalence among pregnant women in Busia County, and this necessitates integrated disease control measures.

Keywords: Malaria, Helminthiasis, Co-infection, Anaemia, Pregnant Women, Busia County, Kenya

34.

THE EFFECTS OF PRO/SYNBIOTICS AND ENGAGEMENT IN A CLINICAL TRIAL ON GROWTH DURING INFANCY IN WESTERN KENYA

Authors: Alloys O K'Oloo (KEMRI-CGHR)*; Iwaret Otiti (Kenya Medical Research Institute- Centre for Global Health Research, Kisumu, Kenya); Micah June (Kenya Medical Research Institute- Centre for Global Health Research, Kisumu, Kenya); Simon Kariuki (KEMRI); Kephas Otieno (Kenya Medical Research Institute- Centre for Global Health Research, Kisumu, Kenya); James Dodd (Department of Clinical Sciences, Liverpool School of Tropical Medicine, UK); Stephen Allen (Department of Clinical Sciences, Liverpool School of Tropical Medicine, UK); Feiko ter Kuile (Department of Clinical Sciences, Liverpool School of Tropical Medicine, UK)

Background: Growth faltering among under-5s is common in poor resource countries, and undernutrition is implicated in almost 45% of deaths. The 2022 KDHS reported that 13% of under-5s in Homa Bay County, western Kenya, were stunted (length-for-age z score <-2), and 1.8% were wasted (weight-for-length z score <-2), indicating poor growth in this region.

Methods: In an open-label, randomized, controlled trial in western Kenya, we assessed whether administering pro/synbiotics from 0-6 months improved gut health and growth. Newborns <4 days old were enrolled and randomly allocated (1:1:1:1), stratified by HIV exposure, to one of 4 study arms to receive 32 doses given daily for the first 10 days then weekly to age 6 months of either one of 2 synbiotics, a probiotic, or no intervention (controls). All doses were supervised and administered during home visits, when participant's caregivers also received education and advise on breastfeeding and WASH-Benefit practices. Control infants received the same home visits as those receiving pro/synbiotics. Anthropometric indices at age 12 months were compared with WHO reference data (WHO 2016) and between study arms.

Results: Six hundred children were enrolled between October 2020 and January 2022. At age 12 months, anthropometric indices in the controls were close to WHO standards (Figure). Overally, mean (SD) z score for weight-for-age was -0.24 (1.08), length-for-age was -0.57 (1.03), weight-for-length was 0.06 (1.13) and head circumference-for-age was 0.01 (1.01). Among the HIV-exposed infants (99/545; 18.2%), the mean (SD) z score for weight-for-age was -0.55 (1.16), length-for-age was -0.74 (1.06), weight-for-length was

-0.25 (1.19) and head circumference-for-age was -0.15 (1.04). 10/99 (10.1%) were stunted, 9/99 (9.1%) wasted and 11/99 (11.1) infants were underweight among the HIV-exposed infants. Overally, stunting occurred in 12/132 (9.1%) controls and in 9/140 (6.4%) infants in the Labinic synbiotic arm (RR=0.71, p=0.44), 11/134 (8.2%) with Lab4b synbiotic (RR=0.90, p=0.81), and 9/139 (6.5%) with Lab4b probiotic (RR=0.71, p=0.45). Wasting occurred in 6/132 (4.5%) control infants, and 6/140 (4.3%; RR=0.94, p=0.92), 5/134 (3.7%; RR=0.82, p=0.76), and 4/139 (2.9%; RR=0.63, p=0.50) in the Labinic synbiotic, Lab4b synbiotic and La4b probiotic arms respectively.

Conclusions: Participation in the trial with frequent home visits by a research staff providing advice and support but no specific intervention improved growth. Further research should evaluate the impact of community-based support in improving growth. In addition, the effects of engaging in clinical trials on early growth that is not due to specific interventions need to be considered in trial design. The potential of pro/synbiotics to improve growth should be explored in further trials.

Keywords: Growth faltering

SCIENTIFIC SESSION 4:

MALARIA-1

35.

PREVALENCE AND PREDICTORS OF ASYMPTOMATIC MALARIA INFECTION IN THE BORICHA DISTRICT, SIDAMA REGION, ETHIOPIA: IMPLICATIONS FOR ELIMINATION STRATEGIES

Authors: Desalegn Dabaro Dangiso (Jimma University)*

Background: Malaria remains a major public health threat in Ethiopia despite the tremendous progress made toward the 2030 elimination targets. Silent transmission of asymptomatic infection is one of many factors that enhance the persistence of disease as a public health issue and impede efforts to eliminate it. Therefore, we investigated the prevalence and risk factors of asymptomatic malaria in the Boricha district, Sidama region, Ethiopia.

Methods: A community-based cross-sectional study was conducted in eight selected kebeles (smallest administrative unit) in the district. A multi-stage sampling technique was used to select representative households. Rapid diagnostic testing (RDT) and light microscopy were used for diagnosis. Socio-demographic data were gathered using a structured questionnaire.

Results: Of the 573 presumably healthy participants tested, 6.1% (95% confidence interval (CI): 4.3–8.4) and 4.0% (95% CI: 2.6–6.0) were found to be positive by RDT and microscopy, respectively. Participants aged under five years (AOR = 1.57, 95 CI: 0.46–5.39) and 5–14 years (AOR = 2.42, 95% CI: 1.08–5.40), insecticide-treated net use (AOR = 8.41, 95% CI: 1.09–65.08), travel history (AOR = 6.85, 95% CI: 2.32–20.26), and living in houses with windows (AOR = 2.11, 95% CI: 1.02-4.36) were significantly associated with asymptomatic malaria infection.

Conclusion: The findings revealed that asymptomatic malaria was prevalent in the study area. Therefore, rigorous implementation of the existing interventions as well as the development of new ones that are tailored to the identified factors is strongly recommended to achieve the intended goal of elimination.

Keywords: Prevalence, Asymptomatic malaria, Boricha, Ethiopia

36.

COMPARATIVE ANALYSIS OF PERIPHERAL WHOLE BLOOD TRANSCRIPTOME FROM ASYMPTOMATIC CARRIERS REVEALS UPREGULATION OF SUBSETS OF SURFACE PROTEINS IMPLICATED IN *PLASMODIUM FALCIPARUM PHENOTYPIC PLASTICITY*

Authors: Joseph Gisaina Amwoma (University of Embu)*

The molecular mechanism underlying Plasmodium falciparum's persistence in the asymptomatic phase of infection remains largely unknown. However, large-scale shifts in the parasites' gene expression during asymptomatic infections may enhance phenotypic plasticity, maximizing their fitness and leading to the persistence of the asymptomatic infections. To uncover these mechanisms, we aimed to identify parasite genetic factors implicated in asymptomatic infections through bioinformatics analyses. We performed comparative transcriptome analyses on publicly available transcriptome datasets containing three different sample types: asymptomatic malaria (ASM), uncomplicated malaria (UM), and malaria-naïve (NM) from 35 subjects. Uncomplicated malaria samples were obtained from consenting participants enrolled in healthcare facilities in Timika, Papua Province, Indonesia. Asymptomatic and naïve malaria sample were obtained from children in health facilities in Mali. Total RNA was extracted from leucocyte depleted whole blood samples and sequenced on 2500-HT Hiseq. Our analysis identified 755 and 1773 differentially expressed genes (DEGs) in ASM vs UM and NM, respectively. These DEGs revealed sets of genes coding for proteins of unknown functions (PUFs) upregulated in ASM vs UM and ASM, suggesting their role in underlying fundamental molecular mechanisms during asymptomatic infections. Upregulated genes in ASM vs UM revealed a subset of 24 clonal variant genes (CVGs) involved in host-parasite and symbiotic interactions and modulation of the symbiont of host erythrocyte aggregation pathways. Moreover, we identified 237 differentially expressed noncoding RNAs in ASM vs UM, of which 11 were found to interact with CVGs, suggesting their possible role in regulating the expression of CVGs. Our results suggest that P. falciparum utilizes phenotypic plasticity as an adaptive mechanism during asymptomatic infections by upregulating clonal variant genes, with long noncoding RNAs possibly playing a crucial role in their regulation. Thus, our study provides insights into the parasites' genetic factors that confer a fitness advantage during asymptomatic infections.

Keywords: Malaria, Asymptomatic, Phenotypic plasticity, Ontology, Clonal variant

37.

RED BLOOD CELL TENSION PROTECTS AGAINST SEVERE MALARIA IN THE DANTU BLOOD GROUP.

Authors: Brian Kabugu Tawa (Kemri-wellcome)*

Background: Malaria has had a major effect on the human genome, many protective polymorphisms such as sickle cell trait having been selected to high frequencies in malaria endemic regions. Recently, it was shown that the blood group variant Dantu provides 74% protection against all forms of severe malaria in homozygous individuals. This is a similar degree of protection to sickle cell trait and considerably greater than the best malaria vaccine, but until now the protective mechanism has been unknown. The Dantu polymorphism has been fine-mapped to a structural rearrangement in the glycophorin (GYP) gene cluster. This rearrangement of the GYPA and GYPB genes creates two copies of a hybrid gene that encodes the Dantu blood group antigen. Both GYPA and GYPB play important functional roles in the invasion of P. falciparum merozoites into RBCs.

Methods: To investigate the impact of Dantu on P. falciparum invasion, we collected RBC samples from 42 healthy children from Kilifi in Kenya. To eliminate any possible confounding influences of other large-effect malaria-protective polymorphisms, we excluded samples from those children with either βs or homozygous α-thalassaemia. We quantified RBC invasion over one life cycle using a fluorescence-activated cell sorting (FACS). Parasites were co-cultured with differentially labelled Dantu-heterozygous, Dantu-homozygous and non-Dantu RBCs, and we measured invasion events into each using a fluorescent DNA dye.

Findings: We observed significantly lower invasion of Dantu RBCs than of non-Dantu RBCs by three parasite strains (3D7, Dd2 and SAO75). We also observed a trend towards greater invasion resistance by Dantu-homozygous than Dantu-heterozygous RBCs, suggesting a dose-dependent effect. To investigate the specific step at which invasion was impaired, we used time-lapse video microscopy to study the invasion process. We found a strong link between RBC tension and merozoite invasion and identified a tension threshold above which invasion rarely occurred, even in non-Dantu RBCs. Dantu RBCs had higher average tension, meaning that a greater proportion resisted invasion.

Conclusion: These findings provide both an explanation for the malaria-protective effect of Dantu, and fresh insights into why the efficiency of *P. falciparum* invasion might vary across the heterogenous populations of RBCs both within and between individuals.

Keywords: Dantu polymorphism, *Plasmodium falciparum* invasion, Fluorescence-activated cell sorting (FACS).

38.

ADVANCING ACTIVE MALARIA CASE DETECTION VIA CONTACT TESTING IN NYAMIRA, KENYA: A STRATEGIC APPROACH

Authors: Wayne O Otieno (Catholic Medical Mission Board)*

Background: Despite extensive efforts in malaria control and community management, persistent malaria threats persist in various landscapes. Community Health Promoters (CHPs) have been instrumental, yet underreported cases hinder interventions in Nyamira County, known for highland malaria despite low transmission. Economic activities like brick making worsen this. Challenges persist with unreported cases among contacts, risking ongoing transmission. A pilot study aimed to evaluate contact testing's effectiveness in enhancing active malaria case detection in Nyamira.

Method: Over a nine-month period, a pilot program was conducted across eight Community Health Units (CHUs) with higher malaria prevalence in Nyamira. The program involved training 80 Community Health Volunteers (CHVs) from Manga and Nyamira North in active case detection alongside routine community management of malaria. Contact testing for malaria was executed by systematically screening and testing individuals near confirmed malaria patients. Community Health Practitioners (CHPs) employed mRDTs known for their higher sensitivity in testing, occasionally validated by quality assurance teams for confirmed positive cases. Rigorous data collection via kobocollect and subsequent analysis facilitated the assessment of the method's efficacy in identifying new malaria cases beyond the initial cases.

Results: Pilot findings present encouraging results regarding the application of contact testing to enhance active case detection within the Community Case Management (CCM) for malaria in Nyamira. This method notably amplified the identification of new malaria cases among individuals in close contact with confirmed patients, leading to earlier diagnosis and subsequent treatment of infections. Over a nine-month period, the collective positivity rate within the eight Community Health Units (CHUs) averaged at 41%, with Manga CHUs exhibiting notably higher rates exceeding 70%. As a result of contact testing, 4,372 individuals were subjected to parasitological tests using mRDT at their households, revealing an overall 6% positivity rate (264) among contacts. These findings highlight the significance of identifying these cases, which would have otherwise remained undetected, perpetuating disease transmission. Specifically, CHUs in Manga sub-county, such as Morako and Engo'a, demonstrated substantially higher positivity rates among contacts at 16% and 11% respectively, emphasizing the critical impact of contact testing in identifying potential sources of transmission.

Conclusion: The utilization of contact testing for malaria offers a promising avenue to enhance active case detection in Nyamira, Kenya. This strategy demonstrates potential for improving disease surveillance and prompt intervention, ultimately contributing to more effective malaria control and management in endemic regions. Proper commodity management is key to realizing this innovative practice.

Keywords: Mobilization, Service access, Adolescent girls and young women

39.

EVIDENCE AND LESSONS LEARNED FROM THE MALARIA VACCINE IMPLEMENTATION PROGRAMME (2019-2023)

Authors: Jonathan S Schultz**,** Titus Kwambai (Malaria Branch, Center for Global Health, US Centers for Disease Control and Prevention, Kisumu, Kenya); Jonathan S Schultz (CDC-Kenya)*; Nelli Westercamp (Malaria Branch, Division of Parasitic Diseases and Malaria, Center for Global Health, Centers for Disease Control and Prevention, Atlanta GA, USA); Aaron Samuels (Malaria Branch, Center for Global Health, US Centers for Disease Control and Prevention, Kisumu, Kenya); Samuel Akech (Centers for Disease Control and Prevention)

Background: RTS,S/AS01E malaria vaccine (RTS,S) was introduced by national immunization programmes in Ghana, Kenya, and Malawi in 2019 in large-scale pilot schemes. Prospective evaluations were conducted to address questions about feasibility and effectiveness, and to assess safety signals from the phase 3 trial, before recommending wider use. One hundred-fifty-eight clusters were randomized to early or delayed introduction of RTS,S, with three doses to be administered between the ages of 5 and 59 months and a fourth dose at 2 years. Primary outcomes of the evaluation were all-cause mortality, hospital admission with severe malaria, meningitis or cerebral malaria, deaths in girls compared to boys, and vaccination coverage.

Methods: Mortality surveillance was undertaken in children aged 1-59 months throughout the pilot areas. Surveillance for meningitis and severe malaria was established in 8 hospitals in Ghana, 6 in Kenya, and 4 in Malawi. Vaccine uptake was measured in surveys of children aged 12-23 months, for the primary series, about 18 months after vaccine introduction and in children aged 30-41 months for the fourth dose. We estimated incidence rate ratios (IRRs) by comparing the ratio of the number of events in children age-eligible to have received at least one dose of the vaccine (safety outcomes), or age-eligible to have received three doses (impact), to that in non-eligible age groups, between implementation and comparison areas. To determine if there was evidence of a difference between girls and boys in mortality, the female:male mortality ratio in age groups eligible to receive the vaccine relative to non-eligible children was compared.

Results: There was moderate coverage of the three primary doses during the endline survey in 2022 (75% in Ghana, 69% in Kenya, and 63% in Malawi) and relatively low uptake of the fourth dose (in Ghana 54%, 34% in Kenya and 33% in Malawi). Among children eligible to have received at least one dose of RTS,S, there was no evidence of an excess of meningitis or cerebral malaria cases (IRR (Implementation: comparison areas) for hospital admission with meningitis was 1.04, 95% CI 0·62,1·75 and with cerebral malaria 0.91, 95% CI 0·63,1·32), and the impact of RTS,S introduction on mortality was similar for girls and boys (relative mortality ratio 0.89, 95% CI 0·81,0.98). Among children eligible for three vaccine doses, RTS,S introduction was associated with a 22% (95% CI 4%, 37%) reduction in hospital admission with severe malaria, and a 13% (95% CI 2%, 22%) reduction in all-cause mortality excluding injury.

Conclusions: During the four years of RTS,S implementation, high coverage was achieved with the primary series in all the three countries through routine immunization systems. There was no evidence of the safety signals that had been observed in the phase 3 trial, and introduction of the vaccine was associated with substantial reductions in all-cause mortality and hospital admission with severe malaria.

Keywords: RTS,S/AS01 (RTS,S), Malaria, Vaccine Evaluation, Pilot Implementation

40.

PFKELCH-13 SEQUENCING STRATEGY ON IDENTIFYING ARTEMISININ RESISTANCE IN BUSIA COUNTY, KENYA

Authors: Mark Makau (Mount Kenya University)*; Benard Kanoi (Mount Kenya University); Michael Maina (MKU); Calvin Mgawe (MKU); Jesse Gitaka (Mount Kenya University)

Background: *Plasmodium falciparum* is the leading cause of severe malaria globally. It is prevalent in sub-Saharan Africa and is responsible for more than 220 million malaria cases globally. More than 90% of these cases were from Africa. Artemisinin and artemisinin combination therapy have been the first-line drugs against *Plasmodium* malaria. Despite the efficacy of the drug, case of delayed parasite clearance has been reported globally and this has been defined by the WHO as artemisinin resistance.

Mutations in the *PfK13* gene have been an important marker for artemisinin resistance. Most of these mutations have been reported in Southeast Asia. These mutations have also been reported in other regions with R561H being reported in three East African countries, Rwanda, Uganda, and Tanzania. No validated mutation has previously been reported in Kenya.

Methods: Busia County is a malaria-endemic region and is a border county to Uganda. This study was conducted in Alupe sub county hospital in Busia County and aimed to confirm the presence of K13 mutations and their potential link to artemisinin resistance. Among 502 microscopy-confirmed malaria-positive individuals, parasitemia levels were monitored 24 hours post-administration of artemether-lumefantrine. DNA extracted via the Chelex boiling method enabled a nested PCR approach amplifying the *K-13 propeller region* in 100 samples, subsequently sequenced using Sanger sequencing. Multiple Sequence Alignment was then done against the 3D7 reference.

Results: While the cohort exhibited an average 92% parasite clearance rate, a subset displayed delayed or failed parasite clearance within 24 hours, indicative of possible artemisinin resistance. Surprisingly, molecular analysis of the sequenced samples revealed no mutations within the *PfK13* gene, challenging the assumption of widespread artemisinin resistance in this region. However, the observed treatment response variation necessitates further investigation beyond K-13 mutations. Factors encompassing host immunity, broader parasite genetic diversity, or drug metabolism variations might be influencing treatment outcomes, warranting comprehensive exploration. Recognizing the limitation of sequencing only 100 samples, out of the 502 collected, emphasizes the necessity for a more expansive sample size to comprehensively understand K-13 mutations' prevalence and their potential association with treatment response.

Conclusion: In conclusion, while this study did not identify *PfK13* mutations linked to artemisinin resistance in Busia County, the findings underscore the complexity of treatment outcomes and advocate for continued surveillance and expanded research to unravel the intricate dynamics of resistance in malaria-endemic regions. This study provides a foundational framework for future investigations aimed at unraveling the complexities surrounding malaria treatment outcomes and the multifaceted nature of resistance patterns in similar regions.

Keywords: *PfK13*, artemisinin Resistance,*Plasmodium Falciparum*

41.

SPECIFICITY AND SENSITIVITY OF MICROSCOPY AND MALARIA DIAGNOSTIC KIT (MRDT FIRST RESPONSE™) AMONG PREGNANT WOMEN PRESENTING FOR DELIVERY IN BUSIA COUNTY, WESTERN KENYA

Authors: Dickson Kipchirchir (KEMRI-CGHR)*; Bartholomew Ondigo (Laboratory of Malaria Immunology and Vaccinology, National Institute of Allergy and Infectious Disease, NIH, Bethesda, Maryland, USA;); Stellah A Chumbe (Maseno University/KEMRI); Duncan M Wakoli (Department of Biochemistry and Molecular Biology Egerton University, US Army Medical Research Directorate-Africa); GEORGE N IMBUSI (EGERTON UNIVERSITY); EVERLYNE CHIMWANI KHALIVINZWA (Jaramogi Oginga Odinga University of Science and Technology); Odhiambo Caleb (Egerton University); DANIEL SIKUKU (Egerton University)

Introduction: Placental malaria is caused by infiltration of malaria-infected erythrocytes into the placental intervillous space during pregnancy. Effective malaria treatment relies greatly on diagnosis, a main support of malaria control and elimination efforts. All suspected cases of malaria should be confirmed using microscopy or malaria rapid diagnostic tests (mRDTs). This study sought to investigate the prevalence of malaria in pregnant women presenting for delivery at Port Victoria and Sio-Port Sub-County Hospitals, Busia County using microscopy and mRDT techniques.

Methods: Pregnant women presenting at Port Victoria and Sio Port Sub-County hospitals for delivery between April and October 2023 were enrolled in this cross-sectional study after consenting. About 2 mL of peripheral blood was collected from 236 women for the detection of gestational malaria using microscopy and mRDT. Placental blood was also collected for the placental malaria screening using microscopy. Maternal haemoglobin (HB) was determined using Mission plus® HB machine. The measure of agreement (Cohens Kappa statistic) between microscopy and mRDT was also calculated.

Results: 114 (48.3%) were from Sio Port Sub-County Hospital while 122 (51.7%) were from Port Victoria Sub-County Hospital. Participants mean age was 24.0 ± 5.9 years. Out of 236 women enrolled, primigravida were 93 (39.4%), secundigravida were 66 (28.0%) whereas multigravida were 77 (32.6%). 39/236 (16.5%) and 52/236 (22.0%) of peripheral blood samples collected at delivery were positive for malaria by microscopy and mRDT, respectively. 27/236 (11.4%) of placental blood samples were malaria positive by microscopy. The specificity and sensitivity of microscopy and mRDT was 90.3% and 82.7% respectively. The mean hemoglobin was 10.2 ± 1.8 and blood group O+ was the most prevalent. Additionally, anaemia (HB£11.0g/dL) was significantly reported at a prevalence of 196/236 (83.1%), $P < 0.0001$). Anaemia was defined as; Severe anaemia: HB < 7g/dL, moderate anemia: HB 7-9.9 g/dL, and mild anemia: HB 10-10.9 g/dL. A fair agreement between microscopy and mRDT was also shown (Kappa = 0.25). Malaria infection intensities were 8 (20.5%), 14 (35.9%), 13 (33.3%), and 4 (10.3%) for very low, low, moderate, and high parasitaemia, respectively.

Conclusion: A significant number of pregnant women still present with malaria infections during delivery calling for enhanced diagnosis, treatment and preventative measures during the routine antenatal clinics.

Key words: Placental malaria, gestational malaria, microscopy, malaria rapid diagnostic tests(mRDT)

42.

EVALUATION OF MALARIA SURVEILLANCE SYSTEM IN HOMA BAY COUNTY, KENYA, JANUARY—MARCH 2023

Authors: Diana Rose W Mwaura (FELTP)*; Maria Thuita (FELTP- MOH); Elvis Oyugi (MOH- NMCP); Maurice O Owiny (Kenya FELTP)

Introduction: Surveillance helps in tracking progress towards the target of reduction of malaria burden by 75% of the 2016 levels by 2023 in Kenya. Homa Bay County has had an increasing malaria incidence with 106.7 cases per 1000 in 2020 to 308 cases per 1000 in 2022 despite the implementation of intervention measures. We evaluated the surveillance system to ascertain the veracity of the data and propose areas for improvement.

Methods: We used the updated CDC guidelines for evaluating disease surveillance systems to assess qualitative (simplicity, acceptability, and flexibility) and quantitative (timeliness and completeness of data) attributes. We conducted key informant interviews by administering a 5-point Likert scale questionnaire to 28 healthcare workers from the county, sub-county, and health facility levels and summarized the responses thematically in proportions. We reviewed data from KHIS and compared malaria cases in Electronic medical records (EMR) and paper-based primary registers with data captured by the surveillance system during the first quarter of 2023. We analyzed the data and responses using MS Excel and Epi Info. Verification Factor (VF) values of less than 0.9 (90%) or greater than 1.1 (110%) were indicative of data quality problems.

Results: Twenty-seven (97%) of the respondents reported the ease of use of the malaria surveillance guidelines and correctly described the information flow at three levels (facility, county, and, national). For primary registers, 20/28 (71%) utilized both paper-based and electronic, 5/28 (18%) manual systems only, and 3/28 (11%) electronic systems only. The introduction of the new variable "tested for malaria" in 2018 was reported in the Health Information System. The timeliness and completeness of data was 100%. The average verification factor for the quarter was 0.7 for facilities that utilized paper-based and 0.9 for facilities that utilized both EMR and paper-based primary registers.

Conclusion: The system was simple, flexible, and acceptable. There were different primary sources of patient data. We recommend streamlining documentation by ensuring all malaria indicators are included in the various primary sources, for uniformity across the county to improve data quality.

Keywords: Data accuracy, Malaria, Health Information Systems, Electronic Health records

SCIENTIFIC SESSION 5: HEALTH SYSTEMS -1

43.

INFLUENCE OF HEALTH SYSTEM MANAGEMENT ON OCCURRENCE OF POSTPARTUM HAEMORRHAGE AMONG WOMEN OF REPRODUCTIVE AGE 15 - 49 YEARS IN HOMA BAY COUNTY, KENYA

Authors: Ottoman W. Adel (Medical Academy of Research and Training for Community Empowerment, Kenya (MARTCOME-KENYA))*

Background: In Kenya, 34% of maternal deaths are because of postpartum haemorrhage. In Homa Bay County, postpartum haemorrhage remains the number one contributor of maternal mortality. Thirty eight percent of all maternal deaths are attributed to postpartum haemorrhage despite several strategies by the ministry of health to reduce its occurrence. Poor health care provision have been cited in some studies as contributing factor to high postpartum haemorrhage. No study, however, has explored the possible determinants, impacts, and challenges of health system management on occurrence of postpartum haemorrhage in the County. The main objective of this study was to establish the influence of health system management on the occurrence of postpartum haemorrhage.

Methods: The study was cross-sectional design in which mixed research methods were used. The study population were women who had childbirth at level four public hospitals in Homa Bay County. A sample size of 400 was arrived at using Cochran 1977 formula. The instruments for data collection were: questionnaire, observation checklist, and key informant interview guide. Information was gathered on: socio-demographics, maternal health characteristics, postpartum haemorrhage occurrences, health system determinants, effects, and challenges of health system management.

Results: The study had 90.75% response rate. Respondents were between 15 years to 44 years of age. The mean age was 27 years while standard deviation of the ages was ±11.18. Socio-demographic profile of respondents was as follows; 77.8% were married; 20.5% had monthly income less than Ksh.1,000; salaried respondents were 8%; while 69.6% of respondents were protestants. The prevalence of postpartum haemorrhage was 9.9% with 95% CI (7.2% - 13.5%). Determinants of occurrence of postpartum haemorrhage were: previous experience of postpartum haemorrhage (p-value=0.01), parity (p-value=0.004), trimester of initiation of antenatal care visit (p-value=0.0494), health care provider to client level of attention (p-value=0.046), change of work station by health care providers (p-value=0.017), and availability of quality healthcare services (p-value=0.017). Health systems associated with occurrence of postpartum haemorrhage were: health financing (p-value=0.049); medicines and technologies (p-value=0.027) and; health service delivery (p-value=0.001) while the challenges of health system management were: inadequate number and skilled human resource for health (p-value=0.01); low quality and insufficient diagnostic services: lack of essential tests (p-value=0.01), venereal disease research laboratory (p-value=0.003). Inadequate essential obstetric and perinatal drugs, obstructed labour (p-value=0.001), and traditional birth attendants (p-value=0.034).

Conclusion: Health system management have a positive influence on occurrence of postpartum haemorrhage**.**

Keywords: INFLUENCE, HEALTH SYSTEM MANAGEMENT, POSPARTUM, HAEMORRHAGE, WOMEN OF REPRODUCTIVE AGE

44.

PATTERNS OF FACILITY AND PATIENT RELATED FACTORS TO THE ORTHOPEDIC AND TRAUMA ADMISSIONS AT THE KENYATTA NATIONAL HOSPITAL: A QUALITATIVE ASSESSMENT

Authors: Maxwell P omondi (University of Nairobi)*

Inappropriate utilization of higher-level health facilities and ineffective management of the referral processes in resource-limited settings is increasingly becoming a concern in health care management in developing countries. This is characterized by self-referrals and frequent bypassing of nearest health facilities coupled with low formal referral mechanisms. This scenario lends itself to a situation where uncomplicated medical conditions are unnecessarily managed in a high-cost health facility. This compromises the ability and capacity of Kenyatta National Hospital to function as a referral facility as envisioned by Kenya Health Sector Referral Implementation Guidelines of 2014, Kenya 201 constitution and Kenyatta National Hospital legal statue of 1987. The study objective was to assess the patterns of facility and patient related factors to the orthopedic and trauma admissions at the Kenyatta National Hospital. This was a descriptive qualitative study design. The study was conducted amongst the orthopedic and trauma admission caseload for 2021. Data collection was done through a) data abstraction from 905 patients charts admitted during February to December 2021 and b) 10 (ten)semi-structured interviews with 10 major health facilities that refer to KNH to understand the reasons for referral to KNH. Quantitative data was analyzed using Statistical Package for Social Science version 21.0 to calculate the frequency distribution. Qualitative data from the data abstraction and transcripts from the KIIs were analyzed using NVivo version 12. The major facility and patient related factors to the orthopedic and trauma admissions at Kenyatta National Hospital were inadequate human resource capacity and availability (42.7%), financial constraints

(23.3%), inadequate Orthopedic equipment's and implants availability (20.0%) and inadequate health facility infrastructure (6.3%) while the major patient related factor was patient's preference (23.4%). In conclusion, to decongest Kenyatta National Hospital requires that the lower-level health facilities need to be better equipped and resourced, improve the health infrastructure and their operative capacity and improve human resource capacity and availability including addressing the MoH culture of absenteeism at work to avoid unnecessary referrals of patients and also for timely management of orthopedic and trauma patients.

Keywords: Patterns, orthopaedic and trauma, admissions

45.

LABORATORY SAMPLES ONLINE REMOTE LOGGING, A KEY TOOL FOR IMPROVING TURNAROUND TIME AND MONITORING PATIENTS CARE: A CASE STUDY IN SEME SUB COUNTY KENYA

Authors: CELLINE A OKUTA (MINISTRY OF HEALTH-KISUMU COUNTY)*; ARTHY YONGO (HJFMRI)

Background: Laboratory samples online remote logging from the satellite referring laboratory to the central testing hub laboratory is a laboratory information management system (LIMS) which allows users to manage samples and their associated data more effectively. In this case a software is installed in the satellite laboratory and linked to the central hub laboratory where samples are to be referred and tested. The system has an inbuilt sample manifest. The referral lab is expected to submit the sample details and request online before sample transportation. The information is automatically received at the central reference lab. Seme Sub County with the support of Henry Jackson Medical Research International (HJFMRI) implemented this process in order to improve the turnaround time (TAT) of viral load and early infant diagnosis (EID) samples, to monitor patients care management by making the results available to clinicians in a timely manner and to reduce transcription errors.

Methods: In the year 2020 to date, HJFMRI installed computers and printers in three health facilities(Manyuada sub county hospital, Ratta health Centre and Kombewa county hospital) to support sample remote logging before shipping the samples to the testing laboratory. Each facility is expected to key in sample details and request in the system under the dashboard sample manifest and submit the sample on the website before shipping the samples to the referral laboratory. This system is applicable to viral load and EID samples. The facilities are also able to download and print results from the website ones the testing laboratory is through. A unique batch number is given for each set samples being remote logged. The respective medical laboratory officers were capacity built to perform the activity. A data clerk at Kombewa county referral hospital was employed to support and oversees the remote log-in process in the entire sub county.

Results and Discussions: At the baseline the TAT of viral load samples was between 2 to 3months, whereas for EID samples the TAT was between 3 to 6 months. This lead to delayed patients management and also gave poor outcome for the exposed infants. 3 months after the implementation of remote log-in process the viral TAT has be reduced to 9 days in average. Whereas EID TAT has been reduced to 13 days in average. The process has also improved in flagging of patients with High viral load, positive EID patients and also facilitated data analysis process in the laboratory.

Conclusions: Sample remote logging is a good practice and can support in effective client management and reducing TAT of different testing processes such as Tuberculosis testing. Remote logging for samples being shipped to National reference and county laboratories is recommended for effective and timely management of the clients. The next step is to scale up the remote logging and laboratory manifest implementation process from three facilities to at least six in the year 2024.

Keywords: TAT, EID, LIMS

46.

EXPLORING THE VIABILITY OF COMMUNITY PUBLIC-PRIVATE PARTNERSHIPS FOR CHRONIC ILLNESS DIAGNOSTIC SERVICES IN EAST AFRICA

Authors: JAMES N. KARIUKI (KENYA MEDICAL RESEARCH INSTITUTE)*; David Mathu (KENYA MEDICAL RESEARCH INSTITUTE (KEMRI)); Joseph Mutai (KENYA MEDICAL RESEARCH INSTITUTE (KEMRI)); Richard Mutisya (KENYA MEDICAL RESEARCH INSTITUTE (KEMRI))

Introduction: There exists public-private partnership (PPPs) ventures, but little is known about their level of engagement in diagnostic services provision in the East Africa Partner States. The objective was to conduct an assessment of PPPs in health service delivery within East African countries with a view to suggest options and innovative approaches for engaging PPPs undertaking diagnostic services.

Methodology: A mixed-method (convergence) design was used. The team triangulated multiple sources namely: questionnaire, observation, key informant interviews and desk-top review to collect data. The study was conducted during the months of June to December 2019. One (1) urban and one (1) cross-border towns were purposively selected in each country. A total of twenty-eight laboratory facilities were visited by the study team across the four East African countries.

Key Findings: Over 50% of the private laboratories offered Ziehl-Neelsen (ZN) microscopy, over 60% offered malaria screening, bacteria culture and sensitivity was carried out in 37% of the facilities. Private laboratories did not send specimens to neighbouring public laboratories and vice versa but opted to refer patients instead. All laboratories sent specimens to their respective national reference laboratories for external quality assurance (EQA). In Kenya, 15.4% of private laboratories, 33% in Tanzania and 25% in Uganda had been accredited. Noted high PPP risks namely performance, governance, suitability and capacity risks which may revise the gains already made in realization of PPP ventures in diagnostic services.

Conclusion: The evidence is suggestive that there exists an informal laboratory partnership between the public and private facilities in as far as the provision of diagnostic services is concerned. However, there were critical knowledge gaps that would require research. Recommendation: A modified output-based approach (OBA) type of partnership would be the idle form of public-private partnership for diagnostic service provision.

Keywords: public-private partnerships, community, diagnostic services

47.

RELATIONSHIP BETWEEN STRATEGIC LEADERSHIP STYLE AND THE ADOPTION OF CLINICAL INNOVATIONS BY PUBLIC REFERRAL HOSPITALS IN NAIROBI COUNTY, KENYA

Authors: *Kirigi, G., Kinuthia, J., and Muigai, R. G.

Background : It is obscure if there is a significant relationship between strategic leadership style and the adoption of clinical innovations. Effective strategic leadership is crucial for the successful implementation of clinical innovations in hospitals to improve healthcare. Specifically, the study was to investigate the relationship between strategic leadership style and the adoption of clinical innovations by public referral hospitals in Nairobi County.

Methods : The specific objectives were to examine the relationship between elements of strategic leadership style: organisational capabilities, cultivating innovation-oriented attributes, managers' behavioural preferences, fostering innovation in organisations, and the adoption of clinical innovations. The research used a nomothetic, descriptive and cross-sectional survey research design and surveyed 189 target populations of healthcare leaders in four public referral hospitals because it has the advantage over idiographic approach in terms of study context and achieving a wide understanding of the general laws, patterns, or trends, with large population application. The data was collected through a digitized questionnaire. The samplings conducted included stratified random sampling of public referral hospitals and purposive sampling procedures for healthcare leaders in the study to constitute a final sample. The primary data was initially used to explain exploratory factor analysis and then multivariate linear regression performed. The collected data was then analyzed, aided by the statistical software STATA version 15.1.

Results : Descriptive and inferential results were presented numerically in text or tables and graphically in their figures. The findings have shown statistically significant with demonstrations of positive and negative relationships with some outcome inconsistencies that are now acknowledged in existing literature. The multi-regression values for each variable ($\alpha = 0.05$) was: Organizational capabilities(β 0.2145,$p<0.010$), cultivating innovation-oriented attributes($\beta=0.0857$,$p=0.195$) managers' behavioral preferences($\beta=-0.0783$,$p=0.045$) and fostering innovation in the organization($\beta=0.2259$,p=<0.001). Overall, the analysis allowed the study to reasonably support the developed hypotheses.

Conclusion : To sum up, organizational capabilities have shown the most statistically significant and positive factors in relation to the adoption of clinical innovations by public referral hospitals in Nairobi County. Kirigi: http://orcid.org/0000-0002-4324-6137.

Keywords: strategic leadership style, adoption of clinical innovations, public hospital

48.

IMPACT OF USING WEB REMOTE LOGGING SYSTEM TO IMPROVE TUBERCULOSIS CULTURE SAMPLES REFERRAL TO KISUMU KEMRI CGHR LAB IN WESTERN KENYA

Authors: Ben Odhiambo

Background: Tuberculosis (TB) remains a global health emergency. There are programmatic challenges associated with high levels of drug resistance the world over. Access to accurate tracking of TB patient samples electronically still remains a challenge. Use of paper based sample request forms has proved to be tedious and unreliable. The hard copies are received in the lab with missing patient information despite clear instructions that all fields are mandatory. Remote logging system (RLS) web based system, addresses these challenges by ensuring all critical patient information are captured as they are mandatorily enforced by the system. All patient information is captured at facility level by clinicians or laboratory personnel before dispatching samples to Kisian lab for testing. The objective of this study was to evaluate manual request form completion rate versus online request form.

Methods: Pilot testing was done in select facilities in Kisumu County. After a successful pilot, it was then rolled out to five other counties out of seventeen supported counties. The facilities had web remote system installed in their computers. All laboratory staff handling TB samples were given access credentials and trained on sample referral using remote logging system. Data was extracted from Labware LIMS database and analyzed in excel. Data variables were: number of samples remotely logged, request form completion with respect to mandatory patient demographics; patient treatment number, gender, name, HIV status, age and Patient category.

Results: Total samples received between May 2022 and June 2023 were 5828. Before full implementation of RLS, the proportion of samples received by the web-based system compared with conventional manual system were 17.2% and 82.2% respectively. Request form data completion was as follows; patient treatment number (TB MDR No.) 7%, Gender 1%, patient name 100%, HIV status 70%, age 10%, TB type 1% and patient category 4%. After full implementation of RLS, request form data completion rate in LIMS for the above variables was 100%. Information captured at source is easily verifiable and can be corrected before reaching the testing lab. RLS improves specimens tracking and testing within the network and also completeness of patient details in the LIMS.

Conclusion: RLS proved to be the panacea to incomplete/missing data on patient request forms as it enforces system rules to ensure 100% compliance for sample request form completion. Consideration for adoption of web remote logging is recommended to improve data documentation and quality of patient information for program decision making.

49.

SOCIODEMOGRAPHIC FACTORS INFLUENCING HEALTH WORKER UTILIZATION OF ELECTRONIC HEALTH INFORMATION SYSTEM: A CASE OF DISTRICT HEALTH INFORMATION SOFTWARE IN BURUNDI

Authors: Innocent Yandemye (Ministry of Health)*

Background: Under the umbrella of strengthening the District Health Information System, Burundi introduced the District Health Information Software (DHIS2) as an electronic reporting data tool since a decade as a solution to solve challenges from paper-based records. Despite the efforts gathered, DHIS2 implementation is still facing many challenges. This study aimed to identify the socio-demographic factors associated to DHIS2 utilization among health workers in Burundi.

Methodology: We conducted a cross-sectional study among health professionals involved in health data collection and validation in three provinces of Burundi. Trained research assistants were used to collect data. Data analysis included descriptive and Chi-square tests using SPSS version 25.

Results: Eighty-four participants responded to the questionnaire. Most of them were male (82.1%), secondary level (66.7%) and from health Centre (79.8%). Male and married men were significantly the most satisfied with DHIS2 effect on improvement of health

information access from DHIS2 (p=.005), information quality (p=.008) and health information management (p=.020). Health workers with lower time travel were satisfied significantly with DHIS2 effect on improvement of information quality (p=.001), number of training received (p=.000), DHIS2 in line with current health facility management tools (p=.030), and Personal privacy (p=.000). Education level and profession were significantly associated with reduction of information error (p=.007) and ease of learning (p=.041) and DHIS2 in line with the vision of Ministry of Health (p=.034).

Conclusion: There is a need for gender, education and professional equity assurance in designing and implementing e-health projects while motivating health professionals with living support and travel means to reach their workplace.

Keywords: Healthcare ;Electronic health information;DHIS2 ; Sociodemographic factors

SCIENTIFIC SESSION 6: MENTAL HEALTH

50.

A RANDOMIZED TRIAL OF NON-SPECIALIST, PSYCHOTHERAPY OR PSYCHOPHARMACOLOGICAL TREATMENT OF MAJOR DEPRESSION AND POSTTRAUMATIC STRESS DISORDER IN KISUMU, KENYA

Authors: Linnet Ongeri (Kenya Medical Research Institute)*; Susan Meffert (University of California, San Francisco); Muthoni Mathai (University of Nairobi); Thomas Neylan (University of California, San Francisco); Daniel Mwai (University of Nairobi); Dickens Onyango (Kisumu County,MOH); Dickens Akena (Makerere University); Grace Rota (University of Nairobi); Ammon Otieno (University of Nairobi); Anne Mbwayo (University of Nairobi); Jim Khan (University of California, San Francisco); Craig Cohen (University of California, San Francisco); David Bukusi (Kenyatta National Referral Hospital); Gregory Aarons (University of California, San Diego); Rachel Burger (University of California, San Francisco); Chengshi Jin (University of California, San Francisco); Charles Mc Culloch (University of California); Simon Njuguna (Ministry of Health, Mental Health Division)

Background: Mental disorders are a leading cause of global disability, driven largely by depression and anxiety. This study tests strategies to integrate evidence-based psychotherapy and modern psychopharmacological treatments for major depression and Posttraumatic-Stress Disorder (PTSD) within public-sector outpatient settings in Kisumu, Kenya.

Methods: We randomized participants using a Sequential Multiple Assignment Randomized Trial (SMART) design to 12-weekly Interpersonal Psychotherapy (IPT) sessions or 6 months of fluoxetine for treatment of major depression and PTSD. Treatments were delivered by non-specialists at Kisumu County Referral Hospital (KCRH). Participants were age 18 or older with major depression, PTSD, or both. We analyzed first line treatment outcomes using a modified intent-to-treat analysis, requiring attendance of at least one treatment session. Generalized estimating equations were used for a logistic regression model with robust standard errors and an exchangeable correlation structure for repeated measures. ClinicalTrials.gov NCT03466346.

Findings: Between September 2020 and Oct 2021, 2162 participants were enrolled and randomized –1082 to IPT and 1079 to fluoxetine. Average age of participants was 36 years and the majority were married women with some primary or secondary education. At baseline, over 90% of participants had a diagnosis of major depression; approximately 52% had PTSD. The most common co-morbidity was HIV (39·4%). At treatment end, approximately 13% (IPT) and 10% (fluoxetine) met threshold score for major depression. The odds ratios (ORs) were 0.024 (IPT) and 0.017 (fluoxetine); no significant group difference. At treatment end, approximately 18% (IPT) and 12% (fluoxetine) met threshold score for PTSD. The ORs for PTSD were 0.028 (IPT) and 0.018 (fluoxetine). Fluoxetine was more effective than IPT for reducing PTSD (ratio of ORs 0.645, p=0.015). Among those who remitted (1532), 91% of IPT and 96% of fluoxetine participants were in remission for both disorders six months after treatment end.

Interpretation. Non-specialist delivery of IPT and fluoxetine integrated with public sector primary care in Kenya is highly effective for remission of major depression and PTSD. This study provides evidence that modern mental health treatment options can be integrated at scale within public-sector facilities to improve population mental health in low-resource settings.

Keywords: Post Traumatic Stress Disorder (PTSD), Depression, Psychotherapy, SMART Trials, Integrated mental health care

51.

MENTAL HEALTH DISORDERS AMONG SUDANESE MEDICAL STUDENTS IN THE MIDST OF 2023 CONFLICT: PREVALENCE, PREDICTORS, AND IMPLICATIONS

Authors: Esraa S Alfadul (University of Khartoum)*; Salma Alrawa (University of Khartoum); Badria Tebaig (University of Khartoum); Abdelgadir Osman (University of Khartoum); Andrew Molodynski (Consultant Psychiatrist and honorary senior lecturer, Oxford Health NHS Foundation Trust and Oxford University, United Kingdom.)

Background: Prolonged upheaval continues to deeply affect the Middle East and Africa, with ongoing military conflict in Sudan since April 2023.

Aim: This study investigates the prevalence of anxiety, depression, and posttraumatic stress disorder (PTSD) and their predictors in Sudanese medical students during this crisis.

Methods:A cross-sectional study was conducted among Sudanese medical students in conflict-affected regions. Participants completed an online questionnaire covering demographics, education, coping strategies, and mental health using the Hospital Anxiety and Depression Scale (HADS) and Posttraumatic Stress Checklist (PCL-5). Statistical analyses involved Wilcoxon rank sum tests, Fisher's exact tests, and multiple linear regression.

Results: Among 4185 medical students, alarming rates of anxiety (61.98%), depression (65.5%), and PTSD (36.7%) were reported. Associated factors included age (OR: 0.44, 95% CI: 0.20-0.67), being male (OR: 0.70 for depression, 2.3 for anxiety, 95% CI: -0.95 to -0.44), from a public university (OR: -0.80, 95% CI: -0.63 to -0.16), financial stability (OR: 2.2, 95% CI: 0.22-4.3), traumatic experiences (death: OR: 6.7, 95% CI: 5.0-8.3; financial damage: OR: 6.0, 95% CI: 4.9-7.1), coping strategies (religious practices: OR: -0.18 for depression, 95% CI: -0.29 to -0.06), and being in preclinical years (OR: 0.45, 95% CI: 0.09-0.80). Individuals with stable internet access and clean water reported reduced levels of depression and anxiety. Conversely, lacking plans for continuing education was associated with heightened stress and depression. Conflict-displaced students faced amplified PTSD risks.

Conclusion: This study found high rates of distressing mental health disorders among Sudanese medical students during the ongoing conflict. Associated factors include demographic factors, personal economic stability, coping strategies, and trauma. Urgent interventions are vital to target the aforementioned factors. Prioritizing students' mental well-being is critical for their resilience and also to ensure their contributions to post-conflict nation-building efforts.

Keywords: Anxiety, depression, PTSD, conflict, Middle East, Developing countries.

52.

CHARACTERIZING ALCOHOL AND OTHER SUBSTANCE USE DISORDER AMONG IN-PATIENTS AT THE PORTREITZ MENTAL HOSPITAL IN MOMBASA - KENYA 2021-2022

Authors: Abdalla H Mpigabao (DoHs, Mombasa County)*; Caren Ndeta (Kenya FELTP); Nassoro J Mwanyalu (Kenya FELTP); Maurice O Owiny (Kenya FELTP)

Introduction – Globally Alcohol and other substance use disorder is estimated to affect 36.3 million people. In Kenya, a decline of 10.4% to 9.7% in Alcohol Use Disorder is reported, however, a double increase in Cannabis Use Disorder is reported from 0.8% to 1.6%. Scarcity of data in Mombasa on substance use disorders precipitated the study whereby We described the sociodemographic, and clinical characteristics and determined the prevalence of Alcohol and other substance use disorders among patients admitted to Portreitz Mental Hospital, Mombasa, Kenya.

Methods -We conducted a retrospective records review for patients enrolled between 2021-2022. Using a data abstraction tool, we collected data on socio-demographic and clinical characteristics. We performed descriptive analysis, for continuous variables we calculated the mean and median. While for categorical data we calculated frequencies and proportions. We used Epi Info version 7.2.5.0.

Results- A total of 302 records were reviewed, mean age was 29.3 SD ± 8.7 years. Males were the majority at 287 (95%). Most of the patients were not in a relationship at 246(81.7%), and 205(66.8%) had a secondary-tertiary education. Patients working in the Informal sector were 240 (82.2%). and most lacked health insurance coverage at 249(82.6%). Slightly more than half of the patients resided in Mombasa at 167(55.5%). Polysubstance use disorder was predominant at 293(97%), and the common drug combination was Bhang-Tobacco-khat/Muguka at 131/219 (61.6%). Heroin-alcohol-Muguka at 10(4.6%) and Cocaine-Bhang were the least at 5(2.3%). Patients previously diagnosed with substance use disorder were 102/122(88.5%). Polysubstance Use Disorder co-occurred with Schizophrenia at 24(7.9%), Drug-Induced Psychosis at 22(7.3%) and Bipolar Mood Disorders at 16(5.3%).

Conclusion: We found a high prevalence of polysubstance Use Disorders, the most used drugs were Bhang-Tobacco-khat. Mental health disorders co-occurred with substance use disorder. We suggest Public Health awareness and intervention programs tailored towards those at risk. Further research on the co-occurrence between substance use disorder and other mental health conditions is needed.

Keywords: substance related Disorder, cannabis ,schizophrenia ,bipolar disorders, kenya

53.

THE ROLE OF SOCIAL SUPPORT ON MENTAL HEALTH AMONG PARENTING ADOLESCENT GIRLS AND YOUNG WOMEN: A NESTED CROSS-SECTIONAL STUDY IN SOUTH-WESTERN KENYA

Authors: Nita C Akech (Kenya Medical Research Institute - Research Care and Training Programme (KEMRI-RCTP))*; George O Otieno (KEMRI); Elizabeth Bukusi (KEMRI); Ruanne Barnabas (University of Washington); Nelly Mugo (KEMRI); Imeldah N Wakhungu (Kenya Medical Research Institute (KEMRI)- Research Care and Training Programme (RCTP)); Mercelline Onyando (KEMRI); Maricianah Onono (KEMRI)

Background: Adolescence, a critical developmental phase characterized by physical, psychological, and social changes, presents distinct challenges for girls and young women (AGYWs) managing pregnancy and parenthood. This study aims to ascertain the prevalence of Common Mental Disorders (CMDs) in Parenting AGYWs and investigate the impact of Social Support on their mental health, specifically focusing on CMD severity.

Methods: We conducted s a comparative quantitative cross-sectional study nested within the single-dose HPV clinical trial (KEN SHE). Social support was measured using the Multidimensional Scale of Perceived Social Support (MPSS), assessing support from Friends, Family, and significant others. CMDs, including anxiety disorders, depression, and trauma experiences, were evaluated using the Harvard Trauma Questionnaire, Primary Health Questionnaire, and Generalized Anxiety Disorder Scale. Modified Poisson Regression and Logistic Regression models were employed to analyze the relationship between CMDs, social support, and its severity.

Results: In both parenting and non-parenting AGYWs, participants had a mean age of 20 years (SD=1.4), with over 80% having a Secondary level of education. High social support correlated with a 33% relative decrease in depression levels among parenting AGYWs. Having a child before marriage and cohabiting increased depression levels (PR=2.41, 95% CI: 1.44, 4.03) and (PR=2.99, 95% CI: 1.55, 5.76) respectively. High social support also corresponded to a 90% relative decrease in general anxiety (PR=0.10, 95% CI: 0.14-0.88), while experiencing a loss resulted in a 4.3 relative increase in general anxiety (PR=4.26, 95% CI: 1.67-11.05). However, PTSD was not significantly associated with social support. Regarding the severity of mental health disorders, those with high social support had a 93% significant reduction in severe depression (OR=0.07, 95% CI: 0.02, 0.32), whereas having a child before marriage and suffering loss increased the odds of severe depression, (OR=2.45, 95% CI: 1.04, 5.75) and (OR=2.91, 95% CI: 1.24 - 6.86) respectively.

Conclusion: High social support significantly reduced severe depression and anxiety among AGYW, underscoring the complex interplay between support networks, relationship dynamics, and life events in shaping their mental health, particularly in parenting roles. These findings advocate for targeted interventions that enhance social support and address specific risk factors to improve mental health outcomes for AGYW.

Keywords: MPSS, CMDs, AGYW, PTSD

54.

EFFECT OF PREGNANCY INTENDEDNESS ON MATERNAL ATTITUDE, ADJUSTMENT AND BONDING POST-PREGNANCY AMONG ADOLESCENT GIRLS AND YOUNG WOMEN IN SOUTHWESTERN KENYA

Authors: Dennis Kegode (KEMRI RCTP)*; Nita Aketch (KEMRI- RCTP); George Omondi Otieno (KEMRI); Elizabeth Bukusi (KEMRI-RCTP); Ruanne Barnabas (Havard University); Mercelline Onyando (KEMRI-RCTP); Maricianah Onono (KEMRI-RCTP)

Background: The prenatal period is pivotal for shaping future parent-child relationships, particularly for adolescent girls and young women (AGYWs). Despite the significance of pregnancy intendedness, limited research explores its association with maternal adjustment, attitude, and bonding post-pregnancy. This study investigates the impact of pregnancy intendedness on these aspects among AGYWs in Southwestern Kenya.

Methods: Data were extracted from an ongoing comparative cross-sectional perinatal mental health study nested in a single-dose HPV vaccine trial (KEN SHE). The Maternal Adjustment and Maternal Attitudes (MAMA) questionnaire and Postpartum Bonding questionnaire were utilized to assess maternal adjustment, attitude, and mother-infant bonding. Multiple linear and logistic regression models were employed to analyze the associations between unintended pregnancy and MAMA, as well as unintended pregnancy and postpartum bonding, respectively. Covariates, two-way interactions, and potential confounding effects were addressed through backward elimination. Analysis and comparisons were done at a 5% level of significance

Results: The analysis encompassed 209 participants aged 18 to 24 years (median 20 years), predominantly with secondary education. Seventy-eight percent experienced unintended pregnancies. AGYWs with unintended pregnancies exhibited a 1.36 increase in negative

attitudes toward sex (β=1.36, 95% CI: 0.21, 2.50, p=0.021). Older AGYWs (20-24 years) demonstrated 1.34 times higher negative attitudes toward sex than younger mothers (18-19 years) (β=1.34, 95% CI: 0.38, 2.30, p=0.004). Participants who had a forced marriage and from a lower household socio-economic position had > 5 increase in negative attitude to sex (β= 5.21, 95% CI: 0.63, 9.79, p= 0.026). Unintended pregnancy correlated with a >5-fold likelihood of impaired postpartum bonding (OR=5.48, 95% CI: 1.01, 29.81). Similarly, older AGYWs and those with higher parity were associated with impaired bonding (OR=3.92, 95% CI: 1.22, 12.63) and (OR=2.73, 95% CI: 1.22, 6.13), respectively.

Conclusion: Unintended pregnancies, forced marriages, and lower socioeconomic status adversely affect maternal attitudes, adjustments, and postpartum bonding among AGYWs. Future studies should delve into these factors to enable the formulation of targeted strategies for enhancing maternal adjustment and infant bonding during pregnancy and postpartum periods among AGYWs.

Keywords: AGYWs, MAMAs

55.

INTIMATE PARTNER VIOLENCE AMONG GAY, BISEXUAL, AND OTHER MEN WHO HAVE SEX WITH MEN IN SOUTH-WESTERN KENYA: PREVALENCE AND RISK FACTORS

Authors: Vincent KIPCHUMBA SALANO (KEMRI)*; George Omondi Otieno (KEMRI); Fredrick Otieno (Nyanza Reproductive Health Society(NRHS)-Kenya); Imeldah N Wakhungu (Kenya Medical Research Institute (KEMRI)- Research Care and Training Programme (RCTP)); Mercelline Onyando (KEMRI); Maricianah Onono (KEMRI)

Background: Intimate Partner Violence (IPV) affects Gay, Bisexual, and other Men who have sex with Men (GBMSM) but remains understudied. GBMSM may experience comparable or higher prevalence rates than heterosexual couples. This study aims to determine the prevalence, frequency, and risk factors of intimate partner violence (IPV) and assess the association between IPV and common mental disorders (CMD) within the GBMSM community in southwestern Kenya.

Methods: Quantitative baseline data was extracted from a prospective longitudinal cohort study assessing oral human papillomavirus prevalence, incidence, persistence, and risk factors in HIV-infected and at-risk HIV-uninfected men in southwestern Kenya. Chi-squared/ Fisher's exact tests assessed categorical variables, and t-tests or Wilcoxon rank-sum tests evaluated continuous variables based on data type and distribution. Log-binomial regression determined prevalence ratios for IPV-associated risk factors.

Results: Data from 315 participants were analysed, with the majority (44%) aged 24-29 years. Eighty-six percent identified as male, while 10% were transgender females. Only 12% were married at enrolment. IPV prevalence was 29%. Demographic factors such as age, cohabitation with a female partner, frequency of casual partner intercourse, and alcohol consumption predicted IPV among men who have sex with men (MSM). IPV increased with age, with MSM≥40 years having over a 5-fold higher likelihood of IPV prevalence compared to younger individuals (PR=5.3, 95%CI:1.28-21.93). The prevalence of IPV was also higher among those cohabiting with a female partner (PR=1.90, 95%CI:1.24-2.90). Each additional instance of intercourse with a casual partner resulted in a 3.3 relative increase in IPV (PR=3.28, 95%CI:1.16-9.28). Individuals expressing concern about their drinking had a 2.1 relative increase in IPV prevalence (PR=2.08, 95% CI: 1.33-3.27). IPV participants exhibited higher rates of severe depression symptoms (50% vs. 14%, p <0.001), severe anxiety symptoms, and high perceived stress (44% vs. 20%, p=0.001) and (9% vs. 4%, p=0.002) respectively.

Conclusion: These findings highlight the intersectionality of sexual behavior, substance use, and mental health in mitigating IPV among MSM. Future research should explore the nuanced interplay of these factors to inform comprehensive strategies for IPV prevention and support within this population.

Keywords: IPV(Intimate Partner Violence), MSM(Men having sex with men), CMD(Common Mental Disorders)

SCIENTIFIC SESSION 7: TB

56.

HIGH NUMBER OF TB RELAPSE CASES IN AN MDR SURVEILLANCE IN WESTERN KENYA

Authors: JOSEPH J.O ORURE (KEMRICGHR)*; Ruth N Sitati (KEMRI/CGHR); CAROLINE OCHOLA DANDE (KENYA MEDICAL RESEARCH INSTITUTE-CENTRE FOR GLOBAL HEALTH RESEARCH); Laureen Nyongesa (KEMRICGHR); Joan Tonui (KEMRI/CGHR); Cecilia Wagoro (KEMRI/CGHR); Ronald Odero (AMREF); ALBERT O OKUMU (KEMRI); Steve Wandiga (KEMRI)

Background: Data from the World health Organization show that Kenya is one of the 22 countries that contribute to about 80% of world TB cases. In Kenya, Multi drug resistant TB (MDR-TB) burden is estimated at 3.1% of new and 10% of re-treatment cases (2015 Kenya Drug Survey). In 2018, those who developed Drug Resistant TB were 2500 out of which 19% (470/2500) was put on treatment and 74% (346/470) successfully treated. We therefore sought to determine the proportion of relapse cases by age, sex or HIV status if it could be contributing factors

Methodology: This was a cross sectional study that incorporated samples received for the MDR TB surveillance from relapse cases who were previously declared cured between the month of June and September 2022. All MDR samples were referred to KEMRI TB Laboratory testing facility from three counties (Nyanza, Western and Rift valley). Well-labelled spot sputum samples in 50ml falcon tubes received at KEMRI TB lab accompanied by their respective request forms for culture and line probe assay (LPA). All samples received as per acceptance and rejection SOP. Samples then processed using 4% sodium hydroxide + 2.9% sodium citrate and NALC. The processed samples then inoculated in MGIT culture, LPA and FM done. History on MDR TB treatment retrieved from the request

Results: A total of 1266 samples with request form were received, out of which 24% (298/1266) were relapse cases after successful treatment. Further, of the 298 cases, 56% (50/168) were male and 44% (130/298) female. Out of the 298 relapsed cases, 30% (50/168) and 34% (44/130) HIV positive were men and female respectively while 5 % (16/298) females and 15% (46/298) males did not have HIV status

Conclusion: From the study, we noted a significantly high number of relapse cases with men mostly affected compared to females. Patients, who have been declared cured, should be done for longitudinal follow up for one year at the interval of two months, to establish the cause and period in which the relapse occurs.

Keywords: TB, Relapse, Follow up.

57.

EFFECTS OF SPUTUM VOLUME AND QUALITY ON MTB YIELD AND SMEAR POSITIVITY FROM SAMPLES RECEIVED AT KEMRI TB LAB WESTERN KENYA

Authors: Ruth N Sitati (KEMRI/CGHR)*; Joan tonui (KEMRI/CGHR); JOSEPH J.O ORURE (KEMRICGHR); Laureen Nyongesa (KEMRI/CGHR); Isaiah Omondi (KEMRI/welcom-trust); BEN ODHIAMBO OKOTH (KEMRI); ALBERT O OKUMU (KEMRI); Steve Wandiga (KEMRI)

Introduction: Tuberculosis diagnosis, management of patients with the disease, rely on accurate and timely laboratory test results. International guidelines have emphasized macroscopic sputum quality as an important determinant of performance of smear microscopy and culture, thus Sputum quality assessment is routinely performed in testing laboratories. However, evidence about how it affects performance of TB diagnostic tests is limited. We sought to assess the impact of sputum quality and volume on smear positivity and MTB yield by culture in presumptive TB patients

Methodology: This was a cross sectional study where samples received between January and December 2022 as part of TB multidrug surveillance were used. Well-labelled samples in 50ml falcon tubes were received at KEMRI TB lab accompanied by their request forms. Sputum quality and volume was captured in electronic database. 2% N-acetyl-l-cysteine-sodium hydroxide was used to decontaminate the samples in the ratio of 1:1. Concentrated sediment was re-suspended in 2.0 ml sterile phosphate-buffered saline (pH 6.8) and used for MGIT culture and FM smear

Result: Samples used were 4098, and quality was as follows; 1319 (32.2%) salivary, 1922 (46.9%) mucoid, 658 (16.1%) tenacious and 199 (4.9%) were not indicated. Moreover, 223 (16.9%), 594 (30.9%) and 233 (35.4%) of salivary, mucoid and tenacious samples respectively turned positive for smear. While 22 (1.9), 446 (26.3) and 165 (28.4) of salivary, mucoid and tenacious samples, respectively turned positive for MTBC by culture. Sputum volume was categorised into three categories; 3ml and above 1-3mls and less than 1ml.

Logistic regression was used to evaluate the magnitude of association between sample quality and Smear positivity and the results indicated that Mucoid and tenacious samples were associated with 2.20 and 2.69 times increased odds of turning positive by smear compared to salivary samples. While by culture, Mucoid and tenacious samples were associated with 1.84 and 2.50 times respectively increased odds of turning positive compared to salivary samples.

Samples volume of 1-3mls were associated with 0.83 times reduced odds of smear positivity compared to the volume above 3mls. By age, compared to those aged >60yrs,30 years and below had 3.34 increased odds of turning positive while males had 1.67 times increased odd of turning positive compared to women.

Conclusion/Recommendation: Good quality sputum is good predictor of identifying mycobacteria in sputum by smear microscopy and culture highlighting the importance of sputum quality assessment. However, sample volume is poor predictor and should not be used to exclude sputum samples for TB testing by culture as MTB was recovered in samples with 1ml and less volume.

Keywords: TB, culture, MTBC

58.

EFFECTIVENESS OF ANTI-TUBERCULOSIS TREATMENT AMONG PATIENTS RECEIVING HIGHLY ACTIVE ANTI-RETROVIRAL THERAPY

Authors: Moses Y Parmeyian (Kenya Medical Research Institute (KEMRI))*

Introduction: Tuberculosis (TB) remains the leading cause of death among HIV-infected people. HIV-infected people are 18 (15–21) times more likely to develop active TB disease than those who are HIV-non-infected. Even when on antiretroviral therapy (ART), HIV-infected are 3 times more likely to die during TB treatment. In Kenya, there is need for proper coordination of antiretroviral therapy (ART) and tuberculosis (TB) treatment as most (60%) of the TB patients are also human immunodeficiency virus (HIV) infected.

Objective: This study aims to determine the difference in response to TB treatment among HIV-infected TB patients and HIV-non-infected TB patients receiving delayed highly active antiretroviral therapy (HAART) in Nairobi-Kenya.

Materials and Methods: A total of 116 patients were diagnosed using direct smears from sputum prepared and stained using the Ziehl-Neelsen procedure. The patients were offered HIV testing and counseling and then categorized into category A (PTB with HIV n =50) and category B (PTB without HIV co-infection n =66). They were put on the same TB chemotherapy of a short course comprising of: Two months of Rifampicin-R, Isoniazid-H, Pyrazinamide-Z, and plain Ethambutol-E, followed by six months of Ethambutol and Isoniazid. The main outcome measured was the sputum conversion rate from positive sputum to negative sputum. One-way analysis of variance (ANOVA) was used to test the null hypothesis.

Results: Of the 116 patients recruited for the study, 50 patients (43%) were found to be HIV positive and were put on HAART. The other 66 patients (57%) were HIV-negative. The sputum conversion rate for HIV-positive TB patients after two months and five months of chemotherapy was 88% and 94%, respectively. The sputum conversion rate for HIV-negative TB patients at two months and after five months of chemotherapy was 92 and 97%, respectively. However, there was no significant difference in the bacteriological outcome responses to TB chemotherapy between the two groups.

Conclusion: The high sputum conversion rates in the two groups indicated good control and management of TB. Findings in this study indicated that delayed use of HAART during TB treatment leads to better outcomes in TB treatment. The study recommends more concerted efforts to provide TB treatment to HIV-positive TB patients in Kenya.

Keywords: Highly Active Anti-Retroviral Therapy

59.

GENETIC DISTRIBUTION OF MYCOBACTERIUM TUBERCULOSIS COMPLEX, DRUG RESISTANCE AND TRANSMISSION AMONG PRESUMPTIVE TUBERCULOSIS PATIENTS IN WESTERN KENYA

Authors: Albert Okumu1, 2, James Orwa3, Jeremiah Ogoro4, Benjamin Ochieng1, Steve Wandiga1, Collins Ouma2

Introduction: The burden of Tuberculosis (TB) is high, however, knowledge on the genetic diversity of *Mycobacterium tuberculosis* complex (Mtb) strains and transmission dynamics is sparse, especially in the western region of Kenya. Understanding Mtb global lineages, and Single nucleotide polymorphisms (SNPs), are critical in providing phylogenetic information of Mtb strains and their relationships.

This study therefore sought to demonstrate Mtb strains genetic diversity, drug resistance markers, and possible transmission clusters.

Methods: We analyzed 57 clinical Mtb isolates collected between March through October 2020. Sputum samples collected were processed for standard culture (MGIT), the positively identified Mtb, had DNA extractions carried, conventional PCR performed and thereafter sequencing using Mycobacterial interspersed repetitive units-Variable number tandem repeats (MIRU-VNTR) technique was carried out. Data was analysed using multivariate and logistic regressions presented in tables and frequencies.

Results: The study showed presence of eight (8) strains of Mtb population. A further analysis revealed that the strains were predominantly from three (3) lineages (L) of medical importance. In addition, 3 clusters comprising of two (2) strains each, n = 6 (10.5%), showing a possibility of recent patient-to-patient Mtb transmission. Moreover, n = 14 (24.6) of the strains were multidrug-resistant (MDR). Moreover, HIV infected patients had 9.31 times risk of being infected with Beijing strains, compared to HIV uninfected (p= 0.020). Isolates with mono RIF resistance had an increased risk of being a Beijing strain (12.5 [p= 0.014]) and previously treated patients had decreased risk of having this strain, (0.04 [p= 0.004]).

Conclusion: Our study show that L3 strains are the main causative agent of TB in western Kenya, with MDR strain transmission is becoming an emerging concern in this region. This reaffirms the need to put a lot of effort towards infection control strategies and contact tracing of patients with MDR-TB to break the transmission chains as well as initiating adequate and appropriate management options for the diagnosed patients.

Keywords: Genotypic, Multidrug resistance, *Mycobacterium tuberculosis*, diversity, Strains, MIRU, Polymorphism, Lineages, Sequencing

60.

SCALING UPTAKE OF TB PREVENTIVE THERAPY AMONGST HEALTHCARE WORKERS IN MIGORI COUNTY

Authors: Emelder Auma Ngani (Ciheb/MOH)*

Background: Mariwa health centre is a health facility in Awendo Sub-County in Migori County with catchment population of 5,375. Majority of health care workers (HCWs) have not openly come up for both screening and tuberculosis (TB) preventive therapy (TPT) in the county and not consistent in implementing of infection prevention and control in their facilities. According to the mid term review (MTR) 2013 report, for every three health facilities, at least one health care workers (HCW) has TB disease mostly from ongoing transmission within facilities. Another study done in Kiambu County, found that 78% of HCWs were infected with latent TB infection (LTBI) and these are a “seedbed” for TB in the community from World Health Organisation (WHO) TB guideline 2019 hence need for TPT.

The aims of the study were to sensitize HCWs on TPT, screen and start eligible workers on TPT and to identify barriers to health care initiation on TPT.

Methodology: This was cross sectional study done from August 2022 to March 2023. TPT sensitization sessions were done to HCWs on weekly basis at the facility. All the HCWs were screened for eligibility using a intensive case finding card, HIV status then previous exposure to TPT especially isoniazid taken daily for 6 months, and eligible ones were initiated of TPT and followed up to completion while addressing adverse drug reactions. Weekly phone reminders were done for those on TPT, facility support group used and drugs were taken at the facility. Use of HCWs who were on TPT as champions to help reduce stigma and fear among other HCWs. Weekly TPT data reviews.

Results: The number of health care workers sensitized was 62 of which 52(83.9%) were eligible for TPT. Ten(10) (16.1%) were not eligible due to previous use of isoniazid prophylaxis. Of the 52 eligible clients 47 (90.3%) were initiated on TPT i.e. 4 (10%) clinical officers, 6(12%) nurses, 1(4%) HIV testing counselor, 1(4%) HIV testing service screener, 5 (10.6%) Youth peer providers, 1(4%)-adherence counsellor, 1(2%) lab technologists1 (2%) data clerk, 27 (62%) Community health promoters. The 5 (9.6%)eligible and not started on TPT due to the following reasons 1(20%) pregnancy, 2(40%) fear side effects, 1 (20%) fear of poor adherence, 1(20%) commodity stock out 46 (97.8%) have completed treatment, 1 (2.1%) defaulted on treatment due to side effects.

Conclusion: Multifaceted approaches are needed to scale up TPT uptake amongst health care workers and promote adherence.

Recommendation: Need for proper sensitization of TPT among HCWs, scale up of TPT advocacy to alleviate fear of unknown and stigma related with TB medication.

Need for HCWs to lead and be champions for TB prevention to reduce myths and stigma on TPT and scale up biannual TB screening, TB programme to avail enough TPT commodities to avoid stock outs.

Keywords: It’s better and cheaper to prevent and control disease in the community

61.

LEVERAGING SUPPORT NETWORKS: ASSESSING SUPPORT GROUP IMPACT ON SUSTAINED TREATMENT ADHERENCE AMONG TUBERCULOSIS PATIENTS IN MAKUENI AND MACHAKOS COUNTIES

Authors: Elizabeth Atieno Odhiambo (Catholic Medical Mission Board)*; Wayne Otieno (Catholic Medical Mission Board); Hilary Ngeso (Catholic Medical Mission Board); Kennedy Kioko (Catholic Medical Mission Board); Gladys M Njaka (Catholic Medical Mission Board)

Background: Tuberculosis (TB) necessitates a meticulous treatment regimen lasting 6-24 months. Successful treatment hinges significantly on adhering strictly to medication, attending clinics punctually, and maintaining proper nutrition. However, this extended treatment period poses challenges for patients, including medication side effects, financial limitations, stigma, and feelings of isolation, all contributing to treatment disruptions. For optimal outcomes, collaborative patient involvement with healthcare providers is essential. Recognizing these challenges, the Catholic Medical Missions Board (CMMB) in partnership with AMREF proactively initiated supportive networks through a Global Fund TB project aimed at bolstering comprehensive TB care. Specifically designed for Makueni and Machakos counties, these networks seek to fortify treatment adherence, fostering improved health outcomes among TB patients.

Method: 17 support networks were established spanning 17 level four and five facilities in Machakos and Makueni counties. Each group, comprising 7-20 members in intensive TB treatment, fostered patient interaction and engagement with peers and healthcare workers. Clients were recruited into the support group voluntarily by the facility clinical staff. Two meetings were held—one at treatment onset and another at the second month—to address challenges, share experiences, and provide crucial TB treatment information. Healthcare workers led discussions during meetings aimed at enhancing treatment literacy and addressing challenges. Assessment, through various qualitative and quantitative measures (review of the community and facility level data) like provider observations, and treatment adherence tracking respectively evaluated the groups' impact on patient well-being, adherence, and overall health outcomes in the specified regions.

Results: The program level data reviewed overtime showcased a declining trend in TB treatment interruptions, attributable to the support networks. From January to October 2023, the instances of treatment interrupters notably decreased to 192, reflecting a substantial 32.3% decline compared to the 284 cases reported during the same period in 2022. In addition, qualitative feedback from clients have demonstrated likability and usefulness of this support networks. This decline is indicative of effectiveness of the support networks in mitigating treatment interruptions among TB patients in the specified timeframe.

Conclusion: Patient support network significantly contributed to positive treatment outcomes among TB patients. When effectively utilized by patients and healthcare workers, these groups serve as catalysts for motivation and encouragement, enhancing treatment success, and potentially reducing TB transmission rates in the long term.

Keywords: Support Networks, Treatment Interrupters, Tuberculosis, Patients

62.

THE BURDEN OF MYCOBACTERIUM INTRACELLULARE TB AMONG PRESUMPTIVE TB PATIENTS IN WESTERN KENYA; KEMRI-TB LABORATORY BASED SURVEILLANCE

Authors: Caroline Ochola Dande (Kenya Medical Research Institute-centre for Global Health Research)*; Ruth N Sitati (KEMRI/CGHR); Daniel Matete (KEMRI-CGHR); Laureen Nyongesa (KEMRI-CGHR); Patrice Madara (KEMRI-CGHR); Cecilia Wagoro (KEMRI-CGHR); JOSEPH J.O ORURE (KEMRICGHR); ALBERT O OKUMU (KEMRI); Steve Wandiga (KEMRI)

Background: It is an increasing problem around the world to handle non-tuberculous Mycobacteria infection (NTM). In addition it is also indistinguishable from tuberculosis (TB). Further, the clinical implication is quiet largely unidentified. We sort to understand the trends and characterize NTM as a major priority to guide on optimizing effective patient treatment and control approaches.

Methods: A cross sectional study of patients with Non Tuberculous *Mycobacterium* Tb from 40 Ministry of health facilities in Western Kenya referring samples to KEMRI-TB laboratory between Jan, 2022 to Oct, 2023 was done. We used liquid culture (Mycobacterial growth indicator tube (MGIT)) system to culture mycobacteria from clinical samples. Positive work up procedures was done including BD TBcID identification done to differentiate between Mycobacterium tuberculosis complex and NTM species for further molecular characterization of NTM. GenoType® Mycobacterium Common Mycobacteria (CM) assay kit (HAIN Life Science, Nehren, Germany) was used following the manufacturer's protocol.

Results: A total of 332 patients were tested, the medium age was 38 years and 55% (183/332) were males. Of the total patients tested, 259 Non Tuberculous *Mycobacterium* isolates were identified using GenoType(®) Mycobacterium CM/AS and 73 tested negative.

Among the species identified M. Intracellulare significantly increased from 34 %(20/58) in 2022 to 67 %(134/201) in 2023. The proportion of NTMs identified also grew from 22% (58/259) in 2022 to 78 %(201/259) in 2023, with *Mycobacterium Spp*. at 11 %(28/259), M abcessus at 10 %(25/259) and M. Interjectum at 7% (18/259). Other Species identified included M.Scrofuleceum 3% (8/259) and M.Malmoense (8/259) both at 3%, M.Gordonae at 2 %(5/259), M Kansasii at 2% (6/259), M.Fortuitumat 2 %(5/259), and M.Avium at 1% (2/259)

Conclusion: From the study, there is significantly growing high number of M intracellulare Tb infections playing a vital role in causing Non Tuberculous *Mycobacterium* TB. Correct and timely diagnosis will optimize treatment and inform control strategies.

Keywords: Nontuberculous mycobacteria; GenoType(®) Mycobacterium CM/AS

63.

INTEGRATING TUBERCULOSIS ACTIVE CASE FINDING IN INDEX TESTING SERVICES TO AID IN EARLY TB DIAGNOSIS IN AROMBE DISPENSARY, MIGORI COUNTY

Authors: Loriet M Otieno (CIHEB-K)*; Isaiah Angwanga (CIHEB-K); Peter P.O.O Omware (Ministry of health); Omune Everlyn Adhiambo (Ministry of health); Joyce Otieno (CIHEB-K)

Back ground: Arombe Dispensary is a health facility in Migori County, Suna West Sub County with a catchment population of 11,490. It has been implementing TB case finding alongside HIV Testing Services for hospital, non hospital and index testing modalities, however, case notification has been low at index testing modality. TB being the leading cause of morbidity and mortality amongst People Living with HIV, it prompted the facility to identify knowledge gap as a challenge in TB Active Case Finding.

Objectives: To increase TB case finding by 20% and pediatric TB case finding to 10%

Methodology: This is a retrospective study comparing data collected at the facility TB4 register and HIV testing and linkage Lab register MOH 362 before interventions and 2022 after interventions. The number of TB cases diagnosed was then analyzed. Strategies employed were Continuous Medical Education to sensitize HIV Testing Services Counselors on TB active case finding. On job training and mentorship on screening and TB management. Monthly and quarterly active case finding data review meetings.

Results: TB cases notified through index testing 2020 0/49 (0%), 2021 1/65 (1.5%), 2022 12/76 (16%). Pediatric TB case finding.

2020 0/0(0%), 2021 1/10 (10%), 2022 3/7 (42%)

Conclusion: Integrating TB active case finding at index testing modality has increased early diagnosis of TB cases and helped reduce mortality and morbidity at Arombe dispensary.

Recommendations: We recommend integrating TB active case finding through index testing services in all facility set up to improve early TB diagnosis and reduce morbidity and mortality.

Keywords: PLHIV - People Living with HIV TB - Tuberculosis HTS - HIV Testing Services

64.

SCREENING OF MINERS USING DIGITAL CHEST X-RAY IN MASARA SUNA WEST SUB COUNTY

Authors: Peter P.O.O Omware (Ministry of health)*

Back ground: Masara area in Suna west found in wiga ward has a mixed population of approximately 12,400 and its major economic activity is mining with little small scale farming being done. It has 6 major mines I.e. Korwath, Kanyabope , Ka Walter, Ka futi, kolongo and Kayungo.The area has approximately 1000 miners.

Objectives: To screen for TB and other mining related lung health complications, to establish prevalence of TB amongst miners.

Methodology: The outreaches were done in 2 mines but mobilization done across the 6 mines and the surrounding communities.

This is an operational research in which 179 miners mobilized by community health promoters were clerked, screened using a digital x-rays and all presumptive TB cases identified both clinically and x-rays were entered into the presumptive TB registers and sent for sputum analysis (microscopy and gene expert) the data analyzed. Exclusion criteria being non miners) (1 boda boda, 1 business person, 3 charcoal sellers).

127 males and 52 females miners participated in the study. Age segregation of miners 18-25 years male-30,females-9, 26-35 years males -44,females 15, 36-45 years-13 males, females 11, 46-55 years-25 males, females -14, 56-65 years 9 males, females 3 and 66-75 years-6male,females -0

Results: (a) Clerkship (work load)

59 (33%) miners had complaint of chest pain, 4 (2%) difficulty in breathing (asthma) 1 (1%) Chronic obstructive pulmonary diseases and 1(1%) cold sensitivity the rest had no complaint (63%).

Miners ever treated for TB 30 (17%).

(b) Screening with digital x-ray

144 (81 %) miners had normal chest x-rays, 33 (18 %) x-rays suggestive of TB, 2 (1%) other abnormal finding (bronchitis and pneumonitis)

(c) Presumptive TB case identification

A total of 38 miners were sent for both gene expert and microscopy (33 suggestive -x-rays and 5 symptomatic but with normal chest x-ray.

(d) No of TB cases diagnosed

10(5.7%) TB cases diagnosed, 6 bacteriologically confirmed TB cases and 4 clinically diagnosed cases.

All the TB cases were started on treatment

14 (46.7%) cases of post TB sequlae (12 with suggestive chest x-rays, 2 with normal chest x-ray

Conclusion: The TB prevalence amongst miners is high.

Most miners experience respiratory symptoms.

Recommendations: Biannual screening of miners for TB and other respiratory disorders.

Multi agency approach to enhance occupational safety and health in relation to lung health amongst miner. An enhanced mandatory social insurance cover that covers imaging such as x-rays ,CT scans.

Keywords: TB-Tuberculosis

65.

LEVERAGING ON COMMUNITY TB ACTIVITIES TO SCALE UP TB CASE FINDING IN SUNA WEST, MIGORI COUNTY.

Authors: Peter P.O.O Omware (Ministry of health)*

Back ground: Suna West is ranked third in terms of contribution to tuberculosis (TB) case finding amongst the 8 sub counties in Migori County .The sub county has an annual TB case finding target of 617 but up to 2021 only 208 cases were diagnosed hence still a large proportion of undiagnosed cases in the community.

According to World Health Organisation (WHO), Kenya is listed among the 30 high TB, TB/HIV and MDR burden countries in the world. The 2015/2016 Kenya TB prevalence survey, found an overall national prevalence of 426/100,000 and demonstrated that Kenya misses approximately 40% of people with TB

Objective: To increase TB case yield from community activities from 8% to 10% by December 2022.

Methodology: This was a mixed method study design comparing data collected from the facility TB patient registers and contact management from 2021 before interventions and 2022 to 2023 during implementation of interventions as routine data collection occurred , then the number of TB cases diagnosed was then analyzed.

Strategies employed were

1.Training community health promoters (CHP) on screening, contact tracing and community facility referrals of suspects (30) across all the four wards (4) .

2. Training of CHPs on infection prevention, proper sample handling and providing them with cooler boxes to ferry samples from the field (30) to ensure clients reluctant to come to facility access TB testing across all the four wards.

3.Leveraging on home visit activities to screen households for TB e.g. social network strategy (SNS), Partner notification strategy (PNS) and defaulter tracing.

4.Facility based outreaches and national TB outreaches in mines.

5.Screening of schools for TB.

Results: In 2021 out of the 208 TB cases diagnosed 16(8%) were from community activities i.e. 2 contact invitation, 9 contact tracing and 5 routine community health promoter referrals.

During the implementation : In 2022 out of the 377 TB cases diagnosed 53 (14%) were from community activities i.e. 1 contact invitation, 35 contact tracing and 17 routine community health promoter referrals

In 2023 out of the 385 TB cases diagnosed 60 (16%) were from community activities i.e. 12 contact invitation,25 contact tracing ,10 routine community health promoter refferals,11 outreaches and 2 from home visits of clients during SNS and PNS sessions.

Conclusion: Increasing of TB screening activities in the community resulted in an increase in the proportion of clients diagnosed from the community from 8% in 2021 to 16% by end of 2023.

Recommendation: Multifaceted approach to increase screening in the community in high TB burden areas is essential to increase TB case finding.

Keywords: TB-Tuberculosis

66.

ENHANCING PUBLIC HEALTH: COMPREHENSIVE STRATEGIES FOR IMPROVED SURVEILLANCE IN TB CONTACT INVESTIGATION.

Authors: Gladys M Njaka (Catholic Medical Mission Board)*; Wayne Otieno (Catholic Medical Mission Board); Elizabeth Atieno Odhiambo (Catholic Medical Mission Board); Hilary Ngeso (Catholic Medical Mission Board)

Background: The effective identification and treatment of Tuberculosis (TB) via contact investigation play a crucial role in reducing its spread. The End TB strategy (2015) by the World Health Organization emphasizes regular screening of individuals closely associated with TB patients for early detection. In Kenya, contact screening for TB takes place at the household level with support from community health volunteers, facing challenges such as the reluctance of household members due to stigma. To address this, Catholic Medical Missions Board (CMMB), in collaboration with Amref Health Africa and the National TB program, launched a program for household contact screening and referral to improve patient notification rates in Makueni County. The objective was to assess the impact of Community Health Promoters (CHPs) on TB patient notification rates in Makueni through household contact screening and referral.

Method: On-job training to 49 (19 male,30 female) Community Health Promoters (CHPs) regarding contact investigation procedures was provided across the targeted 49 community units of Makueni (an average of 8 CHPs Per Sub county).Vital outcomes were identified to guarantee thorough coverage, such as directing all household contacts for screening at healthcare facilities, ensuring a sufficient stock of Ministry of Health referral resources, and promoting cooperation among stakeholders to maintain precise record-keeping. Experiential lessons as well as service access data from community and facility were collected and analyzed to gain insights into the TB patient notification rates through household contact screening and referral.

Results: Analysis revealed a notable increase in contacts referred to health facilities by CHPs, rising from 65% in 2022 to 77% in 2023. This increase corresponded with the identification of 54 new TB cases in 2023, up from 25 in 2022. Moreover, 2,555 contacts commenced Tb Preventive Therapy (TPT) in 2023, compared to 631 in 2022, signifying the substantial risk of Latent TB Infection (LTBI) and active TB among those exposed to TB patients. Effective contact tracing and screening significantly contribute to identifying the 40% of missing TB cases, complementing existing TB strategies.

Conclusion: Moving forward, we advocate for a universal 100% household contact referral system post-contact tracing. Systematic and active investigation of TB contacts is crucial for early detection, treatment, and halting further transmission of TB. Contact investigation remains a pivotal strategy in identifying TB cases, ensuring prompt treatment, and preventing its spread.

Keywords: Contact tracing, community Health Promoters, Health Facility, Tuberculosis, Community, Referral

SCIENTIFIC SESSION 8: HEALTH SYSTEMS-2

67.

COMPARISON BETWEEN THE SMART TRIAGE MODEL AND THE EMERGENCY TRIAGE ASSESSMENT AND TREATMENT (ETAT) GUIDELINES IN TRIAGING CHILDREN PRESENTING TO THE EMERGENCY DEPARTMENTS OF TWO PUBLIC HOSPITALS IN KENYA

Authors: Stephen Kamau (KEMRI Wellcome Trust)*, Joyce Kigo (KEMRI Wellcome Trust), Paul Mwaniki (KEMRI Wellcome Trust), Dustin Dunsmuir (UBC), Yashodani Pillay (UBC), Cherri Zhang (UBC), Brian Nyamwaya (KEMRI Wellcome Trust), David Kimutai (Mbagathi Hospital), Mary Ouma (Mbagathi Hospital), Ismael Mohammed (Mbagathi Hospital), Mary Chege (Kiambu L5 Hospital), Lydia Thuranira (Kiambu L5 Hospital), J Mark Ansermino (UBC), Samuel Akech (KEMRI Wellcome Trust)

Introduction: Several triage systems have been developed, but little is known about their performance in low-resource settings. Evaluating and comparing novel triage systems to existing triage scales provides essential information about their added value, reliability, safety, and effectiveness before adoption.

Methods: This prospective observational study included children aged < 15 years who presented to the emergency departments of two public hospitals in Kenya between February and December 2021. We compared the performance of Emergency Triage Assessment and Treatment (ETAT) guidelines and Smart Triage (ST) models (ST-only model, ST model with independent triggers, and recalibrated ST model with independent triggers) in categorizing children into emergency, priority, and non-urgent triage categories. We visualized changes in the classification of participants using Sankey diagrams.

Results: 5618 children were enrolled, and the majority (3113, 55.4%) were aged between one and five years of age. Overall admission and mortality rates were 7% and 0.9%, respectively. ETAT classified fewer children, 513 (9.2%), into the emergency category compared to 790 (14.1%), 1163 (20.8%), and 1161 (20.7%) by the ST-only model, ST model with independent triggers, and recalibrated model with independent triggers, respectively. ETAT also classified more children, 3089 (55.1%), into the non-urgent triage category compared to 2442 (43.6%), 2097 (37.4%), and 2617 (46.7%) for the respective ST models. ETAT classified 191/395 (48.4%) of admitted patients as emergency, compared to more than half in all the ST models. ETAT and the ST-only model classified 25/49 (51%) children who died as emergencies, while the ST models with independent triggers classified 39/49 (79.6%) children as emergencies.

Conclusion: Smart Triage shows potential for identifying critically ill children in low-resource settings, particularly when combined with independent triggers. Additionally, it performs comparably to ETAT. Evaluation of Smart Triage in other contexts and comparison to other triage systems is required.

Keywords: Triage, digital health, Smart triage, paediatrics, ETAT

68.

SPATIAL ANALYSIS OF PUBLIC HEALTH FACILITIES UTILIZATION ON TUBERCULOSIS PATIENT MANAGEMENT IN NAIROBI COUNTY: PRELIMINARY ANALYSIS OF CHARACTERISTICS OF TUBERCULOSIS DIAGNOSED PATIENTS ATTENDING RHODES CHEST CLINIC

Authors: Orina F*1,2., Songoro E2., Nyerere A2., Abisinwa E1., Muthoni L3., Meme H1.

Kenya Medical Research Institute-Center for Respiratory Diseases Research, 2. Jomo Kenyatta University of Agriculture and Technology, 3. Nairobi county Government

Background: Various tuberculosis (TB) strategies have been implemented by TB control programs to stop the transmission of the disease. However, low middle income countries including Kenya continue to dominate as high burden countries even with free diagnosis and treatment in public health facilities (PHFs). Subsequent TB prevalence surveys have indicated a large number of undiagnosed TB patients in the communities. Health system delivery can be negatively impacted through bypassing of nearest PHFs by TB patients. This is due to the infectiousness of *Mycobacterium tuberculosis*, compounded by transmission of resistant strains and mode of transmission. Generally, hospital bypassing is usually influenced by distance, service quality, availability of resources, stigma and patient preferences. In this study we investigated patients' related factors, their residences and PHFs bypass for tuberculosis management.

Methodology: This was a cross-sectional study whereby a comprehensive Nairobi County public health facilities map was developed together with residences of participants attending Rhodes Chest Clinic – Nairobi using point coordinates by Geographic information system software - QGIS. Clinical measurements and demographic information of participants were collected using a standard questionnaire. Data was analysed to illustrate the spatial pattern of PHFs utilization and categorical data, assessed using the chi-square ($\chi 2$) test.

Results: Data from 100 participants was analysed whereby 76.2% participants were males. The mean and standard deviation (SD) for: age of participants diagnosed with TB at the clinic was 36 years (SD 15.3); body mass 18.9 (SD 2.8); oxygen concentration 94.2% (S.D 4.7); traveling a distance of 13KM (S.D 8.5) across the Nairobi Metropolitan area. Most of the patients regardless of sex 78% (women 84.2% (16/19)) by-passed their local PHFs (from the analyzed 82 Nairobi County PHFs) to Rhodes Chest Clinic for TB management. There was a positive correlation between oxygen saturation (SPO2), patient temperature and number of meals consumed ($p<0.05$).

Conclusion: There is a substantial inclination among TB patients attending Rhodes Chest Clinic-Nairobi for tuberculosis management, irrespective of gender, to bypass their nearest Public Health Facilities. Additionally, a significant positive correlation, underscores the interplay between oxygen saturation, patient temperature, and dietary intake in TB disease progression. There is need to further evaluate TB biomarkers and service delivery of public health facilities in Nairobi County for tuberculosis control.

Keywords: tuberculosis, *Mycobacterium tuberculosis*, spatial distribution, health system bypass

69.

CONNECTED DIAGNOSTICS FOR SEMI-REAL TIME EPIDEMIOLOGICAL SURVEILLANCE OF INFECTIOUS DISEASES IN AFRICA: KISUMU COUNTY MALARIA CASE STUDY.

Authors: Felix Bahati (KEMRI)*; Kevin O Owuor (KEMRI); Patricia Gomez (PharmAccess Foundation); Lisette Schutte (PharmAccess Foundation); Emmanuel Milimo (PharmAccess Foundation); Alloys K'Oloo (KEMRI); Cem Koyuncu (PharmAccess Foundation); Simon Kariuki (KEMRI); Jonathan Cooper (University of Glasgow); Julien Reboud (University of Glasgow); Gregory Ganda (Ministry of Health, Kisumu County); Tobias Rinke (Amsterdam Institute for Global Health and Development/)

Background: Point of care (POC) Lateral Flow Tests (LFTs) are widely used for the diagnosis of infectious diseases. The LFTs can target antigens, antibodies, or the nucleic acid material of respective organisms after amplification. The tests are rapid, low cost and relatively simple to use. Accordingly, LFTs are crucial in low and-Middle-income-countries (LMICs) with disproportionate high burden of infectious diseases yet inadequate access to laboratory diagnosis. Effective use of POC LFTs could help target therapeutic interventions and early detection of disease outbreaks. We report on the use of Artificial Intelligence (AI) to accelerate malaria monitoring by interpreting malaria LFTs and providing semi-real-time data for epidemiological surveillance through dashboards.

Methods: Connected diagnostics (ConnDx) project began in April 2023, and we continue to collect malaria Rapid Diagnostic Test (RDT) data across 27 health facilities in Kisumu County. We position ConnDx as part of healthcare routine where clinicians suspecting malaria cases request patients to have malaria RDT done. The results of malaria RDT are digitalized through mobile phone photography and uploaded to a cloud for AI interpretation. The AI-interpreted results are then displayed on digital dashboards accessible to healthcare providers and decision makers. The digital dashboards are built on Microsoft's Power BI software (version 2.123.684.0) which leverages patients' data such as age, sex, facility coordinates and malaria RDT test outcome to present proportion summaries. Finally, we evaluate the AI RDT interpretation accuracy by calculating the sensitivity and specificity using human RDT interpretation as the gold standard.

Results: Since ConnDx inception, 3,237 malaria RDT were reported from the 27 health facilities enrolled in the project. The prevalence of malaria in Kisumu County based on human interpreted RDT results is 25.1% (805/3,209). Of the 3,237 RDT results submitted, due to a shift in procurement of malaria RDTs, only 23.8% (n=770) were eligible for interpretation by AI. The AI RDT classification shows substantial agreement with healthcare workers' interpretation with a sensitivity and specificity of 86.6% (95% CI: 79.6-92.1) and 98.0% (95% CI: 96.6-98.9) respectively, (Cohen's kappa 0.85, 95% CI (0.78-0.92). Overall, the False Negativity Rate (FNR) is 13.4% while False Positivity Rate is 2%.

Conclusion: Given the growing need for semi-real time data-driven healthcare solutions and policies in LMICs, disease surveillance dashboards are indispensable. This paper indicates that well-trained machine learning algorithms linked to free dashboards have great potential in this space.

Keywords: Connected diagnostics, malaria, dashboard, sensitivity, specificity, AI

70.

COSTS ASSOCIATED WITH ANTIMICROBIAL RESISTANCE AMONG PEDIATRIC IN-PATIENTS AT THE KENYATTA NATIONAL HOSPITAL

Authors: Teresa Ita (Washington State University Global Health - Kenya)*

Background: In Kenya, where only 19% of patients have health insurance, healthcare costs are primarily borne out-of-pocket. Consequently, patients often forego or suspend treatment to minimize healthcare costs low. These actions can be catastrophic for antibiotic-resistant infections, which are often associated with significantly higher costs. We conducted a cost analysis study to estimate the extraneous costs associated with antimicrobial-resistant infections among pediatric inpatients.

Methods: Patients of up to 13 years of age diagnosed primarily with a bacterial infection and admitted for > 2 days between 2014 and 2019 were identified through medical record reviews. For retrieval of relevant patient files from the record archiving system, specific codes corresponding with urinary tract infections, bacterial sepsis, gastroenteritis, tonsilitis, bacterial pneumonia, and bacterial meningitis were be identified from the list of ICD 10 codes available at the Kenyatta National Hospital Records Department. Costs associated with hospital bed use, clinical procedures, medical devices, and other administrative costs were compared between patients with resistant infections versus those with susceptible infections.

Results: In total, 1469 records including 831 (57%) of patients with susceptible infections and 638 (43%) of those with resistant infections were reviewed. Infants were the most affected by resistant infections.The median treatment cost was higher for those with resistant infections compared to those with susceptible infections (Kes. 47,562 vs. 20,150; $p < 0.001$). Bacterial sepsis imparted the highest treatment cost for resistant versus susceptible infections (Kes. 79,911 vs. 26,890; $p < 0.001$) compared to other diagnosis.

Conclusion: Antibiotic-resistant infections were significantly associated with higher treatment costs than susceptible infections. Strategies to increase targeted antibiotic therapy among hospitalized infants in Kenya and optimizing treatment costs for patients with resistant infections are recommended, particularly among poor populations.

Keywords: Antimicrobial resistance, Burden of antimicrobial resistance, Financial cost of antimicrobial resistance

71.

OUTCOME OF LABORATORY QUALITY MANAGEMENT SYSTEMS IN REDUCING ERRORS: A CASE STUDY OF RANGWE SUB COUNTY, HOMABAY COUNTY

Authors: EVERLYNE AKINYI MBOGA (MOH,HOMABAY)*

Introducttion: Laboratory Quality Management System (LQMS) refers to a set of policies, procedures, and practices implemented in a laboratory to ensure consistent quality and accuracy. Turnaround time (TAT) is the time from when a test is ordered to when results are delivered. This study aimed at determining the sample rejection rates and TAT at Rangwe Sub County Laboratories and characterized pre-analytical errors that contribute to it.

Method: This was a retrospective review of monthly laboratory workload reports in 9 QMS labs within the sub county during the pre QMS period (Jan to November 2021) and post introduction of QMS period (Jan 2021 to November 2023. Data on Rejection rates and TAT was collected using standard questionnaire. The descriptive data was presented as counts and percentages. Pearson's Chi square was used to test for change in the periods before the implementation of this intervention, during intervention, and at post intervention.

Results: Descriptive data analysis depicted a reduction of rejections and reduced TATs in all the tests especially viral load, EID and CD4 samples since the onset of implementation of QMS coupled with effective root cause analysis. There was significant improvement on monthly workload for all the tests conducted from 2056 to 8784. Rejection rates reduced from 34% to 2%, and TAT of 30 days for VL samples to 12 days, 54 days for EID to 7days and from 5days to 1 Day for CD4 samples. On rejections, clotted specimen [85%] was the major cause of blood specimen rejection followed by hemolysis (79%). However, insufficient volume of the specimen and labelling errors accounted the least as causes of blood specimen rejection (22%) and (13%) respectively.

Conclusion: Implementation of QMS has reduced the rejections and improve the TAT. Further training in phlebotomy and blood samples transportation can reduce the high number of samples rejected due to clotting. This can be done through regular, continuous medical education (CME), OJT and mentorships to clinicians and laboratory personnel.

Keywords: QMS, PRE ACCREDITATION, ACCREDITATION

72.

EVALUATING SPECIMEN REJECTION AS A QUALITY ASSESSMENT TOOL FOR INTERVENTION AT KEMRI-TB REFERENCE LABORATORY.

Authors: Elizabeth Awuor Okoth (Kenya Medical Research Institute)*; Steve Wandiga (KEMRI); Fred Ogumbo (kemri); ALBERT O OKUMU (KEMRI); BEN ODHIAMBO OKOTH (KEMRI)

Introduction: Tuberculosis (TB) remains a major global health concern. Accurate and timely diagnosis is crucial for effective treatment and control. Specimen rejection can lead to delays in diagnosis and treatment initiation and can have serious public health implications. Quality management of TB encompasses good quality specimen. Inappropriate specimen collection technique packaging and transportation may lead to specimen rejection.

Methodology: This study was conducted as part of the baseline internal quality improvement initiative at the KEMRI-Tuberculosis Referral Laboratory. The study aimed to assess the effectiveness of using specimen rejection as a quality assessment tool for implementing innovation at KEMRI-TB Reference Laboratory. A retrospective search was conducted using TB LabWare information system (LIMs) as our data source. rejected specimens were extracted, capturing the period between January to December 2022. Indicators such as, reasons for rejection, patient location and type of test requested were assessed. The total number of specimens that were rejected during this time period was presented in percentage by county, test type and reasons for rejection.

Results: 19 (32%) out of 59 samples were rejected from Kisii County,Vihiga 12(20%), Migori 9(15%), Siaya 5(9%), Homa Bay 5(8%), Kisumu 3(5%), Uasin Gishu 2(3%) and 1(2%) Bomet, Kericho, Kakamega and Busia based on test type. Rejection due to Leakage Kisii at 12(40%), Vihiga 7(23%), Migori 3(18%), Homa Bay 3(10%), Uasin Gishu 2((7%) Kisumu, Bomet and Siaya 1(3%).

Conclusion: The findings of the study justify that specimen rejection has significant clinical consequences, including significant delay in result availability, delayed intervention and possibility of specimen/ test abandonment which could lead to rapid speed of MDR and XDR stain of Tuberculosis to the general public. Monitoring of specimen acceptability is an important quality assurance measure within the clinical laboratory.

Keywords: Tuberculosis, Quality Assessment .Intervention, Monitoring,of specimens Rejection, Indicators, Reference Laboratory

73.

MIMBA PREGNANCY EXPOSURE REGISTRY IN WESTERN KENYA: COHORT DESCRIPTION, CHALLENGES, AND OPPORTUNITIES FOR SCALABILITY.

Authors: Benard Omondi (Kenya Medical Research Institute(KEMRI))*; Hellen Barsosio (Liverpool School of Tropical Medicine (LSTM)); Kennedy Maube (Kenya Medical Research Institute(KEMRI)); Benard Opiyo (Kenya Medical Research Institute(kemri)); Titus Ochieng' (Kenya Medical Research Institute(Kemri)); Mercy Terer (KEMRI-CGHR); Michael Alaw (Kemri); Stephanie Dellicour (Liverpool School of Tropical Medicine(LSTM))

Background: Until now, pregnant women have usually been excluded from clinical trials during drug development for fear of harming the developing foetus. Many essential medicines, therefore, get licensed without safety information during pregnancy, resulting in delays for pregnant women to access safe and effective therapeutics. Active pharmacovigilance studies are key in assessing the risk-benefit profiles for medicines and therapeutics, especially for groups such as pregnant women where there is a lack of safety information. This presentation will explore the methodological challenges in setting up active pharmacovigilance studies in LMICs, solutions to these challenges and opportunities for leveraging data from routine healthcare.

Methods: The "MiMBa pregnancy exposure registry" is a multi-centre prospective cohort study in Homa Bay county, Kenya, and Nanoro district in Burkina Faso. The aim is to assess the safety of antimalarials taken during pregnancy, focusing on the first trimester. In order to identify pregnancies early, women of childbearing age (WOCBAs) are enrolled before conception, screened for pregnancy periodically and referred to routine antenatal care when identified as pregnant. An ultrasound scan is offered to all participants to assess gestational age. Information on antimalarial and other therapeutic exposure during pregnancy is collected through the extraction of data from routine care and complemented by structured interviews. Participants are followed up until delivery and all infants up to 8 weeks post-partum. The safety outcomes of interest include the following adverse pregnancy outcomes: pregnancy losses, congenital anomalies, preterm birth and low birth weight. Suspected cases of congenital anomalies are reviewed by an independent expert committee to confirm the diagnosis. A sub-group of infants exposed to antimalarials in-utero in the first trimester and matched unexposed controls are followed up for neurodevelopment assessment at months 6 and 12.

Results: From February 2021 to November 2023, 50,351 WOCBAs have been enrolled in Kenya, 11,804 of whom have been pregnant, and 8,256 have delivered with documented pregnancy outcomes. The cohort has a mean gestational age at pregnancy detection of 23.6 (SD=13.1) weeks. Key challenges include record linkage, late detection of pregnancies and incomplete ascertainment of early pregnancy losses.

Conclusions: Community health systems can be optimised to improve the early detection of pregnancies and pregnancy losses by community health promoters. Electronic community health information systems, the roll-out of the national unique patient identifiers and standard electronic medical record systems as provided for in the Kenya Digital Health Bill 2023 present opportunities to scale up active pharmacovigilance across disease areas, with wider geographical coverage and in a sustainable manner.

Keywords: Pharmacovigilance, Malaria,

74.

PROVISION OF ADOLESCENT AND YOUTH-FRIENDLY SERVICES IN PUBLIC HEALTH FACILITIES IN MIGORI COUNTY, KENYA

Authors: Lillian N Nyaga (Ministry of health)*; Eunice mwangi (Aga Khan University-East Africa)

Background: According to the World Health Organization (WHO), adolescents and youth (AY) are individuals aged 10-19 and 15–24 years, respectively. It is imperative to respond to the needs of AY by providing friendly health services. Global and national guidelines on provision of adolescent and youth-friendly services (AYFS) exist. Kenya's devolved governance structure, including the health system, provide renewed attention to address long-standing challenges in the provision of AYFS. However, the extent to which these services are provided in Kenya, is unknown. Therefore, this study aimed to assess provision of AYFS in public health facilities in Migori County, Kenya.

Methods: Provision of AYFS was measured by determining if the AYFS were equitable, accessible, acceptable, appropriate, and effective. Data collection took place between March and May 2023. The study setting was public health facilities in Migori County and the county has 159 public health facilities. Determination of the sample size of the facilities and the HCPs to participate was calculated using the Taro Yamane method.

A multistage sampling was done ,114 public health facilities were identified. The total health care providers (HCPs) were 455 within the 114 facilities. Further, using the taro Yamane method 210 HCPs were sampled. Three facility in-charges were purposively selected to represent each Level of healthcare delivery system. Data was collected using structured questionnaires, key informant interviews guide, and Health facility observation checklists as per Kenya AYFS 2016 guidelines.

Results: Statistical Package for Social Sciences data entry program was used to enter coded questionnaires and analyzed using SPSS Version 24.0 while NVivo 9 software was used for transcribing and coding the qualitative data. 0n equitable AYFS, nearly all facilities 110(98%) were administering AYFS without discrimination; while for accessible AYFS Majority of facilities 87(78%) were offering free AYFS. Further on acceptability, nearly all the facilities 110(98%), HCPs were respectful and non-judgmental to AY clients and on appropriateness 63(56%) had a package that fulfills the needs of AY. Results on the effectiveness, 71(63%) had HCPs with the required competencies to provide AYFS. However, less than half 29(26%) of the facilities had required AYFS policies available for use during provision of AYFS and 49(44%) had HCPs trained on AYFS.

Conclusion: Public health facilities in Migori County provide equitable, accessible, acceptable, appropriate, and effective AYFS. However, the inadequate availability of required AYFS policies and trained HCPS on AYFS within the public health facilities hinder the effective provision of AYFS. The county needs to avail , disseminate AYFS policies and capacity build HCPs within the health facilities on AYFS.

Keywords: Accessible, acceptable, appropriate, equitable, and effective AYFS, Sexual Reproductive Health Services

75.

FACTORS IDENTIFYING IDEAL SCIENTIFIC COMMUNICATION CHANNELS AT KENYA MEDICAL RESEARCH INSTITUTE: VIEW POINT

Authors: Isaac Joseph Muthotho (KEMRI)*

Background: Communication channels for conveying scientific outcomes to stakeholders are critical in research institutions. Kenya Medical Research Institute's (KEMRI) core mandate is to conduct human health research and communicate findings through, research innovation services and capacity building. Corporate Affairs in liaison with KEMRI scientists disseminate their findings to various target groups in different fora. These has posed challenges in packing messages so as to communicate to these stakeholders. The scientific jargon remains a challenge in communicating research findings. The main objective was; To identify preferred communication channels used at KEMRI.

Methodology: The study utilized mixed method approach anchored on Communication theory, Stakeholders theory and Media Dependency Theory (MDT). Convenient non-probabilistic sampling was used to random identify and pick respondents in KEMRI, Nairobi centres. Data collection was done through semi structured questioners, desk review, alongside in-depth interviews (IDI) were carried out using a check list on key informants from; a) KEMRI's Corporate Affairs, b) KEMRI scientists and collaborators c) select study participants from on-going KEMRI Nairobi projects.

Sample size: 76

Study design: Descriptive.

Results: The study identified 11 diverse channels comprising; Scientific Conferences such as KEMRI Annual Scientific and Health Conference - (18%), Knowledge Café Meetings (12%), Digital and Tradition Media (Television, Radio - Formal and Vernacular Stations) – 14%, Print Media (Newspapers) (10%), Peer Reviewed Publications (6%), Bulletins (5%), Dashboard Visualization (Infographics) (7%), Social Media (Tweeter and Linkedin) (14%), Oral Dissemination – Barazas (Informal Community Meetings and Storytelling) (6%), Podcasts (Youtube) (5%), Exhibitions and Trade Fairs examples, Nairobi and Mombasa Agricultural Society of Kenya (ASK) international shows (3%).The study highlighted three broad categories based on tools utilized and impact. These KEMRI's communication channels were based on these three factors: (i) Teaching pedagogy (Graduate School learning instruction) 28%; (ii) Knowledge capitalization for sharing internally example departmental meetings, internal seminar (32%); (iii) The target audience (40%).

Conclusion: The study concluded that conferences were the most preferred communication channels followed by digital and traditional channels. The paper discussed the challenge interpreting the esoteric language while retaining the scientific accuracy of disseminated findings in communication channels. Furthermore, identified the need to maintain visibility and relevance by increasing media outreach content, utilizing the digital and broadcast media. The study recommended periodic review of the channels packaged to stakeholder preference.

Key Words: Communication channels, knowledge capitalization, target audience, teaching pedagogy

SCIENTIFIC SESSION 9:

MALARIA-2

76.

HSP90 AS A POTENTIAL BIOMARKER: EXPLORING THE COMPLEX RELATIONSHIP BETWEEN ANTIMALARIAL TREATMENT AND *PLASMODIUM FALCIPARUM* HEAT SHOCK PROTEIN 90 EXPRESSION

Authors: Lewis k Mbabu (Kenya Medical Research Institute)*; Dorcas Wachira (Kenya Medical Research Institute); Rukiya Haji (Kenya Medical Research Institute); Japheth Lusweti (Kenya Medical Research Institute); Rosemary Githae (Kenya Medical Research Institute); Nancy Kinyatta (Kenya Medical Research Institute); Francis T Kimani (KEMRI); Christine Ichugu (Kenya Medical Research Institute)

Background: The protozoan parasite adapts to its environment by translocating Heat Shock Proteins Hsps for survival. Hsp90 is a chaperone protein that enables the parasite to circumvent challenges such as febrile episodes and drug pressure in the host. Subsequently, Hsp90 may constitute the hub that drives drug resistance in malaria parasites. The study aimed to determine if there were significant differences in expression levels of Hsp90 in untreated and treated malaria cases and whether the difference could be used as a marker of drug efficacy based on clinical outcomes providing important insights into ACT action against malaria.

Methodology: RNA was extracted from forty-five Whatman dried blood spots from archived clinical isolates for day 0 (before treatment) and day 2 (after treatment) and purified. qPCR was used to amplify the Hsp90 gene. Each sample was amplified in duplicate with a housekeeping gene, Beta-actin included. Average Ct was calculated and the fold change between Hsp90 expression at day 0 and day 2 was computed using the $2^{-(\Delta\Delta Ct)}$ method.

Results: 15/45 (33%) samples showed at least a twofold increase in expression levels. 8/15 (53.3%) had a twofold increase. 3/15 (20%) had a threefold increase, with single samples out of the 15 (6.7%) showing a 4-, 5-, 7-, and 9-fold increase. From the samples analyzed, 12 of the 45 (27%) showed a downregulation in Hsp90 expression between the febrile and treated samples while 18 samples (40%) showed no difference in expression levels. Hsp90 expression at day 0 and admission temperature of the sampling individual gave a correlation value of -0.0984(p=0.0717) while the association with parasitemia at admission gave a correlation value of -0.0633 (p= 0.00000135). Comparing the fold change in HSP90 expression with parasitemia at day 0 gave a correlation value of 0.1596 (p= 0.2951) while the correlation with parasitemia after treatment gave a coefficient of -0.0733 (p =0.6324). Correlated with temperature at sampling, the fold change in HSP90 expression gave a coefficient of 0.1908 (p = 0.2092).

Conclusion: The association of Hsp90 expression at day 0 with admission temperature shows a weak negative correlation with no statistical significance p = 0.0717 while the correlation with parasitemia at admission shows a significant negative correlation at a p-value of 0.00000135 ($p < 0.05$). This shows that parasitemia and (not temperature) may be a confident predictor for Hsp90 expression at the febrile stage. Correlating the fold change with parasitemia at day 0 highlights a weak negative correlation with no statistical significance, p=0.2951. Correlated with temperature at sampling, the fold change shows a weak positive correlation that is similarly not statistically significant p=0.2092. Overall, the data suggests that Hsp90 expression is not an ideal biomarker for treatment outcomes based on Artemisinin Combination Therapies in managing clinical malaria.

Keywords: Heat shock protein, *Plasmodium falciparum*, ACT

77.

EVIDENCE OF *P. VIVAX* IN NORTHERN KENYA, AN EMERGING MALARIA CONTROL THREAT; AN INCIDENCE REPORT FROM THE OUTCOME OF THE MID-2023 EPIDEMIC RESPONSE SURVEY.

Authors: Francis T Kimani (KEMRI)*; Kelvin Thiongó (KEMRI); Lewis k Mbabu (Kenya Medical Research Institute); Moreen Otinga (KEMRI); Mary Ombati (KEMRI); Luna Kamau (Kemri); Damaris Matoke (KEMRI)

Background: Malaria mortality and morbidity in Kenya has all along been largely due to *Plasmodium falciparum* infections with no cases attributed to P.vivax. The epidemiology in northern Kenya counties is traditionally classified as zero to low risk transmission zones. A recent upsurge in febrile illnesses was reported in the counties of Marsabit, Mandera and Turkana, in mid 2023. which required an emergency pandemic response. An analysis determining the presence of *Plasmodium* infection and the species present in this rapid response are hereby reported.

Methods: A total of 89 blood samples were collected from patients suspected of malaria in the Northern Kenya counties, after which they were analysed. Positivity and speciation was performed using 18S rRNA and qPCR TaqMan® probes with species specific primers

Results: From 3 health facilities in Marsabit, Mandera and Turkana counties a total of 24, 50 and 15 dried blood spot samples were received respectively. There were 11, 40 and 15 *Plasmodium* positive samples in the three county health facilities respectively. This translated to a total positivity of 74.2%. Speciation analysis was done for the four common *Plasmodium species*. This analysis recorded

a total of 60 *P. falciparum* positive samples, 2 samples with a mixed infection of P. malariae and P. falciparum, 2 P.vivax mono infection samples, and 2 P. vivax P. falciparum co-infected samples. No *P.ovale* was observed in any of the facilities. Three of the P.vivax infections were in Marsabit county while the remaining case was from Mandera County translating to an incidence rate of 12.5% (3/24)and 2%(1/50) respectively. No P.vivax infection was identified in Turkana county.

Conclusion: The findings of this analysis show that the incidence of malaria from the response sites was quite high, at 74.2%. Although the burden of *P. vivax* in these counties is undetermined, the presence of the observed proportions in such a small sample size is an indicator of an underlying problem of cases that are rarely diagnosed in a clinical setting and may often be asymptomatic. The presence of *Anopheles stephensi* that was recently identified for the first time in Kenya in the same study region, implies the potential expansion of a highly competent vector here, which could dramatically enhance the transmission of P. vivax and reverse all the malaria control gains made over the years.

Keywords: *P. Vivax*, Emerging, upsurge, febrile illnesses

78.

EFFECTIVENESS OF INDOOR RESIDUAL SPRAY ON MALARIA CONTROL; A REVIEW OF THE MALARIA CASES AMONG CHILDREN UNDER FIVE YEARS IN RACHUONYO NORTH SUB COUNTY, HOMA BAY COUNTY AND NYAKACH SUB COUNTY KISUMU COUNTY, KENYA.

Authors: GABRIEL O KOTEWAS (MoH - Homa Bay County)*

Background: Indoor residual spraying (IRS) is one of the core interventions implemented in western Kenya for prevention of malaria. . IRS has been implemented in Homa Bay County in western Kenya from 2018 to 2023.The objective of this study was to assess the effect of IRS on malaria cases among children under 5 in areas sprayed with organophosphates and neonicotinoids and without IRS.

Methods: A retrospective study was conducted to assess the trend of malaria incidence over the last four years (2019 – 2022) using recorded blood smear reports in laboratory registers in health facilities. Data was retrieved from health facilities in Rachuonyo North sub-county in Homa Bay County (IRS plus pyrethroid-only ITNs) and Nyakach sub-county in Kisumu County (pyrethroid-only ITNs). Descriptive analysis was performed, and malaria incidence rates estimated for each sub-county. The association between the incidence rates, sub-county and season were determined by regression analysis.

Results: Over the last four years, a total of 37,008 and 37,295 malaria-suspected cases were tested for malaria in Rachuonyo North and Nyakach, respectively. In Rachuonyo North, the highest incidence was observed in 2020 (12 per 1000 population) and lowest in 2021 (8.3 per 1000 population). In Nyakach, the highest incidence was recorded in 2022 (295 per 1000 population and lowest in 2019 (223 per 1000 population). Malaria was recorded all year round with two major malaria peak seasons observed: one from January to March and September to November. A significant variation of malaria cases was observed across the sub-counties ($p<0.05$).

Conclusion: Malaria reduction in Rachuonyo North seemed to be associated with the implementation of IRS and standard ITNs since 2018. Although a reduction in malaria cases has been recorded in Rachuonyo North where IRS was conducted, additional interventions beyond ITNs may need to be put in place in Nyakach to facilitate further burden reduction as was the case in Rachuonyo North.

Keywords: Effectiveness, IRS, Malaria, Control

79.

DETECTION OF TWELVE *PLASMODIUM FALCIPARUM KELCH 13* GENE MUTATIONS IN CLINICALS SAMPLES FROM FOUR SITES ACROSS KENYA REVEALS INTENSE GENOMIC EVENTS

Authors: Hosea Akala (USAMRD-K/KEMRI); Benjamin Opot (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI))*; Dennis Juma (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI)); Raphael Okoth (USAMRD-K/KEMRI); Redemptah A Yeda (usamru-k-KEMRI); Edwin W Mwakio (USAMRD-A/K); Gladys Chemwor (Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI)); Jackline Juma (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI)); Agnes Cheruiyot (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya

Medical Research Institute (KEMRI)); Michal Ohaga (KEMRI/USAMRU-K); Doris Njoroge (KEMRI/USAMRD-A); Timothy E. Egbo (USAMRD-A); Ben Andagalu (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI)); Edwin Kamae (3Department of Pathology and Area Laboratory Service, Tripler Army Medical Center, Honolulu, USA); Bernhards Ogutu (Kenya Medical Research Institute)

In the recent past, parasites that harbor mutations conferring delayed clearance by artemisinin-based combination therapy have been reported in Africa, though at low frequency therefore needing largescale characterization of samples from wide geographic range. This study determined the polymorphisms of *Plasmodium falciparum Kelch 13 (PfK13)* gene that is associated with artemisinin resistance alongside other malaria drug resistance markers in clinical samples collected at six geographically distinct locations in Kenya.

Methods: Blood samples collected between 2018 and 2022 from individuals presenting with uncomplicated malaria were analyzed by Sanger sequencing to detect polymorphisms in PfK13. Each sample was further assayed for single nucleotide polymorphisms in putative drug resistance genes namely *Pfcrt, Pfmdr1, Pfdhfr, Pfdhps*, and *Pfcytb* on the Agena MassARRAY platform.

Genomic analyses of PfK13 polymorphisms in 375 from Busia (n=100), Kisii (n=80), Kisumu (n=87), Kombewa (n=86), Marigat (n=18) and Kericho (n=5) revealed 14 mutations in 20/375 (5.6%) infections. Eight nonsynonymous mutations were detected at P553L, E612D, V637I, S600F, F483L and F491L from Kericho, Kisii, Busia and Kombewa; ten synonymous *at V637D, V637V, C469C, A504A*, and *L488L* from Kisumu, Busia, Kombewa and Kisii. One sample from Kisii site harbored two mutations at P553L and G497G. Nonsynonymous mutations at E612D, S546F and F491L, synonymous mutation A504A have not been previously reported elsewhere. Mutations in other validated malaria drug resistance markers Pfcrt, Pfmdr1, Pfdhfr, Pfdhps, and Pfcytb remained stable during this period. In vitro drug resistance data for these compounds showed modest in vitro response to a panel of 12 antimalarials.

Mutations in the K13 gene were detected across all the study sites depicting widespread dispersion of these variants. Though most of most of these polymorphisms had been reported elsewhere in Africa, non-synonymous mutation *F491L* and *S600F* as well as synonymous mutations K455E, G497G detected by this study appear to have not been reported elsewhere, revealing the depth of diversity in parasite genomic backgrounds across the continent. Mutations *A578S* and *L505F* previously reported in at high frequency in Kenya were not detected. This identification of multiple nonsynonymous mutations in multiple loci presents intense genomic activities within the *Pfk13* propeller gene, evocative of progress towards the mutant status involving multiple genome regions once fitness of the new variant is attained.

Keywords: Polymorphisms, *Plasmodium falciparum*, *Kelch 13 (PfK13)* gene

80.

UTILITY OF EX VIVO MALARIA SYBR GREEN L ASSAY IN SUSCEPTIBILITY PROFILES OF *PLASMODIUM FALCIPARUM* AND NON-*FALCIPARUM* CO-INFECTIONS IN WESTERN KENYA

Authors: Agnes C Cheruiyot (usamru-k)*; FARID S ABDI (USAMRD-A); Hoseah Akala (KEMRI/USAMRD-A/K); Dennis Juma (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI)); Benjamin Opot (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI)); Redemptah A Yeda (usamru-k-KEMRI); Raphael Okoth (USAMRD-K/KEMRI); Edwin W Mwakio (USAMRD-A/K); Jackline Juma (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI)); Risper Maisiba (USAMRD-A/Walter Reed Project); Maurine Mwalo (USAMRD-A/Walter Reed Project); Timothy Egbo (USAMRD-A)

Background: Ex vivo drug testing (testing parasites without culture adaptation) has been proved to be effective in examining drug susceptibility in *Plasmodium falciparum* (P.f) field isolates. There are concerns regarding its utility in testing non-Plasmodium falciparum species in endemic regions where non-Plasmodium falciparum infections are increasingly being reported. We retrospectively analyzed data for malaria field samples under approved surveillance protocol KEMRI #3628, WRAIR #2454 collected between 2008 and 2022 at Kisumu County Hospital and Kombewa Sub County Hospital.

Methods: A total of 135 samples were assessed by ex vivo testing and molecular marker analysis. Samples were screened against chloroquine (CQ), quinine (QN), atovaquone (AV), primaquine (PQ), artemether (AR), artesunic acid (AS), amodiaquine (AMQ), artemisinin (ART), doxycline (DX) halofantrine (HAL) and tafenoquine (TAF) using Malaria SYBR green l. Drug response curves were obtained from relative florescence units (RFU) using Graph Pad Prism (San, CA, USA) and single nucleotide polymorphisms were obtained using Sanger sequencing.

Results: Median drug concentration for CQ were 10.22 ng/ml (6.543-17.03) in samples with falciparum only and 9.545 ng/ml (5.495-15.36) P=0.19 in *falciparum-malariae* co-infection, 7.810 ng/ml (3.782-16.24) P=0.7 in *falciparum–ovale* co-infection. QN had 21.26 ng/ml (13.11-35.33) in falciparum only and 25.59 ng/ml (9.828-57.36) P=0.6 in *falciparum-malariae*. AV had 2.680 ng/ml (1.368-4.647) in *falciparum* only and 1.963 ng/ml (1.026-6.163) P=0.9 in *falciparum-malariae*. PQ had 592.9 ng/ml (116.6-794.5) in *falciparum* only and 611.9 ng/ml (179.9-1027) p=0.4 in falciparum-malariae. DX, 2952 ng/ml (737.3-7252) in *falciparum* only and 6794 ng/ml (1201-9222), p=0.2 in *falciparum-malariae.* ART had 2.875 ng/ml (1.608 -4.780) in *falciparum* only and 3.739 ng/ml (2.949-6.907), p=0.07 in *falciparum*-malariae. HAL had 3.2220 ng/ml (1.775-23.73) in *falciparum* only and 2.843 ng/ml (1.798-7.989), p=0.5 in *falciparum-malariae*. TAF had 414 ng/ml (156.4-617.8) in falciparum only, 425.1 ng/ml (262.0-570.0), p=0.9 in falciparum- malariae. *P. falciparum* only with *falciparum* –ovale CQ median of 12.39 ng/ml (7.753-20.93) in falciparum only and 5.790 ng/ml (3.910-17.27), p=0.1 in falciparum –ovale.

Conclusion: Median IC50s in all the drugs tested for falciparum only compared with non-falciparum co-infection had no significant variation, a similar finding in drug marker analysis. This finding argues for inclusion of non-falciparum species profiling using ex vivo SYBR Green 1 to step up surveillance of antimalarial resistance.

Keywords: *Plasmodium*

SCIENTIFIC SESSION 10: PUBLIC HEALTH-1

81.

FACTORS ASSOCIATED WITH LOW MEASLES-RUBELLA VACCINATION COVERAGE: AN ASSESSMENT OF POST OUTBREAK VACCINATION CAMPAIGN IN ASAL COUNTIES, KENYA, 2022.

Authors: Serah Nduta Itotia (FELTP-NVIP)*

Background: Kenya confirmed a Measles outbreak in seven counties in June 2022, with 150 confirmed cases as of December 2022. A reactive supplementary immunization activity was conducted in December 2022. However, estimated coverage had not been established. The main objective of the survey was to determine vaccination coverage and evaluate strategies used in the campaign (fixed post, fixed temporary and hard-to-reach areas strategies.

Method: A population-based survey was conducted in December 2022 in the seven outbreak-stricken counties of Garissa, Wajir, Mandera, Marsabit, West Pokot, Turkana and Nairobi. Children aged nine (9) months to fifty-nine (59) months who were the target population for the vaccination in the seven counties were enrolled. A multi-stage probability proportionate to the cluster size sampling strategy was used to determine the number of clusters per sub-county. Seven (7) households per cluster were randomly selected and a total of 78 clusters were surveyed. Data were collected using electronic-based semi-structured questionnaires, analyzed using MS Excel and Stata software, and presented in frequencies and proportions.

Result: We visited 544 households with 953 eligible participants, of whom 88% (839/953) had been vaccinated during the campaign. Those aged 1–2 years were 20% (168/839), and females were 49% (407/839). Among the caregivers, 92% (499/544) were female, 55% (300/544) had no formal education, and 47% (258/544) were unemployed. Nearly 79% (660/839) were vaccinated at Fixed Temporary sites, 22% (170/839) and 2% (20/839) were vaccinated at Fixed Permanent sites and Hard-to-reach areas. About 57% (311/544) of the caregivers were aware of the campaign before it happened, and 28% (151/544) were aware during the campaign. Challenges noted were the communities' nomadic nature, the counties' vastness, and the easily fading ink- markers used.

Conclusion: The coverage was below the desired threshold of 95% coverage. Community Health Volunteers (CHV) and mobile vaccination sites were integral in the vaccination campaign. The use of fixed temporary points should be adopted in arid pastoral areas of Garissa, Wajir, West Pokot, Turkana, Mandera and West Pokot to strengthen routine vaccination activities.

Keywords: Kenya, Measles-Rubella, Survey, Vaccination, Immunization Program

82.

KNOWLEDGE, ATTITUDES AND PRACTICES AND SOURCES OF INFORMATION TOWARD ANTHRAX AMONG HIGH RISK OCCUPATIONAL GROUPS IN MURANG'A AND MERU COUNTIES, KENYA

Authors: Juster Mungiria (Chuka University)*; John Njeru (KEMRI); Haddison Mureithi (KEMRI); Kenneth Malombe (KEMRI)

Background: Anthrax is an important zoonotic disease in the horn of Africa, causing high morbidity and mortality in human, wildlife and livestock. It's often reported in many parts of horn of Africa such as Somalia, Kenya, Ethiopia and Eritrea. This study hoped to assess the knowledge, attitudes, practices and the main sources of information on anthrax (KAPS) among farmers and butchers in selected high risk counties of Kenya based on the reported cases of Anthrax

Methods: A cross-sectional study was conducted among 388 adult farmers (Meru; 83 and Murang'a; 93) and 176 adult butchers (Meru; 210 and Murang'a; 178) counties from June 2019 and June 2021.Data was collected through questionnaires and administered through face to face interviews and accuracy checked using an epicollect

Results: In terms of the distribution, more butcher and farmer participants were drawn from Mikinduri, Mitumbiri, and Karama and Nginda wards in Meru and Murang'a respectively. Butcher's knowledge assessment found that the respondent's gender, education level, household head, production system and period of anthrax knowledge level were significantly associated with good anthrax knowledge level. Significant differences in knowledge were reported on period working in butchery ($t = -2.46; p = 0.015$), age ($t = -3.74; p = <0.001$) whether or not meat traders confirmed meat source ($\chi2 = 15.6; p = <0.001$), and the availability of a slaughter slab near the business site ($\chi2 = 5.28; p = 0.022$). Assessment of butchers practices showed that the participants' level of education ($\chi2 = 1.55; p = 0.461$) did not translate to good practices. Significant differences in practices were found among the duration on butchery occupation ($t = -2.61; p = 0.01$), region ($\chi2 = 4.48; p = 0.0342$), and site of business ($\chi2 = 12.2; p = 0.002$). Assessment of farmers practice, found that the participants' gender and education level ($\chi2 = 3.45; p = 0.063$ & $\chi2 = 1.95; p = 0.583$) did not translate to good practices. Significant differences in practices were reported among study region, household head, production system and respondents' period of anthrax knowledge. In addition, assessment of the farmers knowledge found that the respondent's gender p=0.015, education p=0.006 level, household head p=0.026, production system and period of anthrax knowledge level were significantly associated with good anthrax knowledge level p=0.001 and p<0.001 respectively. Overall, radio (42%) was ranked as the most effective modes of communicating information on anthrax.

Conclusion: The findings imply that, butchers and farmers with low knowledge levels may have inappropriate attitudes/practices towards anthrax. The data will enable government and other stakeholders to take transparent and evidence-based planning for intervention measures to improve the health of community. Also, it may help to inform policies to mitigate the public health and economic impact of anthrax and help to change the behavior of people.

Keywords: Anthrax; Knowledge; Attitude; Practices

83.

EVALUATION OF THE INFLUENZA SENTINEL SURVEILLANCE SYSTEM IN KENYA, 2021–2022

Authors: Valentine N. Kabita (FELTP)*

Introduction: Influenza sentinel surveillance entails the systematic collection of influenza data routinely from a select number of surveillance sites. In Kenya, influenza sentinel surveillance was established in 2007 to monitor circulating influenza viruses. There's need for periodic evaluations to identify areas for improvement and provide evidence of data reliability for policymaking.

Methods: We used CDC guidelines to evaluate performance of the influenza surveillance system, Kenya, 2021-2022. MS Excel data abstraction tool used to extract data from influenza database register. Variables collected; demographic, clinical and laboratory data. Descriptive statistics performed. Performance was evaluated using 9 attributes; simplicity, timeliness, acceptability, flexibility, stability, usefulness, data quality and completeness, positive-predictive-value and representativeness. For each attribute specific indicators were developed and described using quantitative and qualitative methods. We used scale from 1 to 3 to provide score for each indicator and attribute: 1 (weak performance); 2 (moderate performance); 3 (good performance). Overall score for each attribute and the system was obtained by averaging the scores of all evaluated attributes.

Results: Records reviewed for 8 sentinel sites had 7538 cases tested, majority 6586 (87.4%) were below 5yrs, males were 4307 (57.1%), influenza positive cases were 998 (13.2%), of which 835 (83.7%) were SARI patients, Kakuma site had most 354 (35.5%) positive cases. Samples tested within one week from receipt 5451 (72.3%), type A was most common 710/998 (71.1%). Majority 5183 (95%) had not received influenza vaccine. The overall mean score for the system was 2.5 (moderate-to-good performance). Key strengths of the system were data quality (2.8) stability (2.9) and usefulness (2.8). Representativeness had moderate (2.0) performance.

Conclusion: The system performed moderately well and provided reliable timely data. Gaps in data quality and low uptake of influenza vaccine noted. We recommend sensitization on influenza vaccine, key improvements on timeliness of sample testing and increase sentinel sites to expand geographical coverage.

Keywords: Influenza, Surveillance, Evaluation, Kenya

84.

COMMUNITY PREFERRED DRUG DELIVERY APPROACHES FOR ROLL-OUT OF NOVEL PAEDIATRIC SCHISTOSOMIASIS TREATMENT OPTION IN TWO ENDEMIC COUNTIES OF KENYA; A MIXED METHODS STUDY

Authors: Janet M Masaku (Kemri)*; John Gachohi (Jomo Kenyatta University of Agriculture and Technology (JKUAT)); Alice Sickeet (African Institute for Health and Development); Mary Maghanga (African Institute for Health and Developmen); Florence Wakesho (Division of Vector Borne and Neglected Tropical Diseases (DVB/NTDs), Ministry of Health (MoH), Nairobi,); Wyckliff Omondi (Division of Vector Borne and Neglected Tropical Diseases (DVB/NTDs), Ministry of Health (MoH), Nairob); Nora Monnier (Tropical and Public Health Institute, Basel,); Peter Steinmann (Tropical and Public Health Institute, Basel); Lisa Reigl (Technical University of Munich (TUM),); Isabelle Lange (Technical University of Munich (TUM),); Andrea Winkler (Institute of Health and Society,Harvard Medical School, Boston, MA); Sammy Njenga (Kenya Medical Research Institute (KEMRI)); Mary Nyamongo (African Institute for Health and Development)

Background: Treating preschool age children (PSAC) for schistosomiasis has remained a challenge over the years due to lack of a pediatric formulation. In response to this unmet need, the Paediatric Praziquantel Consortium has developed a novel paediatric treatment option. In advance to its roll-out, we conducted a social science study to gather information on preferred drug delivery approaches to inform implementation.

Methods: A cross-sectional study was conducted in eight villages in two purposively selected Kenyan counties: Homa Bay and Kwale. A questionnaire was administered on 690 parents/guardians of PSAC at household level. Preferred drug delivery approaches were analyzed using frequencies and proportions. We conducted key informant interviews with 17 opinion leaders and 28 healthcare workers, and 12 focus group discussions with parents/guardians of PSAC and 7 with community health volunteers (CHVs). Thematic data analysis was performed on the qualitative data.

Results: Majority of the 690 respondents were women 594 (86.1%) with a mean age of 34.1 (SD=11.3, min-max=18-86). Community-based mass drug administration (cMDA) was the most preferred drug delivery method by 598 participants (86.7%), followed by health facility/fixed points by 398 participants (57.7%). Similarly, in the qualitative data study participants in both counties indicated that they would prefer cMDA. The reasons were that CHVs are familiar with households with PSAC and are trusted to explain the drug effects. Also, health facilities/fixed points were the second most preferred drug delivery approach in the qualitative analysis, but there were concerns with understaffing and overcrowding from the healthcare workers category as a limitation for this approach. Timing of the drug distribution was mentioned by all categories of study participants to be very critical, irrespective of the approach used.

Conclusion: All profiles of study participants preferred cMDA over the other delivery approaches due to the convenience of receiving drugs at home and providing explanations about the new drug to the recipients. For positive outcomes, adequate planning, proper timings and community involvement are highly recommended.

Keywords: Schistosomiasis, Pre-school age children, delivery approaches

85.

COMMUNITY SMEARING DAY IN PREVENTION AND CONTROL OF TUNGIASIS, A CASE OF EMANYINYA CU IN EMUHAYA SUBCOUNTY, VIHIGA COUNTY

Author: Fanuel Khaingaa

Background: Antenatal care is a crucial component in maternal and child health as it helps in monitoring and ensuring healthy growth of the pregnancy. Apart from healthcare system factors like distance to health facilities, male partners are a key contributor in reduced ANC attendance since they are majorly the decision makers at the household. This happens since most women seek permission from their male partners before taking action. The objective of the study was to improve access and utilization of ANC services. **Methodology:** Cohort study design was used to select pregnant mothers for the study. 62 pregnant mothers attending clinic at Ekwanda Health Centre were mapped and visitation made to their households by healthcare workers. Their male partners were taken through the importance of attending all the ANC visits. They were then grouped into Father-to-Father groups consisting of 10 people each. These groups were scheduled to be meeting on monthly basis to discuss matters maternal health with the help of a nursing officer from the MCH. “Anzilisha” as a key component was discussed with an aim of making the men understand the care of the mother and the child in the first 1000 days since conception. They were encouraged to be accompanying their female partners for ANC visits and providing any possible support during the pregnancy. Focused Group Discussions were also conducted to asses men’s knowledge on importance of ANC. **Results:** The study showed a large proportion of men had denied their partners a chance to attend antenatal clinics or allowed them to attend only once since they didn’t know the importance. In comparison to ANC data of February 2022, evaluation done in February 2023 showed an immense increase in mothers attending at least 4 ANC visits by 90%. It was also noted that uptake of Iron and Folic Acid Supplements (IFAS) and other health interventions during pregnancy had increased by 85% and unskilled delivery dropped to 1%. It was also noted that most men had feared to accompany their partners to clinic due to stigma and negative community perspective. **Conclusion:** Men involvement in maternal health issues improves uptake of health services by pregnant mothers. Men should be sensitized more on matters maternal health and Father-to-Father groups formed in all the communities as they give men an opportunity to share challenges and experiences thus improving maternal health.

Keywords*:* Community Smearing day, community engagement, behavior change, locally available resources

86.

INFLUENCE OF RADIO PROGRAMS IN CREATING AWARENESS ON COVID-19 PANDEMIC AMONG RESIDENTS OF LUNGA LUNGA SUB COUNTY, KWALE COUNTY, KENYA

Authors: Richard R.K Korir (KEMRI)*

Introduction: The fear associated with misinformation on the reality of Covid-19 was of great public concern during the pandemic. Kenyans thrived on myths regarding corona virus and scientific facts were exaggerated hence had a negative implications which impart fears and mistrusts. This study assessed the influence of radio programs in creating awareness and reactions to covid-19 among residents of Lunga-Lunga Sub County, Kwale County. The study was anchored on cultivation theory as it was concerned with the audience influence on radio programs. Cultivation theory is a sociological and communications framework designed to unravel the enduring impacts of media consumption, with a primary focus on radio in this case. **Methods:** This was a cross sectional research study that was carried out among participants who were radio listeners and were engaging actively in interactive basis. The impact of these interactions was assessed through qualitative methods. Qualitative and quantitative data was collected using structured and semi structured questionnaires. Analysis was done using simple percentages and frequencies.

Results: A total of 100 community members participated in this study giving a response rate of 100% with 51.0% males and 49.0% females. Most (58.4%) participants were farmers while 5.9% were in full time employment. A good number (31) of the participants were fetching water from the rivers while 5.0% were connected with piped water in their houses. All participants were aware of corona virus causing Covid-19 disease in the community and the world at large. However some argued that they had not seen any person who was suffering or had died from the disease in the community. Majority (90.0%) of the participants confirmed that they first knew about the Covid-19 disease through radio programs aired in the local dialect. Discussion: In this study, more than 85.0% of the participants were educated on the need to keep social distance and the benefits of washing hands in order to prevent the spread of corona virus through their preferred radio stations among other preventive measures. In order to prevent the spread of corona virus, 100% of the participants were washing hands, while 90.0% were wearing masks to prevent the spread of the Covid-19 disease. Majority (84.0%) were using mask to prevent themselves from contracting corona virus while some were afraid of police beatings, arrest and quarantine.

Conclusion: We concluded that radio programs helped in creating awareness about Covid-19 pandemic among the community members.

Recommendations: The study therefore recommends the government to aggressively use radio programs in local dialect to create awareness during emergencies and pandemics in future in order to reduce their spread. They can utilize this media strategically before the beginning and the end of any program including news readings.

Key words: Covid-19, awareness, pandemic, influence, participants, radio programs, public health

SCIENTIFIC SESSION 11: VECTOR BIOLOGY-1

87.

FIRST REPORT OF *ANOPHELES STEPHENSI* IN SOUTHERN ETHIOPIA

Authors: Dawit Hawaria (Hawassa University)*

Background: Anopheles stephensi is an emerging urban vector of malaria in East Africa. The World Health Organization recently announced an initiative to take concerted actions to limit this vector's expansion by strengthening mosquito surveillance and control in Africa. This study sought to determine the geographic distribution of An. stephensi in southern Ethiopia.

Methods: A targeted entomological survey, both larvae and adult, was conducted in Hawassa city, Southern Ethiopia between November 2022 and February 2023. Larval anophelines were reared to adults for species identification. CDC light traps and BG Pro traps were used overnight both indoors and outdoors at selected houses to collect adult mosquitoes in the study area. Prokopack Aspirator was employed to sample indoor resting mosquitoes in the morning. Adults of An. stephensi was identified using morphological keys, and then verified by PCR.

Results: Larvae of *An. stephensi* were found in 28 (16.6%) of the 169 potential mosquito breeding sites surveyed. Out of 558 adult female *Anopheles* mosquitoes reared from larvae, 234 (42.7%) were identified to be An. stephensi morphologically. A total of 434 female anophelines were caught, of which 53 (12.2%) were *An. stephensi*. Additional *anopheline* species present in the study area included *An. gambiae (s.l.), An. pharoensis, An. coustani*, and *An. demeilloni.*

Conclusion: The study, for the first time, confirmed the presence of *An. stephensi* in southern Ethiopia. The presence of both larval and adult stages of this mosquito attest that this species has established a sympatric colonization with native vector species such as *An. gambiae* (s.l.) in Southern Ethiopia. The findings underscore the need for more research on the ecology, behavior, population genetics, and role of *An. stephensi* in malaria transmission in Ethiopia.

Keywords: *Anopheles stephensi*, malaria, mosquito breeding, mosquito habitat, Ethiopia

88.

EVALUATION OF PASSIVE COOLING OPTIONS AND VECTOR PROOFING FOR INDOOR HEAT REDUCTION AND MOSQUITO CONTROL IN WESTERN KENYA

Authors: Bernard O Abong'o (Kenya Medical Research Institute (Kemri))*

Introduction: Doors, eaves and fenestrations facilitate heat transfers between the indoor and outdoor environment through stack and cross ventilation and allow light into the house. Unfortunately, these also serve as the entry routes for disease-carrying vectors such as mosquitoes. These fenestrations are usually not oriented or are disproportionate in size to the indoor environment to achieve meaningful cooling. Screening of these openings has the potential of increasing indoor temperatures hence jeopardizing the comfort of the occupants. We assessed the impact of combining passive cooling options with vector proofing for indoor temperature reduction and mosquito control in Siaya County, western Kenya.

Methodology: A randomized control study with ten houses in each arm allocated to either a cool roof, cross ventilation or mat ceiling was used to assess the impact of the modification on indoor temperatures compared to unmodified ones. Houses with passive cooling options were combined with door, window and eave screening. Indoor temperatures were monitored daily using data loggers while mosquito numbers were assessed by indoor CDC light traps collected monthly before and after modification. Community knowledge, attitude, and perception of house modification for temperature and mosquito reduction were assessed using structured questionnaires while an infrared camera was used for thermal imaging of the houses.

Results: The number of An. funestus were 54% lower in screened compared to unscreened houses and 5 lower than before screening. Houses with cool roofs had the lowest mean daily temperature of 26.18°C ±2.80 at the hottest hour of the day compared to control, 28.62°C±3.99 whereas, houses with mat ceilings had the least mean daily temperature variation of between 27.56°C - 25.18°C compared to control 28.62°C-23.38°C.

Conclusion and recommendation: The combination of passive cooling options and vector proofing provides practical opportunities for mitigation of the impact of rising temperatures due to global warming and malaria control in rural African communities. Further investigation is recommended to assess the impact of the modification on health outcomes including sleep quality, heat rate, heat stress and malaria among others.

Keywords: Housing modification, Temperature, mosquitoes

89.

INFLUENCE OF BLOOD MEAL ORIGINS ON REPRODUCTIVE OUTCOMES IN *ANOPHELES GAMBIAE*: ENHANCING FECUNDITY IN A MASS REARING ENVIRONMENT.

Authors: Celestine N Wekesa (KEMRI)*; Eric O Ochomo (Kenya Medical Research institute); Maxwell Machani (KEMRI)

Background: Blood feeding host with sufficient production levels for mass rearing of An. gambiae is indispensable for continuous research operations. High rates in feeding, egg laying, hatchability and survivorship are essential parameters to consider when selecting a blood host for mass production of *An. gambiae*. Rearing *An. gambiae* is faced with challenges of determining the optimal source of blood that results in successful mass production for downstream experiments and colony maintenance. Consequently, the study investigated feeding success, reproduction performance and survivorship of An. gambiae under laboratory conditions for mass rearing. These aspects were compared across five different hosts (cow, goat, sheep, pig and chicken) with the human host as the control.

Methodology: Female An. *gambiae* mosquitoes, aged three days, were provided six host blood meals and subsequently allowed to lay eggs individually. Feeding success was assessed by examining the abdomen's engorgement status, categorized as either fully fed or unfed. Egg laying was established by counting eggs laid by individual mosquito per gonotrophic cycle. The hatchability of eggs was established by counting neonate larvae that hatched and then monitored for pupation rate and time. The emerged adult mosquitoes were monitored for their survival rate and longevity by daily tallying the number of individuals that were alive versus those that had died until the last one.

Results: There was a significant difference across host blood-meal performance when compared with human blood meal. There was no significant difference in feeding success when mosquitoes were provided with pig blood meal (123 ± 7.93 cm, $p<0.010$) versus human blood meal (125.25 ± 3.86 cm, $P<0.010$). Similarly, the average number of eggs laid per mosquito when fed with pig blood meal (100.46 ± 6.36 cm, $p<0.010$) was comparable to that observed with human blood meal (111.65 ± 5.75 cm, $p<0.010$). However, all the blood-meals showed significant difference in hatchability (F (5, 114) = 37.63368, P=1.24E-22), pupation time (F (5,18) =5.532763, P=0.002941) and pupation rates (F (5,18) =8.26, P=0.0003). The mean larval survival rates across different blood meals (F (5,92) = 0.130404, P=0.985079) did not significantly differ between blood groups. Nevertheless, pig blood meal (M=0.5684375, SD= 0.112) survived longer than the rest. Survival rates for the adult F1 *An. gambiae* were significantly different (F (6,346) =133.1909, P= 8.90284E-87) between blood meals. Pig blood meal M= (0.670808, SE= 0.043) survived longer but goat (0.861301± 0.37) had the highest mean surviving at median.

Conclusion: Blood feeding, fecundity and adult survivorship were positively performed in pig blood when compared with human blood meal. This study revealed pig blood meal as the most recommendable host blood for mass rearing and production of *An. gambiae* though it has not been largely investigated.

Keywords: Blood-meal, fecundity, colony, An. gambiae reproduction, mass production.

90.

IDENTIFICATION OF INSECTICIDE RESISTANCE MARKERS IN *ANOPHELES ARABIENSIS* AND *ANOPHELES GAMBIAE* FROM KENYA AND BENIN USING WEIGHTED GENE CORRELATION NETWORK ANALYSIS

Authors: Cynthia Odhiambo

Background: Indoor Residual Spraying (IRS) and Insecticide-Treated Nets (ITN) are the two main methods used to control mosquito populations for malaria prevention. Currently, efficacy of these strategies is threatened insecticide resistance (IR) which may compromise malaria control efforts. Studies of the genetic evolution leading to insecticide resistance could enable an identification of molecular markers that can be used for IR surveillance and an improved understanding of the molecular mechanisms associated with IR. This study aimed to use a Weighted Gene Co-Expression Network Analysis (WGCNA) algorithm, a systems biology method, to identify genes with similar co-expression patterns and hub genes that can be used as molecular markers for insecticide resistance surveillance in Kenya and Benin.

Methods: *Anopheles arabiensis* and *An. gambiae* from Kenya and Benin, respectively, were phenotyped for resistance to alphacypermethrin, permethrin and deltamethrin insecticides. RNA was extracted from unexposed, susceptible and resistant samples followed by Illumina sequencing. WGCNA was conducted on the resulting sequences to evaluate co-expression patterns of genes to identify modules, hub genes and generate a gene co-expression network.

Results: A total of 20 and 26 gene co-expression modules (sft:20,18) were identified via the average linkage hierarchical clustering from *An. arabiensis* (Kenya) and An. gambiae (Benin), respectively. The top modules based on the number of genes in *An. arabiensis* and *An. gambiae* were identified to be salmon (n=3197) and blue (n=3839)

modules. The genes with the strongest connection (hub genes) were found in all modules. Serine protease, E3 ubiquitin-protein ligase, cuticular protein RR2 and leucine-rich immune protein were identified as hub genes in both species. **Conclusion:** This is the first study to conduct WGCNA based on IR transcriptomic data. Four biologically relevant hub genes shared between the two species were identified as potential markers for insecticide resistance. Functional validation of these genes as IR markers should be conducted through in vitro and in vivo studies.

Keywords: Hub genes, insecticide resistance markers, *Anopheles gambiae, Anopheles arabiensis*, Benin, Kenya.

91.

APPLICATION OF MALDI-TOF MS IN PARITY STATUS PREDICTION OF FIELD COLLECTED MALARIA VECTORS

Authors: Mercy J Tuwei (Kemri-Wellcome Trust Research Programme)*; Jonathan Kazungu Karisa (KEMRI-Wellcome Trust Research Programme); zedekiah ondieki ombogo (kemri-wellcometrust research programme); Luis B Constantino (Centro de Investigacao em Saude de Manhica); Gildo Cole (Centro de Investigação em Saúde de Manhiça (Maputo, Mozambique)); Trisa Anastácio (Centro de Investigação em Saúde de Manhiça (Maputo, Mozambique)); Romário Armazia (Centro de Investigação em Saúde de Manhiça (Maputo, Mozambique)); Claida Alves (Centro de Investigação em Saúde de Manhiça (Maputo, Mozambique)); Caroline Kiuru (Barcelona Institute for Global Health, Barcelona, Spain); Caroline Wanjiku (KEMRI Wellcome Trust Research Programme); Regina Rabinovich (Barcelona Institute for Global Health, Barcelona, Spain); Carlos Chaccour (Barcelona Institute for Global Health, Barcelona, Spain); Marta F Maia (KEMRI)

Background: Examining mosquito parity is pivotal in evaluating the efficacy of vector control strategies, influencing mosquito survival. Parity is also used as a surrogate for age. Therefore, it is a crucial indicator of vector potential. Traditionally, parity status is determined through intricate, labour, and time intensive microscopic examinations of ovarioles (Detinova technique). Within a mosquito, physiological processes including egg formation result in quantifiable proteomic changes. Thus, MALDI-TOF MS, a protein profiling approach, is proposed as an alternative to the complex dissections. Here, we demonstrate its utility in predicting the parity status of wild-caught malaria vectors.

Methods: Adult mosquitoes were collected using CDC light traps in Mopeia, Zambezi region of Mozambique. The samples were morphologically identified. A subsample of the unfed female Anopheline mosquitoes were individually dissected, and their ovaries microscopically examined to distinguish parous from nulliparous mosquitoes using the Detinova technique. Remaining mosquito carcases were individually preserved in RNALater™ and transferred to the KEMRI Wellcome Trust Research Programme laboratories for subsequent analysis. In the laboratory, samples were cleaned using 70% ethanol and HPLC water. Cephalothoraxes (head and thorax (HT)) were separated from the carcasses and longitudinally dissected into two halves. One half was allocated for MALDI-TOF MS analysis for age grading and species identification, while the other half was designated for PCR.

Results: Mosquitoes were mainly composed of *An. funestus s.s* (525) and *An. gambiae s.s* (335). Age prediction accuracies was 76% for An. funestus s.s and 89% for An. gambiae s.s. Overall, the age prediction accuracy was 81%, with sensitivity and specificity at 82% (95% CI 0.79-0.85) and 73% (0.63-0.82), respectively. Overall, there was a fair agreement between MALDI-TOF MS and microscopy (Kappa = 0.37 (0.30-0.45).

Conclusions: The study demonstrates MALDI-TOF MS as a promising tool for efficient mosquito parity determination offering potential advancements in vector control strategies.

Keywords: MALDI-TOF MS, Age grading

92.

LATE MORNING BITING BEHAVIOUR OF ANOPHELES FUNESTUS IS A RISK FACTOR FOR TRANSMISSION IN SCHOOLS IN SIAYA, WESTERN KENYA

Authors: Seline Omondi (Kenya Medical Research Institute)*; Jackline Jeruto Kosgei (KEMRI); George Musula (KEMRI); Margaret Muchoki (KEMRI); Bernard O Abong'o (Kenya Medical Research Institute (Kemri)); Silas Agumba (KEMRI_CGHR); Caroline Ogwang (KEMRI); Daniel McDermott (Liverpool School of Tropical Medicine); Martin Donnelly (Liverpool School of Tropical Medicine); Sarah Staedke (Liverpool School of Tropical Medicine); Jonathan S Schultz (CDC-Kenya); Julie Gutman (CDC); John Gimnig (CDC); Eric O Ochomo (Kenya Medical Research institute)

Background: Children in Kenya spend a substantial amount of time at school, including at dawn and dusk when mosquitoes are active. With changing vector behaviour towards early morning biting, it is important to determine whether there is an additional risk of transmission in schools. This study sought to understand whether late morning biting by Anopheles funestus previously documented in households in western Kenya was replicated in schools.

Methods: From the 4th to the 6th of August 2023, human landing collections were conducted hourly in four schools in Alego Usonga Sub-County, Siaya County. The collections were conducted in and outside five classrooms in each school and ran for 17 hours, starting at 18:00 until 11:00 hours the next morning.

Results: *Anopheles funestus* was the predominant species collected, forming 93·2% (N=727) of the entire collection, with peak landing between 06:00 and 07:00 hours and continuing until 1100 hours. All *An. funestus* were identified as *An. funestus* sensu stricto by PCR. More than half of the collected *An. funestus* were either fed or gravid, potentially indicative of multiple bloodmeals within each gonotrophic cycle, and had a sporozoite rate of 2·05%. Other species collected included *An. gambiae* (n=49; 6.3%), An. coustani (n=2, 0.25%) and An. ziemanni (n=2, 0.25%). *Anopheles arabiensis* comprised of 98% An. arabiensis and the rest as An. gambiae s.s. None of the *An. gambiae* s.l. tested positive for sporozoite infectivity.

Conclusion: School children spend up to 10 hours of their daytime in schools, reporting between 06:00 and 07:00 hours and staying in school until as late as 17:00 hours, meaning that they receive potentially infectious mosquito bites during the morning hours. There is a need to consider vector control approaches targeting schools and other peridomestic spaces in the morning hours when An. funestus is active.

Keywords: *Anopheles funestus*; malaria; mosquito behaviour; primary schools

93.

EXPERIMENTAL HUT AND FIELD EVALUATION OF A METOFLUTHRIN BASED SPATIAL REPELLENT AGAINST PYRETHROID RESISTANT *ANOPHELES FUNESTUS* IN SIAYA COUNTY, WESTERN KENYA.

Authors: Silas Agumba (KEMRI_CGHR)*; Margret Muchoki (KEMRI); VINCENT MOSHI (PTBiKenya); Seline Omondi (Kenya Medical Research Institute); Jackline Jeruto Kosgei (KEMRI); Edward Walker (Michigan State University); Bernard O Abong'o (Kenya Medical Research Institute (Kemri)); Nicole Achee (University of Notre Dame); John Grieco (University of Notre Dame); Eric O Ochomo (Kenya Medical Research institute)

Background: Spatial repellents (SR) may complement current vector control tools and provide additional coverage when people are not under their bednets or are outdoors. Here we assessed the efficacy of a metofluthrin based SR in reducing exposure to pyrethroid-resistant Anopheles funestus in Siaya County, western Kenya.

Methods: Metofluthrin, was vaporized using an emanator configured to a liquid petroleum gas (LPG) canister, placed inside experimental huts (Phase 1) or outdoors (Phase 2) and evaluated for reductions in human landing rate, density, knockdown and mortality rates of An. funestus which have high densities in the area. To demonstrate the mosquito recruiting effect of LPG, a hut with only LPG cooker but no metofluthrin was added as a comparator and compared to an LPG cooker burning alongside the emanator and a third hut with no LPG cooker as control. Phase 2 evaluated the protective range of the SR product while emanating from the centre of a team of mosquito collectors sitting outdoors in north, south, east, and west directions at 5, 10 and 20 feet from the emanating device.

Results: Combustion of LPG with a cook stove increased density of *An. funestus* indoors by 51% over controls with no cook stove. In contrast, huts with metofluthrin vaporized with LPG combustion had lower indoor densities of *An. funestus* (99.3% less than controls), with knockdown and mortality rates of 95.5 and 87.7% respectively in the mosquitoes collected in the treated huts. In the outdoor study (Phase 2), the outdoor landing rate was significantly lower at 5, 10 compared to 20 feet away from the emanator.

Conclusion: Vaporized metofluthrin almost completely prevented *An. funestus* landing indoors and led to 10 times lower landing rates within 10ft of the emanator outdoors, the first product to demonstrate such potential. Cooking with LPG inside the house could increase exposure to Anopheles mosquito bites but the use of the metofluthrin canister eliminates this risk.

Keywords: Anopheles funestus, emanator, metofluthrin, spatial repellent, western Kenya

94.

ADDRESSING MALARIA CHALLENGE THROUGH DURABILITY MONITORING OF LONG LASTING INSECTICIDE NETS: RESULTS FOR ATTRITION AND FABRIC INTEGRITY OVER 12 MONTHS OF NET USE IN KENYA.

Authors: Paul PMG Gichuki (KEMRI)*

Background: The use of long-lasting insecticidal nets (LLINs) is a key strategy for malaria control. LLINs are nets pretreated during manufacturing and should retain their efficacy against mosquito for a minimum of 3 years. However, studies have reported that LLINs protective ability declines with time and may be lost before the three years are over. The nets also develop holes with time affecting their contribution to malaria transmission control. The objective of this study is to monitor durability of LLINs distributed in Kenya in 2021 mass net distribution.

Methodology: Repeated cross sectional surveys of LLINs at 12 months of use in households in 5 counties. The LLINs brands included Yorkool® in Kisumu, MAGNet® in Nandi and Turkana and DuraNet® in Kirinyaga and Taita Taveta Counties. The target population was LLINs distributed during the 2021 mass net distribution. LLIN presence and use in the household was observed. Holes on LLIN were assessed and categorized according to WHO classification (holes smaller than a thumb (0.5–2.0 cm), holes between a thumb and a closed fist (2–10 cm), holes between a closed fist and a head (10–25 cm) and holes bigger than a head (> 25 cm).

Results: A total of 1158 LLINs were sampled in the selected clusters. An attrition of 14.8% was reported, with majority of the LLINs (67%) having been given away. Total 39.4 % of the LLINs had at least one hole with lower side having majority of the holes (86.6%). Kisumu had highest LLINs with at least one hole (77.8%). Overall 72.4% of the nets had been washed with a majority using detergent powder (47.0%). A majority 60.2% reported drying the LLINs under a shade.

Discussion: Attrition of 14.8% was majorly attributed to giving away of the LLINs to relatives. A majority of nets did not have holes at 12 months and those which had holes were still in good condition thus offering protection to the users. A good proportion of the nets were dried under direct sunlight which can have an effect on the net.

Conclusion: A majority of the nets were in good condition after 12 months of use thus offering intended protection to the users.

Keywords: Long lasting insecticide nets, attrition, 12 month

SCIENTIFIC SESSION 12:

MCH-2

95.

AN INTERRELATIONAL STUDY ON HYPERTENSIVE DISORDERS IN PREGNANCY AND NEONATAL HEALTH OUTCOMES AT THIKA LEVEL FIVE HOSPITAL, KENYA

Authors: Jared K Ronoh (Mount Kenya University)*

Background: Hypertensive disorders of pregnancy (HDPs) are the major cause of maternal and neonatal morbidity and mortality worldwide. In Kenya, HDPs affect 5 to 10% of expectant women, and are linked to increased risks of adverse maternal and neonatal outcomes. However, there is limited data on the interrelationship between HDPs and neonatal health outcomes in Kenya.

Objectives: The specific objectives were assess the prevalence of hypertensive disorders during pregnancy, to identify the prevalence of neonatal complications associated with normotensive and hypertensive mothers, and to identify the risk factors associated with neonatal complications in those with hypertensive disorders during pregnancy at Thika Level 5 Hospital.

Methods: This was a cross-sectional study. The quantitative and qualitative data was obtained by interviewing 97 mothers who were admitted at the post-natal ward at the hospital between August and December 2023. The data was collected through interviews and questionnaire filling, and then analyzed using SPSS for levels of significance of various risk factors to the incidence of hypertensive disorders, neonatal complications and their interrelationship.

Results: One-third of the respondents reported neonatal complications post-delivery. One-third of the respondents were diagnosed with hypertension during pregnancy. Advanced maternal age (>35 yrs) is associated with a higher risk of experiencing neonatal complications (p = 0.0386). Visiting the antenatal clinics in the first trimester is associated with decreased risk of neonatal complications (p = 0.0235). Term deliveries are associated with a higher risk for neonatal complications (p = <0.0001). Having more than two babies is associated with a higher risk for experiencing neonatal complications (p = 0.0066).

Conclusion: A considerable proportion of participants were diagnosed with hypertensive disorders during pregnancy. Despite some reporting difficulties in accessing antenatal clinics, most respondents had a positive perception of healthcare access and support, with the majority having medical coverage and the ability to access healthcare facilities during emergencies. This study suggests evidence-based policy and practice recommendations, including targeted support for older pregnant women, promoting early pregnancy recognition and timely initiation of antenatal care, investigating the causes of higher risk for neonatal complications in term deliveries, providing specialized care for families with multiple births, and effective management of hypertensive disorders during pregnancy. These findings emphasize the importance of treatments tailored to each population's unique needs and circumstances and encourage further research to refine these recommendations and develop more targeted interventions. This study serves as a call to action for specialists in research, and maternal and child healthcare, to continue exploring and addressing these critical issues.

Keywords: Hypertension in pregnancy, Maternal health, Neonatal health, Pre-eclampsia

96.

IDENTIFICATION OF CHILDREN WITH WASTING USING A FAMILY MUAC SUPPORTED BY A TWO-WAY SMS PLATFOR

Authors: Benson Singa (KEMRI)*; Kirk Tickell (UW); Catherine A Otieno (KEMRI); Mary Masheti (DNDi); Maureen Okello (KEMRI); Agnes Ndirangu (KEMRI=Wellcome Trust); Mame Diakhate (UW); Emily Yashioka (UW); C Levin (UW); Arianna Rubin Means (UW); Esther Choo (UW); Keshet Ronen (UW); Jeniffer Unger (UW); Barbrar Richardson (UW); Christine McGrath (UW)

Background: Effective prevention and identification methods for childhood wasting are increasingly required to achieve global child health goals. Family mid-upper arm circumference (MUAC) programs are an increasingly popular method of identifying children with wasting (low weight-for-height) among Community Management of Acute Malnutrition (CMAM) programs. We assessed the effectiveness of a two-way short message service (SMS) platform (referred to as the Maternally Administered Malnutrition Monitoring System [MAMMS]) coupled with family MUAC measurements in western Kenya.

Methods: In this individual-level, randomized controlled trial in two rural counties in western Kenya, children (aged 5-12 months) were randomly allocated (1:1) to receive either standard care (SOC) or the MAMMS. Eligible participants were children attending maternal child health clinics with a MUAC between 12·5-14·0 cm. All caregivers with eligible children received a talk on child nutrition and a 10-minute standardized training on MUAC measurements before randomization. The MAMMS group received two MUAC tapes and weekly SMS reminders to screen their child's MUAC. The SOC group received routine community health volunteer services and additional quarterly visits from the study team. A follow-up visit was conducted at the study clinic for the caregiver-child dyad at month six. The primary analysis used a Cox proportional hazards model to compare SOC and MAMMS time-to-diagnosis of wasting (MUAC <12·5cm) confirmed by a health professional during a 6-month follow-up. Secondary outcomes were days from enrolment to treatment initiation among children with wasting, the proportion of all children with wasting who were identified by the two approaches (treatment coverage), mean MUAC at treatment initiation, and duration of wasting treatment.

Results: Between August 1st, 2019, and January 31st, 2022, 1,200 children were enrolled in the study. The incidence of confirmed wasting was 37% lower in the MAMMS group (hazard ratio: 0·63, 95% CI: 0·42-0·94, p=0·022). However, among children with wasting, the median number of days to diagnosis was similar between study groups (MAMMS: 63 days [interquartile range (IQR): 23-92], SOC: 58 days [IQR: 22-94]). Treatment coverage in the MAMMS group was 83·3% (95% CI: 39·9-100·0) while coverage in the SOC group was 55·6% (95% CI: 22·3-88·9%, p=0·300). Treatment duration and mean MUAC at treatment initiation were similar between groups.

Conclusion: Family MUAC supported by SMS was associated with a 37% reduction in wasting among young children. Family MUAC, with the support of two-way SMS, may serve as a useful adjuvant or alternative to community health worker-led screening for wasting, as well as a method for preventing wasting in some settings. Empowering caregivers to monitor their child's nutritional status at home may prevent a substantial proportion of moderate wasting. A cost-effectiveness analysis is recommended for strategic Implementation.

Keywords: Family MUAC, childhood wasting, acute malnutrition

97.

EVALUATING THE PROPORTION OF MORTALITY ASSOCIATED WITH UNDER-NUTRITION AMONG UNDER-FIVE YEAR OLD CHILDREN HOSPITALIZED WITH HYPOXEMIA IN UGANDA

Authors: BENARD O OCHIENG (KEMRI/CGHR)*; Michael Hawkes (University of Alberta)

Background : undernutrition exacerbates disease condition and result in many cases of hospitalization and mortality especially in the Low and Middle Income Countries. Research studies have associated high mortality rates among children suffering various conditions with under-nutrition. We used data for the under-five year old children hospitalized with hypoxemia to determine the proportion of deaths associated with undernutrition and to assess clinical, social and demographic predictors of death.

Methods : Under-five year old children admitted at 20 health facilities across Uganda and presenting with cough and/difficulty in breathing were screened using a portable oximeter. Parents of 1,213 children with oxygen saturation < 92% were consented and enrolled. Basic demographic and clinical data were collected from the case admission records and participants were followed up during their hospital admission. The treatment outcome was captured in a binary format of either "death" or "discharge", the dependent variable. Independent variables were constructed based on the World Health Organization growth standards, anthropometric indices, stunting (HAZ < -2SD), wasting (WHZ < -2SD) and underweight (WAZ < -2SD). Pearson and Fischer's exact chi square were used to test independence between the two groups of children who died and those who were discharged. We evaluated the proportions of deaths associated with various conditions and further assessed predictors using bivariate and multivariate logistic regressions.

Results: We analyzed a total of 1,213 records out of which 56% were males. The underweight, wasted and stunted children were 20.7%, 20.7% and 40.6% respectively. Comorbidities included underweight, wasting, stunting, severe malaria, severe pneumonia, diarrhea, severe anemia, cyanosis and HIV, which were attributed to the following proportions of deaths, 6%, 4.8%, 3%, 2.8%, 2.3%, 4.3%, 3.7%, 5.5% and 20% respectively. Predictors for death were underweight, wasting, diarrhea, cyanosis, HIV and wealth index, OR = 3.88 95% CI: 1.72, 8.79; OR = 2.83 95% CI: 1.24, 6.48; OR = 2.49 95% CI: 1.10, 5.64; OR = 2.99 95% CI: 1.31, 6.85; OR = 13.35 95% CI: 1.34, 133.22 and OR = 10.54 95% CI: 3.35, 33.15 respectively.

Conclusion: Under-nutrition poses mortality danger to under-five year old children hospitalized with hypoxemia, therefore, such children require urgent attention upon admission. Other comorbidities that necessitate urgent attention are diarrhea, cyanosis and HIV infection.

Keywords: Undernutrition, Hypoxemia, Comorbidities, Under-five mortality, Uganda

98.

PERCEIVED BARRIERS AND FACILITATORS TO QUALITY CONTRACEPTIVE DECISION SUPPORT FOR ADOLESCENT GIRLS AND YOUNG WOMEN (AGYW) AMONG PHARMACY STAFF: A QUALITATIVE STUDY IN WESTERN KENYA

Authors: Dismas O CONGO (KEMRI CMR_RCTP)*; Maricianah Onono (KEMRI); Elizabeth Bukusi (KEMRI); ELIZABETH Harrington (University of Washington)

Background: Unintended pregnancy significantly impacts the health and well-being among adolescent girls and young women (AGYW) in sub-Saharan Africa. New strategies to engage and support AGYW in utilizing family planning (FP) services in community-based contexts, such as pharmacies, where they may prefer to receive care are needed.

Method: We conducted a formative study using structured in-depth interviews with pharmacy staff at 20 retail pharmacies in Kisumu, Kenya to assess pharmacy-based contraceptive service delivery to AGYW. Purposive sampling was used to select community pharmacies and pharmacy staff that participated in the study. The community pharmacies were selected if they provided at least four FP methods — emergency pills, daily oral pills, and injectable contraceptives, owner supportive of study procedures, and a private consultation area (at least half of the pharmacies). The pharmacy staff were selected for interview if they were able to speak English Kiswahili, or Dholuo fluently, provided contraceptive methods to AGYW, were willing to provide informed consent in English or Kiswahili and the Pharmacy manager/owner was supportive of study procedures.

Audio recordings of interviews were transcribed and thematically analyzed using Dedoose qualitative data analysis software. A codebook was developed deductively based on prior study findings and inductively from emerging transcript themes.

Results: The majority of pharmacy staff emphasized the importance of contraceptive for young women counseling before dispensing FP methods in the pharmacy. Counseling predominantly occurred in private rooms within the pharmacy or in a counter away from the other clients, addressing privacy concerns. Participants cited various barriers to contraceptive counseling in pharmacies, including lack of time, privacy concerns, inadequate training, shortage of personnel to attend to other paying clients, language barriers, and stigma. Additionally, many AGYW are perceived to be in a hurry and decline counseling. Most staff mentioned concerns about overuse of emergency contraception among AGYW, and a desire to better support their contraceptive decision-making. Potential facilitators to offer quality contraceptive decision support were: the provision of IEC materials, guidelines, additional personnel, FP-specific training, private rooms, and subsidizing services. Staff expressed openness to a tablet-based mobile app focused on decision support as a feasible and acceptable approach to improving the quality of care for AGYW.

Conclusion: Participants in this study provided valuable insights into the role of community pharmacies in the provision of contraceptive services among AGYW in Kisumu County. These findings are currently informing the development of a novel adolescent-centered contraceptive decision support tool designed specifically for the retail pharmacy setting.

Keywords: Contraceptives, Counselling, Community Pharmacy, Adolescent girls, Qualitative

99.

MALNUTRITION ASSOCIATED DEATHS AMONG CHILDREN AGED 1-59 MONTHS IN RURAL AND URBAN WESTERN KENYA, FOR THE PERIOD MAY 2017- DECEMBER 2022: FINDINGS FROM THE CHILD HEALTH MORTALITY PREVENTION SURVEILLANCE (CHAMPS) NETWORK

Authors: SAGAM CALEB KIMUTAI (KENYA MEDICAL RESEARCH INSTITUTE CENTER FOR GLOBAL HEALTH RESEARCH)*; Rael Mwando (County Government of Kisumu); Miriam Teagtmeyer (Liverpool School of Tropical Medicine); Edwin Kiplagat Kiplelgo (Kenya Medical Research Institute); Joyce Akinyi Were (KEMRI); Harun Owuor (Kenya Medical Research Institute (KEMRI)); Dickson Gethi (Kenya Medical Research Institute (KEMRI)); Aggrey Igunza (Kenya Medical Research Institute (KEMRI)); Richard O. Onyando (KEMRI-CGHR); Victor Akelo (8Liverpool School of Tropical Medicine)

Background: Despite reduction in global malnutrition rates, malnutrition in developing countries is poorly assessed largely due to insensitive methods used to ascertain related causes of death in such settings. The Child Health and Mortality Prevention Surveillance (CHAMPS) Network uses minimally invasive tissue sampling (MITS) to provide accurate, timely and reliable data for decision-making on the causes of death (CoD) for children under age 5 and stillbirths in high mortality settings in sub-Saharan Africa and South Asia.

Objective: To describe malnutrition associated mortality among children aged 1-59 months enrolled in the CHAMPS Network site in Kenya.

Methods: Health Demographic Surveillance System (HDSS) was used to track under-5 child deaths from Manyatta informal urban setting, Kisumu County and rural Karemo in Siaya County. Parental or primary caretaker`s consent was obtained for MITS procedure. MITs samples were tested for array of etiologies, deceased and maternal clinical records were abstracted, and verbal autopsy data were reviewed by a panel of experts to decide on the CoD.

Results: Between May 2017 and December 2022, CHAMPS Kenya enrolled 911; 888/911 (97.5%) had CoD determined; infants and children accounted for 42.0% (373/888). One hundred and fifty-seven (42.1%) had at least one form of malnutrition as a cause of death (kwashiorkor (5.6%), marasmus (12.1%), marasmic-kwashiorkor (19.6%)). Ninety-eight (62.4%) of the 157 had malnutrition as an underlying CoD, 32 (20.4%) as a morbid condition and 27 (17.2%) as other significant condition. Sepsis, pneumonia and gastroenteritis were the common immediate causes of death among children with malnutrition as an underlying CoD, accounting for 36.2%, 10.6% and 7.5% respectively. Malnutrition was significantly higher in males (p=0.032) and in HIV positive decedents (p=0.005).

Conclusion: Malnutrition remains a major contributory cause of death in infants and children. Therefore, interventions need to be put in place to reduce malnutrition related mortalities.

Keywords: Malnutrition, Causes of death, Mortality

100.

INCIDENCE AND RISK FACTORS ASSOCIATED WITH CAESAREAN SECTION DELIVERIES: FINDINGS FROM A PROSPECTIVE COHORT STUDY IN WESTERN KENYA, 2020-2022

Authors: Edwin Kiplagat Kiplelgo (Kenya Medical Research Institute)*; Richard Omore (Kenya Medical Research Institute); Gregory Ouma (KEMRI); Joyce Akinyi Were (KEMRI); SAGAM CALEB KIMUTAI (KENYA MEDICAL RESEARCH INSTITUTE CENTER FOR GLOBAL HEALTH RESEARCH); Harun owuor (KEMRI); Victor Akelo (Liverpool School of Tropical Medicine)

Background: Caesarean section is a vital life-saving obstetric intervention when deemed medically necessary during childbirth. Globally, one in every five child-births is a C-section and is expected to rise, with nearly a third of all deliveries likely to occur by caesarean section by 2030. The postulated high rates evoke concerns about the use of C-section among the non-emergency cases. This necessitates close monitoring of possible indicators to ensure targeted dissemination of practical recommendations aimed at improving safe delivery. This study sought to determine the incidence of C-section and its associated risk factors.

Methods: Data from a prospective cohort study, Pregnancy Risk Stratification Innovation and Measurement Alliance (PRISMA) in Western Kenya, was collected from a Health and Demographic Surveillance System (HDSS) area. All deliveries with indicated mode of birth as the outcome variable were included in the analysis. Data was analyzed using descriptive statistics and a Mixed-effects Poison regression model.

Results: Incidence rate of C-section delivery from 2461 births was 13.8%. The median maternal age was 25.0 years (IQR: 22.0, 30.0). Increased risk of C-Section was observed among women with multiple pregnancies (RR: 4.00, se = 1.86), history of C-sections (RR: 7.73, se = 2.78), gestation<37 weeks (RR: 2.12, se = 0.70) and ANC visits >3 (RR: 1.82, se = 0.51). Per unit increase in maternal age elevated the risk: (RR: 1.06, se = 0.03). A unit increase in Hemoglobin measurement and maternal height reduced the risk of C-section; (RR: 0.67, se = 0.03) and (RR: 0.95, se = 0.01) respectively.

Conclusion: History of C-sections, multiple pregnancies, and less gestation at delivery increased the risk of cesarean section. To enhance personalized strategies of providing better care to pregnant women, this study recommends sensitization to the adherence of ANC visits and provision of iron supplements to normalize the hemoglobin levels.

Keywords: C-section, Obstetric, Prevalence, Determinants.

101.

MANAGEMENT OUTCOMES OF BURNS IN PEDIATRIC PATIENTS <13 YEARS AT THIKA LEVEL V HOSPITAL, KIAMBU COUNTY, KENYA.

Authors: Alphonce Oyugi, Betty Mukami, Rotich Brian, Valary Akoth, Joseph Arisi and Daisy Iminza

Background: Management outcomes of burns among pediatric patients <13 years pose a significant public health concern. Seldom data exists on the management outcomes of burns at Thika Level V Hospital, which is of great importance in preventing and evaluating the effectiveness of the available management options and pediatric care protocols. The main aim of the study was to evaluate the management outcomes of burns among pediatric patients<13 years old at Thika Level V Hospital.

Methods: A retrospective cross-sectional study design was conducted, analyzing 41 patient files obtained from Thika Hospital's Medical Records Department between January and December 2022. Out of these, 39 complete files were included in the study, while 2 were excluded due to incompleteness. The study focused on age, gender, management options used, and duration of hospitalization. Only complete files with relevant information were included in the analysis. Data were analyzed using SPSS version 15.0, and the results were presented through tables, bar graphs, and pie charts.

Results : The prevalence of burns at Thika Level V hospital was 3%. Burns are more common within the age bracket of 1-3 years 22(56%) with male 23(59%) being affected. Scald burns accounted for 38(97%). Fluid therapy 23(59%) and silver sulfadiazine 33(84%) were the most commonly used management options. Other management options included pain management, nutritional therapy, grafting among others. Mild degree of burns accounted for 31 (79.5%), while 2nd degree superficial burns were mostly reported 34 (87.2%). The average duration of hospital stay was 15 days. Fluid therapy significantly affected the duration of hospitalization. There was a positive correlation between depth of burns and duration of hospitalization (Spearman's rho ($\rho = 0.245$, $p = 0.133$).

Conclusion: Burns contribute to 5% of disability in pediatric patients, with a prevalence of 3% at Thika Level V Hospital. It primarily affects males and children aged 1-3 years. Dermazine is the main management option, and fluid therapy plays a significant role in hospitalization duration, typically less than 10 days. This suggests that prevention at the household level and effective burn management using pediatric protocols are strongly recommended.

Keywords:

1.Burns 2. Pediatric patients 3. Management outcomes 4.Pediatric burn care 5. Healthcare management 6. Pediatric burn injur

SCIENTIFIC SESSION 13: HEALTH SYSTEM – 3

102.

QUALITY ASSURANCE IN THE KENYA POLIO LABORATORY: CELL SENSITIVITY ASSAY, 2022–2023.

Authors: Shadrack Mr. Barmasai (Kenya Medical Research Institute)*; Peter Maritim (KEMRI); Joanne H Hassan (kemri); Mercy A. Onyango (Kenya Medical Research Institute); DIANA WANJIRU WANJIKU (KEMRI); Paul Muchai (Kemri); Jennifer Lewett (KEMRI); Robert Mainga (KEMRI); Agnes Chepkurui (KEMRI); Jimmy Nyangao (KEMRI); Evans Komen (KEMRI); Benlick Mwangi (KEMRI); Fiona Aluoch Alaii (KEMRI); Collins K Cheruiyot (KEMRI); Samira Ali Katembe (KEMRI); Celine Alice (KEMRI); Janet Ngugi (KEMRI); Casey Asigo (KEMRI); Maureen Njihia (KEMRI); Rosemary Nzunza (KEMRI); samoell A Khamadi (KEMRI); Peter Borus (KEMRI)

Background: The Global Polio Eradication Initiative of the World Health Organization relies on cell culture for poliovirus isolation, as it is considered the "gold standard" in virus isolation. False negative results can seriously harm the endeavor to eradicate poliovirus by preventing virus isolation. A key element of the laboratory's quality assurance strategy is the routine assessment of cell lines' susceptibility to virus isolation. Routine testing is done midway through passaging and when fresh cells are resuscitated or received in the laboratory. This gives comfort in knowing that a cell line can still identify polioviruses, even when they are present at low titre. This study summarizes the quality assurance done in a polio laboratory using the polio virus cell lines L20B and Rhabdomyosarcoma (RD).

Method: The laboratory quality-control (LQC) standards of known and reproducible titres (Sabin 1 and Sabin 3) prepared from authenticated Sabin poliovirus reference strains were used to inoculate L20B and RD cell lines. Before the addition of cells, a serial dilution of the standard from 10^-2 to 10^-8 was performed, and a dilution of 10^-5 to 10^-8 was put on a plate for testing. The development of the cytopathic effect (CPE) was examined using an inverted microscope, and daily readings were recorded for 5–7 days. Calculation of the virus titre by the Kärber formula log CCID50 = L – d (S – 0.5) was used, and the results were compared to the known titre of the LQC standards.

Results: Eight (8) sensitivity assays have been done between 2022 and 2023. Sabin type 1 and Sabin type 3 in the RD cell line had an average of 7.75 and 7.31 of virus titre respectively and were within the expected range of 7.26–8.26 and 6.68–7.68 respectively of virus titre. Sabin type 1 and Sabin type 3 in the L20B cell line had an average of 6.81 and 6.43 of virus titre respectively and were within the expected range of 6.36-7.36 and 5.98-6.98 respectively of virus titre.

Conclusion: To isolate poliovirus, the quality of cell lines plays an important role. Microscopic examination of cells cannot be used to identify a decrease in cell sensitivity. Any laboratory using cells should be able to conduct routine cell sensitivity to be able to isolate a virus at very low concentrations to ensure no virus is missed and use cells free from contamination.

Keywords: Epidemiology, Measles, Case-based Survaillance

103.

LABORATORY AND PUBLIC HEALTH COLLABORATION IN PROMPT MANAGEMENT OF COVID 19 CASES THROUGH HOMEBASED CARE AT NYAHERA SUB COUNTY HOSPITAL, KISUMU COUNTY, KENYA

Authors: duncan odhiambo ongayi (ministry of health)*

Background: COVID 19 pandemic posed a lot of danger and led to influx of patients in hospitals leading to scarcity in the bed capacity in several facilities. With the second and third wave of Covid which were a little bit mild, homebased care played a major role in patient care since most of the patients who didn't meet the case definition threshold were discharged and monitored through homebased care with the assistance of community health volunteers. Laboratory department played a very key role by conducting a prompt and real time referral of clients who tested positive for COVID 19 immediately to public health department for line listing of contacts and homebased care assessment for further management.

Methods: This was a Retrospective study of

45 patients that had tested positive with antibody rapid test for Covid 19 were linked to the public health department who in turn worked closely with CHVs (community health volunteers) based at the community to implement and monitor patients on homebased care. The facilities assessed at home were, handwashing facilities, social distance, nutrition, adherence to medication, ventilation and general hygiene.The data was obtained retrospectively and was analyzed in Microsoft excel and presented in percentages.

Results: of the 45 people followed up ,27(60%) were female 15(33,3%)were males while 3(6.7%) were children of median age of 9,59%(n=16)of females were fully vaccinated while only 33%(n=15) of males were fully vaccinated by AstraZeneca vaccine and progressed well . 41% (n-11)had received only one dose. None of the 3(0%) children was vaccinated.

Conclusion: prompt and real time referral of patients to Homebased care led to clients accessing Covid 19 services at home hence an important strategy to achieving epidemic control.

Keywords: COVID 19

104.

WHAT DOES IT TAKE TO INTEGRATE HIV NCD SERVICES IN PRIMARY HEALTH CARE? A CASE STUDY OF NYALKINYI HOSPITAL HOMABAY COUNTY

Authors: JEFF OMONDI ONYACH (MINISTRY OF HEALTH/LVCT)*; Corneleous Edward Okal (Ministry of Health); MIRIAM OGENDO (MINISTRY OF HEALTH)

Background: Kenya is currently experiencing an increasing burden of non-communicable diseases (NCDs) which account for up to 39% of deaths in the country. HIV infection may increase the risk of NCDs due to the stimulation of inflammatory markers and adverse events associated with some antiretroviral medicines for HIV treatment. The recently released Kenya NCD strategic plan (2021-2025) focuses more on strengthening multisector collaboration and partnerships in NCD management.

Homabay County is a high HIV burden County with a prevalence of 15.2. The Primary health facilities have few staff who are responsible for seeing all the patients. In order to successfully manage NCDs amongst HIV patients in primary health care, integration of NCD clinics into the CCC is key in ensuring the quality of care. This is a case study of Nyalkinyi Health centre that have successfully integrated HIV/NCD clinics.

Methodology: Nyalkinyi Health centre staffs were trained on NCD(Hypertension. Diabetes, Asthma, chronic obstructive pulmonary disease and Epilepsy) through the MSF curriculum. Simplified Information Education Communication materials were developed and issued to service providers and Community Health Volunteers for sensitization. The team held weekly consultative technical working groups/mentorship forums with the facility to track progress. NCD commodities such us pharmaceuticals and laboratory investigations were supplied by the County and buffered by Medicien San Frontières (MSF). We also developed Referral SOPs and shared them with Community Health promoters (CHP). We tracked performance on a weekly basis.

Results: A total of 9 health care providers were trained on NCDs (Clinical officers 2, Nurses 4 and 3 lead CHPs) Nyalkinyi H/C has been able to enroll 344 patients. Females were 64.5%. Median age 50.5 IQR (1-89) and 29.4% of patients on follow-up were HIV positive. About 39.2% of the patients have been enrolled in NHIF. The number of cases with Hypertension was 157(45.6%), Asthma 72 (20.9%), Diabetes 69(20.1%), Epilepsy 36(10.5%) and Chronic Obstructive Pulmonary Disease 10(2.9%) cases. The hospital sees an average of 20 patients with NCD each day and has adequate pharmaceuticals and laboratory commodities for the patients. This shows an increase of service delivery to NCD patients which was as low as 7 patients per month before the interventions.

Conclusion: NCD HIV Integration is achievable in primary health care. We recommend training of service providers on NCD management and ensuring a consistent supply of medication as a prerequisite to a successful integration.

Keywords: NCD/HIV INTERGRATION IN PRIMARY HEALTH CARE

105.

UNDERSTANDING THE TREATMENT BURDEN OF PEOPLE WITH CHRONIC CONDITIONS IN KENYA: A CROSS-SECTIONAL ANALYSIS USING THE PATIENT EXPERIENCE WITH TREATMENT AND SELF- MANAGEMENT (PETS) QUESTIONNAIRE

106.

BARRIERS AND SOLUTIONS TO ACCESSING EYE CARE IN MERU COUNTY, KENYA: A MULTI-PHASED MIXED METHODS STUDY

Authors: Sarah Karanja (KEMRI)*; Luke Allen (London School of Hygiene and Tropical Medicine (LSHTM)); David Macleod (LSHTM); Min Kim (LSHTM); Malebogo Tlhajoane (LSHTM); Cosmas Bunywera (Peek Vision Ltd); Lena Koome (Meru County Department of Health); Michael Gichangi (Ministry of Health, Ophthalmic Services Unit); Andrew Bastawrous (LSHTM/Peek Vision Ltd)

Background: Globally, at least 2.2 billion people have vision impairment, with 1 billion preventable or treatable cases remaining unaddressed. Universal access to eye care is essential to universal health coverage and sustainable development goals. Internal data from a large eye screening project in Kenya shows that only 50% of those referred for eye treatment attended referral clinics. This study assessed the barriers and potential solutions to accessing eye services, as perceived by patients screened at the community level and referred to outreach clinics but failed to attend.

Methods: This was a multi-phased mixed methods study. First, we conducted in-depth interviews with non-attenders selected from groups with the lowest attendance rates. We explored their perceptions of barriers and potential solutions to clinic non-attendance. Second, we conducted a telephone ranking survey with a wider group of non-attenders. This group ranked the potential solutions based on their likely impact to improve attendance and access to eye care services. Finally, we held a meeting with eye health stakeholders to obtain their views on which interventions should be prioritized for testing based on likely impact, feasibility, cost, and potential risks. We used purposive sampling to select the in-depth interviews and stakeholders meeting participants while consecutive sampling was used for the ranking survey. Thematic analysis and simple descriptive statistics were used to analyze data.

Results: A total of 46 non-attenders were interviewed in-depth, while 401 participants completed the ranking survey. The stakeholder meeting had an attendance of 15 participants. The reported barriers to clinic attendance included perceived cost of spectacles, distance to referral site, transportation cost, conflicting work and social engagement, forgetfulness, long queues, lack of clear information, and mixed age groups in queues. Solutions proposed included more clinic locations, extended working hours, specifying opening and closing times, mop-up clinics, reduced wait times, text reminders, clarifying services available and the costs, and adequate and sustained stocking of medicines. Stakeholders suggested both individual and clinic-level interventions to address these challenges. At individual level, they recommended enhanced counseling and effective communication at the point of referral and text message reminders. At the clinic level, stakeholders proposed organizing mop-up clinics and creation of distinct queues for women and children, younger individuals, and older individuals as the most practical interventions.

Conclusion: It is imperative for screening projects in Kenya to anticipate and address the barriers that impede non-attenders from utilizing eye care services. The suggested interventions should be tested and, if proven effective, scaled up.

Keywords: Equity, Access, Eye Health, Barriers, Solutions

107.

FEASIBILITY OF PROVIDER COLLECTED AND PARTICIPANT SELF-COLLECTED VAGINAL SWABS AMONG ADOLESCENT GIRLS AND YOUNG WOMEN PARTICIPATING IN HPV VACCINE TRIAL IN SOUTH WESTERN KENYA

Authors: Imeldah N Wakhungu (Kenya Medical Research Institute (KEMRI)- Research Care and Training Programme (RCTP))*; Ruanne Barnabas (Havard University); Maricianah Onono (Kenya Medical Research Institute (KEMRI)); George Omondi Otieno (KEMRI); Nelly R. Mugo (KEMRI); Elizabeth Bukusi (University of Washington)

Background: Adolescents and Young Women (AGYW) face a heightened risk of acquiring sexually transmitted infections (STIs). There is evidence that self and provider collected swabs have comparable performance in STI testing, more so, self-collected swabs are more cost effective and offer privacy. To enhance STI testing and management in this population, we explored convenient screening and testing strategies by comparing the trends in the uptake of provider-collected swabs versus self-collected swabs over an 36-month study (total

8-expected swabs) period. Additionally, we examined the factors influencing the mode of collection and assessed acceptability among AGYW enrolled in an HPV vaccine study in western Kenya.

Methodology: Data for this analysis was drawn from an ongoing randomized clinical trial testing the efficacy of single-dose HPV vaccine among AGYWs in Kenya aged 15-20 years. We enrolled 1200 participants and followed them up every 6 months during which genital swabs were collected. Genital swabs were collected through both provider and self-collected swabs over a period of 21 months. Pelvic exam by providers was encouraged for participants who came for in person visits. We calculated proportions of self-collected swabs, described trend of provider versus self-collected swab over the study period. Multivariable logistic regression was used to analyse predictors of self-collection of swabs.

Results: Analysis involved 1,113 participants aged 15 to 25 years, median age 17 (IQR: 16-18). Most (88%) attained secondary education. Six out of the expected eight swabs, 5/8 (63%) and 4/8 (50%), were self-collected in visits at month 18 and 24 of follow up. A higher proportion of AGYWs aged <18 years consented to self-collection compared to those ≥18 years (73% vs 27%, p < 0.001), and a higher proportion of singles compared to married participants easily consented to self-collection (99% vs 1%, p= 0.008). Participants ≥18 years were 35% less likely to self-collect compared to minors (OR=0.65, 95% CI: 0.50, 0.85), and married women were less likely than singles (OR=0.19, 95% CI: 0.14, 0.91).

Conclusion: This evaluation adds to literature on the acceptability of both provider and self-collected swabs among AGYW. Implementation of both methods in routine practice and in community- holds significant promise for enhancing the screening and management of STIs. The findings advocate for the incorporation of dual collection methods in public health programs to optimize STI prevention efforts and promote the overall well-being of AGYW. This approach could have a substantial impact on public health outcomes.

Keywords: Swabs, self-collected, HPV, AGYW

108.

ASSESSING HEALTH SYSTEM CAPACITIES FOR MATERNAL AND CHILD NUTRITION: A COMPREHENSIVE STUDY OF MERU, THARAKA NITHI, NYERI, NYANDARUA, AND KIRINYAGA COUNTIES.

Authors: Christine W Nderitu (Helen Keller International)*

Background: The Community Health Strategy outlines the delivery of basic health prevention and promotion services in Kenya. Community health volunteers (CHVs) are critical in providing health services at the household and community levels and making referrals to linked community health units (CHUs) and health facilities. CHVs receive their training and supplies at the CHU and health facilities. The objective of this study was to evaluate the services offered by, and knowledge among CHVs pertaining to maternal and child nutrition, and the services, supplies and equipment available and training provided by health facilities within five Kenyan counties.

Methods: A cross-sectional, mixed methods study was conducted involving 71 health workers and 78 CHVs from Meru, Tharaka Nithi, Nyeri, Nyandarua, and Kirinyaga counties. Structured surveys and interviews were employed to gather data on services related to iron supplementation, deworming practices, nutrition counselling, breastfeeding initiation, child anthropometric assessments, and the availability of essential supplies and equipment in healthcare facilities. The study utilized a two-stage sampling technique for quantitative data collection and purposive sampling for qualitative data.

Results: The health worker's survey revealed that 100% of health facilities provided combined iron and folic acid supplements. However, only 31% and 6% of facilities had ready-to-use therapeutic foods for severe and moderate acute malnutrition and supplementary foods, respectively. Only 16.9% of facilities had 50,000 IU vitamin A capsules available. Availability of 100,000 IU and 200,000 IU vitamin A capsules varied significantly across counties (P = 0.000 and P = 0.004, respectively). Health facilities had adult weighing scales, infant scales, and MUAC tapes; however, critical tools like Oral Rehydration Therapy (ORT) corners were only available in 43.7% of facilities. CHVs provided information and counselling on the benefits of the nutrition services to caregivers and delivered Vitamin A supplementation and deworming drugs in the community. The majority of CHVs (82.8%) were trained on the basic CHV modules while less than half (46.6%) were trained on the technical CHV module across the counties.

Conclusions: There is a need for sufficient allocation of resources to ensure consistent supply of essential products, tools, and services, and to strengthen the supply chain management system. Further, healthcare workers need regular training and updates on the delivery of services, including monitoring and reporting to encourage continuous improvement in service delivery. Lastly, CHVs need comprehensive training on the basic and technical CHV modules to build their capacity to both deliver and create demand for services. Moreover, there is need to strengthen collaboration between CHVs and health facilities to enhance delivery of service at the community level.

Keywords: Maternal and Child Nutrition, Community Health Volunteers, Health Care Workers

109.

MISSED OPPORTUNITIES FOR DATA USE IN HEALTH CARE DECISION-MAKING IN KENYA: CROSS SECTIONAL DIGITAL HEALTH LANDSCAPE ASSESSMENT.

Authors: Mercy Terer (KEMRI-CGHR)*; Miriam Taegtmeyer (Liverpool School of Tropical Medicine)

Chepkirui M1,3, Musuva R2, Dellicour S3, Akoth I1, Omondi B1, Barsosio H1, Otiso L2, Okomo G6, Tancred T3, Alhassan Y3, Waweru M4, ter Kuile F1,3, Lesosky M5, Kariuki S1, Taegtmeyer M3

1. Malaria Branch, KEMRI-Center for Global Health Research (CGHR)

2. LVCT Health

3. Liverpool School of Tropical Medicine

4. GIND

5. Imperial College, London, UK

6. Department of Health, Homabay county

Background: Sub-Saharan Countries have a rising uptake of eHealth and mHealth interventions to improve data quality, decision-making, and accelerate healthcare access in the last decade. The proliferation of digital health solutions has led to an e-chaotic situation with electronic medical records (EMR) systems implementation characterized by fragmented implementation, inadequate system linkages, limited data sharing, and reliance on short-term, donor-driven funding. Consequently, there is an exponential growth in health data generation that is underutilized for decision-making, patient-centric care, and research.

Methods: A cross-sectional landscape assessment was carried out in Homabay County in Kenya between June 2022 and Oct 2023 in 113 public health facilities. We used health facility surveys and 33 in-depth interviews with relevant health system stakeholders to map what EMRs were present (and functioning) and explored perspectives on the utility of EMRs for data use in decision-making.

Results: Nine unique EMR systems were identified across the surveyed facilities (1 inactive). Ninety-two percent (104/113) of the health facilities surveyed had KeEMR used for HIV patient care. Seven additional EMR systems (WebADT, USHAURI, Elephant, LIMS, WISECARE, CAREPOINT & FANSOFT) were identified in active use alongside KeEMR. Five out of the eight active EMRs were supported by implementing partners and faith-based organizations. EMR challenges were lack of interoperability, internet connectivity, system downtime, patient workload, power outage, staff turnover, and lack of universal patient identifiers. Data quality checks, reporting, and data reviews were done routinely in 92% of the facilities.

Conclusion: The study findings mirror digital health systems utilization in public health care settings. Despite the heavy skewness towards HIV care and lack of interoperability, there is a huge potential for effective utilization of EMR in low-resource settings. There is a need for the government to take a central leadership in driving EMR implementation, defining scope and purpose to cover the general population. Implementation of a sustainable patient record identification mechanism will allow data sharing amongst platforms and promote inter and intra-facility longitudinal patient follow-up. A centralized secure platform for data access will further facilitate data uptake and use for public health research and decision-making. A journey that will involve developing standardized data quality protocol to enable good quality data use for health care decision making.

Keywords: Digital health, electronic medical records , data sharing, decision making, big data

110.

AVAILABILITY AND UPTAKE OF CERVICAL CANCER SCREENING AND TREATMENT SERVICES AT 19 KENYAN HEALTH FACILITIES

Authors: Catherine M Wexler (University of Kansas Medical Center)*; May Maloba (Global Health Innovations); Natabhona M Mabachi (DARTnet Institute); Nicodemus Maosa (Kenya Medical Research Institute); Shadrack Babu (Kenya Medical Research Institute); Vincent Staggs (IDDI); Sharon Mokua (KEMRI); Kathy Goggin (Children's Mercy Kansas City); Sarah Finocchario-Kessler (University of Kansas Medical Center)

Purpose: In 2012, Kenya announced its commitment to prioritizing cervical cancer (CC) services with the National Cervical Cancer Prevention Program. However, gaps in implementation remain, causing suboptimal uptake. The goal of this manuscript is to provide a

situational analysis of 19 government health facilities in Kenya to assess facilities' capacity to provide CC screening and treatment.

Methods: We conducted a retrospective data review at 19 health facilities in Siaya and Busia counties of Kenya from September 2021-September 2022 to assess availability and uptake of CC services. Key variables included hospital volume, positivity, and numbers of women screened, treated, and referred. Notes were taken to document challenges with service provision and data collection. The retrospective review informed site matching for a proposed cluster-randomized trial.

Results: Across the 19 facilities, 1.2%-70.3% of the women enrolled in care at the hospital were screened during the data collection period. Positivity ranged from 0.4%-13.1%. Of the 19 facilities offering CC screening, five lacked the required equipment to provide same-day treatment; and complex referral pathways were noted for women needing to seek care elsewhere. Several challenges that impact the provision of guidelines-adherent CC care were noted, most notably inconsistent documentation, lack of coordination between multiple screening points, complex referral pathways, and inadequate hospital resources.

Conclusion: Gaps noted were low screening rates and opportunities to improve the efficiency of CC services; structural limitations in implementing the screen-and-treat approach; and poor documentation of cervical cancer services and outcomes. Urgent action is needed to ensure all facilities offering CC screening are equipped with the personnel, supplies and equipment necessary to conduct guideline-adherent same day cryotherapy or thermal-ablation treatment and improve documentation at the facility level to track CC services across the cascade of care.

Keywords: Cervical cancer

111.

SOCIO-BEHAVIORAL FACTORS INFLUENCING SCABIES INFESTATION AMONG CHILDREN UNDER 5 YEARS OF AGE IN KWALE COUNTY, KENYA

Authors: Mariam Macharia (KENYA MEDICAL RESEARCH INSTITUTE)*; Charles Nzioka (University of Nairobi); Bridget Kimani (KEMRI); Doris Njomo (KEMRI)

Background: Scabies, an ecto-parasitic disease caused by mites, is estimated to globally affect over 300 million people living in the tropics and especially in overcrowded places. The disease is highly prevalent in children, the aged and immuno-compromised individuals. In Kenya, scabies is listed as a common water-washed disease with studies showing a prevalence of 8.3%. The World Health Organization has listed it as one of Neglected Tropical Disease (NTDs) targeted for elimination by 2030. Creating awareness on hygiene practices, community support and behavior change are essential for successful elimination. The objective of this study was to assess the socio-behavioural factors influencing scabies infestation in children under five years of age in Kwale County.

Methods: This was a mixed methods cross-sectional survey conducted in six villages of Kwale County that were selected after review of the County's "Diseases of the skin" Pivot Report. A close-ended questionnaire was administered to 301 purposively selected caregivers of children under 5 years with observed signs of scabies or reporting a scabies infestation in the last six months. A total of 4 focus group discussions with community members stratified by age were conducted. Quantitative data was analyzed using Stata version 15.0 and qualitative data by NVIVO version 12.

Results: Scabies infestation was more common in boys (51.8%) than in girls (48.2%). A majority, 56.8% of the infested children were below 36 months of age. The main mode of transmission reported by 59.8% of the respondents was skin contact with an infected person. Itching and lack of sleep for children were the most common symptoms and main consequence of scabies reported by 90.4% and 77.1% of the respondents respectively. Slightly over half of the respondents (54.2%) associated causality with personal hygiene while, 41.5% of them were not aware of the causes. Among the respondents 54.3% of them indicated that they delayed seeking medical care, of these 91.7% reporting that they sought treatment from the local health facilities. The qualitative results showed that there was stigma related to scabies and it was viewed as a sign of HIV and AIDS disease.

Conclusion: There is a need to provide correct information on scabies especially its causes, prevention and management. Behavior change communication with emphasis on good hygiene practices, early detection and treatment is an important step towards scabies elimination.

Keywords: Scabies, Neglected Tropical Diseases, awareness, perceptions, practices, Kwale County

SCIENTIFIC SESSION 14: RISING STAR AWARD-2

112.

CHARACTERISATION OF PROTEUS MIRABILIS ISOLATES FROM TICKS COLLECTED IN ISIOLO COUNTY, KENYA

Authors: Bryson B Kimemia (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI)*; Lillian Musila (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Lang'at Solomon (Centre for Virus Research, Kenya Medical Research Institute (KEMRI)); Erick Odoyo (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Stephanie Cinkovich (United States Armed Forces Health Surveillance Division, Global Emerging Infections Surveillance Branch); Samoel Khamadi (Centre for Virus Research, Kenya Medical Research Institute (KEMRI)); Jaree Johnson (United States Armed Forces Pest Management Board); Timothy Egbo (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Elly Ojwang' (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Eric Garges (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Fredrick Eyase (US Army Medical Research Directorate-Africa)

Background: Ticks are responsible for the transmission of bacteria that cause several human diseases. Previous studies conducted in Kenya have identified many of these bacteria. However, since these studies used molecular screening, they only identified the bacteria without determining viability. Using 16S ribosomal ribonucleic acid (rRNA) sequencing, Proteus mirabilis was identified from ticks collected in Isiolo County. Consequently, the identified bacteria were isolated and characterized.

Methods: Tick homogenates suspected to contain P. mirabilis were cultured on Cysteine Lactose Electrolyte Deficient agar, Sheep Blood Agar (SBA) and MacConkey Agar. Gram staining and microscopy was done before identification and Antimicrobial Susceptibility Testing (AST) done on the Vitek® 2 system. DNA extraction was then performed, and Whole Genome Sequencing (WGS) done on an Illumina MiSeq. Quality control was done on the reads using BBDuK, assembly using SPAdes and Ribosomal Multi-Locus Sequence Typing (rMLST) using the PubMLST platform. Genome annotation was done on PROKKA and Bacterial and Viral Bioinformatics Resource Centre (BV-BRC) platform to identify Virulence Factors (VFs) and Anti-Microbial Resistance (AMR) genes. Phylogenetic analysis was carried out based on core-genome Single Nucleotide Polymorphisms of the study isolates and 64 other isolates obtained from BV-BRC database. Maximum likelihood phylogeny was inferred in IQTREE 2, using 5000 bootstrap replicates.

Results: The isolates as were morphologically characterised as gram negative, non-lactose fermenting and gamma haemolytic cocci. They had mucoid, convex, and medium sized colonies. They all had been recovered from Hyalomma dromedarii ticks. The isolates were biochemically identified as P. mirabilis which was corroborated by rMLST. They were all determined to be closely matched to the rST-227184 profile. The isolates lacked motility indicated by the lack of swarming on both SBA and MacConkey agar. WGS analysis showed that all the isolates had the cheY, fliM, and flhC genes which are involved in motility. However, this genetic finding does not to translate into their phenotypes. In addition, 8 more VFs were identified in the isolates according to the Virulence Factors Database (VFDB). The isolates were found to harbour the tetJ and arnA AMR genes against tetracyclines and Colistin respectively. These genes were expressed and conferred phenotypic when tested with the Vitek® 2 system. The system also flagged the production of Extended Spectrum Beta Lactamases by all the isolates. Phylogenetic analysis of the isolates revealed that they clustered in a clade with isolates collected from humans and pigs, suggesting a possible zoonotic link.

Conclusion: The current study implicates ticks as carriers of viable P. mirabilis. While the competency of H. dromedarii ticks to transmit P. mirabilis between hosts has yet to be determined, there is a potential risk of zoonotic spillover to humans.

Keywords: Tick-Borne Diseases, Vector Borne Diseases, Bacterial Diseases, Proteus mirabilis, One Health

113.

MIXED EFFECTS MODELS IN THE ANALYSIS OF EPSTEIN-BARR VIRUS SEROLOGICAL RESPONSES IN CHILDREN FROM CHULAIMBO, WESTERN KENYA

Authors: Onditi Ian Arao (KEMRI)*; Bonface Ariera (KEMRI-CGHR); Emmily Koech (KEMRI-CGHR); Kevin Waomba (KEMRI-CGHR); Stellah A Chumbe (Maseno University/KEMRI); Jackson Conner (University of Colorado); Katherine Sabourin (University of Colorado); Sidney Ogolla (KEMRI-CGHR); Rosemary Rochford (University of Colorado)

Background: Mixed effects models are feasibly the most preferred techniques in longitudinal data analysis since they flexibly accommodate complex correlation structures, irregularly spaced visits, missing data and mixtures of time-varying and static covariate events which, often complicate the process of analyzing the data. There exist two classes of mixed effects models; linear mixed effects models (LMMs) and nonlinear mixed effects models (NLMMs). Despite the common use of NLMs in the analysis of serological responses, the interpretation of its model parameters in comparison to LMM might not be straight forward due to the conditional mean of its responses being dependent on the random effects in a nonlinear way. Whether LMMs performs sufficiently in scenarios particularly

suitable for NLMMs was therefore evaluated in this study.

Methods: Using EBV specific anti-VCA and anti-EBNA1 IgG data generated using multiplex bead-based assay from samples collected at birth, 6, 10, 14, 18 and 24 weeks from infants born to mothers with (MEU) and without (MUU) malaria infection during pregnancy, model performance was evaluated using Pearson correlation by analyzing observed versus predicted anti-VCA and anti-EBNA1 IgG levels extracted from LMM and NLMM.

Results: Correlations between observed versus predicted VCA and EBNA1 IgG levels demonstrated the competent performance of LMM in fitting both VCA and EBNA1 IgG responses; r: 0.89 and 0.72 respectively compared to NLMM; r: 0.94 and 0.88.

Conclusion: These findings suggest that LMMs performs sufficiently in a scenario particularly suitable for NLMMs, hence reduced specification errors that may lead to invalidated research findings.

Keywords: Malaria exposure, IgG, Epstein-Barr Virus

114.

GENOTYPIC AND PHENOTYPIC PROFILES OF ANTIMICROBIAL RESISTANCE IN PATHOGENIC BACTERIA ISOLATED FROM SEPTICEMIC PATIENTS IN WESTERN KENYA

Authors: Joseph Khamisi Kaingu (U S Army Medical Research Directorate-Kenya/ KEMRI)*; Gathii Kimita (WRAIR-Africa); Amos Onditi (KEMRI/WRAIR-Africa); Kirti Tiwari (KEMRI/WRAIR-Africa); James Nonoh (Maseno University); Carolyne Kifude (KEMRI/WRAIR-Africa); John N Waitumbi (KEMRI/Walter Reed Project)

Background: Antimicrobial resistance (AMR) is a significant global health threat that is estimated to cause 700,000 deaths annually. In Western Kenya and the Lake Region, many hospitals lack adequate AMR testing, with a few relying solely on cultures for bacterial identification without capability for antimicrobial susceptibility testing (AST). In addition, the current phenotypic AST face limitations such as delays and inability to capture the rapidly emerging resistance mechanisms. To address these challenges, we compared the performance of phenotypic AST and whole genome sequencing (WGS) in generating useable AMR profiles in patients with septicemia.

Methodology: This was a retrospective study that utilized WHO-GLASS pathogenic bacterial isolates from the Western and Lake Region County Referral Hospitals (2022- 2023). BD Bactec 9050 and BD Phoenix 100 system were used for blood culture incubation, phenotypic identification and AST. DNA was extracted from the bacteria cultures using the ZymoBIOMICS DNA/RNA Miniprep Kit, followed by WGS using the rapid PCR barcoding kit on the Oxford Nanopore Technologies platform. Bacteria identification was done in EDGE Bioinformatics while detection of AMR genes was done in abritAMR and RGI.

Results: Out of 960 blood cultures, 12.8% (123) had bacteria growth, of which 17/123 (13.8%) had pathogenic bacteria on BD Phoenix. Of the 17, 13 were gram negative (Escherichia coli, n=4; and Salmonella typhi, n=9), while 4 were gram positive (Staphylococcus aureus, n=3 and Streptococcus pneumoniae, n=1). WGS differed from culture only in the identity of S. typhi that was identified as S. typhimurium. Phenotypically, 2/4 E. coli isolates exhibited resistance to all the antibiotics tested. By WGS, these two isolates had a battery of resistance genes, including multidrug resistant (MDR) efflux genes. The other 2 E. coli isolates were completely susceptible to all the tested antibiotics but were found to harbor multiple MDR efflux genes. Salmonella isolates were resistant to multiple antibiotics and by WGS, had multiple MDR efflux genes. 8/9 S. typhi isolates were resistant to Trimethoprim-Sulfamethoxazole but the associated AMR gene was not detected. S. aureus was resistant to Ampicillin, Trimethoprim-Sulfamethoxazole and Penicillin while S. pneumoniae was generally susceptible, but their genotypic AMR were inconclusive due to low reads.

Conclusion: The phenotypic and genotypic identification of bacteria species was concordant, except for the nine S. typhi that WGS classified as S. typhimurium. We noted that BD Phoenix does not have S. typhimurium and most likely phenotypic characteristics of S. typhi resemble S. typhimurium. This study also revealed important disparities between phenotypic and genotypic calls for the presence of AMR.

Keywords: Blood bacteria cultures, AST, AMR, MDR, WGS

115.

MICROSPORIDIA MB RELATIONSHIP WITH ASSOCIATED MICROBIOTA IN THE MIDGUT AND OVARIES OF *ANOPHELES GAMBIAE AND ANOPHELES FUNESTUS*

Authors: Mark T Kivumbi (KEMRI-Wellcome Trust Research Programme)*; Kelly Ominde (KEMRI-Wellcome Trust Research Programme); Haron Musani (KEMRI-WELLCOME TRUST); Leonard Ndwiga (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi); Jonathan Kazungu Karisa (KEMRI-Wellcome Trust Research Programme); Caroline Wanjiku (KEMRI-WELLCOME TRUST); Caroline Kiuru (ISGLOBAL); Lynette Ochola-Oyier (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi); Joseph Mwangangi (KEMRI); Jeremy K Herren (icipe); George Githinji (KEMRI-WELLCOME TRUST); Martin Rono (KEMRI - Wellcome Trust Research Programme); Marta F Maia (KEMRI)

Introduction: Mosquito microbiota are commensal, pathogenic or mutualistic microorganisms located inside and outside of mosquito tissues. They play several roles in the mosquito including growth promotion, digestion, immunity, reproduction and nutrient acquisition. Mosquito microbiota can influence vector competence by altering susceptibility to infection, immune stimulation, or direct inhibition through competition. Microsporidia MB is a naturally occurring symbiont in mosquitoes that can be maternally inherited. It has been associated with blocking Plasmodium transmission. These make a strategic potential candidate for malaria vector control. There is limited knowledge on the composition and diversity of microbiota hosted in midgut and gonads of Microsporidia MB infected *Anopheles* mosquitoes.

Methods: Mosquito DNA was retrieved from the biobank. The mosquitoes were collected in Kwale county, Kenya. Mosquito species identification was by morphology, MALDI-TOF MS and PCR. DNA was extracted using the TRIzol protocol. Screening for Microsporidia MB using conventional PCR targeting the 18S rRNA gene. 24 positive midgut samples and 24 positive ovary samples, 23 negative midgut samples and 23 negative ovary samples were selected for 16S rRNA gene amplification, targeting the V1 to V9 region using 27'F and 1492'R primers. Library preparation was done using the Oxford Nanopore Native barcoding kit 96 v14 and sequencing done on the Grid ION. The raw sequences were trimmed to remove adaptors and primers. Taxa classification and taxa counts were generated using EPI2MElabs/16s-wf pipeline using minimap2 and NCBI 16S and 18S reference databases. Downstream analysis was performed on R version 4.2.2.

Results: Microsporidia MB only had a significant impact on the microbial evenness in the mosquito ovaries. However, the known important bacteria taxa like *Asaia, Pseudomonas*, *Klebsiella, Pantoea* and *Enterobacter* that are known to be of importance to the mosquito survival were not affected by its presence in both compartments. Nevertheless, there were some notable changes. First, there was a reduction in the relative abundance of Gammaproteobacteria in the MMB positive samples. Secondly, Microsporidia MB was negatively correlated with Stenotrophomonas in both midguts and ovaries and Zymobacter genera in the midgut whereas there was a positive correlation with *Shinella* and *Vogesella* genera in the ovaries.

Conclusion: These findings suggest that Microsporidia MB does not have an overall negative impact on the microbial ecosystem of the mosquito midguts and ovaries. The reduction in Gammaproteobacteria was compensated for an increase of Betaproteobacteria which belongs to the same phylum and has similar roles in the ecosystem. *Stenotrophomonas* is associated with antifungal protection in arthropods and Zymobacter is associated with pyruvate metabolism. *Shinella* protects against phytochemicals in nectar and *Vogesella* for sugar metabolism.

Keywords: Microsporidia MB, Microbiota, *Anopheles* mosquitoes

116.

DESIGN AND OPTIMIZATION OF A MALARIA PF/PAN ANTIGEN DETECTION KIT IN KEMRI, KENYA; ADVANCING HEALTHCARE THROUGH LOCAL MANUFACTURING OF MEDICAL DEVICES

Authors: Abdiaziz A Gosar (KEMRI)*; Matoke Damaris (KEMRI); Lameck Motari Nyabuti (Kenya Medical Research Institute); Kevin Thiongo (KEMRI); Maureen Otinga (KEMRI); Francis T Kimani (KEMRI); James H. Kimotho (Kenya Medical Research Institute)

Background: Malaria is a global health concern with 219 million cases and 409,000 deaths reported in 2019 by WHO. Most cases occurred in Sub-Saharan Africa, specifically Kenya with 3.5 million cases and 10,500 deaths. Prompt and accurate malaria diagnosis is crucial for control and elimination. While microscopy is the recommended diagnostic method, it has limitations in low-resource settings. Rapid Diagnostic Tests (RDTs) have been developed as an alternative to microscopy. In Kenya, the demand for malaria RDTs is estimated at 4 million tests per year. This study aimed to develop a locally produced Malaria Pf/Pan rapid diagnostic kit using pHRP II and pLDH antigens.

Methodology: Anti-pHRP II and anti-pLDH monoclonal antibodies were conjugated to 20nM colloidal Gold suspension, dried using a lyophilizer, and coated onto a nitrocellulose membrane with a spraying machine. The conjugates were then blocked and dried. The kit's performance was evaluated using positive and negative malaria samples, with 27 positive and 22 negative samples tested.

Results: Out of 27 positive malaria samples, all tested positive overall, 89% for Pf, and 100% for Pan. All 22 negative samples tested negative. The kit demonstrated a sensitivity of 100% overall, 89% for Pf, and 100% for Pan. The specificity was 100%.

Discussions: The study successfully developed a prototype of a Pf/Pan malaria detection kit with 100% sensitivity and specificity. Further optimization is required to determine the optimal protein dilution for cost-effective production and to consider the use of proteins circulating in Kenya, accounting for mutations in HRP II/III proteins.

Conclusion: The study successfully produced a prototype of a malaria Pf/Pan antigen rapid detection kit, requiring further evaluation.

Keywords: Malaria, Antigen, Rapid Kits, Pf, Pan

117.

ISOLATION AND CHARACTERIZATION OF ENVIRONMENTAL LYTIC BACTERIOPHAGES AGAINST ENDEMIC MULTIDRUG-RESISTANT *ENTEROCOCCUS FAECALIS AND ENTEROCOCCUS FAECIUM* IN KENYA

Authors: Oumarou Soro (Pan African University for Basic Sciences, Technology, and Innovation (PAUSTI))*; Lillian Musila (KEMRI); Andrew Nyerere (JKUAT)

Background: Enterococcus faecalis and Enterococcus faecium, Gram-positive cocci, are a growing cause of nosocomial and antibiotic-resistant infections. Treating drug-resistant E. faecalis and E. faecium requires novel approaches. This study aimed to isolate and characterize lytic bacteriophages (phages) from wastewater in Kenya, evaluate their antibacterial activity against planktonic strains and biofilm formers of clinical multidrug-resistant (MDR) E. faecalis and E. faecium isolates, and establish their genomic characteristics.

Methods: In total, 26 MDR E. faecalis and 11 MDR E. faecium were used to screen for phages from water sampled from Ruai sewage plant, JKUAT dam, Kibera, and Kahawa sewage using spot assays. Phages were purified using plaque assays and phenotypically characterized by host range tests, temperature, and pH stability assays. The crystal violet biomass assay was used to study the phage's effect on biofilm formation and disruption. The genomes of 17 phages were sequenced on the Illumina MiSeq platform. The quality of the raw reads was assessed using fastqc v0.12.1, trimmed with fastp v0.23.4, and assembled with shovill v1.1.0. Genome annotation was performed using pharokka v1.5.1, and lysogeny genes were predicted using the PhageLead platform.

Results: Five E. faecium and 17 E. faecalis phages were isolated. The host range test showed that 10/17 E. faecalis phages had lytic activity against at least 50% of the E. faecalis strains, but the E. faecium phages only lysed the host bacteria. All phages remained infective against their host bacteria at temperatures between -80^{o}C and 50^{o}C and pH between 5 and 11. The biofilm formation assay showed that 24/26 E. faecalis and 1/11 E. faecium isolates could form biofilm. All E. faecalis phages inhibit and disrupt the biofilm of their host. Genomic analyses showed that all the phages belong to group I of Baltimore's classification and varied in length from 17,979 to 147,374 bp, with G+C contents ranging from 33.14% to 40.05%. The genomes contained 28 to 250 coding sequences. Phages were classified into the families Rountreeviridae (2/17), Herelleviridae (2/17), and unclassified (13/17). They lacked AMR, virulence, and lysogeny genes, suggesting they are strictly virulent and have therapeutic potential.

Conclusion: This study demonstrates that natural phages against *Enterococcus sp.* exist in diverse environments in Kenya and that biofilms are associated predominantly with E. faecalis infections. These phages are promising candidates for phage therapy and biofilm control and could be used singly or in cocktails to target endemic *E. faecalis* and *E. faecium* infections.

Keywords: Bacteriophage, multidrug-resistant, *Enterococcus faecalis*, *Enterococcus faecium,* biofilm

118.

COMPARISON BETWEEN SANGER SEQUENCING AND OXFORD NANOPORE SEQUENCING OF POLIOVIRUSES: THE KEMRI POLIO LABORATORY EXPERIENCE.

Authors: Mercy A. Onyango (Kenya Medical Research Institute)*; Joanne Hassan (KEMRI); Agnes Chekurui (KEMRI); Rosemary Nzunza (KEMRI); Evans Komen (KEMRI); Stephen Ochieng Ombija (Kenya Medical Research Institute); Robert Mainga (KEMRI); Janet Ngugi (KEMRI); Samira Ali Katembe (KEMRI); Jenniffer Lewett (KEMRI); Diana Wanjiru (KEMRI); Paul Muchai (KEMRI); Shadrack Mr. Barmasai (Kenya Medical Research Institute); Peter Maritim (KEMRI); James Nyangao (KEMRI); Benlick Mwangi (KEMRI); Collins K Cheruiyot (KEMRI); Maureen Njihia (KEMRI); samoell A Khamadi (KEMRI); Peter Borus (World Health Organization)

Background: Poliovirus (PV) isolates are taken through genetic sequencing to confirm detection, source, monitor geographic trends in transmission and establish vaccination strategies. The increasing incidence of circulating vaccine-derived poliovirus (cVDPV) infections, has highlighted necessity of genetic sequencing and analysis at country level to improve detection and response timeliness.

Kenya Medical Research Institute EPI laboratory is responsible for region-wide diagnosis of poliovirus by virus isolation in cell culture and intratypic differentiation (ITD) through Polymerase Chain Reaction (PCR) techniques. Sanger Sequencing of the PV VP1 capsid region is carried out at a separate laboratory in Atlanta to confirm poliovirus detection and distinguish cVDPV from vaccine strains.

We undertook a comparative study in the KEMRI lab to compare sequencing similarity between Oxford Nanopore sequencing of Polioviruses from stool samples and compared it to the gold standard Sanger sequencing results from our reference lab in Atlanta.

Methods: 48 stool samples, between July-November 2023, which were positive on L20B and RD cell cultures, were typed by ITD qPCR to identify their serotype in accordance to the WHO standard algorithm. Of these, 19 samples containing PV type 2 had the VP1 region sequenced using both platforms. Where consensus cVDPV2 and Sabin 2 VP1 sequences were available from both nanopore and Sanger sequencing of culture isolate for the same sample, the similarity of the sequences generated was determined.

Results: The percentage of similar nucleotide results for PV VP1 sequencing from Nanopore and Sanger sequencing for the 19 samples with results for both methods was 18/19 (94.73%). The only sample with the differing results had 51 reads for PV type 2, which was just above the cut off (50) for a consensus on nanopore, which explains why it was not scored as a PV 2 virus. However, the second specimen collected from the same patient that underwent the same culture process, had identical results on both sanger and nanopore. Additionally, a comparison between virus extraction starting material as stool suspension (extract) versus cell culture supernatant (isolate) was tested on two samples. One sample yielded 100% similar nucleotide sequence results in both isolate and extract, while the second yielded a 2-nucleotide difference between the extract and isolate.

Conclusion: After sequencing, 18/19 isolates yielded 100% similar VP1 nucleotide sequences on both methods. Nanopore sequencing therefore gives highly similar results as those obtained by the gold standard, Sanger. Another advantage of Nanopore sequencing is it allows the identification of multiple polio serotypes from a single sample, which is problematic for the sanger method. Furthermore, at analysis, it enables rapid identification of contamination during the assay. Overall, it is fast and easy to conduct at the lab and therefore improves the timeliness of results generation.

Keywords: polioviruses, oxford nanopore, sanger, VP1

119.

COMPARATIVE EVALUATION OF THE AUTOMATED VITEK 2 AND MICROBROTH DILUTION METHODS ON COLISTIN ANTIBIOTIC SUSCEPTIBILITY TEST RESULTS

Authors: Allan Barasa Wataka (USAMRD-A KEMRI)*; Michelle Atieno Omondi (USAMRD-A/KEMRI); Erick Odoyo (USAMRD-A KEMRI); Lillian Musila (USAMRD-A KEMRI)

Background: Colistin is a polymyxin polycationic antibiotic used as a last-resort antibiotic for treating infections caused by multi-drug resistant (MDR) gram-negative bacteria, including Pseudomonas aeruginosa and Acinetobacter baumannii. Given the global rise in colistin resistance, monitoring its antibiotic resistance is important to evaluate its clinical utility. In Kenya, colistin is not routinely tested but is included in automated platforms such as the VITEK 2 and could be reported for clinical use. However, the Clinical and Laboratory Standards Institute (CLSI) does not recommend VITEK 2 for colistin testing and has recently changed the interpretation breakpoints significantly. Misreporting results may cause treatment failures or withholding of an effective drug, leading to unnecessary mortality for patients with MDR infections. In this study, we compared colistin susceptibility using the CLSI-recommended microbroth dilution method

(MBD) and the VITEK 2 to determine the potential impact of incorrect testing on therapeutic decisions.

Methods: We retested 57 gram-negative clinical bacterial isolates that were colistin-resistant on the VITEK 2 GN AST Card. The isolates were 44 *Pseudomonas aeruginosa, 5 Acinetobacter baumannii, 4 Enterobacter spp, 1 Myroides sp., 1 Aeromonas hydrophila/caviae*, 1 *Klebsiella pneumoniae* and 1 *Sphingomonas paucimobilis.* We included *E. coli* ATCC strain 25922 as the negative control and Proteus mirabilis(intrinsic resistance) as the positive control. The isolates were tested in a microbroth dilution assay using Cation-Adjusted Mueller Hinton Broth (CAMHB). Concentrations of 0 µg/ml, 1 µg/ml, 2 µg/ml and 4 µg/ml were achieved by adding appropriate numbers of 10 µg colistin disks to the media in tubes to which 50µl of the bacterial suspension was added and incubated for 16-20hrs at 35°C. The minimum inhibitory concentrations were obtained, interpreted per the CLSI guidelines 2022, and compared with the VITEK 2 colistin-susceptibility results.

Results: On the VITEK 2, all 57 (100%) isolates were colistin-resistant. By the microbroth dilution assay, 44/57 (77.2%) isolates were classified as intermediate, including 38 P. aeruginosa, 4 A. baumannii isolates, 1 Myroides sp., and 1 *Sphingomonas paucimobilis*. In comparison, 13/57 (22.8%) isolates were consistently classified as colistin-resistant, including 6 P. aeruginosa isolates, 1 A. baumannii, 4 Enterobacter spp, 1 *Aeromonas hydrophila/caviae*, and 1 *Klebsiella pneumoniae ssp pneumoniae.*

Conclusion: The study confirmed that colistin results on the VITEK 2 can be misleading as resistance was over-reported for priority MDR pathogens P. aeruginosa and A. baumannii, which could lead to underuse of this important last-line drug, thus contributing to unnecessary mortality. We recommend the MBD assay should be part of routine microbiology tests in hospitals with high MDR levels despite it being tedious and time-consuming, as colistin is only reliably tested by this method.

Keywords: Colistin, Antibiotic resistance, MDR bacteria, Gram-negative, Last-resort antibiotic,VITEK 2, Microbroth dilution method,

120.

CASE SERIES OF HEMOGLOBINURIA ASSOCIATED WITH MALARIA IN CHILDREN AGED 3-13 YEARS AT SIAYA COUNTY REFERRAL HOSPITAL (SCRH)

Authors: Getrude Kamuyu (KEMRI, CGHR)*; Martina Oneko (KEMRI); Simon Kariuki (KEMRI)

Background: Blackwater fever (BWF) is a known complication of malaria infection with Plasmodium falciparum, presenting with severe anemia, jaundice and hemoglobinuria as a consequence of massive intravascular hemolysis. The disease was considered a rare complication affecting non-immune adults following the use of quinine but has recently been linked to the use of other antimalarials including Artemesinin-based derivatives, lumefantrine, halofantrine and mefloquine. There are recent reports of increasing incidence of hemoglobinuria in children associated with malaria infection and treatment in Uganda. Following anecdotal reports of hemoglobinuria in children of school going age at SCRH in the past 2 years, we retrospectively assessed suspected cases and risk factors of BWF at SCRH.

Methods: We searched inpatient registers at SCRH for cases of BWF using the following primary search criteria: malaria, anemia and hematuria, in patients aged 3-13 years.

Cases that fulfilled the World Health Organization criteria of severe malaria; and/ or severe anemia (hemoglobin ≤5.0 g/dL) and/or hematuria were entered in a pre-specified questionnaire and analyzed. Possible BWF was defined as a case of confirmed malaria during or prior to admission, severe anemia (hemoglobin ≤5.0 g/dL) and hematuria/hemoglobinuria OR high creatinine (104mmol/L) OR oliguria/anuria>24 hours. Confirmed BWF required hematuria/hemoglobinuria AND high creatinine/oliguria/anuria plus confirmed malaria and severe anemia.

Sickle Cell Disease (SCD) was regarded a risk factor.

Results: From January to August 2023, 336 of 1156 admissions fulfilled primary search criteria and 311 cases were available for review. Of these,169 admissions (17 patients having multiple admissions) involving 125 patients fulfilled at least one criterion of entry. Criteria of possible and confirmed BWF was fulfilled by 14 (one admitted three times) and 1 patient respectively. Of these, 7 patients were 3-5, 4 were 7-9 and 4 were 10 to 12 years old. All had severe anemia. Hematuria/hemoglobinuria was described in 16 of 17 episodes, one child had elevated Creatinine. Creatinine values were available in 10 of 17 episodes, with 2 elevated Creatinine levels. Fifteen patients had confirmed malaria at time of admission with parasite densities from 160 to148,048 parasites/microliter, 47% fulfilling criteria of severe malaria. Two children had malaria prior to admission. SCD was clinically diagnosed in 2 children. All cases were treated with artesunate, in 94% it was given in combination with artemether/lumefantrine. Quinine was administered in 1 case following treatment failure with artesunate. All cases required blood transfusion and 41% needed more than one transfusion.

Conclusion: These findings suggest that symptoms suggestive of BWF are common at SCRH but are not systematically documented. A prospective study is needed to assess the incidence, severity and outcome of children with BWF and ascertain the disease's etiology.

Keywords: Malaria Black Water Fever

121.

DEEP LEARNING APPROACHES FOR FUNCTIONAL ANNOTATION OF HYPOTHETICAL CODING SEQUENCES IN PHAGES

Authors: James W Muturi (KEMRI/Walter Reed Programme)*; Collins K Kigen (KEMRI/USAMRD-A); Vanessa Onyonyi (KEMRI/USAMRD-A); Martin MG Omondi (walter reed); Lillian Musila (USAMRD-A, Kenya/KEMRI)

Background: Increasing antimicrobial resistance to existing antibiotics has sparked renewed interest in phages as viable alternatives due to their effectiveness in lysing host bacteria. Although their utility for treating MDR infections is well established, their genomic diversity factors contributing to their overall fitness and activity remain poorly understood due to limited annotation of phage genomic databases compared to bacterial sequences. Novel endemic jumbo phages (>270 kb) against *P. aeruginosa* have phenotypes with therapeutic potential, yet a significant number of their coding sequences (CDS) remain unannotated. To fully understand phage activity, the functions of these unknown proteins need to be elucidated. Existing annotation frameworks rely solely on sequence similarity, which can identify closely related sequences but fails to identify distantly related ones. This study used a pre-trained twin neural network model, TM-Vec, utilizing structural similarity to correlate structure-function homology at larger evolutionary distances to identify the function of hypothetical phage proteins.

Methods: The whole genome of a previously sequenced *P. aeruginosa* jumbo phage isolated from wastewater samples in Kenya was selected for analysis. Annotation was performed using Pharokka, which utilizes the PHROGs (protein orthologous groups) database to infer the function of known proteins. A total of 441 CDS were reported, out of which 347 were unidentified (no PHROG match), hence termed hypothetical proteins. A subset of 93 hypothetical proteins was selected alongside a control sequence (an identified protein) and was queried for similar CATH domain proteins using the deep learning algorithm TM-Vec. The resulting matching domain sequence from CATH was queried against NCBI BLASTp to infer the functions associated with the protein domain.

Results: The HNH endonuclease control sequence resulted in a domain protein with 100% query cover, matching a DNA endonuclease. Of the 93 hypothetical proteins queried, 71 (76.3%) had a matching homologous domain from the CATH database. BLASTp identified one sample domain with a Template Modelling (TM) score of 0.65 (on a scale of 0 – 1), 100% query cover, and 100% domain sequence match as CRISPR-associated endoribonuclease Cas6/Csy4, while another domain with TM score of 0.62 at 53% cover showed 100% domain sequence match as a site-specific integrase thereby suggesting that the corresponding hypothetical proteins are involved in similar functions.

Conclusion: This study serves as proof of concept, illustrating the use of deep learning to enhance functional annotation of phage sequences where existing frameworks fail. This alternate approach will contribute to a deeper understanding of phage biology by unraveling the functions of large proportions of unknown or hypothetical proteins, thereby advancing knowledge on phage lytic mechanisms that could be exploited for optimized therapeutic applications.

Keywords: Antimicrobial Resistance, Phages, Genomics & Proteomics, Deep learning, Annotation

122.

IMMUNE RESPONSES TO RED BLOOD CELL ANTIGENS AMONG TRANSFUSED SICKLE CELL ANAEMIA PATIENTS IN KILIFI, KENYA

Authors: Michael Musembi Muteti (KEMRI-WELLCOME TRUST)*; Steven Nyanjom (JKUAT); Ephy Atieno (KEMRI CGMRC); Sophie Uyoga (KEMRI CGMRC)

Background: Sickle cell anemia (SCA) is a severe monogenic disorder affecting people with Sub-Saharan Africa (SSA) contributing 75% of the global burden. Transfusion remains the mainstay for patient management and prior to transfusions, alloantibody screening or extended matching beyond ABO and RhD is not undertaken in Kenya which is likely to increase the risk of alloantibody development (alloimmunization). The burden of alloimmunization has not been extensively studied and studies within SSA have been cross-sectional which might have missed alloantibodies that become undetectable months' post-transfusion due to lack of follow-up. This study aimed to establishing the burden of alloimmunization in SCA patients in Kilifi County.

Methods: The study utilized two designs; (i) a retrospective cohort of 106 participants with 322 transfusion events where 255 plasma samples were retrieved from Biobank for follow-up. (ii) a cross-sectional survey that recruited 142 participants from the Kilifi County Hospital sickle cell clinics who had received transfusions from 2021-2023. Participants were genotyped for confirmation of the sickle gene. Plasma samples were screened for alloantibody using commercial standard 3-ID-Diacell and ID-LISS/Coombs gel cards. Positive samples for the initial screen were further analysed for alloantibody identification using the Bio-Rad 11-ID-diapanel cells (DiaMed GmbH; Switzerland, Bio-Rad).

Results: In the retrospective cohort, 54% were female and the median age was 4.9 (IQR, 2.3-7.9) years. The number of transfusions ranged from 1 - 13 with the median age at first transfusion being 2.3 (IQR, 1.0-4.8) years. 24 (9.4%) samples were alloantibody positive in the follow-up time period with an alloimmunization rate of 13.2%. Eight alloantibodies were identified; 2-e, E, M, S, s, Lua & Leb. Five participants had pan-reactive alloantibodies and three with antibodies of unidentified specificities (AUS). One participant had an autoantibody identified.

In the cross-sectional survey, 53.5% were male and the mean was 10.7 (range 1-46) years. An alloimmunization rate of 4.9% was reported among the 142 participants. Five alloantibody specificities identified; anti-e, 2-E, D & Lea. 2 participants expressed pan-reactive and AUS. and other 2 were positive for autoantibodies.

Conclusion : The cohort reported a higher rate (13.2%) compared to the reported rates in East Africa region (2.9% - 8%) while the cross-sectional survey reported a rate of 4.9% similar to the rates previously reported by cross-sectional surveys. 75% of the identified alloantibody were from Rh and MNS blood groups. There is need for rigorous follow-up studies to maximize on tracking for alloantibody development post – transfusion. Incorporation of antibody screening and matching especially for the highly immunogenic Rh blood group or provision antigen negative cells for alloimmunized patients prior to transfusion is necessary in regular transfused SCA patients.

Keywords: Sickle cell anemia, Transfusion, Alloantibodies, Alloimmunization

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123.

INTEGRATED APPROACHES TO IMPROVE NUTRITIONAL STATUS OF CHILDREN UNDER FIVE: CASE OF POSITIVE DEVIANCE HEARTH MODEL IN KONOIN SUB-COUNTY, BOMET COUNTY IN KENYA: PRELIMINARY FINDINGS

Authors: Lorraine A Ombogo (KEMRI)*; Violet Wanjihia (KEMRI); Schiller Mbuka (KEMRI); Erastus Muniu (KEMRI); Sarah Karanja (KEMRI); Carolyne Terer (MOH- Bomet County)

Background: Malnutrition in children is responsible for ill health than any other cause. Globally, 149.2 million children below 5 years suffered from stunting, 45.4 million wasted and 38.9 million overweight in 2020, mostly in Central and Southern Asia and sub-Saharan Africa. In Kenya, there was progress in the reduction of malnutrition levels between 2008-09 to 2014, stunting reduced from 35.3% to 26%, underweight from 16.1% to 11%, and wasting from 6.1% to 4%. However, in 2014 Bomet County stunting levels were (36%), wasting (2%) and underweight (12%). Malnutrition causes are diversified and to address them, integrated approaches are required. This study sought to assess the effect of positive deviance hearth model on the weight of children 6- 24 months in Bomet County.

Methods: This was a quasi-experimental non-randomized study with a non-equivalent control group. Information on sociodemographic factors, breastfeeding, complementary feeding, health-seeking, hygiene and caring practices were collected using semi-structured questionnaires and FGDs. Computation of Z-scores was done using WHO AnthroPlus. Exploratory data analysis was employed to uncover the distribution of continuous variables. Quantitative data was analysed using SPSS version 22. Weight gain and difference in Z-scores between baseline and end-line were compared using T-test. Qualitative data were processed and analysed using the framework method.

Results: Out of 110 sampled children, 52.7% were females in the intervention compared to 42.9% in the control group. Mean age was comparable between the study groups at 15.2 and 15.0 months for intervention and control groups respectively. At baseline, there was no significant difference in mean weight and MUAC at ($p>0.05$) however, at the end line, there was a mean positive change in weights at 0.1 for intervention and 0.2 for control groups at ($p<0.05$) and; a positive net MUAC increase of 0.3 for intervention and 0.1 for control groups at ($p<0.05$). A majority of caregivers cited poverty, low health seeking behaviour, dependence and wide use of herbal over contemporary medicine, and consuming a lot of time in the tea farms as opposed to child caregiving as some of the factors that contribute to the poor nutritional status of children.

Conclusion: This study has shown that PD Hearth intervention was successful in reducing underweight in children. The causes of malnutrition identified call for further research to understand the community behaviours and practices that can be tailored into integrated interventions to address malnutrition.

Keywords: Positive Deviance Hearth Model- Bomet

124.

ASSESSING THE RISK OF RIFT VALLEY FEVER AND OTHER ARBOVIRUS TRANSMISSION IN NGURUMAN, KAJIADO COUNTY

Authors: FAITH FAITH CHEROP (Kenya Medical Research Institute)*; Rosemary Sang (International Centre for Insect Physiology and Ecology); David P. Tchouassi (International Centre of Insect Physiology and Ecology); Edith E.L Chepkorir (Kenya Medical Research Institute)

The re-emergence of arboviruses like Rift Valley Fever (RVF), dengue, and yellow fever is a public and veterinary health threat globally resulting in major socio-economic burden. There have been sporadic cases and outbreaks reported in different regions in Kenya with subsequent social-economic implications. Nguruman area, in Kajiado County reported its first RVF outbreak during the 1997/1998 since then, no surveillance studies have been conducted. This study sought to assess the risk of exposure of Rift Valley Fever to the human population and potential for transmission of RVFV and other arboviruses among the mosquito population. This study adopted a cross sectional study design. Entomological sampling was conducted across 12 villages within Nguruman. Adult mosquitoes were collected using CDC light and Biogent sentinel traps. Larvae were collected from the various breeding habitats and reared into adults in the field laboratory. All mosquitoes were preserved and transported in liquid nitrogen to icipe in Nairobi. They were morphologically identified and pooled based on sex, species and sampling site. The mosquitoes were categorized into primary and secondary vectors depending on their role in the transmission of RVF. The pooled mosquitoes were assessed for presence of arboviruses using cell culture and Reverse Transcriptase Polymerase Chain Reaction (RT-PCR). Blood meal analysis was carried out using PCR. The seroprevalance of RVF among the human population was assessed using Plaque Reduction and Neutralization Test (PRNT). Human serum samples were collected from October 2020 to May 2021 from patients attending Entosopia Health Centre, presenting with symptoms associated with RVF infection. Only patients who consented were enrolled into the study, and a structured questionnaire was used to collect demographic data. A total of 13,937 mosquitoes were collected. Based on Shannon and Simpson diversity indices, mosquito abundance and diversity varied across the villages. Aedes mcintoshi (49.72%) was the abundant species and the only primary vector of RVF found in the area while the secondary vectors constituted 26.11%. Both the primary and secondary vectors assessed for blood meal analysis exhibited opportunistic feeding patterns. The seroprevalence study consisted of 179 sera. Antibodies to RVF were detected in 14 (7.8%) participants whereby, 4.4% were males and 3.4% females. The observed difference in exposure between male and female could be attributed to cultural practices and animal husbandry. Therefore, the presence RVF vectors, serological evidence of RVF infections among the human population, and the opportunistic feeding behavior of mosquitoes suggesting spillover transmission of zoonotic diseases to humans, confirms that disease surveillance and stringent vector control measures need to be applied to these at-risk areas with further emphasis on human vaccine and diagnostic kit development to mitigate the effects of possible outbreaks.

Keywords: Rift Valley Fever,Seroprevalence

125.

EXTRA-OCCUPATIONAL PREDICTORS OF COVID-19 DISEASE AMONG HOSPITAL HEALTH WORKERS. FINDINGS FROM A CASE CONTROL STUDY IN KENYA

Authors: John Macharia Kiragu (University of Nairobi)*; Richard Ayah (University of Nairobi)

Background: The spread of COVID-19 cases among HWs has been associated with an acute shortage of health workers (HWs) and overwhelmed health system capacity. Preliminary evidence points to an increased risk of spreading COVID-19 to HWs from exposures in households and non-occupational settings. However, evidence on the role of extra-occupational exposure to COVID-19 among HWs remains incomplete.

Our objective was to identify non-occupational predictors of COVID-19 disease among HWs in a tertiary hospital in Kenya.

Methods: Using a hospital-based and unmatched case-control study design, exposure differences were examined for 39 random COVID-19 cases (SARSCoV2 PCR positive HWs) and 108 convenient HWs without COVID-19 disease as controls (SARSCoV2 PCR negative and COVID-asymptomatic) between November and December 2021. A literature-based and researcher-administered questionnaire was used to assess exposure and was used to assess socio-demographics, occupational, community and health systems' exposure factors.

At 95% Confidence Intervals, multiple imputations for missing data were applied, and multivariable logistic regression and Akaike Information criteria were applied to identify statistically significant exposures.

Results: Controlling for occupational exposure variables, community risk factors associated with COVID-19 disease included being on leave (aOR 2.43, $p<0.05$), self-reported history of non-specific exposure to a COVID-19 case within the study period and in the 2 weeks before PCR testing (aOR 11.14, $p<0.05$) and the symptom-based PCR Covid19 testing protocol for HWs (aOR2.79, $p<0.05$). The model had statistically significant goodness of fit compared to the null and the overall effect size was estimated at 0.36 (Hosmer-Lemeshow pseudo-r-squared).

Conclusion: COVID-19 exposure among HWs is not limited to clinical settings. Our findings are consistent with literature linking non-clinical and non-occupational settings to COVID-19 disease exposure among HWs such as households and communities. Policies enhancing the safety of health workers from COVID-19 disease and similar infectious outbreaks need to be evaluated for extra-occupational exposure precautions. Future studies can confirm these findings and provide more precise evidence on the role of extra-occupational COVID-19 and similar disease exposure in disease transmission among health workers.

Keywords: extra-occupational, COVID-19, health workers, hospital, safety

126.

CHARACTERIZATION OF FETAL VERSUS MATERNAL INNATE IMMUNE RESPONSES AGAINST PLACENTAL MALARIA

Authors: Samuel W Chenge (Jomo Kenyatta university of Agriculture and Technology (JKUAT))*; Harrison Ngure (Mount Kenya University); Melvin Mbalitsi (Maseno University); Moses Obimbo (University of Nairobi); Omu Anzala (KAVI-ICR); Bernard Kanoi (Mount Kenya University); Mourine Kangogo (Jomo Kenyatta University of Agriculture and Technology); Jesse Gitaka (Mount Kenya University); Francis Kobia (Mount Kenya University)

Abstract: Placental malaria (PM) is associated with poor pregnancy outcomes. The mechanisms driving PM in humans are not yet fully understood. Here, we used archived human placental tissues from malaria holoendemic region and found that PM-positive placentas showed differential expression of fetal versus maternal TLR4, TLR7, TLR9 and expressed increased oxidative DNA damage compared to healthy controls.

Introduction: In malaria-endemic regions of sub-Saharan Africa, PM, which is caused by the sequestration of Plasmodium falciparum-infected erythrocytes (Pf-IEs) in placental intervillous spaces, is a leading cause of poor pregnancy outcomes, including low birthweight and stillbirth. However, the mechanisms driving PM are not fully understood. Mouse models have associated Toll-like receptor (TLR)-mediated innate responses to PM with adverse pregnancy outcomes. These studies indicate that PM triggers TLR4-mediated inflammation on the maternal side of the placenta, which is associated with poor pregnancy outcomes. In response, the fetal side is reported to mount a TLR4-mediated innate counterresponse, which improves fetal outcomes. However, such observations have not been made in human PM. Here, we sought to determine whether human PM is associated with differential deployment of innate immune responses on the fetal versus maternal sides of the placenta.

Methods: For this, we leveraged our biobank of term placental tissues donated by mothers with a known history of malaria in pregnancy and mothers without a known history of MiP (each group, n=63). The placenta donors were all residents of Webuye, a malaria-holoendemic region of western Kenya. Formalin-fixed paraffin-embedded (FFPE) placental tissues were used for histopathological (hematoxylin & eosin staining) and immunohistochemistry (IHC) analysis. Their frozen counterparts were separated into fetal (chorionic tissue) and maternal (decidua tissue) sides before RNA was separately extracted from both groups. RNA integrity was checked, and equal amounts were used for RT-qPCR to determine the relative gene expression of TLRs using the $2^{-\Delta\Delta CT}$ method.

Results: Histology revealed that 69 placentas had PM (mean burden of Pf-IEs: 5.3%). Compared with PM-free samples, the fetal side of PM-positive placentas relatively expressed significantly higher levels (fold change) in TLR4 (1.5), TLR7 (1.5), and decreased TLR9 (0.9). Similarly, the maternal side of the PM-positive placentas expressed significantly higher levels of TLR4 (1.2), no change in TLR7 (1.0), and lower levels of TLR9 (0.9). IHC showed that, compared with PM-free controls, PM-positive placentas express markedly higher levels (10 times) of 8-hydroxydeoxyguanosine (8-OHdG), indicating a DNA damage response.

Conclusion: These findings further our understanding of fetal-maternal innate immune responses to human PM and highlight the need to further investigate PM pathogenesis with the aim of developing effective interventions and diagnostics.

Keywords: Placental malaria, Toll like receptors, Innate immune responses, fetal versus maternal, oxidative DNA damage

127.

CHARACTERIZATION OF EBV INFECTION IN TONSILS OF CHILDREN RESIDING IN MALARIA HOLOENDEMIC REGION OF WESTERN KENYA

Background: Epstein Barr virus (EBV) infection usually occurs in early childhood and can persist in palatine and pharyngeal tonsil lymphocytes. The presence of EBV in non-neoplastic lymphoid tissue of the nasopharynx and tonsil has rarely been investigated. We previously reported the changes in tonsillar B cell population in Caucasian children, but there is a paucity of data on EBV infection in tonsils; the site of EBV entry, from children residing in malaria endemic regions. EBV and Plasmodium falciparum (Pf) malaria are the main co-factors in the etiology of endemic Burkitt's lymphoma; which is the most common pediatric cancer in sub–Saharan Africa. **Methods:** This cross-sectional study determined EBV viral loads and EBV type frequency in blood, plasma, saliva and tonsillar mononuclear cells (TMCs) in children aged 1-14 years undergoing tonsillectomy from western Kenya. EBV viral loads and EBV type in the different compartments were determined by quantitative real time PCR and qualitative real time PCR respectively. **Results:** The mean EBV viral loads in TMCs was significantly higher compared to levels in blood (p=0.002). In addition, higher mean EBV viral loads was observed in saliva as compared to mean viral loads in plasma (p=0.046). Although there was no correlation between age and EBV DNA copies in plasma, saliva and blood, a significant negative effect of age on EBV loads was demonstrated in TMCs (r= -0.6875, p<0.0001), indicating that there is reduction of EBV viral particles as age increases. Children co-infected with both EBV type 1 (EBV-1) and EBV-2 had significantly higher viral loads as compared to those infected with only EBV-1 (p= 0.0024) and not EBV-2 in saliva compartment, no difference was observed in the other compartments. **Conclusion:** This data suggests that, children residing in malaria endemic regions have elevated viral loads in tonsils which decreases as age progresses. In addition, coexistence of both EBV-1 and EBV-2 favors increase of EBV infested cells hence increase in EBV viral loads.

Keywords: Tonsil, Burkitt Lymphoma, Epstein-Barr Virus, Malaria.

128.

MALARIA MORBIDITY DUE TO NUTRITION DEFICIENCY IN ENDEMIC ZONES WESTERN, KENYA

Authors: Redemtah Yeda, Hoseah Akala (KEMRI/USAMRD-A/K); Agnes Cheruiyot (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI)); Dennis Juma (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI)); Raphael Okoth (USAMRD-K/KEMRI); Edwin W Mwakio (USAMRD-A/K); Benjamin Opot (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI)); Jackline Juma (1Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI))

Introduction: Malaria and malnutrition are key public health challenges in malaria endemic zones. Recent studies have presented conflicting finding whether malaria is associated with increased or decreased malnutrition. However, the relationship between them is poorly understood. Here, we aimed to assess malaria morbidity due to nutrition deficiency in malaria endemic zones. Assessing the relationship may lead to discovery of low effective ways to malnutrition prevention in malaria endemic areas. **Methods:** This study is part of an on-going surveillance study, where we characterized children aged 6–59 months with baseline of malaria infection upon enrollment. We compared the mal-nourished children from nourished children of the same age for their past exposure to malaria in Kisumu County Kenya. Blood samples were drawn for microscopy and a valid structured questionnaire was used to collect epidemiological data. The collected data were analysed for descriptive statistics using STATA data analysis software.

Results: A total of 300 (70 malnourished and 230 nourished) under-five children participated in the study. Previous exposure to Plasmodium infection was found to be a predictor for the manifestation of malnutrition in under-five children (P=0.02 [OR=1.87, CI=1.115–3.138]). Children with high plasmodium density were 4.5 more likely to be malnourished as compared to nourished children (P=0.001 [OR=0.422, CI=0.181–0.978]).

Conclusion: Study finding reveals exposure to plasmodium falciparum has an impact on nutritional status. The high prevalence of undernutrition in children contributes to malaria morbidity in the region. Therefore, future research should be prioritized to generate data on the individual level. Further, malaria control interventions could be tailored to integrate nutrition programmes to disrupt indigenous malaria transmission in a population.

Keywords: Nutrition,Malnourished , Morbidity,Malaria

SCIENTIFIC SESSION 15:

PUBLIC HEALTH 2

129.

MODELLING COVID-19 WAVES IN KENYA

Authors: Wandera Ogana (AMMSI)*; Victor Juma (The University of British Columbia); Wallace Bulimo (Kenya Medical Research Institute); Vincent Nandwa (University of Nairobi)

Background: COVID-19 is a disease caused by the novel coronavirus SARS-CoV-2 that emerged at the end of December 2019 and has since spread globally. In Kenya, the virus was first detected on 13 March 2020. Soon after, the Kenyan government implemented non-pharmaceutical interventions (NPIs) to slow the spread of the disease. The pandemic continued to spread and it evolved into several waves over the years despite the discovery of vaccines and treatment.

Methods: Mathematical models have been developed to help analyse, predict and simulate the dynamics of the pandemic. These models have, however, mainly been confined to single waves, without ready extension to other waves. In this paper, we develop a compartmental model that can readily be extended to multiple waves using various concepts. Key amongst these is the application of computational and mathematical techniques that convert infection curves with negative gradients to those with positive gradients, in the neighbourhood of the change point, namely, where transition occurs from one wave to the next. This effectively generates a new wave. We then introduce a jump mechanism for the susceptible fraction that allows further computation to align itself with the observed infection curve. To test our models, we analysed the publicly available online daily COVID-19 data from websites of the Ministry of Health, Kenya, and Worldometer.

Results: The method was applied to COVID-19 in Kenya and the computation successfully replicated all the seven waves that appeared from March 2020 to January 2023.. It also identified change points located within the months when COVID-19 variants became dominant.

Conclusion: The findings strengthen the proposition that the dominant COVID-19 variants were the major drivers of the waves. For public health application, the methods enable estimates of the proportions of infected individuals at the peak of the epidemics and at the end of a given interval of intervention. They also enable us to validate to what extent the intervention measures met the proposed targets. The techniques can be extended to new strains of COVID-19 and to influenza and other periodic infectious diseases.

Keywords: Mathematical model, COVID-19, delay functions, multiple waves

130.

MALARIA PREVALENCE AND DETERMINANTS OF OPTIMAL INTERMITTENT PREVENTIVE MALARIA THERAPY AND INSECTICIDE-TREATED NETS AMONG PREGNANT WOMEN IN BUSIA COUNTY, KENYA

Authors: Everlyne Chimwani Khalivinzwa (Jaramogi Oginga Odinga University of Science and Technology)*; Daniel Onguru (Jaramogi Oginga Odinga University of Science and Technology); Bartholomew Ondigo (Laboratory of Malaria Immunology and Vaccinology, National Institute of Allergy and Infectious Disease, NIH, Bethesda, Maryland, USA;); Duncan M Wakoli (Department of Biochemistry and Molecular Biology Egerton University, US Army Medical Research Directorate-Africa); Odhiambo Caleb (Egerton University); GEORGE N IMBUSI (EGERTON UNIVERSITY); Daniel Sikuku (Egerton University); DICKSON KIPCHIRCHIR (KEMRI-CGHR); Stellah A Chumbe (Maseno University/KEMRI); Rakel Makandi (Egerton University); Michael Ong'echa (Centre for Global Health Research, Kenya Medical Research Institute)

Introduction: Malaria during pregnancy is a significant public health concern. Three doses of sulfadoxine-pyrimethamine for intermittent preventive treatment (IPTp-SP) of malaria in pregnancy (MiP) and the use of insecticide-treated nets (ITNs) are recommended for maximum protection. These interventions can avert the adverse effects of malaria in pregnancy-associated maternal anemia, intrauterine deaths, preterm delivery, and low birth weight (LBW).

Methods: This cross-sectional study was aimed at determining the prevalence of malaria and factors influencing the uptake of optimal doses of intermittent preventive malaria therapy and the use of insecticide-treated nets among pregnant women between 15 - 49 years of age attending antenatal and postnatal clinics in Port Victoria and Sio Port Sub County Hospitals, Busia County, Western Kenya. Quantitative data was collected from pregnant and post-delivery women who consented from May to September 2023.

Results: Preliminary findings show that 168/303 (55.5%) women were from Samia sub-county. The participants' mean age was 24.79 ± 5.95 years, 226/303 (74.6%) were protestants, 233/303 (76.9%) were married, 243/303 (80.2%) were unemployed, 148/303 (48.5%) had attained the primary level of education, and 197/303 (65.0%) cited good relations with the healthcare workers. On knowledge, 38/303 (12.5%) knew the dangers of malaria in pregnancy, 130/303 (42.9%) knew the optimal doses, and 108/303 (35.6%) knew when to start using IPTp-SP. The prevalence of malaria was 35.1% (95% CI: 29.7%–40.5%). Optimal IPTp-SP uptake was 55.78% (95% CI: 50.1%–

61.3%), while ITN use was 98% (95% CI: 96.1%–99.3%). Predictors of IPTp-SP optimization were the frequency of antenatal care (ANC) visits ($P<0.001$) and maternal knowledge of IPTp-SP start time ($P< 0.02$). Odds of optimizing IPTp-SP increased among women with ≥ 4 ANC visits (aOR = 5.30, 95% CI 3.0–9.39) and those with knowledge of IPTp-SP start time (aOR = 2.1, 95% CI 1.13–3.7). There were no significant predictors for ITN use.

Conclusion: This study found a high prevalence of malaria and low IPTp-SP optimal uptake, hence underscoring the need for targeted interventions.

Keywords: Malaria in pregnancy, Intermittent preventive treatment , Sulphadoxine pyrimethamine, Busia Kenya

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131.

LEVERAGING ADVOCACY TO REDUCE FREQUENT UPTAKE OF EMERGENCY CONTRACEPTIVE PILLS AMONG STUDENTS OF TERTIARY INSTITUTIONS.

Authors: Lordlaro M Lidoros (Maseno University)*

Background: The uptake of Emergency Contraceptive Pills (ECPs) among students has been on the rise in the recent past due to high rates of irresponsible sexual behavior in the learning institutions. This behavior poses a great threat to their reproductive health. Liver damage, teratogenic and ectopic pregnancies, delayed fertility and irregular menstrual cycles have been linked to the frequent use of ECPs.

Methods: The cross-sectional study was conducted in Sigalagala National Polytechnique and Maseno University in Kenya. Google form-structured anonymized questionnaires were used to collect data. The target population was female students from age of 19-25 who had been admitted in the institutions for at least one academic year. Stratified random sampling according to schools was employed to recruit 200 study participants from each of the institutions. Pivot tables in Microsoft excel were used to analyze and present the data.

Results: In both of the institutions, the study identified that 46% of the participants had used ECPs at least once, while 6% had used ECPs at least once every month in the past six months. The use of ECPs was due to the fear of conceiving and not STDs or side effects of the pills. The study identified that 59% of the participants were either misinformed or had insufficient information about ECPs, long-acting reversible contraceptives (LARCs) and other contraception methods.

Conclusions and Recommendations: There is a pressing need for comprehensive education and awareness programs regarding LARCs among teenagers. Research focus and policy review on Emergency Contraceptive Pills (ECPs) need to be comprehensive, evidence-based, and aligned with current medical guidelines also.

Female students should opt for LARCs and only use ECPs in real emergencies.

Keywords: Emergency Contraceptive Pills, Long Acting Reversible Contraceptives, Sexual Reproductive Health.

132.

THE IMPACT OF HOME - BASED CARE ON INFECTIOUS RESPIRATORY DISEASE: A CASE OF COVID-19

Authors: Henry M. Wanjala (Chuka University)*; Mark Okongo (Chuka University); Jimrise Ochwach (Chuka University)

BACKGROUND: Mathematical models offer a window into real-world events without the need for direct experimentation. They've played a crucial role in various fields, particularly in epidemics, allowing for predictions and analyses of the effects of different strategies in curtailing epidemic transmissions. Coronaviruses, a family of viruses causing respiratory illnesses, have triggered documented epidemics such as the Severe Acute Respiratory Syndrome (SARS-CoV) in 2002, the Mediterranean Respiratory Syndrome (MERS-CoV) in 2012, and the most recent Coronavirus Disease-2019 (COVID-19) outbreak. Given the swift spread of COVID, effective public health interventions aim to minimize its transmission while efficiently managing its impact. Broadly, two main strategies are employed to control its spread: pharmaceutical intervention (PI) and non-pharmaceutical intervention (NPI) strategies.The study aims to evaluate the effects of a rapid contact tracing and testing program, focusing on isolating confirmed cases either through home-based care or traditional isolation methods, on the transmission of the coronavirus within a community.

METHOD: The study developed a deterministic mathematical model of ordinary differential equations. The total population is divided into seven mutuallly exclusive compartments of susceptiles,$S(t)$, exposed,$E(t)$, asymptomatic,$A(t)$,symptomatic,$S(t)$,Home-based care,$H(t)$,Hospitalised,$J(t)$ and Recovered,$R(t)$.The determination of the basic reproduction is through the next generation matrix (NGM).

Local stability of the disease-free equilibrium (DFE) is derived using the trace-determinant method, while its global stability is established employing the Lyapunov-Krasovskii approach.A numerical simulation is conducted using PYTHON program based on the system model. Parameters are adjusted to align with previously reported studies, with some values estimated to ensure a relevant analysis for this particular study.

RESULTS: The study realized that the epidemic was both locally and globally asymptotically stable though the effectiveness of the strategies was unrealistically attainable and thus other strategies were to be applied. The numerical simulations established effective use of home-based care delayed the peak days and lowered the peak population giving time time to public health officials to improve the facilities.

CONCLUSION: Home based care as a strategy by which mild symptomatic cases and the asymptomatic cases are to be managed can be employed. These strategy lowers the burden on the health facilities and personnel to focus on the severe cases. Home-based care is to be co-opted with other non-pharmaceutical strategies to reap maximum benefits.

Keywords: COVID-19, Reproduction Number, Disease Free Equilibrium, Home-Based Care, Numerical Simulation

133.

THE EFFECT OF COVID-19 PANDEMIC ON HEALTHCARE SEEKING IN AN URBAN INFORMAL SETTLEMENT IN NAIROBI AND A RURAL SETTING IN WESTERN KENYA

Authors: George O. Agogo (CDC)*; Patrick K Munywoki (CDC, Nairobi, Kenya); Allan Audi (KEMRI); Joshua Auko (KEMRI); George Aol (KEMRI); Clifford Oduor (KEMRI); Samuel Kiplangat (KEMRI); Alice Ouma (KEMRI); Terry Komo (KEMRI); Amy Herman-Roloff (CDC); Peninah Munyua (CDC); Godfrey Bigogo (KEMRI)

Background: The COVID-19 pandemic caused widespread changes and disruptions to healthcare seeking behavior. There are limited studies on the effect of the COVID-19 pandemic on healthcare seeking patterns in low-and middle-income countries (LMICs), especially in settings with inequitable access to healthcare in rural and urban informal settlements. We investigated the effect of the COVID-19 pandemic on reported healthcare seeking at health facilities and chemists using morbidity data from participants in an ongoing population-based infectious disease surveillance platform in Asembo in Siaya County, a rural setting in western Kenya and Kibera, an urban informal settlement in Nairobi County.

Methods: We described healthcare seeking patterns before (from 1st January 2016 to 12th March 2020) and during the pandemic (from 13th March 2020 to 31st August 2022) by gender and age for any reported illness and select clinical syndromes using frequencies and percentages. We used a generalized estimating equation with an exchangeable correlation structure to assess the effect of the pandemic on healthcare seeking adjusting for gender and age.

Results: Overall, there was a 19% (adjusted odds ratio, aOR: 0.81; 95% Confidence Interval, CI: 0.79 – 0.83) decline in odds of seeking healthcare at health facilities for any illness in Asembo during the pandemic, and a 30% (aOR: 0.70; 95% CI: 0.67 – 0.73) decline in Kibera. Similarly, there was a decline in seeking healthcare by clinical syndromes, e.g., for ARI, aOR: 0.76; 95% CI:0.73–0.79 in Asembo, and aOR: 0.68; 95% CI:0.64–0.72 in Kibera. The pandemic resulted in increased healthcare seeking at chemists (aOR: 1.23; 95% CI: 1.20–1.27 in Asembo, and aOR: 1.40; 95% CI: 1.35 –1.46 in Kibera).

Conclusion: This study highlights interruptions to healthcare seeking in resource-limited settings due to the COVID-19 pandemic. The pandemic resulted in a substantial decline in seeking care at health facilities, and an increase of the same at chemists.

Keywords: Event based surveillance, Indicator-based surveillance, Machine learning,

134.

HEALTH PROVIDERS' PERCEPTIONS OF THE USE OF LONG-ACTING HIV PREVENTION PRODUCTS DURING PREGNANCY AND LACTATION IN KENYA: A QUALITATIVE STUDY

Authors: Cherotich Sharon Mutai (Partners in Health Research and Development, Center for Clinical Research, Kenya Medical Research Institute)*; Vallery Ogello (Centre for Clinical research, Kenya Medical research Institute-PHRD Thika); Nicholas B Thuo (Kenya Medical Research Institute - CCR - PHRD Thika Site); Zachary Kwena (Kenya Medical Research Institute, Center for Microbiology Research, Kisumu); Cynthia Cheptoo (Partners in Health Research and Development, Center for Clinical Research, Kenya Medical Research Institute, Nairobi); Catherine Makokha (Kenya Medical Research Institute, Center for Microbiology Research, Kisumu); Anyango Rennah (Kenya Medical Research Institute, Center for Microbiology Research, Kisumu); Emmah Owidi (Partners in Health Research and Development, Center for Clinical Research, Kenya Medical Research Institute, Nairobi); Catherine Kiptinness (KEMRI); Nelly R. Mugo (KEMRI); Kenneth Ngure (Jomo Kenyatta University of Agriculture and Technology)

Background: Pregnant and lactating women especially from sub-Saharan Africa are at high risk of HIV infection. Long-acting HIV prevention products have the potential to reduce new HIV infections among this population. However, little is known about health providers' perceptions of the use of long-acting HIV prevention products during pregnancy and lactation, and their perceptions might affect uptake despite their important role in delivery of HIV prevention services. We sought to understand health providers' perceptions of the use of long-acting HIV prevention products during pregnancy and lactation.

Methods: From November 2022 to January 2023, we conducted qualitative interviews with purposefully selected health providers representing those working in maternal and child health clinic and those offering HIV prevention services from four public health facilities in central and western Kenya. We used semi-structured interview guides to collect data to assess health providers' perceptions of four long-acting HIV prevention products (monthly oral pill, implant, injectable and vaginal ring). We analyzed data thematically to capture perceived benefits and concerns of the use of long-acting HIV prevention products.

Results: We interviewed 40 health providers; median age was 38 years, (interquartile range [IQR] 31-57) and the majority 82% were female. Specifically,73%(n=29) nurses, 20% (n=8) clinicians, among other cadres. All health providers expressed strong support for the use of long-acting HIV prevention products during pregnancy and lactation, because of their potential to reduce HIV transmission rates. Perceived benefits to the use of long-acting HIV prevention products to clients included; address adherence challenges associated with PrEP pill burden, reduce stigma concerns associated with PrEP pill bottles, offer privacy especially for women who do not want to disclose PrEP use, as well as reduce clinic visits and save costs. In addition, perceived benefits to health providers were that the long-acting HIV prevention products would help address health system barriers such as; heavy workload, less need of adherence counselling and monitoring, and help decongest health facilities due to reduced frequency of clinic visits. However, health providers reported concerns about the use of long-acting HIV prevention products such as potential health risk to the mother and child due to a lack of evidence-based data on safety and efficacy during pregnancy and lactation.

Conclusion: Health providers in this study were supportive of the use of long-acting HIV prevention products during pregnancy and lactation, as they believed that these products could offer several benefits to both clients and health systems. Concerns about the safety and efficacy of these products among pregnant and lactating women may be addressed through more research to provide evidence-based data which would translate to higher acceptability of these products to health providers.

Keywords: Perceptions; Long-acting HIV prevention products; Health providers

135.

THE EPIDEMIOLOGY OF CIRCULATING VACCINE DERIVED POLIOVIRUS TYPE 2 (CVDPV2) IN KENYA IN, 2023.

Authors: Shadrack Mr. Barmasai (Kenya Medical Research Institute)*; Joanne H Hassan (kemri); Mercy A. Onyango (Kenya Medical Research Institute); Collins K Cheruiyot (KEMRI); Agnes Chepkurui (KEMRI); Janet Wanjiru (KEMRI); DIANA WANJIRU WANJIKU (KEMRI); Paul Muchai (KEMRI); Robert Mainga (KEMRI); Peter Maritim (KEMRI); Jimmy Nyangao (KEMRI); Stephen Ochieng Ombija (Kenya Medical Research Institute); Evans Komen (KEMRI); Benlick Mwangi (KEMRI); Fiona Aluoch Alaii (KEMRI); Samira Ali Katembe (KEMRI); Jennifer Lewett (KEMRI); Celine Alice (KEMRI); Casey Asigo (KEMRI); Maureen Njihia (KEMRI); Rosemary Nzunza (KEMRI); samoell A Khamadi (KEMRI); Peter Borus (KEMRI)

Background: The Global Polio Eradication Initiative (GPEI) developed the Polio Eradication Strategy for 2022–2026, with one of its goals being to stop circulating vaccine derived poliovirus type 2 (cVDPV2) transmission and prevent outbreaks in non-endemic countries. Poliovirus can be detected through acute flaccid paralysis (AFP) and environmental surveillance. The isolates can be classified into three

major types: wild, Sabin-like, or vaccine-derived. The wild or vaccine derived poliovirus, when detected, can lead to an emergency, which can be defined as a situation that has the potential to spark an outbreak. The cVDPV2 outbreaks were detected after the withdrawal of type 2 containing oral polio vaccine in April 2016.The study summarizes the epidemiology of cVDPV2 outbreaks between

January and October 2023 in the Kenya Polio surveillance system.

Methods: A retrospective study of confirmed cases of cVDPV2 between January and October 2023 was performed using a Kenyan AFP surveillance case-based database. Epi-Info statistical software

(version 6) was used for the analysis.

Results: A total of 1265 cases of AFP and 165 environmental samples were reported between January and October 2023. Of these, 18 were confirmed as cVDPV2: 13 from AFP samples in Garissa and 5 from environmental samples in Bouralgy and Newmarket (Garissa) and Eastleigh A (Nairobi) environmental sites. 13 (1%) cVDPV2 was confirmed among AFP samples, 8 (61.5%) from AFP cases and 5 (38.5%) from healthy community children. 5 (3%) cVDPV2 was confirmed among environmental samples. All the confirmed AFP cases were <15 years old and 3 (2.4%)

had zero doses of the Oral Polio Vaccine (OPV).

Conclusion: The emergence of cVDPV2 is a result of importation and is genetically linked to Somali origin. Supplementary immunisation activities (SIAs) and mass immunisation campaigns should be enhanced in the border regions. On August 2023, Kenya introduced a novel oral poliovirus vaccine (nOPV2) that is used for outbreak response purposes only. However, strategy on strengthening routine immunisation especially inactivated polio vaccine (IPV) coverage need to be improved to ensure community immunity.

Keywords: poliovirus, circulating vaccine derived poliovirus type 2 (cVDPV2)

136.

COVID 19 TESTING: POSITIVITY RATE IN CONTEXT TO VACCINATION STATUS AT NYAHERA SUB COUNTY HOSPITAL, KISUMU COUNTY, KENYA.

Authors: duncan odhiambo ongayi (ministry of health)*

Background: COVID-19 is overwhelming health systems universally. Increased capacity to combat the epidemic is important, while continuing regular healthcare services in which laboratory testing at the point-of-care is very important. COVID-19 vaccines provide strong protection against serious illness, hospitalization and death. There is also some evidence that being vaccinated will make it less likely that you will pass the virus on to others, which means your decision to get the vaccine also protects those around you. Kenya adapted and administered 4 vaccines namely; AstraZeneca, Modana, Johnson and Johnson and Phzer. An individual is expected to be fully vaccinated if he/she receives 2 doses and a booster dose. The main aim of this study was to determine the positivity rate amongst the vaccinated patients attending Nyahera sub county hospital.

Methodology: This was a Retrospective study conducted from June 2021 to October 2022 by abstracting data from Covid 19 laboratory register ,Digital Health information system (DHIS) and chanjo platform .The data obtained was analyzed in Microsoft excel and presented in percentages.

Results: Out of 435 patients tested for Covid 19, 58(14.3%) were positive, in which 19(32.8%) were males while 39 (67.2%) were females. Children >5 years were 3(8.6%) and both females. On vaccination uptake 24(41.3%) were partially vaccinated having got 1 to 2 doses of the vaccine, of the 58 positives 16(27.6%) had received 2 doses of AstraZeneca, while only 1 (1.7%) had received Phzer vaccine. For the laboratory diagnosis 4(6.9%) were confirmed by PCR test while the rest were done by rapid antigen test.

Conclusion: Timely completion of vaccine doses is very key and paramount in offering the required body protection however not only completion of vaccination offers an individual 100% protection, but should be observed alongside other public health interventions like hand hygiene, proper masking and waste management.

Keywords: COVID 19, Laboratory Testing, Vaccination,DHIS

137.

EXPLORING THE DIVERSITY OF THE HUMAN MITOCHONDRIAL GENOME ALONG THE KENYAN COAST: PROGRESS TOWARDS ESTABLISHING A FORENSIC REFERENCE DATABASE FOR KENYA

Authors: Eva K Aluvaala (KEMRI)*; Wallace Bulimo (KEMRI); Belinda Cherono Azzam (Kenya Medical Research Institute)

Mitochondrial DNA (mtDNA) haplogroups serve as valuable markers for inferring biogeographical ancestry, notably aiding forensic investigations lacking suspect leads or in identifying disaster victims. Across populations, distinct haplogroups indicate ancestral lineages, with haplogroups A, B, C, D, E, F, G, and M commonly associated with Asians, while haplogroups A, B, C, and D predominate among Native Americans. African lineages include haplogroups L0, L1, L2, L3, L4, L5, L6, and L7, while European populations often exhibit haplogroups H, I, J, K, T, U, V, W, and X.

The advent of next-generation sequencing (NGS) has validated its utility in forensic contexts, simplifying the sequencing of the entire human mitochondrial genome. However, its meaningful application relies on accessible reference population databases for statistically interpreting forensic DNA evidence. While mitogenome reference databases are established for Caucasian and Asian populations, African populations are notably underrepresented. Utilizing foreign reference databases in African contexts lacks statistical relevance, highlighting the imperative to develop a mitogenome reference database tailored to the Kenyan population.

To ascertain mitogenome diversity along the Kenyan coast, we analyzed 86 samples from individuals representing 13 ethnolinguistic groups in the coastal region. Maternally inherited ethnicity was determined through self-identification, and next-generation sequencing facilitated mitogenome haplogroup determination. Employing long-range PCR enrichment and the Collibri™ ES DNA Library Prep Kit, sequencing was executed on Illumina MiSeq. Data analysis and haplogroup assignment utilized CLC Genomics Workbench v.22 and the AQME plug-in (AFDIL-QIAGEN mtDNA Expert).

Among the 86 analyzed haplotypes, 55% were unique, revealing a diverse spectrum of haplogroups, notably L0, L1, L2, L3, L4, L5, and M, with respective frequencies of L0 (26.96%), L1 (4.49%), L2 (19.1%), L3 (42.69%), L4 (4.49%), L5 (1.12%), and M (1.12%). Notably, the L3 haplogroup predominated, with sub-haplogroup L3e representing 47% of all L3 haplogroups in this geographic region. These findings significantly contribute to constructing a population-specific forensic reference mitogenome database for the Kenyan population. This database will empower the statistical interpretation of forensic evidence and foster the routine integration of mitochondrial DNA analysis in Kenyan forensic laboratories.

Keywords: Human Mitogenome, reference forensic database, Kenyan Coast

138.

CHALLENGES FACED DURING MASS DRUG ADMINISTRATION FOR TRACHOMA ELIMINATION IN A PASTORAL CONFLICT AREA: EXPERIENCES OF PROGRAM IMPLEMENTERS IN BARINGO COUNTY, KENYA

Authors: Bridget Kimani (KEMRI)*; Tabitha W Kanyui (KEMRI); Doris Njomo (KENYA MEDICAL RESEARCH INSTITUTE); Paul Gichuki (KENYA MEDICAL RESEARCH INSTITUTE); Collins Okoyo (KEMRI); Wycliffe Omondi (Vector Borne and Neglected Tropical Diseases Unit (VBNTDU), Ministry of Health, Kenya); Titus Watiti (Vector Borne and Neglected Tropical Diseases Unit (VBNTDU), Ministry of Health, Kenya)

Introduction: Trachoma is one of the 20 diseases designated by World Health Organization (WHO) as neglected tropical diseases (NTDs). It is the most common infectious cause of blindness, a condition that is irreversible. As guided by the WHO, in areas with a prevalence of > 10%, programmes need to treat the whole population with antibiotics annually and achieve a treatment coverage of at least 80 %. Loyamorok ward in Baringo County was purposively selected due to low treatment coverage of 48% -57%.

Methods: We conducted a qualitative study to identify challenges faced by program implementersduring mass drug administration (MDA) for trachoma elimination. Eight in-depth interviews (IDIs) were conducted with community health extension workers (CHEWs); four semi-structured interviews with county, sub-county NTD program personnel and county trachoma focal person and three focus group discussions (FGDs) with community health volunteers (CHVs). All the study participants were purposively selected due to their involvement in trachoma MDA program. The data were analyzed by QSR NVIVO version 12 according to thematic areas.

Results: The program implementers reported several challenges that impacted on MDA uptake. Inadequate community sensitization and mobilization which led to low levels of knowledge of trachoma, lack of awareness of MDA benefits, negative attitudes towards modern medicine and fear of side effects of the drugs. Other challenges highlighted were failure to use of door-to-door method of drug distribution and inadequate number of community drug distributors (CDDs). Inaccessibility of remote areas due to adverse weather conditions

during the rainy season, insecurity in the area due to tribal conflicts and migration of community members in search of pasture during the extremely dry seasons were further reported to negatively impact on MDA uptake. Other reported challenges included late transmission of data by the CDDs, and insufficiency of drugs allocation caused by incorrect census data.

Conclusion: This study documents important challenges that need to be addressed during the implementation of trachoma MDA campaign. The challenges should be factored in at the planning of implementation to make the program more efficient and achieve the goal of trachoma elimination.

Keywords: Trachoma Elimination, Mass Drug Administration, Health Care Workers

SCIENTIFIC SESSION 16: VECTOR BIOLOGY 2

139.

EFFICACY OF THE PERMANET® DUAL COMPARED TO THE INTERCEPTOR® G2 AND THE PERMANET® 3.0 IN EXPERIMENTAL HUTS IN SIAYA COUNTY, WESTERN KENYA.

Authors: Nashon A Ogutu (Maseno University)*; Silas Agumba (KEMRI_CGHR); VINCENT MOSHI (PTBiKenya); Collins Ouma (Maseno University); Edith Ramaitae (M.O.H); Lenson Kariuki Kinyua (Ministry of Health -NMCP); Bernard O Abong'o (Kenya Medical Research Institute (Kemri)); John Gimnig (CDC/DDPHSIS/CGH/DPDM); Eric O Ochomo (Kenya Medical Research institute)

Introduction: The development and evaluation of new generation long lasting insecticidal nets (LLIN) is critical in ensuring the constant supply of effective products against pyrethroid resistant malaria vectors. Pyrethroid-chlorfenapyr nets have shown significant epidemiological impact over pyrethroid-only and pyrethroid plus piperonyl-butoxide (PBO) LLINs in Africa. Here we describe a non-inferiority evaluation of PermaNet® Dual (PD), a new chlorfenapyr plus deltamethrin LLIN, compared to the Interceptor® G2 (IG2), another pyrethroid plus chlorfenapyr net, and to the PermaNet® 3.0 (PN 3.0) a PBO net, in experimental huts in Siaya, western Kenya against free flying pyrethroid resistant Anopheles funestus.

Methods: The study followed a 7x7 Latin square design with treatments employed as unwashed and 20 times washed LLINs. Sleepers entered the huts in the evening and mosquitoes were aspirated from the huts and window exit traps the following morning. Mosquitoes were assessed for blood feeding and then monitored for immediate knockdown 1-hour post collection and delayed mortality after 72 hours. The primary and secondary outcomes were mortality and blood feeding inhibition, respectively.

Results: A total of 15,144 An. funestus mosquitoes were collected from the experimental huts over the 7 weeks' study period, averaging 44 An. funestus per hut per night. Mortality at 72 hours was 37% for the control net, 56% for PN 3.0, 66% for the IG2 and 68% for the PD. Blood feeding inhibition was highest with PN 3.0 at 49%, and least with PermaNet® Dual (PD) at 12%. PermaNet® Dual (PD) and IG2 had no significant differences in mortality (OR=1.10, 95% CI=1.00 – 1.20) or blood feeding inhibition (OR=1.18, 95% CI=1.04 - 1.33 and the lower confidence bounds were within the non-inferiority margins indicating the PermaNet® Dual (PD) met the WHO criteria for non-inferiority to IG2. Compared to the PN 3.0, the PD superior in inducing mortality, OR=1.81 95%CI=1.65 - 1.97, but inferior in blood feeding inhibition, OR=1.63 95%CI=1.43 - 1.86.

Conclusion: The PD was found to be non-inferior to the IG2 and superior to the PN3.0 LLINs in causing mortality but inferior to PN 3.0 in blood feeding inhibition of the vectors. Therefore, the PD met the WHO criteria for non-inferiority to IG2 and may be considered for deployment for public health use against pyrethroid resistant Anopheles vectors of malaria.

Keywords: PermaNet® Dual, PermaNet® 3.0, Interceptor® G2, non-inferiority, insecticide resistance

140.

COST COMPARISON ANALYSIS OF DIFFERENT WORKFLOWS FOR ENTOMOLOGICAL SURVEILLANCE USING A DECISION-TREE APPROACH

Authors: Jonathan Kazungu Karisa (KEMRI-Wellcome Trust Research Programme)*; Rist Cassidy (Virginia-Maryland College of Veterinary Medicine at Virginia Tech, Blacksburg, USA); Mercy J Tuwei (Kemri-Wellcome Trust Research Programme); zedekiah ondieki ombogo (kemri-wellcometrust research programme); Kelly Ominde (KEMRI-Wellcome Trust Research Programme); Brian K Bartilol (KEMRI-WELLCOME TRUST); Haron Musani (KEMRI-Wellcome Trust Research Programme); Caroline Wanjiku (KEMRI-Wellcome Trust Research Programme); Martin Rono (KEMRI - Wellcome Trust Research Programme); Philip Bejon (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi); Joseph Mwangangi (KEMRI); Marta F Maia (KEMRI)

Background: The use of MALDI-TOF MS for entomological surveillance is growing in popularity. However, the potential cost savings of using MALDI-TOF MS in routine entomological surveillance such as that conducted by the national malaria control programme (NMCP) has never been evaluated. This study compares the costs of current diagnostic methods routinely used for entomological malaria surveillance by the Kenyan NMCP relative to those that would be incurred if MALDI-TOF MS were to be used.

Materials and methods: A decision tree analytic model to provide a systematic process for calculating the costs associated with materials, labour and direct costs, and time-to-results for two workflows: 1) current diagnostic methods, and 2) MALDI-TOF MS platform were developed. The analysis assumed a sample size of 15,000 mosquitoes (representing the average number of mosquitoes analysed annually by the national malaria control programme (NMCP) in Kenya) and accounted for time-to-results and direct costs (materials and labour).

Results: Using the MALDI-TOF MS platform, would result in cost savings on reagents and consumables (materials) of up to 30% and 67% on labour costs, resulting in an overall direct cost savings of 34% and net time savings of 81% based on analysis of 15,000

mosquitoes. In a perfect scenario where MALDI-TOF MS is solely used for mosquito surveillance, the costs on materials and labour further reduced, resulting in a total direct cost savings of 83% compared to the current workflow.

Conclusion: MALDI-TOF MS represents an inexpensive and high throughput platform. Despite the initial high capital cost of purchasing the instrument, the ease of performance, the rapid turn-around time to results, and the modest cost per sample makes it a novel methodology that could bring about a paradigm shift in routine entomological surveillance.

Keywords: Entomological surveillance, cost-comparison, MALDI-TOF MS, decision tree,

141.

HOST-SYMBIONT INTERACTION IN MICROSPORIDIA MB INFECTED ANOPHELES ARABIENSIS MOSQUITOES

Authors: Jacqueline Wahura Waweru (icipe)*; Jeremy K Herren (icipe); Daniel Masiga (icipe); Nicola Mulder (University of Cape Town); Lilian M Ang'ang'o (Rhodes University); Edward Edmond Makhulu (icipe); Thomas O Onchuru (Icipe); Joseph N Gichuhi (icipe)

Microsporidia MB (MB), is a maternally inherited symbiont with a strong Plasmodium transmission-blocking phenotype in Anopheles arabiensis mosquitoes. The ability of MB to block Plasmodium transmission, its vertical transmission and avirulence to A. arabiensis make it a novel candidate for Plasmodium transmission-blocking. However, the existing interaction between MB and its host, that would inform on the established and persistent symbiosis and the endosymbiont's Plasmodium transmission blocking phenotype remain unknown. We used transcriptomics to determine how MB affects host factors across different host tissues predominantly localized by MB i.e., fat bodies, midgut, and ovaries, in sugar fed and blood fed mosquitoes. Our results show that MB affects genes involved in the Plasmodium developmental cycle in the guts of both sets of mosquitoes. In sugar fed mosquitoes, MB infection triggered trypsin and carboxypeptidases downregulation in the guts. Trypsins are categorized as serine proteases and are linked to roles such as digestion, activation of immune responses through processes such as melanization and the activation of Plasmodium falciparum prochitinases which allows Plasmodium to transverse through the periotrophic matrix. Downregulated trypsins could infer Plasmodium ookinete prochitinase remaining inactivated in MB positive guts and thus preventing the parasite from crossing the midgut barrier. In blood fed mosquitoes, Ornithine decarboxylase was downregulated. Ornithine decarboxylase is important in cell growth as it catalyzes the production of polyamines required for stabilizing newly synthesized DNA. Increased polyamine levels increase arginine sequestration making it unavailable for nitric oxide formation needed for immune responses against Plasmodium. Downregulated Ornithine decarboxylase levels in the guts of MB infected mosquitoes could be triggering increased nitric oxide levels thus sterilization and Plasmodium clearance prior crossing the midgut epithelial barrier. Microsporidia MB infected ovaries on the other hand exhibited similar gene expression profiles to the non-infected mosquitoes in both sugar and blood fed mosquitoes. This could be adaptive for the symbiont to maximize transmission and the symbiotic interaction. MB infected fat bodies indicated a systemic gene expression interference. Specifically, MB infected fat bodies from sugar fed mosquitoes were under high oxidative stress as compared to the non-infected fat bodies. High oxidative stress could damage the Plasmodium parasite by encapsulation and melanization. In the blood fed mosquitoes pattern recognition receptors such as galectins were up regulated indicating that the systemic immune response was activated. In summary, these results suggest that MB could be blocking Plasmodium transmission by affecting host midgut physiology or by priming the host immune system at either local or systemic levels.

Keywords: Microsporidia MB, host-symbiont interaction,

142.

MICROSPORIDIA MB INFECTION RATES IN *ANOPHELES GAMBIAE S.S.* AND *ANOPHELES ARABIENSIS* FROM BUSIA, A MALARIA ENDEMIC ZONE OF WESTERN KENYA

Authors: Herzel Tiffany Ms Wandera (KEMRI)*; Edward Edmond Makhulu (icipe); Peter Mutai (KEMRI); Martin Sang (KEMRI); Sharon Nyagaka (KEMRI); Maurice Ombok (KEMRI); Stanley Kitur (KEMRI); Lucy Njeri Wachira (KEMRI); Damaris Matoke-Muhia (KEMRI); Eric Ochomo (KEMRI); Jeremy K Herren (icipe); Luna Kamau (Kemri)

Introduction: Malaria remains a major public health concern despite decades of control efforts. Microsporidia MB has potential in malaria control since studies have shown that infection with Microsporidia MB, results in reduction of vector densities and plasmodium parasite load in mosquitoes. This study aimed at comparing Microsporidia MB infection rates in natural populations of Anopheles gambiae s.s. and Anopheles arabiensis from Busia, a malaria endemic zone of western Kenya.

Methods: In this cross-sectional study, mosquitoes were collected from Busia County in June 2023 during the rainy season. A total of 751 Anopheles gambiae s.l. larvae and indoor-resting adult mosquitoes identified as anopheles based on morphology were collected. Samples were transported to the laboratory where the larvae were reared into adults in the insectary and morphological identification confirmed. DNA extraction and molecular species identification was carried out for both sets of samples and Microsporidia MB detection was done by amplification of the MB 18S region and electrophoresis on 2% agarose gel.

Results: A total of 751 Anopheles gambiae s.l. mosquitoes were analyzed. Of these, 405 were adults reared from field-collected larvae and comprised 263 samples (64.9%) An. gambiae s.s. and 142 samples (35.1%) An. arabiensis. Of the remaining 346 field-caught adult mosquitoes 330 (95.4%) were An. gambiae s.s. and 16 (4.6%) An. arabiensis. Overall, Microsporidia MB infection rates were significantly higher in field-caught adults compared to those sampled as larvae ($z = 3.3378$, $p = 0.00084$) and significantly higher in An. gambiae s.s. compared to An. arabiensis ($z = 2.3426$, $p = 0.01928$ in adult collections; $z = 13.9801$, $p = 0.00001$ for samples collected as larvae). Microsporidia MB positivity in samples collected as larvae was 4.69% (19/405): 95% CI [3, 7.2], with a positivity rate of 4.4% (18/405) 95% CI [2.8, 6.9] in An. gambiae s.s. and 0.25% (1/405): 95% CI [0.044, 1.4] in An. arabiensis. For field-collected adults, Microsporidia MB positivity was 11.2% (39/346): 95% CI [8.4, 15], with a positivity rate of 10.7% (37/346): 95% CI [7.9, 14], in An. gambiae s.s. and 0.58% (2/346): 95% CI [0.16, 2.1], in An. arabiensis.

Discussion: The significantly higher Microsporidia MB infection rates in An. gambiae s.s. compared to An. arabiensis suggests a higher affinity in the former species. This is desirable since An. gambiae s.s. remains the predominant vector species in the study area. The higher Microsporidia MB infection rates in indoor-collected adults compared to the larval collections may suggest higher prevalence in indoor samples although this, alongside environmental factors that could affect variations in infection prevalence and intensity need investigation. Further, analysis of Microsporidia MB strain diversity to understand whether there are any species-related variations, is important in the design of vector control tools employing Microsporidia MB.

Keywords: Vector Control, Malaria, Anopheles Larvae, Anopheles gambiae S.L, Microsporidia MB

143.

SPECIES DIVERSITY AND ABUNDANCE OF TICKS COLLECTED FROM LIVESTOCK IN SELECTED PASTORAL REGIONS IN KENYA

Authors: Hellen S Koka (Kenya Medical Research Institute)*; Solomon K Langat (Kenya Medical Research Institute (KEMRI)); Francis M Musili (KEMRI); James K Mutisya (Kenya Medical Research Institute (KEMRI)); Samuel Owaka (KEMRI); Millicent Sifuna (Texas Tech University); Juliette Ongus (JKUAT); Joel Lutomiah (KEMRI); Rosemary Sang (ICIPE)

Background: Ticks have veterinary and public health importance as they transmit many pathogens. Identification of tick species, diversity and their geographic distribution is critical to understanding the epidemiology of tick-borne diseases and developing targeted interventions.

Methods: Ticks were collected from livestock in Isiolo, Baringo, Turkana and West Pokot counties and identified to species using morphological identification keys. After identification, representative adult ticks of medical importance from each site were randomly selected and subjected to molecular identification. Briefly, DNA was extracted from thirty tick samples of different species from each site and PCR was done using the mitochondrion cytochrome c oxidase 1 (cox1) gene. The PCR products were cleaned using Exo-sap, sequenced and sequences compared with those on GenBank by Blast analysis. Haplotype diversities were determined using DnaSP and phylogenetic relationships were inferred using the Maximum Likelihood algorithm.

Results: A total of 12,206 ticks were collected. Thirteen different tick species were identified across the four sites. However, the highest number of ticks were collected from Turkana (45.4%), followed by Isiolo (23.1%), Baringo (22.7%), while West Pokot had the least collection (8.8%). Rhipicephalus appendiculatus was mainly collected in sheep in Turkana (n= 405), and Hyalomma marginatum from camels in Isiolo (n=182). From the 120 tick DNA extracts, 73 PCR products were amplified by the mitochondrial cox1 gene and sequenced. The morphological and molecular identification for Amblyomma tick species were consistent. However, incongruence was reported in the identification and classification of some Hyalomma and Rhipicephalus tick species.

Conclusion: Species of medical importance were reported in this study and many are well known vectors of arboviruses such Crimean Congo Haemorrhagic fever virus, Dugbe, Ngari, Thogoto amongst others and rickettsial infections such as Rickettsia africae, R. conorii and Coxiella burnetii. The data for morphological and molecular identification for Hyalomma species was not consistent and this may be due to introgressive hybridization. Ticks are dynamic and therefore, this findings adds to baseline data available on tick species in pastoral ecologies in Kenya. It also shows the need for continous updating in order to assess the risk of tick-borne diseases.

Keywords: Tick, species diversity, molecular diversity

144.

INSECTICIDE RESISTANCE, RESTING BEHAVIOR AND SPOROZOITE INFECTION RATES IN ANOPHELES GAMBIAE AND ANOPHELES FUNESTUS IN TESO SUB-COUNTY, WESTERN KENYA.

Authors: Sarah Nyasende1*, Daniel Kiboi2, Stanley Kitur3, Lucy Wachira3, Charles Mbogo6, Luna Ka

Background: Malaria transmission in Kenya is driven mainly by Anopheles gambiae, Anopheles arabiensis and Anopheles funestus mosquitoes, vectors which have been reported to adapt in diverse climatic conditions and seasonality. Chromosomal inversions have been reported to play a major role in mosquito's adaptive behavior. This study sought to understand the association between 2La chromosomal inversion, with sporozoite infection rates, and insecticide resistance in Anopheles gambiae mosquitoes from Teso, a malaria-endemic area, in Western, Kenya.

Methods: Both adult and larvae mosquitoes were collected during short rains October-December 2015, and long rains April-June 2016. Mosquitoes were identified morphologically using Taxonomical keys by Gillies and De Meillon, (1968) Gillies M.T. and Coetzee,M. (1987) and molecular analysis (Collins et al., (1987) Scott et al., (1993) and Koekemoer et al., (2002) protocols. Knockdown resistance allele genotyping (Bass et al., 2007 and Ochomo et al., 2015), and 2La chromosomal inversion analysis (White et al., 2007). Plasmodium falciparum sporozoite infection analysis, and host bloodmeal analyses, was performed using Enzyme-Linked Immunosorbent Assays (Wirtz et al., (1987). The determination of mosquito susceptibility levels to pyrethroids followed the WHO 2016 guidelines for insecticide resistance monitoring.

Results: Total collections were 2,306 Anopheles mosquitoes, An. arabiensis constituted 48.4% and An. gambiae s.s. 51.6%. Plasmodium falciparum infection in An. arabiensis and An. gambiae s.s. was 0.6% and 0.4% respectively. Susceptibility to deltamethrin and permethrin by An. gambiae mosquitoes was less than 90% indicating resistance. Knockdown East mutation was dominant in all An. gambiae mosquitoes analyzed, there was no KDR west mutations in the samples analyzed. Mosquitoes with chromosomal inversion standard karyotype was found more indoors than outdoors. The correlation of An. gambiae mosquitoes with 2La chromosomal inversion and Plasmodium falciparum sporozoite infection showed a significant association with Chi-square test of association($\chi 2$=9.150, df=1, P<0.01). The feeding preference by An. gambiae mosquitoes was human host.

Conclusion: An. gambiae s.s. and An. arabiensis was found to be the predominant malaria vectors in Teso Western Kenya. We observe an association of 2La chromosomal inversions and Plasmodium falciparum sporozoite infection in An. gambiae mosquitoes. An. gambiae mosquitoes with 2La inversion rest indoors and are susceptible to sporozoite infections, and thus may play a role in continuous malaria transmission in the region.

Keywords: Bioassays, Pyrethroids, Sporozoites, Knockdown resistance, Chromosomal inversion

145.

ENTOMOLOGICAL SURVEILLANCE OF MALARIA VECTORS IN BARINGO COUNTY, KENYA

Authors: Lucy Wachira1,Lenson Kariuki2, Stanely Kitur1, Edith Ramaita2, Kiambo Njagi2, Luna Kamau1, Charles Mbogo3, Damaris Matoke-Muhia1

1Center for Biotechnology Research and Development, KEMRI, Nairobi

2 Division of National Malaria Program, Ministry of Health, Nairobi

3 Centre for Geographical Medicine Research-Coast, KEMRI, Kilifi

*corresponding author lwachira@kemri.go.ke

Introduction: Baringo County is an arid and semi - arid region that is prone to seasonal transmissions of malaria mostly in rainy seasons. Recently, there have been reports of malaria outbreaks in the area, necessitating vector surveillance and its associated risk factors to inform control strategies. In this study, we undertook vector surveillance in Baringo County to determine malaria vector species, blood feeding behavior and parasite infection rates.

Methodology: Mosquito sampling was conducted in June 2018 and February 2022 in three Sub-counties 6 villages in Baringo County. Adult mosquitoes were sampled using CDC light traps and procopack while scoopers were used for larvae collection. Taxonomical keys were used for mosquito morphological identification. Specimens were preserved in silica gel in labeled eppendorf tubes. Anopheles gambiae and An. funestus complex mosquitoes were further analyzed for sub-species identification following DNA extraction and PCR. We did sporozoite and blood meal analysis using ELISA technique.

Results: We sampled 84 households where a total of 1063 anopheles mosquitoes were collected. Of these 21% were identified as An. funestus while 78.9 % were An. gambiae. 1.2% were positive of malaria sporozoites. On blood feeding preference, 11.7% had fed on human.

Conclusion: There is presence of malaria vectors in the entire three sub - counties in Baringo sampled. An. funestus is the most prevalent vector in the region. Malaria control interventions need to be implemented in the county despite it being categorized as a seasonal or epidemic prone zone.

Keywords: Species identification, Bloodmeal ELISA, Sporozoite ELISA

146.

CLIMATE CHANGE ASSOCIATED ECOLOGICAL IMPACTS ON VECTOR-BORNE DISEASE TRANSMISSION - A CONTEMPORARY GLOBAL PERSPECTIVE ON

DISPARATE CLIMATE VULNERABILITY

Authors: James M Mutunga (Pennsylvania State University)*; Esther Obonyo (Pennsylvania State University)

Background: The impacts of climate change on natural and built environments are highly varied at local and global scale. Arthropod disease vectors such as mosquitoes, ticks, tsetse flies, blackflies and sand flies have varied clonal and ecological niches influenced by multiple factors that propagate their bionomics and disease transmission. Climate change impacts therefore affect disease transmission landscape through intrinsic and extrinsic effects on vertebrates hosts, the vectors and the pathogens they transmit. Climate and non-climate drivers of vector borne disease transmission present complex interactions posing dynamic health risks across regions. In this study, we examine the documented global ecological changes in both natural and built environments and analyze the trends of vector-borne disease (VBD) occurrence and spread across time and space.

Methods: Guided by a formulated research question, scientific literature was searched from Web of Science, Scopus, Wiley Online Library, Google Scholar and PubMed. Keywords used were “environment”, “climate change”, “vector borne”, “disease” and their combinations. Initial search results (n = 565) were subjected to a prescribed inclusion criteria to obtain selected set of articles that were used for information appraisal, evidence synthesis and analysis to generate the findings described here-in. A spatial-temporal rendering of the main subject areas, regions and disciplines are graphically presented.

Results: We report localized climate change induced disease risks with variability at regional and global scale. Contributing factors to this variability include disparities in socioeconomic status, vector bionomics, ecotypes and ecosystem disturbance, natural and built environment parameters, and intrinsic vector-pathogen biological attributes. We report existing deficiencies in datasets for predictive modeling of VBD outbreaks and propose steps to meet these needs. Trends of disease transmission indicate a higher vulnerability of the global south and calls for urgent interventions to reduce disproportionate climate impacts on underserved communities. The expanding urbanization in global south is associated with escalating effects of climate risks, hence research and development investments are needed to minimize the costs and consequences of climate impacts while protecting urban development gains.

Conclusion: We recommend increased investment in data on vector dynamics and evolution of natural and built environments under climate change pressures. Enhanced interdisciplinary integration of diverse skillsets is needed. Deployment of experimental and theoretical modeling of “climate superbugs” will allow development of adaptive and multi-ecosystem disease prevention strategies. The physiological plasticity of vectors and their environmental drivers contribute to climate attribution science required in predictive responses to disease outbreaks.

Keywords: climate change vector-borne disease transmission environment

147.

VALIDATION USING ATTRACTIVE SUGAR BAITS (ASBS) CONTAINING A FLUORESCENT DYE IN SIAYA COUNTY, WESTERN KENYA: AN EVALUATION OF ANOPHELES FEEDING RATES

Authors: Jackline Jeruto

Background: Vector control is an essential component of malaria prevention. Additional mosquito control tools are urgently needed to further suppress malaria transmission worldwide. Attractive targeted sugar baits (ATSBs) exploit the sugar feeding behavior of mosquitoes. Prior to epidemiological trials on ATSBs, validation studies were conducted in rural villages of western Kenya to assess the levels of mosquito feeding on attractive sugar baits (ASBs) with uranine fluorescent dye and were made to assess whether the deployment of two versus three bait stations per building structure led to a significantly different daily feeding rate by the local vectors of malaria as a proxy for ATSBs, and to compare this with the minimum rate for an epidemiological effect, according to separate modelling studies. **Methods:** The study followed a cross-over design in ten treatment clusters with two control clusters in Rarieda Sub-County, western Kenya. Either two or three ASBs were deployed to all structures within the ten clusters (5 each) and switched over at two months' time point so that clusters which initially received two ASBs were given three and vice versa. Sample collection and ASB monitoring for durability was done for four months from initial deployment then an additional four months for extended monitoring of ASBs. Mosquitoes were collected using UV light traps and Prokopack aspiration indoors and outdoors then screened for morphological characteristics and fluorescence due to the uranine dye. Samples of mosquitoes collected were processed for molecular species identification and sporozoite infectivity. Data was managed on CommCare® (Dimagi, Inc, Massachusetts, USA) platform and analysis was performed using R statistical software platform and analysis was performed using R statistical software. **Results:** An. funestus s.s. was the predominant malaria vector in the twelve clusters, with overall proportion with dye feeding of 11.2% while the overall proportion with dye for An. gambiae s.l. averaged 3.5%, translating to daily feeding rates of 4.8% (2.4-9.4%) in An. funestus and 1.2% (0.51%-2.8%) in An. gambiae with no significant differences detected between two and three ASB stations. An. funestus s.l. comprised 82% (n=1086) An. funestus s.s. while 6.3% (n=83) were An. Leesoni. Anopheles arabiensis comprised 68% (n=1,342) of the An. gambiae s.l. sampled with An. arabiensis with 21% (n=407) being An. gambiae s.s. An. funestus s.l. samples had a sporozoite positivity rate of 2.28% (n=29) while An. gambiae s.l. samples recorded a sporozoite positivity rate of 1.00% (n=19). **Conclusion:** Anopheles funestus s.s., the dominant malaria vector in the study site demonstrated higher rates of feeding on ASBs compared to An. gambiae s.l. No significant difference was detected between deploying two or three bait stations per structure. The study provided important information utilized in the subsequent deployment of ATSBs in epidemiological trials.

Keywords*:* Anopheles, control, ASB,

SCIENTIFIC SESSION 17:

MCH -3

148.

CHILDHOOD HOSPITAL READMISSION FOLLOWING ACUTE ILLNESS IN AFRICA AND SOUTH ASIA: A SECONDARY ANALYSIS OF CHAIN COHORT.

Authors: Moses M Ngari (KEMRI Wellcome Trust Research Programme)*; Voskuijl Wieger (Amsterdam Centre for Global Child Health & Emma Children's Hospital, Amsterdam, Netherlands); Narshion Ngao (KEMRI Wellcome Trust Research Programme); Benson Singa (KEMRI); Robert Bandsma (Department of Gastroenterology, University of Toronto, Toronto, Canada.); Hama Diallo (Department of Public Health, University Joseph Ki-Zerbo, Ouagadougou, Burkina Faso.); Ezekiel Mupere (Department of Paediatrics and Child Health, Makerere University College of Health Sciences, Kampala, Uganda.); Christina Lancioni (Department of Pediatrics, Oregon Health and Science University, Portland, Oregon, USA.); Abu Sadat Md. Sayeem (Nutrition Research Division, International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b); Dhaka, Bangladesh.); Mohammod Jobayer Chist (Nutrition Research Division, International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b); Dhaka, Bangladesh.); Judd Walson (University of Washington); James Berkley (KEMRI - Wellcome Trust Research Programme)

Background: In low and middle-income (LMIC) settings, children remain vulnerable following hospital-discharge, but little data exist on hospital readmission in this population. To better understand risk of readmission, we estimated the incidence and correlates of hospital readmission among children aged 2–23 months in LMIC settings.

Methods: This is a secondary analysis of the Childhood Acute Illness and Nutrition (CHAIN) Network, a prospective cohort which recruited 3101 children aged 2–23 months admitted with acute illness to nine hospitals in sub-Saharan Africa and South Asia. Children discharged alive after the index admission were analysed for a primary outcome of hospital readmission within 180-days from discharge. Using models with death as the competing event, we evaluated whether demographic, nutritional, clinical and socioeconomic factors were associated with readmission.

Results: Of 2874 children discharged alive, 655 readmission episodes among 506 children occurred: 391 (14%) with one admission and 115 (4%) with multiple readmissions; 41·0 (95%CI 38·0–44·3) readmissions/1000 child-months. Median time to readmission was 42 (IQR 15–93) days. One-third (N=213/655, 33%) of readmissions occurred within one month and two-thirds (N=433/655, 66%) within three months after index discharge respectively. Most readmissions were for the same illness as the index admission with the following percentages of children readmitted with the same condition; pneumonia 72%, gastroenteritis 42%, sepsis 46%, malaria 50% and anaemia 53%.. High illness severity, prior hospitalization, chronic conditions and high maternal mental health score, but not child nutritional status, were associated with readmission. Readmission rates varied significant across sites and sites with the fewest readmissions had the highest mortality.

Conclusion: Hospital readmission occurred in almost 20% of all children in the CHAIN cohort, of which two-thirds occurred more than 30 days after index discharge. Sites differed between their rates of readmission, likely reflecting differential care quality and ability and willingness to access healthcare. Targeting children at risk for poor outcomes following discharge should be a priority and should include optimizing discharge planning as well as interventions targeting post-discharge care and caregiver support.

Keywords: Child Health, Hospital admission, Africa, South-Asia

149.

BURDEN, TIMING, CAUSES AND FACTORS ASSOCIATED WITH STILLBIRTH AND NEONATAL MORTALITIES IN A HEALTH AND DEMOGRAPHIC SURVEILLANCE SYSTEM IN RURAL WESTERN KENYA, 2018-2022.

Authors: GEORGE AOL OTIENO (KEMRI)*; Richard O. Onyando (KEMRI-CGHR); GODFREY BIGOGO (KEMRI); VICTOR AKELO (LSTMED); JOSHUA AUKO (KEMRI); THOMAS MISORE (KEMRI); BRIAN GENGA (KEMMRI); Stephen Munga (Kenya Medical Research Institute (Kemri))

Introduction: Sub-Saharan Africa has the highest stillbirth and neonatal mortality rates worldwide. We sought to understand the burden, timing, causes and factors associated with stillbirth and neonatal mortality in western Kenya.

Methods: We analyzed data from a Health and Demographic Surveillance System that monitors population dynamics of approximately 208,766 individuals. Households are interviewed every six months using a standardized questionnaire about events that happened since prior visit. All women of reproductive age (15-49 years) are asked about their pregnancy status and outcome. Verbal autopsies were done for stillbirth and neonatal deaths using WHO VA 2016 questionnaire and causes of death generated using Inter VA5 algorithm. Data were analyzed using logistic regression in STATA; results were stratified by maternal age.

Results: The stillbirth mortality rates in Asembo, Karemo and Manyatta were 15.6, 17.6 and 12.5 deaths per 1,000 livebirths respectively; the neonatal mortality rates were 18.9, 22.0 and 18.4 deaths per 1,000 live births respectively. Overall, 60% of the stillbirth deaths happened to fetuses over 38 weeks old; 62% of neonatal deaths happened on the delivery day. The leading causes of death were birth asphyxia (41.4%) and prematurity (39.2%) for neonates; fresh stillbirth (52.0%) and macerated stillbirth (30.0%) for stillbirths. Factors associated with stillbirths among women aged 20-24 were no ANC visits (OR 10.31, 95% CI [2.3-45.8]) or attending 1-3 ANC visits (OR 2.0, 95% CI [1.1-3.8]); for women aged 25-29, rural residence (OR 1.7, 95% CI [1.0-2.9]) or attending 1-3 ANC visits (OR 3.9, 95% CI [1.6-9.4]); for women aged 30-34, never married (OR 2.5, 95% CI [1.2-5.0]) or attending 1-3 ANC visits (OR 2.2, 95% CI [1.1-4.3]); for women aged 35-39, attending 1-3 ANC visits (OR 3.8, 95% CI [1.1-12.9]). Factors associated with neonatal deaths among women aged 16-19 were divorce/separation (OR 4.1, 95% CI [1.2-14.5]), less than primary education (OR 17.5, 95% CI [3.1-98.2]), no ANC visits (OR 8.1, 95% CI [2.2-29.6]) and home delivery (OR 4.3, 95% CI [1.9-9.9]); divorce/ separation (OR 2.4, 95% CI [1.0-5.6]) for women aged 20-24; high SES (OR 3.6, 95% CI [1.0-12.9]) for women aged 30-34; no religion (OR 7.5, 95% CI [1.7-34.1]) for women aged 35-39 and divorce/separation (OR 9.2, 95% CI [2.2-37.8]) for women aged 40-49.

Conclusion: We observed high stillbirths and neonatal mortality rates in the study area with most deaths occurring around time of delivery. Most causes of stillbirths and neonatal deaths were preventable. Divorce/separation and ANC attendance were risk factors for stillbirths and neonatal deaths. There is need for improved maternal care before, during and immediately after birth.

Keywords: BURDEN, TIMING, CAUSES, FACTORS, STILLBIRTH, NEONATAL, MORTALITY RATES

150.

IMPACT OF HIV INFECTION AND MALARIA PARASITEMIA ON IMMUNOGENICITY OF INACTIVATED INFLUENZA VACCINE IN PREGNANT WOMEN AND ON MOTHER-TO-CHILD VACCINE-INDUCED ANTIBODY TRANSFER

Authors: MICHAEL O OTIENO (kemri cghr)*; NANCY OTIENO (KEMRI); BRYAN NYAWANDA (KEMRI); SHIRLEY LIDECHI (KEMRI); SIMON KARIUKI (KEMRI); SAMUEL OMONDI (MOH)

Background: Vaccinating pregnant women with seasonal influenza vaccines is recommended by the World Health Organization. However, impact of HIV infection and malaria parasitemia on the immunogenicity of inactivated influenza vaccines and trans-placental transfer of antibodies has not been well-explored.

Methods: At two hospitals in western Kenya, immune responses to influenza vaccination and vertical antibody transfer were assessed in three groups of pregnant women (at <31 weeks gestation): 1) HIV-positive; 2) malaria positive with parasitemia at enrolment (malaria(+ve)); and 3) HIV-uninfected without malaria parasitemia (comparison group). All women received trivalent inactivated influenza vaccine. Hemagglutination inhibition assay (HAI) antibody titers were measured at enrolment and vaccine administration (day 0), day 16 post-vaccination (range 14-24 days), and at delivery. For infants, HAI titers were measured in cord blood, at week 16 and 24 weeks post-delivery. Seroconversion against each virus subtype was defined as four-fold rise in HAI titer with post-vaccination titer ≥1:40, and vaccine-induced antibody transfer as infant HAI titers ≥1:40.

Results: Between June 2018 – January 2020, 355 pregnant women were enrolled and vaccinated (89 HIV+, 77 malaria(+ve) and 189 HIV-/malaria(-ve). Two to four weeks post-vaccination, >86% and >83% of women in all three groups achieved protective HAI titers (≥1:40) against A/H1N1pdm09 and A/H3N2, respectively; lower proportions achieved titers ≥1:40 against influenza B/Victoria: HIV+ (53%), malaria(+ve) (56%) and HIV-/malaria(-ve) (71%). A/H1N1pdm09 was the most immunogenic subtype and most women (>77%) had HAI titers ≥1:40 at delivery. Trans-placental antibody transfer was similar across groups of women. At birth, 84%, 75% and 56% of newborns had HAI titers ≥1:40 against A/H1N1pdm09, A/H3N2, and B strains.

Conclusion: This study provided additional evidence of immunogenicity of influenza vaccination during pregnancy among HIV-infected and malaria-infected women, high levels of vertical antibody transfer in all groups and potential protection of infants during the first six months of life.

Keywords: HIV Infection, Malaria Parasitemia, Immunogenicity, Inactivated Influenza Vaccine, Pregnant Women

151.

PRENATAL EXPOSURE TO SARS-COV-2 INFECTION DURING PREGNANCY AND NEURODEVELOPMENTAL OUTCOMES AMONG INFANTS IN WESTERN KENYA AT 6 MONTHS OF AGE

Authors: NANCY OTIENO (KEMRI CGHR); Bryan BN Nyawanda (KEMRI); paul otieno jaoko (KEMRI CGHR)*; MICHAEL OTIENO (KEMRI CGHR); EUNICE ORERI (MOH)

Background: Diagnosis of COVID-19 during pregnancy is associated with adverse pregnancy and neonatal outcomes. However, knowledge on the effect of exposure to COVID-19 during pregnancy on infant development is limited. We assessed the risk of developmental delay at 6 months of age in infants exposed to COVID-19 during pregnancy.

Methods: We enrolled pregnant women (under 31 weeks of gestation) and contacted them weekly to identify cases of COVID-like illness (CLI). We followed them until delivery, and together with

their infants for 6 months. Nasopharyngeal and oropharyngeal swabs were obtained from patients with CLI and tested for SARS-CoV-2 by real-time reverse transcription polymerase chain reaction. We performed growth and developmental evaluations for all infants at 6 months using the Caregiver Reported Early Development Instruments (CREDI), assessed through four domains: cognitive, language, motor and socio-emotional. Failure was flagged when -2< z-score >2. Differences in developmental outcomes by maternal prenatal COVID-19 exposure were assessed using chi-square tests.

Results: Between February 1 – December 2, 2022, we enrolled 1,988 pregnant women and 1641 (82.5%) gave birth. Of the 1,641 women, 360 (22.2%) reported ARI/CLI during pregnancy; 345 (95.8%) were tested for SARS-CoV-2; and 54 (15.7%) were positive. Of the 345 infants whose mothers had been tested for SARS-CoV-2 during pregnancy, 156 (45.2%) infants had their CREDI

assessment done at 6 months. Of these, 26 (16.7%) were born to mothers who had COVID-19 during pregnancy. Infants whose mothers had COVID-19 during pregnancy were more likely to have delays in cognitive (11.5% vs 2.3%; p-value=0.03) and socio-emotional development

(15.4% vs 4.6%; p-value=0.04).

Conclusion: Maternal prenatal COVID-19 exposure was associated with lower CREDI cognitive and socio- emotional scores in infants at 6 months. Further analyses are needed to determine if such findings are identified through Bayley testing, if they persist through toddlerhood, and are preventable through COVID-19 vaccination.

Keywords: Prenatal, SARS-CoV-2 Exposure, Pregnancy, Neurodevelopmental Outcome Infants

152.

ASSESSMENT OF SOCIAL SUPPORT LEVELS AND ASSOCIATED FACTORS AMONG WOMEN ATTENDING POSTNATAL CLINIC AT GULU REGIONAL REFERRAL HOSPITAL, UGANDA

Authors: Nannungi Christine (GULU UNIVERSITY)*

Background: Social support is an important factor which can affect mental health as well as general wellbeing of postpartum mothers via its protective role against postpartum complications. In this study, we assessed Social Support levels and Associated Factors among Women Attending Postnatal Clinic at Gulu Regional Referral Hospital, Uganda.

Methods: This was a facility-based cross-sectional study with a quantitative approach among 223 postpartum mothers attending the postnatal clinic at Gulu Regional Referral Hospital. Data were collected using interviewer guided questionnaires. Oslo-3 social support scale was used to assess social support levels. Oslo-3 social support scale score of 3-8, 9-11 and 12-14 defined poor, moderate and strong social support respectively. Multivariate analysis was used to identify factors associated with achievement of statistical significance at $P \leq 0.05$.

Results: Of the 223postpartum mothers, 165(74.0%) were aged 20-35years, and (177)79.4% married. Overall, majority of the study participants experienced moderate social support 115(51.6%) and poor social support 86(38.6%). Only 22(9.9%) had strong social support. The factors associated with social support levels were emotional violence, major financial crisis, being Anglican and technical/vocational education as the highest level of education.

Conclusion: In this study, most of the postpartum mothers experienced moderate social support with emotional violence and major financial crisis among postpartum mothers, Anglican postpartum mothers and postpartum mothers whose highest level of education was technical/vocational education found to have a statistically significant correlation with the levels of social support among the postpartum mothers.

Keywords: Social support, social support levels, postpartum mothers, postnatal clinic

153.

MATERNAL HIV STATUS AND THE RISK OF ADVERSE PREGNANCY OUTCOMES: A COHORT OF WOMEN PARTICIPATING IN IMPROVE 1 AND IMPROVE 2 STUDIES.

Authors: EVERLYNE D ONDIEKI (KEMRI/CGHR)*; Hellen Barsosio (Liverpool School of Tropical Medicine (LSTM)); George O Otieno (KEMRI); Henry Aura (KEMRI); Eric Onyango (Kemri)

Everlyne Delylah Ondieki1, Hellen Barsosio1,2, George Olilo1, Henry Aura1, Eric Donald1

Affiliations

1. KEMRI, Centre for Global Health Research, Kenya

2. Liverpool School of Tropical Medicine, UK

Background: The intersection of maternal HIV infection and pregnancy outcomes has been a subject of critical importance in the realm of maternal and child health. The IMPROVE 1 and IMPROVE 2 studies have provided a comprehensive platform to investigate the intricate relationship between maternal HIV status and the risk of adverse pregnancy outcomes. These will be essential for informing evidence-based interventions that may prevent negative fetal and/or infant consequences.

Methodology: Data for HIV-negative pregnant women were extracted from IMPROVE 1, a randomized, double-blind, three-arm trial conducted in regions with elevated sulfadoxine-pyrimethamine resistance in Kenya, Malawi, and Tanzania. For HIV-positive pregnant women, data were extracted from IMPROVE 2, a randomized, double-blind, two-arm, placebo-controlled trial focused on monthly IPTp with dihydroartemisinin-piperaquine for malaria in HIV-infected participants on daily cotrimoxazole eligible for (or on) daily tenofovir-lamivudine-dolutegravir (TLD) and with an undetectable viral load.In these trials, women with viable singleton pregnancies between 16-28 weeks gestation were enrolled. Multivariable logistic regression was employed to identify associations between maternal HIV status and adverse pregnancy outcomes.

Results: The median age at enrolment was 25 years, with an interquartile range (IQR) of 21 to 30 years. Women in the Improve 2 group were notably older than those in the Improve 1 group, with a median age of 30 compared to 24 ($p < 0.001$). Less than half of the women (48%) had attained a primary level of education, and only 34% had completed secondary education. Compared with their HIV-negative counterparts, HIV-positive women were more likely to experience an adverse pregnancy outcome, odds ratio (OR) 1.3[95% confidence interval (CI): 1.06–1.58]; miscarriage OR 1.83, 95% CI: 1.06, 2.77; or a stillbirth, OR 1.80 [95% CI: 1.16–3.09]. Cohabiting women exhibited nearly a two-fold increase in the odds of adverse pregnancy outcomes (OR = 1.75, 95% CI: 1.08, 2.82). The odds of experiencing adverse outcomes decreased with an increase in the level of education, for those with a primary education (OR = 0.71, 95% CI: 0.55, 0.91) and those with a secondary education (OR = 0.64, 95% CI: 0.49, 0.85). Women in urban settings had 53% increased odds of adverse outcomes compared to those in rural settings (OR = 1.53, 95% CI: 1.11, 2.11).

Conclusion: HIV-positive pregnant women continue to have an increased risk of adverse pregnancy outcome compared to their HIV negative counterparts.Therefore, more research is required to investigate the causes of this ongoing discrepancy to enable interventions to improve pregnancy outcomes among HIV-positive women and their children.

Keywords: HIV,pregnancy,adverse pregnancy outcomes

154.

DEVELOPMENT OF A SHIGELLA MULTIVALENT BIOCONJUGATE VACCINE: A PHASE I/II RANDOMIZED, CONTROLLED AND AGE DESCENDING STUDY INCLUDING DOSE FINDING IN KENYAN INFANTS

Authors: Jane Adetifa 1, Linet Cherono 2, Chinaza Ezirim 3, Cristina Alaimo 3, Patricia Martin 3, Josphat Kosgei 2, Mainga Hamaluba 1.

1 KEMRI-CGMRC, Kilifi, Kenya, 2 KEMRI-USAMRD-K, Kericho, Kenya, 3 LimmaTech Biologics AG, Schlieren, Switzerland.

Background: Shigella is among the most common causes of severe diarrhea and dysentery worldwide, especially among young children from lower resourced countries and travelers. Although several oral Shigella vaccines have been clinically evaluated, risk of reactogenicity and potential reversion back to a pathogenic phenotype have proven challenging. Thus, a new type of vaccine to prevent shigellosis is key.

The O-antigen serotype-specific immune response detected in association with convalescence from shigellosis has encouraged development of a new generation of glycoconjugates as an alternative vaccine strategy against Shigella.

A Shigella flexneri 2a bioconjugate has shown, in a controlled human infection model, protection from the most severe form of the disease after challenge with S. flexneri 2a strain 2457T. In addition, immune responses post vaccination were associated with a lower disease severity score.

Methods: The potential of bioconjugation to develop a high fidelity and cost-effective multivalent Shigella vaccine targeting the most common serotypes contributing to global morbidity and mortality has been exploited. The tetravalent Shigella4V bioconjugate, including O-antigens from S. flexneri 2a, 3a, 6 and sonnei, has been evaluated for safety and immunogenicity in the target population of 9 months old infants. The trial was conducted in Kenya starting with a step 1, age descending and dose-escalating cohort, followed by a step 2 dose finding cohort where the target population received a 3dose schedule of the bioconjugate delivered with and without alum adjuvant.

Results: The last patient last visit occurred in Q4 2022 and immunogenicity and safety data (from the target population) from the interim analysis (IA) was made available in Q3 2022, the remaining data will be available in Q4 2023.

Conclusion: The IA data has shown good immunogenicity 1 month post 2nd vaccination across all treatment groups and serotypes along with well distributed and mostly mild safety events. Following the positive IA results, we have progressed towards the next steps.

Keywords: Safety and immunogenicity of Shigella-tetravalent biconjugate vaccine.

155.

IMPACT OF MALNUTRITION ON CLINICAL OUTCOMES AMONG CHILDREN WITH SEVERE ACUTE RESPIRATORY ILLNESS IN KAKUMA, KENYA

Authors: JOEL A MACHUKI (Henry Jackson Foundation Of Medical Research International)*; Lilian Waiboci (University of Nairobi); Jorim Mr Ayugi (KEMRI-CGHR); Elizabeth Simiyu (IRC); Peter M kinuthia (HJFMRI); Raphael Nyonje (University of Nairobi); Nancy Otieno (KEMRI-CGHR)

Background: Malnutrition is common among children under 5 years of age, particularly in refugee settings, and is an important risk factor for acute respiratory infection. Moreover, severe acute respiratory illness (SARI) contributes to significant morbidity and mortality in young children. However, the impact of malnutrition on clinical outcomes in children hospitalized with acute respiratory illness is under recognized, especially in sub-Saharan Africa. We assessed the prevalence of malnutrition and patient outcomes among children hospitalized with acute respiratory illness at Kakuma Refugee Camp, northern Kenya.

Methods: We analyzed data collected as part of sentinel surveillance for SARI. Between January 2019 and December 2022, we identified children <5 years from Kakuma refugee camp with SARI (defined as acute illness in the last 10 days with fever (measured (≥38°C) or history of fever), cough and requiring hospitalization). Malnourished cases were identified through clinical assessment using the mid-upper arm circumference evaluation. Influenza infection was confirmed through real-time reverse transcription polymerase-chain reaction. Measures for severity of malnutrition included duration of hospital stay and death. We used chi-square tests to assess differences in clinical outcomes.

Results: Out of 2981 SARI cases, 1101 (36.9%) had malnutrition. Half of the malnourished children (510/1101, 46.3%) were under one year of age. Influenza infection was detected in 378 (12.7%) of all SARI patients. Malnourished cases were more likely to have influenza (15.3% vs 11.2%; p=0.001), stay longer (7 days or more) in the hospital (23.3% vs 12.9%; p<0.001) or die during hospitalization (2.5% vs 1.2%; p=0.005) compared with cases without malnutrition.

Conclusions: Malnourished children with SARI were more likely to have influenza, prolonged hospital stay or die. The findings highlight the need to prioritize the management of malnourished children to reduce poor outcomes among young children, including influenza vaccination.

Keywords: Malnutrition, Clinical Outcomes, Kakuma

SCIENTIFIC SESSION 18:

NCDS

156.

PATTERNS OF ORTHOPEDIC AND TRAUMA ADMISSIONS TO A TERTIARY TEACHING AND REFERRAL HEALTH FACILITY IN KENYA: CHART REVIEW

Authors: Maxwell P Omondi (University of Nairobi)*

In Kenya, the incidence of injuries and violence is high, with mortality levels increasing over the years to account for 3.5% of all deaths in 2009, and mainly affecting the productive and younger population. There is need to strengthen a national referral system for primary, secondary and tertiary care and reduce the burden and mortalities of violence and injuries by 27% by 2030. Tertiary hospitals in resource-limited countries should treat referred patients but in reality, are the first level of care for the vast majority of patients. As a result, the tertiary facility effectively functions as a primary health care facility. The urban phenomenon of widespread self-referral results in congestion and inappropriate utilization of tertiary care facilities. Kenyatta National Hospital (KNH) was established as a National Referral and Teaching Hospital, to provide training and medical research and provide specialized health care to referred patients as per KNH Board order of 1987 contained in the Legal Notice No. 109. The study objective was to determine the patterns of orthopedic and trauma admissions to KNH. This was descriptive study design. 905 patient charts were reviewed in 2021. Majority 66.3% were between 25 – 64 years with those above 65 years being 40 (4.4%). Children 0-14 years comprised 10.9% of the admissions. Of the 905 admissions, 80.7% were accident and trauma-related admissions while 17.1% were non-trauma related admissions. About 50.1% were facility referrals while 49.9% were walk-ins. Majority of admissions were through Accident and Emergency Department 78.1% while the rest from the clinics. About 78.7% were emergency admissions while 20.8% were elective admissions. Approximately 48.5% were due to Road Traffic Accidents and 20.9% due to falls. Close to 44.8% were casual workers and 20.2% unemployed. About 34.0% attained primary education and 35.0% secondary education. Female admissions were due to non-trauma conditions as compared to male admissions ($p<0.001$). Admissions for those aged 25 – 64 years were 3.5 more likely to have emergency admission as compared to those aged 0 – 14 years. Male were 65.1% less likely to have elective admissions compared to female ($p<0.001$). Whereas lower limb injuries and non-trauma related conditions were the most commonly admitted conditions, Lower limb injury and spine cases were mostly facility referred while non-trauma conditions were walk-in patients. Vast majority (89.2%) of admissions were from Nairobi Metropolitan region. This means the catchment population for KNH is mostly within Nairobi county and its environs. Therefore, there is need to educate the general public on the role of KNH as a referral health facility and patients encouraged to visit lower-tier health facilities for essential orthopedic and trauma care, upscale the training of spine surgeons and set-up trauma registry at KNH to monitor trauma case load and to feed policy makers for corrective action.

Keywords: Patterns, orthopaedic and trauma, admissions

157.

EVALUATION OF BACTERIAL PATHOGENS FROM SELECTED DIABETIC FOOT ULCER PATIENTS AT THIKA LEVEL 5 HOSPITAL, KIAMBU COUNTY, KENYA.

Authors: Ameyo Daglus (Kenya Medical Research Institute)*

Abstract: In this study, Bacterial pathogens were identified and evaluated in diabetic patients with foot ulcers at Thika Level 5 Hospital. The study uncovered a correlation between bacterial pathogens and foot ulcer progression, as well as the spectra of bacteria, the stage of diabetic foot ulcers, and demographic factors.

Introduction: Diabetic foot ulcers have a major impact on the morbidity and mortality of patients with diabetes in Kenya. There is lack of up-to-date information on microbial isolates from diabetic foot ulcers in Kiambu County. Timely diagnosis of diabetes mellitus and prognosis of diabetic foot ulcers is very important to reduce disease progression and other infections (Mutonga et al., 2019). This study aims to evaluate this data that will help clinicians diagnose and treat patients with foot ulcers. A laboratory-based cross-sectional study design was used. The study was conducted at Thika Level 5 Hospital for 3 months. Twenty-five patients were selected through Consecutive sampling and informed consent was taken. Sterile cotton swabs were moistened in normal saline and used to obtain pus swabs aseptically. The swabs were cultured on blood agar and MacConkey agar and incubated aerobically for 24 hours. Suspect Pure colonies were gram stained and a series of biochemical tests were carried out to further identify the bacterial isolates.

Results and Discussions: From the 25 patients,24 (96%) had infected diabetic foot ulcers. 13(52%) were women and 12(48%) were male. 40% of infected individuals were from age 51-60 years which is the productive age. A total of 64 bacterial isolates were obtained. 96% of the patients with foot ulcers had poly-bacteria and 4% had monobacteria. The predominant bacteria were Escherichia coli 21/25(84%) followed by Staphylococcus aureus 11/25 (44%). Most patients were at Wagner grade 2 (40%) and Wagner grade 3 (32%) foot ulcer stages. Neuroischemic was the most predominant clinical foot ulcer (40%), followed by ischemic foot ulcers (35%) and lastly neuropathic foot ulcers (25%).

Conclusion: From these findings, it is evident that physicians should emphasize the need and routine carrying out of culture on the infected diabetic foot ulcers before treatment. This approach will enable accurate identification of wound-infecting pathogens. Subsequently, correct diagnosis and treatment will be achieved.

Keywords: Diabetic,foot ulcers,Immunosuppression

158.

UNDERSTANDING THE AFTER VIOLENCE CARE FOR ADOLESCENT GIRLS AND YOUNG WOMEN EXPERIENCING GENDER BASED VIOLENCE IN KISUMU COUNTY

Authors: Omollo Mevis (KEMRI/CGHR)*; Isdorah Akoth (KEMRI/CGHR); Hellen Barsosio (Liverpool School of Tropical Medicine (LSTM)); Eucabeth A Awuonda (KEMRI-CGHR); Peter Ochere (KEMRI/CGHR); Ruby Reed (Stanford University); Jennifer Lang (Stanford University); Clea Sarnquist (Stanford Univeristy)

Background: Cases of Gender Based violence (GBV) have over time increased in Kisumu County despite the various advocacies on eliminating the shadow pandemic hence increasing the burden of mental health. In a region where there are only two Gender Based Violence and Recovery Centers (GBVRC) located in Kisumu Central and Kisumu East Sub Counties, it is important to understand what happens to majority of the Adolescent Girls and Young Women (AGYW) who are not able to access the GBVRC after experiencing GBV. This paper aims to understand the existing After-Violence care available to AGYW facing GBV, and possible ways of improving the services for better mental health outcomes.

Methods: We conducted 4 Focus Group Discussions with AGYW consisting of 10 respondents in each FGD and 16 Key Informant Interviews (KIIs) with healthcare providers. The 4 FGDs were categorized geographically considering AGYW from urban, peri-urban, and rural areas and accessing HIV Care services from selected health facilities in Kisumu East, Kisumu Central, Kisumu West and Nyando Sub-Counties. Further stratification was according to age, 2 FGDs with 16-19 years, and 2 FGDs with 20 -24 years. The KII respondents consisted of the healthcare workers affiliated to the health facilities with AGYW. Data collection was done at the respective health facilities of choice. Data saturation was attained upon no new emerging information. Interviews were conducted in either English, Swahili or Luo, and were audio-taped with backup of field notes. Data transcription was done in verbatim and there were a total of 20 transcripts. Data was analyzed thematically using Nvivo 12 software. There were two independent coders. All ethical and confidentiality codes were observed.

Results: The existing After-Violence Care comprised of reporting the incident either to the village administrators, community based human rights groups, trusted persons, church leaders, nearest health facilities, police stations or children's offices. Following that, depending on where the reporting was done the After-Violence care that was availed included referrals to either to the health facility for Sexual and Reproductive Health Services (SRH) and/or Legal and Police departments for justice-related services. The After-violence care was made possible from the support in referral received upon reporting and the availability of SRH or legal services at the facilities. The major barriers to after violence care were failure to report the incident, inadequate referral and follow-up system, bureaucracy at the legal and police department that resulted in delayed justice, and the survivor's trauma of narrating the GVB story again.

Conclusion: The existing After-Violence care for the AGYW who experienced GBV was anchored on reporting and referral aspects. For effective improvement of After-Violence care, there is need to address the challenges that are related to reporting to facilitate a better mental health outcome.

Keywords: Gender Based Violence, After Violence Care, Adolescent Girls and Young Women, reporting

159.

PREVALENCE OF HYPERTENSION AMONG DIABETES CLIENTS: A CASE STUDY OF DIABETIC CLINIC, HOMA BAY COUNTY REFERRAL HOSPITAL.

Authors: Evans Odoyo Ondiek (Ministry of Health Homabay)*; Corneleous Edward Okal (Ministry of Health)

Background: Globally the number of people with diabetes rose from 108 million in 1980 to 422 million in 2014. The International Diabetes Federation ranked Kenya as the 31st African country in terms of diabetes with a prevalence of about 460 diabetic cases per 10,000 population. Diabetes hypertension comorbidity increases morbidity and mortality of cardiovascular diseases. However, no clear data is available on the prevalence of hypertension among people living with diabetes nationally and in Homabay County. The purpose of this study was to establish the prevalence of hypertension among people with diabetes attending a medical outpatient clinic at Homa Bay County Referral Hospital.

Methodology: We did a retrospective review of the records of all clients who presented with Diabetes at Homabay County Referral Hospital Medical Outpatient from January 2018 to December 2020. Sociodemographic and clinical variables were collected using Microsoft Excel. Sociodemographic variables of interest were age, sex, and sub-county of residence while clinic variables included diabetes and hypertension. Hypertension was defined as having an average of two BP readings above 140/90mmHg or being on medications for lowering BP. We did descriptive analytics using SPSS and assessed the prevalence of hypertension among people living with diabetes

Results: A total of 169 diabetic records were reviewed in the period. Females accounted for 65.7 %(111/169) and 60.4% (102/169) of the clients were between the ages of 50- 69. Homabay Town Sub-county Diabetic cases were 59.2% (100/169). The overall prevalence of hypertension amongst people living with diabetes was 63.9% (108/169). Female patients had a hypertensive caseload of 72.2% (78/108)

Conclusion: About six of every ten people living with diabetes had hypertension in the study. Most of the cases were female. We recommend regular screening for hypertension among people living with diabetes.

Keywords: Diabetes, Hypertension, Diabetic clinic

160.

CLINICAL OUTCOMES OF PATIENTS HOSPITALIZED WITH FEMORAL FRACTURES AT GULU REGIONAL REFERRAL HOSPITAL-UGANDA: A RETROSPECTIVE COHORT STUDY

Authors: Yakobo Nsubuga (Gulu University)*; Julius Tumwiine (Gulu University); Edward Kironde (Gulu University); Keneth Mwesiga (Gulu University); Jerom Okot (Gulu University); Moris Ojara (Gulu Regional Referral Hospital); Felix Bongomin (Gulu University)

Background: Femoral fractures are very common injuries following traumatic events associated with high morbidity and mortality. However, data on the burden of complications, mortality and associated factors in northern Uganda remains unknown. The main objective of the study was to determine in-hospital clinical outcomes of femoral fractures at Gulu Regional Referral Hospital (GRRH) in Gulu district in Uganda.

Methods: This was a retrospective cohort study of patients hospitalized at the surgical ward of GRRH, Gulu, Uganda. Data of patients who were admitted between January 2021 to December 2022 with a diagnosis of femoral fracture was collected on clinical outcomes as a composite of complications and survival. Logistic regression analysis was used to determine predictors of treatment failure defined as the occurrence of complications or death. $P<0.05$ was considered statistically significant.

Results: We included 248 participants, with a median age of 33 (interquartile range [IQR]: 15.5-54.5) years and duration of hospitalization of 19 days (IQR: 15-22). More than half were female (63.3%, n=157), 104 (43.1%) had no formal education and 84 (33.9%) had attained primary education. Most participants had closed fractures (90.7%, n=225) and fracture of the shaft (76.6%, n=190).Less than a third had complications (26.7%, n=66). Twenty-one (8.5%) participants died. For complications, with individuals with closed fractures having 81% lower odds compared to those with open fractures (adjusted odds ratio [aOR] = 0.19, 95% confidence interval [CI]: 0.07 — 0.53, $p< 0.001$). For mortality, compared to those with no formal education, the odds of death were 4.7-fold higher among those who had attained primary education (aOR: 4.7, 95%CI: 1.48 — 15.05, $p=0.009$)

Conclusion: In this study, among patients hospitalized with femoral fractures, about 1 in 4 had complications and 1 in 10 of the victims died. Moreover, those with lower level of education were more likely to die. These findings contribute to our understanding of the multifaceted nature of healthcare outcomes and underscore the importance of considering various factors when designing interventions and healthcare policies to improve patient outcomes in similar populations.

Keywords: Femoral fracture, complications, mortality

161.

EVALUATION OF CHEMICALS OF CONCERN IN SELECTED HAIR RELAXERS USED BY WOMEN IN EMBU COUNTY.

Authors: Beatrice Irungu (kemri)*; Cecilia Kimani (KEMRI); Esther Matu (Kenya Medical Research Institute); Mary Nyangi (Kenya Medical Research Institute); Teresa Olisa (Kenya Medical Research Institute); Adana Llanos (Columbia University)

Background: Emerging data from studies carried out in the United States and Ghana show that use of personal care products (PCPs) and hair products (permanent hair dyes and chemical relaxers) may be associated with increased risk of breast cancer. In this study, which is part of a larger study examining the prevalence of hair product use and attitudes and perceptions about potential health risks associated with use of certain hair products and other PCPs among women residing in two counties in Kenya, we documented chemicals of concern (COCs) in hair relaxers widely used in Embu County.

Methods: A total of 366 women aged 15-50 years consented and enrolled in questionnaire-based study, which ascertained participants' sociodemographic characteristics, use of hair products and other PCPs in the last 7-14 days, and ever use of hair dyes and chemical relaxers. Based on respondents' responses, we purchased eight hair relaxer products that were commonly used. We reviewed information captured on the label and recorded relaxer strength, ingredients list, manufacturer and location, and other claims made on the label. We then cross-checked the list of ingredients against the Campaign for Safe Cosmetics' Red List – a list of (COCs) in cosmetics and PCPs – to evaluate the frequency and proportion of COCs (out of the total number of ingredients) listed on each product. The Red List categorizes COCs into three categories (based on authoritative lists including the International Agency for Research on Cancer and the US National Toxicology Program): Tier 1, COCs that should be prohibited from use; Tier 2, COCs that are emerging and harmful to the environment; and Tier 3, COCs that are classified as asthmagens, allergens, and irritants that should be avoided in PCPs whenever possible.

Results: Eight hair relaxers were purchased (regular, 3 [37.5%]; super, 3 [37.5%]; and mild, 2 [25%]). Six (75%) were manufactured in Kenya and two (25%) were manufactured in Uganda and South Africa respectively. Five (62.5%) were labelled 'professional use only'. Among the eight products, 11 different COCs were identified: Tier 1, 2 (18.2%); Tier 2, 8 (72.7%); and Tier 3, 1 (9.1%). Notably, petrolatum and sodium hydroxide (Tier 2) were present in 100% and 87.5% of the relaxer products, respectively. Two relaxers from the same manufacturer contained both formaldehyde and isoeugenol (Tier 1).

Conclusion: Our preliminary analysis documented relaxers that contained CoCs that should not be used in PCPs. Hence, there is need for a review of PCP regulatory frameworks in the context of PCPs and cancer risk. Secondly, there is need for public education on the chemical composition of PCPs and their likely adverse health effects. Such awareness will help consumers make informed choices when purchasing and using these products. Our future work will include analysis of CoCs in other PCPs available in the Kenyan market and an assessment of hair relaxers' regulatory requirements in Kenya.

Keywords: hair relaxers, chemicals of concern, breast cancer risk, Embu County, Kenya

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162.

PREVALENCE OF OVERWEIGHT AND OBESITY AMONGST PRIMARY SCHOOL CHILDREN AGED 8 - 11 IN THIKA WEST SUB- COUNTY, KENYA

Authors: Margaret Mburu

Background: Childhood over nutrition is a growing public health challenge in the 21st century as a risk factor for adult over nutrition and non-communicable diseases. If the status quo remains unchanged, it is estimated that by 2035, 51% of the world's population >5 years of age will be overweight or obese. We sought to determine the prevalence of over nutrition among school-going children aged 8 - 11 years.

Methods: We employed a cross-sectional study design and a multistage sampling procedure. We recruited 281 children aged 8 –11 from five schools in Thika West Sub-County. Weight and height measurements for the children were assessed. The WHO growth standards of body mass index (BMI) for age z-scores were used as the reference indicator for nutrition status. We used the chi-square test to determine the association between overweight/obesity and other study variables. A p-value <0.05 was considered significant.

Results: The mean age of the respondents was 9.88 (±0.05) years. More than half of the respondents i.e., 55% (n=155) were girls, while 45% (n=128) were boys. Respondents were drawn from public 47.7% (n=135) and private schools (52.3%, n=148). The prevalence of overweight and obesity was 10.3% and 0.7% respectively. Conversely, 22.4% of the children were underweight. There was a significant association between the type of school attended and over nutrition ($\chi2=9.050$, p= 0.004). There was no significant association between gender and over nutrition ($\chi2=1.233$, p= 0.267).

Conclusion: We found the coexistence of both undernutrition and over nutrition. It is paramount that the existing school nutrition programs take up an integrated approach aimed at prevention, early detection, and effective management of both forms of malnutrition to achieve the SDG targets.

Keywords: Overweight, obesity, underweight, Kenya, primary school children, the double burden of malnutrition

163.

SEVERE ACUTE RESPIRATORY ILLNESS IN PATIENTS WITH SICKLE CELL DISEASE HOSPITALIZED IN TWO WESTERN KENYA REFERRAL HOSPITALS.

Authors: Peter M Kinuthia (HJFMRI)*; Lilian Waiboci (UON); Titus Chelulei (HJFMRI); Jackline Benta (KEMRI); James Ougo (KEMRI); Joel Machuki (HJFMRI); Nancy Otieno (KEMRI)

Background: Patients with sickle cell disease (SCD) are at a greater risk of acute respiratory infection and associated complications. There is limited data on the clinical outcomes of SCD patients hospitalized with acute respiratory illness. We describe characteristics and illness outcomes among SCD patients hospitalized with acute respiratory illness at two county referral hospitals in western Kenya.

Methods: We utilized data collected from Siaya County and Kakamega County Referral and Teaching Hospitals, as part of sentinel surveillance for severe acute respiratory illness (SARI). Between January 2019 and December 2022, patients of all ages were enrolled at the two hospitals with SARI, defined as cough or difficulty in breathing, history of or measured fever (≥38°C) and requiring hospitalization. SCD status of the patients was documented as part of risk factor data collected on the surveillance platform. Inpatient follow-up was conducted to determine the outcome of the hospital admission. We used chi-square tests to assess differences in patient characteristics and clinical outcomes.

Results: A total of 1925 SARI patients were enrolled; 66 (3.4%) had SCD and most of these (46, 69.7%) were aged younger than 5 years. SARI patients with SCD were more likely to required mechanical ventilation (3% Vs 0.3%; p=0.028) or get admitted to the intensive care unit (ICU) (54.6% vs 34.6%; p< 0.001) compared with patients without SCD. There was no difference in the duration of hospital stay or death between patients with and those without SCD.

Conclusions: SARI patients with SCD were more likely to require mechanical ventilation or be referred for ICU care. Our findings highlight the need to prioritize care and management of patients with SCD, particularly those hospitalized with SARI.

Keywords: sickle cell disease, severe respiratory illness.

164.

PREDICTORS OF MORTALITY AMONG PATIENTS ON MAINTENANCE HEMODIALYSIS ATTENDING NAKURU COUNTY REFERRAL AND TEACHING HOSPITAL

Authors: Zachary Mwambi Abere (EGERTON UNIVERSITY)*

Introduction: Hemodialysis is one of the main treatment options for patients with end-stage renal disease and chronic kidney failure. However, the number of patients dying while on maintenance hemodialysis has been due to multiple reasons either secondary to the hemodialysis process or due to complications of end-stage renal disease. These predictors of mortality among hemodialysis patients seem to differ based on geographical regions and even county-to-county. This study aimed to determine the specific predictors of mortality among patients at Nakuru Teaching and Referral Hospital.

Methods: A descriptive cross-sectional study was done among patients on maintenance and medical records review of patients' demographic, clinical, biological, and anthropometric data between January 2017 and January 2022. Statistical analyses with the assistance of Statistical Package for the Social Sciences (SPSS) version 29.0 software program (SPSS). The hazard proportional regression analysis model was done for association on survival time of patients.

Results: The study findings indicate that the year 2022 had an uptake trend of females (59.4%) compared to males (40.6%). Cox proportional hazard regression model and Kaplan survival curves analysis showed cardiovascular disease (hazard ratio (HR) =0.73), hypertension (HR=0.88), diabetes (HR=0.77), pneumonia (HR=2.25), and HIV (HR=1.56) as independent predictors of mortality among hemodialysis maintenance patients. One of the study limitations was poor medical records documentation and loss of records over time.

Discussion: The study recommends that interventions such as early initiation of medical treatment of comorbid conditions will assist in reducing the mortality rate of patients in their first year of hemodialysis initiation. The County should strengthen public education on the uptake of maintenance hemodialysis among patients with end-stage renal disease. The adoption of electronic health records (EHRs) will improve documentation, storage, and available patient data for health research.

Keywords: maintenance hemodialysis, predictors, mortality, morbidity, dialysis

165.

A TRANSCRIPTOME ANALYSIS OF BREAST TUMORS FROM KENYAN WOMEN

Authors: Francis W. Makokha (Mount Kenya University)*

Background: Breast cancer genomic studies in indigenous African populations are limited, despite recording the highest mortality rates worldwide. Evaluating gene signatures and mutational profiles could help to understand the biological pathways that might be amenable for the treatment of more aggressive breast cancers. We aimed to assess the transcriptomes of tumor and adjacent non-tumor tissue pairs from Kenyan women diagnosed with breast cancer to identify altered genomic pathways.

Methods: We performed RNA sequencing on 22 pairs of fresh frozen breast tumor and adjacent normal breast tissues from Kenyan women to investigate their gene expression profiles. Differentially expressed genes (DEGs) were identified at a cut-off using an adjusted $P < 0.05$, and an absolute fold change ≥ 2. In a gene set enrichment analysis (GSEA), Hallmark and Kyoto Encyclopedia of Genes and Genomes (KEGG)-defined gene sets (n=50 and 186, respectively) were selected within the GSEA molecular signature database, and those with a False Discovery Rate (FDR) < 0.25 were included in our data analysis.

Results: RNA sequencing identified 884 DEGs, including 348 upregulated and 536 downregulated protein-coding transcripts. Generally, the most upregulated genes in Kenyan tumors are associated with cell cycle control. Hallmark-defined E2F targets and the G2M checkpoint were identified as the most significantly enriched gene sets using GSEA. The top five upregulated genes in tumors were H2BC5, H2BC21, H3C4, H2BC18, and PAQR4, while the top five downregulated genes were PLAC9, SPTBN1, SORBS1, MTURN, and CLDN5. PLK1, TOP2A, NUSAP1, and CDC20 were the most upregulated genes.

Conclusion: Our findings suggest that gene sets involved in E2F signaling and G2M checkpoint pathways are significantly enriched in the breast tumors of Kenyan patients. This observation will require further validation in a larger study to assess if these pathways constitute vulnerabilities that can be targeted as biomarkers and therapy for breast cancer.

Keywords: Breast Cancer, Transcriptome, Upregulated, Downregulated, E2F Signaling, G2M Checkpoint

166.

PREVALENCE OF MINOR RED BLOOD GROUP ANTIGENS AMONG SICKLE CELL ANAEMIA PATIENTS IN KILIFI, KENYA

Authors: Ephy A Akoko (Kenya medical Research Institute- Centre for Geographic Medicine Research Coast)*; Michael Muteti (KEMRI-Wellcome Trust Research Programme); Sophie Uyoga (KEMRI CGMRC)

Background: Sickle cell anaemia (SCA) patients rely on transfusions as an intervention for the management of the disease. Before transfusion, matching is only done for major ABO and Rhesus without extended matching for clinically significant minor blood groups and screening for alloantibodies. This could possibly increase the risk of developing antibodies against the minor antigens (alloimmunization). The World Health Organization and American Society of Hematology recommend that red blood cell antigen profiling and matching for clinically significant antigens are necessary to reduce the risks of alloimmunization. The diversity of these antigens among patients has not been established. The study aimed to establish the prevalence of red blood cell (RBC) antigens and phenotypic diversities in SCA patients in Kilifi.

Methods: This was a cross-sectional study where 142 SCA patients attending the Kilifi County Hospital sickle cell clinic were recruited. Phenotyping for RBC blood group systems, including ABO, Rh (C, c, D, E, e), Kell (K, k, Kpa, Kpb), Duffy (Fya, Fyb) Kidd (Jka, Jkb); Lewis (Lea, Leb), Lutheran (Lua, Lub), P1, and MNS (M, N, S, s) was done on the patient's red cells using the Bio-Rad phenotyping gel-cards.

Results: 53.5% were male, and the median age was 10.7 years (age range 1-46 years). 137 (96.5%) participants were Rhesus-positive.

The prevalence of blood groups O, A, B, and AB was 54.9%, 18.3%, 23.7% and 3.1% respectively. Highly expressed antigens were D, c, e, Kpb, k, and Jka while Fya, Fyb and K were the rare antigens. The Rhesus blood group showed seven diverse phenotypes presented by the patients. R0r (ccD.ee) had the highest frequency of 54.9% while R1R1 (CCD.ee), R1R2 (CcD.Ee) and R2Rz (CCD.EE) were the rarely expressed phenotypes. The MNS blood group system presented 11 phenotypes with M+N+S-s+ expressed at 26.7% and M+N+S+s-, M-N-S-s+ rarely expressed (<1%). Other rare phenotypes in Kell, Lewis and Duffy were K+k+, Le(a+b+) and Fy(a+b+) respectively.

Conclusion: The study establishes evidence for the distribution of the antigens and phenotypes for the nine clinically significant blood groups among the regularly transfused SCA patients in Kilifi. The antigen frequencies reported in the Rhesus and MNS blood groups were comparable to those of Ghanaian sickle cell anaemia patients. Lowly expressed (rare) RBC antigens (Fya, Fyb and K) and phenotypes (CCD.ee, CcD.Ee, CCD.EE, M+N+S+s-, M-N-S-s+, K+k+, Le(a+b+), and Fy(a+b+)) can potentially pose a risk of alloimmunization. Studies to investigate RBC alloimmunization post-transfusion are needed to improve the safety of blood transfusion, especially in multiply-transfused patients.

Keywords: sickle cell anemia, transfusion, red blood cell antigens, phenotyping

SCIENTIFIC SESSION 19:

PUBLIC HEALTH 3

167.

QUALITATIVE STUDY EXPLORING CHALLENGES AND INFLUENCES ON AZITHROMYCIN MASS TREATMENT UPTAKE IN TURKANA PASTORAL COMMUNITIES IN KENYA, 2023.

Authors: Stephen J.O. Olubulyera (Ministry of Health, Kenya-FELTP)*; Faith Yego (Moi University); Maurice O Owiny (Kenya FELTP)

Background: Kenya is one of the countries with high trachoma burden globally. Of the 47 counties, 12 are endemic to trachoma, with 7 million people at risk of exposure. Turkana County has the highest trachoma burden in Kenya, with a primarily nomadic population. Despite significant progress made by the national program on trachoma control and elimination, consistency and sustainable treatment campaigns in pastoral communities have been difficult to achieve. The study aimed to explore the community and program challenges and factors influencing azithromycin mass treatment (AMT) uptake for trachoma in Turkana County.

Methods: We conducted a qualitative study exploring the challenges and factors influencing AMT uptake conducted in September 2022. In-depth and key-informant interviews were conducted with community drug distributors (CDDs) from sampled villages and experts from the Trachoma Program, respectively. We generated significant themes related to the subject matter from the data using QSR Nvivo software.

Results: We conducted twenty-two in-depth and four key-informant interviews. We identified compliance strategy, convincing powers of CDDs and community sensitization and mobilization themes influencing AMT uptake. In addition, we identified the motivation of CDDs, technical support to CDDs, logistics for AMT, capacity building and season timings themes challenging uptake of AMT.

Conclusion: Compliance strategy, community sensitization and mobilization and the CDD's influence play a significant role in AMT uptake in pastoral communities. However, lack of motivation, limited training and technical support for CDDs, inadequate logistics for AMT, and season timing were barriers to AMT uptake. We recommend enhanced collaboration between health support partners to improve logistical support on AMT and the provision of requisite training and technical support for CDDs during AMT.

Keywords: Azithromycin, Motivation, Trachoma, Capacity Building, Seasons, Kenya, Trachoma, Neglected Tropical Disease

168.

A PRELIMINARY SCOPING REVIEW ON THE ETIOLOGY AND DISTRIBUTION OF DIARRHEAL DISEASES IN KENYA.

Authors: Latifah Benta Mukanga (Kenya Medical Research Institute)*; Brian Kimutai (Kenya Medical Research Institute); JOSEPH OUMA MUGAH (KENYA MEDICAL RESEARCH INSTITUTE); Eddy Johnson Owino (Center for Global Health Research, Kenya Medical Research Institute); Fredrick A Ogumbo (Kenya Medical Research Institute); Steve Wandiga (Kenya Medical Research Institute); Lillian Musila (Kenya Medical Research Institute/United States Army Medical Research Directorate- Africa)

Background: Approximately 1.6 million deaths occur due to diarrheal diseases annually, with the highest burden reported in Sub-Saharan Africa. There is no comprehensive review of the etiology and distribution of diarrheal diseases in Kenya. This gap hinders understanding of the factors contributing to the prevalence, geographic spread, and diversity of diarrhea etiology within the country that would guide appropriate response and diagnostic tools to deploy in clinical settings and outbreak situations. Therefore, we conducted a scoping review of existing literature to determine the prevalence, etiology, and risk factors associated with diarrheal diseases among all age groups across Kenya.

Methods: This scoping review was conducted according to the framework outlined by Arksey and O'Malley. We searched for studies conducted from 2016 to 2023 using the search string "Prevalence" AND "Causes" AND "Diarrhea" AND "Risk Factors" AND "Kenya" in the databases PUBMED, Google Scholar, Web of Science, SCOPUS, CINAHL, EMBASE, and MedRvix. The retrieved articles were reviewed based on the abstract to ensure they met the inclusion criteria. They were further evaluated based on full-text review to identify articles from which to extract data for the scoping review.

Results: An initial data extraction from seven cross-sectional studies was used for this report. The studies were conducted in Kilifi, Kisii, Murang'a, Homabay, Marsabit, and Nairobi counties. The studies showed a total population of children under five years (70%; n = 1713) and a combined population of children and adults (30%; n= 748) with diarrhea. 908 of the population had at least one enteric bacterial or viral infection. In the articles, different counties differed in the etiologies of diarrhea. In two articles, Rotavirus, Sapovirus, and Norovirus exhibited heightened prevalence during the rainy season, whereas Adenovirus peaked during the dry season. In two studies, vancomycin and metronidazole reduced diarrhea due to C. difficile by 62 % and 45%, respectively, while ceftriaxone reduced Typhoid fever-induced diarrhea by 76% in another. Among the seven studies, two focusing on the rotavirus vaccine showed that Rotarix, a monovalent Rotavirus vaccine, reduces the prevalence of Rotavirus by 35% and 9.5%, respectively. The common risk factors for diarrhea identified were poor sanitation, nutritional problems, and clinical factors.

Conclusion: Our scoping review underscores the need to adopt diagnostic procedures to identify all causes of diarrhea because most studies focus only on known or typical diarrheal etiologies. To combat diarrhea, a multifaceted approach encompassing vaccination programs for preventable causes, targeted antibiotic therapy, and seasonal variations is needed to reduce morbidity significantly. Adopting metagenomic approaches would further elucidate other etiologies that could be missed, contributing to the burden of diarrheal disease.

Keywords: Prevalence, distribution, etiology,risk factors and treatment/AMR of diarrheal diseases

169.

ASSESSING THE COVERAGE OF VITAMIN A SUPPLEMENTATION AND DEWORMING AMONG CHILDREN AGED 6-59 MONTHS IN SELECTED COUNTIES OF KENYA

Authors: Caleb M Ombati (Helen Keller International)*; Asa Lelei (Helen Keller International); Esther Njeri (Helen Keller International); Solomon Omariba (Helen Keller International); Benjamin Kihika (Helen Keller International); Beth Mungai (Helen Keller International); Robinson Mochoni (Helen Keller International); Christine W Nderitu (Helen Keller International)

Background: Globally, Vitamin A Deficiency affects 30% of children under-5 years and 2% of the deaths are associated and Soil-Transmitted Helminth. WHO recommends biannual dosage for Vitamin A supplementation (VAS) and deworming interventions targeting over 80% coverage. Kenya through the Ministry of Health implements the delivery of the interventions through routine health facility services, Malezi Bora (MB) events, community outreaches and early childhood development centres. A post-event coverage survey was conducted in July 2023 to estimate the true coverage of VAS and deworming and effectiveness of MB event done in June 2023 in the study area.

Methods: A cross-sectional survey employed the WHO (2015) two-stage stratified cluster using both quantitative and qualitative methods. Clusters were selected by probability proportionate to size sampling and households randomly selected. The survey had 2 strata: Statum 1 (Meru, Tharakanithi, Nyeri, Nyandarua, Kirinyaga) and Stratum 2 (Kilifi). The selection stratum 1 was purposive due to Helen Keller support and similarities in population characteristics, proximity and socioeconomic activities, while stratum 2 was a donor request. Health workers and community health promoters (CHPs) were purposively selected due to their involvement in MB. Overall interviews done were for 1,642 caregivers reaching 1,934 children, 149 CHPs and 111 health workers interviews.

Results: The VAS semester coverages were 83% (999) and 92.7% (935), for stratum 1 and 2 respectively, while deworming coverage was 75% (883) and 93.1% (810) respectively. The primary reasons for not receiving both interventions in both strata were statistically significant as indicated: community health promoters not visiting the homes (VAS=39%; OR=1.336; p=0.041], and deworming =37% [OR=1.027; p=0.050) and caregivers not informed (VAS=31%; OR=1.161; p=0.039], and deworming =27%; OR=0.938; p=0.029]). The VAS malezi bora coverage was in stratum 1 was +5.8% and stratum 2 was +30% higher than the administrative coverage in June 2023. Less than half (48%) of the respondents were aware of the Malezi Bora event, and they got the information from CHPS= 45% and health workers=25%. The Caregivers had high familiarity (87%) with Vitamin A, however, there were variations in awareness of the benefits and dosing frequency.

Conclusion: VAS and deworming coverage remain a crucial public health challenge in Kenya. The survey results indicated that VAS coverage wase satisfactory, as it was >80% national target, the deworming coverage was 75% in stratum 1 below the national target. Notably, coverages were significantly higher during the MB events. The low knowledge for the caregivers is associated with missed opportunities and low coverage rates in some areas. Therefore, the use of these strategies are effective in increasing the coverage of the two interventions. Recommendations to improve CHP home visits and caregiver information will increase coverage.

Keywords: Vitamin A supplementation, Deworming

170.

CONCURRENT SEXUAL RELATIONSHIPS AND PARTNER'S HIV STATUS AWARENESS AMONG GIRLS AND YOUNG WOMEN AGED 15-24 YEARS OLD

Authors: George O Otieno (KEMRI)*; Joan Ongere (KEMRI-RCTP); Imeldah N Wakhungu (Kenya Medical Research Institute (KEMRI)-Research Care and Training Programme (RCTP)); Ruanne Barnabas (Havard University); Nelly R. Mugo (KEMRI); Elizabeth Bukusi (University of Washington); Maricianah Onono (Kenya Medical Research Institute (KEMRI)

Background: Concurrent sexual relationships among girls and young women (aged 15-24) and their male partners are a significant public health concern. The link between such relationships and awareness of a partner's HIV status is vital for shaping effective preventive strategies such as comprehensive sexual education programs that not only provide information on safe practices but also foster open communication about HIV status between partners. Research exploring the connection between concurrent sexual relationships and a partner's HIV status awareness can provide valuable insights into the determinants of sexual behavior in these vulnerable age group

Methods: This study evaluated ConceptPrEP-on-demand, a digital health service delivery model for adolescent girls and young women (AGYW) in Kisumu. Using a quasi-experimental design, 200 AGYW aged 15-24 were enrolled, initiated on PrEP and contraceptives, and followed up for six months. The analysis aimed to uncover the prevalence and determinants of concurrent sexual relationships, including the partner's HIV status awareness. Fixed-effect Poisson regression was employed to model the predictors of sexual concurrency.

Results: The analysis focused on 192 AGYW with complete information on both main and casual sex partners. The median age was 21 years (IQR: 20-23). At enrollment, only 39% of AGYWs were students. Sexual overlap prevalence was 27% at baseline and 29% at the end line. AGYW who were unaware of their partners' HIV status had a 11% significant increase in the risk of engaging in concurrent sexual relationships (Relative Risk [RR] = 1.11, 95% CI: 1.02, 1.20). AGYWs who were students and engaged in transactional sex demonstrated a 76% higher risk of sexual overlap (RR = 1.76, 95% CI: 1.28, 2.52). Conversely, employed AGYWs involved in transactional sex had a two-fold increased risk of engaging in concurrent sexual relationships (RR = 2.03, 95% CI: 1.63, 2.55). Additionally, AGYW who reported no continuation of pre-exposure prophylaxis (PrEP) but used condoms consistently had a 47% lower risk of sexual concurrency. AGYWs who lived with their sexual partners had a 42% lower risk of sexual concurrency (RR = 0.68, 95% CI: 0.50, 0.91).

Conclusion: Awareness of and communication about HIV status emerges as a key factor in influencing sexual behavior among AGYW. Individuals who are informed about and confident in their partner's HIV-negative status may be more likely to make choices that reduce the risk of concurrent sexual relationships.

Keywords: Sexual Concurrency, HIV, AGYW

171.

THE IMPACT OF COMMUNICATION AND ADVOCACY THROUGH STORYTELLING ON THE ROAD TO ZERO NEGLECTED TROPICAL DISEASES (NTDS)

Authors: Mercy K Mumo (Drugs for Neglected Diseases initiative)*; Linet Otieno (Drugs for Neglected Diseases initiative); Edith Magak (Drugs for Neglected Diseases initiative); Ilan Moss (Drugs for Neglected Diseases initiative)

Objective: This abstract investigates how storytelling contributes to the advancement of global initiatives aimed at eradicating neglected tropical diseases (NTDs).

Introduction: Storytelling is a powerful tool in the global fight against NTDs: it helps shape narratives, raise awareness, and drive action. This abstract examines the impact of storytelling by emphasizing three crucial aspects: the training of journalists and scientists to amplify visibility and awareness of NTDs, the contribution of stories of change to fundraising for pharmaceutical research and development for neglected diseases, and the role of storytelling in communication and advocacy to influence policy change.

Methods and results: Stories of change in NTDs provide a compelling platform to engage individuals, communities, influence policymakers, and organizations, inspiring them to contribute to the fight against NTDs. By highlighting personal experiences, successful interventions, and breakthroughs in treatment and prevention, these stories instill hope and can facilitate the mobilization of resources. In 2022, a former visceral leishmaniasis patient, Luke Kanyang'areng', who works as a nurse in Kacheliba, West Pokot County in Kenya, participated in the annual Norwegian solidarity fundraising campaign TV-Aksjonen and raised more than $26 million towards leishmaniasis and sleeping sickness. This example demonstrates how impactful storytelling plays a pivotal role in fundraising for research and development, enabling the discovery of innovative treatments, improved diagnostics, and sustainable interventions to eliminate NTDs.

Training journalists to become advocates and effective communicators is essential in raising visibility and awareness of NTDs. In Africa, between 2018-2022, DNDi trained over 50 journalists from Kenya, Uganda, Tanzania, Ethiopia, Ghana, the Democratic Republic of Congo, South Africa, Sudan, Burkina Faso, Côte d' Ivoire, Cameroon, Togo, Mali, Guinea, and Somalia. As a result of the training, DNDi has seen an increase in impactful stories on NTDs in the region across various media platforms. DNDi continues to invest in physical and virtual training of scientists and researchers on how to synthesize complex scientific information to enable its dissemination to the media, policy makers, communities, and other stakeholders. An example of the positive effect of global communication and advocacy efforts through stories is the inclusion of mycetoma and noma diseases in the WHO's list of NTDs. Opinion pieces and films have also played a key role in raising awareness on NTDs.

Conclusion: Storytelling is a potent force and contributor to the realization of the WHO roadmap on NTDs and Africa's New Public Health Order. By sharing stories, we can fuel fundraising efforts for R&D that drive action, influence policy, strengthens collaborations, promote behaviour change, build community engagement and ultimately pave the way for the elimination of NTDs globally.

Keywords: Storytelling, neglected tropical diseases, policy change, advocacy, communications, leishmaniasis, mycetoma, fundraising

172.

BRIDGING FACILITIES, EMPOWERING LIVES: THE IMPACT OF PSYCHOSOCIAL SUPPORT GROUPS IN PMTCT (PREVENTION OF MOTHER-TO-CHILD TRANSMISSION) IN THE COMMUNITY IN KASIPUL SUB COUNTY

Authors: Millicent Achieng Ongidi (MOH)*

Background: Homabay County is a high HIV burden county with a prevalence of 15.2%. The County Elimination of mother-to-child transmission (EMTCT rate) is at 5.3% while that of Kasipul Sub-county is 4.5%. Maternal viremia contributes to most of the pediatric transmission in the County. We implemented interfacility PMTCT Psychosocial groups (PSSGs) in Kasipul Sub-county to address maternal viremia.

Methods: We implemented PSSGs for mothers with high viral load and poor adherence across five facilities in the Sub-county in the year 2021 – 2022. The group interventions included treatment literacy sessions, sharing of experiences, a buddy system, and income-generating activities. Group members acted as reminders to peers on adherence issues and maintaining bonds beyond the facility.

Results: The program enrolled 41 clients in the PMTCT PSSGs. Median age was 27(IQR 10-44) Married 28(68%) 6(14%) widows and 5(12%) Single. Parity ranged between 1-4 with an average of 2 children. Viral load at baseline, 16(39.0%) had High viral load 3(7.3%) low-level viremia, and 23(56.0%) were virally suppressed. All the mothers had a viral load of less than 50 copies after the intervention

Conclusion: Integrating psychosocial support across facilities can help improve maternal viral suppression and eventually reduce pediatric infections

Keywords: eMTCT, Psychosocial support groups

173.

SEXUAL RELATIONSHIP POWER AND SAFE SEX PRACTICES AMONG KENYAN ADOLESCENT GIRLS AND YOUNG WOMEN IN SOUTH-WESTERN KENYA

Authors: Teresia A Otieno (KEMRI-RCTP)*; George O Otieno (KEMRI); Imeldah N Wakhungu (Kenya Medical Research Institute (KEMRI)- Research Care and Training Programme (RCTP)); Nelly R. Mugo (KEMRI); Elizabeth Bukusi (KEMRI); Ruanne Barnabas (Harvard University); Maricianah Onono (KEMRI)

Background: Multiple factors contribute to the escalating risk of HIV acquisition among adolescent girls and young women (AGYW). Existing HIV prevention strategies often overlook the impact of gender dynamics, specifically the power imbalances within intimate relationships. Sexual relationship power encompasses one partner exerting control, making decisions, or influencing the other partner's behaviour. This study aimed to investigate the association between sexual relationship power and safe sex practices among AGYW.

Methods: This was a cross-sectional, quantitative study targeting AGYWs aged 15 to 24 years old initiating PrEP and contraceptive, and followed up for a period of 6 months in south-western Kenya. Data analysis focused on participants who could identify their primary sexual partners. Safe sex practice was defined as consistent condom use with main partners or having only one sexual partner. Sexual relationship power, assessed with 16 questions, considered imbalance if participants answered >8. Fixed-effect Poisson regression models evaluated the relationship between safe sex and sexual relationship power.

Results: Analysis included 175 participants, aged 17 to 24, median age 21 (IQR: 20-23). Most (64%) were single. Low sexual relationship power among AGYWs was 40%. Those in relationships where male partners held more power were 97% less likely to practice safe sex [RR=0.03, 95% CI: 0.00, 0.36]. Increased age correlated with a 15% greater likelihood of safe sex among those with lower sexual relationship power [RR=1.15, 95% CI: 1.03, 1.30]. Living with a non-sexual family member significantly increased the risk of practicing safe sex by 14% [RR=1.14, 95% CI: 1.04, 1.26], while staying with sexual partners resulted in an 82% decreased risk [RR=0.12, 95% CI: 0.02, 0.66]. Continuing PrEP showed a 42% decrease in safe sex practice [RR=0.58, 95% CI: 0.57, 0.58]. Unemployed AGYWs were more likely to practice safe sex compared to those in school [RR=1.41, 95% CI: 1.12, 1.77].

Conclusion: The association between sexual relationship power and safe sex practices underscores its pivotal role among AGYWs. These findings advocate for incorporating empowerment strategies, encompassing social, economic, and educational options, into risk reduction and HIV prevention programs for AGYW.

Keywords: Safe sex,sexual relationship power,AGYW

174.

CLINICAL AND SEROLOGICAL CHARACTERISTICS OF THE POST-COVID-19 STATUS OF HEALTHY VOLUNTEERS FROM KENYATTA UNIVERSITY

Authors: Martin W Theuri (Department of Medical Laboratory Science, Kenyatta University)*; Eric Ndombi (Department of Medical Microbiology and Parasitology, Kenyatta University); Peris Thamaini (Department of Human Pathology, Kenyatta University); James Ogutu (Department of Medical Microbiology and Parasitology, Kenyatta University); Lister Onsongo (Department of Community and Reproductive Health Nursing, Kenyatta University); June Madete (Department of Biomedical Engineering, Kenyatta University); Victor Mr Ofula (KEMRI); Samuel Gitau (Department of Pharmacology and Clinical Pharmacy, Kenyatta University); Gladys Mwangi (Department of Pharmacology and Clinical Pharmacy, Kenyatta University); Paul Okemo (Department of Plant and Microbial Sciences, Kenyatta University)

Background: Post-coronavirus disease 2019 (COVID-19) is associated with considerable morbidity and reduced quality of life. This condition is reported to present with diverse symptoms across individuals. In addition, elevated levels of anti-severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) IgG antibodies have been observed in individuals with persisting symptoms of COVID-19. However, studies characterizing the post-COVID-19 condition in Kenya and describing the potential association of anti-SARS-CoV-2 antibodies with the post-COVID-19 status are limited. This study aimed to determine the prevalence of post-COVID-19 condition and assess the association between post-COVID-19 condition and anti-SARS-CoV-2 among healthy volunteers from Kenyatta University community.

Methods: This was a descriptive cross-sectional study conducted at the Directorate of Kenyatta University Health Services. Demographic and clinical data were collected using a questionnaire. The levels of anti-SARS-CoV-2 antibodies in serum were quantified using the Human SARS-CoV-2 Spike IgG ELISA kit. Descriptive statistics were used to analyze the clinical symptoms of the participants. Chi-square test was used to compare the anti-SARS-CoV-2 IgG titers between the participants with and without the post-COVID-19 symptoms. Statistical significance was set at p value < 0.05.

Results: A total of 189 volunteers were included in this study (median age: 21 years, range: 18–71 years; male, 49.2%). Forty individuals had COVID-19, out of which 12 (30%) complained of post-COVID-19 symptoms (persistence of symptoms: n=6, emergence of new symptoms: n=7). The persisting symptoms were cough, sore throat, fatigue, runny/stuffy nose, and diarrhea, whereas the new symptoms included loss of smell/taste, heart palpitation, fatigue, joint pain, muscle aches, alteration in menstrual cycle, shortness of breath, and mental distress. The antibody titers showed no significant differences between the participants with and without the post-COVID-19 symptoms (P>0.05). Additional assays will be conducted to measure two morbidity markers associated with post-COVID-19 condition, that is, C-reactive protein and interleukin 6.

Conclusion: These findings show that post-COVID-19 condition is a health concern in the population and requires attention from healthcare stakeholders. Future longitudinal research should follow up patients diagnosed with COVID-19 to identify any persisting or emerging symptoms.

Keywords: emerging symptoms, IgG antibodies, persisting symptoms, post-COVID-19 condition, SARS-CoV-2

175.

REVOLUTIONIZING GLOBAL HEALTH: BRIDGING INNOVATIONS, EMERGING TECHNOLOGIES, AND VACCINES FOR SUSTAINABLE PRODUCT DEVELOPMENT

Authors: John M Giteru (Technical University of Mombasa)*

This abstract explores the confluence of global health, technology, and vaccine development, presenting a roadmap for transformative and sustainable progress. In a rapidly advancing era, the synergy of these elements holds immense potential to reshape healthcare worldwide. The paper delves into emerging technologies, emphasizing their role in diagnostics, treatment, and preventive measures. Artificial intelligence, biotechnology, and data analytics are identified as key drivers in this paradigm shift.

Vaccine development takes center stage as a cornerstone of preventive healthcare. The abstract underscores the need for an agile approach to research and manufacturing, aligning with the dynamic nature of infectious diseases. Advances in mRNA technology, nanotechnology, and novel adjuvants are discussed for their impact on vaccine efficacy and production timelines. Global collaboration is highlighted as crucial for accelerating vaccine accessibility, especially in resource-constrained regions.

The abstract also addresses sustainable product development to mitigate health disparities. It explores eco-friendly manufacturing, ethical clinical trial practices, and the integration of circular economy principles in healthcare. The interconnectedness of environmental sustainability and public health is emphasized, advocating for an approach that considers both immediate health outcomes and long-term ecological impact.

In conclusion, revolutionizing global health requires a strategic fusion of innovations, emerging technologies, and vaccine development. This multidimensional perspective, incorporating scientific advancements, ethical considerations, and environmental stewardship, aims to pave the way for a sustainable and equitable future in healthcare.

Keywords: Climate change, health, Nutrition, food security ,Health systems

176.

MODELLING HEAT STRESS IN CONJUNCTION WITH OTHER STRESSORS: IDENTIFICATION OF VULNERABLE POPULATIONS

BERNICE SCHOLTEN (TNO)*; BAS HENZING (TNO); ANJOEKA PRONK (TNO); BORIS KINGMA (TNO)

Background: Global average temperatures are increasing worldwide due to climate change. Africa’s climate has warmed more than the global average since pre-industrial times . Besides the negative health effects of heat stress, high temperatures can also aggravate the effects of other stressors including air pollution and airborne allergenic pollen. Because these stressors interact and can have a combined effect on human health, it is important to consider them jointly.

Methods: Hourly exposure data for the three factors were sourced from three models (air pollution: LOTOS-EUROS, pollen: Copernicus, meteo: ECMWF) for the period between 01-05-2022 until 31-08-2022. Thresholds for each stressor were based on official values or literature recommendations. The result is a 1km2 resolution grid for each factor, with each cell representing whether exposure met or exceeded the threshold. To account for differences in experienced heat stress amongst groups, the heat-stress index was adjusted to resemble a worker involved in heavy labour whilst wearing a full working outfit.

Results: We present a map that indicates where people are living that are vulnerable to heat stress based on the meteorological and pollution data and their personal characteristics, and in addition might be exposed to other stressors that can also negatively affect their health. Male and female workers with a high-risk profile for heat stress are at increased risk for simultaneous exposure as the area of co-exposure hotspots in Europe is over three to six times higher for these worker groups, respectively.

Conclusion: This work lays out a robust approach to assess simultaneous threshold exceedances of multiple environmental risk stressors. This framework can be extended to other vulnerable groups (i.e., pregnant women) and other continents. Further collaboration on this work could be explored in the Air Pollution Center of Excellence of KEMRI.

Keywords: heat, multiple stressors, air pollution, vulnerable populations

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177.

BARRIERS OF PARTICIPATION AND ACCESS TO MASS DRUG ADMINISTRATION FOR TRACHOMA ELIMINATION AMONG PASTORAL COMMUNITIES OF BARINGO COUNTY, KENYA

Authors: Tabitha W Kanyui (KEMRI)*; Bridget Kimani (KEMRI); Paul Gichuki (KEMRI); Titus Waititu (MOH); Collins Okoyo (KEMRI); Wyckliff Omondi (MOH); Doris Njomo (KEMRI)

Background: Trachoma is the second leading cause of avoidable blindness in Kenya. It is mostly found in dry and dusty climates and affects about 11 million people in the country. Baseline surveys conducted in the year 2004 showed a prevalence of active trachoma in Baringo County, 33.3% in selected clusters. Mass drug administration (MDA) is recommended where active trachoma (TF) is >30% for 5 years with a minimum coverage of 80% for maximum effect. In Loyamorok ward, Baringo County, treatment coverage trends have ranged between 48% to 57% which is below the recommended threshold. This study sought to assess the barriers of community participation and access to MDA for trachoma elimination among pastoral communities of Baringo County.

Methods: Twelve focus group discussions (FGDs) were conducted with purposively selected adult participants, segregated by age and gender. The number of FGDs was determined by the saturation model and a thematic framework method for content analysis was used. The identified themes included; knowledge of trachoma causes, prevention, transmission and control, risk perceptions, awareness of MDA and treatment benefits and perceptions towards treatment.

Results: Although community members were aware of trachoma and the benefits of MDA, there was poor knowledge of disease etiology, and risk susceptibility. Trachoma infection was attributed to dirt, dust and flies, with some participants reporting that it is caused by witchcraft. Women, children and elderly persons were perceived to be at a higher risk of infection. Community members noted that awareness creation efforts were centered near markets and main roads and did not penetrate to remote villages and towns, thus not all were reached. Uptake of MDA was negatively affected by trachoma drugs side effects, such as, diarrhoea, nausea, headache and drowsiness and the perception that the drugs are too large in size and have a bad taste.

Conclusions: MDA efforts would benefit from awareness creation to dispel myths and misconceptions and improve knowledge on trachoma etiology. Awareness creation should be conducted in the interior parts of Loyamorok Ward and not just in towns which are along the main roads. All side effects experienced thus far should be well documented and communicated during MDA awareness creation campaigns and also distribution exercises. Results from this study will have implications for MDA programs among pastoralist populations.

Keywords: Barriers, Trachoma, Elimination, Pastoral Communities

178.

REPORTING AND METHODOLOGICAL QUALITY OF CLINICAL PRACTICE GUIDELINES FOR MANAGEMENT OF MALNUTRITION IN THE EAST AFRICAN COMMUNITY. A SYSTEMATIC REVIEW

Authors: Sagam Caleb Kimutai (Kenya Medical Research Institute Center for Global Health Research)*; Eddy Johnson Owino (Center for Global Health Research, Kenya Medical Research Institute); Jenifer A. Otieno (Kenya Medical Research Institute); Lisa Were (Kenya Medical Research Institute (KEMRI)); Moriasi Nyanchoka (Centre for Global Health Research, Kenya Medical Research Institute); Belyse Munezero (University of Burundi); Jean Marie Butoyi (Light University of Bujumbura); Oscar Nyabenda (Ministry of Public Health Burundi); Gildas Ndibanje (Mount Kenya University, Burundi); Jonathan Niyukuri (University of Burundi); Maurice Felo (University of Kinshasa); Eleanor Ochodo (Kenya Medical Research Institute (KEMRI))

Background: Childhood undernutrition remains a public health concern in the East African Community (EAC). With efforts to combat childhood undernutrition, there has been an increased interest in the clinical practice guidelines (CPGs) use in management of malnutrition. This review aimed to critically appraise the methodological quality and reporting of CPGs for managing malnutrition within the EAC.

Methods: We searched the Ministry of Health websites of the EAC countries. We used the search terms “clinical practice guidelines, “nutrition guidelines”, “nutrition protocols”, “health guidelines”,” “IMAM”, “CIMAM” and “country”. Five reviewers independently selected CPGs and extracted data in English and French guidelines. We conducted a quality assessment of the included CPGs using the online version of the AGREE II tool across six domains and using the RIGHT reporting checklist.

Results: We retrieved 47 documents from the Ministry of Health and Health Associations’ websites. The average mean scores were as follows: clarity of presentation 93.4%, with all guidelines scoring above 80%. Scope and purpose: 76.6%, with one guideline scoring less than 50%. Stakeholder involvement was 47.1%, with one CPG scoring more than 60%. The applicability domain 51% with only two CPGs scoring above 60%. Editorial independence was the poorest at (8.9%), with the highest CPG scoring 13%. Only 8 items were reported in all the guidelines, and 11 items were partially reported. Most items were not fully reported in the majority of the guidelines, pointing out serious problems that could be contributing to the low scores in AGREE II.

Conclusion: Utilizing the AGREE II tool and RIGHT checklist allows for a comprehensive evaluation of the strengths and weaknesses of the guidelines. In the current review, the scope, purpose, and clarity of presentation were areas of strength, whereas the rigor of development, editorial independence and generally the reporting transparency require improvement.

Keywords: Childhood malnutrition, clinical practice guidelines, AGREE II and RIGHT

179.

MENTORSHIP AS A PATHWAY TO GENERATING HIGH QUALITY CANCER DATA FOR DECISION MAKING IN SUB-SAHARAN AFRICA

Authors: Evans Tanui (KEMRI)*, Kiptanui E1, Chesumbai G2, Koskei A1, Obuya M1, Okerosi N1, Gathere S1, Korir A1

Institutional Affiliations:

1Nairobi Population-based Cancer Registry, Kenya Medical Research Institute

2Eldoret Population-based Cancer Registry.

Mentorship as a pathway to generating high quality cancer data for decision making in sub-Saharan Africa

Introduction: Cancer surveillance coverage in sub-Saharan Africa (SSA) is currently insufficient, and this calls for concerted efforts geared towards building strong functional, efficient, resourced and well-equipped registries at the same time advocating for strengthening the existing registries with the aim of generating high quality, reliable, accurate data for quality decision making. Nairobi population-based cancer registry was inaugurated as the International Agency for Research on Cancer- Global Initiative for Cancer Registries (IARC-GICR) Collaborating Centre for Sub-Saharan region mandated to conduct trainings, develop and implement mentorship program, and offer technical support to different registries in the SSA region. We share lessons learned from the first cohort of training and mentorship as part of innovative approach towards attaining high quality data.

Methods: We adopted both virtual and onsite training and mentorship modules from the month of November 2022 to May 2023. Pre- and post-assessment surveys were administered at different stages of the training. Throughout the training and mentorship program, emphasis was made on the quality of data generated and measures of data quality that include completeness, validity, accuracy, timeliness among many others.

Results: A total of 58 surveillance officers from 22 registries in the region participated in the program. Thirty four percent (n=15) have never participated in any cancer registry training apart from the on-the-job trainings. About 70% (n=31) reported lack of a continuous training /mentorship program, such as refresher courses or quarterly trainings. In addition, 30% (n=13) responded not having an idea whether they conduct data cleaning or not. Only 57% (n=25) have institutional support to access trainings and capacity building efforts. An assessment of the training outcomes indicated that a significant proportion, 82% were confident that training and mentorship experience will be very much useful for their work, 68% strongly agreed the objectives of the training were clearly defined, and 75% strongly agreed the trainers were well knowledgeable of the topics.

Discussion and Conclusion: For the region to attain high impact surveillance data with accurate information on cancer burden; training and mentorship frameworks, institutional support, and leveraging on the lower hanging fruit -partnership and collaboration for robust utilization of resources, and expertise is inevitable.

Keywords: Cancer Surveillance Mentorship Data

180.

TRANSFORMING DATA SYSTEMS TO IMPROVE PANDEMIC READINESS AND RESPONSE 2020-2023

Authors: George O. Agogo (CDC); Anne Njoroge (ITECH); Emmanuel Okunga (Ministry of Health); Bonventure Juma (CDC); Nelson Akenga (APHL); Rufus Nyaga (APHL); David Kareko (Ministry of Health); George Owiso (ITECH); Elvis Kirui (Ministry of Health); John Mwihia (Ministry of Health); Hillary Limo (Ministry of Health); Amy Herman-Roloff (CDC); Peninah Munyua (CDC)*

Background: While high-quality data serve a foundational role in surveillance and response, producing these data from semi-automated and siloed information systems is challenging. In Kenya, the Ministry of Health (MOH) struggled to gather data to support COVID-19 response and global reporting requirements. Data were transmitted through phone calls and spreadsheets via email. Over time, electronic data capture tools and application programming interfaces (APIs) were developed to facilitate data transmission to the national District Health Information (DHIS-2) platform, with limited uptake.

Method: To resolve this, MOH and CDC-Kenya developed secure web-based portals with the requisite cybersecurity standards and access management were then created. We developed a simple spreadsheet template with the minimum data variables needed for COVID testing and COVID 19 in-patient case management. Users were trained to to download the template, populate it with the data needed and then upload it to the same portal and submit the data to MOH. Users were linked to facilities to federate access, therefore a facility only has access to the data they have uploaded.

Results: A total of 124 private and 417 public laboratories submitted over 3 million test results through the portal. These case-level testing data were the primary information source for the daily sitreps on COVID-19 case counts in the country. For case management, the portal, hosted on DHIS allowed private hospitals, which managed most patients, to submit case-level data to MOH. Web-based portals were viewed positively by users compared to APIs as they did not involve sharing the system details to enable data transfer.

Conclusion: While web-based portals were semi-automated, their uptake and utilization by the private healthcare providers was remarkable and data were utilized to inform response. Expansion of web-portals for transmission of case-level data for different surveillance use cases is on-going.

Keywords: District Health Information (DHIS-2), Electronic data capture, Information systems,

181.

UTILIZATION OF SUB-NATIONAL PUBLIC HEALTH EMERGENCY OPERATIONS CENTERS TO RESPOND TO PUBLIC HEALTH EVENTS IN KENYA, 2020-2023

Authors: Daniel Wako (CDC)*; hillary limo (MoH)

Introduction: During the COVID-19 pandemic, CDC supported the Kenya Ministry of Health to establish sub-national (i.e., county) public health emergency operations centers (PHEOCs) in 18 (of 47) counties.

Context & Aim: Prior to COVID-19, Kenya had only a national PHEOC. In addition to helping coordinate county COVID-19 response, county PHEOCs have responded to other public health events (i.e., outbreaks). We describe how county PHEOCs have been used to respond to outbreaks at a sub-national level.

Methods: We collected information from county PHEOC staff using a outbreak matrix tool. This enabled the team to find out about outbreaks that were responded to from 2020 to 2023. Outbreak data were analyzed by location (county), time, and type of outbreak.

Findings: Between 2020-2023, there were 87 PHEs responded to by county PHEOCs across 18 counties (median = 6 events; range: 0-10). The number of PHEs responded to by PHEOCs increased each year, from 7 in 2020 to 45 in 2023. The most common PHE types were cholera (18), measles (13), and COVID-19 (6).

Innovative contribution to policy, practice and/or research: County PHEOCs have been leveraged to respond to a variety of events in Kenya. The increasing number of events responded to might indicate growing adoption of public health emergency response principles in the country. Continued institutionalization of PHEOC operations might further enhance outbreak response in Kenya.

Keywords: Emergency Management, Outbreak response

182.

HEALTH AND DEMOGRAPHIC SURVEILLANCE SYSTEM (HDSS) PROFILE: A POPULATION-BASED SURVEILLANCE PLATFORM IN KIBERA URBAN INFORMAL SETTLEMENT.

Authors: Clifford Oduor1, Alice Ouma1, Samuel Kiplangat1, Robert Mutinda1, Godfrey Bigogo1, George O. Agogo2,Peninah Munyua2, Patrick K Munywoki2

Affiliations

1 Center for Global Health Research, Kenya Medical Research Institute (KEMRI), Kisumu, Kenya

2Division of Global Health Protection, U.S. Centers for Disease Control and Prevention (CDC), Nairobi, Kenya

Background: Health and demographic surveillance systems (HDSSs) play an important role in public health intervention evaluation by providing important longitudinal data on population dynamics, disease burden, and mortality in resource poor settings.

Methods: The surveillance platform was established in 2015 in two villages in Kibera (Soweto West and Gatwekera), covering 0.42 km2. The area residents have participated in a population- based infectious disease surveillance which included routine household visits to consented household. In 2022 the households were visited by trained fieldworkers every 4 months. During the routine visits demographic data including vital statistics and socio-economic status data were collected. In addition, verbal autopsy (VA) interviews were conducted for all reported deaths.

Results: In 2022 the mid-year population was 23,546 with under 5 years constituting 11.7% of the population. The median number of individuals per household was 4. The sex ratio was 93 males :100 females. The general fertility rate was 59 births/1,000 women aged 15-49 years and the crude birth rate was 18.7/1000 person-years-observation (pyo). The crude death rate was 2.0/1000 pyo. Infant and under-5 mortality ratios were 27.3 and 31.8/1000 live births, respectively. Crude out-and in-migration rates were 66.4/1000 pyo and 64.3/1000 pyo respectively. The most common probable cause of death was acute respiratory infections/pneumonia.

Conclusions: This platform provides valuable information for monitoring population dynamics. The Under-5 mortality rate is high in this setting and acute respiratory infection including pneumonia remains a leading cause of death. Evidence generated here may help inform targeted interventions aimed at reducing under-five mortality and respiratory illnesses in urban informal settlements.

Keywords: Informal settlement,survaillance,rates

183.

QUALITY HEALTHCARE REDEFINED: NATIONAL HOSPITAL INSURANCE FUND (NHIF)'S INFLUENCE ON SERVICE STANDARDS AT PUBLIC HOSPITAL IN KENYA

Authors: Ndirangu Ngunjiri (University of Nairobi)*

The National Hospital Insurance Fund (NHIF) has been credited with improving access to healthcare in Kenya, particularly for low-income earners. Kenya has a six-tiered healthcare system, with facilities ranging from dispensaries offering basic care to national referral hospitals providing specialized services. Generally, higher-level facilities have better infrastructure, equipment, and staffing. The Kenyan government is committed to achieving Universal Health Coverage (UHC). Initiatives like mamacare and investments in primary healthcare aim to improve the overall state of facilities. The study used a mixed-method approach, combining quantitative and qualitative data collection methods to capture a comprehensive picture. Used quantitative methods like surveys and audits to gather numerical data on performance indicators (e.g., waiting time, and medication availability). Used qualitative methods like interviews and focus group discussions to understand patients' and healthcare workers' experiences and perceptions. We Used validated questionnaires and data collection forms to ensure consistency and reliability of data across different hospitals and periods, using existing tools such as the Service Provision Assessment (SPA) tool. Developed specific questions that directly address the impact of NHIF on service standards. The quantitative data was analyzed using descriptive statistics, such as means, standard deviations, and frequencies. Select a representative sample of 73 public hospitals across different regions and levels of care. The qualitative data was analyzed using thematic analysis, which involved identifying and coding recurring themes in the data. The study's findings inform policy decisions and improve the quality of healthcare in public hospitals in Kenya. NHIF provides financial support to public hospitals through the contributions made by its members. This financial assistance helps public hospitals improve infrastructure, acquire medical equipment, and enhance their overall capacity to deliver quality healthcare services. NHIF has implemented quality assurance programs to monitor and assess the performance of public hospitals. These programs include regular inspections, audits, and patient satisfaction surveys. NHIF has the potential to influence service standards at public hospitals in several ways. By providing financial support, establishing accreditation standards, creating provider networks, implementing quality assurance programs, and offering capacity-building initiatives, NHIF can contribute to improving the quality of healthcare services at public hospitals.

Keywords: Quality, NHIF, healthcare, standards, universal health,

SCIENTIFIC SESSION 21:

HIV

184.

EFFECT OF STATUS DISCLOSURE ON QUALITY OF LIFE AMONG PEOPLE LIVING WITH HIV/AIDS IN GHANA: A HEALTH FACILITY-BASED CROSS-SECTIONAL STUDY

Authors: Farrukh I Saah (Ministry of Health Rwanda)*; Kizito Aidam (University of Health and Allied Sciences); Abdul-Aziz Seidu (College of Public Health, Medical and Veterinary Services, James Cook University); Hubert Amu (University of Health and Allied Sciences); Luchuo Bain (International Development Research Centre)

Background: HIV/AIDS is notorious for hindering quality of life (QoL). The availability of care and social support from family and close friends is a significant determinant of the quality of life of people living with HIV/AIDS (PLWHA) in developing countries like Ghana. Only through HIV/AIDS status disclosure can PLWHA access social and material support to help them cope and recover from physical illness and lessen depressive symptoms due to the disease. However, due to fear of discrimination and stigmatisation, status disclosure remains a difficult task for most PLWHA in Ghana. We examined HIV/AIDS status disclosure and its influence on QoL among PLWHA.

Methods: This health facility-based cross-sectional study involved 124 PLWHA aged 18 years or older and accessing antiretroviral therapy at a hospital in the Obuasi Municipality of Ghana. This population was chosen because they are experiencing services that are meant to impact their decision to disclose their HIV/AIDS status and quality of life. Using the exit strategy to recruit the respondents, a pre-tested questionnaire that adopted the WHOHIV-QOL BREF tool was deployed to collect their sociodemographic, HIV/AIDS, status disclosure, and social support information. The tool was used to appraise QoL and respondents' overall perception of their health using 31 questions evaluating QoL from six domains, namely; physical, psychological, level of independence, social relations, environmental, and spiritual domains, scored on a 5-point Likert scale. The data analysis included descriptive statistics and linear regression tests, with statistical significance set at p-value<0.05 at a 95% confidence interval using STATA v15.0.

Results: 42% had disclosed their HIV status. Social support, encompassing financial support for medical expenses, upkeep, and the provision of shelter and emotional support, was available for 76.9% of those who had disclosed their status. The mean QoL was highest for the physical domain (14.3±2.9) and lowest for the psychological domain (11.03±3.26). About 47.6% attained the mean overall QoL score (73.18). Being a male predicted lower QoL in all domains than females. Being a Muslim, having tertiary education, and being an urban resident significantly predicted better QoL than being a Christian, having no formal education, and being a rural resident, respectively. Respondents' age negatively predicted overall QoL. Although disclosing HIV/AIDS status positively predicted QoL, the difference was not statistically significant.

Conclusion: This significantly poor quality of life and low HIV/AIDS status disclosure can drag efforts by Ghana towards achieving the Sustainable Development Goal of reducing the HIV/AIDS pandemic and its associated mortality. Stakeholders in AIDS prevention should employ innovative methods such as peer support to encourage status disclosure and intensify education on the provision of social and emotional support for PLWHA.

Keywords: Quality of life; People living with HIV/AIDS; Status disclosure; Social support

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185.

THE BURDEN OF OVERNUTRITION AMONG ADULT PLHIVS ON CARE AT HOMABAY COUNTY AND REFERRAL HOSPITAL 2023

Authors: Nancy Atieno Osewe (Ministry of Health)*

Background: According to WHO, being overweight and obese is a key risk factor for non-communicable diseases (NCDs). Evidence shows that overweight/obesity is increasing among people living with HIV (PLHIV) on antiretroviral (ARVs).The weight gains have also been attributed to immunological response, and lifestyle. Homabay County Teaching and Referral Hospital (HBCTRH) has 6844 active adults on ART treatment. The clinic reviews at least 5 new and 108 known hypertensive every month.

The current reporting tools focus on undernutrition and not overnutrition.it is therefore important to determine the prevalence of overnutrition among PLHIV so as to come up with an intervention to prevent NCDs.

Objective: To establish the prevalence of overnutrition amongst Adult PLHIVs being followed at HBCTRH.

Methodology: We did a cross-sectional study assessing the BMIs of all active Adult PLHIVs being followed up at HBCTRH. Overnutrition was categorized into two groups, overweight and obese. Overweight was defined as a BMI > 24.9 and < 30 while obesity was a BMI of 30 and above. We further graded obese as grade 1(30 to<35), grade 2(35 to <40) and grade 3 > 40.Sociodemographic and clinical variables were abstracted from the electronic medical record in use (KEMR) into a database with enforced data quality and consistency checks. We conducted descriptive data analysis and assessed the prevalence of overweight and obesity

Results: We reviewed 6844 records of active PLHIVs 18 years and above. Females were 64% (4366/6844). Median age 46 IQR (18-87). Overnutrition was found in 33.2% (2272/6844) while undernutrition cases were 11.3% (770/6844). Of the overnutrition cases, 67.4% (1532/2272) were overweight and 33% (720/2272) were obese. Of the obese clients, 79% (572) were graded 1, 15% (111) were graded 2, and 5% (37) were graded 3. About 40% of the patients with hypertension have overnutrition.

Conclusion/Recommendations/Implications: Overnutrition was evident in every three of ten patients being followed up in the clinic. We recommend more sensitization on lifestyle and diet as an underlying cause of overnutrition to prevent NCDs.

Keywords: overnutrition, hypertension, step up more focus on addressing overnutrition, hypertension.

186.

AN ASSESSMENT OF ANTIRETROVIRAL (ART) RESISTANCE AMONGST PATIENTS ON SALVAGE AND THIRD LINE REGIMENS, HOMABAY COUNTY KENYA 2023

Authors: Corneleous Edward Okal (Ministry of Health)*; Daniel Mumelo (EGPAF); Dr Willis Omwoyo (Ngima Mogen); Steve Obunga (Ministry of Health); Dr Gordon Okomo (Ministry of Health)

Background: HIV drug resistance can affect the efficacy of antiretroviral (ART) leading to an increased number of new HIV infections, morbidity, and deaths

Homabay County is a high HIV burden County with a prevalence of 15.2 % and has the highest number of People living with HIV (PLHIVs) on third-line ART. We assessed antiretroviral resistance amongst patients on third-line and salvage ART regimens

Methodology: We retrospectively abstracted treatment records and ART drug resistance results of PLHIV on third-line ART on follow-up in, Homa Bay County. Sociodemographic and clinical variables were extracted from Kenya Electronic Medical records into a database with enforced data quality and consistency checks. ART drug resistance was classified as High, Intermediate, and low. We conducted descriptive data analysis and assessed the prevalence of ART resistance

Results: We included all 115 people living with HIV on third line and salvage treatment in the study. The median age was 37 years (SD 3.1). Males accounted for 52.0% and 37.6% were from Homabay Town Sub County. The mean duration of ART was 8.3 years (SD 3.1). Protease inhibitors (PI) major mutations were 56%. High-level resistance to Atazanavir was 38.4%, Lopinavir 23.2% and Darunavir 2.4%. For nucleoside and non-nucleoside reverse transcriptase inhibitors, high-level resistance was at 38.4% for Abacavir, 27.2% zidovudine, 60.8% lamivudine, 10.4% Tenofovir, 40% Efavirenz, and 51.2% Nevirapine. For Integrase inhibitors, high-level resistance to Dolutegravir was 3.2%.

Conclusion: Most third-line patients have high-level resistance to Protease inhibitors and other Antiretroviral. Dolutegravir and Darunavir were the least affected.

Keywords: Third line ART, Salvage regimens, ART resistance

187.

ART EXPERIENCE, VL SUPPRESSION AND CD4 STATUS OF HIV PATIENTS ADMITTED TO HOMABAY COUNTY HOSPITAL INPATIENT DEPARTMENT IN 2021

Authors: Corneleous Edward Okal (Ministry of Health)*; Sarah Jebitok (LVCT Vukisha 95)

Background: Despite advancements in antiretroviral therapy (ART) uptake, AIDS-related morbidity has increased in recent years, and those living with advanced HIV disease face a greater risk of death. Advanced HIV is usually associated with ART treatment failure, treatment interruptions, and late diagnoses.

We did an assessment in the Homabay County inpatient department to check ART use, Viral Load (VL) suppression, and CD4 status among patients admitted to the Inpatient Department in 2021 (IPD)

Methodology: We retrospectively abstracted records of People Living With HIV on ART admitted in the medical wards at HCTRH, Homa

Bay County in Kenya from January to December 2021. Sociodemographic and clinical variables were abstracted from Ministry of Health registers into a database with enforced data quality and consistency checks. We conducted descriptive data analysis and assessed ART use, viral load suppression, and CD4 status of patients.

Results: A total of 1007 people living with HIV were admitted in 2021. The mean age was 42 with an SD of 14.7. Females HIV positive were 54% (540/1007). Previous ART use was confirmed in 71% (713/1007) of the patients and 3% (32/1007) being ART Naïve. Missing ART documentation in 26% (261/1007) of the patients. Viral load and CD4 uptake in the IPD was 589(58%). Of the patients done VL, 71%(346/589) were LDL write in full, 8% (50/589) had low-risk LLV write in full, 7% (39/589) had high-risk LLV and 26% (154/589) had VLs >1000copies.CD4 < 200 was identified in 31% of LDL Clients, 56% of low-risk LLVs, 54% of high-risk LLVs, and 78% of patients with VL> 1000 copies

Conclusions: About three-quarters of people living with HIV admitted to IPD in 2021 had used ART and more than half of the clients done viral load were suppressed. Three in every ten patients who had LDL VL had a CD4 less than 200. We recommend the need to track patient CD4 in the wards to help in identifying advanced disease among people living with HIV.

Keywords: ART, Viral load,CD4

188.

ROLE OF THE ORPHANS AND VULNERABLE COMMUNITY INTERVENTIONS IN ADDRESSING VIRAL SUPPRESSION AMONGST CHILDREN AND ADOLESCENTS LIVING WITH HIV IN HOMA BAY, KENYA.

Authors: Victor O Owuor (Ministry of Health)*; Purity Muia (PATH); Justus Amayo (IDF); Corneleous Edward Okal (Ministry of Health)

Background: HIV is one of the leading causes of morbidities and mortalities in children and adolescents in Homa Bay County. Rachuonyo North sub-county had an HIV prevalence rate of 22% with 2,277 children and adolescents living with HIV in 2019.

Viral suppression amongst Children and Adolescents Living with HIV (CALHIV) was 85% in 2019. A community model targeting Orphans and Vulnerable Children was initiated to address socioeconomic, psychosocial, and structural gaps to help in viral suppression.

Objective: To assess the overall contributions of the community Orphans and Vulnerable Children (OVC) interventions in viral load (V.L) suppression among Children and Adolescents Living with HIV on care in Rachuonyo North Sub County, Homa Bay County.

Methods: Retrospective data review of 1,935 children and adolescents on follow-up in Rachuonyo North sub-county across the 37 ART sites from January 2019 to August 2023. Sociodemographic and clinical variables were abstracted from the Kenya Electronic Medical Records and the OVC database.

The clinical variables of interest were viral load and linkage rate to the OVC program. All the linked CALHIVs benefited from case management, psychosocial counseling, and structural support based on individual needs. Data quality assessment was done using a Field Epidemiology and Laboratory Training Program (FELTP) standard tool, and descriptive statistics and the corresponding percentages were used to summarize categorical variables.

Results: Of the 1,935 CALHIV records reviewed, females accounted for 57%. The median age was 13 years with a range of 19 (20 – 1).

In 2019; 27% of the CALHIV were linked to the Orphans and Vulnerable Children program with a viral suppression rate of 85%. In 2020, the linkage was 34%, a suppression rate of 88%. In 2021, the linkage was 36%, and the suppression rate was 86.5%, in 2022 linkage was 47%, with suppression of 88.8%, and in 2023 the viral suppression rate was 92% with a linkage of 53%.

Viral suppression among the CALHIV enrolled in the OVC program benefiting from the community intervention was on an average of 90.4% within the review period.

Conclusion: The OVC community model helped improve VL suppression amongst the Children and Adolescents Living with HIV (CALHIV) enrolled in the program. It’s therefore recommendable that the program be optimized into pediatric and adolescent clinical care.

Keywords: OVC,vulnerable,viral supression,community

189.

AN EVALUATION OF EARLY INFANT DIAGNOSIS OF HIV AMONG INFANTS ATTENDING SELECTED LEVEL 4 AND LEVEL 5 HEALTH FACILITIES IN KENYA.

Authors: Emily C.R Barsito (KEMRI Graduate School)*

Background- An estimated 38.4 million people were living with HIV worldwide in 2021. 2.73 million were children aged 0-19years. In sub- Saharan Africa women and girls account for 63% of all new infections, Over 90% of HIV infections in children are through Mother-To-Child Transmission. High rates of HIV infection among women and failure to utilize available PMTCT interventions translate to high rates of HIV transmission. EID of HIV is critical for timely intervention. Currently HIV infections of children born to HIV positive mothers is about 14%, this trend needs to reversed. The study sought to evaluate EID of HIV utilization among infants attending selected level 4 and level 5 health facilities in Kenya. Its' determinants, to compare health outcomes among those utilizing EID and those diagnosed later and to describe the role of healthcare workers on EID utilization.

Methods- Study Sites: six counties of Kenya. Mixed Methods research design was used in this study, QUAN-QUAL. Quantitative methods consisted of case-control. Qualitative methods used were FGDs and in-depth interviews. Two stage sampling was done, first stage involved grouping counties based on NASCOP HIV prevalence. Two counties randomly selected from each category.

Results- Findings were 59% of the respondents were aged below 30years, 73% were married, 13% were single.48% of the respondents had attained primary level as the highest level of education and only 1% had studied up to university level. Caretaker's knowledge of HIV, its transmission, diagnosis and treatment were significantly different between cases and controls. Awareness of HIV treatment was significantly different between cases and controls. Controls were more aware (OR=1.439, p=0.4264). There was significant difference in knowledge on effects of HIV infection on infants' life (OR=1.357, p=0.341) thus the odds for exposure among cases is greater than the odds of exposure among controls. The controls had better health outcome of HIV than cases (OR=1.28, P value= 0.2206). Regional difference in HIV prevalence, in terms of location of the region, urban or rural, presented differences in knowledge levels of EID services utilization. Disclosure, stigma and intimate partner violence were reported as major challenges facing EID by most caregivers. Caretakers perceived EID to be 'good' as infants received care, demonstrated understanding of benefits of EID. Respondents in rural counties reported less knowledge and awareness of EID compared to those from Urban counties. Neutral provider attitude significant, p<0.001.

Conclusions- Need for clear signages on where services were being provided as an enabler Confidentiality is important in addressing fear. Shorter queues, reduced waiting times at facilities are critical factors for compliance with facility visits. Timely HIV intervention in infants will help address SDGs 3 on child mortality, contribute to achieving the social pillar Kenya vision 2030 goal and strengthen PMTCT.

Keywords: EID- Early Infant Diagnosis of HIV. PMTCT-prevention of mother-to-child transmission. FGDs- focused group discussions

190.

UNRAVELING THE THREADS OF HIV/AIDS: A COMPREHENSIVE STUDY OF PATIENTS AT THE KEMRI CLINIC IN KISUMU COUNTY, KENYA

Authors: Cindy A Nyandiko (KEMRI)*; elizabeth ochola (KEMRI); farid salim (usamrd-k); Sean Oduor (Embu University); wycliffe Moracha (Astrakhan state medical university)

Background: This research delves into the intricate origins and dynamics of Human Immunodeficiency Virus 1 and 2 (HIV-1, HIV-2), which attacks the immune system, particularly CD4 cells, weakening it and leading to opportunistic infections and cancers. Antiretroviral treatment (ART) is crucial for diagnosed cases, not only for personal health but also as a preventive measure against HIV transmission. However, adherence to treatment is still challenging due to religious beliefs and social stigma, potentially contributing to a resurgence of HIV/AIDS in Kisumu County. This research aims to address the alarming rise in new HIV infections in Kisumu County, and the uneven HIV treatment coverage among adolescents and disruptions in mother-to-child transmission prevention that may contribute to this complexity. As such, this study explores driving factors of the current upward trend in infection rates, focusing on adherence challenges and the social context of HIV/AIDS management. Addressing these issues is crucial for sustaining progress through comprehensive research and targeted interventions and preventing a potentially new pandemic.

Methods: This research uses a cross-sectional design to assess HIV/AIDS prevalence among 544 outpatients seeking Voluntary Counselling and Testing (VCT) and Provider-Initiated Testing and Counselling (PITC) services at the KEMRI clinic in Kisumu. The study targeted patients testing positive for HIV/AIDS. The primary data collection occurred at various clinic stations where information was extracted from registers, while secondary data was gathered from reports and journals for contextual information.

Results: Data was analyzed from 187 out of the total number of patients who sought HIV testing at the clinic. The results indicate that 50.3% of the patients were males and 49.7% were females. The prevalence of HIV/AIDS was 4.25% among males and 9.68% among females, with one result noted as inconclusive. Notably, 102 out of 187 individuals were tested individually, and only 85 tested as a couple. Four out of the nine positive females were in polygamous marriages. The results suggest a higher prevalence among females which may be as a result of epidemiological trends or influences such as healthcare access and risk behaviors.

Conclusion: The HIV/AIDS epidemic remains a significant public health challenge in Sub-Saharan Africa and particularly in Kisumu. Therefore, this study recommends strengthening local prevention efforts, increasing access to testing and treatment, addressing stigma and discrimination, empowering vulnerable groups, enhancing data collection and monitoring, and fostering collaboration among stakeholders for a comprehensive response to HIV. A concerted effort is crucial to achieving progress towards an AIDS-free Kisumu.

Keywords: HIV/AIDS, TRENDS, ANTIRETROVIRALS THERAPY, ADHERANCE, HIV TESTING, KISUMU COUNTY

191.

EMPOWERING ADOLESCENT GIRLS AND YOUNG WOMEN (AGYW): PEER-LED MOBILIZATION FOR ENHANCED HIV PREVENTION SERVICES IN SIAYA COUNTY, KENYA

Authors: Wayne O Otieno (Catholic Medical Mission Board)*

Background: High rates of new HIV infections among adolescents and young people, particularly young women, underscore the urgent need for improved access to HIV prevention services and sexual reproductive health knowledge in Kenya. In response, the CMMB, through the Global Fund HIV program, aimed to amplify access and scale up HIV services specifically for adolescent girls and young women (AGYWs) in Siaya County. This study showcases the efficacy of leveraging AGYW peers as peer educators (PEs) to bolster the demand and uptake of HIV-related services among AGYWs.

Method: Drawing insights from the program's initial phase (2018-2019), the involvement of AGYW PEs as mobilizers for HIV biomedical and behavioral services emerged as a pivotal lesson. Recognizing that AGYWs congregated in social settings and faced discomfort engaging with community health volunteers (CHVs), the program established a selection criterion and recruited AGYW PEs. These PEs underwent comprehensive training on HIV, gender-based violence, and peer education methodologies, adhering to national guidelines. Their primary task involved sensitizing peers in the community, mobilizing them to access HIV prevention services during community outreaches, and facilitating client flow processes and referrals. Monthly review meetings with the PEs and service delivery data analysis facilitated comparisons between service access and uptake from 2018/2019 to 2020/2021.

Results: The outcomes in 2020/2021 showcased a remarkable 222.8% surge in access and uptake of HIV prevention services, including a substantial 166.5% increase in access to HIV Testing Services. Screening for additional critical services like STIs, TB, and cervical cancer also notably improved by 93-97%. These findings highlight the potency of AGYWs in strengthening referrals for services among their peers.

Conclusion: The use of AGYW PEs significantly outperformed CHVs in augmenting the demand and uptake of HIV services among AGYWs, presenting a commendable return on investment. This successful model advocates for further implementation and scale-up to fortify HIV prevention efforts within AGYW communities.

Keywords: Mobilization, Service access, Adolescent girls and young women

192.

PROGRESS TOWARDS EMTCT: A COMPARISON OF STUDY OUTCOMES FROM 2014-2015 VS 2020-2023

Authors: Catherine M Wexler (University of Kansas Medical Center)*; Sharon Mokua (KEMRI); May Maloba (Global Health Innovations); Nicodemus Maosa (Kenya Medical Research Institute); Shadrack Babu (Kenya Medical Research Institute); Kathy Goggin (Children's Mercy Kansas City); VIncent Staggs (IDDI); Samoel Khamadi (KEMRI); Sarah Finocchario-Kessler (University of Kansas Medical Center)

Background: From 2014-2015, our team conducted a study evaluating the impact of the HITSystem on early infant diagnosis services. In this study, 3.6% of infants (32/895) tested positive and 90% initiated ART at a median age of 17.5-25.1 weeks. It took approximately 11-14 weeks from the time of sample collection to ART initiation. PMTCT guidelines changed to recommend more frequent ANC visits and more frequent infant testing. Our team is currently evaluating a modified version of HITSystem targeting maternal viral load suppression

and retention in care. The goal of this analysis is to (1) evaluate EID services and positivity from 2020-2023 and (2) qualitatively compare the proportion of infants diagnosed with HIV, initiated on ART, and the median time to ART initiation among a mother-infant pairs enrolled in PMTCT approximately 5 years later.

Methods: Data were collected from 1640 pregnant women living with HIV enrolled in PMTCT care at 12 Kenyan hospitals from Oct 2020 to Nov 2023. Demographic surveys were conducted at baseline and key clinical outcomes were prospectively tracked until 6 months postpartum. We used descriptive statistics to calculate infant testing and ART initiation outcomes. Associations between demographic and clinical data were assessed using Fisher's Exact Test.

Results: Of the 1640 women enrolled in the study from 2020-2023, 1495 women (91.1%) had documented deliveries of 1531 infants and 1432 infants (93.5%) had at least one HIV test. 9 infants (<1%) tested HIV positive. Maternal ART initiation within the past year and unsuppressed VL within 6 months of delivery were associated with an increased likelihood of infant positivity. Other trends appeared large enough to be clinically meaningful, but the small number of positives limited the power to detect significance. Of the 9 infants diagnosed with HIV, 8 infants started ART. Among all infants, median infant age at first HIV test was 7.7 weeks and was 10.9 weeks among infants with a positive HIV test. Median infant age at ART initiation was 17.0 weeks (range: 7.8-68.9) and median time from sample collection to ART initiation was 6.14 weeks (range 0.8 weeks – 12.3 weeks).

Discussion: HIV transmission rates from the 2020-2023 period were lower (3.6% vs 0.6%) and ART initiation among infants with a positive result was faster (11-14 vs 6.14 weeks) than the 2014-2015 time period. These data represent clinically meaningful changes that could be attributed to the significant investment Kenya has put into PMTCT and EID services. The HITSystem was designed to support standard of care services and the addition of algorithms to support PMTCT (in addition to EID) may have contributed to some of the improved outcomes since the initial study. Further gains could be achieved by enhancing follow up among women newly initiated on ART and among those with high viral loads.

Keywords: HIV, eHealth

193.

IN SILICO GENOMIC RECOMBINATION ANALYSIS REVEALS HIV-1 AND HIV-2 MOSAIC GENOMES IN CIRCULATION

Authors: Edwin Magomere (University of Ghana)*; Peter Quashie (University of Ghana -

WACCBIP); George Kyei (University of Ghana - Noguchi)

Recombination is a shared feature among retroviruses, which occurs when reverse transcriptase enzyme transfers between the two RNA templates in diploid virions. Recombination events result in a progeny of viruses carrying genomic fragments from two genetically distinct parental strains. Currently, more than 118 HIV-1 inter-subtype recombinants have been documented but there is no record of inter-type (HIV-1 and HIV-2) recombinants. We hypothesized that interaction between HIV-1 and HIV-2 in dually infected individuals could result in inter-type recombinants. To test this hypothesis, we developed a bioinformatic pipeline to analyze HIV near-full length genomes (NFLGs) for evidence of recombination. NFLGs were downloaded from the Los Alamos HIV-DB and visualized in UGENE. We wrote R-scripts for multiple sequence analysis in R. The resultant multiple sequence alignment was used as input file in RDP4 for full exploratory scanning to detect recombinant sequences. Identified recombinant sequences were confirmed by phylogenetic analysis. In total, 504 NFLGs from 6 west African countries were included in this study. RDP4 detected 19 potential HIV1/HIV2 recombinants out of which 6 sequences passed all the seven statistical tests built in RDP4. Three of the 6 sequences were further confirmed as recombinants by phylogenetic analysis. Recombination hotspots were found to be located between nucleotide position 4502 and 6754, spanning from integrase to Env genomic regions. The affected genes code for integrase, protease, vif, vpr, tat, Rev, vpx/vpu, and Env. The largest genomic fragment transferred from minor to major parent was 1566 nucleotides long. We identified three putative HIV-1/HIV-2 mosaic sequences. Recombination hotspots were dense in the region between 4502 and 6754 nucleotide positions affecting 8 genes. The affected genes including integrase and Env are important drug and/or vaccine targets, hence HIV-1/HIV-2 recombination might confer drug resistance and/or immunological escape.

Keywords: Recombination, HIV-1, HIV-2, NFLGs, Recombination hot spots

194.

REVIEW OF GENERATIONAL HIV STATUS CHANGE FROM HIV POSITIVE ADOLECENTS TO HIV NEGATIVE CHILDREN IN RACHUONYO EAST SUB COUNTY HOMABAY COUNTY, KENYA

Authors: Nicholas Odiemo Ogone (LVCT health)*

Background: Elimination of mother to child transmission of HIV has been listed as global public health priority. Among the HIV prevention measures undertaken by the Kenyan government, PMTCT has proven to be the most effective intervention.

Problem statement: Study has not been conducted to determine the success rate of PMTCT among a cohort of adolescent girls who were born of HIV and later gave birth and are up bringing HIV negative children above 2 years.

Objective: To determine the success rate of PMTCT among a cohort of adolescent girls who were born of HIV and later gave birth.

Methodology: A data review was conducted among seropositive adolescents attending comprehensive care clinic within Rachuonyo east Sub County and were now mothers with children above 2 years of age. Data was collected from patient files and EMR. Data collected included records of social demographics and HIV status of the mother and child. Data was keyed into excel sheet and analyzed by calculating proportions.

Results: A total of 36 entries of adolescent mothers were reviewed. The age bracket of the adolescent girls studied was 16-23 years. The mean age was 18.4 years. Two thirds 24 (66.7%) of the participants were married while 24 (67.5%) of the women were using family planning. Most women 29 (79.2%) had only one live birth. Majority 35 (97%) of the children studied were HIV negative.

Discussion: According to the study results, there exists a 97% success rate of PMTCT among adolescents who acquired HIV as children in Rachuonyo east Sub County. This rate is majorly attributed to functional and successful OTZ program in the sub county.

Conclusion: This high successful rate indicates that among the key populations, programs designed for this category of PMTCT mothers are greatly contributing towards elimination of MTCT of HIV and should be sustained and strengthened.

Keywords: elimination of vertical transmission

SCIENTIFIC SESSION 22:

PUBLIC HEALTH 4

195.

MATHEMATICAL MODEL OF COVID-19 WITH A DOUBLE-DOSE VACCINE

Authors: Henry M. Wanjala (Chuka University)*; Mark Okongo (Chuka University); Jimrise Ochwach (Chuka University)

BACKGROUND: Mathematical modeling is a tool necessary in epidemiology so as to give understanding of the outcomes of an epidemic in different scenarios. Since, the emergence of Corona Virus 2019 (COVID - 19), there has been devastating effects to all the spheres of our lives. In the absence of a treatment plan, vaccination and Non – Pharmaceutical Interventions like social distancing, handwashing, use of face masks, quarantine, isolation and contact tracing become the control and mitigation measures instituted to lower the COVID-19 burden.. In this study, a deterministic mathematical model is developed so as to understand the dynamics of COVID-19 under the mitigation measures of vaccination, use of face-masks, quarantine and isolation.

METHODS: The model is developed by splitting the total human population at a time (t), denoted by N(t) into nine mutually exclusive compartments of the susceptible (S), vaccinated with first dose (V1), vaccinated with second dose (V2), exposed (E), quarantine (Q), asymptomatic (IA), Symptomatic (IS), isolated (J) and the recovered (R), such that:

$$N(t) = S(t) + V1(t) + V2(t) + E(t) + Q(t) + IA(t) + IS(t) + J(t) + R(t)$$

The basic reproduction equation is obtained by the use of the next generation matrix (NGM). The Jacobian matrix derived from the model equations is used to determine the reproduction number. The local stability analysis is performed by constructing the Jacobian matrix of the model system and solving it at the Disease Free Equilibrium (DFE) and at the Endemic Equilibrium (EE). The ordinary differential equations, which are used to get the numerical solutions were programmed into the PYTHON program and solved using the numpy and scipy solver. To be able to compare and analyze, some of the parameters vary within given set of limits.

RESULTS: It is established that the DFE is both globally and locally asymptotically stable whenever the reproduction number is less than unity and unstable when otherwise. It was also established that the EE was both locally and globally asymptotically stable.

When an initial vaccine of an efficacy of 50% is introduced to a population with no vaccination, the exposed population reduces from 320 suspected cases to 302 but when a vaccine of higher efficacy of 80% is used the exposed population reduces to 284 from the baseline value of 1000. When the vaccine coverage rate is increased from the base-line value of 8 individuals for every 10000 of the exposed to 800, then, with an increase of the efficacy of the vaccine from 50% to 100%, then the exposed population reduces from 256 people to 6 people with the peak delayed from the 94th day to the 114th day.

CONCLUSION: Generally, the success of vaccination drive depends on two factors, these are the efficacy of the vaccine and the fraction of the population vaccinated. When both factors are maximum, then, the disease can be eradicated.

Keywords: Double-dose vaccine, Face-masks, Reproduction number, Equilibrium Analysis

196.

ENHANCING UNIVERSAL HEALTH COVERAGE FOR MALARIA THROUGH WEEKLY HOUSEHOLD SWEEPS BY COMMUNITY HEALTH PROMOTERS IN NYAMIRA, KENYA.

Authors: *Dorah Wafula1, Wayne Otieno1, Salome Ileli1, Hillary Ngeso1, 1Malaria Programs, Catholic Medical Mission Board (CMM

Dorah K Wafula (Catholic Medical Mission Board)*; Wayne Otieno (Catholic Medical Mission Board); Hilary Ngeso (Catholic Medical Mission Board); Salome Ileli (Catholic Medical Mission Board)

BACKGROUND: While strides have been made in maternal and child health, infectious diseases remain a significant issue in Kenya, with pneumonia, malaria, and diarrhea being leading causes of under-five mortality. Community Health Promoters (CHPs) present an opportunity for bolstering Universal Health Care, especially in preventing and treating infectious diseases like malaria. However, the efficacy of malaria interventions is hampered by underreported cases, particularly in Nyamira, a highland malaria epidemic county with high malaria instances despite being a low transmission area. With Kenya's goal of malaria elimination, leveraging existing community structures becomes crucial for assessing malaria burden in such low transmission settings. This study aimed to evaluate the effectiveness of CHP-led weekly Active Case Detection (ACD) household sweeps in managing epidemic malaria in western Kenya's highland region.

METHOD: Between March and September 2023, cross-sectional weekly ACD for malaria was conducted across eight Community Health Units (CHUs) in Nyamira's highlands. Concurrently, 83 other CHUs performed monthly and quarterly household visits for community-based malaria case management. CHPs from the eight CHUs conducted weekly household sweeps, identifying febrile cases, and performing rapid diagnostic tests on suspected malaria cases using finger-prick blood samples. Positive cases were treated with 1st Line Anti-Malaria medication.

RESULTS: In the period of March to September 2023, household sweep data gathered weekly over nine month period exhibited 21.9% higher positivity (2322 cases) compared to 586 cases registered the same seasonal period of March - September 2022 when the same CHUs practiced the normal community case management of malaria. With the moderately stable commodity quantification and supply , household sweeps detected more malaria cases due to the prompt active case detection.

CONCLUSION: The prevalence of underreported malaria cases remains a concern in the community. Implementing active weekly household sweeps could significantly enhance Universal Health Care outcomes, especially in resource-limited settings. Strengthening the Community Health Strategy is crucial for improving Universal Health Outcomes in such contexts, highlighting its significance for the Ministry of Health.

Keywords: Active Weekly Household sweeps, Malaria, Universal Health Coverage, Community Case Management of Malaria

197.

EPIDEMIOLOGY OF CASE-BASED LAB CONFIRMED MEASLES VIRUS CASES IN KENYA, 2021-2023

Authors: DIANA WANJIRU WANJIKU (KEMRI)*; Paul Muchai (KEMRI); Joanne H Hassan (kemri); Mercy A. Onyango (Kenya Medical Research Institute); Shadrack Mr. Barmasai (Kenya Medical Research Institute); Collins K Cheruiyot (KEMRI); Agnes Chepkurui (KEMRI); Janet Wanjiru (KEMRI); Robert Mainga (KEMRI); Peter Maritim (KEMRI); James Nyangao (KEMRI); Stephen Ochieng Ombija (Kenya Medical Research Institute); Evans Komen (KEMRI); Benlick Mwangi (KEMRI); Fiona Aluoch Alaii (KEMRI); Samira Ali Katembe (KEMRI); Jennifer Lewett (KEMRI); Maureen Njihia (KEMRI); Rosemary Nzuza (KEMRI); samoell A Khamadi (KEMRI); Peter Borus (KEMRI)

Background: In Kenya, measles case-based surveillance was introduced in 2002 as a strategy for measles control through laboratory confirmation of suspected cases. This paper shows the distribution of lab-confirmed measles cases that were reported from the 47 counties in Kenya following the pandemic from 2021 to 2023, following the interruption of scheduled measles Supplementary Immunization Activities (SIAs) following the COVID-19 pandemic.

Method: This study takes on a retrospective study design. Serum samples were collected from measles-suspecting cases in community health facilities and hospitals in the sub-counties. Patient information, including age, sex, vaccination status, and residence, was captured in the MOH 502 form, which is the case investigation form (CIF). Samples were transported to the National Measles Laboratory at KEMRI for measles IgM testing through serological assay analysis. Data entry and analysis were done using Epi-Info 3.5.4 software.

Results: A total of 4766 samples from all 47 counties in Kenya were tested for measles IgM using ELISA in the past 3 years, with 857 samples testing positive for measles. Cases aged 1-4 years were found to be the most affected, regardless of sex. The incidence of confirmed measles cases increased from 99 to 174 to 584 in 2021, 2022, and 2023, respectively. The highest percentage of lab-confirmed cases were found in 2023: 584. There was an increase in incidence in cases over 15 years old in 2023. Measles was found to be distributed throughout the country. The highest number of confirmed cases in 2023 were found in Turkana, Mombasa, Garissa, and Isiolo counties.

Conclusion: COVID-19 pandemic-affected public health intervention strategies for diseases of public health importance including scheduled Supplementary Immunization Activities (SIAs) for measles, which are designed to interrupt measles virus transmission and keep measles incidence low. The interruption of SIAs has devastating consequences. The incidence was highest at ages 1-4 years. The incidence increased in 2023 compared to 2022 and 2021 combined. Additional research is needed to determine the genotype of the circulating measles virus as well as the changes in the epidemiology of measles disease. A wide age-group measles vaccination campaign is highly recommended.

Keywords: Epidemiology, Measles, Case-based Survaillance

198.

COMMUNITY ACCEPTABILITY OF ATTRACTIVE TARGETED SUGAR BAITS IN A CLUSTER RANDOMIZED CONTROLLED TRIAL IN WESTERN KENYA

Authors: Caroline Ogwang (KEMRI CGHR)*; Teresa Bange (KEMRI CGHR); Dominic Ouma (KEMRI CGHR); Omollo Mevis (KEMRI/CGHR); Brian Seda (KEMRI CGHR); Julia Janssen (CDC); Julie Gutman (CDC); Jonathan S Schultz (CDC-Kenya); Aaron Samwels (CDC); Eric O Ochomo (Kenya Medical Research institute); Simon Kariuki (KEMRI); Feiko ter Kuile (LSTM); Sarah Staedke (LSTM); George Okello (LSTM); Sarah Staedke (LSTM)

Background: Attractive Targeted Sugar Baits (ATSBs) are a promising intervention containing a thickened fruit syrup laced with an insecticide (dinotefuran) designed to attract and kill mosquitoes. We are currently conducting a cluster-randomised trial to evaluate the impact of ATSBs on the burden of malaria. Households in the intervention clusters receive two ATSB bait stations per structure on exterior walls that are replaced every six months over two years. Understanding factors that influence ATSB coverage and acceptability of this new intervention by community members, is important for guiding future implementation of ATSBs, if they prove to be effective. Here, we report the results of a qualitative evaluation of community perceptions of ATSBs, utilizing rapid ethnographic methods.

Methods: Between May 2023 and October 2023 we conducted in-depth interviews and FGDs with a purposive sample of community participants from intervention clusters to assess factors influencing acceptance of ATSBs.

Interviews were recorded and transcribed verbatim into MS word then data quality checks were done. Data was analysed using a thematic analysis whereby transcripts were interrogated for specific and emergent themes. The interview guides, conceptual framework and evaluation objectives were used to create an initial set of predetermined codes for the domains of potential barriers and facilitators to high ATSB coverage. Data was coded and organized by theme using Nvivo 12 software then a synthesis of data within each code was drafted. Patterns among themes and across types of respondents were identified and interpreted.

Results: Community members described some misconceptions about ATSBs including the expectation that ATSBs would eradicate mosquitoes and misunderstandings that they trap mosquitoes stemming from the local name of 'Otego suna', which translates as 'mosquito trap'. This led some community members to perceive them as ineffective, while others perceived an increase in mosquitoes in association with ATSBs, when installation was done during the rainy season. Some participants were negatively influenced by other experiences that involved random selection to participate in other trial activities. Factors enhancing community acceptability of ATSBs included: active community engagement strategies including sensitization meetings highlighting key messages; positive experiences following installation of ATSBs, such as reduction in mosquitoes and malaria cases; and trust in KEMRI and the government to conduct research for the benefit of the population.

Conclusion: The information on barriers to community acceptance of ATSBs can guide future sensitization and education of communities about ATSBs. Community engagement to understand and address community concerns is essential to improve acceptability of this new malaria control intervention.

Keywords: Malaria control; acceptability

199.

FACTORS ASSOCIATED WITH POOR TREATMENT OUTCOMES AMONG TUBERCULOSIS PATIENTS IN MERU COUNTY, KENYA ,2022

Authors: Abdiaziz M Mohamud (Kenya Field Epidemiology and Laboratory Training Program)*; Fredrick Odhiambo (Kenya Field Epidemiology and Laboratory Training Program); Catherine Githinji (Division of National Tuberculosis, Leprosy and Lung diseases, Ministry of Health,Kenya); Maria Nunga (Kenya Field Epidemiology and Laboratory Training Program)

Background: Tuberculosis (TB) remains a major public health burden globally, with 10.6 million cases and 1.6 million deaths reported by the World Health Organization (WHO) in 2021. Kenya is ranked among the 30 high-burden TB/Human Immunodeficiency Virus (HIV) countries in the world. The incidence of TB in Meru County is among the highest in the country. The aim of this study was to determine factors associated with poor treatment outcomes among TB patients in Meru County.

Methods: We conducted a cross-sectional study design among TB cases enrolled in clinic care between January and December 2022. We collected socio-demographic, clinical, and exposure information from the Treatment Information Basic Unit (TIBU) register. We defined poor treatment outcomes as cases whose outcomes of interest were recorded as death, treatment failure, and loss to follow-up. We calculated proportions and frequency for categorical variables, measures of central tendency, and spread for continuous variables. We used prevalence odds ratios to test for association, with a p-value of <0.05 considered statistically significant.

Results: We reviewed 3,462 TB records. The mean age of the cases was 34(±16) years, males were 2,537(73%), pulmonary TB cases were 3,159(91%), and those with poor treatment outcomes were 439 (13%). Of those with poor treatment outcomes, 245(7%) patients died, 30(1%) failed treatment and164(5%) defaulted. Factors associated with poor treatment outcome were being HIV positive [OR 2.1669, (CI: 1.7009-2.7606)], age ≥55 years [OR 2.0804, (CI: 1.6015-2.7026)], having a positive sputum smear at the second-month follow-up [OR 2.7685, (CI: 1.8035-4.2498)], and body mass index (BMI) <18.5 [OR 1.4896, (CI: 1.1849-1.8728)].

Conclusion: We recommend that targeted measures be considered to reduce the rate of poor treatment outcomes among high-risk groups and using identified parameters of poor treatment outcomes.

Keywords: Tuberculosis, Cross-sectional studies, Incidence, Treatment failure

200.

FACILITATORS AND BARRIERS TO IMPLEMENTATION OF LONG-ACTING HIV PREVENTION PRODUCTS AMONG PREGNANT AND LACTATING WOMEN IN KENYA: A HEALTH CARE PROVIDER AND NATIONAL STAKEHOLDER PERSPECTIVES

Authors: Maryeve N Gikwa (Partners in Health and Research Development, Center for Clinical Research, Kenya Medical Research Institute, Nairobi, Kenya)*; Vallery Ogello (Centre for Clinical research, Kenya Medical research Institute-PHRD Thika); Nicholas B Thuo (Kenya Medical Research Institute - CCR - PHRD Thika Site); Zachary Kwena (Kenya Medical Research Institute, Center for Microbiology Research, Kisumu, Kenya); Catherine Makokha (Kenya Medical Research Institute, Center for Microbiology Research, Kisumu, Kenya); Rennah Anyango (Kenya Medical Research Institute, Center for Microbiology Research, Kisumu, Kenya); Emmah Owidi (Partners in Health Research and Development, Center for Clinical Research, Kenya Medical Research Institute, Nairobi, Kenya); Catherine Kiptinness (KEMRI); Nelly R. Mugo (KEMRI); Kenneth Ngure (Jomo Kenyatta University of Agriculture and Technology)

Background: Women face challenges with oral PrEP persistence and/or adherence attributed to individual, social, and biological factors. Implementation of long-acting HIV prevention products promises to expand HIV prevention options and potentially address adherence challenges. We conducted qualitative interviews among healthcare providers (HCPs) and national stakeholders to assess facilitators and barriers to implementation of long-acting HIV prevention products among pregnant and lactating women.

Methods: From November 2022 to March 2023, we conducted in-person and virtual interviews using in-depth interview guides with HCPs(n=40) and national stakeholders (n=20). We purposively selected HCPs, sampled to include those working in maternal and child health clinics and HIV care clinics, from four public health facilities in western and central Kenya. Public health facilities were selected given the HIV prevalence in the regions and high client volume in the facilities. National stakeholders had a representation of policymakers, researchers, implementers, and ethical review bodies. In-depth interviews were audio recorded, transcribed, and translated simultaneously. We analyzed data thematically and found three key organizing themes to understand barriers and facilitators 1) community factors, 2) health facility factors, and 3) policy requirements.

Results: Overall, the majority 83% (n= 33) of HCPs were female, 73% (n= 29) nurses, and 20% (n= 4) clinical officers among other cadres. Both HCPs and national stakeholders perceived that creating public awareness through community education, adequate HCPs training, and integrating long-acting HIV prevention products within existing services e.g. family planning could potentially facilitate implementation. HCPs added that existing knowledge and experience with oral PrEP delivery would aid in the delivery of these products, while national stakeholders expressed the need for clear guidelines and administrative support. Additionally, HCPs reported potential barriers to implementation associated with product shortage, workload as they perceived integration of long-acting products in the facility would increase workload, cost to clients, accessibility challenges, and stigma among clients. Further, national stakeholders perceived barriers related to provider training, partner involvement, and lack of evidence-based data on long- acting HIV prevention products among pregnant and lactating women. Both HCPs and national stakeholders felt adopting long-acting HIV prevention products into policy documents could support implementation.

Conclusion: Our study found important facilitators such as awareness, provider training, and service integration to support implementation of long-acting HIV prevention products. However, facility factors such as workload, stigma, and cost may impede implementation. Policymakers, resource allocators, and implementors may consider these factors during implementation to yield success.

Keywords: Long-acting HIV prevention products; Pregnant and Breastfeeding women; HIV prevention

201.

KNOWLEDGE AND ADHERENCE TO THE NATIONAL MALARIA TREATMENT GUIDELINES FOR MALARIA DIAGNOSIS IN PREGNANCY AMONG HEALTH-CARE WORKERS IN RANGWE SUB COUNTY, HOMABAY COUNTY.

Authors: EVERLYNE AKINYI MBOGA (MOH,HOMABAY)*

Malaria in pregnancy remains a significant contributor to maternal morbidity and mortality in malaria-endemic countries. Malaria case management is a critical strategy for malaria elimination. This entails early diagnosis and prompt treatment with effective antimalarial medicines recommended for use in the country. We identified the knowledge and adherence to national guidelines on malaria treatment in pregnant women by health workers regarding uncomplicated malaria treatment in all public health facilities in Rangwe Sub County, Homabay county.

METHODOLOGY: A cross-sectional survey was carried out in 21 public facilities among all the 255 clinicians at the facilities . Provider's age, gender, years of experience, cadre and knowledge of national diagnostic guidelines for uncomplicated malaria in pregnant women was assessed using standardized questionnaires.

RESULTS: Overall, we had 255/255 (100%) responses .Majority 248/255 (97.2%)of respondents accurately described clinical malaria signs and symptoms. All 255/255 (100%) malaria cases were parasitological confirmed before treatment. either through Malaria Rapid Tests or Microscopy. Most clinicians (94.9%) 242/255 knew the drug of choice for malaria prophylactic in pregnancy. Majority 243/255 (95.2%) accurately administered prophylactic antimalarial drugs. 100% of them were aware that microscopy was the gold standard for malaria treatment.

CONCLUSION: The study highlights crucial gaps among public health providers in diagnostic knowledge and adherence to the National guideline in malaria treatment. Interventions to improve health workers' capacity to diagnose treat malaria and implementation of the National guidelines should be prioritized.

Keywords: Malaria, Prophylaxis, Pregnancy

202. Air quality monitoring based on low-cost sensors and labelled air pollution modelling; Bas Henzing

Introduction: The WHO estimates there are around 400,000 early deaths each year in Europe related to air pollution, globally an astonishing 7 million premature deaths are counted. In Europe an estimated 80-90% of the population is exposed to concentrations above the WHO guidance values, arguably this percentage number is higher in other parts of the world. Global warming may lead to droughts, wildfires and extreme weather all with consequent modifications to air pollution. Air pollution strategies to lower exposures to pollution requires insight in concentration levels and the responsible emission sources. Our measurement based monitoring system foresees in this need.

Method: The availability and use of low-cost air pollution sensors has been increasing in recent years. We explored the potential of the sensor data to monitor air pollution on different spatial scales. For this purpose, we used three levels of observational data. The first level is based on high-end equipment (gravimetric mass determination and BAM monitors) in specially designed monitoring stations for official reporting according to EU standards. The mid-cost network contains hardware-modified Shinyea PPD42 sensors reading out the (filter's) voltage outputs and relate generated pulses via Mie theory to particle size. The third level of data consist of low-cost sensors operated by citizens, dominated by NOVA SDS011 and Sensirion SPS030. Typically this latter network of sensors contains many unknown uncertainties and outliers. In our study all three levels of data are used to 'calibrate' air quality simulation by various data assimilation techniques. Despite the uncertainties of low-cost sensors, we will demonstrate the obtained added value of low-cost sensor observation especially when an exuberant amount of observations is available.

Results: We will discuss the results from an implementation in the open-source LOTOS-EUROS model. This model is equipped with label capability which means every source category (e.g. industry, traffic, households etc.) and emission source origin (e.g. local, county, country) is tracked over time and space. In this manner everywhere for every location within the model domain, it is known what part of the pollution is local and what sources categories are dominating the concentration levels. This approach reveals action perspective thus supporting local policy development and implementation. A local application over a Dutch city reduced the simulated concentration bias from -36% without observational data, to -20% using the high-end, to +6% bias using sensors.

Discussion: Our measurement based air pollution monitoring system provides insight in current air pollution levels and is supporting air pollution mitigation policies. Our approach is frequently used to perform (predictive) simulations in our changing climate. We will show results from an applications over the Netherlands and Colombia. We will discuss the potential for application over Kenia

SCIENTIFIC SESSION 23:

VIROLOGY

203.

COMPARATIVE ANALYSIS OF CELL-CULTURE BASED METHOD AND DIRECT DETECTION METHOD IN POLIOVIRUS SURVEILLANCE.

Authors: Collins K Cheruiyot (KEMRI)*; Joanne Hassan (kemri); Rosemary Nzunza (KEMRI); Agnes Chepkirui (KEMRI); Mercy A. Onyango (Kenya Medical Research Institute); Jim Nyangao (KEMRI); Evans Komen (KEMRI); Stephen Ochieng Ombija (Kenya Medical Research Institute); Benlick Mwangi (KEMRI); Robert Mainga (KEMRI); Janet Wanjiru (KEMRI); Samira Ali Katembe (KEMRI); Diana Wanjiku (KEMRI); Maureen Njihia (KEMRI); Paul Muchai (KEMRI); Jennifer Lewett (KEMRI); Peter Maritim (KEMRI); Shadrack Mr. Barmasai (Kenya Medical Research Institute); samoell A Khamadi (KEMRI); Peter Borus (WHO)

Background: Poliovirus (PV) is one of the vaccine preventable diseases targeted for eradication globally. Since the launch of Global Polio Eradication Initiative (GPEI) in 1988, there has been a 99% decline in polio cases as of April 2023. Globally, all countries except Pakistan and Afghanistan have managed to interrupt the transmission of wild PVs. However, the expanding outbreaks of vaccine-derived PV (VDPV) in Africa pose the risk of reversing progress made by GPEI. Kenya reported the last case of indigenous wild type PV (WPV) in 1984 and last case of importations of WPV1 in July 2013. In July 2023, Kenya reported outbreaks of circulating vaccine-derived PV type 2 (cVDPV2) in Hagadera refugee camp. Cell culture is the gold-standard for detection of PV . Limitations of this method are; virus mutation during growth in cell culture, biocontainment concerns of poliovirus grown in culture and competitive exclusion of low fitness variants of viruses in samples containing PV mixtures. Direct detection method aims to reduce the turnaround time of PV detection from 4 weeks to 1 week.

Methods: PV isolation was done from stool samples. A total of 438 stool samples collected from AFP cases, their contacts and community children were processed according to the WHO manual, 2004. The resultant stool suspension were analyzed using both cell-culture and direct detection methods. For cell culture, stool suspensions were inoculated onto monolayer of rhabdomyosarcoma (RD) and L20B cells and observed daily for the appearance of cytopathic effect (CPE). Negative cultures were observed for five days and re-passaged onto a new monolayer for additional five days. Isolates showing CPE on L20B were selected as polioviruses and subjected are intratypic differentiation using RT-PCR. For direct detection method, PV RNA was extracted directly from the stool suspension and characterized using RT-PCR.Sequencing of the VP1 region was done to distinguish vaccine-derived Poliovirus (VDPV) and wild-type polioviruses.

Results: Of the 438 samples analyzed, 324 (74%) had matching results in both methods; Non-Enterovirus(NEV) 284, Non-Polio Enterovirus(NPENT) 27 and suspected poliovirus(SP) 13. Cell culture reported; NEV 338, NPENT 87 and SP 13. On the mis-matching results, 46 samples reported NEV by cell culture were reported NPENT in direct detection, while 57 reported NPENT by culture were reported NEV by direct detection. Important to note is that there was no mismatch in the detection of suspected poliovirus (both=13) between the two methods.

Conclusion: The specificity of direct detection method and cell culture methods were 100% for suspected polioviruses. However, their sensitivities varied. As compared to cell culture, direct detection reported 84% sensitivity for NEV and 31% for NPENT. Further studies are warranted on sensitivity of direct detection.

Keywords: Cell Culture based method and direct detection method

204.

CHARACTERIZATION OF WEST NILE VIRUS KOUTANGO LINEAGE ISOLATED FROM PHLEBOTOMINE SAND FLIES IN KENYA 2021

Authors: Jane W Thiiru (Jomo Kenyatta University of Agriculture and Technology)*; Solomon Langat (Centre for Virus Research, Kenya Medical Research Institute); Francis Mulwa (Centre for Virus Research, Kenya Medical Research Institute); Stephanie Cinkovich (Armed Forces Health Surveillance Division, Global Emerging Infections Surveillance Branch); Hellen Koka (Centre for Virus Research, Kenya Medical Research Institute); Santos J Yalwala (KEMRI/USAMRD-AK); samoell A Khamadi (KEMRI); Justus Onguso (Jomo Kenyatta University of Agriculture and Technology); Nicholas Odemba (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Francis Ngere (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Jaree Johnson (Armed Forces Pest Management Board); Timothy Egbo (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Eric Garges (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Elly Ojwang (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Fredrick Eyase (US Army Medical Research Directorate-Africa)

Background: Sand flies are important vectors that are suspected to transmit a number of arboviruses. Recent studies in parts of Africa, including Kenya have revealed the circulation of several of these arboviruses among sand fly populations making the vector of great public health importance in the region. The present study sought to isolate and characterize viruses from female sand flies recently collected from

different geographical regions in Kenya.

Methods: Female sand flies recently collected from different geographical regions were tested for presence of arboviruses using cell culture in Vero CCL-81 cells. Ribonucleic acid (RNA) from the viral isolate was sequenced on an Illumina iSeq 100. Genome obtained from the reads were subjected to BLAST analysis for taxonomic identification. Comparative analyses of amino acid sequences were conducted to identify crucial changes in the protein sequence. Subsequent phylogenetic and molecular clock analyses were performed to decipher the virus's evolutionary relationships and confirm its phylogenetic placement. Evolutionary pressure analysis investigated episodic/point selection. Protein modeling in Pymol was carried out to elucidate changes in important protein regions. In vitro experiments were performed to investigate the isolated virus's viral growth kinetics in mammalian (Vero-E6) and mosquito (C636) cells.

Results: We report the isolation of West Nile Virus Koutango lineage (KOUTV) from sand flies collected in Baringo County within the Kenyan Rift Valley in 2021. The isolated KOUTV formed a single clade with others previously isolated/identified in West Africa. Diversifying pressure was acting at position 1772 (codon 267) within NS3 of the KOUTV. Protein models revealed unique differences for the current strain at position 3181 (codon 653) within NS5 when compared to other KOUTV and West Nile virus genomes. Growth kinetic analyses show that the current KOUTV replicates efficiently in Vero-E6 and C636 cells compared to West Nile virus Lineage 1a, previously isolated from mosquitoes in Kenya. No significant differences were observed between the growth profiles of the two viruses.

Conclusion The isolation of KOUTV in sand flies points to them as potential vectors, however vector competence studies would confirm this. The replication of isolated KOUTV strain in both mammalian cells and mosquito cells demonstrates its adaptability to both the host and the vector. We speculate the close evolutionary relationship KOUTV in East and West Africa to be enabled by the bird migratory route between the two regions. If proved, this may point to a potential future pandemic pathway for these viruses.

Keywords: West Nile Virus, Koutango Virus, Sand Fly Viruses

205.

CLOSED OR OPEN CANAL IN ENVIRONMENTAL SAMPLING? EVIDENCE FROM RETROSPECTIVE ANALYSIS OF SARS-COV2 AND ENTERIC VIRUS ISOLATION

Authors: Stephen Ochieng Ombija (Kenya Medical Research Institute)*; DIANA WANJIRU WANJIKU (KEMRI); Paul Muchai (KEMRI); Jennifer Lewett (KEMRI); Robert Mainga (KEMRI); Peter Maritim (KEMRI); Agnes Chepkurui (KEMRI); Jimmy Nyangao (KEMRI); Mercy A. Onyango (Kenya Medical Research Institute); Evans Komen (KEMRI); Benlick Mwangi (KEMRI); Joanne H Hassan (kemri); Shadrack Mr. Barmasai (Kenya Medical Research Institute); Janet Wanjiru (KEMRI); Rosemary Nzunza (KEMRI); Fiona Aluoch Alaii (KEMRI); Samira Ali Katembe (KEMRI); Collins K Cheruiyot (KEMRI); Maureen Njihia (KEMRI); Celine Alice (KEMRI); Casey Asigo (KEMRI); Samoel Khamadi (KEMRI); Peter Borus (KEMRI)

Background: Environmental sampling (ES) is a strategic tool for identification of infectious agents or substances of interest present in the environment. ES is being used for various diseases baseline determination such as Poliovirus, SARS- CoV-2 and Anti-Microbial Resistance surveillance. ES sampling uses closed and open systems as main types of drainage canal where samples are obtained. To increase efficiency in selection of site choice, this study sought to find if canal type is empirically linked to SARS-CoV-2 and Poliovirus isolation.

Methodology: A retrospective analysis of data stored on EPI info v 3.5 in 2022 was used in data collection. We included all open and closed canal sites from Nairobi. Thirty-five samples were collected by grab sampling technique and concentrated by two phase separation method. Enteric virus was isolated using chloroform RNA extraction and cell culture. SARS CoV-2 was extracted using RADI kit and rPCR performed. Chi-square tests were conducted to test statistically significant differences between canal type and the test results for both SARS-Cov-2 and Enteric virus at 5% significance. Data were analyzed using STATA v15.

Results: There was no statistically significant relationship between canal type and enteric virus test results ($\chi 2$ =2.9167, p=0.08). The relationship between SARS-CoV-2 test results and canal type was also not statistically significant ($\chi 2$ =0.7721, p=0.38).

Conclusion and Recommendation: There is no superior test between closed and open canal types for testing SARS-COV-2 and enteric virus. A person has a discretion to choose whether of them to use since the canal type is not positively or negatively associated with SARS CoV2 or enteric virus isolation outcome. We recommend larger sample size for analysis in future for precise considerations.

Keywords: Environmental Sampling, Open Canal, Closed Canal, Virus Isolation

206.

TRENDS IN ACUTE FLACCID PARALYSIS CASES FROM KENYA AND SOMALIA: A RETROSPECTIVE SECONDARY DATA ANALYSIS USING EPI-INFO STATISTICAL SOFTWARE (VERSION 7).

Authors: Samira Ali Katembe (KEMRI)*; samoell A Khamadi (KEMRI); Raphael Lihana (KEMRI); Peter Borus (KEMRI); Rosemary Nzunza (KEMRI); Joanne Hassan (KEMRI); Jimmy Nyangao (KEMRI); Evans Komen (KEMRI); Janet Wanjiru (KEMRI); Robert Mainga (KEMRI); Peter Maritim (KEMRI); Agnes Chepkurui (KEMRI); Jeniffer Lewett (KEMRI); Benlick Mwangi (KEMRI); Mercy A. Onyango (Kenya Medical Research Institute); Collins K Cheruiyot (KEMRI); Paul Muchai (KEMRI); Steve Ombija (KEMRI); Diana Wanjiku (KEMRI); Maureen Njihia (KEMRI); Fiona Alaii (KEMRI); Celine Adhiambo (KEMRI); Casey Isigo (KEMRI); Shadrack Mr. Barmasai (Kenya Medical Research Institute)

Background: Polio is highly infectious causing total paralysis in hours and killing youngsters aged 15 and below. On April 6, 2018, KEMRI found live polio type 2 viruses in sewage samples from Nairobi's Eastleigh state. The sample had been collected in March during a routine investigation. In December 2020, January 2021, and July 2023, circulating vaccine-derived poliovirus type 2 cases were identified. For a country that had almost forgotten what polio looks like, with conviction that it had been eradicated and had hoped to be certified polio-free, this was a major setback. A series of vaccination campaigns was carried out in Nairobi and other high-risk counties. Somalia was declared polio-free in 2007 after a series of anti-polio campaigns but it returned in 2013 when poliovirus type 1 was confirmed from the southern and central areas. Children were administered with bivalent OPV but in 2017, circulating vaccine-derived poliovirus type 2 was detected and has been the world's longest ongoing outbreak. Could free movement along the Kenya-Somalia border be the problem? Garissa County of Kenya is at a high risk of polio spread due to its proximity to the country's border. The presence of the Dadaab camp and poor sanitation challenges help the spread of the virus. Poliovirus survives only in humans, spreading from person to person through the fecal-oral route. One confirmed positive case is declared an outbreak.

Methodology: Retrospective secondary data analysis of all suspected polio cases from Kenya and Somalia was conducted using Epi-Info Statistical Software (version 7): from 2021 to 2023. The software captures information such as acute flaccid paralysis (AFP) positive or negative, age, sex, residence, clinical presentation, and vaccination status of the patient.

Results: A total of 9397 AFP samples were received from 2021 to September 2023. Of the 9397 cases reported, 236 (2.5%) were true AFP cases, 7968 (84.8%) negative, and 1193 (12.7%) were non-polio AFP cases. A total of 4658 cases were from Kenya (72 positive, 4012 negative, and 574 non-polio AFP cases). A total of 4739 were from Somalia (164 positive, 3956 negative, and 619 non-polio AFP cases). The data shows that both countries are actively doing AFP surveillance with Somalia having twice the number of AFP positives detected than Kenya.

Conclusion : Poliovirus is a vaccine-preventable disease. Inadequate vaccine coverage leads to mutations of the vaccine virus in children from war-torn areas of Somalia. Despite Kenya having good vaccination coverage, we experienced a recent outbreak in 2023 in Garissa County. Sequencing linked the virus to Somalia's origin, due to our porous borders. Vaccination efforts need to be enhanced regionally for the virus to be eradicated. Non-polio AFP cases can be due to cross-over myelitis and traumatic neuritis.

Keywords: KASH2024

207.

LINEAGE DIVERSITY OF RIFT VALLEY FEVER VIRUS ASSOCIATED WITH HUMAN OUTBREAKS IN KENYA.

Authors: Konogoi Limbaso (KEMRI)*; John Juma (International Livestock Resaerch Institute); Solomon K Langat (Kenya Medical Research Institute (KEMRI)); Kristina Roesel (International Livestock Research Institute); Edith E.L Chepkorir (Kenya Medical Research Institute); Rosemary Sang (International Centre of Insect Physiology and Ecology); Klaus Osterrieder (4. Freie Universität Berlin, Institut für Virologie); Bernard Bett (International Livestock Resaerch Institute); Samuel Oyola (International Livestock Research Institute)

Background: Prompt pathogen detection and characterization is key in monitoring disease events, outcomes and informing response strategies. Rift valley fever (RVF) disease is a priority disease in Kenya with multiple outbreaks documented over increasingly wide geographical areas. RVFV evolution is attributed to its segmented genome, which can result in reassortment contributing to its evolutionary diversity. Monitoring evolution during and between outbreaks is critical towards identifying drivers of genetic diversity that may impact epidemiology of the disease.

Methods: RVF samples collected from different regions between 1997 and 2020 were screened and processed for virus isolation and

real time PCR (qPCR). Positive isolates were subjected to whole genome sequencing utilizing the illumina high throughput sequencing technologies. Maximum likelihood (ML) phylogenetic analysis was undertaken on the aligned sequences and visualized in FigTree. Recombination analysis was done by visual inspection of the phylogeny and validation by RDP4 software.

Results: Whole genome sequences were obtained from 17 isolates representing 8 counties. All isolates clustered within lineage C forming 2 distinct clusters; Kenya-1 and Kenya-2. Differences in clustering patterns were observed across the 3 genome segments. Isolates from 1998 (1), 2007 (1) and the most recent isolates from 2018-2020 (5) had all their segments clustering within the Kenya 2 sub lineage, while the other 10 isolates clustered in both the Kenya 1 and Kenya 2 sub lineages with differences in individual segment clustering patterns. Reassortment events between lineages were observed in 7 isolates.

Conclusion: The findings suggest that lineage C is the most predominant lineage associated with multiple RVF outbreaks in Kenya. The detection of reassortment events highlights the importance of constant monitoring and detection of events that may alter the biological characteristics of the virus with impacts on virulence, transmission, diagnostics, and control of RVF outbreaks.

Keywords: Rift valley fever, lineags, re assortment

208.

PREVIOUS EXPOSURE OF CAMELS TO MERS-COV VIRUS AS INDICATED BY SERO-POSITIVITY IN MANDERA EAST

Authors: Guyo H Sora (Kenya Medical Research Institute)*; Abdiaziz A Gosar (KEMRI); japhet jk katana (kenya medical research institute); EDWARD Kithela (KEMRI); Musa Otieno (Kenya Medical Research Institute); Shingo Inoue (Nagasaki University Institute of Tropical Medicine)

Background: The Middle East respiratory syndrome (MERS) is a viral respiratory disease caused by a novel coronavirus (MERS-CoV) that was first identified in Saudi Arabia in 2012. It is one of the major zoonotic Emerging Infectious Diseases (EIDs) that has occurred over the last two decades. This study aimed to detect the MERS-CoV virus in camels through both serological and molecular analyses.

Method: Both serum and nasopharyngeal swabs were collected in this study. In this first phase of the study the collected seventy-six nasopharyngeal swabs were analyzed using real-time Reverse Transcriptase Polymerase Chain Reaction(rtRT-PCR) targeting the MERS-Orf1a gene while 20 serum samples which were collected in this phase were analyzed using a Commercial MERS-CoV IgG detection kit utilizing MERS-CoV N antigen. Camel age, gender, and owner details were also taken during sampling and recruitment. Data analysis was done using STATA version 14.

Results: Out of the 76 Nasopharyngeal swabs analyzed using rtRT-PCR, none tested positive for the MERS-Orf1a gene. On the other hand, out of 20 serum samples analyzed 7 were positive for IgG antibodies. This accounted for 35% of the samples analyzed.

Conclusion: The result of this ongoing study revealed a previous exposure of the camels with MERS-CoV virus. We recommend further examination of more samples from Mandera County to understand role camels play in the epidemiology of MERS.

Keywords: MERS-CoV, IgG, Seroprevalence, RT-PCR, Camels

209.

MOLECULAR CHARACTERISATION OF VIRULENT STRAINS OF NEWCASTLE DISEASE VIRUS ISOLATED FROM DEAD CHICKENS COLLECTED IN SOUTHERN HIGHLANDS AND EASTERN ZONE OF TANZANIA

Authors: Charlie Franck Amoia (Sokoine University of Agriculture)*

Background: Newcastle disease (ND) is a viral disease affecting a wide range of avian species and has a major impact on poultry production worldwide, due to the significant economic consequences for the poultry industry that this disease can cause. Newcastle disease virus (NDV) has the capacity to infect at least 250 species of birds and all avian species are considered susceptible. Evidence of ND infections has been reported in other non-avian hosts such as cattle and sheep, mink, hamsters, mice, rabbits, camels, pigs, monkeys and humans. In humans, the virus has already been isolated from a patient with no apparent signs of the disease and can cause fatal encephalitis in children.

Objectives: The main aim of the current study was to investigate the NDV genotypes circulating in backyard poultry flocks.

Methods: Reverse transcription polymerase chain reaction (RT-PCR) based on the fusion (F) and hemagglutinin-neuraminidase (HN) genes amplification was conducted on 2 tissues samples collected from chickens during a suspected ND outbreak. Sanger sequencing was performed on the purified PCR products by Macrogen (Maastricht, Netherlands). Geneious Prime 2023.0 was used to assess the quality of the chromatograms, assemble and edit the obtained nucleotide sequences. NCBI BLAST was used to compare the sequences with those found on the NCBI nucleotide database. MEGA X software was used for nucleotide alignments using the ClustalW method. Phylogenetic analysis based on the F and HN gene was performed using the Maximum Likelihood method with General Time-Reversible (GTR) model with a discrete gamma distribution (+G), allowing for invariant sites (+I) and 1000 bootstrap resampling.

Results: A phylogenetic analysis using the full F and HN genes sequences revealed that the viruses belong to genotype VII and showed a higher genetic similarity to NDVs from Mozambique, South Africa, Zambia, Zimbabwe, Botswana, Southeast Asia (Malaysia, Indonesia), and China. The common F protein aa cleavage site motif for the studied NDV isolates was 112R–R–Q/K–K–R–F117, indicating that these viruses are virulent.

Conclusion: Newcastle Disease Virus (NDV) genotype VII is a highly pathogenic Orthoavulavirus that has caused multiple outbreaks among poultry in the world. Given the problems posed by genotype VII elsewhere, regular monitoring and characterization of circulating strains, as well as expansion of the study to other regions of Tanzania will provide a more accurate picture of the ND situation and contribute to improved disease control. In addition, these results should be considered as a warning because of the possibility for the emergence of new NDV sub-genotypes and the occurrence of uncontrolled epidemics in the future.

Keywords: Newcastle disease virus; genotypes; virulence; phylogeography, Africa

210.

ILLNESS OUTCOMES OF IN-AND-OUT PATIENTS CO-INFECTED WITH SARS-COV-2 AND MALARIA, 2020-2022

Authors: Jorim Mr Ayugi (KEMRI-CGHR)*; Bryan BN Nyawanda (KEMRI); Peter M Kinuthia (HJFMRI); Jeanette Dawa (WSU); Rosalia Kalani (MOH); Elizabeth Kiptoo (MOH); Emmanuel Okunga (MOH); Nancy Otieno (Kenya Medical Research Institute (kemri))

Background: There is paucity of data on the impact of co-infection of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) and malaria on illness outcomes, especially in Sub-Saharan Africa where malaria is common. We assessed illness outcomes among inpatients presenting with respiratory illness who were infected with SARS-CoV-2 or malaria compared to those coinfected with SARS-CoV-2 and malaria.

Methods: We analyzed data collected from eight severe acute respiratory illness (SARI) and influenza like illness (ILI) sentinel surveillance sites in Kenya. SARI was defined as hospitalization with a cough and fever (reported or documented) within the last 10 days , whereas ILI was defined as presentation with cough and measured fever ≥ 38o C within the last 10 days. Severe outcomes were defined as either death, intensive care unit (ICU) or acute care unit (ACU) admission, or use of supplemental oxygen. SARS-CoV-2 infection was confirmed through reverse transcription polymerase-chain reaction (rtPCR) while malaria infection was confirmed through microscopy or rapid diagnostic tests (RDT). Differences in severe outcomes were assessed using Odds ratios (OR) while adjusting for age of patient, site and month of data collection.

Results: During the period March 2020 to December 2022, we enrolled a total of 4922 patients (4000 inpatients and 922 outpatients); of which 3880 (78.8%) were aged <5 years and 2702 (54.9%) were males. The prevalence of SARS-CoV-2 infections was 7.7 % (381/4922): 6.1% (238/3880) and 13.7% (143/1042) among patients aged <5 and ≥5 years, respectively. Malaria infections were detected in 25.4% (1252/4922) of the patients: 23.7% (921/3880) among children <5 years and 31.8% (331/1042) among older patients. There were higher malaria prevalence in Siaya and Kakamega for sites that routinely test for malaria. On the other hand, there were higher SARS-CoV-2 prevalence (above 10%) in Nyeri, Siaya and Nakuru sites. Co-infections of SARS-CoV-2 and malaria were detected in 1.5% (76/4922) of the patients (36 (4.0% among outpatients and 40 (1.0%) among inpatients) . Co-infected inpatients of any age were more likely to die during admission as compared to those infected with malaria alone (11.79 (2.59-53.67), p<0.01).

Conclusion: Understanding the effect of SARS-CoV-2 and malaria co-infection is important in advising effective patient management practices. Co-infected patients require more attention and should be prioritized.

Keywords: Coinfection, malaria, Covid-19, severity

211.

WHOLE GENOME CHARACTERIZATION OF G8P[14] ROTAVIRUS STRAIN DETECTED IN KENYA: EVIDENCE FOR ARTIODACTYL -TO-HUMAN INTERSPECIES TRANSMISSION AND REASSORTMENT

Authors: Ernest A Wandera (Kenya Medical Research Institute)*; Yuki Akari (Fujita Health University School of Medicine); Carlene Sang (KEMRI); Pamela Njugu (Kenya Medical Research Institute); Samoel Khamadi (Kenya Medical Research Institute); Satoshi Komoto (Oita University); James Nyangao (Kenya Medical Research Institute)

Background: Rotaviruses (RVs) are a major cause of acute gastroenteritis in children and young animals globally. Although RVs are generally host-restricted, there is increasing evidence supporting animal-to-human zoonotic transmission and reassortment events. During our routine RV surveillance, we detected for the first time in Kenya a human RV strain A75 (G8P[14]) in a pediatric diarrheal patient. Employing the next generation sequencing, we aimed to determine the whole genome sequence of all 11 segments of this strain and clarify its phylogenetic relationship with known human and animal RV strains.

Method: Stool sample was collected from pediatric diarrhea patients at Aga Khan University Hospital Kenya in 2000. Genomic dsRNA was extracted from the G8P[14] strain and subjected to Illumina MiSeq next-generation sequencing. Analyses of the sequence data were carried out using CLC Genomics Workbench v8.0.1 (CLC Bio). Maximum-likelihood phylogenetic trees were constructed for all 11 genes using MEGA7.0.26.

Results: The VP7 gene of the strain A75 was most similar (97.3%) to the Slovenian deer RV D110-15 strain (G8P[14]). The VP4 gene was most similar (92.2%) to the South African buffalo RV 4426 strain (G29P[14]). The 11 genes of strain A75 were assigned as G8-P[14]-I2-R2-C2-M2-A11-N2-T6-E2-H3. A11, T6 and H3 were typical artiodactyl RV genotypes. Furthermore, Phylogenetic analysis showed that remaining eight genes were also closely related to artiodactyl RV and artiodactyl-like human RV.

Conclusion: We report compelling evidence to suggest that the Kenyan G8P[14] strain may have been derived through interspecies transmission and reassortment events involving artiodactyl and human rotavirus strains. This is the first report of G8P[14] detected in Kenya and it is a rare human G/P genotype worldwide. Due to the close proximity between humans and animals in developing countries such as Kenya, it is essential to continue monitoring the spread of zoonotic RV strains in the human population to enhance data-driven public health interventions.

Keywords: Kenya; Whole genome analysis; Rotavirus; G8P[14] strains; Artiodactyl-to-human interspecies transmission.

212.

LONGITUDINAL STUDY FOR SARS-COV-2 AND NEUTRALIZING ANTIBODIES BETWEEN APRIL 2021 AND MARCH 2022 IN KOMBEWA, WESTERN KENYA

Authors: Esther A Omuseni (KEMRI-Walter Reed Project)*

Background: The coronavirus disease-2019 (COVID-19) pandemic disrupted global health systems, causing widespread illness. Being a new disease, there was a need to understand its transmission dynamics to help manage citizens' anxiety and to hopefully contain its spread. While SARS-CoV-2 is the best indicator of ongoing infection, neutralizing antibodies (nAbs) produced in response to infection or vaccination are the best correlate of protection.

Methods: This study evaluated the temporal kinetics of SARS-CoV-2 and anti-SARS-CoV-2 nAbs between April 2021 (wave 3) and April 2022 (end of wave 5) at the Human Demographic Surveillance System (HDSS) site in Kombewa, Kisumu county, western Kenya. Participants were consented to provide nasopharyngeal or oropharyngeal samples and serum every fortnight for detection of SARS-CoV-2 by reverse transcriptase real time PCR (RT-qPCR) and nAbs to SARS-CoV-2 RBD (Receptor Binding Domain) protein.

Results: A total of 1385cross-section samples were provided by 939 females (68.1%), 439 males (31.9%) and 7 (0.5%) unknown gender of age bands: <9 (26.9%), 10-19 (15.4%), 20-39 (28.4%), 40-59 (16.6%), >60 (0.1%) and 4 (0.3%) unknown age out of which 1342 were analyzed. At survey one, April 2021, proportion of samples positive for nAbs and RT-qPCR were 18.7% (n=214) and 3.3% (n=214) respectively. The nAbs positivity rate continued to increase reaching 88.9% (n=227) by the 6th survey (March 2022). Positivity by RT-qPCR increased to 26.3% (n=217) by second survey (June 2021), and thereafter decreased as nAb positivity rate increased, decreasing to 0% by survey 4 (October 2021), up to 0.1% by survey 5 (December 2021) and then 0% by survey 6 (March 2022). Likewise, the quantity of nAbs increased over time: 0.42U/mL at survey 1, 1.28U/ml by survey 2, 2.65U/ml by survey 3, a slight decline recorded at survey 4 1.71U/ml with an increase onwards, 4.48U/ml by survey 5 and 9.39U/ml by survey 6. Females had higher mean levels of nAbs (3.734U/ml, CV of 277.6% at 95% CI) than males (1.976U/ml, CV of 374.1% at 95% CI, p= 0.0146). Neutralizing antibody levels increased with age with a mean of 2.125U/ml, 2.620U/ml, 3.302U/ml, 3.737U/ml and 4.680U/ml for ages <9 Years, 10-19 years, 20-39 years, 40.59 years and >60years age bands respectively. Although these differences were statistically significant, the effect sizes were minimal with R2 values of less than 0.1.

Conclusion: Our study found a strong presence of nAbs in the study population with a steady increase over time. However, absence of vaccination data was a major limitation to differentiate vaccine and disease-mediated nAbs response.

Keywords: COVID-19, SARS-CoV-2, Neutralizing antibodies

213.

PRESENCE OF SARS-COV-2 RNA IN WASTEWATER AND CORRELATION WITH REPORTED COVID-19 PREVALENCE IN THE THIKA SUB-COUNTY

Authors: Samuel Ng'ang'a 1, Esther Wanjiru 1, Harrison Waweru 1, Ernest Wandera 1, Bernard Kanoi 1, Hussein M. Abkallo 2, Fatma Guerfali 3, Jesse Gitaka 1

1 Center for Research in Infectious Diseases, Mount Kenya University (MKU), Thika, Kenya

2 Animal and Human Health Program, International Livestock Research Institute (ILRI), Nairobi, Kenya

3 Laboratory of Transmission, Control, and Immunobiology of Infections, Institut Pasteur de Tunis, Tunisia

Wastewater-based epidemiology (WBE) offers real-time monitoring capabilities. This study established a WBE system in Thika, Kenya, to investigate correlations with clinical data. Long-term monitoring from Nov 2021 to Nov 2022 revealed that 16.5% of 200 wastewater(WW) samples were positive for SARS-CoV-2 RNA. Higher viral shedding, indicated by lower Cycle threshold(Ct) values and increased prevalence in Nov 2021, Dec 2021, and Jan 2022, coincided with higher COVID-19 case prevalence. This suggests that WBE could serve as an early warning system for infection trends.

Introduction: Infectious disease outbreaks in densely populated areas are hard to predict with existing surveillance strategies. WBE is a promising technique to monitor health status in real-time. This study sought to established a WBE system for SARS-CoV-2 in Thika, Kenya, to complement clinical surveillance. Long-term monitoring was carried out from November 2021 to November 2022.

Methods: Wastewater sampling was done using Moore swabs in 13 sites, 4 in Thika wastewater sampling site, 5 in Mount Kenya University, 3 in Thika level 5 hospital and 2 apartments. Total nuclei acid was extracted and qRT-PCR proceeded targeting, N, S and the ORF1ab SARS-CoV-2 genes. A sample was deemed positive if at least 2 of the targeted genes had a Ct< 37.

Results and Discussion: 33 (16.5%) of 200 WW samples were positive for both N and ORF1ab gene targets, with frequencies of detection being 47 and 35, respectively. The N gene displayed lower Ct values, attributed to its higher abundance and lower genetic variability. No sample amplified the spike (S) protein gene, indicating decreased shedding, or high genetic variability.

Recording lower Ct values and higher prevalence in Nov 2021(50%), Dec 2021(69%), and Jan 2022(42%) coincided with more precipitation and warmer temperatures compared to May-Nov 2022(8.6%). This indicates increased viral shedding and higher viral load in WW, suggesting potential transmission. Low Ct values correlated with high COVID-19 prevalence in Nov 2021(1.35%), Dec 2021(21%), and Jan 2022(16%). WBE could provide an early warning for infection trends.

Conclusion: This study demonstrated SARS-CoV-2 RNA detection in WW, correlating with COVID-19 reported cases. High viral shedding, due to prevalence, determined viral concentration, masking weather effects. WBE offers insight into changing infection trends.

Keywords: SARS-CoV-2, wastewater, RNA-Seq, Wastewater Based Epidemiology

214.

TEMPORAL DYNAMICS OF DENGUE VIRUS 1 MUTANT POPULATIONS DURING A DENGUE FEVER OUTBREAK AT THE KENYAN COAST

Authors: Josphat N Nyataya (Kenya Medical Research Institute)*; Eavalyne Wambugu (Kenya Medical Research Institute); John N Waitumbi (KEMRI/Walter Reed Project); George Waitumbi (Kenya Medical Research Institute); Gathii Kimita (WRAIR-Africa); Eric M Muthanje (KEMRI/Walter Reed Project)

Background: Dengue is a viral disease that causes dengue fever (DF), an emerging public health concern, that causes more than 390 million infections globally, 96 million of which have clinical manifestations. In Kenya DF is rampant in the coastal region of the Indian Ocean. DF is caused by four antigenically distinct serotypes (DENV–1-4), which are further subdivided into genotypes. This study evaluated the temporal dynamics of mutant populations that were associated with November 2019 to September 2022 DF outbreak.

Methods: We collected 1,951 plasma samples between November 2019 to September 2022 from study subjects presenting with febrile illness at hospitals in south and north coast of Kenya. DENV serotypes were identified by RT-qPCR and whole genomes obtained by next generation sequencing. Complete genomes were used for phylogenetic analysis and envelope genes used to identify genetic mutants.

Results: Of the 1,951 samples, 350 tested positive for DENV-1 serotype. Few cases of DENV-2 (highest=12 cases) and DENV-3 (highest=7 cases) were observed at the onset of the study (early 2019) but they quickly disappeared from circulation. Two waves of DENV-1 infections were observed that were interspersed with a prolonged period of very low infections. The first wave occurred between November2019-June 2020 and the second wave between September 2021-May 2022.The burden of infection was highest in males (67.4%) of ages 19-39 years (53.1%) and the most common clinical symptoms included headache 85.4% (299/350), joint ache 74.6% (261/350), chills 73.7%% (258/350), muscle pain 72.3% (253/350) and eye pain 56.0% (196/350). From the 350 DENV-1 positive samples, complete genomes were obtained in 180 samples. DENV-1 genotypes I and III were co-circulating during wave 1. Thereafter, genotype I that was characterized by a homogenous mutant population disappeared and the heterogenous genotype III dominated the second wave.

Conclusion: Our findings provide data on the complex temporal dynamics of DENV mutant populations during a DF outbreak at the Kenya coast

Keywords: Dengue, Fever, Dengu Virus

SCIENTIFIC SESSION 24:

AMR

215.

MONITORING THE BATTLEGROUND: EXPLORING ANTIMICROBIAL RESISTANCE, ANTIBIOFILM TRENDS, AND VIRULENCE FACTORS IN WOUND BACTERIAL ISOLATES

Authors: Silas O Awuor (Jaramogi Oginga Odinga teaching & Referral Hospital)*

Background: There is an alarming increase in antibiotic resistance, especially in common bacterial infections that could be attributed to extensive and indiscriminate use of antibiotics.   Continuous strategic monitoring of antibiotic use and AMR trends becomes imperative. Chronic wound infection remains a public concern in this era of AMR. This motivates a thorough evaluation of wound isolates for relevant bacteria and assessing their drug susceptibility patterns, which we report herein. The study aimed to decipher antibacterial resistance by examining samples collected from patients with chronic wounds seeking medication at Jaramogi Oginga Odinga Teaching and Referral Hospital (JOOTRH).

Methodology: This was cross-sectional study among the patients with chronic wounds seeking medication at Jaramogi Oginga Odinga Teaching and Referral Hospital (JOOTRH). Standard microbiological methods were employed to identify and characterize the bacterial pathogens.

Results: Analysis of the wound isolates revealed a significant presence of microbial growth, with a higher prevalence of 59% isolates in male patients. Staphylococcus aureus 20.7% emerged as the most predominant pathogen, followed by Klebsiella spp.14.8%, P. aeruginosa spp. 14.8%, and E. coli 4.4% in the wound samples. Notably, Cotrimoxazole exhibited the highest antibacterial resistance 48.1%, followed by Clindamycin 25.9% and Erythromycin 25.9%, affecting both Gram-positive and Gram-negative bacteria. Furthermore, among the isolates, 75% were capable of producing haemolysin and protease, while 50% produced lipase and phospholipase, factors that enhance virulence and survival.

Conclusion and recommendation: These findings provide crucial insights into antimicrobial resistance in chronic wounds among patients attending JOOTRH, thus the importance of creating awareness and emphasis on responsible antibacterial use in wound management and shedding light on the need to developing more potent antibiotics to treat chronic wounds effectively.

Keywords: Antibiofilm, Antimicrobial resistance, human pathogens, susceptibility, virulence,

216.

FUNGAL SPORE AIR POLLUTION IN VARIOUS ENVIRONMENTS IN NAIROBI KENYA

Authors: Vincent Kiprop (Kemri)*; Christine Bii (KEMRI); Anthony Nyamache (KU); Sally N Loronyokie (KEMRI)

Background: Fungal spores constitute a majority of bioaerosols and are important indicators for bio-pollution. According to WHO, rural-urban migration explosion has increased human-caused air pollution in several cities across developing nations causing up to 6.5 million annual mortalities. Nevertheless, existing literature on air pollution research primarily focuses on inorganic pollutants, evidently leaving out bio-pollutants. This study focuses on the load, distribution, and diversity of fungal spores in selected sites within Nairobi County, Kenya during dry and wet seasons as well as their relationship with meteorological parameters. **Methods:** Air sampling was conducted in markets, roads, recreational, and dumping sites of Nairobi using the Settle plate method. Petri dishes with prepared Sabouraud Dextrose Agar were aseptically exposed for 5 minutes at the sampling sites before transporting for incubation at 28 °C. Meanwhile, meteorological parameters, i.e., temperature, humidity, and windspeed were recorded at the sampling sites using the AccuWeather App. After monitoring and recording fungal growth for 3-7 days, fungal concentration was computed, and the isolates were identified using macroscopic and microscopic techniques. All statistical analyses were performed in SPSS v. 27. P values with less than 0.05 ($p<0.05$) were considered statistically significant.

Results: The wet season had the highest number of fungal spores, averaging 6716.738 CFU m^{-3}, compared to the dry season whose average concentration was 1929.576 CFU m^{-3}. A total of 511 isolates were isolated across two seasons, with 58 genera and 69 species comprising Ascomycota (96.30%), Zycomycota (1.65%), Deuteromycota (1.44%), and Basidiomycota (0.62%). Stepwise regression analysis revealed that temperature among all the other meteorological parameters had the biggest influence on fungal concentration. Pearson correlation analysis showed that temperature negatively correlated with the fungal concentration significantly, humidity positively correlated with the fungal concentration but was not statistically significant, and wind speed negatively correlated with fungal concentration significantly.

Conclusion: Our findings signify the importance of fungal air pollution, the possible risks of human respiratory infections and spore allergies, providing the necessary valuable insights to the policymakers. More studies will shed light on airborne fungal spores and human mycoses with changing weather patterns and climate change.

Keywords: Fungal Spore Pollution

217.

PHENOTYPIC AND MOLECULAR CHARACTERIZATION OF Β-LACTAMASE-PRODUCING KLEBSIELLA SPECIES AMONG CHILDREN DISCHARGED FROM HOSPITAL IN WESTERN KENYA.

Authors: Doreen Wanjira Rwigi (KEMRI-Graduate School)*

Background: The emergence and spread of β-lactamase-producing Klebsiella spp. has been associated with a substantial healthcare burden resulting from therapeutic failures. We sought to describe the proportion of phenotypic resistance to commonly used antibiotics, characterize β-lactamase genes among isolates with antimicrobial resistance (AMR), and assess the correlates of phenotypic AMR in Klebsiella spp. isolated from stool samples collected from children being discharged from hospitals in Western Kenya.

Methods: We conducted a cross-sectional study involving 245 children aged 1-59 months who were being discharged from Kisii and Homabay Referral hospitals in Western Kenya between June 2016 and November 2019. Rectal swabs were collected and Klebsiella spp. isolated by standard microbiological culture. β-lactamase genes were detected by polymerase chain reaction whilst phenotypic antimicrobial susceptibility was determined using the Kirby Bauer disc diffusion technique following standard microbiology protocols. Sociodemographic and clinical data on sex, child age, HIV exposure, length of hospital stay, antibiotic use during hospitalization, water source, and treatment were also collected through questionnaires. Descriptive analyses were used to calculate proportions (percentages) and confidence intervals to characterize phenotypic AMR and carriage of β-lactamase-producing genes. Univariate and multivariable poison regression models were used to calculate correlates of phenotypic AMR.

Results: The prevalence of β-lactamase carriage among Klebsiella spp. isolates at hospital discharge was 62.9% (154/245). More than half of the Klebsiella spp. isolates (62.8%) were resistant to at least one of the third-generation cephalosporins; Ceftriaxone, 155 (63.2%) Cefotaxime, 154 (62.8%) and Ceftaxidime,146 (59.6%). Resistance to cefoxitin was only 4.9% while 58.0% were resistant to gentamicin. Among the less commonly prescribed antibiotics in Kenya hospitals, 42% were resistant to Chloramphenicol, 32% to Ciprofloxacin, and 24% to azithromycin while 90% were susceptible to Meropenem and imipenem. Antibiotic use during hospitalization (adjusted prevalence ratio [aPR]=4.51; 95% CI: 1.79-11.4, $p<0.001$), longer duration of hospitalization (aPR=1.42; 95% CI: 1.14-1.77, $p<0.002$), and access to treated water (aPR=1.38; 95% CI: 1.12-1.71, $p<0.003$), were significant predictors of phenotypically determined β-lactamase. The most prevalent genes were bla CTX-M (92.2%; 95%CI: 86.8–95.9) and blaSHV (92.2%; 95%CI: 86.8–95.9) followed by blaTEM (57.1%; 95%CI: 48.9–65.1) and blaOXA (31.2%; 95%CI: 24.0–39.1), respectively.

Conclusion: Carriage of β-lactamase producing Klebsiella spp. was associated with a longer duration of hospitalization, antibiotic use, and access to treated water. These findings emphasize the need for continued monitoring of antimicrobial susceptibility patterns to inform the development and implementation of appropriate treatment guidelines.

Keywords: Antimicrobial Resistance, beta-lactams, Klebsiella spp, Extended Spectrum Beta lactamases, Cephalosporins

218.

SURVEILLANCE OF NON-TYPHOIDAL SALMONELLA FROM ENVIRONMENTAL SOURCES IN A DISEASE ENDEMIC SETTING IN NAIROBI, KENYA

Author: Collins Kebenei

Background: Non-typhoidal (NTS) causes self-limiting gastroenteritis in most developed Countries but is associated with severe bacteremia in sub-Saharan Africa, especially in children under five years of age and immune-compromised individuals. Lack of clean water, poor sanitation, and hygiene are environmental factors reported to be associated with the disease. However, our understanding of the potential role of the environment as a reservoir for community transmission of NTS in disease-endemic settings is limited.

Methods: This study aimed to screen for NTS in various environmental samples (drinking water, household wastewater, soil, and raw sewers) in a disease-endemic Mukuru settlement and investigate seasonal variations. Samples were collected throughout 2022, and real-time quantitative Polymerase Chain Reaction was used for screening.

Results: Out of 274 collected samples, 82 (34.6%) were contaminated with NTS, with Salmonella Enteritidis being the most ubiquitous at 54/274 (19.7%) compared to Salmonella Typhimurium 28/274 (10.2%). Raw sewers exhibited higher contamination levels (12/86 (75%) S. Enteritidis and 11/86 (68.8%) S. Typhimurium) compared to the household wastewater (21/86 (24.4%) S. Enteritidis and 10/86 (11.6%) S. Typhimurium), drinking water (12/86 (14%) S. Enteritidis and 3/86 (3.5%) S. Typhimurium), and soil samples (9/86 (10.5%) S. Enteritidis and 4/86 (4.7%) S. Typhimurium). NTS detection was more frequent during wet seasons (April-June, October-December) than during periods of lower precipitation (July-September, January-April). **Conclusion:** Detection of NTS in different ecological niches may indicate their potential to persist longer in the environment, elevating the risk of community transmission in Mukuru settlement. Contamination across various niches underscores a significant public health concern, emphasizing the need for a comprehensive surveillance system to understand NTS dynamics, inform prevention strategies, and control its spread within the community.

Keywords: Non-Typhoidal Salmonella; Environmental Contamination; Seasonal Variations; NTS Surveillance

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219.

ANTIMICROBIAL RESISTANCE IN A CHANGING CLIMATIC CONTEXT: AN EMERGING PUBLIC HEALTH THREAT IN AFRICA

Authors: Collins Otieno Asweto (University of Embu)*

Background: Although there are improvements in human survival as a result of the accessibility of powerful antibiotics, this gain is approaching its limit due to the changing climate and antimicrobial resistance (AMR) development. African countries are hardest affected, since they have less access to new antibiotics, are under more financial strain, and are unable to pay for second-line antibiotics.

Objective: The aim of this review was to provide an evidence base for understanding AMR and climate change in a public health-focused approach. Specifically, it aims to shed light on aspects of climate change on the spread and proliferation of antibiotic resistance in Africa.

Methodology: Systematic review was conducted using PRISMA-ScR Checklist. We compiled the information that has been published on the emerging antimicrobial resistance in Africa. Relevant articles published between 2010 and 2022 were rigorously searched for using Scopus, Web of Science, and Google Scholar. Only research that met the following criteria was included in this review: (a) it must have been conducted in Africa; (b) it must have estimated the prevalence or incidence of antimicrobial resistance pathogens; (c) it must have described at least some of the measures taken to prevent and/or control the spread of AMR pathogens; and (d) it must have reported quantitative or qualitative data of antimicrobial resistance pathogens in the humans and or domestic animals.

Findings: Our results show that regional consumption drives selection for the carriage of genes conferring resistance to most antimicrobials. There were diverse patterns of resistance seen in the isolates and the prevalence of AMR in the wake of climate warming in Africa. Many African countries do not effectively implement existing policies and legislation, most notably the prohibition of over-the-counter antimicrobials, and monitoring AMR in agriculture and food production systems across the continent.

Conclusion: Actions are needed to combat AMR in all settings with the One Health concept in mind. It is important to increase the regulatory capacity of African countries to monitor AMR in agriculture and food production systems. The appropriate use and prescription of antibiotics must be addressed to target audiences in human health, animal health, and agriculture. Lastly, there is a need to develop new public health strategies for addressing climate change and infectious diseases together.

Keywords: Antimicrobial resistance, Climate change, Africa, AMR monitoring

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220.

ANTIMICROBIAL RESISTANCE AND INTESTINAL SHEDDING OF NON-TYPHOIDAL SALMONELLA AMONG CHILDREN UNDER FIVE YEARS AND CARRIAGE IN ASYMPTOMATIC HOSTS IN KENYA

Authors: Kelvin Kering (KEMRI)*; celestine w wairimu (Kenya Medical Research institute); Georgina A Odityo (Kenya Medical Research Institute); Collins Kebenei (KEMRI); Kariuki Njaanake (Univeristy of Nairobi); Marianne Mureithi (University of Nairobi); Cecilia Mbae (KEMRI); Samuel Kariuki (KENYA MEDICAL RESEARCH INSTITUTE)

Background: Nontyphoidal Salmonella (NTS) infection is characterized by self-limiting enterocolitis, but can become invasive resulting in bacteremia. Salmonella enterica serovars Typhimurium and Enteritidis (S. Typhimurium and S. Enteritidis) are the most common causes of NTS with the highest incidences reported in sub-Saharan Africa and in children ≤ 5 years. Since intestinal shedding could serve as a potential source of new infections in vulnerable individuals, this study aimed to determine rates of post-convalescent shedding in children under five years of age and corresponding age-matched controls in the community.

Methods: This was a prospective case-control study in children from the Mukuru Informal settlement in Nairobi, between June 2021 and April 2023. Children presenting with fever for > 24 hours with or without diarrhoea and not on antibiotics were recruited. Blood and stool were collected, subjected to culture for NTS isolation, biochemical testing, and identified through serology and PCR). Kirby Bauer Disk diffusion method was used to determine the antimicrobial susceptibility to 14 commonly used antibiotics. Fourteen days post-treatment, index cases, their household contacts, and randomly selected controls (neighbours to the index cases) were followed up for a minimum of one month. Thereafter, follow-up was stopped after three consecutive negative cultures from the stool.

Results: Of the recruited participants, 1.5% (49/3,216) were NTS-positive with 58.7% (27/46) being male. The positivity rate per age group was: ≤ 12 months, 1.8% (18/853), 13-24 months 1.6%(15/939), 25-36 months, 1.1% (6/563), 37-48 months, 0.8% (4/475), and 49-60 months, 2.3% (9/386). Intestinal shedding was observed in 26.5% (13/49) of the index cases with 66.7% (9/13) of those being male. The longest duration of intestinal shedding was three months post-treatment. Among the healthy individuals, 3.9% (7/190) were found to be shedding NTS. Resistance to Azithromycin, the current drug of choice for the treatment of invasive NTS, was observed in 13.8% of S. Typhimurium and 8.9% of S. Enteritidis with reduced susceptibility in 72.4% of S. Typhimurium and 82.2% of S. Enteritidis.

Conclusion: The presence of NTS carriage in children within informal settlements is a risk as they can be sources of transmission to vulnerable immunosuppressed populations. This study demonstrates the need for vaccine introduction in the prevention of invasive NTS infections especially among young children in endemic settings.

Keywords: Shedding; Carriage; Salmonella; Children; Asymptomatic; Antimicrobial resistance

221.

ROLE OF GALLSTONES IN SALMONELLA TYPHI CARRIAGE AND FECAL SHEDDING, ANTIMICROBIAL RESISTANCE AND BIOFILM FORMATION

Authors: Peter Muturi (KEMRI)*; Peter Wachira (Department of Biology, University of Nairobi, Kenya); Maina Wagacha (Department of Biology, University of Nairobi, Kenya); Cecilia Mbae (KEMRI); SUSAN M KAVAI (KENYA MEDICAL RESEARCH INSTITUTE); Musa Muhammed (Medical Services, Nairobi City County); John Gunn (Nationwide Children’s Hospital and Ohio State University); Samuel Kariuki (KENYA MEDICAL RESEARCH INSTITUTE)

Background: Even after successful treatment approximately 3-5% of patients with typhoid fail to clear the bacteria within one year and become chronic carriers. Such carriers can become a source of transmission of typhoid in the community through fecal shedding of the bacteria into the environment. 95% of typhoid carriers have gallstones in their gallbladder. Biofilm formation on gallstones is highly correlated with chronic carriage. Although highly contagious, carriers are typically asymptomatic and shed the infectious bacteria intermittently in their feces for an ill-defined period of time and thus serve as a reservoir of infection.

The aim of this study was to determine prevalence of chronic typhoid carriers, the longitudinal shedding dynamics, and whether antimicrobial resistance or the isolates biofilm forming ability is associated with the duration of shedding.

Methods: A cohort of typhoid fever patients identified through blood and stool culture in Mukuru slums and Mama Lucy Kibaki Hospital, Nairobi, from December 2020 to July 2023 were followed up after treatment. Stool samples were collected at least once monthly for 12 months to detect S. Typhi stool shedding from cases and contacts at home. An abdominal ultrasound scan was used to identify individuals with gallstones. Antimicrobial susceptibility to commonly used antibiotics was tested for all isolates followed by in vitro biofilm formation assays.

Results: A total of 30 typhoid fever cases aged >12 years and their contacts at home were successfully followed up. Stool shedding was observed in 26.7% (8/30) of the cases and seven household contacts during the first and/or the second month of follow-ups. Only 13.3% (4/30) of the cases continued to shed S. Typhi after the second month; these four cases and one asymptomatic contact were found to have gallstones in their gallbladder.

Salmonella Typhi isolates showed highest resistance to nalidixic acid at 90%. Multidrug resistance was observed in 38.3% of the isolates while 83.3% showed reduced susceptibility to ciprofloxacin, the drug of choice for treatment of typhoid. All S. Typhi isolates from carriers that were found to be having gallstones had reduced susceptibility to ciprofloxacin. Out of the 5 carriers with gallstones, one was shedding MDR S. Typhi, three shed S. Typhi strains that showed both resistance to nalidixic acid and reduced susceptibility to ciprofloxacin while one shed S. Typhi susceptible to all antibiotics.

Isolates from 4/5 of the carriers with gallstones formed stronger biofilms compared to biofilms formed by most of the S. Typhi from non-carriers/acute cases.

Conclusion: There is a strong correlation between duration of S. Typhi shedding, presence of gallstones and biofilm forming ability. Asymptomatic carriers at household level are a potential reservoir for typhoid and may be responsible for persistence and spread of MDR S. Typhi in Nairobi.

Keywords: Typhoid carriage, Gallstones, Antimicrobial resistance, Biofilms

222.

UNVEILING THE RESILIENCE MECHANISMS OF ACINETOBACTER BAUMANNII IN NOSOCOMIAL SETTINGS: INSIGHTS FROM AMR AND VIRULENCE GENE CARRIAGE

Authors: Vanessa N Onyonyi (KEMRI/USAMRD-A)*; Collins K Kigen (KEMRI/USAMRD-A); Lillian Musila (USAMRD-A, Kenya/KEMRI)

Background: Multi-drug resistant (MDR) Acinetobacter baumannii (A. baumannii) has been associated with high morbidity and mortality rates globally, especially as a hospital-acquired infection (HAI). A. baumannii demonstrates high stress tolerance with high genome plasticity at acquiring foreign resistance genes. Current research on A. baumannii has explored the characterization of antimicrobial resistance (AMR) and virulence genes separately. As a result, the virulence and AMR gene associations have not been well understood. Understanding this relationship is crucial for more optimized infection prevention and control approaches

Methods: In an ongoing surveillance study spanning from 2015 - 2021, 124 A. baumannii isolates were collected from clinical samples across nine hospitals in Kenya. Clinical and demographic data, along with patient consent, were also obtained. Bacterial culture and DNA extraction were performed, followed by Whole-Genome Sequencing using the Illumina MiSeq platform. The reads were pre-processed on FastQC and assembled using Shovill. Screening for AMR and virulence genes was on AbritAMR software and plasmid replicons were screened with the Abricate software against the PlamsidFinder database.

Results: Out of the 124 isolates, 112 (90%) carried the blaADC gene that intrinsically encodes Cephalosporins resistance, while 96(77%) showed resistance genes against Aminoglycosides. Carbapenem-related resistance genes, including blaOXA-23 79(64%) and blaPER-7 7 (5%), were also identified. The gene blaPER-7 is an emerging gene with more hydrolytic activity against Cephalosporins and Aztreonam. Interestingly plasmids were absent in 123(99%) of the isolates. While all 124 isolates possessed virulence genes related to metal surfaces, with 112(90%) featuring the nickel resistance gene nreB. Biocide resistance was observed in 31(25%) of the isolates, and 2 showed resistance genes against heat.

Conclusion: Pathogens with high genetic plasticity readily acquire fitness genes to boost their survival yet, contrary to current research, all virulence and AMR genes in the isolates were chromosomally and not plasmid-encoded. This could explain the clonal and persistent nature of nosocomial outbreaks of A. baumannii. This study observed that all the isolates had a variety of chromosomally-encoded AMR and virulence genes that enhance their resilience when exposed to antiseptics, heat and antibiotics in nosocomial environments. The predominance of the nreB gene could explain the association of A. baumannii with device-associated infections as medical equipment is typically composed of nickel. Understanding the specific mechanisms underlying the coexistence of AMR and virulence genes in A. baumannii could guide the development of effective infection control strategies in hospital settings such as using copper surfaces.

Keywords: AMR surveillance of MDR A. baumannii in nosocomial settings

223.

GENOMIC CHARACTERIZATION OF LYTIC BACTERIOPHAGES ISOLATED IN KENYA IDENTIFIES CANDIDATE PHAGES FOR TREATMENT OF PSEUDOMONAS AERUGINOSA INFECTIONS

Authors: Collins K Kigen (KEMRI/USAMRD-A)*; Martin MG Omondi (walter reed); James Wachira (KEMRI/USAMRD-A); Vanessa Natasha (KEMRI/USAMRD-A); Erick Odoyo (KEMRI/USAMRD-A); Mikeljon Nikolich (Walter Reed Army Institute of Research); Lillian Musila (KEMRI/USAMRD-A)

Background: P. aeruginosa is a WHO priority pathogen due to rising antibiotic resistance and presence of various virulence factors which pose treatment challenges for nosocomial infections it causes. The global spread of multidrug-resistant, extensively drug-resistant, and pan-resistant infections has limited/exhausted treatment options with conventional antibiotics, urging the development of alternative treatments. Bacteriophages specifically infect and kill bacteria and possess therapeutic potential. Ideal therapeutic phages should have broad host ranges, lytic lifecycles, and lack toxin, AMR and virulence genes. Genomic characterization of phages is therefore essential to ensure clinical safety, in addition to enhancing a better understanding of phage biology, diversity, and host specificity.

Method: Thirty-five plaque-purified bacteriophages, isolated from wastewater samples in Kenya and exhibiting lytic activity against clinical P. aeruginosa isolates by spot test, were evaluated through whole-genome sequencing. The phages underwent amplification, filtration (0.22 µm) and DNAse treatment prior to phage DNA extraction, library preparation, and sequencing on a Nanopore platform. Raw reads were assembled using Flye and the genomes annotated using Pharokka to determine genome length, GC%, taxonomy, AMR and virulence genes, CRISPR sites, and tRNAs. Lysogeny markers was determined using PhageLeads.

Results: The 35 plaque-purified phage samples from isolation and enrichment, harbored 1 to 5 distinct complete genomes each, indicating the presence of both pure, single phages and morphologically indistinguishable composite phages. Genome lengths varied from small (25kb) to large jumbo phages (>277 kb). Eight distinct taxonomic groups were identified: Phikmvvirus, Pifdecavirus, Pakpunavirus, Kochitakasuvirus, Phikzvirus, Septimatrevirus, Bruynoghevirus, and an unclassified category. Single-genome phage (89 – 93 kb) in the Papkunavirus genus, demonstrate lysis and replication capabilities independent of other phages, while the jumbo phages, all from Phikvirus genus, had a partner Papkinavirus phage suggesting a dependence for functionality. GC composition correlated with genome lengths: jumbo phages (277 – 281 kb) having the lowest GC% of 36 – 37 %, the 89-93 kb phages with 49%, while the smaller size phages (25 – 64 kb) had higher GC% of 53 – 62%. Notably, the phages with lower GC% than their P. aeruginosa host GC% of ~ 65%, carried tRNAs, with the 89 – 93kb phages having 12 -17, and jumbo phages 6 – 7 acting as codon compensation for less frequently used host codons. All the phages lacked lysogeny markers, CRISPRs, AMR, virulence, and toxin genes, posing no adverse risks to humans.

Conclusion: Genomic characterization of phages from Kenya revealed 7 distinct and 1 novel taxa, and potentially symbiotic phages with diverse genomic features. Importantly, all the phages lacked undesirable genomic features, making them good candidates for phage therapy.

Keywords: Phage therapy, Genomics, AMR

224.

HOST RANGE DETERMINATION OF LYTIC PSEUDOMONAS AERUGINOSA PHAGES ISOLATED FROM KENYAN WASTEWATER IDENTIFIES SIX PHAGES WITH BROAD ACTIVITY ACROSS ENDEMIC STRAIN TYPES.

Autors: Martin MG Omondi (walter reed)*; Ivy J. Mutai (Institute of Primate Research/USAMRD-A); Erick Odoyo (Kenya Medical Research Institute/United States Army Medical Research Directorate-Africa, Nairobi, Kenya); Mikeljon Nikolich (Walter Reed Army Institute of Research, Silver Spring, Maryland, USA); Lillian Musila (Kenya Medical Research Institute/United States Army Medical Research Directorate-Africa, Nairobi, Kenya)

Background: Pseudomonas aeruginosa (PA) is a significant hospital-acquired infection (HAI) pathogen increasingly resistant to multiple antibiotic classes. Bacteriophages (phages), viruses that infect bacteria, have been proposed as a potential therapeutic option to treat multidrug-resistant (MDR) bacteria, including PA. A major challenge to phage therapy is the narrow spectrum of many individual phages, which have limited strain specificity. This study assessed the host range of PA phages obtained from Kenyan wastewater against multiple PA clinical isolates that are endemic in Kenya to determine if they have broad therapeutic value.

Methods: The phage hunting targeted six non-endemic PA strains (PAO1, MRSN 3705, MRSN 4841, MRSN 9718, and ATCC 10145) and produced 25 phages. To determine their lytic activity against endemic strains, a host range assay using the direct spot test was conducted on 51 clinical PA isolates belonging to 51 distinct multilocus sequence strain types representative of the strains causing infections in different Kenyan counties: Nairobi (15), Kisumu (19), Kericho (3), Kisii (9), and Kilifi (5). The lytic activity of phages with the broadest host range by spot test was quantified by the efficiency of plaquing (EOP) assay. Phages with EOP values of >1 compared to their screening host were considered good candidates.

Results: From the spot tests, Ø8 was the least effective as it could not lyse any of the endemic strains. The most susceptible bacterial strains were ST 850 (Nairobi), 3672 (Nairobi), 3671(Malindi), 267 (Kisii), and 3666 (Nairobi). Strain types 654,455, 285, 3675, 233, 2143, 2037, 17, 2483, 2483, 41, 2025, and 871 were not susceptible to any of the 25 phages.

The 15/25 phages with the broadest host range by spot test were selected for EOP. The phages were able to lyse 76.4 % of the endemic isolates efficiently. Six phages showed the broadest host range among the isolates tested: Ø19 (47.06%), Ø20 (43.14%), Ø21 (35.29%), Ø23 (45.10%), Ø24 (49.02%), Ø25 (39.22%).

Discussion: The study's findings suggest that six PA phages isolated from Kenyan wastewater samples exhibit the broadest host range, making them potentially effective against a significant proportion of clinical isolates. Identifying phages with high productivity against endemic strains is promising for developing a cocktail phage therapy that could be used as an alternative treatment for drug-resistant PA infections. As some endemic strains are not targets of the identified phages, additional phages with a more diverse host range will be identified for more tailored approaches to address the challenge of strain specificity/narrow spectrum in phage therapy.

Conclusion: This study contributes valuable information on the feasibility and limitations of using phages as a therapeutic option for combating multidrug-resistant P. aeruginosa infections in the context of the Kenyan healthcare system.

Keywords: Pseudomonas aeruginosa, bacteriophages, host range

225.

ANTIMICROBIAL RESISTANCE AMONG SHIGELLA ISOLATES FROM CHILDREN AGED 6-35MONTHS WITH MEDICALLY ATTENDED DIARRHEA (MAD) IN RURAL WESTERN, KENYA: FINDINGS FROM THE ENTERICS FOR GLOBAL HEALTH SHIGELLA SURVEILLANCE STUDY (EFGH) 2022-2023.

Authors: Alex O. Awuor1*, Bi Alex o Awuor (KENYA MEDICAL RSEARCH INSTITUTE)*; Richard O. Onyando (KEMRI-CGHR)

Background: Shigella is the second leading cause of diarrheal mortality in children under five years residing in Sub-Saharan Africa and Asian countries. Although antibiotics can shorten the duration of illness caused by Shigella, the emerging resistance of Shigella isolates to the WHO recommended drugs (ciprofloxacin, azithromycin and ceftriaxone) can pose a challenge to effective treatment. We assessed antimicrobial resistance patterns of Shigella Isolates among children aged 6-35 months with medically attended diarrhea (MAD) in rural western Kenya.

Methods: This study leveraged data from the Kenyan site of the Enterics for Global Health: Shigella surveillance study (EFGH). A MAD case was defined as a child aged 6-35 months with ≥3 loose stools in the previous 24 hours who sought care for a diarrhea episode at a designated sentinel health facility. Rectal swabs collected at enrollment were tested for Shigella using standard culture methods. Antimicrobial resistance of Shigella isolates to a panel of antimicrobial agents was determined by Kirby-Bauer disk diffusion method and interpreted according to Clinical and Laboratory Standards Institute guidelines. Multi-drug resistance (MDR) was defined as resistance to at least one agent in three or more antimicrobial categories. The results of the Shigella positive cases were relayed back to clinicians to inform modifications to treatment as per the Integrated Management of Childhood Illnesses guidelines.

Results: Between August 2022 to October 2023, there were 868 enrolled cases with MAD of which 47 (5.4%) had Shigella isolated. Shigella isolates were most resistant to nalidixic acid (6 [12.8%]), ciprofloxacin (3 [6.4%]), azithromycin (2 [4.3%]) and ceftriaxone (2 [4.3%]). No isolate was resistant to all the 3 WHO recommended treatments but 5/47 (10.6%) Shigella isolates were MDR. The most prescribed WHO recommended drugs to shigellosis cases were ciprofloxacin (32 [68.1%]), azithromycin (8 [17.0%]) and ceftriaxone (1 [2.1%]). While no Shigella cases prescribed azithromycin or ceftriaxone resistance to those drugs was detected., Of the 32 cases who were prescribed ciprofloxacin, 3 (9.4%) had resistant Shigella isolates. The distribution of Shigella serogroups among the 47 positive cases was as follows: S. flexneri was the most common (30 [63.8%]), followed by S. sonnei (12 [25.5%]), S. boydii (3 [6.4%]), S. dysenteriae (1 [2.1%]), and undetermined (1 [2.1%]). S. sonnei was the only serogroup in resistance to ceftriaxone (2/2 [100.0%]), while S. flexneri was the leading serogroup in resistance to ciprofloxacin (2/3 [66.7%]) and nalidixic acid (3/6 [50.0%]). The resistance to azithromycin was equally distributed between S. flexneri (1/2 [50.0%]) and S. sonnei (1/2 [50.0])

Conclusion: We observed an emerging resistance pattern to the current WHO recommended antibiotics for treatment of Shigellosis. Monitoring of Shigella AMR trends for effective clinical treatment is important in this setting.

Keywords: Antimicrobial resistance shigella isolates

SCIENTIFIC SESSION 25:

NTDS AND ONE HEALTH

226.

PREVALENCE AND ECONOMIC IMPACT OF CYSTIC ECHINOCOCCOSIS IN NAROK COUNTY, KENYA.

Authors: Tonny T Nyandwaro (KEMRI)*; Eberhard Zeyhle (Meru University of Science and Technology); Mathew Mutinda (KEMRI); Caroline Njoroge (Kenya medical Research Institute); Anne Mwangi (KEMRI); Joanne J Yego (Kenya Medical Research Institute); Peter Rotich (KEMRI); Doris Njomo (KEMRI); Vincent K Ruttoh (Kenya Medical Research Institute); Robinson M Irekwa (Kenya Medical Research Institute); Nicole Sian (KEMRI); Grace Ng'endo (KEMRI); Muuo Nzou (KEMRI)

Background: Cystic echinococcosis (CE) is a zoonotic parasitic disease transmitted by the canine tapeworms of Echinococcus spp. The economic burden of CE in humans is associated with the direct losses resulting from treatment, while in livestock losses include condemnation of infected organs. This current study attempted to quantify the financial losses associated with CE in humans and livestock in Narok County, Kenya.

Methods: This was a retrospective cross-sectional survey of 62 CE patients diagnosed for CE and treated at Narok County Referral Hospital, Tenwek Mission Hospital and Kijabe Mission Hospital between 2010 and 2022. Additionally, a total of 954 animals (293 cattle, 370 sheep and 291 goat) were studied using a prospective cross-sectional study design. In August 2022, post-mortem investigations were performed on carcasses of livestock slaughtered at Narok County's main abattoirs, Ewaso Nyiro, Mulot, and Narok. Internal organs were visually inspected, palpated, and incised to identify the presence of cysts. The direct losses due to livestock organ condemnation and human losses associated with treatment were estimated to quantify the economic losses of CE.

Results: CE is estimated to cause $7,808,077.99 per year in direct losses to livestock traders in Narok County, Kenya, with cattle liver condemnation accounting for the majority of the loss. CE prevalence was highest in sheep (40%), followed by cattle (32%) and goats (24%). The total direct human loss from CE in Narok County is estimated at $50,507 per year.

Conclusions: This study demonstrated that CE is a severe public health problem that causes significant economic losses in Narok County. To reduce the parasite's economic impact, there is need for appropriate locally accepted interventions by the respective government authorities and communities to avoid these losses and improve the livestock industry and the health of people.

Keywords: CYSTIC ECHINOCOCCOSIS, ECONOMIC LOSSES, HUMAN, LIVESTOCK, SURGERY

227.

PREVALENCE AND SPECTRUM OF FUNGAL PATHOGENS ISOLATED FROM INMATES WITH RESPIRATORY AND URINARY TRACT INFECTIONS

Authors: Larry Afundi Jackson (KEMRI / JKUAT)*; Sally N Loronyokie (KEMRI); Samson Chebon (JOMOKENYATA UNIVERSITY OF AGRICULTURE AND TECHNOLOGY(JKUAT)); Christine Bii (KEMRI)

Introduction: Fungal etiological agents play an important role in the morbidity and mortality of patients with respiratory diseases. Fungal infections and antifungal resistance highlight the need for local epidemiological data to guide empirical therapy in the clinical setup. Research findings on fungal and antifungal drug resistance are limiting in developing countries due to inadequate funding hence the burden estimation in low- and middle-income countries is not well defined. The study aims to determine the spectrum of fungal pathogens in inmates with respiratory and urinary tract infections.

Methodology: A cross-sectional study design was carried out in Nairobi County whereby sputum and urine samples were obtained from inmates presenting with symptoms of respiratory and urogenital infections at the prison's outpatient clinic. 162 samples were investigated at the mycology division at the Center for Microbiology Research-KEMRI between March 2023 and May 2023. Samples for fungal culture were inoculated on sabouraud dextrose agar plates (Oxoid, UK) supplemented with chloramphenicol at a concentration of 0.5 mg/mL to inhibit bacterial contamination and incubated at 35o Celsius for 7-14 days. Yeast isolates were differentiated on CHROMagar® Candida and corn meal agar and mold identification was done using colony macroscopic and microscopic morphological features. Histoplasmosis was detected with Clarus Histoplasma GM Enzyme Immunoassay Kit. Clinical and socio-demographic data was collected using a structured questionnaire

Results: Of the 162 participants from two prisons, (94: 68), 12(23%) respiratory samples from prison A and 7(21%) from prison B tested positive for molds, 27(51%) respiratory samples from prison A and 14(42%) from prison B tested positive for yeast infections. The mycological agents isolated from prison A included Aspergillus fumigatus which accounted for 3 prisoners (3.2%), Aspergillus flavus 4 (4.3%), Candida albicans 3 (3.2%), other Candida spp (25%) and from prison B included Aspergillus fumigatus which accounted for 2 prisoners(2.9%), Aspergillus flavus 3(4.4%), Candida albicans 5 (7.3%), other candida spp (13.2%), 19(46%), In the urine samples from

prison A, Histoplasma accounted for 3(3.2%), Candida albicans 3(3.2%), other Candida spp 13(13.8) and from prison B Histoplasma accounted for 2(2.9%), Candida albicans (7.4%), other candida spp 8(12%). There was a statistical difference between the respiratory tract and urogenital tract for microbes isolated from both genders at $p<0.05$. However, there was no statistical difference in fungal infections between Male and female groups $p> 0.05$.

Conclusion: Mycological agents are significant causes of respiratory and UTI infections among prison inmates that could be misdiagnosed as bacterial infections without proper detection. Considering the results, specific control measures are to be taken against fungal infections in prisons and in the general population.

Keywords: Prison inmates, Aspergillus spp, Histoplasma, Cryptococcus, Histoplasma GM Enzyme Immunoassay Kit, Respiratory and UTI

228.

PREVENTIVE CHEMOTHERAPY WITH IVERMECTIN, DIETHYLCARBAMAZINE AND ALBENDAZOLE TRIPLE-DRUG THERAPY FOR THE ELIMINATION OF LYMPHATIC FILARIASIS IN KENYA: PROGRAMMATIC IMPLEMENTATION AND RESULTS OF BASELINE SURVEY AND THE FIRST IMPACT SURVEILLANCE

Authors: Sammy Njenga (Kenya Medical Research Institute (KEMRI))*

Sammy M. Njenga, Henry Kanyi, Collins Okoyo, Edward Githinji, Cassian Mwatele, Patrick N. Gitahi, Hadley S. Matendechero, Wyckliff P. Omondi, Chrispin Owaga, Joyce Onsongo, Katherine Gass

Background: Lymphatic filariasis (LF) is a mosquito-borne neglected tropical disease (NTD) caused by infection with the filarial nematode species Wuchereria bancrofti, Brugia malayi or B. timori. In 2017, the World Health Organization (WHO) recommended triple-drug co-administration of ivermectin, diethylcarbamazine and albendazole (IDA) as an alternative mass drug administration (MDA) regimen for the acceleration of LF elimination. In 2018, Lamu County and Jomvu Sub-county in Kenya were selected for the acceleration of LF elimination using IDA. An operational research study was established to determine target populations, infection indicators, sampling strategies, and/or thresholds required to determine when it is safe to stop IDA.

Methods: Two rounds of MDA with IDA were conducted in November 2018 and November 2019. Cross-sectional population-based epidemiological and entomological surveys were conducted at baseline and endline in 30 and 5-10 randomly and purposively sampled villages, respectively. Blood specimens were tested for circulating filarial antigen (CFA) in the field using the Filariasis Test Strip (FTS). Statistical analyses were performed using STATA version 16.1 (STATA Corporation, College Station, TX, USA. MDA with IDA, study sites, and participants age and gender were the independent variables whereas the FTS test result was the dependent variable. Graphs were developed using the ggplot package implemented in R. Village locations were mapped using ArcGIS Desktop version 10.2.2 software (Environmental Systems Research Institute Inc., Redlands, CA, USA).

Results: Treatment coverage was above 80% during each year. Baseline CFA rates were generally low in both implementation units, but comparatively higher in Jomvu (1.4%) than in Lamu (0.5%). Relative reduction (%) in LF prevalence following the two rounds of MDA with IDA was significant in both Jomvu (52.45%, $P<0.02$) and Lamu (52.71%, $P<0.05$). Heterogeneity was observed in the LF prevalence reduction between random and purposive clusters as well as between adult and child populations.

Conclusion: The results of the study show that IDA accelerated elimination of LF as a public health problem in the two implementation units. When compared with the WHO recommended 30-cluster transmission assessment survey, the endline results showed that IDA could be safely stopped. Purposively sampled sites might be adequate for assessing LF endemicity in areas where MDA has been ongoing and acceleration with IDA is considered.

Keywords: Kenya, lymphatic filariasis, circulating filarial infection, triple therapy, ivermectin, diethylcarbamazine and albendazole

229.

CLIMATE ADAPTATION APPROACHES AND PROPOSED MODELING OF CLIMATIC VARIABLES TO PREDICT VL TRANSMISSION AND INFORMING OUTBREAK PREVENTION AND EARLY RESPONSE IN MARIGAT SUB-COUNTY, BARINGO COUNTY IN KENYA

Author: Bernard Ong'ondo

Background: Visceral Leishmaniasis (VL) transmissions are linked to the presence of sand-fly vectors and reservoir hosts. Communities affected are found in rural areas with limited awareness of disease transmission and prevention, poor socioeconomic conditions, limited access to healthcare, inadequate housing, and lack of capacity to diagnose in healthcare centers. VL transmission exhibits seasonal patterns which complicates prevention and response to outbreaks. Temperature rise affects the survival, reproduction, abundance, and distribution of Leishmania parasites, vectors (sandflies), and reservoir hosts. Studies have demonstrated that an increase in temperature leads to an increase in endemic sites and prolongs the seasonal transmission period of VL. Hence unstable unpredictable climate change can drive emergence, resurgence and redistribution, outbreak frequency, and severity of VL in Kenya. Reports Rabai village is characterized by poor infrastructure (mud/stick walled houses, grass thatched roofs) predisposing 60% of the residents to the bite of the infected sand fly. Infected sandflies have been reported to fly from the breeding sites into the houses where they enter through cracks, spaces of uncompleted roofs, or stick walls. The Perkerra site is characterized by irrigation canals that feed water to plots of the National Irrigation Board. This irrigation scheme was potentially implemented to influence income, production, employment, and provision of water to residents. However, the site is infested with sandflies. The 36 houses earmarked for upgrading were constructed using corrugated iron sheets and timber poles. Both the walls and roofs were built using corrugated iron sheets and the houses were two-room units with concrete floors and fitted lockable wooden windows and doors.

Methodology: sand flies were trapped using a CDC light trap in both upgraded and un-upgraded houses. The sand flies were aspirated, counted, and recorded for each type of house.

Results: Sand-fly density was reduced in the improved house structures. The number of sand flies trapped indoors before and after house improvement were significantly different ($p< 0.05$). Proposed modeling: develop a mathematical modeling tool for predicting and informing prevention and early response to VL outbreaks. The modeling tool will also be able to evaluate the potential impact of VL response interventions, tools, and strategies, and determine optimal ways of integrating/co-deploying existing and novel interventions for outbreak prevention and response. Data on the geographical distribution of VL cases, sand-fly habitats, sandflies' interactions with humans and reservoir hosts, and the impact of environmental factors like temperature and humidity on their abundance of sandflies can help identify high-risk areas, inform targeted interventions, inform vector control strategies and predict seasonal variations in transmission and help authorities prepare for outbreaks during favorable conditions.

Keywords: Sandflies, Visceral Leishmaniasis, climate change and adaptation, Modeling, house upgrading

230.

INVESTIGATION OF AN ACUTE FEBRILE ILLNESS OUTBREAK IN LAISAMIS SUB- COUNTY, MARSABIT COUNTY, MAY 2023

Authors: Victor Mr Ofula (KEMRI)*; Albert O Nyunja (KEMRI); Maureen Otinga (KEMRI); Konogoi Limbaso (KEMRI); Francis T Kimani (KEMRI); Damaris Matoke (KEMRI); Solomon K Langat (Kenya Medical Research Institute (KEMRI)); Edith C Koskei (KEMRI); Hellen S Koka (Kenya Medical Research Institute); Joel Lutomiah (KEMRI); Seth Okeyo (KEMRI); Edith Chepkorir (KEMRI); Samuel Owaka (KEMRI); Francis Mulwa (KEMRI); James K Mutisya (Kenya Medical Research Institute (KEMRI)); Richard M Kimenye (FELTP Kenya); James M Maragia (Turkana County Governmennt-MOH); Evelyne Kanyina (MOH); Emmanuel Okunga (MOH); samoell A Khamadi (KEMRI); Ahmed Abade (FELPT-K); Nelly Mugo (KEMRI); Elijah Songok (KEMRI); Stephen J.O. Olubulyera (Ministry of Health, Kenya-FELTP)

On 11th May 2023, the Ministry of Health Kenya, received reports from Marsabit county of a suspected outbreak of an acute febrile illness. Patients were presenting with fever of unknown origin, a few had tested positive for malaria by rapid diagnostic method (RDT), however there was a big portion of the sick population that was not responding to the malaria treatment. The number of those who were presenting with the febrile condition kept increasing and there was need to conduct an active investigation to ascertain the possible cause of the outbreak the geographic areas affected. An outbreak investigation team was team was formed and sent out to conduct the investigation. The febrile cases were being reported from Kargi location, Laisamis and Korr-Ngurunit wards all in Laisamis Sub County. The objective

of this investigation was to determine the cause and magnitude of the outbreak in these areas. Questionnaires were administered to all who presented with febrile symptoms and consented to the investigation. A total of 76 blood samples and eight (8) nasal and oral pharyngeal samples were collected from persons who presented with the febrile illness symptoms. The blood samples were all subjected to qPCR for Dengue, Chikungunya and Yellow Fever and malaria parasites. They were also tested for the same viruses using IgM ELISA. The OP/NP were subjected to qPCR for respiratory syncytial virus's panel, SARS-COV-2, Adenovirus, Influenza A & B, Rhinovirus. A total of 11/76 tested positive for P. falciparum, 1/11 being positive for both P. faliciparum and P. vivax. 18/76 tested positive for Chikungunya virus by IgM ELISA, five (5) tested positive for both P. falciparum and Chikungunya virus (IgM). All the eight samples were negative for respiratory viruses tested. The findings of this investigation indicate that the most likely cause of this outbreak was a co-infection of Chikungunya virus and malaria. It is the first time Chikungunya virus and P. vivax are being reported in this area. Kargi location was the most affected in this outbreak. More studies are needed to determine active circulation of these pathogens in this area and the neighboring regions.

Keywords: Marsabit County, Outbreak, Chikungunya, Malaria

231.

EVALUATION OF LYMPHATIC FILARIASIS SEROPREVALENCE FOLLOWING TRIPLE THERAPY MASS TREATMENT WITH IVERMECTIN, DIETHYLCARBAMAZINE AND ALBENDAZOLE IN COASTAL KENYA

Authors: Henry Kanyi1,2, David Odongo2, Walter Jaoko2, Richelle Kihoro1, Henry Emisiko1, Brook Goodhew3, Katherine Gass4 and Sammy M. Njenga1

Affiliations:

1Kenya Medical Research Institute (KEMRI), Nairobi, Kenya

2University of Nairobi, Kenya

3Centers for Disease Control and Prevention, Atlanta, USA

4NTD Support Center, Task Force for Global Health, Atlanta, USA

Background: World Health Organization recommended adoption of Ivermectin, Diethylcarbamazine and Albendazole (IDA) triple therapy for the mass drugs administration (MDA) of lymphatic filariasis (LF) with the aim of accelerating its elimination in the endemic areas in 2017. Consequently, the treatment was used for mass drugs administration (MDA) in Lamu and Jomvu LF endemic areas in Kenya in 2018 and 2019. Multiplex beads assay (MBA), a technique that is capable of analyzing antibody responses against up to 100 antigens in a single sample, is considered to be an important serological platform for evaluating the exposure, seroprevalence and transmission dynamics of different diseases in a geographical area. As a result, the assay was used to evaluate antibody responses against three LF antigens to establish the impact of the IDA treatment to LF infection in two endemic areas along the Kenyan coast.

Methods: Two rounds of MDA with IDA were delivered in Lamu County and Jomvu sub-county in Mombasa in 2018 and 2019. Baseline cross-sectional surveys were conducted in 2018 (before the MDA with IDA) while impact assessment survey in 2021 after the second MDA. A total of 18076 participants were recruited in the two surveys. Dried blood spot (DBS) specimens were prepared using finger prick whole blood samples. The DBS specimens were used to test for antifilarial antibodies against 3 Wuchereria bancrofti recombinant antigens, namely Wb123, Bm14 and Bm33 using a multiplex bead assay platform.

Results: The overall LF seroprevalence by the three antigens reduced from 0.3% (95%CI: 0.17-0.43) at baseline to 0.1% (95%CI: 0.05-0.17) at impact assessment. Similarly, there was reduction of seroprevalence by Bm33 and Wb123 individual antigens from 20.2% (95%CI: 19.3-21.2) and 3.6% (95%CI: 3.2-4.1) to 16.1% (95%CI: 15.4-16.7) and 2.5% (95%CI: 2.2-2.7) respectively. However, the seroprevalence by Bm14 remained the same at 0.7% (95%CI: 0.5-0.9) at baseline and 0.7% (95%CI: 0.5-0.08) at impact assessment level.

Conclusion: This study reports on the importance of antifilarial antibody testing against multiple antigens for monitoring MDA for LF using IDA. It also underscores the importance of using multiple antigens to generate robust data on a single platform. Additionally, the study exemplifies the utility and possibility of using MBA for serosurveillance of diseases undergoing elimination interventions in an area.

Keywords: lymphatic filariasis , Baseline, IDA, triple therapy, Multiplex beads assay, Wuchereria bancrofti, serosurveillance

232.

IMPACT OF DEWORMING ON THE PREVALENCE OF INTESTINAL PARASITIC INFECTIONS IN OLOISUKUT CONSERVANCY COMMUNITY, NAROK COUNTY, KENYA.

Author: Zipporah NJERI Gitau (University Of Nairobi)*; Erastus Mulinge (Kenya Medical Research Institute); Eberhard Zeyhle (Meru University of Science and Technology); Jackson Mpario (Oloisukut Conservancy, Narok, Kenya); Tabitha Irungu (Kenya Medical Research Institute); Joyce Nyambura (Kenya Medical Research Institute); Japheth Magambo (Meru University of Science and Technology, Meru, Kenya); Malika Kachani (College of Veterinary Medicine, Western University of Health Sciences); David Odongo (School of Biological Sciences, University of Nairobi)

Background: Globally, intestinal parasitic infections (IPIs) are a major public health concern among social-economically deprived communities in most developing countries. Mass drug administration (MDA) remains the World Health Organization recommended control strategy along with routine monitoring and surveillance and Water, Sanitation and Hygiene (WASH) approach. Many countries including Kenya have launched national control programs on soil transmitted helminths (STH) aimed at achieving deworming coverage rates of 75% of all school going children. Despite the elaborate measures deployed for control of STH, the prevalence of parasitic infections remains high.

Method: A cross-sectional community-based descriptive study was conducted between the months of August to December 2021 to evaluate the impact of deworming on prevalence of STHs among the community living in Oloisukut Conservancy, Narok County, Kenya. Human fecal samples were collected from 411 people at baseline and examined microscopically to detect IPIs using the Kato-Katz and formal-ether concentration methods. After 3 months, 245 mebendazole-treated people were re-examined.

Results: The overall prevalence of IPIs (protozoa and helminths) was 62.5% at baseline and 53.9% at end line. The prevalence of intestinal helminths was 39.9% at baseline survey. Following deworming, helminth infections reduced to 19.2%, with a relative reduction rate of 58.4%. The prevalence of Trichuris trichiura decreased from 36.7% at baseline to 15.9% at end line survey with a relative reduction rate of 56.7%. For Ascaris lumbricoides, the prevalence reduced from 5.6% to 4.9% with a relative reduction rate of 12.5%. All individuals infected with hookworm (2.7%), Hymenolepis nana (1.2%) and Strongyloides stercolaris (0.2%) did not have detectable ova/parasite in stool after deworming. Infection with Taenia spp. increased from 0.7% at base line to 2.9% at the end line survey. New infections were mostly observed in T. trichiura and A. lumbricoides [9/245 (3.7%)] followed by Taenia spp. 6/245 (2.5%). The intensity of infection based on egg per gram (EPG) of STH was light (86.8%) to moderate (11.9%) with only two cases (1.3%) of heavy intensity detected. At end line survey, STHs were light-moderate (76.5%-23.5%) in intensity.

Conclusion: There was a marked reduction of hookworm prevalence compared to the other intestinal parasites following deworming which is in agreement with previous studies in Kenya. While deworming resulted in decline of infections, high rate of re-infections (43%) remained a problem in this study. This finding implies that in the long run, deworming program alone maybe not sustainable since it is unable to protect treated individuals from re-infection. For maximum benefit, there is need to integrate MDA

Keywords: Intestinal parasites (IPIs), Soil transmitted helminths (STH), Parasites, Mass drug administration (MDA)

233.

CO-INFECTIONS OF LEISHMANIA DONOVANI AND LEISHMANIA MAJOR IN BLOOD OF PATIENTS WITH VISCERAL LEISHMANIASIS FROM GARISSA COUNTY, NORTHERN KENYA

Authors: Vane K Omwenga (Walter Reed Army Institute of Research - Africa)*; Cyrus Ayieko (Maseno University); Clement Masakhwe (Walter Reed Army Institute of Research - Africa); Gathii Kimita (WRAIR-Africa); John N Waitumbi (KEMRI/Walter Reed Project)

Introduction: Leishmaniasis is endemic in many countries, including Kenya. Globally, around 350 million people are at risk of contracting the disease. Despite an increased frequency of visceral leishmaniasis (VL) outbreaks in Northern Kenya (Garissa county) in recent years, there is little data on the genetic structure and epidemiology of Leishmania parasites in the region. This study investigated the inter-species diversity and evolutionary relationships of Leishmania parasites collected from Northern Kenya (Garissa county) during the 2019 - 2022 visceral leishmaniasis outbreak.

Methods: 286 archived blood samples collected from patients suspected of having VL at Garissa Referral County Hospital between 2019 and 2022 were analyzed. Leishmania parasites were screened at genus and species level by quantitative real-time PCR (qRT-PCR). To characterize the parasites genotypes, amplicons of Hsp70 (~2000nt) and ITS (1,400nt) genes generated through conventional PCR were fragmented into suitable library sizes, sequenced and analyzed using phylogenetic tools. To deconvolute unexpected observation of

mixed infections of L. donovani and L. major, we designed a deep sequencing assay targeting un-fragmented 350nt region of ITS1 gene. Sequencing was performed on the Illumina MiSeq platform. Sequences were analyzed using the ngs mapper pipeline and Dada2 in R.

Results: By qRT-PCR, 128/286 (45%) blood specimens tested positive for Leishmania at the genus level. Upon speciation, 48/128 (17%) had mono-infections of L. donovani, 2/128 (1%) had mono-infections of L. major while 78/128 (27%) were co-infected with L. donovani and L. major. On sequencing using the fragmented amplicons, we obtained 86/128 Hsp70 and 79/128 ITS gene sequences which on phylogenetic analysis clustered with L. donovani complex. On sequencing the full 350nt ITS fragments, mixed infection of L. donovani and L. major were detected.

Conclusion: This study reveals the complex nature of Leishmania epidemiology in Kenya. It also sheds light on the possible inter-species interaction that may have significant implications on diagnosis and pharmaco-therapy.

Keywords: Leishmaniasis, Visceral leishmaniasis, Northern Kenya, Hsp70, ITS, ITS1, Inter-species diversity, Co-infection, Phylogenetic

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234.

COMMUNITY PERCEPTION ON FACTORS ASSOCIATED WITH SCHISTOSOMA MANSONI PREVALENCE AND INTENSITY IN THE ENDEMIC PARTS OF SIAYA COUNTY

Authors: Austine O Okinyo (KEMRI)*; Isaac Okeyo (Technical University of Kenya); Erick Muok (KEMRI); Eric Ndombi (Kenyatta University); Francis Oguya (Technical University of Kenya); Michael Mbata (KEMRI); PETER R OLILAH (KEMRI)

Background: Schistosomiasis also known as bilharzia or ‘snail fever’ is one of the most prevalent parasitic diseases in the world. This disease is transmitted through contact with water containing the infective forms of the parasite called cercariae which develop in the snail and penetrate the unbroken skin. About 800 million people globally are at risk of schistosomiasis of which 250 million are infected and 97% of these are in Africa. In Africa, about 50 million preschool children live with schistosomiasis. The highest intensity of the infection is usually observed in children but chronic consequences of infection may last into adulthood.

Methodology: The study was conducted in hot-spot and non-hot-spot areas of Siaya County. A cross-sectional study design adopting both quantitative and qualitative techniques was employed. The target population consisted of both Primary School-aged children and adults in ten (10) selected villages from hot spot and non-hot spot villages of in Siaya County. A purposive sampling technique was used to select the ten (10) villages after which 200 participants were randomly selected from the clustered villages. Kato Katz technique was then used for the diagnosis of S. mansoni. Quantitative data was obtained using a structured self-administered questionnaire. Key Informant Interviews were conducted to obtain qualitative information from the selected teachers and community health workers.

Results: Data tables presenting categorical data as percentages with observed proportions were analyzed by prop test, while continuous data was presented using model means with 95% Confidence Intervals (95% CI). Of the 200 participants, 81 (40.5%) tested positive for Schistosomiasis. Prevalence was found to be high in hotspots 59% compared to non-hotspot villages 22%. Intensity levels were found to be higher in females compared to males 0.95 (95% CI = 0.48, 1.4, P = 0.03) and in adults compared to children 1.1 (95% CI = 0.64, 1.6, P <0.01) The proportion of infected participants was found to be significantly higher in males compared to females 48% vs 33% (P = 0.04) and in participants aged > 18 years compared to those aged < 18, 50 vs 31 (P = 0.001) The odds of having schistosomiasis was lower among, children with knowledge on schistosomiasis compared to those without 0.34 (95% CI = 0.14, 0.83 P = 0.02), those with knowledge on the causes 0.32 (95% CI = 0.13, 0.76 P = 0.01) and among those with knowledge on factors associated with schistosomiasis 0.35 (95% CI = 0.15, 0.84 P = 0.02)

Conclusion: Lack of knowledge and community perception of the disease were associated with higher exposure to schistosomiasis. Despite mass drug administration with praziquantel for the control of schistosomiasis in the endemic parts of Siaya County, the disease remains prevalent, necessitating the adoption of additional control and prevention measures, including public education and water, hygiene, and sanitation-based control strategies.

Keywords: Schistosomiasis, Bilharzia, Prevalence, Intensity, endemic, hot spot, non-hot spot, community perception, praziquantel

235.

DELAY IN LEPROSY DIAGNOSIS IN KILIFI AND KWALE COUNTIES IN KENYA

Author: Bakhita Barbara (KEMRI)*

Introduction: Leprosy, a chronic infectious disease caused by the bacterium Mycobacterium leprae, continues to be a significant public health concern in several regions of the world. Early diagnosis and prompt initiation of treatment are crucial to prevent disabilities and reduce transmission. However, delay in diagnosing leprosy remains a major challenge, contributing to the persistence of the disease burden. This study aimed to determine the factors contributing to delayed leprosy diagnosis in Kwale and Kilifi counties in Kenya.

Methods: This was a cross-sectional study carried out between July 2019 and March 2020. Leprosy patients diagnosed between January 2014 to December 2019 were identified retrospectively from health facility leprosy treatment registers. Data abstracted from these registers included demographics, type of leprosy clinical diagnosis, health seeking behavior, time to diagnosis and the time treatment was initiated. A questionnaire was also administered to the leprosy index cases. Results:

A total of 81 index patients out of the 118 traced were enrolled in the study. There were more females at 49 (60%) than males. Among the patients, 72(88.9%) had multibacillary type of leprosy at time of diagnosis. The median age at the time of diagnosis was 53 years (IQR 38-68). The delay in diagnosis was measured in months and represented the time elapsed between the onset of leprosy symptoms and the actual diagnosis. The median delay of diagnosis in months was 24 (IQR 10-100). While the majority of patients (79%) were initiated on treatment promptly after diagnosis (0-2 weeks), there were significant delays in diagnosing leprosy for a substantial number of individuals (21%), with some experiencing delays of more than a decade. The results also suggest that a significant portion of individuals with leprosy 44 (54%) initially sought care from informal sources and 26 (31%) sought care from sources other than hospitals and health centers.

Conclusion: Findings from this study showed that delay in leprosy diagnosis still persists in Kenya and should therefore be a priority of the leprosy program. Addressing this requires a multi-faceted approach, involving coordinated efforts from governments, healthcare organizations, and communities. Interventions should focus on determinants of delayed case detection such as misdiagnosis, health-service-seeking behavior, and should consider relevant individual, socioeconomic, and community factors, including stigmatization.

Keywords: Leprosy, Delayed diagnosis, Disability

236.

ONE HEALTH IN PRACTICE: ANTHRAX OUTBREAK INVESTIGATION IN MURANG'A COUNTY, KENYA, MAY 2023.

MARK N MATHEKA (FELTP)*; FREDRICK ODHIAMBO (FELTP); JANE AKALE (FELTP); PIUS N MUTUKU (FELTP-K); MATHEW MUTURI (ZOONOTIC DISEASE UNIT); ATHMAN MWATONDO (ZOONOTIC DISEASE UNIT)

Authors: Mark Matheka1,2*, Fredrick Odhiambo1, Jane Akale1,2, Pius Mutuku1, Athman Mwatondo2, Mathew Muturi2.

1Field Epidemiology and Laboratory Training Program, 2Zoonotic Disease Unit – Ministry of Health and Ministry of Agriculture and Livestock.

*Correspondence email: macndosh@gmail.com

Background: Anthrax is a priority zoonotic disease in Kenya. Humans get infected through consumption or contact with infected animal tissues. Globally, world health organisation (WHO) estimates 20,000–100,000 cases of human anthrax annually. In Kenya, at least 10 human and animal outbreaks are reported every year. In May 2023, we investigated an anthrax outbreak in Murang'a County to establish its magnitude, possible exposure and implement interventions.

Methods: We conducted retrospective record review in health facilities that reported suspect cases, contact tracing and active case search at the community level. A case was defined by acute illness with a painless skin lesion developing over 1 to 7 days, fever and/or malaise and lymphadenopathy in a person of any age residing in Murang'a County. A structured questionnaire was used to collect information. Data were extracted into an MS Excel for analysis.

Results: Out of 26 contacts, 13 were cases. Males were most affected at 62.5% (9) with a Median age of 39 years. Case Fatality Rate was 23.1% (3). Cases were reported in four sub Counties: Kigumo, Kandra, Mathioya and Gatanga. Overall attack rate was 2.2/100,000: Kigumo sub County at 4.9/100,000. All cases were epidemiologically linked to dead cattle. Slaughtering/ skinning exposed 69% (9) of the cases to Anthrax. Four (4) slaughter points identified: 75% (3) involving slaughter of dead animals. Most cases presented with the cutaneous form at 85% (11), with a majority affected on the upper limbs at 73% (8). Fever was in 62% (8) while headache, abdominal pains and convulsions were in 31% (4) of the cases.

Conclusion: Anthrax was linked to carcasses from dead animals. Poor handling of animal carcasses was a major area of concern for its transmission. Better handling of suspect animal carcasses and implementation of prevention and control measures in animals will help prevent recurrence.

Keywords: Zoonotic diseases, Anthrax, endemic, transmission, prevention and control.

237.

COMPARING INFECTION SUSCEPTIBILITY BETWEEN EXPOSED LABORATORY INBRED LINES AND THIRD GENERATION FROM THE FIELD ON BIOMPHALARIA SUDANICA AND BIOMPHALARIA CHOANOMPHALA IN WESTERN KENYA: PRELIMINARY RESULTS.

Authors: George Ogara (KEMRI)*

George Ogara1, Fredrick Rawago1, Maurice R. Odiere1 , Kennedy Andiego1, Boaz Mulonga1, Meredith Odhiambo1, Isaac Onkanga1, Tom Pennance2 , Michelle L. Steinauer2

1 Centre for Global Health Research, Kenya Medical Research Institute (KEMRI), Kisumu, Kenya

2 College of Osteopathic Medicine of the Pacific – Northwest, Western University of Health Sciences, Lebanon, OR, United States

Background: Schistosomiasis control measures have focused largely on the definitive host with very little attention on the snail, which is the natural intermediate host. A gene responsible for resistance to schistosomiasis infection has previously been documented in one of the snail species in South America and this has led to increased interest to further explore approaches for vector control through use of laboratory models combined with field testing. We compared susceptibility (measured in terms of attrition and infectivity rates) to S. mansoni infection between exposed laboratory inbred and third generation wild Biomphalaria snails in western Kenya.

Methods: B. sudanica (Bc) and B. choanomphala (Bc) snails were collected from Lake Victoria in western Kenya through scooping and dredging. Third generation of both inbred and freely living wild snails were challenged with miracidia. First screening was done at week six to confirm on susceptibility or resistant.

Results: Following S. mansoni infection, the infectivity rates in Bc wild (third generation) and Bc inbred colonies were 50.4% and 71.7%, respectively. The attrition rates in Bc wild and Bc inbred snails were 50.0% and 64.7%, respectively. Although both the infectivity and attrition rates were higher in Bc inbred colonies compared to Bc wild snails, the differences were not significant. In the Bc snails, the infectivity rates were 36.9% and 37.8% in the wild and inbred snails, respectively, whereas the attrition rates following S. mansoni infection were 69.7% and 53.2% for the wild and inbred colonies, respectively. The differences in both the infectivity and attrition rates in Bc wild and Bc inbred snails were not significant.

Conclusion: Both the infectivity and attrition rates were comparable between wild and inbred colonies in both Bc and Bc snails. The preliminary data coupled with the low samples size preclude any solid conclusions on susceptibility as the results may change as more data is generated.

Keywords: BIOMPHALARIA SPP

SCIENTIFIC SESSION 26: VICTOR BIOLOGY 3

238.

SEASONAL DYNAMICS OF AEDES AEGYPTI AND ASSESSMENT OF DENGUE VIRUS INFECTION PREVALENCE

Authors: David P. Tchouassi (International Centre of Insect Physiology and Ecology)*; Josephine Osalla (International Centre of Insect Physiology and Ecology); Caroline Getugi (International Centre of Insect Physiology and Ecology)

Background: Arboviral diseases are increasingly important contributors to global human mortality and morbidity. This exemplified by unprecedented emergence and re-emergence of epidemic arboviral diseases in the recent past such as dengue, chikungunya, Rift Valley fever and yellow fever. In many African countries, the impact of arboviral diseases is undetermined due to paucity of active surveillance, poor disease reporting systems, and lack of appropriate diagnosis. Surveillance targeting vectors is essential to provide an early warning of the presence of viruses to reduce the potential for human disease.

Methods: Both eggs and adult populations of Aedes aegypti were monitored through a longitudinal study in an urban focus of coastal Kenya (Ukunda, Kwale County), endemic for dengue. The adult mosquitoes (including those reared from eggs) were tested in pools by RT-PCR and virus culture for infection with dengue and other viruses (flavi- and alphaviruses). Blood fed specimens were also screened for viruses in addition to determining the vertebrate host meal sources by PCR.

Results: We found monthly variation in the abundance of Ae. aegypti. Dengue 2 and insect specific viruses were detected in the samples. Analysis of blood meals found high rates of human feeding (>70%) followed by feeding on rodents and other livestock hosts.

Conclusions: Detection of the virus is indicative active circulation between epidemics. The study sheds light on influence of seasons on important vector bionomic attributes - abundance, oviposition rates, blood host utilisation and infection rates, important for risk mapping of dengue disease spread.

Keywords: dengue-2 virus, arbovirus risk assessment, Aedes aegypti, climate change, blood feeding patterns

239.

HARNESSING MOSQUITO SYMBIONTS FOR MALARIA TRANSMISSION BLOCKING

Author: Jeremy K Herren (icipe)*

Introduction: The recently discovered Anopheles symbiont, Microsporidia MB, is maternally inherited and has a strong malaria transmission-blocking phenotype in Anopheles arabiensis the predominant Anopheles gambiae species complex member in many active transmission areas in eastern Africa. The ability of Microsporidia MB to block Plasmodium transmission together with vertical transmission and avirulence makes it a candidate for developing a strategy for transmission blocking by vector population replacement.

Methods: We used fluorescence confocal microscopy and qPCR to investigate the characteristics and efficiencies of Microsporidia MB transmission between Anopheles arabiensis mosquitoes. The patterns of Microsporidia MB localization over the development of Anopheles arabiensis were investigated by confocal microscopy and qPCR.

Results: We show using qPCR that Microsporidia has high rates of vertical transmission (75%). Microscopy demonstrated that >95% of mosquito eggs are infected by Microsporidia MB. Both qPCR and Microscopy demonstrate that Microsporidia MB can be transmitted paternally and sexually and that there is Microsporidia MB accumulation in tissues linked to transmission routes, specifically the germ line.

Conclusions: The confirmation of high rates of vertical and sexual transmission indicate that Microsporidia MB uses different methods to spread through host mosquito populations. The implementation of Microsporidia MB for malaria control will benefit from finding ways to exploit and enhance these natural transmission routes.

Keywords: malaria anopheles microsporidia mb

240.

ENTOMOLOGICAL SURVEILLANCE OF MALARIA VECTORS IN TURKANA COUNTY, AN ARID AND SEMI-ARID REGION IN KENYA

Authors: Lucy Wachira1, Lenson Kariuki2, Stanely Kitur1, Jacinta Muli4, Kiambo Njagi2, Luna Kamau1, Charles Mbogo3,4, Damaris Matoke-Muhia1,4

1Center for Biotechnology Research and Development, KEMRI, Nairobi

2 Division of National Malaria Program, Ministry of Health, Nairobi

3 Centre for Geographical Medicine Research-Coast, KEMRI, Kilifi

4 Pan Africa mosquito Control Association

*corresponding author lwachira@kemri.go.ke

Introduction: Turkana County is arid and semi-arid region in Kenya which is sparsely populated with predominantly semi-nomadic population, hardly reached with convectional malaria control. Recently, there have been reports of malaria outbreaks in Kenya with emerging new foci including Turkana County. There is the need to survey malaria vectors and its associated risk factors to inform control strategies. In this study, we sought to determine prevalence, parasite infection rates and blood feeding preference on malaria vectors in Turkana County.

Methodology: Mosquito collections were done in 2017 and 2020 in 6 villages in Turkana County. Adult mosquitoes were sampled using CDC light traps while scoopers were used for larvae collection. Taxonomical keys by Gillies and De Meillon, (1968) and Gillies M.T. and Coetzee M. (1987) were used for mosquito morphological identification. Anopheles gambiae and An. funestus complex mosquitoes were further analyzed for sub-species identification following DNA extraction by Collins et al., (1987) and PCR by Scott et al., (1993) and Koekemoer et al., (2002) protocols. Sporozoite and blood meal analysis was done using ELISA technique described by Wirtz et al., (1987).

Results: A total of 484 were collected. For 2017, 86.5% were An. arabiensis 13.5% did not amplify. In 2020, 54.2% were identified as An. arabiensis 6.2% An. gambiae s.s while 39.6% did not amplify. 42.9% fed on human and 1.5% were positive of Plasmodium falciparum.

Conclusion: Anopheles arabiensis is the dominant vector in Turkana County. 40% of anophelines were not identified as An. gambiae or An. funestus complexes, the dominant malaria vectors in Kenya indicating possibility of new species in the county requiring further investigation. The mosquitoes were infected with Plasmodium falciparum and feeding on human indicating local transmission, therefore, malaria control strategies need to be implemented in the County.

Keywords: vector surveillance, taxony, sporozoite Elisa

241.

DIVERSITY OF ANOPHELES MOSQUITOES IN VERY LOW MALARIA TRANSMISSION EPIDEMIOLOGICAL ZONES IN KENYA

Authors: Jacinta M Muli (PAMCA)*; Lucy Njeri Wachira (KEMRI); Lenson Kariuki Kinyua (Ministry of Health -NMCP); Stanley Kitur (KEMRI); Edith Ramaita (MOH); Kiambo Njagi (MOH); Luna Kamau (KEMRI); Charles Mbogo (KEMRI); Matoke Damaris (KEMRI)

Introduction: Anopheline mosquitoes play either a primary or secondary role in malaria transmission and this necessitates understanding of the species. Malaria transmission in Kenya is categorized into different epidemiological zones requiring continuous surveillance for better control strategies. This study aimed to assess the species composition, sporozoite infection and blood meal status of malaria mosquitoes in low transmission Counties in Kenya.

Methodology: Adult mosquitoes were sampled from indoor and outdoor settings using CDC light traps while larvae were collected from water pools using scoopers. Taxonomical keys were used for mosquito morphological identification. An. gambiae and An. funestus complex mosquitoes were further analyzed for sub-species identification following DNA extraction and PCR procedures. Sporozoite and blood meal analysis was done using ELISA technique.

Results: A total of 7526 mosquitoes were collected. Of the total 64.78% were An. arabiensis, 1.81%. An. funestus and 1.13% An. gambiae. For sporozoite infection rates 0.06% were positive for Plasmodium falciparum, infection was distributed across species. Blood

meal analysis revealed diverse feeding with 3.31% feeding on human, 3.76% on goat, 1.18% on bovine, 0.32% on dog, and 0.88% on cat. For mixed blood meals, 3.03% had fed on both goat and bovine, 0.12% on human and bovine and 0.11% on human and dog.

Conclusion: Anopheles arabiensis is the dominant vector in low malaria transmission Counties. 30.6% of anophelines were not identified as An. gambiae or An. funestus complexes, requiring further investigation through genome sequencing. The mosquitoes were infected with P. falciparum and feeding on human and domestic animals indicating local transmission, therefore, malaria control strategies need to be implemented in very low transmission Counties.

Keywords: Mosquito, Species, Low transmission zones

242.

SPECIES COMPOSITION AND INSECTICIDE RESISTANCE PROFILES OF MAIN MALARIA VECTORS IN KWALE COUNTY, KENYA

Authors: Miguel Gerson1,4 Caroline Kiuru2 Jonathan Karisa3 Rehema Gona1 Tobias Odongo1 Bruno Otieno1 Festus Yaa1 Faiz shee4 Caroline Wanjiku3 Carlos Chaccour2 Marta Maia3

1Kenya Medical Research Institute Center for Vector Disease Control

2 Barcelona Institute for Global Health

3 Kenya Medical Research Institute Wellcome-Trust

4 Pwani University

Background: Malaria has been on the decline, however, since 2015, the progress has stagnated. This is partly due to the development of resistance by the main malaria vectors towards the mostly commonly classes of insecticides. The aim of the study was to understand the malaria vectors profile and their insecticide resistance status in Kwale county. This study is part of the BOHEMIA clinical trial that evaluates the Impact of ivermectin MDA on malaria transmission in Kwale county, Kenya.

Methods: Adult mosquitoes were collected using CDC Light trap, Prokopack aspirator whereas larval sampling was performed using dippers in Lunga Lunga and Msambweni sub counties where the trial is taking place. Adult Anopheles mosquitoes were morphotyped into species and grouped according to according physiological status. Larvae were reared to adult and exposed to four classes of insecticides: deltamethrin, permethrin, DDT, Bendiocarb and Pirimiphos methyl using the WHO tube assay. To check for the occurrence of metabolic resistance a synergistic assay using PBO was used. GLMM (negative binomial regression models) was used to identify factors influencing the density/number of anopheles vectors.

Results: So far, a total of 8302 mosquitoes have been collected. These were composed of An. funestus (70%), An. gambiae (17%) and other anopheles (13%). Several predictors significantly influenced the count of An. funestus and An. gambiae. The presence of ITNs in households significantly reduced An. funestus count by 65% (IRR = 0.35, 95% CI 0.13-0.97, P<0.044). Moreover, Palm leaves roof type (IRR = 4.46, 95% CI 2.30-8.64, P<0.001) and mud walls (IRR = 6.74, 95% CI 2.81-16.17, P<0.001) significantly increased An. funestus count. In Anopheles gambiae complex, there was no statistically significant difference in fixed effects.

Anopheles gambiae complex showed resistance to Deltamethrin and Permethrin but was susceptible to DDT, Pirimiphos methyl and Bendiocarb. How the resistance was reversed when synergistic assay with PBO was performed, confirms the possibility of metabolic form of resistance.

Conclusion: The study showed that An. gambiae and An. funestus were collected in higher numbers and they are the potential malaria vectors in Kwale. House characteristics such as presences of nets, palm leaves roofs and mud walled houses significantly influenced An. funestus count. Furthermore, phenotypic resistance Anopheles gambiae complex might lead to dominance of the species in Kwale.

Key Word Insecticide Resistance, ITNs, Malaria vector

Keywords: Insecticide Resistance, Insecticide Treated Nets, Malaria Vector

243.

PREVALENCE, AND SEASONALITY OF MICROSPORIDIA MB IN ANOPHELES MOSQUITOES IN KWALE, COASTAL KENYA

Authors: Kelly Ominde (KEMRI-Wellcome Trust Research Programme)*; Mark T Kivumbi (KEMRI-Wellcome Trust Research Programme); Haron Musani (KEMRI-Wellcome Trust Research Programme); Festus Yaah (KEMRI-Kwale); Jonathan Kazungu Karisa (KEMRI-Wellcome Trust Research Programme); Martin Rono (KEMRI - Wellcome Trust Research Programme); Isabella Oyier (KEMRI-Wellcome Trust Research Programme); Simon Muriu (PAMCA); Joseph Mwangangi (KEMRI); Jeremy K Herren (icipe); Caroline Kiuru (Barcelona Institute of Global Health (IS Global)); Caroline Wanjiku (KEMRI-Wellcome Trust Research Programme); Marta F Maia (KEMRI)

Background: Microsporidia MB (MMB) is an endosymbiont shown to naturally block Plasmodium transmission in Anopheles arabiensis and therefore a potential novel malaria control tool. However, its prevalence, and seasonality in wild anophelines is poorly understood. To address this gap, this study evaluated the prevalence and seasonality of MMB infections in wild anopheline populations from coastal Kenya.

Methods: A cross sectional survey of anophelines was done during wet (long and short rains) and dry season in two villages in Msambweni (Fihoni) and LungaLunga (Jego) sub counties of Kwale, Kenya. Adults were sampled using CDC light traps (LT) and deployed indoors/outdoors (livestock enclosures) across 20 households in two villages. Adults collected were morphotyped, dissected to separate gonads (testes/ovaries), midguts and cephalothoraxes. DNA was extracted from tissues to screen for MMB by PCR targeting MMB 18sRNA gene. Cephalothoraxes were divided into two halves for species identification by MALDI-TOF MS and sporozoite detection. Data collected was used to calculate MMB prevalence rate.

Results: Sample processing and data collection is ongoing. So far, a total of 675 whole mosquitoes (1350 individual tissues) from the dry (n = 104/675), short rainy (n= 86/675) and long rainy season (n=485/675) have been screened for MMB. None of the of the dry and short rainy season mosquitoes were positive for MMB. Only 4.77% of the long rainy season mosquitoes tested positive, with an overall prevalence of 8.64% for An. gambiae s.l (n=30/347) and An. funestus s.l 1.88% (n=9/480). From dry season, a total of 104 whole mosquitoes (208 tissues) have been screened and none tested positive for MMB. Similarly, from short rainy season, none of 86 whole mosquitoes (172 tissues) screened, tested positive.

Conclusion: MMB infections appears most prevalent during long rainy season. However, prevalence rate in this study is slightly lower than that previously reported in anophelines from Western Kenya (Herren J et al, 2020), implying that presence of MMB could serve as a potential novel malaria control strategy.

Keywords: Microsporidia MB, Prevalence, Seasonality, Kwale

SCIENTIFIC SESSION 27: HEALTH SYSTEMS 5

244.

SUPPLY-SIDE FACTORS INFLUENCING INFORMAL PAYMENTS FOR HEALTHCARE AT PUBLIC HEALTH FACILITIES IN KENYA

Authors: Evelyn Kagure Kabia (KEMRI Wellcome Trust Research Programme)*; Dina Balabanova (London School of Hygiene and Tropical Medicine); Eleanor Hutchinson (London School of Hygiene and Tropical Medicine); Edwine Barasa (KEMRI Wellcome Trust)

Background: Informal payments are payments made by a patient to a health provider in addition to the officially determined service fees. They are considered a form of petty corruption. 17% of Kenyans had paid a bribe to access health services at public facilities. Informal payments limit progress toward universal health coverage because they limit access to care and expose individuals to financial hardship. Various demand-side (individual/household/community), supply-side (related to the production of health services), and contextual factors are associated with informal payments.

Objective: This study examined supply-side factors influencing informal payments at public health facilities in Kenya.

Methods: We conducted a qualitative study in 2022/23 at 8 public health facilities (4 hospitals and 4 health centres) in two counties (urban and rural). Study participants were identified through purposive sampling. We conducted 8 focus group discussions with male (n=4) and female patients (n=4) who were seeking different health services at the study facilities, and in-depth interviews (n=35) with health workers and non-clinical staff of various cadres and sub-county and county health managers. Data were analyzed using a thematic approach based on the main (and emerging) themes such as health service, health worker and health facility factors.

Results: Health service factors: Charging of informal payments cut across most services and were more common for services that were charged user fees compared to free services, outpatient services (especially consultation, laboratory and radiology), specialist services, non-routine/seasonal services such as voluntary medical male circumcision, filling of school medical forms, especially at primary health facilities and pregnancy termination. Health worker factors included, low, delayed, and lack of salaries for some cadres such as community health promoters, delayed and unfair promotions, understaffing, poor working conditions such as long working hours, and individual health worker morals. There was collaboration mainly across cadres to charge informally. Health facility factors comprised of high patient workloads, long waiting lists, especially for specialized services, lack of drugs/supplies/services, and inadequate supervision. Informal charging was more common at public, urban, and higher-level facilities.

Conclusions and recommendations: Supply-side factors associated with informal payments were largely linked to health system inadequacies and inefficiencies in health financing and governance functions. Policy considerations include increasing public spending on health to ensure the availability of drugs, medical supplies, and equipment, ensuring adequate numbers of health workers and fair remuneration, strengthening oversight over health workers, enhancing public awareness of grievance redress mechanisms, and ensuring that they are effective.

Keywords: Informal payments, corruption, supply-side, health, Kenya

245.

PROFILING OF HUMAN BIOLOGICAL SAMPLES EXPORTED BY KEMRI RESEARCHERS BETWEEN 2018 AND 2020

Authors: Timothy Kipkosgei Kiplagat (KEMRI)*; Gideon Msee (KEMRI); Serah Gitome (KEMRI); Enock Kebenei (KEMRI); Daisy Cheruiyot (KEMRI); Maryanne Metto (KEMRI); Judy Waithera (KEMRI); James Nguya (KEMRI); Geoffrey Sang (KEMRI); Victoria Soi (KEMRI); Cyprian Kisienya (KEMRI); Lilian Achacha (KEMRI); Daisy Mudegu (KEMRI)

Background: Sub-Saharan African countries have recorded increased exportation of human biological samples to foreign high-income countries for analysis and storage. Among the justifications for such export include a need for further analysis of biological samples due to a lack of capacity for analyzing the samples locally. In this study, we profiled the reasons for export, the types of samples exported, and types of tests to be done, and the destinations of the samples exported.

Methods: A data collection tool was developed in MS Excel and abstraction was done from 439 archived SERU records of requests for biological sample export for the period January 2018 to May 2020. We excluded records that did not contain human biological samples and those that were never approved. The period from January 2018 to May 2020 was selected because it had complete records of the profiles of the human biological samples (types of samples, types of tests, reasons for export, destination of export, and duration of storage). R statistical was used to perform data analysis. Frequency distributions, and measures of central tendency (mean, median, and mode) were used to describe profiles of the samples shipped and the type of analysis to be performed outside Kenya.

Results: A total of 816 requests for the export of various samples were abstracted from the 439 records. A majority, 613 (75%) were for blood-related samples. Of these, the majority were plasma samples 194 (23.7%), followed by serum samples 136 (16.6%), whole blood samples, 102 (12. %), and 48% (387) included other human tissues and DNA extracts. The most common reason provided for export was further analysis (n=272) with varied assays: Pharmacokinetic/Pharmacodynamics (n=72), Quality assurance and Control (QA/QC) n=58, Immunologic Testing n=48, Endpoints Analysis (n=44), genotyping (n=42, drug level analysis (n=40), molecular analysis (n=38), PCR (n=36), antibody testing (n=30) among others. Most of the requests were for samples being exported to the USA, 327 (53%) followed by South Africa 104 (17%), Switzerland 45(7%) United Kingdom 43(7%) while the remaining n=97 (23 %) we shipped to other countries in Africa, Asia, Australia and Europe.

Conclusion: This study shows that most of the requests for export are to the USA for Pharmacokinetic/Pharmacodynamics, Quality assurance and Control (QA/QC), Immunologic Testing, and Endpoints Analysis. There is a need to build local infrastructural and human resource capacity to run some of the assays in Kenya to minimize the frequent requests for the export of samples where possible.

Keywords: Samples, Export, Analysis,

246.

RECOMMENDATION FOR EARLY PREPARATION TOWARD THE AGEING SOCIETY – SUGGESTION FROM HEALTH AND DEMOGRAPHIC SURVEILLANCE SYSTEM (HDSS) DATA FROM KWALE COUNTY

Authors: Hideki YAMAMOTO (Teikyo University School of Pharmacy)*; Ken Masuda (Nagasaki Univeristy); RYUJI YOSHINO (NUITM-KEMRI); Ssatoko Horii (Nagasaki University); Haruko Noguchi (Waseda University); Shinji Miyamoto (Okayama University of Science); Kazuchiyo MIYAMICHI (Nagasaki University); Nanae TAKEDA (Embassy of Japan in Tanzania); Satoshi Kaneko (Nagasaki University); Violet Wanjihia (KEMRI)

Introduction: Population ageing is the emerging challenge in African countries. Due to economic development and public health improvement, life expectancy at birth in Kenya has been improved by 12.2 years from 53.9 years in 2000 to 66.1 years in 2019. Joint research on Ageing society was organized between Kenya and Japan was organized. Kuwale county was chosen as the study site where HDSS has been managed by KEMRI and Nagasaki University.

Methods: A quantitative survey was conducted in Kwale county from October to December 2022 by using the Open Data Kit (ODK) to focus on socioeconomic status, social network, self-rated health, disability, mental health, and medical history. About 4,300 people aged over 40 years old and over were selected from the Health and Demographic Surveillance (2021) dataset conducted by Nagasaki University and KEMRI, and 50% (approximately 5000 people) were sampled per Community Health Unit (CU) to be eligible.12 local research assistants (RAs) conducted household visit with Community Health Volunteers (CHVs).

The research protocol was approved by IRB in the School of Tropical Medicine and global Health in Nagasaki University (NU_TMGH_2021_154_1) and Kenya Medical Research Institute (No. 4234).

Results: The average ageing rate (60 years or above) for the entire study area exceeded 6%, suggesting that out- migration pushed population ageing and the demographic structure is already entering the ageing stage. The results also revealed large differences in population composition among Community Health Units (CUs), with some CUs having an aging population rate of over 8%. Economic conditions are generally poor among older persons, with some elderly households living in extreme poverty. However, only 42% of older people aged 70 and over receive older persons cash transfer (inua jamii). As for the helath problems, ophthalmologic problems and hip and joint pains are dominate. Among those aged 60 years and over, 34.0% (30.2% of men and 37.2% of women) had a disability or limitation in their lives for more than six months. The highest rates of disability were in walking, memory and seeing, in that order.

Conclusion: Based on the results of this survey, public policy making is recommended as well as public health issues, such as cash transfer receipt, living arrangements, and family-care support, empowerment of community-based organizations.

Acknowledgement: This study was funded by Japan Society for the Promotion of Science (JSPS) 18H03604(2018-2022), 19K217219(2019-2023) and JSPS 25300048 (2013-2017).

Keywords: Ageing, Kuwale,HDSS, NCD, UHC, Japan,

247.

CONTINUOUS QUALITY IMPROVEMENT, TRIPLE R APPROACH TO SCALE UP CASE IDENTIFICATION THROUGH SOCIAL NETWORK STRATEGY AT AROMBE DISPENSARY, MIGORI COUNTY.

Authors: Loriet M Otieno (CIHEB-K)*; Isaiah Angwanga (CIHEB-K); Beatrice Yugi (CIHEB -K); Joyce Otieno (CIHEB-K); Omune Everlyn Adhiambo (Ministry of health)

Background: Arombe Dispensary, a health facility in Migori County, has been implementing strategies to achieve the 1st 95 in the 95-95-95 cascade with the aim of preventing new HIV infections and reduction of HIV prevalence among all populations. However, the uptake of social network strategy (SNS) for the general population has been suboptimal leading to low identification of new HIV infections amongst social networks. SNS screening uptake as of 2020 was at 3.1% with a 1% positivity and a 78% screening with a 3.9% positivity in 2021 respectively. This prompted the facility to identify screening as a challenge in SNS case identification. The aim of this CQI project was to improve SNS screening to more than 95%, and improve yield from SNS to more than 3% by the end of 12 months.

Method: At the beginning of 2022 a CQI Triple R (Rescreening, Rebooking, Recording/reviewing) approach to improve SNS was initiated, after conducting a root cause analysis following a Plan-Do-Study-Act (PDSA) approach. The strategy focused on line listing clients who had not elicited any social conducts and Rescreening them, rebooking missed opportunities for testing within the month and continuously updating the testing status and reviewing performance on a weekly basis. The project progress was tracked using a CQI dashboard. A retrospective review to compare data collected at the facility SNS register and HIV testing and linkage Lab register MOH 362 in 2021 before intervention and 2022 after intervention was conducted.

Results: After the 12 months of intervention, SNS screening improved from 78% (57/73) before CQI to 100% (74/74; $\chi 2=24.4$ $p<0.001$) after implementing triple R CQI intervention. The yield from SNS improved from 1% before intervention to 12% (9/74; $\chi 2=9.95$ $p<0.05$) after CQI. Following rescreening (5/9) 55.6% of the positives from SNS strategy were identified. Out of 184 contacts tested negative 21 were initiated on PrEP.

Conclusion: SNS strategy for general population can yield in identifying people living with HIV who have not been reached. CQI interventions enhanced the screening process achieving uptake and timely service for early interventions for identified clients.

Recommendations: PDSA cycle is an effective model for upscaling indicators with suboptimal performance especially on quality of care to aid in access to HIV care and other services. Health facilities can implement the triple R approach (rescreening, rebooking, recording/ reviewing) to improve screening outcomes especially for index clients not eliciting contacts.

Keywords: SNS- Social Network Strategy PDSA- plan Do Study Act

248.

QUALITY IMPROVEMENT APPROACH TO SCALE UP FAMILY PLANNING UPTAKE AMONGST WOMEN AND ADOLESCENTS OF REPRODUCTIVE AGE THE CASE OF SUNA RAGANA DISPENSARY

Authors: JAIRUS M ONYONI (MOH)*

Background: Suna ragana dispensary is a health facility in Migori County which perennially has high teenage pregnancy of approximately 19.7%. The facility has catchment population of 10,500 whose economic main activity include small scale farming and business .In January 2022 The facility identified this challenge during a data review meeting , formed a work improvement team and Using a fish bone the following root causes were identified: ignorance on family planning amongst adolescents , early marriages, Myths and misconceptions about family planning, illiteracy and poverty

Objective: To increase family planning uptake by 50% amongst adolescents in suna ragana by 50% by December 2022.

Methodology: This is a retrospective study comparing data collected from the facility FP registers from 2019 to 2021 before implementing quality improvement(QI) and 2022 during its implementation.

After identifying the root causes through the fish borne, change ideas were generated using a tree diagram then scored using a decision matrix and the following Strategies were employed :

i. Monthly community dialogues to sensitize to communities on teenage pregnancies and family planning.

ii.Health education targeting schools and market places to sensitize community on effects of unwanted pregnancies.

iii.Engagement of youth peer providers (YPP) to help reduce stigma on various family planning methods.

iv.Partner support for in reaches (12) and weakly outreaches (36) to offer FP services to adolescents and young women.

v.Forming adolescent support groups with age segregation so as to offer age appropriate reproductive health messages.

vi.Teen mum sessions once a month to help prevent recurrences of unwanted pregnancies by having knowledge of family planning .

vii.Use of roving health care providers to offer FP after mobilization by Youth peer providers (YPP) in the community.

viii. Monthly data review to ensure adequate documentation, reporting and to monitor progress.

Results: In 2019 the facility was able to start a total of 562 including 208 adolescents, in 2020 it reduced slightly to a total of 521 starting FP including 200 adolescents. In the year 2021 (baseline) the facility experienced a slight increase of 611 but a decline to 78 in the adolescents starting FP. The teenage pregnancy in that year (2021) increase markedly from 16.4% to 19.7% from the subsequent year (2020).

In 2022 while integrating QI and implementing the above measures the facility was able to Increase the general FP uptake to 1504(246 %) and adolescents on FP to 687 (881%).

Conclusion: Quality improvement played a vital role in the scale up of FP uptake amongst adolescents(881%).

Partners support was essential to supplement government efforts to scale up family planning amongst adolescents.

Recommendations: The government should adopt quality improvement in adolescent and young women reproductive health programmes to improve indicators especially family planning.

Keywords: nil

249.

STRENGTHENING THE DIAGNOSTIC CAPACITY AND QUALITY TESTING OF RURAL LABORATORIES IN LINE WITH UNIVERSAL HEALTH COVERAGE: LESSONS FROM HOMA BAY COUNTY INTER-LABORATORY COMPARISON PROGRAM.

Authors: GABRIEL O KOTEWAS (MoH - Homa Bay County)*; Francis Ngati (MOH - Homa Bay); Nelson Ondenge (MoH - Homa Bay County)

Background: Participation in an external quality assessment (EQA) program or Inter-laboratory comparison (ILC) as required by ISO 15189 standards provides a useful external supplement to the various internal quality controls procedures, which must be employed in the laboratory to maintain a high degree of reliability in the production of results. In this study, we developed ILC in 2020 as a customized approach to assess the testing phase of Laboratories.

Method Biannual surveys comprising of 3-5 Tuberculosis smear slides, Malaria blood slides, Serum sample for syphilis and Hepatitis, whole blood for CD4 and complete Blood Count (CBC) were prepared by the liaison committee using standard procedures and validated by an accredited laboratory then distributed to enrolled participants, tested and result submitted by email to the committee. Results were analyzed and feedback reports sent back with advice for corrective action on unsatisfactory performance.

Results: Six surveys have been conducted with participant enrollment increasing from 10 at pilot to 60 at survey six. Malaria parasite species identification performance increased from 30%(3/10) at survey one to 79%(37/47) in survey six. Parasite quantification remained poor at 21%(10/47). Errors of High false negative in TB microscopy were the highest at 14%(33/235). Serology has sustained a performance of 100% across the surveys; however, participation in CD4 and CBC has not been optimal due to inconsistent reagent supplies. Mentorship was utilized to support unsatisfactory performance to initiate corrective actions across sites with quarterly performance review incorporating all the stakeholders.

Conclusion: ILC has proved to be an important tool in process improvement and its utilization by accredited laboratories during assessments have demonstrated a cost effective means of achieving quality while also reaching out to expanded participation. Effective implementation of this program can be used to assess staff competency, performance of equipment and reagents as part of post-market surveillance.

Keywords: Strengthening, Diagnostic, Capacity, ILC

250.

BEYOND ENEMY LINES: A STRATEGY TO PROVIDING HIV PREVENTION CARE AND TREATMENT SERVICES IN MIGINGO ISLAND, MIGORI COUNTY

Authors: Eugene Ariya

Background: Migingo Island is a unique community in the East African region, being a disputed island between Kenya and Uganda, it is home to nationals from Kenya, Uganda, and Tanzania. Despite having a population of about 500 individuals, the island faces several challenges in the provision of healthcare services, including HIV prevention care and treatment services. However, Muhuru sub-county hospital has been providing integrated outreach services to support the residents every month.

Methodology: Data was collected through interviews with healthcare workers and community members, medical records review, and observations of healthcare service delivery.

Results: The study found that the main activity on the island is fishing, and the island has a mobile population of approximately 500 people, with a HIV prevalence of 39 people, 8%. The study also found that Muhuru sub-county hospital has been providing integrated outreach services to support the residents every month, and the Kenyan facility does not discriminate any client as services are provided irrespective of nationality.

Conclusion: The study recommends increased HIV testing services, especially to the mobile population that visits the island frequently. There is also a need for continued support and funding from the government and non-governmental organizations to ensure sustainability of the healthcare services provided. Additionally, efforts should be made to provide adequate training and resources to healthcare workers, including peer educators, to ensure the provision of quality healthcare services. Finally, the government should work towards resolving the territorial dispute over the island to facilitate effective healthcare service delivery.

Keywords: HIV

POSTER SESSION 1: SCREEN 1-PUBLIC HEALTH

1.

CLIMATE CHANGE AWARENESS AND ITS EFFECTS ON HUMAN HEALTH AMONG RESIDENTS IN MAVOKO SUB COUNTY IN ATHI-RIVER.

Authors: SHARON KHANGUHA (KEMRI)*; Salome Biwott (KEMRI KWALE)

Background: Climate change is the single biggest human health threat, humanity is facing. The impacts are already harming health through air pollution, disease, extreme weather events, forced displacement, food insecurity and pressures on mental health. It constitutes key challenges to development. This is an area that is in dire need of publicity to help the public make informed decisions in its adaptations and mitigation.

Objective: To assess major factors of climate change awareness creation and health threats in Mavoko sub county, in Athi-river ward.

Methodology: Data collection was done among residents at Mavoko sub-county through a semi structured questionnaire with seven question in 2022. This is a descriptive cross sectional study. A sample size of 213 respondents was determined using simple random sampling method (120female,93male,103 young ,110 elderly).

Results: Up to 60%, (36% are young,24%were elderly) of the population had knowledge on environment and its effects to population and health however there exist gaps in their knowledge, mental health, denial. 40% were female and 20%were male. Approximately 80% of the population, 54% female and 26%male had currently or in the past suffered from respiratory illnesses and lung conditions. About 50% of the participants did not consider climate change as a health threat or crisis**.**

Conclusion: Majority of the population had knowledge on climate change, however they were not able to relate climate change and health threats. Air pollution in the area plays a role in causing respiratory diseases.

Recommendation: These findings necessitates need for sensitization and capacity building to improve the population's quality of knowledge on the subject, for informed action. Knowledge is a vital contribution to the subject. Government should formulate strategies to help reduce vulnerability to the impacts of climate change by building adaptive capacity and enhancing climate change resilience. The stakeholders should build partnerships and collaborations to educate the societies on matters of climate change and health and practical ways to take action at a local level for a better future.

Keywords: Climate change, health, awareness, air pollution, environment,factors,knowledge, threats.

2.

AFP SURVEILLANCE SYSTEM EVALUATION, KENYA, 2020-2021

Authors:

Serah Nduta Itotia (FELTP-NVIP)*

Background: Polioviruses are human enteroviruses with three serotypes. They invade the nervous system, causing total paralysis. Poliovirus is targeted for eradication through a sensitive surveillance system for Acute Flaccid paralysis(AFP) and environmental surveillance. Kenya suffered an outbreak of circulating vaccine-derived poliovirus type 2 in 2018. Globally, poliovirus has been targeted for eradication since 1988. The study aims to evaluate the AFP surveillance system.

Methods: We conducted a retrospective review and analysis of 2020-2021 records for AFP, where an adequate surveillance system was described as sensitive and timely. Detection of Non-Polio AFP rate of ≥2 was considered sensitive, with notification of cases within seven days of onset and specimen sent for analysis within 72 hours of collection. All targets set at ≥ 80% are considered timely. Completeness was assessed by sending two adequate stool samples. Variables collected include Demographic characteristics, Stool adequacy, and Non-Polio AFP rates.

Results: 1129 AFP records were reviewed. Cases presented with fever at 538 (84.19%), sudden flaccid paralysis at 99% (953/962). The final classification discarded most cases at 96% (854/893). Sensitivity was lower in 2020, with 74 % (35/47) of the counties reporting less than 2/100000 cases and 15 % in 2021, respectively. Samples were sent after 72 hours from 25% of counties in 2020 and 19 in 2021, while a second stool sample collection reduction was reduced to 40% in 2021 from 25% in 2020.

Conclusion: The Study revealed that Kenya has a quality AFP surveillance system capable of detecting suspected AFP cases; however, some attributes like sensitivity, timeliness, and completeness of the surveillance system were impacted in 2020 by the COVID pandemic, as depicted by more counties with lower performance. We recommend active case finding, strengthening timely reporting notification and investigation of the cases, and training more clinicians on the importance of surveillance.

Keywords: Polioviruses, Acute Flaccid paralysis (AFP), Surveillance, retrospective review, Kenya

3.

EVALUATION OF MENINGOCOCCAL MENINGITIS SURVEILLANCE SYSTEM IN WEST POKOT COUNTY KENYA, 2017-2021.

Authors: Pius N Mutuku1*. Owiny M.1, Nganga F2, Okunga E.2, Tarus W.3

1.Field Epidemiology and Laboratory Training Kenya (FELTP-K) 2. Division of Disease Surveillance and Response (MOH), 3. County Government of West Pokot.

Corresponding author: *Nthwao@gmail.com

Background: Meningitis is the inflammation of the tissues covering the brain and spinal cord. Bacterial meningitis is the commonest severe form of meningitis. Meningococcal Meningitis can cause death and disability in less than 24 hours. Epidemic meningococcal meningitis remains a public health threat in the ‘meningitis belt’ of Africa. Mortality rates range from 8-15% with treatment to 50% if untreated. From 2017- 2021, the enhanced surveillance system in West Pokot County reported 82 suspected cases. We evaluated the system over a five-year period to investigate if it was achieving its objectives of systematic collection and analysis of data for early detection and prevention of meningitis outbreaks.

Methods: A retrospective review of records in West Pokot County was done and Key informants interviewed. Data abstracted from KHIS and registers in Kapenguria County Referral Hospital from January 2017 and December 2021 was analyzed. Data collected was analyzed using Microsoft Excel, continuous variables using frequencies and proportions. Descriptive analysis was done to determine mean ages, periodicity of disease occurrence and gender distribution. Responses of KIIs were used to evaluate system attributes.

Results: The attacks rate for the 5-year period was 36.81/100,000. The annual incidence of meningitis ranged from 0.45/100,000 in 2017 to a peak of 29.88/100,000 in 2019. Female gender was most affected 58.54%. The most affected age group was 1-10 years (38%). The median age was 5 years with a range of 1- 73 years.

Ten system users were interviewed. The system was useful, simple, stable and flexible. Acceptability was moderate, data quality was good.

Conclusions: The meningitis surveillance system in West Pokot County is useful. It meets its main objective of early detection of outbreaks and generating data useful for planning. However, inadequate laboratory support system and lack of case-based data elements limit the usefulness of the system.

Keywords: Meningitis, Epidemics, Surveillance, Evaluation, West Pokot, Kenya

4.

MYCOLOGICAL AND AFLATOXIN ANALYSIS OF Camellia sinensis FROM SELECTED COUNTIES IN KENYA

Authors:

Sally N Loronyokie (KEMRI)*; Anthony Nyamache Kebira (Kenyatta University); Vincent Kiprop (Kemri); Abdi Mohamed (KEMRI); Evage.ine Gatumwa Mathiu (KEMRI); Hannah Kariuki (KEMRI); Christine Bii (KEMRI)

Introduction: Mycotoxin contamination affects approximately 25% of global food, exposing half a billion people to these harmful substances. Aflatoxin, classified as a Group 1 carcinogen by the International Agency for Research on Cancer (IARC), is known to cause adverse health effects, including immunosuppression and cancer. The unprecedented outbreak of acute aflatoxicosis in Kenya in 2004 highlighted the serious consequences of human aflatoxin poisoning. Camellia sinensis tea, the world's second most popular beverage after water and known for its health-promoting properties, is susceptible to fungal and mycotoxin contamination due to poor storage practices. Despite its significance, there is limited research on fungal and mycotoxin contamination in C. sinensis black tea in Kenya.

Objective: The aim of this study is to investigate fungal infestation and aflatoxin contamination in Camellia sinensis black tea retailed in selected counties in Kenya.

Methodology: Forty brands of C. sinensis tea were sampled from 20 retail shops in Bomet and Kericho counties. Fungal infestation was determined through fungal culture and identification based on phenotypic features. Aflatoxin quantification was conducted using ELISA (Envirologix quicktox kit) following the manufacturer's instructions.

Results: The study revealed that C. sinensis harbors toxigenic fungi, including Aspergillus flavus, Aspergillus fumigatus, Aspergillus niger, Rhizopus, Penicillium spp., and other toxigenic Aspergillus spp. Notably, 14.29% of the samples exhibited aflatoxin levels above 30 ppb, and 85.71% exceeded 20 ppb. These levels significantly surpass the established standard of 10 ppb for aflatoxin residues in black tea.

Conclusion: The findings emphasize the presence of toxigenic fungi in C. sinensis, with a concerning percentage of samples exceeding recommended aflatoxin levels. This poses a substantial health risk due to the carcinogenic nature of aflatoxins, underscoring the urgent need for stringent quality control measures in tea production. The study advocates for further research on mycotoxin contamination in non-cereal foods to ensure human and animal safety.

Keywords: Aflatoxin food safety

5.

INFLUENZA-LIKE-ILLNESS AND SEVERE ACUTE RESPIRATORY ILLNESS CASES IN KENYA: BURDEN ESTIMATES AND ASSOCIATED FACTORS 2019 – APRIL 2023

Authors: Mercy Cheptoo (Ministry of Health)*; Maria Nunga (Kenya Field Epidemiology and Laboratory Training Program, Ministry of Health); Rosalia Kalani (Division of Disease Surveillance and Emergency Response, Ministry of Health); Lucy Njoki Munyeki (County Government of Nyandarua); Emmanuel Okunga (Division of Disease Surveillance and Emergency Response, Ministry of Health)

Background: Influenza is a highly infectious respiratory illness of significant public health concern due to its potential for widespread outbreaks. In Kenya, influenza cases occur year-round, with intermittent upsurges. Current information on influenza characteristics and associated factors is limited. We aimed to describe the characteristics of influenza-like illness (ILI) and severe acute respiratory illness (SARI) and assess influenza-related risk factors.

Methods: We conducted a retrospective review of electronic data from the influenza sentinel surveillance system, covering the period from 2019 to April 2023. Descriptive statistics were performed using Epi Info to characterize ILI and SARI cases, and the incident rate ratios (IRRs) were calculated to estimate influenza burden. A chi-square test was performed to evaluate the risk factors for influenza and prevalence odds ratios (POR), with p-values <0.05 considered statistically significant.

Results: We analyzed records of 14,826 influenza suspect cases from January 2019 to April 2023, comprising 13,102 (88.4%) SARI cases and 1,724 (11.6%) ILI cases. Among the enrolled influenza suspect cases, the male cases were 8,269 (55.8%), and the overall median age was 1.11 years (IQR = 0.58, 2.53). The overall influenza positivity rate was 11.8% (1,536/12,969), with influenza-associated deaths of 2.3% (30/1,317). High incidence rates were observed in Nakuru and Kakamega County referral hospitals with IRRs of 103.36 and 34.20, respectively (Ref, Incident Rate/100,000 population = 453). Risk factors for influenza positivity included coming into close contact with an ARI case 14 days before symptoms, POR = 2.06 (95% Cl, 1.7–2.5), and pregnancy, POR = 2.8 (95% Cl, 1.1–7.3).

Conclusion: The burden of ILI and SARI cases disproportionately affects children, with influenza burden estimates indicating Nakuru and Kakamega county referral hospitals have higher incidence rates. We recommend prioritizing vaccination for children and pregnant individuals, promoting public awareness of safe practices around ARI cases, and strengthening healthcare worker capacity.

Keywords: Influenza, burden estimates, SARI, ILI

6.

FACTORS ASSOCIATED WITH NONTYPHOIDAL SALMONELLA INFECTION IN CHILDREN BELOW 5 YEARS IN AN URBAN INFORMAL SETTLEMENT IN NAIROBI, KENYA

Authors: Georgina A Odityo (Kenya Medical Research Institute)*

Background: Non-Typhoidal Salmonella (NTS) is a significant global health challenge, particularly in low- and middle-income countries in Asia and sub-Saharan Africa. In Kenya, Salmonella enterica serovars Enteritidis and Typhimurium accounts for a substantial burden of bacteremia cases in children ≤ 5 years. Populations in urban informal settlements are particularly vulnerable to NTS due to limited access to clean water, poor sanitation and hygiene. We aimed to investigate the factors associated with NTS infection in children under 5 years of age living in Mukuru informal settlements in Nairobi, Kenya.

Methods: This was a cross-sectional study conducted in Mukuru informal settlement in Nairobi, Kenya. Children presenting with fever (≥ 38° C) for more than 24 hours, with or without diarrhea and had not taken antibiotics, at four outpatient health facilities were recruited. A thorough medical history and physical examination of the participants was documented on a structured data form. A structured electronic questionnaire was administered to the guardians which captured data on their social-economic-environmental, co-morbidities, clinical characteristics and demographic factors. Rectal swabs and blood samples collected from the children, were subjected to enrichment, culture and biochemical tests. Additionally, NTS identification was done through serotyping. Data was then subjected to descriptive statistics, chi-square tests, odds ratio calculations, and multivariable binary logistic regression to identify associations and risk factors for NTS infection.

Results: A total of 3071 participants were recruited. The isolation rate of Salmonella Enteritidis and Salmonella Typhimurium was 1.4% (43/3071); Salmonella Enteritidis 0.8 %(25/3071) and Salmonella Typhimurium 0.6 %(18/3071). There was no significant association between the occurrence of Salmonella Enteritidis and Typhimurium with gender, age, and contact with animals. The use of drums for storage of drinking water potentially predicted infection with NTS (2.0%; aOR=1.95, p=0.040). Having malignancy as a comorbidity was predictive of contracting NTS in children (33.3%; aOR=39.10, p=0.003).

Conclusion: This study highlights the importance of improving WASH infrastructure to reduce risk factors associated with transmission of NTS in the community. In the long term, there is need for introduction of vaccine in the prevention and control of NTS.

Keywords: Nontyphoidal Salmonella; Children; Informal settlement; Risk factors; Bacteremia; Hygiene practices

7.

DEVELOPMENT OF A SPECIFIC IMMUNE LATERAL FLOW ASSAY FOR CHOLERA DETECTION

Authors: Freek van't Hoen (TNO)*

Background: Cholera is an acute diarrheal disease caused by Vibrio cholerae, that can be lethal within hours if left untreated. People are usually infected with V. cholerae by using contaminated water or food. UNICEF indicate that every year there are as many as 4 million cholera cases globally and as many as 143,000 deaths. Young children, especially those under the age of 5, are at risk. Rapid detection and identification is essential for the most effective response to an infectious disease outbreak. Therefore, our goal is to develop a more specific Point-of-Care test.

Methods: The following steps were taken for development of a specific Point-of-Care diagnostic test:

1. Determine a specific biomarker of the epidemic V. cholerae strain.

2. Analyze with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) different V. cholerae isolates.

3. Determine if a specific biomarker can be discovered.

4. Develop and test mono-clonal antibodies (mABs) against this specific biomarker.

5.Currently, a prototype immuno-lateral flow assay is being developed.

6. Evaluation and validation of the lateral flow assay.

Results: 1. Cholera is caused by a pandemic strain of Vibrio cholerae. The strain can have a O1 or a O139 serotype and produces the cholera toxin (Figure 1). Other V. cholerae isolates aren't O1 or O139 or are O1 but don't produce the cholera toxin. The complexity is to detect a biomarker that discriminates the pandemic strain from other V. cholerae isolates.

2. Using MALDI-TOF MS a biomarker was found, which is specific for the pandemic V. cholerae strain. Moreover, by using Ferulic Acid as a MALDI matrix a specific protein for the V. cholerae pandemic strain was discovered (Figure 2 and 3).

3. After a band at 35kDa was cut out of a SDS-PAGE gel and analyzed with LC-MS.MS the protein was identified as OmpU. A abundantly expressed outer membrane protein of V. cholerae (Figure 4).

4. Monoclonal antibodies (mABs) were developed and tested. A dotblot confirmed that the mABSs specifically bind to the pandemic V, cholerae strain.

5. The development of the immuno-lateral flow assay is ongoing.

After the prototype is developed its performance will be evaluated in a laboratory against different bacteria. Next, if successful, the immuno-lateral flow assay's will be validated in the field, in an area where cholera is endemic.

Conclusion: Using MALDI-TOF MS a specific biomarker for the pandemic V. cholerae strain was detected. The abundantly expressed outer membrane protein OmpU is a promising candidate to develop a imunno-later-flow assay. Therefore, specific monoclonal antibodies were developed against OpmU. The specific mABs are now used to develop a LFA-prototype. Next, the LFA will be evaluated in the lab and if successful field tests will be conducted in areas where cholera is endemic.

Keywords: Cholera, Vibrio cholerae, Lateral Flow Assay, LFA, infectious diseases, diagnostics, detection, test, Point Of Car

8.

EVALUATION OF ACUTE FLACCID PARALYSIS SURVEILLANCE SYSTEM IN EIGHT PRIORITY COUNTIES IN KENYA, 2020 TO 2022

Authors: lydiakhalayi M Khalayi (MOH)*; Maria Nunga (K-FELTP)

Background: Acute Flaccid Paralysis (AFP) affects children under 15 years old due to various causes, including poliovirus. The country implemented a surveillance system to identify cases and assess their connection to the wild poliovirus. We evaluated the system in eight priority counties from 2020 to 2022, analyzing data and assessing its effectiveness in meeting objectives.

Methodology: We conducted a retrospective descriptive review of data from WHO database, followed by a qualitative study. The population under review was AFP cases meeting the case definition: child aged below 15 years or any person with paralytic illness if polio is suspected. We analyzed continuous demographic and clinical variables using means and medians. System attributes such as sensitivity, timeliness and data quality, as per CDC's MMWR document, were evaluated through proportions and frequencies. We interviewed County Disease Surveillance Officers in the qualitative study, employing thematic analysis to assess the system's stability and representativeness.

Results: We abstracted 375 cases; the median age was 3.25 (IQR 5) years, with age group ≤ 5 years being the most affected (62.2%). Males accounted for the majority of cases, 56.8%. The mean of Polio vaccine doses was 3.8(±1.9). Surveillance was conducted throughout the year, with the peak in January of each year. Sensitivity was lowest in 2020, notification within 24 hours at 100%, sample arrival to the laboratory in ≤ 3 days and feedback ≤ 14 days at 66.1% and 58.6%, respectively. Clinical data indicators were below the 80% completeness threshold. The system is representative of age groups, gender and rural and urban areas. However, it is unstable as per the qualitative interview responses.

Conclusion: This evaluation highlights the system's sensitivity but lacks timely feedback to the counties. It also exhibits low stability and consistency in reporting. We recommend allocating additional resources to the system for undisrupted surveillance.

Keywords: Child, Male, Poliovirus, Vaccines

9.

SURPASSING THE TARGETS OF ORAL CHOLERA VACCINATION CAMPAIGN "A BOON FOR FUTURE OUTBREAKS"- IN KENYA,

Authors: Oscar Gaunya1 E. Salat1, C. Musumba1, M. Matheka1, P. Mutuku1, V. Kabati1, J. Akale1, J. Ondiege1, Abade,1 F. Odhiambo1, M. Owiny1, M. Nanyingi,5A. M. Livinus5, A. Haji, 5I. Obara3, J. Magige3, C. Kiama4, H. Limo3 S. Kadivane2, E. Okunga2, D. Langat2, P. Amoth2.

Affiliation: 1Kenya Field Epidemiology and Laboratory Training Programme (KFELTP), 2Division Of Disease Surveillance and Response (DDSR), 3Public Health Emergency Operations Centre (PHEOC), 4Washington State University (WSU), 5World Health Organisation (WHO)
*Correspondence email: ogaunya2012@gmail.com

Background: In Kenya, cholera remains a disease of public health importance and one of the priority diseases reported immediately in Kenya's Integrated Disease Surveillance and Response. Over the years, the country has reported a yearly increase in cholera cases with spread to different regions and counties. In the recent cholera outbreak, the first case was reported on 21st October 2022. As of 3rd December 2023, twenty-eight (28) counties have reported cases. Nine Sub-counties and the Dadaab refugee camps in four counties were prioritized to implement OCV reactive campaigns in February 2023. This was followed by a second phase of the OCV vaccination campaign during the Month of August 2023 that was implemented in the seven sub-counties. These sites were included in the reactive cholera vaccination campaign due to their high cholera caseloads, high case fatality rates (CFR) coupled with high attack rates. **Methods:** The OCV campaign was conducted between the 2nd to 11th of August 2023. The target population were individuals aged one year and above at the time of vaccination. Mixed strategies were applied to reach the target population i.e. door to door and fixed posts. **Results**: An administrative coverage of 105.1% (1,675,043/1,590,378) was attained. Five sub-counties surpassed the 100% coverage. The lowest coverage was in the GK prisons at 94.2% (2,931/3,111). A coverage of 105.3% for the general population was achieved. Embakasi Central was the highest at 119.1% (336,257/282,225) while Moyale sub-county was the lowest at 96.7% (161,510/167,003). The administrative coverage of the special population was 95% (3,422/3,604) with the school for the deaf attaining 99.6% (491/493) and the GK prisons at 94.2% (2,931/3,111). A total of 1, 675, 284 OCV doses were issued. Nairobi County consumed the largest number of OCV doses 41% (687,489). In terms of wastage, all the counties had very low wastage rates averaging 0.01%. A total of eight suspected cholera cases were reported in two sub-counties. **Conclusion:** Reactive cholera vaccination campaigns are targeted immunization efforts triggered by the occurrence of a cholera outbreak or the identification of high-risk areas for cholera transmission & contain the spread of the disease and prevent further cases.

Keywords: Cholera, Pandemics, Disease Outbreaks, Global Health, Vomiting

10.

EVALUATION OF FACTORS CONTRIBUTING TO LOW RECENCY UPTAKE BASED ON ONLINE RECENCY DASHBOARD DATA IN KABONDO SUB COUNTY HOSPITAL

Authors: Nicholas odiemo ogone (LVCT health)*

Background: Recent infection testing can differentiate recently acquired infection from long term infection. This is majorly done to identify population and areas where HIV transmission is occurring or an incidence has occurred. Sample collection for recency testing is done at the spokes facilities and testing done at the central Lab. This however is faced by several challenges which lead to low uptake of recency hence hindering recent infection surveillance.

Objective: To ascertain the contributing factor to low recency uptake despite high positivity rate as demonstrated by online recency dashboard data in Kabondo sub county.

Methodology: A cross sectional study was conducted in two steps in kabondo Sub County by identifying the reasons for failure to conduct recency test for clients despite having turned HIV positive. In the first step, data on reasons for test not done after enrollment of client into recency surveillance was collected from the recency test laboratory request forms submitted between January to June 2023. In the next step, a short questionnaire with multiple choice questions was administered to the HIV testers in the 17 spokes facilities. Data collected was keyed into excel and analyzed to get proportions. This data was then presented on pie charts.

Results: A total of 285 records were reviewed in the study period. Number found to have missed testing were 53(18%) Five major factors were identified to be contributing to recency testing not conducted. Samples collected but not tested as a result of overstaying contributed 3(6%) while poor quality hence not tested were 2(4%), declined and sample not collected 41(77%) , samples not collected due to lack of commodities 5(9%) and 2(2%) due to lack of phlebotomist. In further analysis among the declining clients, reasons for declining were lack of time 7(17%), fearing needle 12(29%), mentally challenged 1(2%) , myths 6(15%), deemed not beneficial 15(37) and provider knowledge gap 1(2%).

Conclusion: Major contributor to low recency uptake is clients decline to be offered recency while on further analysis major contributor to declining cases was study not deemed beneficial to participants.

Keywords: RECENCY TESTING

11.

DEPRESSION PREVALENCE AND ASSOCIATED FACTORS AMONG UNDERGRADUATE STUDENTS AT GULU UNIVERSITY, UGANDA

Authors: Nansubuga Federes (Gulu university)*

Background: Depression is common among university students and negatively affects their school performance. In this study, we investigated the prevalence and factors associated with depression among undergraduate students at Gulu University, Uganda.

Methods: In this cross-sectional study, we enrolled undergraduate students of Gulu University, Gulu, Uganda between January and April 2023. Data was collected using self-administered questionnaires. Patient Health Questionnaire- 9 (PHQ-9) was used to assess depression. Depression was defined as a PHQ-9 score ≥ 5. Multivariable logistic regression analysis was used to identify independent predictors of depression. P< 0.05 was considered statistically significant.

Results: We included data of 513 participants 199 (38.8%) female, and 113(22.0%) medical students, with a median age of 23 (interquartile range: 22-25) years. Of this, 296 (57.7%) had symptoms of depression. Factors significantly associated with depression were female gender (adjusted odds ratio [aOR]=2.08, 95% Confidence Interval [CI]= 1.28 —3.38, p=0.003) and being a Muslim (aOR=15.89, 95%CI=2.02-124.5, p=0.008).

Conclusions: Almost 3 in 5 of the participants exhibited symptoms of depression, emphasizing the importance of addressing mental health concerns within the university setting. Our findings emphasize the need for targeted interventions and support systems to address the mental health challenges faced by female students and those from specific religious backgrounds. Therefore, Interventions for active screening, diagnosis, and management of depression among undergraduate university students are recommended.

Keywords: depression, religion, gender, university students, Uganda

12.

CASE REPORT: AMELY Y, DYS576 AND DYS570, DYS481 AND DYS458 DROP OUT ENCOUNTERED DURING ROUTINE PATERNITY TESTING.

Authors: Ngure Kirosh Mwiwawi (KEMRI-HID LAB)*; Herzel Tiffany Ms Wandera (KEMRI); Belinda Azzam (KEMRI); Eva K Aluvaala (KEMRI)

Background: The incorporation of the gender determination marker amelogenin in commercial autosomal STR kits used in forensic laboratories is standard practice. A male sample is expected to type as XY and a female sample type as XX. However, in some instances a male may be falsely genotyped as female due to amelogenin Y-allele drop out. Previously autosomal STR kits only incorporated the amelogenin gene for sex determination. However, with improved technologies and increased multiplexing capabilities current STR kits have additional Y chromosome loci to ensure accurate gender testing.

Methods: Here we report a case of multiple Y allele drop outs observed in a male child during a routine paternity test conducted in KEMRI Human Identification lab. Multiplex autosomal STR amplification was carried out using the VersaPlex® 27PY System and the STR loci resolved on the thermofisher 3500 genetic analyzer, allele sizes were assigned using the Gene Mapper IDX version 1.6. The Power Plex® Y23 System was used to further confirm the gender.

Results: Allele drop outs were observed in both Autosomal STR and YSTR typing of the male child's sample despite optimum DNA concentration. In Autosomal STR typing the drop outs were observed in the SRY (Sex determining region of the Y-chromosome) that includes the amelogenin gene, DYS576 and DYS570 as included in the VersaPlex® 27PY kit. However, the DYS391 locus that is present on the non-recombining region of the Y was successfully typed. Y STR typing of the of the male child sample further revealed drop out of additional alleles in the SRY region this include the DYS481 and DYS458 loci. No dropouts were observed in the alleged father sample in both Autosomal STR and YSTR typing. The alleged father was not the biological father of the child.

Conclusion: The YSTR Typing confirmed that the child's gender was male. The loci present on the SRY region of the Y chromosome were not present in the male child indicating non inheritance from his biological father. This case though rare, demonstrates the need of having additional Y chromosome loci in Autosomal STR kits to ensure accurate gender determination in forensic cases.

Keywords: AMELY Y, DYS576 and DYS570, DYS481 and DYS458 Drop out encountered during routine Paternity testing.

13.

EXPLORING THE EXPRESSION PROFILE OF GENES ASSOCIATED WITH SALT-SENSITIVE HYPERTENSION AMONG KENYAN WOMEN DIAGNOSED WITH BREAST CANCER

Authors: John Gitau (African Institute for Mathematical Sciences)*; Godfrey Wagutu (Mount Kenya University); Francis W. Makokha (Mount Kenya University

Background: Breast cancer remains the most common cancer among women globally, with an estimated 2.26 million new cases diagnosed in 2020. Growing evidence suggests a complex bidirectional relationship between breast cancer and cardiovascular diseases, characterized by shared risk factors and systemic inflammation. Salt-sensitive hypertension, a condition with multifactorial underpinnings related to impaired sodium regulation, further complicates this interplay. Notably, chemotherapy and hormone therapy commonly prescribed for breast cancer can also induce hypertension, creating a unique phenomenon termed “onco-hypertension.” This study delved into the expression profiles of genes associated with salt-sensitive hypertension in Kenyan women diagnosed with breast cancer.

Methods: We analyzed differential gene expression from 23 RNA-Seq datasets of breast cancer patients. A cutoff of +/-1 log fold change was applied to identify significant changes in the expression of JAK-STAT and inflammatory pathway genes for further analysis. Subsequently, we employed R software to perform a gene-level correlation analysis on the identified JAK-STAT and inflammatory genes. Additionally, we leveraged clinical information, including systolic and diastolic blood pressure, heart rate, weight, and BMI. We constructed a correlational matrix to uncover crucial insights into the relationship between breast cancer and salt-sensitive hypertension.

Results: Our analysis revealed 27 differentially expressed genes between tumor and adjacent normal tissues. Out of these, 13 genes belonged to the JAK-STAT pathway, while 14 genes were associated with the inflammatory pathway. Within the JAK-STAT pathway, NOX1 gene was significantly upreguled, while TGFBR3, SOCS3, and PPARG genes were downregulated. In the inflammatory pathway, CXCL10 gene was significantly upregulated, while CCL24, CXCL2, and IL6 genes were downregulated. We further demonstrated that the dysregulation of these genes was associated with vascular dysfunction, sodium imbalance, oxidative stress, and inflammation, ultimately contributing to elevated blood pressure.

Conclusion: Our study identified a potential synergistic and antagonistic molecular mechanism underpinning the dysregulation of differentially expressed genes between breast cancer and salt-sensitive hypertension. These findings highlight the critical importance of closely monitoring and managing salt intake in Kenyan breast cancer patients to mitigate cardiovascular complications.

Keywords: Breast Cancer, Onco-hypertension, RNAseq, salt sensitivity

14.

ACUTE FEBRILE ILLNESS OUTBREAK IN NORTHERN KENYA: EMERGING PLASMODIUM VIVAX SPP. MALARIA

Authors: Richard Kimenye (FELTP Kenya Stephen, Olubulyera (Ministry of Health, Kenya-FELTP) , James Maragia (Turkana County Government-MOH) ,Boku Bodha (MarsabitCounty Government-Department of Health) ,Ahmed Abade (FELTP Kenya) ,Fredrick Odhiambo (FELTP Kenya), Victor Ofula (KEMRI) ,Maureen Otinga (KEMRI)

Background: Acute Febrile Illness (AFI), referring to fever occurring within a short period may follow many infections, delaying timely management. Globally, Malaria parasite infection accounted for 247 million cases and 619,000 deaths in 2021, 90% of which occured in Sub-Saharan Africa. In Kenya, 3.4 million cases and over 12,000 related deaths occurred between 2000-2021. Laisamis Sub-county in Marsabit, Northern Kenya, reported increased cases of an unknown illness with fever and related deaths in May 2023. We purposed to investigate the increased cases of AFI to determine the cause and inform public health action.

Methods: We conducted a retrospective review of data in MOH204 outpatient and MOH240 laboratory registers at three health facilities to line-list AFI cases. Line-listed cases were mapped to the village level, where active case search (ACS) was extended to the community. A case was defined as ‘any person presenting with symptoms including fever (hotness of the body), headache and cough between March to May 2023’. Line-listed cases from each village were interviewed using a semi-structured questionnaire and verbal autopsies conducted for those who had died. Variables collected included demographics, health-seeking behaviour, and utilization of insecticide-treated nets (ITNs). Blood samples were collected from the active cases and subjected to expert malaria microscopy. MS Excel was used to summarize categorical variables into frequencies and proportions and continuous variables into mean and standard deviation (SD).

Results: Total line-listed cases were 212. The index case was reported on March 29th, 2023. Cases propagated with the highest peak on May 8th (50), including 1 related death. Of 141 line-listed cases interviewed following ACS in 17 villages, Males were 57% (80/141). The mean age was 22 years (SD 1.6; 95% CI 19.4–25.7). 67% (94/141) were from the Kargi Ward. 6 deaths

were verified with a case fatality rate of 4% (6/141). 51% (72/141) were subjected to expert malaria microscopy, resulting in a malaria positivity rate of 13.89% (10/72). 12.5% (9/72) were Plasmodium falciparum spp. and 1.4% (1/72) were Plasmodium vivax spp. Malaria. ITNs utilization was 34% (48/141), while 64% (90/141) sought medical attention at the health facilities. **Conclusion:** Plasmodium falciparum and Plasmodium vivax spp. Malaria infection likely caused the outbreak. Not using ITNs, among other methods of vector control to prevent malaria infection, and Poor health-seeking behaviour were potential risk factors for morbidity and mortality. Reports of the invasion of Anopheles stephensi mosquito vector and preceding seasonal rainfall in this non-endemic malaria zone were potential contributors. We recommended enhanced vector control methods and community health education to prevent vector bites and improve health-seeking to control the outbreak. Also strengthened curative health services, including community outreaches, to control related deaths.

Key Words: Acute Febrile Illness, Malaria Microscopy, Plasmodium vivax Spp. Malaria, Emerging disease

POSTER SESSION **2:** SCREEN 2-HEALTH SYSTEMS

15.

EVALUATING THE MORPHOLOGICAL TRAITS OF RED BLOOD CELLS AND THEIR RELEVANCE IN PREDICTING PATIENT PROGNOSIS WITHIN HEMATOLOGICAL DISORDERS

Authors: Dan DN Ngugi (KEMRI graduate school)*; Sospeter Njeru (KEMRI); Dorcas Wachira (Kenya Medical Research Institute)

Background: Haematological disorders encompass a wide range of conditions that affect the blood and its components. This study aimed to investigate the association and regression patterns of atypical red blood cell structural features, with a particular focus on evaluating how changes in cell dimensions (anisocytosis), morphology (poikilocytosis), and the existence of inclusion bodies in RBCs might influence the prognosis of patients with haematological disorders over a three-month period

Methodology: The study was conducted between May 15 and August 30, 2023, at Coast General Teaching and Referral Hospital and utilized a Dynamic Progressive cohort design. A diverse group of 73 hematological disorder participants of various ages and both genders were carefully selected to minimize biases. Data collected included anisocytosis and categorized as low, moderate, or high from Full blood count based on RDW%. Poikilocytosis and inclusion bodies in RBC cells in PBF were categorized as low, moderate, or high. Patient prognosis was categorized as excellent, moderate, or low, based on participant prognosis. The data were recorded in an Excel spreadsheet and analyzed using R 4.3.1.

Results: The correlation between Anisocytosis and Prognosis was -0.911, that between poikilocytosis and prognosis was-0.66, and that between inclusion bodies and prognosis was-0.12. Multinomial regression analysis was performed on the same data. The coefficient associated with a fair prognosis in the presence of anisocytosis-low was -10.74, whereas for anisocytosis-moderate, the coefficient was 46.53. Conversely, for poor prognosis, the anisocytosis coefficient was 31.02, anisocytosis-low was -87.64, and anisocytosis-moderate was -19.06. Regarding poikilocytosis, the coefficients for a fair prognosis were -3.43 for poikilocytosis-low and -11.07 for poikilocytosis-moderate. For poor prognosis with poikilocytosis, the coefficients was -22.92 for poikilocytosis-low and -27.42 for poikilocytosis-moderate. Furthermore, the coefficients for a fair prognosis with inclusion bodies were -9.56 for inclusionBodies-low and 1.2 for inclusionBodies-moderate. On the other hand, the coefficients for a poor prognosis with inclusion bodies were 13.5 for inclusionBodies-low and -2.10 for inclusionBodies-moderate.

Conclusion: The analysis in R 4.3.1 showed that anisocytosis strongly correlated with poorer prognosis, as did poikilocytosis, although to a slightly lesser extent. The inclusion Bodies had a milder impact. Multinomial regression analysis supported these findings: high anisocytosis was linked to a poorest prognosis, high poikilocytosis to a poorer prognosis, and more Inclusion Bodies to a fair prognosis. In fine, anisocytosis and poikilocytosis are significant predictors of prognosis in hematological disorders, with anisocytosis being the most influential. Inclusion Bodies also play a role but to a lesser extent. This information can aid in patient management and treatment decisions.

Keywords: Red Blood Cells and Their Relevance in Predicting Patient Prognosis within Hematological Disorders

16.

USE OF A DIGITAL PLATFORM AND BEHAVIOURAL INSIGHTS TO EMPOWER AND MOTIVATE ADOLESCENTS AND YOUNG PEOPLE, TO ACCESS SRH SERVICES IN SELECTED COUNTIES IN KENYA

Authors: Hilina Hailemariam (Triggerise)*; Stanley Gichiri (Triggerise); Hildah Essendi (Triggerise); Rono Clinton (Triggerise)

Background: Kenya has one of the highest teenage pregnancies rates affecting underserved adolescents who lack access to contraception within the health system. Adolescent girls, in particular, require high-quality adolescent and youth-friendly health services as they bear a significant burden of adverse sexual and reproductive health (SRH) outcomes. Use of behavioural science has been credited in reducing some of the challenges girls face accessing SRH services through carefully crafted interventions designed for the local context. Triggerise uses a digital platform, Tiko, to motivate adolescent girls and young women (AGYWs) to adopt SRH services and uses behavioural science to motivate health-seeking behaviours. It combines this with electronic vouchers, managed by mobile technology, which enable AGYWs to access SRH services from a provider of their choice. When users digitally engage with Triggerise's platform, they generate data, which we use to design nudges that encourage healthy behaviour.

Methods: Triggerise's digital platform serves 15-24-year-old AGYWs in Kenya who are linked to a network of public, private clinics and pharmacies that offer quality-assured services. The client user journey from the platform allows application of behavioural insights to overcome existing behaviour change barriers such as knowledge on SRH services, misconceptions, proximity of care, and commitment for consistent use. Real-time insights collected from our programmes are utilised to adjust interventions, thus ensuring the effectiveness and impact of our programmes. The utilisation of nudges – such as reminders, follow ups, subsidies and reward points – together with rating

of the service by users encourages repeat use of our services and enhances the quality of service.

Results: Between January 2019 and March 2023, Triggerise's platform has provided services to a total of 681,000 girls and offered 1,075,000 services to Adolescent Girls and Young Women (AGYWs) in Kenya. According to the data collected from the platform, 58% of AGYWs served with contraceptive services continued using FP, with 85% of those taking long-acting reversible contraceptive methods (LARCs) is 85% and 15% of those taking short-acting methods (SAMs) continuing to use the methods. The target is to increase the continuation rate for SAMs to 30% by the end of 2024. Furthermore, the platform rating on the quality of service received has an impressive satisfaction score of 4.88 out of a maximum of 5 points. As a result of applying SBCC strategies, Triggerise's model demonstrates programme ability to achieve scale.

Conclusion: Triggerise's digital platform, Tiko, leverages behavioural science to motivate adolescent girls and young women in Kenya to adopt SRH services. By utilizing real-time data and applying nudges, the platform effectively encourages healthy behaviours, resulting in increased utilization, satisfaction rates, and improved quality of services.

Keywords: Triggerise,Tiko Digital platform Behavioural science Adolescent girls and young women (AGYWs) Sexual and reproductive health

17.

AN ASSESSMENT OF COMMODITY MANAGEMENT SYSTEM INDICATORS IN CASE MANAGEMENT OF TUBERCULOSIS IN SELECTED HIGH TUBERCULOSIS BURDEN COUNTIES JANUARY 2020 – MARCH 2023

Authors: Carey Abuya Othoo (Field Epidemiology and Laboratory Training Program)*

Background: Tuberculosis (TB) is a highly infectious disease with an estimated 10.6 million cases and 1.4 million deaths globally in 2022; TB is treatable through standard treatment regimens over predetermined periods depending on the type of TB. An efficient and reliable logistic management information system (LMIS) ensures commodity availability and access for TB patients. The national TB allocation tool is an LMIS that manages 4808 Health facilities that report on TB commodities in Kenya. We assessed the National TB program's TB allocation tool to determine if the system meets its set objectives in commodity management.

Methods: Key informant interviews of Stakeholders assessing the system attributes at sub-county, county and National levels using the TB allocation tool, internal data consistency checks across TB commodity reporting tools for Meru County and Data abstraction of reported commodity data from January 2020 to March 2023 for Kiambu, Meru, Nairobi and Siaya Counties. Variables collected included reporting rates, reporting rates on time, beginning balance, quantity received, quantity dispensed, positive adjustments, negative adjustments, losses, and physical count. Data abstracted was cleaned and analysed using MS Excel and Epi info.

Results: We reviewed 1781 records, representing 659 to 663 health facilities reporting on TB commodities between January 2020 to March 2023. The LMIS has a simple data flow from the facility to the TB allocation tool, with over 90% reporting rates and on-time reporting, 80% flexibility, and 33% of those interviewed agreeing the system was stable. Reported TB patient pack consumption between the daily activity register (DAR) and Kenya health information system (KHIS 2) was 53%, the Monthly Summary form (MSF) and KHIS 2 was 101%, and MSF and TB allocation tool was 100%. The average internal data consistency of consumed TB patient packs was 40%, for Rifampicin/Isoniazid/Pyrazinamide 75/50/150 mg was 73%, and Ethambutol 100mg was 79% for the facilities that reported for the four counties.

Conclusion: The system assessment concluded that the LMIS is simple and correctly mines commodity data to the TB allocation tool; commodity-related indicators can accurately be determined from the LMIS, with identified gaps in internal data consistency of reported consumed TB commodities and perceived instability of the system as per key informants interviewed. Therefore, to improve TB commodities' accountability and strengthen TB commodities' availability for treatment of all TB clients plus commodity-related indicators, the National TB program should incorporate internal data consistency and strengthen the capacity of stakeholders to adequately utilize the system for reported TB commodities in the TB allocation tool.

Keywords: Tuberculosis,health Information sytems

18.

BEHAVIORAL CHANGE STILL REMAINS AN IMPEDIMENT TO ENDING HIV EPIDEMIC IN KENYA, ANALYSIS OF REASONS FOR POST EXPOSURE PROPHYLAXIS USE AT KENDU SUB-COUNTY HOSPITAL, RACHUONYO NORTH SUB COUNTY, HOMA BAY COUNTY, KENYA.

Authors: Kevin Mimba1, Gabriel Kotewas1, Phanuel Otieno1

Affliation: MoH-Homa Bay County, Kenya1

Corresponding Author: Kevin Mimba, Email: kevinmimba@gmail.com, 0701099726

Introduction: In recent decades, there have been major advances in the prevention of HIV and sexually transmitted infections (STIs), however there has been a rise in new HIV infections in Kenya and people below 29 years formed 61% of the new infections. Post-exposure prophylaxis (PEP) means taking HIV medicines within 72 hours (3 days) after a possible exposure to HIV to prevent HIV infection We assessed the behavioral intervention among PEP user at Kendu Sub County Hospital.

Method: A retrospective study was conducted on the determinant of PEP use. Data was obtained from the PEP register at the Pharmacy from February 2022 – October 2023. Descriptive analysis was performed on demographics; age and gender and reason for wanting to take PEP. Data was then presented using simple frequencies.

Results: Over the last 21 months, a total of 325 people were issued with PEP drugs at the pharmacy with varied reason for taking PEP, these included; having unprotected sex, condom burst experience, rape cases, defilement, needle stick injuries and mixed feeding in infants. Male were the majority at 58% (188/325) and female 42% (137/325). Out of 325 clients analyzed, 47% (153/325) clients had previously engaged in unprotected sex, 32% (104/325) clients experienced condom burst, Defilement 7% (22/325) and rape 4% (12/235). Unprotected sex was common among the age of below 29 years at 69% (105/153), whereas condom burst experience was common among the age group of above 35 years (35/104). The male reported a significant higher number of those who engage in unprotected sex and turned up for PEP at 61% (94/153) against the female counterparts at 39% (59/153).

Conclusion: Despite the numerous publicity and awareness creation that has been done in HIV prevention, the data on PEP use still indicate prominence of risky sexual behaviors within the population. These findings support the need to design combination prevention interventions which simultaneously address socio-behavioral drivers of the HIV epidemic, promote condom use education, equity and access to condoms, and target age-disparate partnerships in creating awareness, consistent and correct condom use and avoiding risky behavior like unprotected sex.

Keywords: Behavioral change still remains an impediment to ending HIV epidemic in Kenya, Analysis of reasons for Post Exposure Prophyla

19.

A REVIEW OF THE DEVELOPMENT AND UTILIZATION OF COMMUNITY-BASED HEALTH INFORMATION SYSTEMS (CBHIS) IN KENYA.

Authors: Beatrice K Kuvuna (Health Economics Research Unit, KEMRI- Wellcome Trust Research Programme, Nairobi)*; Moriasi Nyanchoka (Health Economics Research Unit, KEMRI- Wellcome Trust Research Programme, Nairobi); Fatuma Guleid (Health Economics Research Unit, KEMRI- Wellcome Trust Research Programme, Nairobi); Michael Ogutu (Health Systems and Research Ethics Department, KEMRI-Wellcome Trust Research Programme, Kilifi); Benjamin Tsofa (KEMRI-Welcome); Jacinta Nzinga (Health Economics Research Unit, KEMRI- Wellcome Trust Research Programme, Nairobi)

Background: At the community level, health information is generated through community-based health information systems (CBHIS), a subset of health information systems (HIS). The CBHIS is crucial in generating extensive data that can be used to inform evidence-based decision-making and enhance healthcare service delivery in community health systems (CHS). With the government of Kenya prioritizing community and primary healthcare approaches to improve the CHS's effectiveness, it's imperative to strengthen CBHIS to provide timely, accurate, and quality data for community health. This review comprehensively examines the CBHIS, focusing on its data sources, processes, utilization, and accessibility of CBHIS data to the community members to empower them in health decision-making processes in Kenya.

Methods: This review followed Arksey and O'Malley's Framework. The search and study selection were guided by the Population, Concept, and Context (PCC) framework. We searched six databases: PubMed, EMBASE, HINARI, Cochrane Library, Google Scholar, and grey literature databases. Data was synthesized using thematic analysis.

Results: Our search yielded 4115 records, with eight studies included for synthesis. Community outreach and household visits were the predominant data sources for CBHIS in Kenya. Most of the studies in this review reported community health promoters (CHPs) as key actors in data generation by using household registers as data-collection tools. CHP supervisors (Community Health Assistants/Officers) were key in summarizing CHW-generated data; however, most studies underreported data management details. The review found that CBHIS data in Kenya is utilized for decision-making, community health program monitoring and evaluation, community dialogues planning, emergency preparedness and responses to disease outbreaks and epidemics, and identifying health services utilization gaps. Community involvement in data utilization mainly occurred through sharing data during community dialogues and health action days. Data collection tools stock-outs, manual systems operations, delayed and limited feedback from the higher levels, and inadequate capacity-building for CHPs were identified as challenges limiting data quality and using CBHIS data during decision-making.

Conclusion: CBHIS across communities and health systems, is essential in bolstering primary health care in Kenya. However, there is notable underutilization of data at the community level and threats to data quality that impede the use of these data to inform decisions. Optimizing the use of CBHIS in Kenya demands robust strategies such as full digitization of CBHIS, integration of user-friendly technology for high-quality and real-time data, capacity-building for communities and CHPs, and building in continuous feedback loops.

Keywords: Community-based health information systems (CBHIS), Community health systems (CHS), Health systems, Data utilization, EIDM

20.

UPTAKE OF DIGITAL HEALTH SYSTEMS IN PUBLIC HOSPITALS IN KENYA

Authors: Pauline Ombiri Omutere (Maseno University)*

Background: High income countries have in the past two decades adopted digital health systems, a move to reduce the usual manual (paper) storage and retrieval of health information. Low and middle income countries,Kenya in this case, are making strides in embracing digital health systems. The aim of the study was to explore the uptake of digital health systems in public hospitals in Kenya.

Methodology: A mixed-method survey conducted in Kenya aimed at providing health decision makers with information on digital systems and how to better develop this fast-rising technology in Kenya.urveys of County Health Records and Information Officers (CHRIOs) to establish the level of IT adoption across public hospitals were done. This was at a National CHRIO meeting that was organized by the Ministry of Health. Snowballing played a major role in identifying suppliers of health systems to hospitals. Data was collected between April 2014 and November 2016.

Results: Through the various data collection methods, information was obtained from 39 CHRIOs, 58 hospital managers , 9 health system vendorsabd 13 hospitals where Electronic Health Records (EHR) was implemented in various departments.

Out of the information provided by the CHRIOs on 121 public health facilities (level 4-level 6),the Comprehensive Care Centre(CCC) was the most computerized(106 facilities-88%), outpatient department (46 facilities - 38%), pharmacy and laboratory (28 facilities- 23%), the least computerized department was inpatient (8 facilities - 7%).It was revealed that all the surveyed facilities purchased a digital health system primarily for administrative purposes. The issue of financial accountability as a primary reason for purchasing EHR systems was sites by hospital managers during the interviews. Issues such as usability, inadequate training and system support were raised by users.

The in-depth interviews revealed 6 key themes that are essential for health systems to work: Acquisition history, Usability, Report generation and Data issues, Infrastructure, System support and training, Departmental communication and System interoperability. From the vendors, it came out clear that a wide range of modules were available but implementation was hindered by priority of service, lack of confidence in new technologies and lack of appropriate data policies.

Conclusion and Recommendations: Public hospitals in Kenya are embracing digital health systems to support administrative duties and also reporting, a good example being the Kenya Health Information System (KHIS).The study also noted challenges faced by system users and vendors. It is recommended that adequate training on digital systems be offered to users as this will improve their confidence in the systems and prioritization of work. Data policies will help in protecting the data being managed.

Keywords: Community-based health information systems (CBHIS), Community health systems (CHS), Health systems, Data utilization, EIDM

21.

MODELLING COUNT DATA FOR HIV-POSITIVE PATIENTS ON ANTIRETROVIRAL TREATMENT (ART) IN KENYA.

Authors: Muricho N Anna (KEMRI)*

Background: The National AIDS Control Programme (NASCOP) guidelines advise patients to begin antiretroviral therapy (ART) when an individual`s CD4+ cell count is below 350 cells/ml or when they begin to exhibit symptoms of HIV infection, as defined by WHO stages I through IV. To achieve HIV viral suppression, antiretroviral drug adherence is essential.

Methodology: A Retrospective Longitudinal study of HIV-Positive patients enrolled on ART from 2018 to 2021 those above 9 years when they sign up for ART. In total, 1489 individuals were involved during research. Data was examined by descriptive statistics. A generalized linear mixed effect model was fitted which took into account the within and between variations due to its flexibility.

Results: The number of patients enrolled on ART increases by Age and Gender over the four years. In 2018, 2019, 2020, and 2021 ART coverage was 22.4%, 24.2%,26.1%, and 27.3% respectively. A correlation that is negative (-0.12) was exhibited among ART count with gender, this implied that the model's predictive and analytical capabilities would be enhanced by the inclusion of this predictors. There existed a positive correlation (0.14) between ART count and age groups. Additionally, there existed a negative correlation (-0.023) between ART count and years. Consequently, there existed a negative correlation (-0.025) between ART count and county regions. A male is 25% less likely to enroll on ART as compared to a female patient. Patient aged 15-19 is 5% less likely to enroll on ART as compared to a patient aged 10-14. An individual aged 20-24 is 9% less likely to enroll on ART as compared to a patient aged 10-14. In 2019 patients were 6% less likely to enroll on ART as compared to the year 2018. In 2021 patients were 16% less likely to enroll on ART as compared to the year 2018. Comparing each of the coefficient's p-values to the level of significance of 0.05, age groups (15-19, 25+), gender and year were found to be significant predictors of ART count at alpha<0.05. Under random effects the standard deviation of 0.9626 a measure of the amount of variation in the dependent measure due to county. Additionally, the variance estimate of random effect county is 0.9811. Due to this difference from zero, it implies that ART count varies for the different patients based on gender, age groups and year. Results demonstrated the AIC for Mixed Model-NB is 6833 while the AIC in the GLM-NB is 8103.

Conclusion: The distinctions between the two GLMMs and GLM when modeling a count response were examined for parameter interpretation. The study found Age and Gender to be significant predictors of ART count under both models. The model with fixed and random effects had a lower AIC and BIC, making it the better model. The study recommends education that is extensive regarding ART and HIV in general should be delivered to all group levels from a wider range.

Keywords: ART- Antiretroviral Treatment, GLM-Generalized Linear Models, GLMM-Generalized Linear Mixed Models

POSTER SESSION 3: SCREEN 3-VIROLOGY

22.

ISOLATION AND GROWTH KINETICS OF BOGORIA VIRUS FROM PHLEBOTOMINE SAND FLIES SAMPLED IN BARINGO KENYA

Authors: Jane W Thiiru (Jomo Kenyatta University of Agriculture and Technology)*; Solomon Langat (Centre for Virus Research, Kenya Medical Research Institute); Francis Mulwa (Centre for Virus Research, Kenya Medical Research Institute); Stephanie Cinkovich (Armed Forces Health Surveillance Division, Global Emerging Infections Surveillance Branch); Santos J Yalwala (KEMRI/USAMRD-AK); Hellen Koka (Centre for Virus Research, Kenya Medical Research Institute); samoell A Khamadi (KEMRI); Justus Onguso (Jomo Kenyatta University of Agriculture and Technology); Nicholas Odemba (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Francis Ngere (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Jaree Johnson (Armed Forces Pest Management Board); Timothy Egbo (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Eric Garges (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Elly Ojwang (Walter Reed Army Institute of Research-Africa (WRAIR-Africa), KEMRI); Fredrick Eyase (US Army Medical Research Directorate-Africa)

Background: Phleboviruses pose emerging threats to public health. While most Sand fly phleboviruses induce self-limiting febrile diseases, some can lead to severe neuroinvasive conditions. The number of newly identified sand fly phleboviruses has increased over the last decade, some of unknown health risks. Recent studies in Kenya revealed five novel sand fly phleboviruses, including Nteppes virus, capable of infecting humans. However, comprehensive information on the diversity, distribution, pathogenic potential, ecological cycles, maintenance mechanisms, and presence in vertebrate reservoirs of sand fly phleboviruses remain limited in Kenya.

Methods: In this study, a total of 8,742 female sandflies from diverse geographical regions were inoculated into culture using mammalian (VERO-CCL) for virus isolation. Consequently Library preparation was performed followed by next-generation sequencing. BLAST analyses were used to determine the identity of the isolate. Phylogenetic analyses were conducted determine for placement of the virus strain. Lastly, in vitro growth kinetics was done on mammalian (Vero E6) and mosquito (C6/36) cell lines to assess viral growth kinetics.

Results: Reproducible cytopathic effects (CPE) was observed in one pool of 10 sandflies of the genus Phlebotomus collected in Baringo County 2021. Next Generation sequencing resulted in the identification of the Bogoria Virus (BOGV). The current virus aligned together in a single phylogenetic clade with other BOGVs identified in 2016 as well as Perkerra virus and Embossos virus. In vitro growth kinetics demonstrated efficient BOGV replication in both Vero E6 and C6/36 cells.

Conclusion: The current isolation of BOGV underscores its probable circulation in Baringo County, having been earlier identified twice in 2016 in the same region. Furthermore, replication of BOGV in both mammalian and mosquito cell lines indicates amenability both to vector and host. As such, the potential involvement of multiple vectors portends major public health implications. Taken together these data points to the need to carry out surveillance for these uncharacterized sand fly viruses.

Keywords: Phlebovirus, Bogoria virus, Sand fly borne-phleboviruses.

23.

METAGENOMIC ANALYSIS OF Aedes aegypti VIROME DIVERSITY DURING A DENGUE OUTBREAK IN KISUMU, KENYA.

Authors: Tabitha W Ng'ang'a (Jomo Kenyatta University of Science and Technology)*; Wallace Bulimo (KEMRI); Solomon Lang'at (KEMRI); Johnson Kinyua (Jomo Kenyatta University of Science and Technology); Nicholas Odemba (US Army Medical Research Directorate-Africa); Santos J Yalwala (KEMRI/USAMRD-AK); Tmothy Egbo (US Army Medical Research Directorate-Africa); Jaree Johnson (US Army Medical Research Directorate- Africa); Elly Ojwang (US Army Medical Research Directorate-Africa); Eric Garges (US Army Medical Research Directorate-Africa); Fredrick Eyase (US Army Medical Research Directorate-Africa)

Background: Aedes aegypti is the main vector for Dengue (DENV) and Chikungunya (CHIKV) viruses in the country. Beyond arboviruses, Aedes aegypti harbours insect-specific viruses (ISVs), which can impact the mosquito's ability to transmit diseases by interfering with viral processes and triggering immune responses. However, the lack of systematic molecular entomological surveillance in Kisumu has left the diversity of viruses in local Ae. aegypti populations largely unknown. This study aimed to address this gap by conducting a retrospective analysis during a dengue outbreak, capturing, and characterizing the viromes of Ae. aegypti in Kisumu.

Method: Adult mosquitoes were collected in Jua Kali area, Kisumu County, using CDC miniature light traps and temporarily immobilized using triethylamine, sorted, preserved in liquid nitrogen and transported to the laboratory at the Kenya Medical Research Institute Kisumu. They were grouped by morphological characteristics and stored at -80 degrees Celsius for virome analysis. RNA extraction, sequencing library preparation, and Illumina Miseq sequencing protocols were carried out. Initial analysis was done on the CZ-ID platform, which is

an integrated pipeline with capabilities to perform quality control, de-hosting, duplicate removal, as well as assembly and identification of viruses.

Findings: A total of 2,142 female Ae. aegypti grouped into 86 pools and 4 superpools were analysed. Metagenomics analysis revealed the presence of a wide range of viruses, including Iflaviridae family members Tesano and Amigeres viruses, Rabai virus, a Negeviruses, and unclassified viruses such as Korlebu, Sassandra, and Hanko Virus. Tesano Aedes virus (TeAV) was prevalent in three out of the four superpools, and Amigeres virus was present in two of the superpools. Significantly, no pathogenic viruses were identified by metagenomic next generation sequencing, suggesting a prevalence of non-pathogenic viral entities in the analyzed Ae. aegypti populations.

Conclusion: In conclusion, our study provides initial insights into the virus diversity within Ae. aegypti mosquitoes in Kisumu, representing the first attempt to uncover this information in the region and particularly during a dengue outbreak. Despite these advancements, understanding the complete impact of ISVs on arbovirus transmission remains challenging due to the intricate and context-dependent nature of these interactions. Ongoing research is imperative to unravel the mechanisms and subtleties governing ISV-arbovirus interactions across diverse environmental settings, contributing to a comprehensive understanding of these complex relationships.

Keywords: Aedes aegypti, Insect Specific Viruses

24.

SEROPREVALENCE OF YELLOW FEVER AND DENGUE VIRUSES AMONG HUMAN POPULATION IN NGURUMAN AND KERIO VALLEY IN KENYA, 2021–2023

Authors: Mercy H Kibathi (International Centre of Insect Physiology and Ecology)*; Edith E.L Chepkorir (Kenya Medical Research Institute); Sepha Mabeya (Jomo Kenyatta University of Agriculture and Technology); David P. Tchouassi (International Centre of Insect Physiology and Ecology); Rosemary Sang (International Centre of Insect Physiology and Ecology)

Background: Dengue (DENV) and yellow fever (YFV) viruses are among emerging and re-emerging arboviral diseases of public health concern. Their incidences and associated burden can be grossly underestimated owing to minimal surveillance and poor diagnosis. This study assessed the exposure risk of humans to yellow fever and dengue viruses in two dryland ecosystems of Kenya, Nguruman and Kerio Valley.

Methods: Human serum samples collected from febrile patients (aged 5-85 years) via a hospital-based cross-sectional study (Nguruman=194, Kerio Valley=286) were tested for neutralizing antibodies to DENV, YFV, and related Flavivirus Zika Virus (ZKV), and West Nile Virus (WNV) using the Plaque reduction neutralization test (PRNT). The seroprevalence was analyzed and compared by sites and associated demographic characteristics.

Results: Overall, at least one of the four viruses was detected in 54.5% (262/480; 95% confidence interval [CI] 50.1–59.0%) of the samples tested, with the percentages significantly higher in Kerio Valley (184/286) than Nguruman (78/194) (P<0.0001). YFV seroprevalence was higher in Kerio Valley than in Nguruman (P<0.0001) with low DENV seropositivity observed only in Nguruman (2%). In contrast, the WNV infection rate was significantly higher in Nguruman (27%) than in Kerio Valley (9%) (P<0.0001); however, with comparable rates of ZIKV (5% vs 6%). A significantly higher virus seropositivity occurred in females than males in Kerio Valley (P<0001) in contrast to Nguruman with higher rates in males (P value=0.049). The highest YFV seroprevalence occurred in the 0-25 age group in Kerio Valley (26%) and Nguruman (3%).

Conclusion: The findings suggest a high circulation rate of the viruses in both study sites that could be contributing to clinical disease. Even though frequent vaccinations following the 1992–1993 outbreak may have contributed to the high YFV incidence in Kerio Valley, the degree of disease protection is still insufficient in the event of an outbreak. To achieve herd immunity, Kerio Valley should consider intensifying YF vaccination to 80%, and Nguruman should consider strengthening vector control strategies to avoid the possible risk of an outbreak.

Keywords: Dengue, Yellow Fever, Flavivirus, Arbovirus surveillance

25.

ENTOMOLOGIC RISK ASSESSMENT OF YELLOW FEVER OUTBREAK IN KENYA 2022

Authors: James K Mutisya (Kenya Medical Research Institute (KEMRI))*; Francis M Musili (KEMRI); Konogoi Limbaso (KEMRI); Betty Chelangat (Kenya Medical Research Institute (KEMRI)); Joel Lutomiah (KEMRI); Rosemary Sang (Kenya Medical Research Institute (KEMRI))

Background: Yellow fever (YF) is a mosquito-borne infection of international public health. It is transmitted to humans through bite of infected Aedes mosquitoes. Following confirmed cases of YF in Isiolo an assessment was carried out in Isiolo and its neighboring counties at risk of spill over. The survey was to ascertain the presence of the Aedes mosquito, its abundance and determine the risk of exposure.

Methodology: Adult mosquitoes were collected through CO2-bated CDC light traps and BG-sentinels traps set during the day and night. Larvae and pupae were collected indoors and outdoors. Door-to-door survey was done to identify the breeding preference of the Aedes species. The data on larval survey were analyzed in R statistics using Chi-square and container index (CI), house index (HI), breteau index (BI), pupal index (PI) calculated as per the WHO procedure.

Results: 487 houses were surveyed with Wajir having the highest house positivity of 27% followed by Isiolo and Garissa having 12% and Meru with 4%. 2,013 containers were inspected and 69 (14.2%) had at least an Aedes larvae or pupae. Overall House Index, Container Index and Breteau Index were 11.3%, 3.4% and 14.2% respectively. Isiolo had the highest Container index (20.3), Breteau index (20.1) followed by Wajir (3.8), 2.5 and 1.7 for Garissa and Meru respectively.

Of the 7,588 adult and 362 larval female mosquitoes collected, Ae. furcifer accounted for 60.2% followed by Ae. aegypti 6.6%, while Ae. simponi accounted for 0.8%., no adult mosquito was collected from Wajir. 245 were collected in ovicups and soil scrapings, while 117 were adult collection. Isiolo had 88(24%) Ae. aegypti, 218(60.2%) Ae, furcifer, 3(0.8%) Ae. simpsoni, 4(1.1%) Ae. chausseri while Ae. aegypti for Garissa and Meru was 48(13.3%) 1(0.3%) respectively.

Conclusions: Overal finding it was evident that the four counties were at risk therefore mitigation measures need to be taken before spill over to the other regions. However, Ae. furcifer was the most abundant in the four counties assessed hence control measures should target breeding preference for the vector to minimize mosquitoes densities.

Keywords: Aedes aegypti, Yellow Fever

26.

METAGENOMIC ANALYSIS OF THE BAT VIROME IN COASTAL AND WESTERN KENYA

Authors: George K Kisoi (Jomo Kenyatta University of Agriculture and Technology (JKUAT), Nairobi.)*; Joel Lutomiah (KEMRI); Solomon Langat (Centre for Virus Research, Kenya Medical Research Institute, Nairobi.); Joel Bargul (Jomo Kenyatta University of Agriculture and Technology (JKUAT), Nairobi.); Johnson Kinyua (Jomo Kenyatta University of Agriculture and Technology (JKUAT), Nairobi.); David Abuom (Armed Forces Health Surveillance Division, Global Emerging Infections Surveillance Branch, United States); Bernard Aqwanda (The National Museums of Kenya, Nairobi, Kenya.); Konogoi Limbaso (KEMRI); Timothy Egbo (Armed Forces Health Surveillance Division, Global Emerging Infections Surveillance Branch, United States); Jaree Johnson (United States Armed Forces Pest Management Board, United States, Silver Spring, Maryland, United States.); Elly Ojwang (Armed Forces Health Surveillance Division, Global Emerging Infections Surveillance Branch, United States); Eric Garges (Armed Forces Health Surveillance Division, Global Emerging Infections Surveillance Branch, United States); Fredrick Eyase (US Army Medical Research Directorate-Africa)

Bats have received considerable attention as they harbor a variety of zoonotic pathogens associated with emerging infectious diseases. The role of bats in the transmission of viruses such as coronaviruses, filoviruses, Nipah virus, and rabies virus is well documented. The link between bats and zoonotic coronaviruses has attracted global attention, especially due to events like the transmission of Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) from bats to humans. The coastal and western regions of Kenya are home to a diverse range of bats, making them important areas for the study of bat-borne viruses. Understanding the bat virome in this region is critical for public health preparedness and intervention strategies. Previous studies have emphasized the need for comprehensive surveillance to characterize the diversity of bat viruses. Therefore, this study aimed to identify and genetically characterize viruses harboured by different bat species in coastal and western Kenya regions. The study adopted a retrospective approach, a total of 97 whole blood samples from eight different bat species were collected from nine sites in the coastal and western regions of Kenya. Pre-screening for filoviruses was performed using Real-Time Polymerase Chain Reaction. Ribonucleic acid (RNA) was then extracted from the filovirus-negative samples using the QIAamp Viral RNA Minikit, followed by library preparation for metagenomic sequencing to identify zoonotic bat viral load pathogens. Libraries were prepared using the Illumina RNA Prep with Enrichment (L) Tagmentation Kit and then sequenced on the Illumina Miseq platform using 2X300 PE chemistry. Raw sequence data were analyzed on the CZ-ID bioinformatics platform for quality control, dehosting, deduplication, and virus assembly and identification. Phylogenetic analysis of the identified viruses was performed with IQ-TREE 2, and the generated trees were visualized using Figtree v1.3. A total of 13,093,710 sequencing reads were generated in the study, with a total of 5,493,521 reads that passed the filtering and quality control steps to be used for subsequent analyses. The viruses identified in different bat populations include, Hepacivirus which was detected in Cardioderma cor bats from Lamu (Mokowe), Pegivirus B detected in Mops condylurus bats from Lamu (Manda Barracks), and Human Mastadenovirus identified in Chaerophon ssp bats from Mombasa (Mtongwe). No viruses were detected in Coleura afra from Kisumu (Kombewa)and Mt. Elgon (Makhonge), Epomophorous labiatus from Kakamega (Kalro), Epomophorous wahlbergi from Lamu (Lamu Island), Rousettus aegyptiacus and Rhinolophus spp from Kwale (Shimoni), and Rousettus aegyptiacus from Mt. Elgon (Ruanda). Therefore, this study has identified different viruses some of which are considered to be important to public health. Continuous surveillance should be carried out to understand the diversity of bat viruses in Kenya and their public health importance.

Keywords: Metagenomics, Bat viruses, zoonotic

27.

ROTAVIRUS DIARRHOEA OUTBREAK IN KIAMBU AND MOMBASA COUNTIES, KENYA, APRIL-MAY 2023

Authors: Carlene Sang (KEMRI)*; Ernest wandera (KEMRI); Pamela Njugu (KEMRI); James Nyangao (KEMRI), Centre for Virus Research, Kenya Medical Research Institute, Nairobi, Kenya

Background: Rotaviruses are the major etiological agent of acute gastroenteritis in children under the age of five years globally. Safe and effective vaccines are a high-impact and cost-effective public health intervention tool to greatly reduce the burden of rotavirus disease. A monovalent rotavirus vaccine was introduced into the National Immunization Program in Kenya in July 2014. There was a long shortage of the vaccine in the country from 2022 lasting for more than a year. In April-May 2023, there were reports of a spike in the number of children aged below 5 years presenting with severe watery diarrhoea, vomiting and high fevers at health facilities in Kiambu and Mombasa Counties.

Objectives: We aimed to investigate the outbreak with a view to determining the causative agent and its molecular epidemiology.

Methods: A total of 28 stool samples were collected from children presenting with diarrheal illness at Coast General Hospital and Ganjoni Hospital in Mombasa County and Gathanga Health Centre in Kiambu County. The samples were tested for group A rotavirus using ProsPect ELISA kit. RNA was extracted from the rotavirus-positive samples and subjected to SDS-PAGE to determine their electrophoretypes and genotyped using multiplex semi-nested RT-PCR.

Results at 33.3% (2/6, 95% CI: 6.0-73.8%). The rates of detection are more than triple the national range of 9-13% [1,2]. The highest rate of rotavirus infection was observed in children between 0-12 months (vaccine-eligible group) at 60%. Long electrophoretypes were predominant as compared to the: Of the 22 samples obtained from Mombasa County, 7 tested positive for group A rotavirus representing a prevalence of 31.8% (95% CI: 15.1-53.1%). In Kiambu County, rotavirus was detected short electropherotypes. The investigation found a higher infection rate in males than females at 56% and 44%, respectively. G3P[8] was the most predominant strain, accounting for 66.7% (95% CI: 33.2-90.7%) of all the circulating strains. The remaining strains were non-typeable.

Conclusion: The strikingly high rate of detection of rotavirus during the diarrhoea outbreak in Kiambu and Mombasa Counties, coinciding temporally with a yearlong stockout of rotavirus vaccines in the country, and which were most pronounced among the vaccine-eligible children and caused predominantly by a single strain, provide compelling evidence to indicate that the outbreak was due to rotavirus infection.

Keywords: Diarrhoea; Outbreak; Rotavirus; Vaccine; Kenya.

28.

SEROPREVALENCE OF NGARI VIRUS IN THE HUMAN POPULATION RESIDING IN SELECTED SITES OF BARINGO AND KAJIADO COUNTIES

Authors: Titus Kitonyo Munywoki (ICIPE)*; Edith E.L Chepkorir (Kenya Medical Research Institute); Sepha Mabeya (JKUAT); David P. Tchouassi (International Centre of Insect Physiology and Ecology); Rosemary Sang (International Centre of Insect Physiology and Ecology)

Background: Viruses transmitted by blood-sucking arthropods (arboviruses) infect people and livestock worldwide and impose a significant social and economic burden on society. Ngari virus (NRIV) spread by mosquitoes has been reported to cause severe febrile illness and hemorrhagic fever in people and small ruminants. Although previously detected during sporadic Rift Valley fever virus outbreaks, a recent study found evidence of active virus circulation of the virus in livestock hosts between epidemics. To date, there is limited data on the Ngari virus in Kenya, particularly human population residing in pastoral areas. This study aimed to investigate whether this virus affects human populations in Baringo and Kajiado counties in Kenya.

Methods: The study employed a cross-sectional design, specifically targeting health facilities in the study areas. Serum samples were collected from human patients experiencing a fever of unknown origin during the period from January 2021 to June 2022. The samples were analyzed by plaque reduction neutralization test to detect neutralizing antibodies to NRIV. The seropositivity rate of the virus was compared between the study areas and considering demographic factors. Data was analyzed using R version 4.2.2.

Results: Overall, 289 and 186 human samples from Marigat, Baringo County, and Nguruman, Kajiado County respectively, were analyzed. The seroprevalence of NRIV was significantly higher in Nguruman (42.5%) than in Marigat (28.4%) (P=0.002). The most affected age group in Marigat was between the ages of 11 and 20 years (18.6% positivity rate). In Nguruman, infection risk was highest in the age group of 21-30 years (20.5%) All affected individuals had contact with either cows, goats, or both.

Conclusions: The results show evidence of human infection in both locations that could be associated with disease. The variation in the prevalence rates between the locations suggests differences in factors influencing the transmission and spread of the virus in these areas. This data likely impacts human health and calls for studies to unravel the potential health burden and mitigation strategies.

Keywords: Arbovirus, Ngari, seroprevalence mosquito-borne diseases blood-sucking arthropods,zoonotic viruses,seroprevalence, human

29.

ANALYSIS OF PHYTOCHEMICAL COMPOSITION OF ANTIVIR-H AND IMB HERBAL SUPPLEMENTS USED FOR MANAGEMENT OF COVID -19

Authors: athuman chiguzo (KEMRI)*

Background: The coronavirus disease (COVID -19) is a new zoonotic coronary system RNA virus that is highly infectious and has resulted in many deaths globally. Traditional medicines have been in use over decades in many parts of the World for management of different health disorders. The aim of this study was to carry out phytochemical analysis of two herbal supplements Antiviral H and Immune Booster (IMB) used for management of COVID-19. The two supplements have been registered by Kenya Pharmacy and Poisons Board as herbal treatment for Covid-19.

Methodology: An experimental study to evaluate the phytochemical profile of Antivir H and IMB herbal combinations of natural products was carried out in the laboratory to assess their phytochemical profiles. Mixed herbal powders for Antivir-H and IMB were screened to determine the presence of different classes of phytocompounds. The powders were extracted in organic and inorganic solvents. The Thin Layer Chromatography (TLC) fingerprinting of the extracts were carried out to determine the phytochemical profiles. Thin-layer chromatography (TLC) is a chromatography technique that separates components in non-volatile mixtures. It is performed on a TLC plate made up of a non-reactive solid coated with a thin layer of adsorbent material.

Results: The results revealed that methanol-dichloromethane (DCM) of Antivir H had moderate presence of phenols, tannins and quinones(++) while the aqueous extracts of the same show a high presence of flavonoids, phenols and saponins (+++) with moderate steroids (++). IMB showed high levels of alkaloids (+++) with moderate phenols, tannins and quinones(++) while aqueous extracts of IMB showed a high levels of flavonoids, phenols and saponins (+++)with moderate tannins (++)

Discussion: Antivir H and IMB contain phytochemicals able to exhibit antiviral activities that could be used to manage respiratory viral

infections including SARS-CoV and COVID -19. Antivir H and IMB contain antibiotic properties useful for infections like pneumonia. Therefore, the two herbal supplements are possible traditional remedy for the treatment of COVID-19 because they have displayed a powerful antiviral effect against SARS-CoV. Further, it has been demonstrated from other studies that two viruses, which use different viral attachment proteins are blocked from binding to saponin-treated cells.

Conclusion: In conclusion, most compounds were extractable using distilled water. However, the products are consumed wholesome orally and hence patients benefit from all the phytochemical compounds composed in the drug. Recommendation: Further studies to be carried out to isolate pure compounds and determine their efficacies separately and in combination.

Keywords: Antivir-H, IMB, Phytochemical, Analysis

30.

PREDICTING FACTORS OF COVID-19 VACCINE UPTAKE AMONG PERSONS AGED 18 YEARS AND ABOVE IN KIAMBU COUNTY, KENYA

Authors: SAID M ABDULLA (JKUAT)*; Reagan Chweya (IRC); Charles Wafula (TICH); Simon Karanja (JKUAT)

Introduction: COVID-19 is still a major public health threat associated with the global burden of diseases, and economic losses especially in developing countries. Rolling out vaccines against COVID-19 is crucial in halting its burden. We investigate predictors of COVID-19 vaccine uptake among persons (≥18 years) in Kiambu County.

Methods: We used cross-sectional study design to determine the COVID-19 vaccine uptake. Using multi-stage sampling, Ruiru and Githunguri sub-counties were randomly selected from 12 sub-counties in Kiambu. Within these sub-counties, Mwihoko and Kamothai wards were then randomly selected. Study participants were selected using cluster sampling in household within the wards and their characteristics and COVID-19 vaccination status obtained using a semi-structured questionnaire. Ordinal logistic regression was used to determine predictors of the vaccine uptake using statistical R software.

Results: We recruited 537 participants of which 313 (58.3%) were female. Of the 537 participants, 421 (78%) received COVID-19 vaccine, in descending order, include AstraZeneca 168 (39.9%), Moderna 113 (26.8%), Johnson & Johnson 101 (24%), Pfizer 25 (5.9%) and Sinopharm vaccine (0.2%). 366 (87%) and 55 (13%) of the 421 vaccinated participants completed or received partial vaccinations irrespective of the vaccine type respectively. Vaccine uptake was associated with being aged 31-45 years (OR=0.46, 95% Confidence interval (CI) 0.28, 0.74), 18-30yrs (OR=0.50, 95%CI0.30, 0.83), doubts on vaccine efficacy (OR=0.24, 95% CI 0.16, 0.35) and vaccine side effects concerns (OR=0.59, 95% CI 0.40, 0.87).

Conclusion: The uptake of COVID-19 vaccine was (78%) against the National target of 100%, associated with increasing age while decreasing with doubts on vaccine efficacy and vaccine side effects concerns. To enhance vaccine coverage, interventions targeting younger age groups are needed to bolster overall community immunity while also addressing vaccine side effect and efficacy concerns through campaigns and awareness.

Keywords: COVID-19 vaccine uptake, Predictors, Kiambu County, Cross-sectional study, Public health, Vaccine hesitancy

31.

SARS-COV2 BEYOND THE PANDEMIC ERA

Authors: Gathii Kimita (WRAIR-Africa)*; Eric M Muthanje (KEMRI/Walter Reed Project); Esther Omuseni (WRAIR-Africa); Stephen Ocholla (WRAIR-Africa); Allan P Lemtudo (KEMRI/USAMRD-K); George Awinda (WRAID-Africa); Rachel Githii (WRAIR-Africa); Beth Mutai (WRAIR-Africa); John N Waitumbi (KEMRI/Walter Reed Project)

The period between 2020 to 2022 witnessed the prominent emergence of SARS-CoV-2, fundamentally shaping the trajectory of global events. During this time, socio-economic aspects of society were gravely disrupted as economies fell, lives tragically lost, and a sense of suspended time persisted for two years due to a disease whose origins remain contested. While Kenya did not experience the high number of infections and mortalities as those witnessed in the Western world, the impact of the disease on our day-to-day lives is still fresh in our minds. Although COVID-19 has since fallen off the "pandemic" list, and no-longer attracts the attention it had carved out for itself, it still lingers on. In 2023 we tested 6,252 respiratory specimens for SARS-CoV-2, of which 112 (1.8%) were positive by RT-qPCR and 50 yielded useable whole genomes. Using the 2023 genome data from our surveillance sites (n=50), and those from Kenya available in public databases (n=297), we show that SARS-CoV-2 still lingers on albeit in small numbers. Omicron is still King, and its lineages dominated 2023. The most abundant lineages were FY.4* (190/347), XBB.1* (60/347) and GE.1* (60/347) accounting for >89% of all lineages detected. These dominant lineages were responsible for the outbreak that occurred between March and July 2023. While other lineages have since declined in frequency, lineage GE.1 has persisted and seems to be slowly gaining the edge over the others, as at late November 2023. A lone variant EG.5.1 (a descendant of XBB.1.9.2) was detected by our Lab in Kisumu in a patient with history of travel to the US and Europe. It's the only genome from Kenya in the GISAID, indicating that it probably did not propagate beyond this case. Lastly, as we navigate the COVID-19 post-pandemic landscape, its important to reflect on lessons learnt during the pandemic, especially the importance of continued genome surveillance in identifying novel lineages to inform COVID-19 prevention measures.

Keywords: SARS-COV-2, COVID-19, Omicron, Genome surveillance, Kenya

32.

EVALUATING COVID-19 VACCINATION UPTAKE IN HEALTHCARE WORKERS: RESULTS FROM A SURVEY IN KENYA

Authors: Abigael Awuor (ICAP)*; Peninah Munyua (CDC); Kelvin Ndede (ICAP); Steve Akoth (ICAP); Jared Opudo (ICAP); Duncan Chege (ICAP); Doris Naitore (ICAP); George O. Agogo (CDC); Amy Herman-Roloff (CDC); Emmanuel Okunga (Ministry of Health); Mark Hawken (ICAP)

Background: Healthcare workers (HCW) have been on the front line in the fight against COVID-19, which put them at high risk of exposure to infection. Vaccination of HCW plays a key role in preventing severe COVID-19 infection. HCW also play a pivotal role in the successful uptake of COVID-19 vaccinations within the general population as they often serve as trusted sources of information for their patients. We conducted a survey to estimate COVID-19 vaccination uptake among HCW within four selected health facilities in Kenya and described their knowledge, attitudes, and perceptions of the COVID-19 vaccine.

Methods: Between April and July 2023, a structured questionnaire and focus group discussions (FGD) were conducted among 274 HCW in four purposively selected healthcare facilities: Loitokitok Sub-County, Marsabit County, Coast General Teaching, and Busia County Referral Hospitals. HCW were categorized as clinical or non-clinical then stratified into four cadre groups, two from each category then a random sample was selected from each stratum. Vaccination status was self-reported. A bivariate logistic regression analysis was performed to determine factors associated with uptake.

Results: Of the 274 HCW, 133 (49%) were female. A majority 238 (87%) reported having received at least one dose of COVID-19 vaccine. The lowest vaccination uptake (71%) was observed among participants aged 18-24 years and the highest uptake (95%) among those aged 35+ years (OR=7.5, 95% CI: 2.2-25.9). COVID-19 uptake was associated with easy access to COVID-19 vaccine (OR=11.6, 95% CI:3.2-47.8) and a perception that the vaccine is safe (OR=20.7, 95% CI: 9.1-49.5) or important (OR=72.8, 95% CI: 24.3-275). Among those that were initially hesitant but got vaccinated, their hesitancy was overcome when anticipated negative side effects were not observed in those vaccinated earlier.

Conclusion: COVID-19 vaccine uptake was high amongst HCW from survey sites. Easy access to the vaccine was the main reason for high vaccination uptake however non-vaccination was largely attributed to vaccine safety concerns. Availing vaccines at workplaces, disseminating information on vaccine safety, and using early vaccine adopters as champions may help improve vaccine safety and overcome vaccine hesitancy. Findings from this survey can provide valuable insights into areas to target during future vaccination campaigns to help effect universal COVID-19 vaccination coverage amongst HCW.

Keywords: COVID-19, Health Care Worker, Vaccine Uptake, hesitancy, perceptions, Kenya

POSTER SESSION 4: SCREEN 4-MALARIA

33.

TRENDS IN INSECTICIDE-TREATED NET INDICES AND EFFECT ON COMMUNITY MALARIA PREVALENCE — WESTERN KENYA, 2015-2020

Authors: Jonathan S Schultz (CDC-Kenya)*; Julia Janssen (3 Malaria Branch, Division of Parasitic Diseases and Malaria, U.S. Centers for Disease Control and Prevention, Atlanta, GA); Ryan Wiegand (Malaria Branch, Division of Parasitic Diseases and Malaria, U.S. Centers for Disease Control and Prevention, Atlanta, GA); Brian Seda (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Kelvin Onoka (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Oliver Towett (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Titus Kwambai (Malaria Branch, Division of Parasitic Diseases and Malaria, Center for Global Health, Centers for Disease Control and Prevention, Kisumu Kenya); Simon Kariuki (KEMRI); Aaron Samuels (Malaria Branch, Division of Parasitic Diseases and Malaria, Center for Global Health, Centers for Disease Control and Prevention, Kisumu Kenya)

Background: Decreases in malaria morbidity and mortality since 2000 have largely been attributed to insecticide-treated nets (ITNs). In western Kenya, where transmission is perennial and high, we modelled the effect of increased ITN ownership, use, and integrity on malaria prevalence to quantify the benefit of maintaining ITN indices at levels achieved after a July 2017 mass ITN distribution campaign.

Methods: We used malaria surveillance data from annual year-round household surveys among residents aged ≥1 month. During the first three months following the campaign, 16.3% of participants used damaged (holes larger than an adult fist) ITNs, 72.1% used 'good' ITNs, 0.4% used ITNs with unknown integrity (ITN not inspected), and 11.2% did not use ITNs. These values were set as the maintenance scenario. To estimate the malaria prevalence reduction if the maintence scenario was sustained, we compared adjusted observed monthly malaria prevalence rates, obtained using logistic regression (controlling for seasonality, rainfall, and ITN indices), to predicted monthly malaria prevalence rates in the maintenance scenario, obtained using the regression coefficients.

Results: From April 2015 to March 2020, 21,754 residents from 3,086 compounds were interviewed. The observed annualized malaria prevalence ranged from 27%–34%. 'Good', 'damaged' and no ITN use ranged from 42%–64%, 20%–35%, and 14%–24%, respectively. Sustaining the maintenance scenario resulted in a decrease in annual malaria prevalence of 1.5 percentage points (95% CI: 1.1–1.8 percentage points) from April 2015-July 2017 and 0.8 percentage points (95% CI: 0.4–1.2 percentage points) from August 2017-March 2020. Increased 'good' ITN use was associated with minimizing the malaria prevalence difference between the observed and maintence scenarios.

Conclusions: ITNs are critical for maintaining malaria burden reduction. Sustaining the maintenance scenario did not result in further malaria burden reduction from what has already been achieved primarily through ITN distribution campaigns and education.

Keywords: Malaria, Insecticide-Treated Net, Western Kenya

34.

PLASMODIUM FALCIPARUM HISTIDINE RICH PROTEIN-2 LEVELS IN BLOOD BUT NOT SALIVA AS A PREDICTOR OF PARASITE DENSITY AND CLINICAL MALARIA STATUS IN PATIENTS WITH ACUTE UNCOMPLICATED MALARIA IN CHULAIMBO, WESTERN KENYA

Authors: Ruth Awuor Omingo (Maseno University)*; Cyrus Ayieko (Maseno University); Patrick Onyango (Maseno University); Sydney Ogolla (KEMRI)

Background: Globally, malaria is the leading cause of death and economic burden. Diagnosis currently relies on microscopy and blood-based rapid diagnostic tests (RDTs). However, both methods are invasive, which increases the risk of accidental infection and is painful. Non-invasive approaches are thus required. Commonly used RDT targets include Plasmodium falciparum Histidine Rich Protein-2 (Pf.HRP-2) which is a parasite enzyme released into the host blood during clinical malaria infection and have been demonstrated in saliva though with inconsistent results. This pilot study detected and quantified the levels of Pf.HRP-2 antigens in blood and saliva, and determined their relationship with age, parasite density and clinical malaria status in a high malaria endemic zone of Western Kenya.

Methods: This was a cross-sectional study involving 30 children aged between (3.3-12.8) years and 6 adult participants aged between (19.3-66.1) years respectively, presenting with clinical malaria at Chulaimbo Sub- County hospital. Blood and saliva samples were collected at enrollment and repeat samples were collected 4-week post recovery. Malaria infection status and P. falciparum parasites density were determined by microscopy and levels of P. falciparum antigens in saliva and blood measured by ELISA. Generalized linear model was done to assess the relationship between the levels of P. falciparum antigen to parasite densities. Logistics regression model was used to determine the relationship between clinical malaria status and antigen levels. Correlation between levels of Pf. HRP-2 in blood and saliva were evaluated using Pearson's correlation.

Results: During clinical malaria, the levels of Pf.HRP-2 antigens were significantly higher compared to recovery period in both plasma (p= 0.000) and saliva (p=0.009). Pf.HRP-2 levels in plasma but not in saliva was a predictor of parasite density (F=10.048, p=0.003; F=0.900, p=0.350 respectively) when data was controlled for age. A significant association of Pf.HRP-2 levels with age of patient was observed for the plasma but not saliva (F=5.427, p=0.027; F=3.539, p=0.070 respectively). Furthermore, Pf.HRP-2 levels in plasma could accurately predict clinical malaria status (p=0.018) yet the levels in saliva could not (p=0.104). Finally, no significant association was observed between the levels of Pf.HRP-2 in plasma and saliva of individuals with acute malaria (r=-0.236, p=0.180).

Conclusion: Measurement of Pf.HRP-2 in saliva may not be a good proxy measure of infection in individuals with acute malaria.

Keywords: Invasive, Parasite density, endemic, Clinical malaria, Cross-sectional, Malaria infection status.

35.

VAR ACIDIC TERMINAL SEQUENCE (VARATS) SCREENING FOR SUB-PATENT MALARIA IN PERIPHERAL BLOOD OF WOMEN ATTENDING ANTENATAL CARE IN LAGOS, NIGERIA

Authors: Aminat Olamide Shokunbi (Instituto Politécnico Nacional- Centro de Biotecnología Genómica)*; Kolapo Oyebola (University of Lagos)

Background: In high malaria transmission settings, levels of acquired immunity are high and Plasmodium falciparum infection is usually asymptomatic even during pregnancy. Malaria arasites may be present in the blood of a pregnant woman, contributing to maternal anaemia even when rapid diagnostic test (RDT) and microscopy results are negative. To prevent malaria-related complications during pregnancy, it is important to adopt highly sensitive techniques for prompt detection of infections. In this study, we tested a molecular diagnostic tool targeting the var acidic terminal sequence (varATS) of the parasite genome for the detection of asymptomatic malaria in women attending antenatal care (ANC) in Lagos, Nigeria.

Methods: An active malaria screening was carried out among seemingly healthy pregnant women attending ANC. A semi-structured questionnaire was used to obtain socio-demographic profiles of the enrollees. Peripheral blood samples were collected for laboratory analysis and anaemic status of the patients was defined by haemoglobin concentration. P. falciparum infection was diagnosed using RDT and microscopy followed by molecular diagnosis using highly sensitive varATS polymerase chain reaction (PCR) to detect sub-microscopic infections.

Results: Among the 225 women screened for asymptomatic malaria infection, 155 (68.8%) were anaemic. Five (2.20%) RDT/microscopy positive samples were also varATS positive. However, varATS detected no additional infection. Previous history of malaria during pregnancy 118 (52.4%) represented a risk factor for asymptomatic carriage and anaemia 155(68.9%) was an important complication associated with asymptomatic malaria.

Conclusion: Our findings have revealed low prevalence of asymptomatic malaria among pregnant women in the study population and RDT/microscopy sensitivity gave comparable results with varATS quantitative PCR diagnosis.

Keywords: Pregnancy, varATS, Asymptomatic Malaria, Sub-microscopic infections, Anaemia

36.

MALARIA MORBIDITY IN CHILDREN LESS THAN FIVE YEARS FOLLOWING VACCINATION WITH RTS S VACCINE AT LIKINDU HEALTH CENTRE IN VIHIGA COUNTY.

Authors: Diana Omboko Andeyo (Likindu health center)*

Introduction: Despite WHO Recommendation that all suspected malaria cases be confirmed before treatment, malaria remains a major public health concern killing approximately 400,000 people a year mainly children under five in Sub-Saharan Africa. The RTS S vaccine targets the liver stage of the parasite life cycle and comprises three doses with a booster administered between ages 5 and 38 months. Following promising results of efficacy trial with estimated 30% reduction in severe malaria in infants, WHO recently recommended the inclusion this vaccine into national malaria prevention portfolios. To ensure its effectiveness, a study was done to evaluate the impact of

RTS S vaccine on malaria burden in children 0-3 years.

Methodology: A retrospective analysis of routine monthly health facility malaria data of children (under 3) who attend outpatient services at Likindu health centre and suspected to have malaria from March to October 2023 after the vaccine rollout were enrolled. Malaria vaccine data was obtained from the (MCH CWC) register of all doses administered during the study period. Questionnaire on use of nets was also incorporated during the study

Results: Out of 772 suspected malaria cases in under 3, 353(45.7%) cases were confirmed positive and a total of 753 vaccine doses (MV1-305, MV2- 264, MV3-184 And MV4 32) had been administered to 520 children during that period. The results were compared to 2022 data of the same period after mass net distribution in june 2021 where 2617 nets were distributed in 829 households and before the rollout of the vaccine at Likindu health centre. Out of 822 suspected cases in 2022, 392(47.6%)cases were confirmed positive.

Conclusion: There was a decrease by 1.9% in malaria severe cases and morbidity in children 0-3 years following rollout of RTS S vaccine. Therefore, combined efforts on community health education on acceptability of RTS S vaccine, use of LLIN and ITN will help reduce malaria morbidity by a greater percentage.

Recommendation: Complete doses of 4 MV in future will have a great impact on malaria elimination together with the use of LLIN and ITNS

Keywords: RTS S vaccine, Morbidity, LLINS, ITNs

37.

MALARIA TEST POSITIVITY RATES IN COMMUNITY SURVEILLANCE AS COMPARED TO HEALTH FACILITY SURVEILLANCE IN MALARIA ENDEMIC AREA RARIEDA SUB-COUNTY, WESTERN KENYA

Authors: Brian Seda (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Wycliffe Odongo (Malaria Branch, Division of Parasitic Diseases and Malaria, Center for Global Health, Centers for Disease Control and Prevention, Atlanta GA, USA); Towett Towett (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Kizito Obiet (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Victoria Seffren (Malaria Branch, Division of Parasitic Diseases and Malaria, Center for Global Health, Centers for Disease Control and Prevention, Atlanta GA, USA); Jonathan S Schultz (CDC-Kenya)*; Aaron Samuels (Malaria Branch, Center for Global Health, US Centers for Disease Control and Prevention, Kisumu, Kenya); Simon Kariuki (KEMRI); Feiko terKuile (Department of Clinical Sciences, Liverpool School of Tropical Medicine, Liverpool, UK); Julie Gutman (Malaria Branch, Division of Parasitic Diseases and Malaria, Center for Global Health, Centers for Disease Control and Prevention, Atlanta GA, USA); Titus Kwambai (Malaria Branch, Center for Global Health, US Centers for Disease Control and Prevention, Kisumu, Kenya)

Background: In malaria endemic western Kenya, community case management (CCM) for malaria is a key strategy to increase access to care and provide prompt diagnosis and treatment. However, there are few data assessing the proportion of malaria cases identified by community health volunteers (CHV) compared to facility out-patient departments (OPD) in our setting. In Kenya, CHVs are organized in community units (CUs), which consists of a number of villages and the health facilities that they are linked to. CHVs visit households with reported malaria symptoms, and test and treat them for malaria and other health conditions. These data are recorded in CHV Activity Registers (CHV-AR) which was digitized using ocular character recognition technology (ScanForm) to enhance quality, timeliness, and data use of information collected in this register.

Methods: We analyzed data collected between January 2021–December 2022 from 35 health facility OPD ScanForm registers (stratified by age to <5yrs, 5–14yrs and 15+yrs) and CHV-ARs from the corresponding 39 CUs covering 397 villages with a total population of about 128,926 people in Rarieda sub-county, western Kenya. We reviewed the number of persons tested for malaria and calculated test positivity rates (TPR).

Results: Overall, 229,511 malaria tests were performed, including 203,208 at OPD (5yrs=40,326, 5–14yrs=63,321, 15+yrs=99,435) and 26,598 in the community (<5yrs=7,770, 5–14yrs= 9,453, and 15+yrs=9,080)The overall TPR was 56.4% at OPD (<5yrs=51.9%, 5–14yrs=69.3%, 15+yrs=48.1%) and 81.1% in the community (<5yrs=85.3%, 5–14yrs=82.5%, 15+yrs=76.0%). Community cases accounted for 11.5% of all malaria tests but 16.1% of all positive cases, highlighting the high TPR in the community. Appropriate provision of artemisinin-based combination therapy for test positive cases was 92.4% at OPD and 95.1% at the community. **Conclusions:** Despite significant utilization of health facilities, the burden of symptomatic malaria in the community remains high. Our data suggest that CHVs appropriately follow testing and treatment guidelines and reach a population in need. Further support for the CCM should be considered to increase the reach of CHVs.

Keywords: Malaria, community health volunteers (CHV), community case management (CCM)

38.

IMPLEMENTING HIGH QUALITY COMMUNITY CASE MANAGEMENT & DATA REPORTING: LESSONS FROM THE FIELD IN SIAYA, WESTERN KENYA

Authors: Kizito Obiet (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Wycliff Odongo (Malaria Branch, Division of Parasitic Diseases and Malaria, Center for Global Health, Centers for Disease Control and Prevention, Atlanta GA, USA); Brian Seda (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Victoria Seffren (Malaria Branch, Division of Parasitic Diseases and Malaria, Center for Global Health, Centers for Disease Control and Prevention, Atlanta GA, USA); Oliver Towett (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Jonathan S Schultz (CDC-Kenya)*; Simon Kariuki (KEMRI); Feiko terKuile (Department of Clinical Sciences, Liverpool School of Tropical Medicine, Liverpool, UK); Titus Kwambai (Malaria Branch, Center for Global Health, US Centers for Disease Control and Prevention, Kisumu, Kenya); Julie Gutman (Malaria Branch, Division of Parasitic Diseases and Malaria, Center for Global Health, Centers for Disease Control and Prevention, Atlanta GA, USA)

Background: Malaria is still a major cause of mortality and morbidity in western Kenya, despite implementation of recommended malaria control interventions. Community case management of malaria (CCM), implemented by Community Health Volunteers (CHVs), is a key strategy for timely identification of fever cases and management. However, inadequate data capture tools, training and supervision affect the quality of data.

Methods: We aimed to track access to diagnostics, treatment, and referral services offered by CHVs using scannable registers to enhance accurate data capture and reporting.

Results: In 2021, we deployed scannable registers in 2 sub-counties, in Siaya County, western Kenya. 914 CHVs covering 975 villages in 89 community units (CU) attached to 95 health facilities were trained on the use of scannable registers and senior MoH staff trained on supervision and data quality review, including summary dashboards. 34 CUs up from 22 CUs in Alego Usonga began reporting during the implementation period (out of 50). In Rarieda, which has received support since 2021, all CUs are reporting (n= 39). There was an increase in the number of malaria positive cases reported by CHVs, from 8653 in 2021 to 12955 in 2022. While cases seen at the health facility decreased (from 61370 to 51842), the proportion of overall cases seen by a CHV increased from 12.4% in 2021 to 20%. More frequent (Monthly) data reviews at CU level as opposed to quarterly at sub-county level improved reporting timeliness.

Conclusions: We uncovered gaps in data collection, review, tallying and reporting. Delayed reports prevented action on critical interventions e.g., restocking malaria testing and treatment commodities. Multiple registers collecting similar indicators presented challenges for CHVs. Therefore, streamlining existing data tools and ensuring partner coordination could reduce CHV workload and improve efficiency. Routine data reviews provide opportunities for supportive supervision and could improve quality of care and data. Integrating and automating tallies from CHV line-listed data into DHIS2 could enhance data quality and facilitate analyses for more targeted malaria control interventions.

Keywords: Malaria, Community case management (CCM), Community Health Volunteers (CHVs), Western Kenya

39.

ASSESSMENT OF GENETIC DIVERSITY OF P. FALCIPARUM CHONDROITIN SULFATE A LIGAND; A PREGNANCY-ASSOCIATED MALARIA VACCINE ANTIGEN

Authors: Rotich K Alex (Mt.Kenya University)*; Bernard Kanoi (Mt. Kenya University); Jesse Gitaka (Mount Kenya University); Kevin Mbogo (JKUAT)

Plasmodium falciparum malaria poses a substantial threat to global health, particularly affecting vulnerable populations such as children and pregnant women. Pregnancy-associated malaria (PAM) is primarily driven by the sequestration of infected erythrocytes in deep vascular beds, facilitated by parasite-derived ligands like VAR2CSA. Developing interventions against PAM requires a comprehensive understanding of these mechanisms. This study focused on the genetic analysis of CSA-L, a ligand associated with sequestration, to explore its potential as a vaccine candidate.

Methods: Sampling, DNA preparation, and whole-genome sequencing were conducted on archived whole blood samples from patients enrolled in a drug resistance surveillance study on selected islands in Lake Victoria and a coastal mainland area. The study spanned from July 2014 to July 2016, with a total of 26 samples.

Read mapping and coverage involved aligning sequence reads against the Plasmodium falciparum 3D7 reference genome using the Burrows-Wheeler Alignment tool (BWA). Subsequent processing with Samtools and Picard removed duplicates. SNPs were called using the Genome Analysis Toolkit (GATK) HaplotypeCaller. Variant analysis utilized the VCF file containing quality-tested samples.

Functional annotation of high-quality SNPs in CSA-L was performed using the SNPEFF tool, and ARTEMIS software was employed for further analysis. Multiple sequence alignment and translation of nucleotide sequences to amino acid sequences were conducted using MUSCLE in MEGA 11.

Results: Genetic analysis of CSA-L revealed conservation, supported by Tajima's D of -1.73363 and Pi of 0.00033. Comparative analysis with Var2csa and Pfadsl genes demonstrated CSA-L's higher conservation. Fu & Li's tests indicated significant values for CSA-L, suggesting potential selective pressure.

Discussion: The observed negative Tajima's D, Fu and Li's D* and Fu and Li's F* statistics from the Homabay population indicated an excess of rare variants and do not suggest balancing selection (Ndwiga et. al 2021). Genes with a significant negative Tajima's D value indicate that the parasites population has a limited potential to retain polymorphisms, especially Csa-l and Pfadsl gene (Amambua et. al 2012).

These findings are consistent with previous studies of P. falciparum in the African population, which showed a majority of genes having a negative Tajima's D value, suggesting a historical parasite population expansion event (Ocholla et. al 2000)

Conclusion: The observed genetic conservation of CSA-L underscores its significance, urging further investigation into its functional relevance as a potential vaccine candidate. Understanding the genetic dynamics of ligands associated with sequestration is crucial for developing targeted interventions against pregnancy-associated malaria.

Keywords: CSA-L, Plasmodium falciparum, VAR2CSA , Pregnancy malaria

40.

ASSESSMENT OF REPEATED MALARIA INFECTIONS IN SIAYA COUNTY, JUNE 2021-MAY 2022

Authors: Cynthia A Musumba (Field Epidemiology and Laboratory Training Programme)*; Githinji Geoffrey (MOH KENYA - FELTP); Winfred Wanjiku (MOH KENYA-FELTP); Fredrick Odhiambo (MOH KENYA-FELTP); Maurice O Owiny (Kenya FELTP)

Cynthia Musumba 1*, Geoffrey Githinji 1 Winfred Wanjiku 1 Fredrick Odhiambo 1, Maurice Owiny 1, Elvis Oyugi 2

1Field Epidemiology and Laboratory Training Program

2Division of National Malaria Program

*Corresponding author email: musumbacynthia@gmail.com

Background: Repeat Malaria cases are defined as laboratory-confirmed infections occurring after seven days of treatment. Kenya's overall malaria prevalence among children aged six months to 14 years was 6%, while Siaya was 28.8%, Busia 38.5%, and Kisumu 15.6% in the 2020 malaria indicator survey. There is limited data on the prevalence of repeat cases. This investigation aimed at evaluating the characteristics of repeat cases.

Methods: Retrospective record reviews were done in select hospitals in Siaya, sampled based on high incidence. Patient records in the outpatient, laboratory and inpatient registers were abstracted into MS Excel including date of visit, age, sex, residence, and malaria tests. Categorical data were analyzed using frequencies and percentages. Continuous variables were analyzed using the median and interquartile range.

Results: A total 7903 cases were listed. Children under 15 years old contributed 64% (5103), females 54% (4277). Malaria was majorly diagnosed by microscopy at 73% (4277). Alego Usonga contributed 58% (n=4599), Bondo 29% (n=2295) of the cases. Repeat cases were 514 representing 6.5% of total cases. Children under 15 were 76% (395), and females 50.58% (260). Alego Usonga contributed 74% (n=383) while Bondo contributed 12% (n=66). The duration between the first and second malaria incidence exceeded 28 days in 78% (400) of repeat cases, while time between second to third infections exceeded 28 days in 66% (76). Repeat malaria diagnoses in less than seven days were 6%(31) in the second visit, 9%(8) in the third visit.

Conclusion: Repeat malaria cases represented 6.5% of the total cases, depicting similar distribution in person, diagnosis method and place. Children < 15 years and females contributed majority of the repeat cases. The burden could be underestimated as lower-level facilities were not investigated. There is need to conduct further research on specific risk factors for repeat cases and employ both community and facility-based studies.

Keywords: Malaria, Incidence, prevalence

41.

IDENTIFICATION OF CONSERVED CROSS-SPECIES B-CELL LINEAR EPITOPES IN HUMAN MALARIA: A SUBTRACTIVE PROTEOMICS AND IMMUNO-INFORMATICS APPROACH TARGETING MEROZOITE STAGE PROTEINS

Authors: Sebastian Musundi (Mount Kenya University)*; Jesse Gitaka (Mount Kenya University); Bernard Kanoi (Mount Kenya University)

Background: Human malaria, caused by five Plasmodium species (P. falciparum, P. vivax, P. malariae, P. ovale, and P. knowlesi), remains a significant global health burden. While most interventions target P. falciparum, the species associated with high mortality rates and severe clinical symptoms, non-falciparum species exhibit different transmission dynamics, remain hugely neglected, and pose a significant challenge to malaria elimination efforts. Recent studies have reported the presence of antigens associated with cross-protective immunity, which can potentially disrupt the transmission of various Plasmodium species. With the sequencing of the Plasmodium genome and the development of immunoinformatic tools, in this study, we sought to exploit the evolutionary history of Plasmodium species to identify conserved cross-species B-cell linear epitopes in merozoite proteins.

Method: We retrieved Plasmodium proteomes associated with human malaria and applied a subtractive proteomics approach focusing on merozoite stage proteins. Bepipred 2.0 and Epidope were used to predict B-cell linear epitopes using P. falciparum as the reference species. The predictions were further compared against human and non-falciparum databases and their antigenicity, toxicity, and allergenicity assessed. Subsequently, epitope conservation was carried out using locally sequenced isolates from a malaria-endemic region in western Kenya (n=27) and Kenyan isolates from MalariaGEN version 6 (n=131). Finally, physiochemical characteristics and tertiary structure of the B-cell linear epitopes were determined.

Results: The analysis revealed eight epitopes that showed high similarity (70-100%) between falciparum and non-falciparum species. These epitopes were highly conserved when assessed across local isolates and those from the MalariaGEN database and showed desirable physiochemical properties.

Conclusion: Our results show the presence of conserved cross-species B-cell linear epitopes that could aid in targeting multiple Plasmodium species. Nevertheless, validating their efficacy in-vitro and in-vivo experimentally is essential.

Keywords: Conserved cross-species, Plasmodium falciparum, subtractive proteomics

42.

ATTRACTIVE TARGETED SUGAR BAITS FOR MALARIA CONTROL IN WESTERN KENYA (ATSB-KENYA): COHORT STUDY RECRUITMENT

Authors: Alice Kamau (KEMRI-Centre for Global Health Research)*; Kizito Obiet (KEMRI-Centre for Global Health Research); Caroline Ogwang (KEMRI-Centre for Global Health Research); Brian Seda (KEMRI-Centre for Global Health Research); Daniel McDermott (Liverpool School of Tropical Medicine); Wycliffe Odongo (CDC); Julie Gutman (CDC); Jonathan S Schultz (CDC-Kenya); Frank Aduwo (KEMRI-Centre for Global Health Research); Mercy Terer (KEMRI-CGHR); Maia Lesosky (Imperial College London); Martin Donnelly (Liverpool School of Tropical Medicine); Simon Kariuki (KEMRI); Aaron Samuels (CDC-Kenya); Feiko ter Kuile (Liverpool School of Tropical Medicine); Sarah Staedke (Liverpool School of Tropical Medicine)

Background: In areas of intense malaria transmission, conventional vector control tools including long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS) are challenged by widespread insecticide resistance and dynamic vector behaviours. Attractive Targeted Sugar Baits (ATSBs), A4-sized panels filled with thickened fruit syrup laced with a neonicotinoid insecticide (dinotefuran), are a novel outdoor intervention designed to attract and kill mosquitoes. We are conducting a Phase III open-label, cluster-randomised controlled trial to evaluate the impact of combining ATSBs with LLINs, compared to LLINs alone, on malaria incidence in a cohort of children residing in Siaya County, western Kenya. Here, we describe the characteristics of children, households, and factors associated with parasitaemia at enrolment.

Methods: Children aged 1 to <15 years old were randomly selected from a census database for recruitment. Residents of households within study clusters who met all selection criteria were enrolled. At enrolment, a fingerpick blood sample was obtained from all consenting participants for a rapid diagnostic test (RDT) for malaria. Households of participating children were surveyed by trained staff. To examine risk factors for malaria prevalence at enrolment, a generalised linear mixed model was used.

Results: Between August 2021 and April 2023, 3,658 children aged 1 to < 15 years were enrolled. The median age of participants was 8.8 years (IQR: 5.4, 11.9), and 1,745 (48%) were female. LLIN use the prior evening was more commonly reported in children aged 1-4 years (95%) than in those aged 5-15 years (83%). A household survey was carried out for 3,535 (97%) participants, including 3,297 households. Only 8% of households were classified as 'improved', as most had open eaves, or were constructed with traditional materials. Nearly all households owned at least one LLIN (99%), but only half (54%) were adequately covered with at least one LLIN for every 2 residents. Of 1,687 children enrolled prior to delivery of ATSB, 874 (52%) were RDT positive. In a multivariate analysis, factors associated with parasitaemia at baseline included house construction (less improved vs improved, adjusted odds ratio [aOR]=2.2; 95% CI: 1.5-3.3; $p < 0.001$), household location (Alego-Usonga sub-county vs Rarieda, aOR=3.2; 95% CI: 2.2-4.9; $p < 0.001$), older age (5 to <15 years vs 1-4 years, aOR=1.6; 95% CI: 1.2-2.1; $p = 0.001$), and lower socioeconomic status (poor vs least poor, aOR=1.6; 95% CI: 1.2-2.1; $p = 0.004$).

Conclusion: The burden of malaria in western Kenya remains high. Although most households owned a LLIN, adequate LLIN coverage was low. Older children, those residing in Alego Usonga, and those with lower socioeconomic status or traditionally constructed households were more likely to test positive by RDT. Additional tools, such as ATSBs, are needed to control malaria in this area.

Keywords: Malaria, ATSB, LLINs, western Kenya

43.

DESCRIBING BIRTH OUTCOME IN WOMEN WITH MALARIA IN PREGNANCY IN MATUNGU SUB- COUNTY, JANUARY 2019 TO DECEMBER 2021

Authors: lydiakhalayi M Khalayi (MOH)*; Faustina Sakari (County Government of Kakamega); Bridget Wesonga (MOH/FELTP); Edith Akinyi (Matungu Sub-county, Kakamega)

Background: Malaria in pregnancy adversely affects both the mother and the newborn, elevating the risk of poor birth outcomes, including low birth weight, miscarriage, intrauterine fetal death (IUFD), and spontaneous abortions. World Health Organization (WHO) recommends administering ≥ 3 doses of Sulfadoxine-pyrimethamine (SP) for intermittent preventive treatment and the use of Long-Lasting Insecticide Treated Nets (LLINs) in regions with moderate to high transmission. This study examined the birth outcomes of pregnant women with malaria in pregnancy (MiP) at Matungu sub-county Hospital.

Methods: We abstracted data from in-patient files of pregnant women diagnosed with malaria from January 2019 to December 2012. We categorized variables into socio-demographic and clinical aspects. We analyzed continuous variables via means and medians while categorical ones through proportions and frequencies. We assessed data completeness using the K-FELTP data audit tool.

Results: We abstracted 417 medical records. The mean birth weight was 3190 (±1770.0) grams, gestation age 36.8 (±3.94) weeks and the mean age of the mother 23.4 (±5.8) years. Live births accounted for 94% (385), Spontaneous abortion was 2.3% (8), Miscarriage was 1.3% (5), Stillbirth was 0.8% (3), and IUFD was 0.3% (2). We established that of those who did not receive preventive measures during the Antenatal Clinic:2% (5) did not attend, 6% (23) did not receive LLIN, and 8% (16) did not receive IPT. Three variables did not meet the lower threshold required in reporting: Occupation, level of education and number of ANC attended.

Conclusion: The study emphasizes active adherence to antenatal care and targeted interventions for malaria prevention, stressing the necessity of thorough documentation. The study recommends targeted education to enhance ANC attendance, promote preventive measures and improve data capture. The study further suggests an investigation into the impact of preventive measures, examining factors influencing attendance and proposing solutions for enhanced compliance during antenatal clinics.

Keywords: Malaria, Pregnant Women, Birth Weight, Live Birth

44.

ASSESSMENT OF ANTIMALARIAL DRUG SUSCEPTIBILITY PATTERNS IN KISUMU AND MARIGAT BETWEEN 2018 AND 2023 BASED ON IN VITRO TESTING, GENOMIC ANALYSES AND PASSIVE MONITORING OF TREATMENT OUTCOMES

Authors: Doris Njoroge

Background: Malaria remains a major public health threat globally affecting 241 million people annually. Persistent malaria burden has been attributed to rapid emergence and spread of parasite resistance to policy recommended drugs. Consequently, timeliness of detecting drug resistance in diverse transmission regions is critical. This established susceptibility of Plasmodium falciparum parasites from Kisumu and Marigat between 2018 and 2023 using in vitro testing, genomic analyses and passive monitoring of treatment outcomes. **Methods:** A total of 649 consenting individuals aged 6 months and over, presenting with uncomplicated malaria were treated with Coartem® according to weight band and monitored on Day 7 to assess treatment outcomes. Up to 5mL whole blood samples collected from each individual prior to start of medication were latter tested for in vitro susceptibility to 14 antimalarial drugs. Each sample was tested for species composition, single nucleotide polymorphisms (SNPs) in drug resistance genes, and presence of residual parasitemia on day seven using genomic analyses techniques. **Results:** 475/ 649 individuals comprising 385 from Kombewa and 90 from Marigat tested positive for malaria by polymerase chain reaction (PCR) assay. In vitro susceptibility showed mean ±standard deviation values of 5.64 ± 23.78ng/ml for chloroquine, 13.95±41.16 ng/ml for quinine, 1.34±3.35 ng/ml for artemether and 40.0±38.3 ng/ml for lumefantrine. 37% of the infections contained P. falciparum single species infection while 37% were contained P. falciparum species alongside other nonfalciparum species as multiple species infections. SNPs analyses showed three nonsynonymous mutation Pfk13 gene V568G, T508N and N554S in two samples and 41% mutation in PfMDR1-Y184F and Pfcrt A76C showed 33% mutation with Pfcrt K76T were wild-type for the entire study period for Marigat samples. None of the day 7 visit samples tested positive for malaria by molecular diagnosis suggesting that all infections resolved after treatment with coartem®. **Conclusion:** Continuous monitoring of changing parasite susceptibility by in vitro and molecular methods is essential for early detection of resistance

Keywords: Malaria, susceptibility, parasite

45.

ASSOCIATION BETWEEN BEDNET USE AND MALARIA PREVALENCE BY AGE GROUP IN RARIEDA SUB-COUNTY, WESTERN KENYA (2015-2020)

Authors: Oliver Towett (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Victoria Seffren (Malaria Branch, Division of Parasitic Diseases and Malaria, U.S. Centers for Disease Control and Prevention, Atlanta, GA); Brian Seda (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Kelvin Onoka (Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya); Julie Gutman (Malaria Branch, Division of Parasitic Diseases and Malaria, U.S. Centers for Disease Control and Prevention, Atlanta, GA); Jonathan S Schultz (CDC-Kenya)*; Simon Kariuki (KEMRI); Feiko terKuile (Department of Clinical Sciences, Liverpool School of Tropical Medicine, Liverpool, UK); Aaron Samuels (Malaria Branch, Center for Global Health, US Centers for Disease Control and Prevention, Kisumu, Kenya); Titus Kwambai (Malaria Branch, Center for Global Health, US Centers for Disease Control and Prevention, Kisumu, Kenya)

Malaria remains a leading cause of illness in western Kenya, particularly among school-aged children (5–14yrs). Identifying whether lack of insecticide-treated bednet (ITN) use by this age group is a factor driving high prevalence is important to guide targeted public health interventions.

From April 2015–March 2020, year-round household surveys were conducted in Rarieda sub-county to assess malaria prevalence and ITN use. An average of 1,330 households (HH) were randomly selected to be surveyed each year. A questionnaire was administered to each HH member (or caregiver) to collect data on sleeping structure characteristics, ITN ownership and use, and self-reported fever in the past 2 weeks. Participants were tested with a pLDH/HRP2-based malaria rapid diagnostic test (RDT) irrespective of the presence of fever. Prevalence ratios were obtained by modified Poisson regression.

Overall, 21,837 questionnaires and malaria tests were administered in 6,419 enrolled HH. ITN access (≥1 ITN/2 people per HH) was 41.2%. Reported ITN use the night before the survey was 81.0%: 87.5% (<5yrs), 74.7% (5–14yrs), 83.1% (15+yrs). Malaria prevalence was 29.7%: 32.0% in <5yrs, 46.1% in 5–14yrs, 18.8% in 15+yrs and 19.0% of cases reported fever in the past 2 weeks (25.1% in <5yrs; 19.8% in 5–14yrs; 15.8% in 15+yrs). Not sleeping under an ITN the night before the survey was associated with higher malaria risk (41.6% vs 27.1%, PR=1.5, 95% CI 1.4 – 1.6, p=0.001). This was significant (p=0.001) in all age groups (<5yrs: PR: 1.6 [95% CI: 1.3 – 1.7];

5–14yrs: PR: 1.2 [95% CI: 1.1 – 1.3]; 15+yrs: PR: 1.2 [95% CI: 1.1 – 1.3]). Fever in the past 2 weeks was associated with higher RDT positivity versus those without a fever (42.9% vs 27.7%, P=1.6, 95% CI 1.5 – 1.6, p<0.001) in all age groups (<5yrs: PR: 1.7 [95% CI: 1.5 – 1.9]; 5–14yrs: PR: 1.5 [95% CI: 1.4 – 1.6]; 15+yrs: PR: 1.4 [95% CI: 1.3 – 1.6]).

ITN access remains well below globally accepted targets in western Kenya. Non-use of ITNs was associated with malaria among all ages. Children 5–14yrs had the highest malaria prevalence and reported the lowest ITN use. Improving ITN access and use could help to reduce malaria prevalence in this age group.

Keywords: Malaria, insecticide-treated bednet (ITN), rapid diagnostic test (RDT)

POSTER SESSION 5: SCREEN 5-VECTOR BIOLOGY

46.

MOSQUITO SPECIES DIVERSITY AND HUMAN BITE RATES AS A MEASURE OF RISK OF DISEASE EMERGENCE, MOMBASA, KENYA

Authors: Francis M Musili (KEMRI)*

Francis Mulwa1, Edith Limbaso1, James Mutisya1, Hellen Koka1, Samuel Owaka1, Langat Solomon1, Edith Koskei1, Albert Nyunja1, Victor Ofula1, Betty Chelangat1, Konongoi Limbaso1, Rosemary Sang1, Joel Lutomiah1,1Centre for Virus Research, KEMRI, Kenya

Background: Mosquito-borne viral infections are spread globally driven by, environmental, human and socio-economic factors including international travel. The presence of vectors due to anthropogenic activities facilitate emergence of mosquito-borne diseases due to human-mosquito interactions. Naïve human populations such as migrating populations or tourists with no previous exposure to exotic diseases are constantly at high risk of infection with vector-borne disease agents. The present study was conducted on an island in Mombasa County, a global tourist destination at risk of emergence of multiple vector-borne diseases**.**

Methods: Mosquitoes were collected using Co2 baited BG sentinel traps at night, during the long rainy season in Mombasa County. Systematic sampling approach was used to directly measure attractiveness of Ae. aegypti to human odors using human landing collection (HLC). The mosquito's species were identified morphologically. The data was analyzed in Microsoft excel and R Statistics software

Results: A total of 4185 mosquitoes were collected by HLC, Aedes aegypti (n=2216; 53%) was the most abundant, followed by Ae. vittatus (n=1438; 33%) and other mosquito species (n=531; 22%). For the anthropogenic vectors Ae. aegypti mosquitoes had a 3.2 bite per person per hour (b/p/h) followed by Ae. vittatus (2.1 b/p/h), Cx. pipiens (0.4 b/p/h) and other species (0.3 b/p/h). From the BG sentinel traps, a total of 7250 mosquitoes were collected comprising of five genera (Aedes, Culex, Anopheles, Eretmophidites and Mansonia). Culex pipiens (n=3395; 47%) were most abundant followed by Ae. vittatus (n=1551; 22%) and Ae. aegypti (n=1509; 21%).

Conclusions: The County is at a significant risk of disease outbreaks due to the abundanceof dengue and chikungunya vectors with a strong propensity to bite people. By aiding in spillover transmission events, vectors that are known to display opportunistic feeding may increase the risk of human exposure to zoonotic infections. In order to reduce the risk of transmission, preventative and control strategies for vector-borne diseases including dengue, chikungunya, and malaria should take into account generated data on species composition and human bite rates.

Keywords: Keywords: Aedes aegypti, human biting rate, abundance, mosquito species

47.

VECTOR COMPETENCE OF Aedes (STEGOMYIA) SPECIES FOR TRANSMISSION OF YELLOW FEVER VIRUS IN KERIO VALLEY, BARINGO COUNTY AND NGURUMAN, KAJIADO COUNTY, KENYA

Authors: Cynthia Chelangat Ruttoh (International Centre of Insect Physiology and Ecology)*; Edith E.L Chepkorir (Kenya Medical Research Institute); Sepha Mabeya (Jomo Kenyatta University of Agriculture and Technology); David P. Tchouassi (International Centre of Insect Physiology and Ecology); Rosemary Sang (International Centre of Insect Physiology and Ecology)

Background: Yellow fever (yf) constitutes a public health threat. Over the past decade, frequent outbreaks of the disease have been reported in different parts of the globe especially in Africa, despite the availability of an efficacious vaccine to protect humans. A recent YF outbreak in Isiolo County (2022) after a lull of 30 years since the 1992/93 outbreak in Kerio Valley, is indicative of active circulation of the causative virus, yf virus. Although spread of the virus has been associated with Aedes (Stegomyia) mosquitoes, the specific driving vectors in different ecological areas remains poorly elucidated.

Objective/Aim: To determine the vector competence of selected Aedes (Stegomyia) species in transmitting yellow fever virus in the dryland ecosystems of Kerio Valley and Nguruman.

Methodology: An experimental study design was conducted and the minimum sample size for YFV was 100 for Aedes agypti per study site. Other Aedes (Stegomyia) species were incorporated after blood feeding since they can't be reared in the laboratory. Mosquito eggs collected using ovicups in both areas during the short rain seasons between February 2022 and May 2023, were reared to adults in KEMRI BSL-2 insectary. Adult females (3-5 D old) were identified to species and orally infected with an infectious blood meal of the virus (East African YFV genotype) using a Hemotek membrane feeder. Subsequently on day 7, 14 and 21 post infection, the body (midgut infection),

legs (disseminated infection) and saliva (transmission) of the mosquito were collected and analysed for virus presence by cell culture. Positive bodies, legs and saliva were subjected also to plaque assay to determine the virus titre. Data was recorded and analysis done using Microsoft Excel.

Results: Low midgut infection was observed for Ae. aegypti both in Kerio Valley (2.27%, n=88), and Nguruman (1.39%, n=144). Similar infection in the midgut was evident among Aedes simpsoni s.l. in Kerio Valley (33.3%, n=3), and Aedes metallicus in Kerio Valley (6.3%, n=16) and Nguruman, (0.9%, n=109). Aedes chausseri sampled in Kerio Valley did not support infection in the midgut. Only one, Ae. aegypti from Kerio Valley had disseminated infection (50%,1/2) but with no evidence of transmission in the saliva.

Conclusion: These findings show that both Nguruman and Kerio Valley mosquitoes appear to be refractory for yellow fever, except for Ae. aegypti from Kerio Valley that was able to disseminate the virus. This confers a potential risk for resurgence of sylvatic YFV in Kenya. This could be due to several factors such as temperature, humidity, mosquito immunity, mosquito genetics, tissue barriers associated with midgut and salivary glands. Further research, including increasing the sample size, ongoing surveillance of species diversity and vector density, and subsequent vector competence investigations, is required to guide policymakers on the appropriate vector management strategies for YFV.

Keywords: Yellow fever, vector competence, Aedes (Stegomyia), dryland ecosystems

48.

DETECTION AND CHARACTERIZATION OF NEGEVIRUSES ISOLATED FROM MOSQUITOES IN KENYA

Authors: Janet M Majanja (Kenya Medical Research Institute)*; Fredrick Eyase (Kenya Medical Research Institute); Edward Muge (Department of Biochemistry, University of Nairobi); Solomon K Langat (Kenya Medical Research Institute (KEMRI)); Rosemary Sang (International Centre of Insect Physiology and Ecology (ICIPE)); Wallace Bulimo (Kenya Medical Research Institute)

Background: Mosquitoes are important vectors of arboviruses. While research primarily focuses on mosquito-borne viruses affecting human and animal health, recent discoveries have revealed insect-specific viruses (ISVs) that replicate exclusively in insects. Next generation sequencing (NGS) and bioinformatics have facilitated the discovery of novel viruses necessitating creation of the Negevirus taxon. Negeviruses are genetically related to plant-infecting viruses of Cilevirus, Blunervirus and Higrevirus genera. The aim of this study was to identify and characterize unknown viruses from archived mosquito isolates.

Methods: Archived virus isolates were obtained from the Kenya Medical Research Institute's Viral Hemorrhagic Fever laboratory repository. These were concurrently inoculated in Aedes albopictus (C6/36) and African Green Monkey kidney cells (Vero). Daily monitoring for cytopathic effect (CPE) was conducted for up to 14 days. Viral RNA was extracted from isolate filtrate and utilized in library preparation using the Illumina Truseq stranded mRNA kit (Illumina, USA). Sequencing was performed on an Illumina MiSeq platform. De novo assembly was achieved using MEGAHIT v0.1 and contigs matched against the NCBI non-redundant nucleotide database using BLASTn. Open reading frames (ORFs) and conserved protein domains were identified using bioinformatics. A phylogenetic tree was constructed based on ORF1 gene, aligned with other Negeviruses available in GenBank.

Results: Nine samples previously isolated from Culex, Mansonia and Aedes mosquito pools exhibited CPE in C636 cells but not Vero cells. These samples yielded 10 genomic sequences designated as Negeviruses. Five genomes resembled Dezidougou virus strain 8345 with nucleotide identities ranging from 73.6 -74.6% and two were similar to Dezidougou virus strain DEZI/Aedes (74.4% identity). The other three genomes shared 87.3% nucleotide sequence identity with Daeseongdong virus strain 8345. Conserved protein domains and ORFs corresponded to those in previously described negeviruses, namely ORF1 (polymerase), ORF2 (glycoproteins) and ORF3 (transmembrane proteins). Phylogenetic analysis grouped Kenyan Dezidougou strains with other Dezidougou strains in Sandewavirus clade. Daeseongdong viruses formed a monophyletic cluster with a German strain of Daeseongdong within the Nelorpivirus clade.

Conclusion: This study identifies Dezidougou and Daeseongdong negeviruses in Kenya for the first time thus underscoring the ubiquity of ISVs across diverse mosquito species. The genetic relationship between negeviruses and plant viruses emphasizes the need to study their evolution as potential sources of emerging viruses. ISVs are being explored as a biological control of arboviruses. Identifying these viruses, their diversity and hosts is an initial step in understanding their roles and implications.

Keywords: Negevirus, Dezidougou virus, Daeseongdong virus

49.

CHILDHOOD TUBERCULOSIS AND FACTORS ASSOCIATED WITH FAVOURABLE TREATMENT OUTCOMES IN NYERI COUNTY, KENYA 2017-2022.

Authors: Grace M Kaluai (Ministry of Health-Nyeri County)*; David Waweru (Ministry of Health-Muranga County); Maria Nunga (KenyaFELTP)

Background: Paediatric tuberculosis (TB) is a leading cause of morbidity and mortality among children. Varied treatment outcomes have been reported in Sub-Saharan Africa with few studies in Kenya particularly in rural settings. Nyeri county has a high TB case notification rate with 22% representation of childhood TB above the 9% national target in year 2022. We aimed to determine treatment outcomes of paediatric TB cases in Nyeri county and identify factors associated with favourable treatment outcomes.

Methods: Retrospective records review of all paediatric (children<15years) data in Nyeri County on the national tuberculosis registry from 2017 through 2022. Sampling was exhaustive with inclusion and exclusion criteria applied. Excel data abstraction tool was used. Socio-demographic and clinical variables were collected. Treatment outcomes were classified as favorable (cure/treatment complete) or unfavorable (failure/loss to follow up-LTFU/death). Data were cleaned in MS-Excel 2016 exported into Epi Info 7.2 for descriptive and analytic analysis. The test of association between outcome and predictors was prevalence odds ratios(OR) for bivariate analysis.

Results: A total of 1257 records were reviewed, males were 56% (698/1257), median age 1.75 years; IQR (1.08-4) and highest proportion of cases 56% (703/1257) from Nyeri municipality. Pulmonary TB cases accounted for 93% (1163/1257) while extra-pulmonary TB among children<5 years was 55% (52/94). The overall treatment success/favourable treatment outcome was 90%(Cured [3.1%, 39] and treatment complete [87%, 1095]). The unfavourable treatment outcomes were (death [4.9%, 61], LTFU [4.9%, 61]and treatment failure [0.1%, 1]). Children <5years had the highest mortality 85% (52/61) with 51% (31/61) of deaths being malnourished. Factors associated with favourable treatment outcomes were normal nutritional status (OR=2.66, CI:1.69,4.18), absence of comorbidity (OR=3.54, CI:2.05,6.11) and HIV negative status (OR=2.85, CI:1.55,5.23).

Conclusion: Despite treatment success being above the national target, targeted public health interventions towards children <5years and those vulnerable are impeative to further reduce TB related mortality.

Keywords: Childhood tuberculosis, Treatment outcomes, Rural setting

50.

HEALTH CARE WORKER RELATED FACTORS ASSOCIATED WITH TUBERCULOSIS TREATMENT NON-ADHERENCE AMONG PATIENTS IN KISUMU EAST SUB-COUNTY, KISUMU KENYA

Authors: Marlyn A. Ochieng (Jomo Kenyatta University of Agriculture and Technology)*; Jackline Nyaberi (Jomo Kenyatta University of Agriculture and Technology); Susan Mambo (Jomo Kenyatta University of Agriculture and Technology); Charles Wafula (Great Lakes University of Kisumu)

Background: Tuberculosis (TB) is a global public health challenge. Sub-Saharan Africa (SSA) contributes 23% of global TB cases while Kenya is ranked among 30 high TB burden countries globally. Treatment non-adherence poses significant risks to health outcomes and impedes the health system's efficiency. Kenya adopted interventions such as Directly Observed Therapy, yet still reports 35% TB treatment non-adherence rates. Treatment non-adherence is among factors curtailing progress toward the end TB strategy under SDG 3.3. Health Care Workers (HCWs) link the population to health services yet little is known about their influence on patients' TB treatment non-adherence in Kenya. This study aimed at determining HCW-related factors associated with TB treatment non-adherence among patients in Kisumu East Sub-County.

Methods: This was a hospital-based analytical cross-sectional mixed-method study. Quantitative data on treatment adherence and HCW-related factors was obtained using a semi-structured questionnaire from a census of 102 consenting eligible TB patients in Kisumu East Sub-county while qualitative data on how HCW-related factors influence treatment adherence was obtained from 12 purposively selected HCWs by rank using a KII guide. Treatment adherence was measured using Morisky Medication Adherence Scale then expressed as a binary variable. Binary logistic regression was adopted at 95% confidence interval while deductive thematic analysis was applied for qualitative data.

Results: TB treatment non-adherence was reported at 26% (95%CI: 18%-36%). The study confirmed that patients' perception of the HCWs critically influenced treatment non-adherence. Patients who found the HCW to be friendly, non-discriminatory, and accommodative reported better odds of treatment adherence. Patients who felt supported by the HCWs in dealing with the illness were

8 times more likely to adhere to treatment compared to those who did not (aOR=7.947, 95%CI: 2.214-28.527, p=0.001). The study highlighted inadequate education and counselling of TB patients, on nutrition and drug interaction with TB treatment, which raised the odds of non-adherence to TB treatment. HCWs reported that heavy workload limited time for patient-centered care and targeted education and counselling of patients.

Conclusion : Kisumu East sub-county reports TB treatment non-adherence rate of 26%. Gaps highlighted on delivery of patient-centered consultation and target-specific education of TB patients that impede treatment adherence. There's need for curriculum developers and trainers, to strengthen and institutionalize capacity building on patient-centered consultation and target-specific education and counselling of patients at the beginning and during treatment to enhance the patients' confidence in addressing challenges that arise during treatment. Additionally, health facility managers' should address the workload at the clinics to facilitate adequate time to deliver patient-centered services.

Keywords: Tuberculosis, Treatment Adherence, Human Resource for Health, Tuberculosis Treatment

51.

TEST RESULT CONCORDANCE RATE BETWEEN TWO DIAGNOSTIC TESTS TB LAM AND GENE-EXPERT USING TB LABORATORY INFORMATION MANAGEMENT SYSTEMS IN KABONDO SUB COUNTY

Authors: Nicholas odiemo ogone (LVCT health)*

Background: The major sample for TB diagnosis has been sputum for a long time. However TB diagnosis using sputum has posed challenges in some instances. In an effort to overcome this, new testing techniques have been introduced. TB LAM which uses urine sample to detect TB has been scaled out for general population diagnosis. This especially the clinically unstable patients, however it has demonstrated great impact for pediatric TB diagnosis. Compared with a molecular test such as Gene-expert, TB LAM is believed to be less sensitive and as such several cases could be missed. This study however has compared the concordance rates of test results between the two tests to determine the extent of variation of positivity rates between TB LAM and Gene-expert.

Objective: To compare test result concordance rate between two diagnostic tests TB LAM and Gene expert for treatment initiation.

Methodology: A cross sectional study was conducted in kabondo sub county hospital among patients tested for TB between Jan to Nov 2023. The study specifically focused on patients whose samples tuned positive for gene expert. the study was accomplished by collecting secondary data from TB registers and TIBU LIMS. Data was collected from patients who were tested for TB LAM and turned positive and later the same sample sent for gene expert. Data was then tabulated and analyzed in excel by using percentages. TB positivity by TB LAM was expressed as a proportion of TB positivity by Gene expert.

Results: A total of 686 records were reviewed in the study period. Out of this number, 112 records were sent for TB LAM test. The proportion who turned positive for TB with TB LAM test were only 28 (20.5%) records. when subjected to gene expert test, 25 turned positive out of 28(89.2%).

Conclusion: TB lam test is relatively comparable with molecular test such as gene expert in positivity rate. existence of slight variation in positivity warrant TB lam test to be used in resource limited areas for tests and prompt decision making awaiting further tests.

Recommendations: TB supporting programs to major on TB diagnosis using TB LAM through sufficient supplies. This is essential especially where prompt sputum sample production on the spot is proving to be a challenge.

Keywords: TB testing

POSTER SESSION:

SCREEN 1-NCDS

52.

PREVALENCE AND DETERMINANTS OF HYPERTENSION AMONG TYPE 2 DIABETES MELLITUS PATIENTS IN MOMBASA COUNTY, KENYA

Authors: Habiba Ramadhan (DoHs, Mombasa County)*; Jack Omolo (3Department of Agriculture, Livestock and Blue Economy,Kilifi); Nassoro J Mwanyalu (Kenya FELTP); Maurice O Owiny (Kenya FELTP); Ahmed Abade (FELTP); Josephine Githaiga (FELTP); Salma Swaleh (DoHs,Mombasa County); Maria Nunga (FELTP)

Background: Hypertension (HTN) and Type 2 Diabetes Mellitus (T2DM) cause over 7.5 million mortalities annually in Africa and 6% of mortality worldwide. The chronic nature of T2DM may either increase the occurrence of other medical complications or influence their response to medication. We aimed to determine the prevalence of HTN and related risk factors among T2DM in Mombasa County.

Method: A retrospective review of records extracted from a digital health platform for tracking diabetic clients (SPICE) between 2018 and 2023. Key variables on social demographics, clinical factors, and treatment outcomes were collected. Unique identifier variables were removed before analysis. Descriptive and inferential analysis were carried out. Factors assessed were sedentary lifestyle, family history of HTN and T2DM, age at diagnosis, smoking of cigarettes, and consumption of alcohol. Bivariate and multivariate regression were used to test for factors associated with HTN; p-values ≤0.05 were considered statistically significant.

Results: A total of 303 records were reviewed. The mean age was 52.7 years (SD ±12.5) and females were majority at 73.9% (224/303). The prevalence of hypertension among the T2DM patients was 56.4% (171/303) and the majority 76%(130/171) were aged between 35–65 years. Patients with health insurance coverage were only 9.2% (28/303). Lost to follow-up (LTFU) was at 44.3% (134/303) and the majority 85.8% (115/134) had no health insurance coverage. Retinopathy was reported at 23.4% (71/303). Factors associated with developing hypertension were age-group ≥65 years (OR=2.9 p-value 0.04), family history of T2DM (OR=2.1 p-value <0.01), family history of HTN (OR=2.4 p-value<0.01), sedentary lifestyle (OR=2.4 p-value 0.002) and smoking (OR=3.1 p-value <0.01). On multivariate analysis, only sedentary lifestyle (AOR=1.9 p-value <0.03) and family history of HTN (AOR=1.3 p-value <0.28) were significant.

Conclusion: HTN was prevalent among T2DM patients. Family history of hypertension and sedentary lifestyle were associated with HTN. We suggest early screening for HTN and T2DM and lifestyle interventions such as modifications to diet, stress management, smoking cessation, and physical activity.

Keywords: Hypertension, type 2 diabetes Mellitus, Mombasa County

53.

TOWARDS THE DEVELOPMENT OF A MICROFLUIDIC DEVICE FOR POINT-OF-CARE DETECTION OF VIABLE CRYPTOCOCCUS NEOFORMANS

Authors: Mary N Wachira (NUITM-KEMRI, Kenyatta University)*

There is a significant diagnostic challenge in differentiating between cryptococcal meningitis (CM) relapse, persistent CM or cryptococcal Immune Reconstitution Inflammatory Syndrome (IRIS), each of which requires specially tailored therapy. We aimed to develop a microfluidic point-of-care device based on the Immiscible Filtration Assisted by Surface Tension and Adenosine Triphosphate (IFAST-ATP) assay for detecting viable Cryptococcus neoformans, the causative agent of CM and IRIS, which would enable appropriate and timely clinical treatment.

Introduction: Cryptococcal meningitis (CM) results from haematogenous spread of Cryptococcus neoformans to the brain and meninges once cellular immunity is compromised especially in HIV/AIDS patients. Current diagnostic methods for detecting the causative agent, C. neoformans, are time-consuming, less sensitive and do not reflect viable C. neoformans, hence not suitable for resource-poor areas. Microfluidic lab-on-a-chip technology based on the specific Immiscible Filtration Assisted by Surface Tension (IFAST) and the sensitive Adenosine Triphosphate (ATP) assay offers the potential to address these challenges [1]. Here, we report the progress in the development of a microfluidic device for the rapid point-of-care detection of viable C. neoformans from cerebral spinal fluid based on IFAST and ATP bioluminescence assay.

Results and Discussion: Our concept for IFAST/ATP assay comprises of two steps: (a) immunomagnetic isolation and (b) detection of viable C. neoformans. First, the immunomagnetic isolation of C. neoformans was investigated. Briefly, functionalised magnetic beads specific to C. neoformans were not commercially available, and were therefore prepared in-house. Anti-C. neoformans antibody binding to C. neoformans cells was confirmed by colony count. A 98.4% immunomagnetic binding efficiency was observed from off-chip tube-based conjugation of biotinylated anti-C. neoformans antibody to streptavidin-magnetic beads via streptavidin-biotin reaction at room temperature for 30 minutes to afford a final concentration of 10 µg antibody per 1 mg magnetic beads. The cells isolated by C. neoformans functionalized magnetic beads were viable. A 75% immunomagnetic capture efficiency was observed from off-chip tube-based isolation of C. neoformans with functionalized anti-C. neoformans antibody at room temperature with 30µl of 10µg antibody per mg beads. A 10-minute incubation time at room temperature gave the highest capture efficiency of 56.5%.

CONCLUSION: A simple and fast system for immunomagnetic detection of C. neoformans has been explored for the first time using IFAST, showing great promise for timely and accurate point-of-care diagnosis of cryptococcal meningitis and cryptococcal immune reconstitution inflammatory syndrome.

Keywords: Detection of viable Cryptococcus neoformans, IFAST/ATP

54.

MALE PARTNER EXPERIENCES AND SOCIAL SUPPORT DURING CERVICAL CANCER SCREENING, TREATMENT AND FOLLOW-UP

Authors: Natabhona M Mabachi (DARTnet Institute)*; May Maloba (Global Health Innovations); Catherine M Wexler (University of Kansas Medical Center); Sarah Finocchario-Kessler (University of Kansas Medical Center); Jill Peltzer (University of Kansas Medical Center); Becky Christian (University of Kansas Medical Center)

Purpose: Male partners can play a significant role in the optimization of CC prevention and treatment including primary prevention by reducing sexual partners and receiving the HPV vaccine. They can also support a woman's decision to access CC screening and treatment as well as offer treatment support while destigmatizing the process. Unfortunately, because this is considered mainly a woman's condition, male involvement has low priority. Highlighted barriers include gaps in knowledge on CC risk factors and prevention, a lack of awareness of the impact of screening and treatment on women's bodies and rigid beliefs about gender norms hindering support. The goal of this study is to understand how males are impacted mentally, emotionally, socially, and culturally and how they consequently support their partners when they are diagnosed with CC.

Methods: We conducted in-depth interviews with 10 male partners to delve deeper their levels of knowledge, emotional and psychosocial responses, and experiences, regarding cervical cancer. These interviews provided a nuanced and richer understanding of the psychological and emotional aspects related to the disease and how they have impacted their understanding of the disease and their importantly, their relationships with their partners. Participants were recruited from healthcare facilities in Siaya and Busia counties whose partners were attending reproductive health services. Qualitative data were analyzed using iterative thematic analysis to identify key themes and patterns in men's knowledge, experiences, and psychosocial and emotional responses.

Results: Initial themes revealed include: 1) Changes in Sexual Relationships, affecting couple intimacy and relationship dynamics 2) Willingness to provide financial and emotional support, 3) Misconceptions and gaps in knowledge especially regarding risk factors, and preventive measures such as HPV vaccination and treatment aftercare for women, 4) Patriarchal tendencies acting as a barrier to seeking screening.

Conclusion: These results indicate that if we are to achieve Kenya's 90:70:90 targets by 2030 it is imperative men are an integral part of the education efforts on CC risk factors and prevention efforts i.e. HPV vaccination. It is important we encourage the provision of social support by male partners through CC screening, treatment, and the cascade of care, while attending to the impact on their emotional and sexual well-being and the forces of patriarchy.

Keywords: Cervical Cancer, Male partners, prevention, treatment, social support, psychosocial, patriarchy, mental health, intimacy

55.

NEOANTIGEN PROFILING IN KENYAN BREAST CANCER PATIENTS USING WHOLE EXOME AND RNA SEQUENCING

Authors: Godfrey Wagutu (Mount Kenya University); John Gitau (Mount Kenya University); Kennedy Mwangi (Mount Kenya University); Mary Murithi (Kabarak University); Francis W. Makokha (Mount Kenya University)*

Background: Immune response against tumors is dependent on the discrimination between self and non-self. Cancer immunotherapy aims to enhance this anti-tumor response for elimination of cancerous cells. Utilization of neoantigens derived from somatic mutations forms the basis for many cancer immunotherapeutic strategies. Given the heterogeneity of breast cancer, understanding its neoantigen landscape becomes crucial for targeted immunotherapeutic interventions. However, there is a scarcity of such information for specific populations, including Kenya. This poses a challenge in tailoring immunotherapeutic strategies for breast cancer patients in the region. This study's objective was to profile neoantigens in Kenyan breast cancer patients for advancing precision medicine and realizing the full potential of immunotherapy within this population.

Methods: Whole-exome sequencing (WES) and RNA-seq data from tumor-normal matched samples of 23 Kenyan breast cancer patients were used. Somatic mutations were identified from the WES data, while tumor RNA-seq data was used to quantify the expression of the identified mutations. Neoantigens prediction focused on human leukocyte antigens (HLA) crucial to cancer, HLA type I. HLA alleles were predicted from each patient's normal sample exome-seq data, with four alleles that were present in 50% of the patients selected. Predicted neoantigens were deemed potentially immunogenic if their median IC50 binding scores were ≤500nM and were expressed (Transcripts per million, TPM>1) in tumor samples.

Results: An average of 1465 neoantigens covering 10260 genes had ≤500nM median IC50 binding score and >1 TPM expressed value for the 23 patients, and were significantly correlated with the somatic mutations (R2=0.570, P=0.001). In a panel of 58 genes reported in the catalog of somatic mutations in cancer (COSMIC, v99) to be mutated in breast cancer, 44 (76%) produced >2 neoantigens, with a mean of 10.52 ranging from 2 to 93. For the 44 genes, a total of 477 putative neoantigens were identified, predominantly derived from missense mutations (88%), indels (6%) and frameshift mutations (6%). Notably, 78% of the putative breast cancer neoantigens were patient specific. HLA-C*06:01 allele was associated with majority of neoantigens (194), followed by HLA-A*30:01 (131), HLA-A*02:01 (103), and HLA-B*58:01 (49). Among the genes of interest that produced putative neoantigens include TP53, GATA3, PIK3CA, MAP3K1, BRCA1&2, and ARID1A.

Conclusion: The unique neoantigen profiles highlight the potential of immunotherapy in personalized breast cancer treatment in the Kenyan population. Furthermore, our findings establish a foundation for increased genomic utilization in breast cancer diagnosis and prognosis.

Keywords: Neoantigen, Breast cancer, exome-seq, RNA-seq, Kenya

56.

PREVALENCE AND DETERMINANTS OF HYPERTENSION AMONG TYPE 2 DIABETES MELLITUS PATIENTS IN MOMBASA COUNTY, KENYA.

Authors: Habiba Ramadhan (DoHs, Mombasa County)*; Jack Omolo (3Department of Agriculture, Livestock and Blue Economy,Kilifi); Nassoro J Mwanyalu (Kenya FELTP); Maurice O Owiny (Kenya FELTP); Ahmed Abade (FELTP); Josephine Githaiga (FELTP); Salma Swaleh (DoHs,Mombasa County); Maria Nunga (FELTP)

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Method: A retrospective review of records extracted from a digital health platform for tracking diabetic clients (SPICE) between 2018 and 2023. Key variables on social demographics, clinical factors, and treatment outcomes were collected. Unique identifier variables were removed before analysis. Descriptive and inferential analysis were carried out. Factors assessed were sedentary lifestyle, family history of HTN and T2DM, age at diagnosis, smoking of cigarettes, and consumption of alcohol. Bivariate and multivariate regression were used to test for factors associated with HTN; p-values ≤0.05 were considered statistically significant.

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Conclusion: HTN was prevalent among T2DM patients. Family history of hypertension and sedentary lifestyle were associated with HTN. We suggest early screening for HTN and T2DM and lifestyle interventions such as modifications to diet, stress management, smoking cessation, and physical activity.

Keywords: Hypertension, type 2 diabetes Mellitus, Mombasa County

57.

WILLINGNESS TO START INSULIN THERAPY AMONG INSULIN-NAÏVE PERSONS WITH TYPE 2 DIABETES MELLITUS AT GULU REGIONAL REFERRAL HOSPITAL, UGANDA

Authors: NAKITTO BRENDA (GULU UNIVERSITY)*

Background: Most patients with type 2 Diabetes Mellitus (DM2) will require insulin for glycemic control during the course of their disease. We evaluated the willingness to start insulin therapy among insulin-naïve persons with DM2 in urban Northern Uganda.

Methods: A facility based cross-sectional study was conducted between June and August 2023, recruiting insulin naïve persons with DM2 at Gulu Regional Referral Hospital (GRRH), Gulu, Uganda. We gauged participants' willingness to use insulin by asking, "If your doctor prescribed insulin for you, would you accept to use it?" with responses categorized as either "Yes" or "No." Poisson regression analysis was performed to assess the factors associated with willingness to start insulin therapy. P<0.05 were considered statistically significant.

Results: We enrolled 190 participants, with a mean age of was 55 ±12.72 years. Most participants were female (63.7%, n=121), attained primary level of education (70.0%, n=133), and were unemployed (84.2%, n=160). Overall, 73.4% (n=138) of the participants were willing to receive insulin therapy if indicated. Participants recently advised on insulin showed a 34% higher willingness (aPR: 1.34, 95%CI: 1.06 — 1.72, p=0.007) , whereas those with a disease duration of 6 years or more were 43% less willing (aPR: 0.57, 95%CI: 0.39 — 0.81, p=0.002) and those concerns about coping with insulin therapy were 55% less willing to commence insulin therapy (aPR: 0.57, 95%CI: 0.39 — 0.81, p=0.002).

Conclusions: About 3 in every 4 participants with DM was willing to receive insulin if indicate. However, healthcare providers should consider personalized counseling strategies to alleviate concerns and enhance informed decision-making regarding insulin initiation. Future interventions should focus on addressing specific barriers associated with prolonged disease duration and apprehensions related to insulin therapy to optimize glycemic control in this population

Keywords: Diabetes mellitus, willingness, insulin naïve, Gulu

POSTER SESSION:

SCREEN 2-NTDS

58.

FIRST SEROLOGICAL EVIDENCE OF LOUSE BORNE RELAPSING FEVER IN NORTHERN KENYA: A RETROSPECTIVE STUDY

Authors: John Njeru (KEMRI)*

Background: Louse-borne relapsing fever (LBRF) is a vector-borne zoonotic disease transmitted to humans by infected body lice and is associated with significant morbidity and mortality in febrile patients in endemic regions. LBRF is caused by a highly motile spirochetes bacterium Borrelia recurrentis. Patients with LBRF present with recurrent high fever and spirochetemia which are accompanied mainly by rigors, headache, dizziness and generalized aches shortly a few days after infection. Frequent outbreaks have been reported in Eritrea, Ethiopia, and South-Sudan mainly in the regions strongly associated with war, famine, poverty, overcrowding and breakdown of personal hygiene. Kenya continues to receive increasing number of refugees from the neighboring countries. Thus, there is a likelihood that refugees may introduce vectors carrying LBRF spirochetes to the communities at the bordering counties of Kenya. Currently, there are no proper epidemiologic data available on the burden of LBRF in Kenya. This study aimed to assess the seroprevalence of LBRF in samples of febrile patients of all ages at the selected hospitals in the Turkana County collected between 2009 and 2010.

Methods: A total of 2,030 Bio-banked, frozen (-80oC) serum samples were thawed to room temperature and screened for the presence of IgG and IgM antibodies against Borrelia recurrentis using a recently validated IgG and IgM based iELISA by our group for serodiagnosis of LBRF.

Results: Overall, 415(20.5%) samples were found to be seropositive for LBRF fever based on a parallel interpretation of the IgG and IgM tests applied. Of these, 328(16.2%) had IgG antibodies while 87(4.3 %) had IgM. An additional 160(7.91%) and 17(0.8%) samples had borderline IgG and IgM antibodies respectively suggesting past exposure. Sixty eight percent of the positive samples were from patients residing from Turkana North (224/328) while 103(31.4% were from Turkana East. Only one sample tested positive among samples from Turkana Central and none from Turkana west. Male accounted for 966(47.6%) of the participants. Of these 153/966 (15.8%) tested positive for LBRF. A total of 175/1064(16.4%) women tested positive for LBRF. Majority (93/328) of positive samples were from participants aged 31-40 years followed by those aged between 41-50 years (79/328).

Conclusions: Our findings provide the first evidence of the presence of LBRF as a serious public health problem in northern Kenya. Considering that LBLF is not systematically considered during routine diagnoses of febrile illnesses in Kenya, due to lack of simple diagnostic assays, such patients often encounter missed opportunities for accurate detection and treatment of their infection. There is therefore a critical need for the deployment of public health awareness about the disease and appropriate management guideline and outbreak preparedness in Kenya.

Keywords: Serological,Louse borne relapsing fever,Northern Kenya

59.

COMPARISON OF INTESTINAL SCHISTOSOMIASIS-RELATED ULTRASOUND DETECTABLE MORBIDITIES IN LOW AND HIGH-RISK AREAS IN WESTERN KENYA

Authors: Dollycate Wanja1*, Anne Straily3, Alfred O. Malit1, Emmy A. Kavere1, Rono Kiplimo1, Jared Rioba1 Solomon Mwangi1, Ryan E. Wiegand3, Susan P. Montgomery1, William E. Secor3, Alex Mwaki1, Alie Eleved1, Maurice R. Odiere 1,2

1. SWAP-Kenya

2. CGHR/KEMRI

3. DPDM-CDC Atlanta, USA

Introduction: Intestinal schistosomiasis remains a public health problem in sub-Saharan Africa, with more than 50% of resultant morbidity found around the African Great Lakes, including Lake Victoria. Chronic intestinal schistosomiasis can cause severe hepatosplenic disease including periportal fibrosis, because of granulomatous inflammatory reactions due to eggs trapped in the liver. Milestones for program performance focus on reductions in prevalence and intensity of infection, rather than actual measures of morbidity. Although use of ultrasound to measure hepatosplenic disease severity is an accepted method of determining schistosomiasis-related morbidity, ultrasound has not historically been considered a field-deployable tool because of equipment limitations and unavailability of expertise.

Methodology: This cross-sectional study was conducted in Siaya (45 villages, high-risk area for intestinal schistosomiasis and Vihiga (29 villages, low-risk area) counties. The prevalence of S. mansoni was determined using the Kato-Katz technique. Tablet-based abdominal ultrasound with Philips Lumify Transducer v 1.8 Device C5-2 broadband curved array was used to examine abdominal internal organs for 6477 participants (4125 in Siaya and 2352 in Vihiga)regardless of S.mansoni status. Participants were grouped Pre-school age children (PSAC) (2-6years), school age children (SAC) (7-14years), adolescents (15-17years) and adults (≥ 18 years). Interpretation of results followed the WHO Niamey protocol.

Results: The prevalence of S. mansoni was 25.6% in Siaya and 0.8% in Vihiga. A higher proportion of individuals had liver image pattern ≥ B in Siaya relative to Vihiga (4.1% vs 1.4%; P = 0.0053). Participants with S. mansoni infection were more likely to present with liver pattern ≥ B compared to uninfected individuals (6.5% vs 3.3%, P < 0.0001). S. mansoni was associated with periportal fibrosis (2.2 vs 1.0, P = 0.008). Adults in Siaya were 8.4 times more likely to have advanced periportal fibrosis + portal hypertension (OR = 8.4, P = 0.04). S. mansoni was associated with splenomegaly (SM) and hepatosplenomegaly (HSM) in all age groups; with periportal vein thickening (PT) in SAC, adolescents and adults, and with Portal vein dilatation (PVD) in adults only.

Conclusion: Ultrasound-detectable morbidity was higher in a S. mansoni high-risk (Siaya) relative to a low-risk area (Vihiga). There was an age-dependent effect of S. mansoni on ultrasound-detectable morbidity, with a preponderance observed in adults. Recent technological advances such as Tablet-based ultrasounds provide a useful tool for the evaluation of schistosomiasis-related morbidity across different risk areas.

Keywords: Periportal fibrosis, Schistosomiasis, morbidity

60.

PLACENTAL METRICS AND PERINATAL OUTCOMES ASSOCIATED WITH MALARIA IN PREGNANCY IN BUSIA, WESTERN KENYA

Authors: Odhiambo Caleb (Egerton University)*; Dancan Wakoli (Egerton University); Sikuku Daniel (Egerton University); DICKSON KIPCHIRCHIR (KEMRI-CGHR); EVERLYNE CHIMWANI KHALIVINZWA (Jaramogi Oginga Odinga University of Science and Technology); Stellah A Chumbe (Maseno University/KEMRI); Makandi Rakel (Egerton University); Michael Ongecha (KEMRI); Bartholomew Ondigo (Laboratory of Malaria Immunology and Vaccinology, National Institute of Allergy and Infectious Disease, NIH, Bethesda, Maryland, USA;)

Introduction: Malaria infection during pregnancy can disrupt placental circulation and impair placental function, reducing infant birth weight. Placenta matrices (placenta weight, longest, shortest diameter, and thickness) are significant indicators of placental function and perinatal outcome. However, the precise impact of placental malaria on placental metrics on term delivery and birthweight remains unclear. This study aimed to determine the relationship between the placental metrics and infant weight by infection status of neonates in Busia, western Kenya.

Method: This study was a cross-sectional whereby, 133 placentae, neonates, and pregnant women from two hospitals in Busia. The weight, size, and malaria status of the placenta were measured using various tools. The gestational age was determined through ultrasound and clinical examination at delivery, and maternal characteristics were recorded. Linear regression was used to analyze the relationship between infant birth weight, placental metrics, gestational age, and maternal BMI.

Results: Out of 133 placental samples,110 (82.7%) were uninfected with malaria, while 23(17.2%) were infected. The mean birth weight of term infants infected and uninfected with malaria was 3129g (95%CI; -256.2-248.2,) and 3125g, respectively(P=0.63). Although not statistically significant, infants infected with placental malaria exhibited lower mean placental weight (444.3g), the longest placental diameter (19.80cm), and placental thickness (2.04cm) (P=0.71, P=0.88, and P=0.26, respectively). Birth weight positively correlated with placental weight (R2 =0.36, p<0.0001), largest placental diameter (R2 =0.27, p =0.002), placental volume (R2 =0.23, p=0.005) and maternal BMI (R2 =0.19, p=0.023). However, there was no significant association between birth weight and gestational age (R2 =0.25, p=0.77). The birthweight/placental weight (BW/PW) ratio and placental weight/birthweight (PW/BW) ratio both exhibited positive correlation with birth weight in both placental malaria-infected and uninfected infants (R2 =0.8, P<0.0001, R2 =0.9, p=0.017). Notably, the odds ratios between placental malaria infection and birth weight, placental metrics, gestational age, and BMI remained at 1 ([OR] 1.000; 95%CI;0.9998-1.001).

Conclusion: While a significant correlation exists between placental weight, the longest placental diameter, and BMI with birthweight, this relationship appears to be independent of placental malaria infection. Therefore, further investigation is warranted to explore other potential factors that influence healthy pregnancy and birth outcomes, enabling more effective public health concerns.

Keywords: Malaria in pregnancy, placental metrics, perinatal outcomes, maternal gestation age, mean birth weight, Busia, western Kenya

61.

PREVALENCE AND RISK FACTORS ASSOCIATED WITH GEO-HELMINTHS AND INTESTINAL PROTOZOA INFECTIONS IN SCHOOL-GOING CHILDREN IN NYERI COUNTY, KENYA. Authors: Anthony M Muthee (KEMRI)* Rael Musili, Joseph Thiong'o, Eric Lelo, Martin Mutuku,

School-age children are at high risk of soil-transmitted helminth (STH) and intestinal protozoa worldwide. In Kenya, STH & protozoa infections in school-going children remain high despite the periodic administration of anthelmintic drugs (MDA). This research was carried out in Nyeri County's Central Kenya lying on 1,340 acres of land which is a swampy plain "no man's land" that has not been demarcated and where residents engage in small-scale non-mechanized farming. Furthermore, there are no latrines (no-man's land), thus there is more likelihood of open defecation leading to frequent contact with the soil, which harbors parasites hence this creates a potential breeding ground for geo-helminths and intestinal protozoa. School Age Children were the study population since they cover a wider range of the population and give a clearer representation of the vast population and thus provide a more accurate picture of the actual population. Most of the research, treatment, and control efforts have centered on this age group, such as in nationwide school deworming programs, which have been demonstrated to have a good influence on children.

Methods: A cross-sectional study on a population of 164 school-going children attending 3 primary schools in the vast low land area (No-man's land) was examined for STH and intestinal protozoa infections by the quantitative Kato-Katz technique and Formal ether concentration techniques.

Results: Among 164 school-going children examined, the prevalence of STH in Kihuro Primary School, Gathuini Primary School, and Gikumbo Primary School was 10.7%, 13%, and 13% respectively. In contrast, the prevalence of intestinal protozoan infections among school-going children in the same schools was 21.4%, 33%, and 20.4% respectively. Protozoan infections were thus higher compared to STH infections (P=0.0107). The odds of being infected with any intestinal protozoa and STH for children in Kihuro Primary School was (odds ratio (OR) = 0.609937; 95% CI 0.17-2.00). Whereas the odds of being infected with any intestinal protozoa and STH for children in Gathuini Primary School was (odds ratio (OR) = 0.8793952; 95% CI 0.32 -2.44). Surprisingly, the odds of being infected with any intestinal protozoa and STH for children in Gikumbo Primary School were similar to Gathuini Primary School. The results of the chi-square test failed to provide evidence of a significant association between gender and infection status, suggesting that there is no relationship between gender and the likelihood of infection of school-going children of three Primary Schools with protozoan and geo-helminths.

Conclusion: The study findings show that STH and intestinal protozoa infection were a health hazard in Nyeri County, the age and gender of pupils had no statistical significance and the associated risk factors(variables) influenced the prevalence of STH and intestinal protozoa infection in the pupils and the environment of school-going children in Nyeri County.

Keywords: Neglected tropical diseases(Geo-helminths)

POSTER SESSION:

SCREEN 3-MCH

62.

MEN INVOLVEMENT IN INCREASED ANC ATTENDANCE AMONG PREGNANT MOTHERS, A CASE OF EKWANDA HEALTH UNIT, VIHIGA COUNTY

Authors: Fanuel O Khainga (MOH)*

Background: Antenatal care is a crucial component in maternal and child health as it helps in monitoring and ensuring healthy growth of the pregnancy. Apart from healthcare system factors like distance to health facilities, male partners are a key contributor in reduced ANC attendance since they are majorly the decision makers at the household. This happens since most women seek permission from their male partners before taking action. The objective of the study was to improve access and utilization of ANC services.

Methodology: Cohort study design was used to select pregnant mothers for the study. 62 pregnant mothers attending clinic at Ekwanda Health Centre were mapped and visitation made to their households by healthcare workers. Their male partners were taken through the importance of attending all the ANC visits. They were then grouped into Father-to-Father groups consisting of 10 people each. These groups were scheduled to be meeting on monthly basis to discuss matters maternal health with the help of a nursing officer from the MCH. “Anzilisha” as a key component was discussed with an aim of making the men understand the care of the mother and the child in the first 1000 days since conception. They were encouraged to be accompanying their female partners for ANC visits and providing any possible support during the pregnancy. Focused Group Discussions were also conducted to asses men’s knowledge on importance of ANC.

Results: The study showed a large proportion of men had denied their partners a chance to attend antenatal clinics or allowed them to attend only once since they didn’t know the importance. In comparison to ANC data of February 2022, evaluation done in February 2023 showed an immense increase in mothers attending atleast 4 ANC visits by 90%. It was also noted that uptake of Iron and Folic Acid Supplements (IFAS) and other health interventions during pregnancy had increased by 85% and unskilled delivery dropped to 1%. It was also noted that most men had feared to accompany their partners to clinic due to stigma and negative community perspective.

Conclusion: Men involvement in maternal health issues improves uptake of health services by pregnant mothers. Men should be sensitized more on matters maternal health and Father-to-Father groups formed in all the communities as they give men an opportunity to share challenges and experiences thus improving maternal health.

Keywords: Father-to-Father, Maternal Health, Behavior change

63.

EFFECTS OF MALARIA EXPOSURE DURING PREGNANCY ON THE LEVELS OF EBV ANTI-GP350 IGA AND ANTI-GP350 IGG AMONG INFANTS IN WESTERN KENYA.

Authors: Stellah A Chumbe (Maseno University/KEMRI)*; Cyrus Ayieko (Maseno University); Sidney Ogolla (Kenya Medical Research Institute (Kemri)); Emmily Koech (Kenya Medical Research Institute (Kemri)); Kevin Waomba (Kenya Medical Research Institute (Kemri)); Boniface Ariera (Kenya Medical Research Institute (Kemri)); Onditi Ian Arao (KEMRI); Rosemary Rochford (University of Colorado)

Background: The Epstein-Barr virus (EBV), a herpes gamma virus, is prevalent in nearly 95% of the global population. Although EBV and malaria infection are both factors in the etiology of Burkitt lymphoma, the precise mechanism underlying the pathogenesis of endemic Burkitt Lymphoma is elusive. In malaria-endemic regions, over 35% of infants are infected with EBV before the age of six months, but it’s unclear why these children are susceptible to early EBV infection. Notably, responses to the viral glycoprotein 350 (gp350) are critical for neutralizing EBV infections. However, it is unknown whether malaria exposure during pregnancy impairs the specific IgA and IgG responses to gp350, thereby predisposing these infants to earlier EBV infection.

Methods: In this longitudinal study, we enrolled pregnant women visiting Chulaimbo Hospital during their antenatal care visit and followed them up to delivery. Upon delivery, their infants were recruited and followed up for 21 months. Venous blood samples were collected from the infants at 6,10,14, and 18 weeks, as well as at 6,9,15, 18, and 21 months of age. DNA was extracted, and EBV loads were assessed using Real-time Polymerase Chain Reaction (Q-PCR). The levels of IgA and IgG against gp350 were quantified through Enzyme-Linked Immunosorbent Assay (ELISA).

Results: The levels of anti-gp350 IgA were significantly higher in infants exposed to malaria during pregnancy at 6, 10 and 18 weeks and at 21 months ($P = 0.04$, $P = 0.02$, $P = 0.01$, and $P = 0.04$, respectively). In contrast, no significant difference in anti-gp350 IgG antibody levels was observed between the infants exposed and unexposed to malaria during pregnancy across all time points. Interestingly, there was no association between EBV load and anti-gp350 IgA antibody levels in both malaria-exposed ($R2 = 0.24$, $P = 0.05$) and unexposed infants (R2= -0.25, P = 0.11). However, a correlation between EBV load and anti-gp350 IgG levels was noted in infants exposed to malaria during pregnancy (R2=0.26, P =0.0037 as well as in unexposed infants (R2= 0.35, P= 0.027).

Conclusion: Maternal malaria during pregnancy impairs the levels of EBV anti-gp350 IgA neutralizing antibodies hence, it may predispose infants to early EBV infection. Exposure of infants to malaria in utero does not affect EBV anti-gp350 IgG, implying that infants have stable protection against systemic EBV.

Keywords: Malaria exposure, gp350, IgA, IgG, Epstein-Barr Virus

64.

ASSESSMENT OF THE PERFORMANCE OF MALARIA DIAGNOSTIC TOOLS IN DIAGNOSING MALARIA IN PREGNANCY AND PLACENTAL MALARIA

Authors: Melvin Mbalitsi (Maseno University)*

Melvin Mbalitsi1,3, Samuel Chenge1,2, Harrison Ngure1, Paul Angienda3, Jesse Gitaka1, Francis Kobia1

1 Center for Malaria Elimination, Mount Kenya University, Thika, Kenya

2 Department of Medical Microbiology, Jomo Kenyatta University of Agriculture and Technology

3 Department of Zoology, Maseno University, Kisumu, Kenya

Introduction: In 2021, >13 million MiP cases occurred in sub-Saharan Africa, with potential placental malaria complications according to WHO. Malaria diagnosis in pregnancy (MiP) and PM is challenging due to high rates of asymptomatic infections and placental sequestration of Plasmodium falciparum (Pf). This is further complicated by the low sensitivities of microscopy and rapid diagnostic tests (RDT), the main methods of malaria diagnosis. Here, we used histology to detect PM in archived placental tissues from a malaria-endemic region of Kenya, and assessed how it correlates with Pf detection rates in maternal blood, placental blood, and placental tissue using PCR, RDT, and Isothermal amplification of identical multirepeat sequences (iso-IMRS).Currently, there are no effective ways of diagnosing PM, mainly because the placenta is inaccessible during pregnancy. High asymptomatic malaria in adults and low microscopy and RDT sensitivity further complicate diagnosis. We evaluated PCR, RDT, and iso-IMRS sensitivities in MiP detection, correlating with histological PM confirmation.

Methods: We studied biobanked maternal blood, placenta blood, and placental tissue from 51 placenta donors from a malaria holoendemic region of Kenya. DNA was extracted using the Chelex method. MiP was tested using PCR on maternal and placental blood. PM was tested using histology, PCR, and iso-IMRS analysis of placental tissues.

Results: PCR detected Pf in 13.7% of maternal blood and 21.6% of placental blood samples, more sensitive than RDT (0%). Iso-IMRS, detecting Pf in 64.7% of placental tissues, surpassed PCR (13.7%) and histology (33.3%). Iso-IMRS and PCR data suggested PM in women with undetectable Pf in maternal blood.

Conclusion: This comprehensive analyses show that iso-IMRS is the most sensitive tool for malaria detection in pregnant residents of malaria-holoendemic regions, where there are high rates of asymptomatic infection. Integrating Iso-IMRS into novel point-of-care tests for MiP may improve the detection of fetal exposure to PM.

Keywords: Malaria in pregnancy, placental malaria

65.

EMPOWERING MALE ENGAGEMENT IN PMTCT: PIONEERING ZERO MOTHER-TO-CHILD HIV TRANSMISSION.

Authors: Wayne O Otieno (Catholic Medical Mission Board)*

Background: The global commitment to eliminating mother-to-child HIV transmission (EMTCT) as a public health priority necessitates addressing sub-optimal care and treatment for HIV-positive pregnant and lactating women, as highlighted in the Kenya Democratic Health Survey (KDHS). Maternal viral suppression remains below optimal levels at 91.5%, potentially due to issues of adherence and retention. Recognizing the influential role of men in household decisions and their impact on pregnant women's access to services and treatment adherence, male involvement in Prevention of Mother-to-Child Transmission (PMTCT) is paramount. The CMMB, in collaboration with the Global Fund HIV program and the Kenya Red Cross Society, initiated community-led monthly psychosocial support groups (PSSGs) involving male partners to augment PMTCT outcomes.

Method: The program tactically integrated men into community PSSGs for PMTCT, specifying criteria for forming PSSGs and fostering discussions conducive to engagement. Each PSSG accommodated a specific number of women, enabling meaningful conversations on pertinent PMTCT topics. Discussions in the group were led by either a healthcare worker from the link facility or trained expert mother. Experiential lessons were gathered from clients and triangulated with service uptake tracking.

Results: Mothers engaged in the PSSGs deemed the discussions invaluable, advocating for their continuation to break down socio-cultural barriers, redefine traditional gender roles, and promote better communication within households. Across Gem and Ugunja, 30 PSSGs were formed, encompassing 980 PMTCT clients. The monthly uptake of PMTCT reproductive health services notably increased by 26%, directly attributed to male participation in the PSSGs. In the implementation sites, 1.6% MTCT rate was recorded, arguably below the national target of 5%. The influence of male involvement in PMTCT was striking, positively affecting women's attendance, ART uptake, services for HIV-exposed infants, and cultivating favorable attitudes among the participating men.

Conclusion/Next Steps: The strategy underscores the criticality of male engagement in PMTCT activities. Their active support contributes significantly to women's adherence to ART, achievement of low viral loads, and healthier lives. This shared responsibility ensures the well-being of both mother and HIV-exposed infant, emphasizing the imperative need to reinforce and prioritize male involvement in PMTCT interventions. Elevating the role of male partners in PMTCT remains pivotal, securing collective responsibility in caring for HIV-exposed infants.

Keywords: Male involvement, PMTCT, Psychosocial support groups

POSTER SESSION:

SCREEN 4-HIV

66.

FACTORS ASSOCIATED WITH VIRAL NON-SUPPRESSION AMONG ADOLESCENTS AND YOUNG ADULTS ON ANTI-RETROVIRAL THERAPY IN NYANDARUA COUNTY, JULY 2023

Authors: Lucy Njoki Munyeki (County Government of Nyandarua)*; Maria Thuita (Kenya FELTP)

Background: The prevalence of HIV among adults in Kenya is approximately 4.9% with 42% new infections among 15–24-year-olds. The Joint United Nations Programme on HIV/AIDS goal is that by 2030, 95% of all persons on antiretroviral therapy achieve viral suppression. Adolescents and young adults on ART in Kenya have shown poor outcomes mostly attributed to behavioral characteristics. This study sought to assess factors associated with viral non-suppression among adolescents and young adults in Nyandarua County.

Methods: We conducted a cross-sectional study. Data was accessed through Comprehensive Care Clinic in-charges and de-identified data abstracted from the Electronic Medical Records (EMR) active line list as of July 2023. Key informant interviews (KII) were conducted with HIV coordinators following an interview guide. Descriptive statistics were conducted. Prevalence odds ratio was used to measure the association between variables and viral load outcome at a 95% confidential level. Data was cleaned on Microsoft Excel® and analyzed on Epi Info®. Associations with p-value <0.05 were considered statistically significant.

Results: We analyzed 642 records. Female cases were 54.05% (370/642), males at 45.95% with a mean age of 18 (±4) years. Overall, viral non-suppression was at 11.41% (73/642), 25 % (13/52) on second-line therapy, and 10% (55/548) on first-line therapy. Of the non-suppressed, 91.7% (67/73) were 15-24 years old. Information from KII established that all comprehensive care centres in the county offered youth-friendly services as part of the HIV Testing Services (HTS) package. Being on second line ART regimen was associated with viral non-suppression (POR=2.9; 95% CI =1.5-5.9)

Conclusion: Viral suppression was sub-optimal with being 15-24 years old and on a second-line ART regimen associated with high viral load. We recommend more education to those between 15-24 years of age on adherence to treatment and further studies on the effect of second-line therapy on viral load outcome.

Keywords: Key words: Adolescents, ART, viral suppression, young adults

67.

BREAKING BARRIERS: ADDRESSING GENDER-BASED VIOLENCE AND IMPROVING TREATMENT ADHERENCE AMONG SERO POSITIVE WOMEN IN DISCORDANT RELATIONSHIPS IN KURIA EAST SUB COUNTY.

Authors: NANCY B MWITA (MOH)*; Benson Okome (CMMB); Isaac Okeyo (TUKICHEKI)

Background:GBV is a concern among women in discordant relationships, particularly the seropositive one, hence a higher risk of violence compared to HIV-negative one. Violence impedes adherence to antiretroviral therapy hindering successful treatment of HIV/AIDS. Healthcare providers play a crucial role in supporting patients' adherence, but it becomes challenging when patients face GBV and stigma, especially from intimate partners.

Methodology: With the help of facility charges, discordant couples peer educators were identified and trained on peer education, communication, and community-facility referrals for HIV services and EBAN K (Evidence based intervention targeting HIV heterosexual discordant couples). Support groups were established, aimed at providing a platform for experiences sharing and support each other while addressing physical and emotional violence. Assessment on experiences of physical and emotional violence was conducted during their routine clinic visits and its impact on treatment adherence was conducted as part of routine HIV care.

Of the 90 discordant couples identified, 65 had women as the seropositive partners. Among them, 46 experienced physical violence, and 55 emotional violence, with three women abandoned by their negative male partners. The establishment of support groups and implementation of training resulted in significant reductions in violence cases over 10 months (January 2023-october 2023), with physical violence cases decreasing from 46 to 10 and emotional violence cases from 55 to 17,all of them were virally suppressed,17 started on PrEP.

Conclusion: Sero positive women in discordant relationships face considerable physical and emotional violence, making them vulnerable in their partnerships. This hampers their adherence to medication and overall treatment outcomes. Therefore, comprehensive psychosocial support, involving male partners, creates healthier living conditions and improves treatment adherence and outcomes. It is imperative that comprehensive psychosocial support be integrated into HIV care programs tailored to address the unique challenges faced by seropositive women in discordant partnerships. This support should extend beyond individual care and actively involve male partners to foster understanding, empathy, and unity in their relationships.

Recommendations: Integrate psychosocial support and training interventions, such as EBAN K, into HIV care programs for seropositive women in discordant relationships. Establishing and sustaining support groups is instrumental in providing ongoing support to these couples. Policy initiatives be developed to promote gender equality, reduce stigma, and raise awareness about GBV in the context of HIV/AIDS, with a goal to end GBV and improve lives of seropositive women in discordant relationships. Stakeholder like healthcare providers, community organizations, and policymakers to collaborate ,address and prevent GBV among this vulnerable population.

Keywords: DISCORDANT COUPLES, SEROPOSITIVE

68.

ROLES OF HEALTH CARE PROVIDERS TOWARD HIV SELF TESTING (HIVST) APPROACH TO ACHIEVE GLOBAL TARGET TO END HIV BY 2030

Authors: Andrea James Hussein (Hubert Kairuki Memorial University)*

Background: HIV self-testing (HIVST) is recommended by the WHO as an innovative strategy to reach UNAIDS targets to end HIV by 2030. This innovative strategy is aimed at achieving zero new HIV infections, zero HIV-related deaths, and zero HIV-related discrimination. In Tanzania at the end of 2018, full-scale HIV self-testing began, with a focus on provision of self-testing kits to all difficult-to-reach populations, such as men and young people

Methods: This was systematic review study conducted from August to September 2022, Dar es salaam, Tanzania. We surveyed literatures published from 2010 to 2021 using two electronic databases (Google Scholar and HIVST.org) and manual search. The inclusion criteria included literature published in english, literature with advantages of HIVST and roles of health care providers on promotion of HIVST. About 22 literatures obtained and analyzed using narrative analysis method after full text reviews. Both qualitative and quantitative results extracted and put into narrative form.

Results: Twenty-two (22) pieces of literature related to HIVST were analyzed, all conducted in Tanzania from 2010 to 2021. Among those, 13 (59.1%) studies discussed the advantages of HIVST, and nine articles described the roles of health care providers in promotion of HIVST approach. In 13 studies, it was reported that HIV self-testing can lead to an increase in the frequency of HIV testing among individuals. 5 out of 13 studies reported that HIVST increases the identification of new HIV diagnoses. Also, 8 out of 13 studies reported that HIVST increases HIV testing uptake and acceptability among populations. Generally, 9 (40.9%) out of 22 studies reviewed revealed that health care providers acting as HIVST educators, counselors, reporters and important agents for distribution of HIV self-testing kits

Conclusion: HIVST is an acceptable, feasible, and helpful program for HIV control. HIVST has challenges such as users' errors as well as linking self-testers to health facilities. The role of the health care providers is to ensure HIVST kit distribution is combined with other services such as confirmatory tests, HIVST education, counseling, and linkage care.

Keywords: HIV, HIV self testing, healthcare providers

69.

EXPLORING THE ROLE OF CHURCHES IN ADDRESSING HIV VIRAL SUPPRESSION IN THREE COMMUNITY SITES,HOMABAY KENYA

Authors: JOAN A ONDIGO (UNTOLD)*; Janet Manyara (UNTOLD); Corneleous Edward Okal (Ministry of Health)

Background: Religion and culture can affect health care, if providers and health care systems are not working together to provide culturally competent care, patients may have negative health consequences. Homabay County has the highest prevalence of HIV in Kenya at 15.2%. The county is yet to achieve the 95% UNAIDS target on viral suppression mainly due to gaps in treatment illiteracy and psychosocial limitations. We implemented a holistic approach in three church centers to address viral suppression. This study assesses the viral load outcome post-implementation.

Methodology: We enrolled 240 clients with high viral loads in three church centers. Healthcare providers used the UNTOLD recruitment matrix to identify the clients for enrolment. Viral load above 1000 copies and the presence of an opportunistic infection were some of the recruitment requirements. All clients received a need-based package of service that included psychosocial support, spiritual counseling, nutritional support skills building, and medical support. Clients were followed up for one year and the viral load at baseline and after intervention was assessed.

Results: Of the 240 clients enrolled in the church centers, 63.9% were female. The mean age was 37SD 9.6. The baseline suppression (VL <200 copies) was 20% (49/240) and the follow-up VL after intervention was 94.2 %(226/240). Baseline low-level viremia (VL200-999) was 7.1% and 1.3 after intervention only three patients had VL > 1000 copies at 1-year graduation.

Conclusion: Collaborations between Churches/faith-based organizations and health care systems can help in improving client viral suppression by addressing treatment illiteracy, and the spiritual psychosocial, and social-economic needs of clients. We recommend consideration of greater partnership initiatives between the health system and religious entities for better healthcare outcomes.

Keywords: Religion,community centres,viral load

POSTER SESSION:

SCREEN 5-HIV

70.

ANTIMICROBIAL SUSCEPTIBILITY AND GENETIC BASIS OF RESISTANCE OF KLEBSIELLA SPP ISOLATED FROM DIARRHEIC AND NON-DIARRHEIC CHILDREN AT HEALTH FACILITIES IN MUKURU INFORMAL SETTLEMENT, NAIROBI, KENYA

Authors: celestine w wairimu (Kenya Medical Research institute)*; Samuel Kariuki (KENYA MEDICAL RESEARCH INSTITUTE)

Background: Antimicrobial resistance (AMR) is a global threat to public health and particularly to children. This study aimed to determine the prevalence of multidrug resistance of fecal Klebsiella spp on selected beta-lactam (3rd generation cephalosporins and carbapenems) and fluoroquinolone classes of drugs in four health facilities serving the Mukuru slum community of Nairobi city in Kenya. Additionally, to determine the genetic basis for the multidrug resistance observed.

Methodology: A cross-sectional laboratory-based study was undertaken where a total of 1171 children below 16 years were selected, from whom stool samples were collected, tested, and analyzed using various microbiological methods namely; culture, biochemical testing, antibiotic sensitivity testing and polymerase chain reaction. A total of 395 (33.73%) Klebsiella spp were isolated, consisting of 365 (92.4%) Klebsiella pneumoniae and 30 (7.6%) Klebsiella oxytoca were isolated. The proportion of multi-drug resistance (MDR) K. pneumoniae and MDR K. oxytoca was 64.1 % (234/365) and 96.67 % (29/30) respectively. MDR was defined as was defined as an isolate non-susceptible to at least one agent in

three or more antibiotic classes K. pneumoniae showed the highest resistance against third-generation cephalosporins namely; cefotaxime 112 (30.7%), ceftriaxone 109 (29.9%), and ceftazidime 100 (27.4%), whereas the least resistance was observed against carbapenems including imipenem 6 (1.6%) and meropenem 6 (1.6%). Out of 365 K. pneumoniae, 42 (11.5%) showed resistance to both third generation cephalosporins and fluoroquinolones. A significant association was observed in diarrheic children (OR =1.88; p=0.01) and those below 50 months (OR = 0.43; p=0.002) and carrying K. pneumoniae resistance to one or more third-generation cephalosporins. Among the K. pneumoniae isolates resistant to both third generation cephalosporins and fluoroquinolones, resistance genes identified included bla TEM 42 (100%), bla CTX-M 40 (95.2%), bla SHV 24 (57.1%), bla OXA-1 28 (66.7%), qnrS 23 (54.1%), qnrB 20 (47.6%) and bla NDM 3 (7.1%). In conclusion, there is a high prevalence of MDR K. pneumoniae carrying genes associated with antibiotic resistance, and this poses a threat to the Mukuru community, especially the vulnerable populations.

Keywords: Klebsiella, Antimicrobial resistance, Community, Children,Urban Settlements, Nairobi,

71.

ENVIRONMENTAL RESERVOIRS OF MULTIDRUG-RESISTANT PSEUDOMONADS IN A GEOGRAPHICAL LOCATION WITH PREDOMINANTLY COMMUNITY-ACQUIRED INFECTIONS IN KENYA

Authors: Polly N Mubassu (Kenyatta University)*; Lillian Musila (Kenya Medical Research Institute/ United States Army Medical Research Directorate-Africa, Nairobi, Kenya); Abednego Musyoki (Kenyatta University); Collins Kigen (Kenya Medical Research Institute/ United States Army Medical Research Directorate-Africa, Nairobi, Kenya); Erick Odoyo (Kenya Medical Research Institute/ United States Army Medical Research Directorate-Africa, Nairobi, Kenya)

Background: Pseudomonads are Gram-negative bacteria associated with life-threatening opportunistic human infections. They readily form biofilms in moist environments, allowing long-term colonization and persistence in sinks, water systems, and swimming pools. Multidrug-resistant (MDR) strains, especially carbapenem non-susceptible isolates, make treatment increasingly difficult. Environmentally persistent MDR strains are typically problematic within healthcare facilities; however, data on MDR pseudomonad reservoirs in settings with community-acquired infections in resource-constrained settings is scarce. Here, we determined reservoirs and antibiotic susceptibility of Pseudomonas species in community and hospital water sources in Kisumu County, Kenya, with reported high levels of community-acquired pseudomonad infections to inform preventive interventions.

Methods: A cross-sectional design was adopted, randomly collecting 297 samples from tap heads, sinks, tanks, water vendors and household storage containers in six selected sub-locations and one hospital (KCRH) within Kisumu County. Standard microbiological procedures were used. Briefly, samples were plated on CHROMagar pseudomonas, presumptive pseudomonad colonies sub-cultured on Mueller Hinton Agar and screened by Gram stain and oxidase tests. Identification and AST were conducted on VITEK 2 automated platform.

Results: We isolated pseudomonads from 14.1% (42/297) of the samples collected, predominantly from the community environments (10.4%, 31/297). Seven different pseudomonads were identified, namely P. aeruginosa, P. fluorescens, P. putida, P. oleovarans, P. mendocina, P. alcaligenes, and P. stutzeri with P. aeruginosa predominating (6.7%, 20/297) overall, in the community samples (5.7%, 17/297), and among isolates from water tanks (21.4%, 7/42). Pseudomonad isolates were 62% (26/42) non-susceptible to piperacillin, 57% (24/42) to tigecycline, 24% (10/42) to meropenem, 21% (9/42) to cefepime, 19% (8/42) to levofloxacin and 14% (6/42) to colistin. Carbapenem resistance was mainly detected in P. aeruginosa 80% (8/10) from the Milimani sub-location 75% (6/8). 45% (19/42) of the isolates recovered were MDR, mainly community-associated carbapenem-resistant P. aeruginosa (CRPA) (42%, 8/19) strains susceptible to colistin. The MDR pseudomonads exhibited high multiple antibiotic resistance indices (MARI), ranging from 0.43 to 1.

Conclusion: This study reveals a higher prevalence of MDR pseudomonads, including CRPA strains, in community water sources. These potential conduits of drug resistance present a critical public health threat, especially among immune-compromised persons. Regular cleaning of water storage facilities, water treatment, maintenance of water piping systems, and strict implementation of antimicrobial stewardship programs are urgently required to prevent a rise in antibiotic resistance and eliminate the environmental reservoirs that put vulnerable populations at risk.

Keywords: Pseudomonads, multidrug resistance, environmental reservoirs, carbapenem-resistant Pseudomonas aeruginosa

72.

TARGETING MYCOBACTERIUM TUBERCULOSIS WITH MYCOBACTERIOPHAGE

Authors: Joseph Gitari (University of Cape Town)*; Elizabeth Kigondu (KEMRI); Mandy Mason (University of Cape Town); Anastasia Koch (University of Cape Town); Digby Warner (University of Cape Town)

The survival of Mycobacterium tuberculosis in dynamic, often hostile, microenvironments during host infection is thought to be partly attributable to the bacillus's capacity for heterogeneity. This trait manifests, too, in the existence of genetically susceptible but antibiotic recalcitrant M. tuberculosis subpopulations – variously referred to as antibiotic tolerant, persistent, or resilient cells which have been implicated in treatment prolongation, and relapse following non-adherence to therapy. There is growing interest, therefore, in the development of innovative interventions to increase the efficiency of M. tuberculosis clearance, including through the application of biologics such as engineered mycobacteriophages.

This study utilizes the lytic mycobacteriophage D29 to investigate the disruption of the complex mycobacterial cell wall to enhance antibiotic efficacy and mycobacterial lysis. We use live-cell time-lapse imaging and flow cytometry to demonstrate phage-mediated lysis and antibiotic uptake in non-pathogenic M. tuberculosis (H37Ra) and M. smegmatis models.

We have determined the efficiency of mycobacteriophage D29 in enhancing mycobacterial cell lysis alone in non-pathogenic M. tuberculosis (H37Ra) and rifampicin-resistant M. smegmatis models, and in combination with cell wall-targeting antimycobacterial drugs in wildtype M. smegmatis. In flow cytometry and live-cell time-lapse microscopy assays utilizing fluorescent M. smegmatis bioreporter mutants, we have demonstrated phage-mediated lysis of single mycobacterial cells under microfluidic culture. Phage adsorption was observed at the poles and septa of actively replicating bacilli, consistent with the known involvement of these sites in the addition of new cell wall material. Notably, phage lysis reduced mycobacterial survival to <0.0001% for all strains tested, with statistically significant differences (p<0.001), supporting the efficiency of phage independent of genetic drug susceptibility.

In ongoing work, we are investigating the use of D29 mycobacteriophage as an adjunct to conventional antibiotic treatment to enhance killing of antibiotic recalcitrant mycobacterial cells.

Keywords: Mycobacteriophage, mycobacterium tuberculosis, antibiotic resistance

73.

ISOLATION AND CHARACTERIZATION OF BACTERIOPHAGES WITH LYTIC ACTIVITY AGAINST DRUG-RESISTANT NON-TYPHOIDAL SALMONELLA FROM NAIROBI CITY COUNTY, KENYA

Authors: Michael Mugo1,2*, Abednego Musyoki2, Angela Makumi3, Ivy Mutai4, Kelvin Kering1, Peter Muturi1, Cecilia Mbae1, Samuel Kariuki1

1.Centre for Microbiology Research, Kenya Medical Research Institute, Nairobi, Kenya.

2.Department of Medical Laboratory Science, Kenyatta University

3.International Livestock Research Institute (ILRI)

4. Phage Biology Laboratory, Institute of Primate Research, Nairobi, Kenya

*Corresponding author: mikemugom@gmail.com

Background: Whereas Non-typhoidal Salmonella (NTS) is a common cause of self-limiting enterocolitis in humans, it has been implicated in life-threatening invasive cases. Emergence of Multidrug-resistant NTS has been reported in Kenya with confirmed cases of resistance to 3rd generation cephalosporin. Due to the emergence of multi-drug resistant (MDR) bacteria coupled with the slowed development pace of new antimicrobial agents, bacteriophages are considered as a feasible alternative to antimicrobials.

Methods: This study, therefore aimed to isolate phages that can be used as an alternative therapy against MDR NTS infections. In vitro assessment of phage efficacy was conducted by host range and efficiency of plating (EOP) assay, using a panel of twelve Salmonella isolates. Phages with the broad host range were selected to determine their efficiency using EOP assay. Later, their physiochemical properties were determined by assessing phage thermal and pH stability. The effects of phages on NTS biofilm was tested by introducing phages on already formed NTS biofilms.

Results: Thirty-one phages were isolated from environmental samples collected within Nairobi city county. They exhibited a narrow to broad host range (8%-100%), with ten phages lysing 80% of the Salmonella strains used for the host range. The ten phages were selected for EOP and physio-chemical characterisation. All phages showed high production efficiency in at least one isolate which was not of their host, apart from two phages. All phages demonstrated relative stability between -80ºC to 40ºC temperature range, with a slight titre reduction at 50ºC for some phages. Relative stability was also observed at pH 5 to 11 with the highest titres recorded at pH 7 to 9. Phages also demonstrated a significant ability to digest NTS biofilms.

Conclusion: This study presents the availability of potential phage-therapy candidates from Nairobi city county, which can be applied against MDR NTS. The Phages lytic activity with broad pH and temperature stability, and biofilm digestion indicates their potential in therapeutic purposes.

Keywords: Bacteriophages, Non-typhoidal salmonella

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