KENYA MEDICAL RESEARCH INSTITUTE
KEMRI

In Search of Better Health

13th

KEMRI ANNUAL SCIENTIFIC & HEALTH (KASH) CONFERENCE

ABSTRACT BOOK

15th - 17th,
FEBRUARY, 2023

SAFARI PARK HOTEL, NAIROBI, KENYA.

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In Search of Better Health

The 13th KEMRI Annual Scientific & Health (KASH) Conference

15th - 17th February 2023
SAFARI PARK HOTEL,
NAIROBI, KENYA

Theme:
Rethinking strategic research-for-health through partnerships, innovation, evidence generation and knowledge sharing in post-pandemic recovery era

Organized by:
Kenya Medical Research Institute (KEMRI)

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

ACKNOWLEDGEMENTS

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MESSAGE FROM DIRECTOR GENERAL KEMRI

PROF. SAM KARIUKI

I am extremely delighted to be part of the the 13th, KEMRI Annual Scientific and Health conference which we popularly refer as "KASH". KASH has had an incredible journey, one which began with its establishment in 2010 at the KEMRI Training Centre with a handful of scientists and mostly KEMRI members of staff. It was incredible that a decade later, over 600 participants, most among the best rated brains, not just in the country, but globally, are meeting in this picturesque auditorium.

Since its humble inception, KASH is today a special event in the Institute's calendar which serves to promote health science through dialogue and exchange among scientists, health practitioners, development partners and policy makers with an average of 500 participation annually.

It is gratifying that findings, conclusions and recommendations from this conference are shared with the various arms of government and policymakers and contribute directly to national discourse including managing pandemics, Universal Health coverage (UHC) and measuring of scientific development trajectories.

It is therefore with great honor that I welcome you to this Conference from this 15th to 17th February 2023 with very rich scientific menu and being held alongside the two-day 4th Kenya National Malaria Forum (KNMF) that brings together experts and stakeholders involved in malaria control in the country. This is significant because both forums – KASH and KNMF seek to address specific, but similar needs that are relevant to contributing new knowledge from research and learnt lessons from key stakeholders in health and disease prevention strategies, control interventions and management that eventually inform policy and practice.

I am happy to note that an apt theme, **"Rethinking strategic research-for-health through partnerships, innovation, evidence generation, and knowledge sharing in post-pandemic recovery era"** is for 13th KASH conference. It also has several other sub-themes including Sustainable health systems, UHC and public health strengthening; Emerging research priorities on mental health and other non-communicable diseases; New frontiers on natural products, drug discovery and therapeutics; Research for effective management of sexual and reproductive health: adolescent, maternal and child health; Emerging and re-emerging infectious and parasitic diseases; Advances in genomics, diagnostics, vaccines and innovations in human health and effects of climate change, environment and one-health.

We are delighted that the Cabinet Secretary for Health, Dr. Susan Nakhumicha spared time to officiate during this joint opening ceremony.

I note with appreciation that 13th KASH recorded one of the highest abstract submissions of 253 that will be presented in 24 parallel oral sessions and 48 posters. The abstracts were received from different countries including the United State of America, Netherlands, Germany, Ghana, Scotland and from our neighbours Tanzania among others.

However, the heroes and heroines of 13th KASH Conference are you the participants who not only submitted abstracts but have also availed yourself to this conference. Indeed, we all know that without your valued participation, then we don't have a conference.
On the same breath, I want on behalf of KEMRI, to appreciate and congratulate all our sponsors and partners, some who have remained steadfast over the last 12 years. There is no doubt that it is this wonderful co-operation and partnership among others which have made this KEMRI what it is today-A pearl in health research development not only in Kenya and Africa, but globally.

I most sincerely appreciate the KEMRI Board of Directors, led by our Chairman, Dr. Daniel M. Mbinda, my colleagues researchers and those in management and members of the KASH Organising Committee led by Dr. Cecilia Mbae. We remain grateful to the Government of Kenya through the Ministry of Health for guidance, financial support and leadership to the Institute and for this conference.

Prof. Sam Kariuki
Ag. Director General,
KENYA MEDICAL RESEARCH INSTITUTE

CONFERENCE OVERVIEW, **DR. CECILIA MBAE**

It is a great honor to welcome you all to the 13th KEMRI Annual Scientific and Health Conference (KASH) 2022 which is being hosted physically as well as - virtually from 15th -17th February, 2023.

For the last 13 years KASH Conference & Exhibition has continued to provide a premier platform bringing together diverse actors in the health research. The 13th KASH conference's main theme is **"Rethinking strategic research-for-health through partnerships, innovation, evidence generation, and knowledge sharing in post-pandemic recovery era".**

The theme is anchored on the following sub-themes: ***Sustainable health systems, UHC and public health strengthening, Emerging evidence on mental health and other non-communicable diseases, New frontiers on natural products, drug discovery and therapeutics, Management of sexual and reproductive health; adolescent, maternal and child health, Emerging and re-emerging infectious and parasitic diseases, Advances in genomics, diagnostics, vaccines and innovations for human health and Effects of climate change, environment and one-health***

The KASH Conference is a core event within KEMRI's calendar of events that aims to bring together researchers, collaborators (local and international), policy makers and other stakeholders in medical research. This year, the Kenya National Malaria Forum is hosting their 4th KNMF Conference alongside the KASH Conference, we are expecting over 600 participants from various local, regional, and international institutions which signifies the importance of this premier scientific event.

The KASH Conference continues to provide great opportunities for sharing, cross-learning and mentoring of upcoming scientists as well as providing a platform for the discussions of the current health research challenges, exchange of new knowledge that will ultimately shape the future of health research in Kenya, Africa and globally.

This year's Conference features a rich and diverse menu of scientific content, with five plenary talks and 10 symposia with discussions on topical issues in health research. I am happy to report that we received a total of 253 abstract submissions which will be presented in 24 parallel oral sessions and 48 posters. These abstracts are from different countries including US, Netherlands, Germany, Ghana, Scotland, Tanzania among others. This means that KASH is now an international conference. We have also given our young scientists to showcase their research findings through the young investigators session which attracted 26 submissions, where the winners will be awarded. Besides this, there will be diverse opportunities to network with colleagues, form new acquaintances, and forge long-term partnerships from both in-person and the virtual interactive platform.

The conference will have distinguished Keynote and plenary speakers who are world class scientists with deep understanding and wealth of knowledge of not only disease burden, but practical knowledge of appropriate health interventions. The **Opening Keynote Address will be given by Dr Mercy Mwangangi, Topic: Spotlighting the essential role of investing in research for Health Systems Strengthening.**

The plenary speakers will be; ***Dr. Roberts Frank who will present the "Relevance of periodontal disease in the context of HIV infection"; Prof Wallace Bulimo "The data revolution, how KEMRI is riding the fourth wave"; Dr. Beth Tippet "Knowledge mobilization for increasing the impact of your research" and Prof. Samson Muuo "Genomics advancements in Vaccine and Diagnostic development in Kenya".***

We wish to thank our sponsors Kenya Commercial Bank (KCB) (Platinum) and Carramore International (Gold), and the more than 20 exhibitors who have partnered with us.

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, WEDNESDAY 15TH FEBRUARY 2023

TIME	OFFICIAL OPENING SESSION & KEYNOTE ADDRESS
0700-0900hrs	**Arrival & Registration**
	Kenya National and East Africa Anthem
0900 - 0910hrs	**KASH Conference overview:** Chair of KASH Organizing Committee, **Dr. Cecilia Mbae** **KNMF Conference overview:** Chair of KNMF Committee, **Prof. Isabella Oyier**
0910 - 0945hrs	**Opening Remarks** Ag. Director General and CEO, KEMRI **Prof. Sam Kariuki** Chairman, KEMRI Board of Directors- **Dr. Daniel Mbinda** USAID Health Population and Nutrition Director - **Dr. John Kuehnle** WHO Representative - **Dr. Abdourahmane Diallo**
0945-0950hrs	**Opening Remarks and welcoming of the Chief Guest** Director General- Ministry of Health - **Dr. Patrick Amoth**
0950hrs-1005hrs	**Address and Official opening by Chief Guest-** Cabinet Secretary- Ministry of Health - **Dr. Susan N. Wafula**
1005 - 1035hrs	Opening Keynote Address: **Dr. Mercy Mwangangi** **Topic: Spotlighting the essential role of investing in research for Health Systems Strengthening**
Master of Ceremony:	**Mr. John Musau**
Session Chair	**Dr. Benjamin Tsofa & Dr. Andrew Mulwa**
Rapporteur	**Dr. Damaris Matoke-Muhia & Dr. Katherine Kilonzo**

1035 – 1115hrs TEA BREAK

SCIENTIFIC SESSION 1 – 6 PARALLEL SESSIONS

1115 - 1245hrs	**1115 - 1245hrs**	**1115 - 1245hrs**	**1115 - 1245hrs**	**1115 - 1245hrs**	**1115 - 1245hrs**
Scientific Session 1: TB-1 **VENUE: Amboseli**	**Scientific Session 2: Vector Biology-1** **VENUE: Tsavo**	**Scientific Session 3: NTDs and One Health** **VENUE: Samburu**	**Scientific Session 4: Natural Products** **VENUE: Bogoria**	**Scientific Session 5: Public Health-1** **VENUE: Mt. Kenya C**	**Scientific Session 6: MCH-1** **VENUE: Mt. Kenya D**
Session Chair: Dr. Jane Onga'ngo **Rapporteur:** Barbara Miheso	**Session Chair:** Dr. Luna Kamau **Rapporteur:** Tiffany Wandera	**Session Chair:** Prof. Samson Muuo **Rapporteur:** Joanne Jepkemei	**Session Chair:** Dr Beatrice Irungu **Rapporteur:** Dr. Sospeter Njeru	**Session Chair:** Dr. Sam Aketch **Rapporteur:** Sharon Mukua	**Session Chair:** Dr Benson Singa **Rapporteur:** Schiller Mbuka

1245-1345HRS: LUNCH BREAK

1345-1430HRS POSTER SESSION (Abstract No. 001-022)

SCIENTIFIC SESSION 7, AND SYMPOSIUM 1-5

1430 – 1700hrs	**1430 – 1700hrs**	**1430 – 1700hrs**	**1430 – 1700hrs**	**1430 – 1700hrs**	**1430 – 1700hrs**
Scientific Session 7: Young Investigators **VENUE: Amboseli**	**Symposium 1 Knowledge Management** **VENUE: Tsavo**	**Symposium 2 PAMCA** **VENUE: Samburu**	**Symposium 3: Family Health Unit (FHU)** **VENUE: Bogoria**	**Symposium 4: NUITM** **VENUE: Mt. Kenya C**	**Symposium 5: Frontiers in Tungiasis** **VENUE: Mt. Kenya D**

Session Chair: Dr. Joseph Mwangangi, Dr. Doris Njomo **Judges:** Dr. Limbaso Konongoi, Francis Kimani	**Session Chair:** Prof. Jennifer Orwa **Rapporteurs:** Dr. Benjamin Tsofa & Eunice Wambui	**Session Chair:** Dr. Simon Muriu **Rapporteur:** Dr. Lydia Kibe & Dr. Damaris Matoke	**Chair:** Dr. Richard Omore **Rapporteur:** Dr. Victor Akelo & Sheila Mbaabu	**Session Chair:** Prof. Satoshi Kaneko **Rapporteur:** Dr. Muuo Nzou & Susan Kavai	**Session Chair:** Dr. Lynne Elson **Rapporteur:** Ulrike Fillinger & Dr. Sophie Uyoga
END OF FIRST DAY					

DAY TWO, THURSDAY 16TH FEBRUARY 2023

TIME	PLENARY SESSION
0700-0830hrs	**Arrival & Registration**
0830- 0855hrs	Plenary Session 1: **Dr. Roberts Frank -** *University of Washington* Topic: Relevance of periodontal disease in the context of HIV infection
0855 - 0920hrs	Plenary Session 2: **Prof. Wallace Bulimo** - *Kenya Medical Research Institute* Topic: The data revolution, how KEMRI is riding the fourth wave
0920 -0945hrs	Plenary session 3: **Dr. Beth Tippet -** *Nyanja Health Research Institute in Malawi* Topic: Knowledge mobilization for increasing the impact of your research
0945-1010hrs	Plenary Session 4: **Prof. Samson Muuo -** *Kenya Medical Research Institute* Topic: Genomics advancements in Vaccine and Diagnostic development in Kenya
Session Chair	**Prof. Charles Mbogo**
Rapporteur	**Susan Kavai**
1010 - 1045hrs	**TEA BREAK**

1045 – 1245hrs	**1045 –1245hrs**	**1045 – 1245hrs**	**1045 – 245hrs**	**1045 – 1245hrs**	**1045 – 1245hrs**
Scientific Session 8: TB-2 **VENUE: Amboseli**	**Scientific Session 9: COVID-19** **VENUE: Tsavo**	**Scientific Session 10: Health Systems-1** **VENUE: Samburu**	**Scientific Session 11: NCDs** **VENUE: Bogoria**	**Scientific Session 12: Vector Biology-2** **VENUE: Mt. Kenya C**	**Scientific Session 13: Sexual Reproductive Health-1** **VENUE: Mt. Kenya D**
Session Chair : Dr. Hellen Meme **Rapporteur :** Barbara Miheso	**Session Chair :** Dr. Samoel Khamadi **Rapporteur:** Janet Majanja	**Session Chair :** Bridget Kimani **Rapporteur :** Tabitha Kanyui	**Session Chair :** Dr Lydia Kaduka **Rapporteur :** Sarah Karanja	**Session Chair:** Dr. Joel Lutomiah **Rapporteur:** Sheila Mbaabu	**Session Chair:** Dr Betty Njoroge **Rapporteur:** Schiller Mbuka
1245-1345HRS: LUNCH BREAK					
1345-1430HRS POSTER SESSION (Abstract No. 023-045)					
SCIENTIFIC SESSION 15, SYPOSIUM 6-10					
1430 – 1700hrs	**1430 – 1700hrs**	**1430 – 1700hrs**	**1430 – 1700hrs**	**1430 – 1700hrss**	**1430 – 1700hrs**
Scientific Session 14: Mental Health **VENUE: Amboseli**	**Symposium 6 SERU** **VENUE: Tsavo**	**Symposium 7: NAPREDA** **VENUE: Samburu**	**Symposium 8: Impact of Climate Change** **VENUE: Bogoria**	**Symposium 9: BOHEMIA** **VENUE: Mt. Kenya C**	**Symposium 10: Nanotechnology** **VENUE: Mt. Kenya D**
Session Chair: Dr. Lucy Chite **Rapporteur:** Dr. Linus Ndegwa	**Session Chair:** Enock Kebenei **Rapporteur:** Carolyne Kithinji & Susan Kavai	**Chair:** Dr. Festus Tolo **Rapporteur:** Dr. Peter Mwitari & Dr. Beatrice Irungu	**Chair:** Prof. Inah Danquah **Rapporteur:** Dr. Eric Muok & Dr. Steve Wandiga	**Chair:** Dr. Marta Maia **Rapporteur:** Dr. Joseph Mwangangi	**Session Chair:** Prof. Bernhards Ogutu **Rapporteur:** Dr. Jeremiah Gathirwa & Kelvin Thiong'o
END OF SECOND DAY					

DAY THREE, FRIDAY 17TH FEBRUARY 2023

TIME	PARALLEL SCIENTIFIC SESSIONS , 15-20
0700 - 0830hrs	**Arrival & Registration**

PARALLEL SCIENTIFIC SESSIONS , 15-20

0830hrs-1000hrs	0830hrs-1000hrs	0830hrs-1000hrs	0830hrs-1000hrs	0830hrs-1000hrs	0830hrs-1000hrs
Scientific Session 15: AMR-1 **VENUE: Amboseli**	**Scientific Session 16:Health Systems-2** **VENUE: Tsavo**	**Scientific Session 17: Genomics** **VENUE: Samburu**	**Scientific Session 18: Public Health-2** **VENUE: Bogoria**	**Scientific Session 19: Sexual Reproductive Health-2** **VENUE: Mt. Kenya C**	**Scientific Session 20: HIV** **VENUE: Mt Kenya D**
Session Chair: Dr John Mwaniki **Rapporteur:** Kelvin Kering	**Session Chair:** Dr Richard Mutisya **Rapporteur:** Ishmael Ahamed	**Session Chair:** Dr Luna Kamau **Rapporteur:** Tiffany Wandera	**Session Chair:** Dr. Sam Aketch **Rapporteur:** Asiko Ong'aya	**Session Chair:** Dr Betty Njoroge **Rapporteur:** Irene Thuo	**Session Chair:** Dr. Samoel Khamadi **Rapporteur:** Hellen Koka

1000 - 1045hrs TEA BREAK

PARALLEL SCIENTIFIC SESSION 21 – 24

1045 – 1245hrs	1045 – 1245hrs	1045 – 1245hrs	1045 – 1245hrs
Scientific Session 21: Health Systems 3 **VENUE: Amboseli**	**Scientific Session 22: MCH-2** **VENUE: Tsavo**	**Session 23: Malaria** **VENUE: Samburu**	**Scientific Session 24: AMR-2** **VENUE: Bogoria**
Session Chair: Dr Richard Mutisya **Rapporteur:** Ishmael Ahamed	**Session Chair:** Dr. Benson Singa **Rapporteur:** Lillian Mayieka	**Session Chair:** Francis Kimani **Rapporteur:** Rukiya M. Haji	**Session Chair:** Dr. John Mwaniki **Rapporteur:** Kelvin Kering

1300-1400HRS: LUNCH BREAK

CLOSING SESSION

1400-1600hrs	Master Of Ceremony: **Dr. Sophie Uyoga**
	Conference outcomes & resolutions Chief Rapporteur: **Dr. Steve Wandiga**
	Awarding Ceremony: **Dr. Vera Manduku**
	Sponsors and Exhibitors Session: **Prof. Charles Mbogo**
	Official Closing remarks **KASH Chair: Dr. Cecilia Mbae** **Ag. Director General & CEO, KEMRI Prof. Sam Kariuki** **Chair KEMRI Board of Directors**
	Vote of thanks - **Dr. Damaris Matoke-Muhia**

END OF CONFERENCE

KEY NOTE SPEAKER

Dr. Mercy Mwangangi

BIO

Dr. Mwangangi is a Health Economist and Policy Analyst with a background in Medicine. She has knowledge and experience in performing high quality Strategic Health Program Planning, Monitoring and Evaluation activities focusing on Universal Health Coverage and Primary Health Care with considerable experience in carrying out in depth Health Situation Analysis and producing of workable recommendations and guidelines on future program directions, incorporating international policies and standards, tailored to local needs

Topic: Spotlighting the essential role of investing in research for Health Systems Strengthening

PLENARY SPEAKER

Dr. Roberts Frank

BIO

Dr. Roberts is a holder of BS, DDS, a certificate in periodontics, and PhD in Microbiology. He is a Professor of Periodontics, the University of Washington, the Associate Dean for Regional & Global Affairs, Director of the Regional Initiatives in Dental Education (RIDE) program and the Pre-doctoral Program Director in the Periodontics Department at the University of Washington School of Dentistry (UWSOD). He has over twenty-five years of experience in research and dental education. He has served as Chief of Periodontics at the Seattle Veterans Administration Medical Center since 1997 where he practices and teaches clinically, with an inter-professional team-care approach. Knowledgeable in experiential learning, Dr. Roberts will serve as a mentor candidate for the Training in Research in Oral Health (TRIOH): A multidisciplinary collaboration between Dentistry, Nursing, and Pediatrics to build up research capacity in global oral health. He has widely published his work in peer review journals.

Topic: Relevance of periodontal disease in the context of HIV infection

Abstract:

Periodontitis is a chronic inflammatory disease that affects the supporting structures of the teeth and leads to early tooth loss and other significant comorbidities. It has been recognized as an early sign of HIV infection with serious complications in untreated HIV patients. This lecture will discuss the presentations of various periodontal infections and potential diagnosis and treatment options available to non-dentists.

PLENARY SPEAKER

Prof. Wallace Bulimo

Topic: The data revolution, how KEMRI is riding the fourth wave

Abstract

How Can Data Science be Leveraged to Improve KEMRI's Research Impact?

The health research ecosystem is constantly evolving, and technology is a key driver in this evolution. One of the most promising technologies is data science, which has wide applicability and potential. The potential application of data science in health research, however, is suboptimal and is not fully appreciated or understood, despite the fact that institute scientists already have and continue to generate massive amounts of health-related research data on a daily basis as they pursue delivery of the institute's mission. Data science is an interdisciplinary field that extracts knowledge and insights from many structural and unstructured data, using scientific methods, data mining techniques, machine-learning algorithms, and big data. It draws upon statistics, computer science, and domain expertise to make sense of and gain new insights out of data. In health research, it can be used to analyze large and diverse amounts of data sets, identify patterns, and make predictions for individuals, populations or disease-causing pathogens. One such application is in precision medicine, a personalized approach to health-care that uses data to determine the most effective treatment options for each patient. Data scientists can guide prediction-medicine by identifying patterns in large amounts of data, such as genetic data, medical records, and clinical trial outcomes to tailor treatment options.

Another key application of data science in health research is in the analysis of population level health data, such as entire communities or countries. By analyzing data on the health of a population, data scientists are able to identify patterns and trends that can aid in the improvement of the population's overall health.

In addition, data science plays a crucial role in the fight against COVID-19. By analyzing data on the virus's spread, data scientists can identify patterns and predict its future spread. These predictions and associations inform public health policies and guide resource allocation.

Prof. Bulimo will discuss the importance of data science in the advancement of healthcare and health research, emphasizing on its applications, benefits, and the exciting future prospects of Data science for KEMRI in this field

PLENARY SPEAKER

Dr. Beth Tippet

BIO

Dr. Barr is an epidemiologist with over 20 years of program and research experience in Southern and Eastern Africa. After completing her secondary school studies in Kenya, she attended university in the US before returning to Africa to serve in the public health arena. She worked with Baylor College of Medicine in Botswana and Malawi establishing training projects in pediatric HIV treatment before joining the US Centers for Disease Control and Prevention (CDC) in Malawi. Dr Tippett Barr then worked for several years in the prevention of mother-to-child transmission of HIV (PMTCT) and was a key team member in the development and implementation of the historic "PMTCT Option B+" approach with the Malawi Ministry of Health, when antiretroviral therapy was first offered to pregnant and breastfeeding women regardless of CD4 count or clinical stage. In 2015, Dr. Barr became the CDC-Zimbabwe Country Director, and in 2018 moved back to Kenya as CDC's Western Kenya Director, working in collaboration with KEMRI's Centre for Global Health Research to establish the Family Health Unit. In 2022 Dr. Barr left CDC-Kenya to found the Nyanja Health Research Institute in Malawi, an organization with a dual mandate to conduct high-impact research, and to train young researchers in how to disseminate their research findings with maximum impact.

Topic: Knowledge mobilization for increasing the impact of your research

Abstract:

Knowledge mobilization is the intentional and coordinated effort to raise awareness of research findings locally, nationally, and internationally. It bridges the historical silos between health research and public sector health programmes, and creates a path through which we can streamline the process of turning research findings into health policy. In this presentation, we will examine how research findings typically move through the research to policy process, and then discuss how researchers can develop and apply a knowledge mobilization framework to their own research studies, positioning their findings to be more readily adopted by **policy-makers.**

PLENARY SPEAKER

Prof. Samson Muuo

BIO

Muuo Nzou is an Assistant Principal Research Scientist, at the Center for Microbiology Research, Kenya Medical Research Institute and a Visiting Associate Professor, Nagasaki University. Previously, He worked as an Associate Professor, Institute of Tropical Medicine and Global Health, Nagasaki University, and a Principal Research Officer Nagasaki University, Institute of Tropical Medicine -Kenya Medical Research Institute Projects (NUITM-KEMRI PROJECT). He holds a MSc in Medical virology from Jomo Kenyatta University of Agriculture and Technology, a PhD in Medical Sciences from Nagasaki University and a Health Research Capacity Strengthening Postdoctoral Grant, Wellcome Trust, His interests in communicable and noncommunicable diseases focus on vaccine and diagnostics development, molecular epidemiology, surveillance and omics leading to drug resistance patterns in humans, where he has published extensively in these areas. He is also a member of surveillance cross-cutting sub-group of the World Health Organization (WHO) Diagnostic Technical Advisory Group (DTAG) for Neglected Tropical Diseases. He has mentored and supervised Masters and PhD students from different institutions internationally

Topic: Genomics advancements in Vaccine and Diagnostic development in Kenya

Abstract:

Abstract Vaccine provide active defence for specific diseases, where's diagnostics provide means of detecting the diseases. Vaccines play a vital role in enhancing the body's immunity to defend against diseases while diagnostics are key in detecting diseases to ensure their treatment, control, surveillance and monitoring systems. Africa and Kenya has lagged behind in coming up with novel vaccines and diagnostics, mostly due to lack of equipment and limited skills. Over, the years, this has change and African scientists have embarked in research to identify candidate vaccine and diagnostic biomarkers. Exploratory research has been enhanced which is key in innovations and technology advancement. KEMRI, has taken lead in research for Vaccine and diagnostic research. This study reports applications of systems biology and immunology through bioinformatics, artificial intelligence and literature guided approaches to identify putative biomarkers that will be validated experimentally using cutting edge and molecular biology techniques including but not limited to next generation genomic sequencing, polymerase chain reaction, cloning and carbodiimide chemistry. The validated biomarkers will be used in pre-clinical testing which is vital in the future development of vaccines and diagnostic kits. To date, the study has been able to identify several putative biomarkers for SARS-COV2 vaccine and diagnostic development. Additionally, it has been able to develop and evaluate over 50 biomarkers for detection of several infectious diseases such as Leishmaniasis, Schistosomiasis, HIV, Trachomatis and Filariasis. Current developments focus on arboviruses, Echinococcosis, and cancer vaccines. Conclusion Development of candidate biomarkers for vaccine and diagnostic against diseases is a holistic manner for Africa nations to have custom made vaccines which might ultimately improve their performance.

Key words Genomics, Polymerase Chain reaction, biomarkers, next generation sequencing

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- Master of Science in Computer Science
- Master of Science in Sustainable Development
- Doctor of Philosophy (PhD)- Education
- Doctor of Philosophy (PhD)- Law and Politics
- Doctor of Philosophy (PhD)- Public Health
- Doctorate of Business Administration (DBA)
- Doctorate of Education (EdD)
- Doctor of Philosophy (PhD) in Accounting and Finance

University of Suffolk

- BA (Hons) Business Management*
- LLB (Hons) Law*
- BSc (Hons) International Nursing (Top Up)
- BSc (Hons) Computing*
- MSc Public Health
- MBA

*Subject to Validation

University of East London

- LLM
- MBA
- MSc International Business Management
- MSc International Relations
- MSc Data Science
- MSc Computer Science
- MSc Big Data Technologies
- MSc Information Security and Digital Forensics
- MSc Construction Engineering Management
- MSc Oil, Gas and Energy Management
- MSc Business Psychology

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- MSc Psychology
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For more information contact:
Mr Samson Kithika Mbondo, Business Development Manager, Unicaf Kenya
at **0714655897** or email at **s.mbondo@kenya.unicaf.org**
link.unicaf.org/KEMRI

In Search of Better Health

POSTGRADUATE COURSES: MAY 2023 INTAKE

Applications are invited for admission into the following programmes for self-sponsored students under the collaborative JKUAT/KEMRI postgraduate training based at the KEMRI Graduate School.

1. Master of Science (M.Sc.)	2-3 Year Programme
2. Doctor of Philosophy (Ph.D.)	3-4 Year Programme

COURSES	*MINIMUM ENTRY REQUIREMENT
MASTER OF SCIENCE (M.SC) **A. PUBLIC HEALTH PROGRAMME** 1. MSc. Public Health 2. MSc. Epidemiology and Biostatistics 3. MSc. Global Health **B. BIOMEDICAL SCIENCES PROGRAMME** 4. MSc. Medical Microbiology 5. MSc. Medical Virology 6. MSc. Medical Mycology 7. MSc. Medical Parasitology and Entomology 8. MSc. Molecular Medicine **C. MEDICINAL CHEMISTRY PROGRAMME** 9. Medicinal Chemistry 10. Medicinal Phytochemistry	The common regulations for all Masters degrees in the University shall apply. The following shall be eligible for admission in KEMRI Graduate School under the JKUAT/KEMRI Collaboration: ○ Bachelor's Degree, Second Class (Upper Division) in a relevant field of study or its equivalent from JKUAT or any other Institution recognized by JKUAT Senate. **OR** ○ Bachelor's Degree, Second class Honors (Lower Division) in a relevant field of study or its equivalent from JKUAT or any other Institution recognized by JKUAT Senate, with at least two years post-qualification work/research experience **OR** ○ Bachelor's Degree with a Pass and a Postgraduate Diploma in a relevant field of study.
DOCTOR OF PHILOSOPHY (Ph.D.) (In the MSc areas above)	The minimum entry requirements of all PhDs in JKUAT shall apply.

More information about the programmes are available on our website: ***www.kemri.go.ke/graduate-school/***

*NB. These are the minimum requirements; other conditions may apply for individual programmes.

Application Procedure and Deadline

Candidates seeking admission are required to fill out application forms obtained from the offices/Website indicated below upon payment of non-refundable application fees of Kshs.1,500/-. Completed application forms and the original receipts for application fees should be returned to the **KEMRI Graduate School** (Located at the Training Centre, KEMRI HQ, not later than **April, 14 2023.**

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The genomics and bioinformatics unit, under the Centre for Biotechnology Research and Development (CBRD), was established in 2020. The facility is equipped with the state-of-the-art Sequencing machines including the Illumina Miseq and Oxford nanopore GridION sequencing platforms. This facility is also equipped with the ability to generate and analyse genome sequences by offering bioinformatics and data management support.

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Bioinformatics and Data Analysis

The process of analysis of sequences generated to make meaningful data and information. Bioinformatics forms an integral part of high throughput sequencing workflow

Training and Capacity Building

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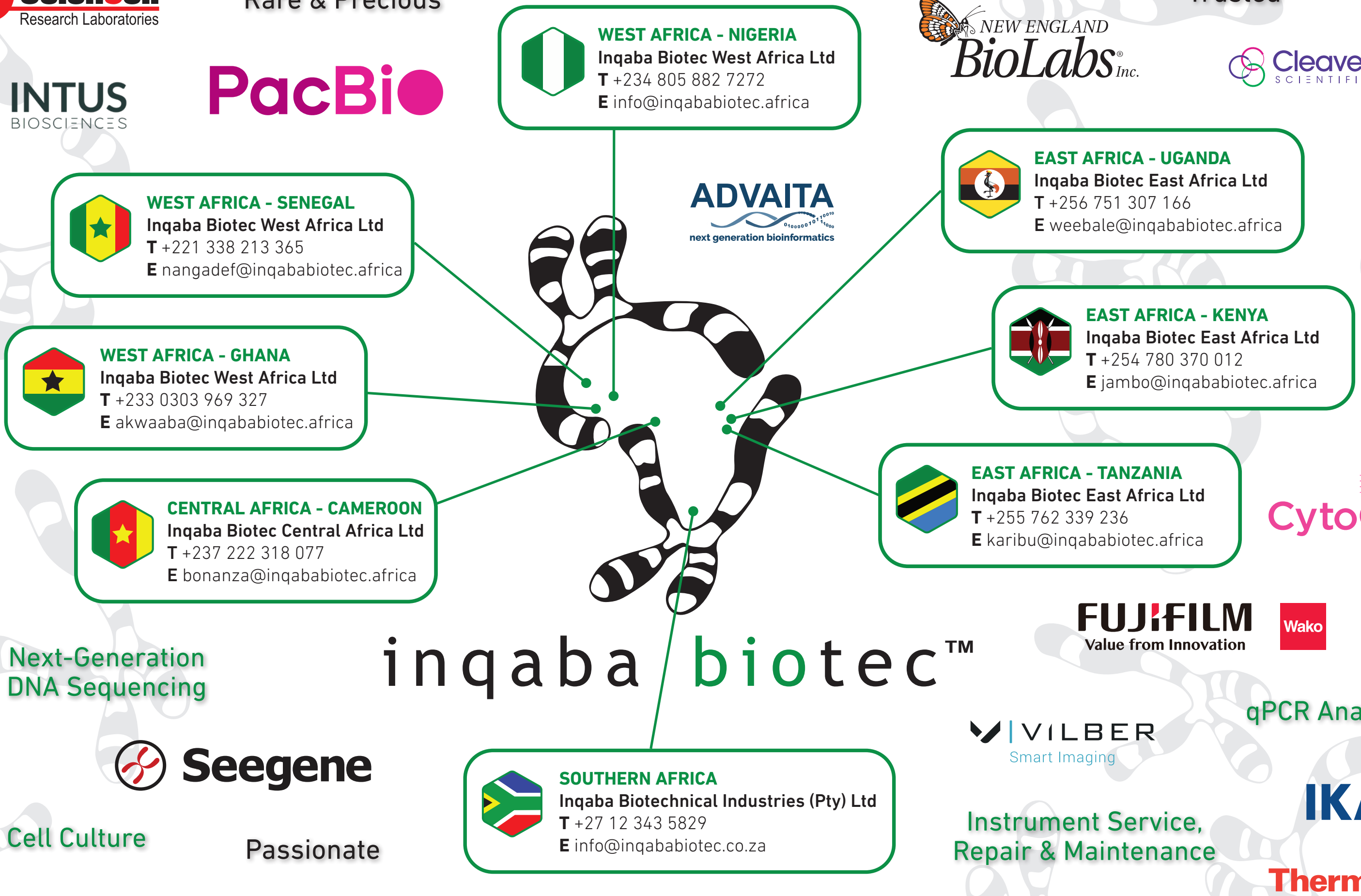
✉ genomics@kemri.go.ke



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FULL PROGRAM

DAY 1, WEDNESDAY, 15th FEBRUARY 2023

TIME	OFFICIAL OPENING SESSION & KEYNOTE ADDRESS
0700-0900hrs	Arrival and Registration of Delegates
	Kenya National and East Africa Anthem
0900 – 0910hrs	**KASH Conference overview:** Chair of KASH Organizing Committee, **Dr. Cecilia Mbae** **KNMF Conference overview:** Chair of KNMF Committee, **Prof. Isabella Oyier**
0910 - 0945hrs	**Opening Remarks** Ag. Director General and CEO, KEMRI **Prof. Sam Kariuki** Chairman, KEMRI Board of Directors- **Dr. Daniel Mbinda** USAID Health Population and Nutrition Director - **Dr. John Kuehnle** WHO Representative - **Dr. Abdourahmane Diallo**
0945-0950hrs	**Opening Remarks and welcoming of the Chief Guest** Director General- Ministry of Health - **Dr. Patrick Amoth**
0950hrs-1005hrs	**Address and Official opening by Chief Guest-** Cabinet Secretary- Ministry of Health - **Dr. Susan N. Wafula**
1005 - 1035hrs	Opening Keynote Address: **Dr Mercy Mwangangi** **Topic: Spotlighting the essential role of investing in research for Health Systems Strengthening**
Master of Ceremony:	**Mr. John Musau**
Session Chair	**Dr. Benjamin Tsofa & Dr. Andrew Mulwa**
Rapporteur	**Dr. Damaris Matoke-Muhia & Dr. Katherine Kilonzo**

1035 – 1115hrs TEA BREAK

1115-1245hrs SCIENTIFIC SESSION 1-6

Time (EAT) 1115hrs-1245hrs	Abstract No	Scientific Session 1: TB-1 VENUE: Amboseli Session Chair: Dr. Jane Ong'ang'o Rapporteur: Barbara Miheso
	1.	Isolation of Non-Tuberculous Mycobacterial Infections among Tuberculosis presumptive cases at the National Tuberculosis Reference Laboratory Kenya, 2018 –2019; **George Kamau**
	2.	Distribution of Mtb genotypes/strains among presumptive multidrug resistant tuberculosis patients in western Kenya; **Albert Okumu**
	3.	Assessing impact of pre-analytical challenges experienced in samples received for TB diagnosis in an MDR surveillance in Western Kenya and North Rift; **Joseph Orure**
	4.	Assessment of TB cases tested using GeneXpert in Ndaragwa Sub county,2021; **Lucy Njoki**
	5.	Spectrum of Fungi Isolated from Sputum of Patients Attending Tuberculosis Reference Facilities in Kenya; **Abdi Mohamed**
	6.	Active Community Transmission for Drug-Resistant Tuberculosis: Are We Safe?; **James Maragia**
	7.	Sputum Smear Conversion rates in relation to HIV status after 6 months of Tuberculosis treatment in Nairobi Kenya; **Dorcas Ihuthia**

Time (EAT) 1115hrs-1245hrs	Abstract No	Scientific Session 2: Vector Biology-1 Venue: Tsavo Chair: Dr. Luna Kamau Rapporteur: Tiffany Wandera
	8.	Mosquitocidal Effect and Pharmacokinetics of Different Ivermectin Dose Regimens in Preparation for Bohemia Cluster Randomized Controlled Trial; **Yvonne Kamau**
	9.	UDP-Glucuronosyltransferase plays a key role in Insecticide Resistance: A study using bioinformatics approaches; **Cynthia Odhiambo**
	10.	Age grading of Afrotropical malaria vectors using MALDI TOF MS; **Mercy Tuwei**
	11.	Resting behaviour of African malaria mosquitoes in an era of high indoor insecticide use; **Kevin Owuor**
	12.	A field bioassay for assessing ivermectin bio-efficacy in malaria vectors; **Kelly Ominde**
	13.	Ivermectin mass drug administration for malaria control (BOHEMIA): updates on trial progress; **Marta Maia**
	14.	Upscaling integrated vector management in the control of malaria and schistosomiasis in Mwea, Kirinyaga County. Baseline Epidemiological and Entomological results; **Paul Gichuki**
	15.	Over-expression of CYP6M2, CYP6P3, CYP4H15 and a cuticular protein is associated with transfluthrin response in Anopheles gambiae ss from Bungoma, Western Kenya; **Stephen Okeyo**
	16.	Controlling malaria from within: Using microbial symbionts to decrease vector competence; **Thomas Onchuru**
Time (EAT) 1115hrs-1245hrs	**Abstract No**	**Scientific Session 3: NTDs and One Health VENUE: Samburu Session Chair: Prof. Samson Muoo Rapporteur: Joan Jepkemei**
	17.	Epidemiological profile of Leprosy cases and the Treatment Outcomes, Kenya January 2011-To December 2021; **Vallerian Karani**
	18.	Production and use of polyclonal antibodies for the diagnosis of human African trypanosomiasis; **Dawala Koromtili**
	19.	Exploring Service Provider Related Determinants of Surgery Non-acceptance Among Women with Trachoma Trichiasis in North Pokot Sub County; **Victoria Akoth**
	20.	Presence of an invasive exotic freshwater snail, Pomacea canaliculata (Gastropoda: Ampullaridae) in Mwea Irrigation Scheme, Kirinyaga County: Potential implications for public health and wetlands biodiversity; **Martin Mutuku**
	21.	Severe dengue in Mandera : a case for event based surveillance; **Albert Nyunja**
Time (EAT) 1115hrs-1245hrs	**Abstract No**	**Scientific Session 4: Natural Products VENUE: Bogoria Session Chair: Dr. Beatrice Irungu Rapporteur: Dr. Sospeter Njeru**
	22.	LC-MS/MS method for simultaneous determination of selected antidiabetic adulterants in formulated herbal remedies being sold in Nairobi and Uasin Gishu Counties, Kenya; **Caroline Maina**
	23.	Antimicrobial activities and phytochemical content of honey and pollen of Meliponula beccarii and Plebeina hildebrandti from Baringo County; **Chepkemoi Christine**
	24.	In silico evaluation and prediction of novel pyrazoline, pyrazole and isoxazoline derivatives of Polygonum senegalense chalcones as anti-cancer agents; **Evans Okemwa**
	25.	Evaluation of Effects of Spirulina Extracts on Immunologic Dysfunction and Inflammation Associated with Aflatoxin B1 Induced Toxicity in Mice; **Gilbert Kipkoech**
	26.	Antimycobacterial Activity of Albizia zygia (Dc.) J.F. Macrb Root Bark Extracts tested singly and in Combination, their Cytotoxicity, and Phytochemicals Profiles; **Kehongo Moses**
	27.	Phytochemical and anti-inflammation activity of *Fagaropsis angolensis and Fagaropsis hildebrandtii* using animal model; **Maloba Mukhunya**

	28.	Anti-inflammatory mechanisms of action of a herbal combination remedy for the management of COVID-19 and other inflammatory diseases incuding arthritis; **Peter Mwitari**
	29.	*In vivo* anti-inflammatory potential, synergy, gene expression profiles and safety of selected medicinal plants on rheumatoid arthritis; **Mercy Jepkorir**
	30.	Formulation, Characterization, and Efficacy Evaluation of *Moringa oleifera* Leaf Polyphenols-Loaded Phytosome Delivery System; **Jecinta Wanjiru**
	31.	Fusidic acid-based drug combination exibit enhanced activity aganist Mycobacterium tuberculosis; **Charles Omollo**
Time (EAT) 1115hrs-1245hrs	**Abstract No**	**Scientific Session 5: Public Health-1 VENUE: Mt. Kenya C Session Chair: Dr. Sam Aketch Rapporteur: Sharon Mukua**
	32.	Preliminary findings from a photovoice study of community members' choice, experiences and perceptions around fuel use and cooking practices in Mukuru (Kenya) and Ndirande (Malawi); **Fred Orina**
	33.	Individual and social level factors influencing repeated pregnancy among unmarried adolescent mothers in Katavi Region—Tanzania: A qualitative study; **Minyahil Tadesse**
	34.	Population, Climate Change, and Sustainable Development in Africa; **Ndirangu Ngunjiri**
	35.	Host transcriptional RNA signatures as predictive markers of outcome in children with severe lung infection; **Angela Maina**
	36.	Association of household food insecurity and malnutrition among caregivers of children attending mother child clinics in western Kenya; **Olieng'o Okoth**
	37.	Evaluation of community event-based surveillance (cebs)in siaya, kenya 2021; **Cynthia Musumba**
	38.	Assessing the transition of campaign delivery of vitamin a supplementation to routine delivery in Côte d'ivoire and Senegal; **Melissa Baker**
	39.	Assessment of health care waste management (hcwm) in context of environmental safeguards in universal health coverage,kisumu west sub county, Nyahera Sub-county hospital; **Duncan Odhiambo**
	40.	Health-seeking behavior for child illnesses in western Kenya: Qualitative findings from the Child Health and Mortality Prevention Surveillance (CHAMPS) Study; **Sarah Ngere**
	41.	Over-The-Counter Antimicrobial Sale in Kenya: A mystery client survey; **John Ndemi**
	42.	Respiratory Syncytial Virus and Vaccination in Kenya; What are the Healthcare Workers' Preference? **Victor Opere**
Time (EAT) 1115hrs-1245hrs	**Abstract No**	**Scientific Session 6: MCH-1 VENUE: Mt. Kenya D Session Chair: Dr. Benson Singa Rapporteur: Schiller Mbuka**
	43.	Dental Visits and Perceived Benefits of Oral Health during Pregnancy Are Associated with Preterm Birth Outcome: Retrospective Analysis of US PRAMS data from 2009 to 2020; **Hyewon Lee**
	44.	Religious Factors Affecting Utilization of Maternal Health Services in Siaya County, Kenya: A Qualitative Study; **Evans Dzenis**
	45.	Knowledge level and associated factors about sexual and reproductive health rights among University of Gondar students, Gondar Ethiopia; **Keflie Yohannes**
	46.	Prevalence and factors associated with anaemia in pregnancy among women attending first ante-natal care clinic between January 2021 and April 2022 at Doldol Subcounty Hospital, Laikipia County: A cross-sectional study; **David Kariuki**
	47.	Developing and Implementing A Vital Signs And Feeds And Fluids Monitoring Chart For Neonatal Hospital Care In LMIC: A Human-Centered Design; **Naomi Muinga**

	48.	Neonatal sepsis incidence at JM Kariuki Memorial County Referal Hospital, Nyandarua; **Michael Chege**
1245-1345hrs: LUNCH BREAK		
1345-1430hrs POSTER SESSION (001-022)		
SCIENTIFIC SESSION 7, SYMPOSIUM 1-5		
Time (EAT) 1345-1430hrs	**Abstract No**	**Scientific Session 7: Young Investigators VENUE: Amboseli Session Chairs: Dr. Joseph Mwangangi & Dr. Doris Njomo Judges: Dr. Limbaso Konongoi & Francis Kimani**
	49.	Epidemiological analysis and diversity of extended spectrum β-lactamases from escherichia coli and klebsiella species feacal isolates in nairobi, Kenya; **Sophia Kuve**
	50.	Red Blood Cell Parameters and Associated Factors among Infants Attending Sangabuye and Makongoro Health Centres, Mwanza,Tanzania; **Rotgen Arnold**
	51.	Behaviors and Sexual Patterns leading to HIV risk among young transgender women in Coastal Kenya; a qualitative Study; **Melanie Awino**
	52.	Dengue fever outbreak at the Kenyan south coast involving serotype 3, genotypes III and V; **Eric Muthanje**
	53.	A comparative analysis of Portable Microbiological Lab (10ml colilert, 1ml pertrifilm) and the Colilert Quanti - tray 2000; **Nancy Chebichii**
	54.	Bacterial Etiologies of Diarrhea in Children Under 5 Years from Mukuru Informal Settlement and their Antimicrobial Sensitivity Profiles; **Susan Kiiru**
	55.	Characterization of Aeromonas species From Dhaka, Bangladesh through whole genome sequencing and phylogeny; **Rahma Golicha**
	56.	Vectorial capacity and TEP1 genotypes of Anopheles gambiae sensu lato mosquitoes on the Kenyan coast; **Brian Bartilol**
	57.	Genetic Diversity of Nontuberculous Mycobacteria among Symptomatic Tuberculosis Negative Patients from Kenya; **Zakayo Mwangi**
	58.	Entomological surveillance of main malaria vectors on the Kenyan coast using MALDI-TOF MS; **Jonathan Kazungu**
	59.	Therapeutic response to artemisinin combination therapies among individuals with Plasmodium falciparum single infection versus mixed Plasmodium species infections in Kisumu County, western Kenya; **Gladys Chemwor**
	60.	Examining the influence of actor interactions and power dynamics on health system responsiveness in Kilifi County, Kenya; **Nancy Kagwanja**
	61.	County governments' capacity of human resources for health in the implementation of Universal Health Coverage in Kenya; **Ismail Adow**
	62.	Patterns and determinants of antibiotic prescription among children admitted to 12 public hospitals in Kenya: A cross-sectional observational study; **Rachel Otuko**
	63.	Profiling Genome-wide Recombination in Epstein Barr Virus reveals Type-Specific Patterns and associations with Endemic-Burkitt Lymphoma; **Eddy Agwati**
	64.	Cytokine profile of a TB and TB/HIV co-infected cohort in Kenya; **Asiko Ongaya**
	65.	Entomological and epidemiological drivers of visceral and cutaneous leishmaniasis outbreak in Kajiado County, Kenya; **Barrack Omondi**
	66.	Association between five-minute apgar scores and adverse short-term outcomes in neonates in the clinical information network hospitals in kenya, 2018-2022; **Pauline Karing'u**
	67.	Advances in The Ambulatory Management of Pneumothorax: A systematic Review and Meta-Analysis; **Vincent Kipkorir**
	68.	The Effect of climate change on Biomphalaria pfeifferi populations in Asao stream, Western Kenya; **Noel Oduor**

Time (EAT) 1430-1700hrs		**Symposium 1: Knowledge Management VENUE: Tsavo Session Chair: Prof Jennifer Orwa Rapporteurs: Dr. Benjamin Tsofa & Lillian Mayieka**

Time (EAT) 1430-1700hrs		**Syposium 2: PAMCA VENUE: Samburu Session Chair: Dr. Simon Muriu Rapporteur: Dr. Lydia Kibe & Dr. Damaris Matoke**

Time (EAT) 1430-1700hrs		**Symposium 3: Family Health Unit VENUE: Bogoria Session Chair: Dr. Richard Omore Rapporteur: Victor Akelo & Sheila Mbaabu**

Time (EAT) 1430-1700hrs		**Symposium 4: NUITM-KEMRI VENUE: Mt. Kenya C Chair: Prof. Satoshi Kaneko Rapporteur: Dr. Muuo Nzou & Ms. Susan Kavai**

Time (EAT) 1430-1700hrs		**Symposium 5: Frontiers in Tungiasis-Wellcome Trust VENUE: Mt. Kenya D Session Chair: Dr. Lynne Elson Rapporteur: Ulrike Fillinger & Dr. Sophie Uyoga**

DAY TWO, THURSDAY 16th FEBRUARY 2023

0700-0830hrs	Arrival & Registration	
	PLENARY SESSION	
0830- 0855hrs	Plenary Session 1: **Dr. Roberts Frank -** *University of Washington* Topic: Relevance of periodontal disease in the context of HIV infection	
0855- 0920hrs	Plenary Session 2: **Prof Wallace Bulimo -** *Kenya Medical Research Institute* Topic: The data revolution, how KEMRI is riding the fourth wave	
0920 -0945hrs	Plenary session 3: **Dr. Beth Tippet -** *Nyanja Health Research Institute in Malawi* Topic: Knowledge mobilization for increasing the impact of your research	
0945-1010hrs	Plenary Session 4: **Prof. Samson Muuo - -** *Kenya Medical Research Institute* Topic: Genomics advancements in Vaccine and Diagnostic development in Kenya	
Session Chair: Rapporteur:	**Prof. Charles Mbogo Susan Kavai**	
1010-1045hrs	**TEA BREAK**	
Time (EAT) 1045 – 1245hrs	**Abstract No**	**Scientific Session 8: TB-2 Venue: Amboseli Chair: Dr. Hellen Meme Rapporteur: Barbara Miheso**
	69.	Identification of Mycobacterium species causing pulmonary tuberculosis in sputum samples from three heath facilities in Nairobi county, Kenya; **Jeremiah Ndeto**
	70.	Novel Approaches for Developing a Highly Sensitive Molecular Assay for the Diagnosis of Tuberculosis; **Clement Likhovole**
	71.	Implementing and Improving the Quality of Tuberculosis Diagnosis in Kenya in 2021; **Solomon Bundi**
	72.	Scaling up active case finding through integrating quality improvement in tb settings the case of suna west sub county; **Peter Omware**

	73.	Treatment outcomes among cases with Drug Resistant TB, Nairobi County TB Treatment Centers, 2016 – 2022; **Selina Marwa**
	74.	Characterization of first line drug resistance for mycobacterium tuberculosis complex by MTBDRplus™ for specimens received at the National Tuberculosis Reference Laboratory Kenya, 2021; **Beatrice Nasimiyu**
Time (EAT) 1045 – 1245hrs	**Abstract No**	**Scientific Session 9: COVID-19 Venue: Tsavo Session Chair: Dr. Samoel Khamadi Rapporteur: Janet Majanja**
	75.	Severe Covid-19 cases in the county hospitals in rural central Kenya, a case study of JM Kariuki hospital, Nyandarua county; **Angelica Kabue**
	76.	Application of isothermal amplification and detection methods for clinical diagnostics; **Bart Keijser**
	77.	Influenza and SARS-CoV-2 co-circulation in Kenya, Apr 2020 – Mar 2022; **Daniel Owusu**
	78.	Occupational correlates for Covid19 disease among Staff at Kenyatta National Hospital; **John Macharia**
	79.	Incidence of SARS-CoV-2 and Influenza Viruses among Pregnant and Postpartum Women and their Infants, Siaya County, Kenya 2020–2021; **Nancy Otieno**
	80.	Wastewater Surveillance of SARS-CoV-2 in Kisumu City, Kenya; **Eric Muthanje**
	81.	Xpert xpress SARSCOV -2 Testing in Kenya; **Mary Mbugua**
	82.	Determinants of COVID-19 vaccine uptake among eligible residents of two populations in Siaya and Nairobi County, Kenya, July 2021 to August 2022; **George Otieno**
	83.	Characteristics of COVID-19 vaccine defaulters in Busia County, 2021; **Jude Oduor**
	84.	Assessment of the Quality of Alcohol-Based Hand Sanitizers, Pre and Peri - COVID-19 Pandemic Outbreak in Kenya; **Samuel Wafula**
Time (EAT) 1045 – 1245hrs	**Abstract No**	**Scientific Session 10: Health Systems-1 VENUE: Samburu Session Chair: Bridget Kimani Rapporteur: Tabitha Kanyui**
	85.	Incorporating mhealth interventions into Kenya's health infrastructure to augment Universal Health Coverage, service delivery improvement approach; **Oduor Otieno**
	86.	Examining the Responsiveness of the National Health Insurance Fund (NHIF) to People Living with Hypertension and Diabetes in Kenya: A qualitative study; **Robinson Oyando**
	87.	Experiences of Pilot Rollout of Web Laboratory Information Management System Remote Sample Login in Western Kenya; **Ben Odhiambo**
	88.	The Experience of rolling out a Mobile Van for conducting Minimally Invasive Autopsy for Community Deaths as part of Child Health and Mortality Prevention Surveillance in Siaya, western Kenya; **Peter Onyango**
	89.	Relationship between caregivers engagement through a 2-way mHealth platform and depressive symptoms in Western Kenya; **Catherine Otieno**
	90.	The Impact of an Integrated Health System Approach in improving access to services for persons with Lymphoedema in Coastal Kenya; **Stella Kepha**
	91.	Strategies to Reduce Informal Payments at Public Health Facilities in Kenya: Patients and Health Workers Perspectives; **Evelyn Kagure**
Time (EAT) 1045 – 1245hrs	**Abstract No**	**Scientific Session 11: NCDs VENUE: Bogoria Session Chair: Dr. Lydia Kaduka Rapporteur: Sarah Karanja**
	92.	Metabolic syndrome and its associated factors among women using hormonal contraceptives in referral hospital, Nekemte, Ethiopia; **Endalo Asefa**
	93.	The Diagnostic Accuracy of Diabetes Retinopathy Screening by Ophthalmic Clinical Officers, Ophthalmic Nurses and County Ophthalmologists against a Retina Specialist in 2 Selected County Referral Hospitals, Kenya; **Jane Ong'ang'o**

	94.	Factors associated with oral healthcare utilization among pregnant women attending antenatal care clinics in Kiambu Level V hospital, Kiambu County, Kenya; **Salome Kinyita**
	95.	Adaptive immune receptor features related to breast cancer in Kenyan patients: High immunoglobulin gene expression and BC-resident gamma-delta T-cells; **Kennedy Mwangi**
	96.	Association between maternal periodontal disease and preterm birth among women in Kisumu County, Kenya; **Linus Ndegwa**
	97.	Complications among Hypertensive cases, Kitui County Referral Hospital, January 2019- March 2022; **Diana Rose**
	98.	Association between nutrition knowledge and practise and cardiovascular disease risk factors among community members in Vihiga County; **Doreen Mitaru**
Time (EAT) 1045 – 1245hrs	**Abstract No**	**Scientific Session 12: Vector Biology-2 VENUE: Mt. Kenya C Session Chair: Dr. Joel Lutomiah Rapporteur: Sheila Mbaabu**
	99.	Whole transcriptomic gene profile of Anopheles arabiensis resistant to pyrethroid and organophosphate from western Kenya reveals overexpression of salivary gland and cuticular proteins; **Diana Omoke**
	100.	Plausibility of skin bacteria as a source of attractive olfactory ecology for Anopheles mosquitoes; **David Mburu**
	101.	The effect of high and low larval growth temperature on microsporidia mb in Anopheles gambiae sl; **Otieno Fidel**
	102.	Vectors of malaria An. arabiensis and An. funestus sampled in Kisumu and Siaya, Kenya, show resistance to permethrin and other insecticides; **Richard Ochieng**
	103.	Environmental factors modulate symbiont-host dynamics: Microsporidia MB in Anopheles arabiensis, at the Ahero Irrigation Scheme, Kenya; **Joseph Gichuhi**
	104.	Community engagement to understand the challenges and opportunities for a Microsporidia MB-based vector control strategy; **Syeda Tullu**
	105.	Isolation of tick-borne viruses in ticks collected from domestic animals in selected Counties Kenya; **Hellen Koka**
	106.	Natural sugar feeding rates of Anopheles mosquitoes collected by different methods in western kenya; **Seline Omondi**
Time (EAT) 1045 – 1245hrs	**Abstract No**	**Scientific Session 13: Sexual Reproductive Health-1 VENUE: Mt. Kenya D Session Chair: Dr. Betty Njoroge Rapporteur: Schiller Mbuka**
	107.	Hybrid rdt for diagonising gonorrhoea and syphillis; **Mathenge Julius**
	108.	Effective management of adolescent health through multisectoral approach; **Onchari Micah**
	109.	Syndromic Verses Laboratory diagnosis of Chlamydia trachomatis and Neisseria gonorrhoea among Adolescent girls and young women aged 15-20 years in South Western Kenya; **Samya Said**
	110.	Pre-exposure prophylaxis (PrEP) uptake & associated factors among adolescent girls and young women (15-20) participating in HPV vaccine trial; **Mildred Obare**
	111.	Repeat pregnancy, incidence & associated risk factors among adolescent girls and young women in Southwestern Kenya; **Erick Aol**
	112.	HIV incidence, trend and associated risk factors among a cohort of adolescents and young women (15-20 years) participating in HPV vaccine study in Kisumu; **George Otieno**
	113.	Prevalence of Chlamydia trachomatis and its associated factors among sexually active women in a high HIV-burden region, Western Kenya using Point-of-Care approach; **Martha Nyakambi**
1245-1345HRS: LUNCH BREAK		

1345-1430HRS POSTER SESSION (Abstract No. 023-045)

AFTERNOON: SCIENTIFIC SESSION 14, & SYMPOSIUM 6-10

Time (EAT) 1430-1700hrs	**Abstract No**	**Scientific Session 14: Mental Health VENUE: Amboseli Session Chair: Dr. Lucy Chite Rapporteur: Dr. Linus Ndegwa**
	114.	A multi-causal pathway to suicide, understanding suicide risk in coastal Kenya: A qualitative study; **Linnet Ongeri**
	115.	Visual arts as a tool to tackle mental health stigma: Findings from the Difu Simo Mental Health Awareness project in Kilifi County, Kenya; **Mary Bitta**
	116.	Design and Evaluation by Action Research of the BoB-programme (Build your Own Buddy) in South Sudan: Mental Health & Psychosocial Support for young children; **Remy Vink**
	117.	Association between maternal depression and child growth in Homa-bay and Migori counties, Kenya; **Julius Onyango**
	118.	Where are the perpetrators? A situational analysis of the Sexual and gender based violence cases among women at Kendu Sub County Hospital, Homa Bay County, Kenya; **Gabriel Kotewas**
	119.	Factors associated with substance abuse among mentally ill outpatients seen in a psychiatric hospital in Nairobi, Kenya: A retrospective study; **Jane Muriuki**

Time (EAT) 1430-1700hrs		**SYMPOSIUM 6: SERU VENUE: Tsavo Session Chair: Enock Kebenei Rapporteur: Carolyne Kithinji & Susan Kavai**

Time (EAT) 1430-1700hrs		**SYMPOSIUM 7: NAPREDA VENUE: Samburu Chair: Dr. Festus Tolo Rapporteur: Dr. Peter Mwitari & Dr. Beatrice Irungu**

Time (EAT) 1430-1700hrs		**SYMPOSIUM 8: IMPACT OF CLIMATE CHANGE VENUE: Bogoria Chair: Prof. Inah Danquah Rapporteur: Dr. Eric Muok & Dr. Steve Wandiga**

Time (EAT) 1430-1700hrs		**SYMPOSIUM 9: BOHEMIA VENUE: Mt. Kenya C Chair: Dr. Marta Maia Rapporteur: Dr. Joseph Mwangangi**

Time (EAT) 1430-1700hrs		**SYMPOSIUM 10: Drug Delivery using Nanotechnology VENUE: Mt. Kenya D Session Chair: Prof. Bernhards Ogutu Rapporteur: Dr. Jeremiah Gathirwa & Kelvin Thiong'o**

DAY THREE FRIDAY 17th FEBRUARY 2023

0700-0830hrs	**Arrival and Registration of Delegates**	
	PARALLEL SCIENTIFIC SESSIONS 15-20	
Time (EAT) 0830-1000hrs	**Abstract No**	**Scientific Session 15: AMR-1 VENUE: Amboseli Session Chair: Dr. John Mwaniki Rapporteur: Kelvin Kering**
	120.	Antimicrobial Resistance Profiles of Bacteria Recovered from Patients seeking COVID-19 PCR Testing in Nairobi; **Japhet Katana**
	121.	Bacteriophages for the treatment and bio control of multidrug resistant Acinetobacter baumannii; **Felix Mwai**
	122.	Low Microbiology Diagnostic Capacity in Kenya Public Hospitals: findings from a cross-sectional survey for 20 facilities; **Brian Nyamwaya**
	123.	First report of colistin resistance gene mcr-10 in Kenya; **Collins Kigen**
	124.	Antibiotic Resistant Vibrio cholerae O1 and its SXT elements associated with cholera outbreaks in Kenya between 2007 and 2016; **Martin Bundi**
	125.	Mutations in MtrR and 23S rRNA genes associated with macrolide resistance in Neisseria gonorrhoeae, Chlamydia trachomatis, and Mycoplasma genitalium among symptomatic women in Busia County, Kenya; **Primrose Ndungu**
Time (EAT) 0830-1000hrs	**Abstract No**	**Scientific Session 16: Health Systems-2 VENUE: Tsavo Session Chair: Dr. Richard Mutisya Rapporteur: Ishmael Ahamed**
	126.	Plan Do Study Act (PDSA) cycle approach to increase yield from contact management the case of Suna West; **Peter Omware**
	127.	Assessing the reception and application of COVID-19 community health messaging in two large diverse urban settlements in Nairobi: a case of Kibra and Nyayo estate Embakasi; **James Wodera**
	128.	Prevalence of hiv drug resistance mutations in hiv patients receiving antiretroviral therapy in Western and Coastal regions in Kenya; **Juster Mungiria**
	129.	Influence of Strategic Leadership Style on Partnerships Implementation in a Medical Research Organisation in Kenya: A Case Study; **George Kirigi**
	130.	Are stories-of-significant change technique useful as a source of capturing experiential evidence for informing policy and practice? Lessons learnt from Kenya; **James Kariuki**
Time (EAT) 0830-1000hrs	**Abstract No**	**Scientific Session 17: Genomics VENUE: Samburu Session Chair: Dr. Luna Kamau Rapporteur: Tiffany Wandera**
	131.	Comprehensive profiling of antibodies against infectious diseases using the protein microarrays; **Elijah Gicheru**
	132.	Whole genome sequencing-based surveillance of rotaviruses in Kenya reveals interspecies transmission, evolution and reassortment events; **Ernest Wandera**
	133.	Proteomics an agnostic approach to detect emerging viruses; **Armand Paauw**
	134.	Characterization of URST7 as a novel prognostic biomarker and therapeutic target for breast cancer; **Regina Wachuka**
	135.	Genomic Analysis of Dengue virus 1 Associated with an Epidemic in Eritrea, 2011; **Victor Ofula**
	136.	The use of unbiased whole genome sequencing for pathogen discovery: A case of Rift Valley Fever in Marigat, Baringo County, Kenya; **Allan Lemtudo**
	137.	Genetic diversity and antigenic variation at vaccine target sites in Rabies Virus collected from different host species in Makueni and Siaya counties, Kenya; **Evalyne Wambugu**

	138.	Development of Thermostable Moloney Murine Leukemia Virus Reverse Transcriptase (MMLV-RT) Enzyme Prototype in Kenya, Utilizing Codon Optimization Strategy; **Abdiaziz Gosar**
Time (EAT) 0830-1000hrs	**Abstract No**	**Scientific Session 18: Public Health-2** **VENUE: Bogoria** **Session Chair: Dr. Sam Aketch** **Rapporteur: Asiko Ong'aya**
	139.	Community members knowledge and perceptions of lung diseases in an urban informal settlement in Nairobi, Kenya; **Cynthia Kairu**
	140.	A mixed-methods study on residents’ treatment-seeking behaviour of tungiasis in Homa Bay County, Kenya; **Kana Suzuki**
	141.	Exploring Gender Based Violence service provision for Adolescent Girls and Young Women during the COVID-19 pandemic in Kisumu County: A qualitative study among service providers; **Isdorah Odero**
	142.	Evaluation of Diabetes and Hypertension Surveillance through the Community Empower Health System in Makueni County, Kenya, 2021; **Dominic Ongaki**
	143.	Using community assets to improve access to cardiovascular disease prevention services: Case study of Health Kiosks in Markets; **Bosire Miriam**
	144.	Burden and Perception of Overweight and Obesity as a Risk Factor to Cardiovascular Diseases in Vihiga County, Kenya; **Melvine Obuya**
	145.	My neighbor my buddy: A strategy to reaching the hard-to-reach defaulters in the HIV Stigma burdened Ntimaru area of Kuria Community in Kenya; **Nancy Mwita**
	146.	Integrated Approaches to empower adolescent girls and young women in Muhuru Ward, Migori County; **Seth Midenyo**
	147.	Lessons from a Ghanaian model of care that addresses antenatal care holistically, focusing on quality, health promotion, and patients' needs; **Jedidia Ayoka**
	148.	The effect of Corn Soy Blend plus Vegetable Oil Enhanced with Fish Oil on Immunological Patterns and Clinical Outcomes Among Children Aged 9 to 24 months with Moderate Acute Malnutrition (MAM): A Randomized Clinical Trial; **Phelgona Otieno**
	149.	Diversity and distribution of fungi in urban and peri-urban residences in Kenya; **Olga Mashedi**
Time (EAT) 0830-1000hrs	**Abstract No**	**Scientific Session 19: Sexual Reproductive Health-2** **VENUE: Mt. Kenya C** **Session Chair: Dr. Betty Njoroge** **Rapporteur: Irene Thuo**
	150.	Prevalence, Progression, and Risk Factors for Abnormal Pap Smear In adolescents and young girls aged 15-20 years in Kenya; **Lizzie Kabete**
	151.	Prevalence, persistence, clearance and associated risk factors of Bacterial Vaginosis in adolescents and young girls aged 15-20 years in South Western Kenya; **Caren Awinja**
	152.	Partner Notification Practice among Kenyan Adolescent Girls and Young women aged 15-20 years diagnosed with sexually transmitted infections; **Teresia Otieno**
	153.	Contraceptive uptake, method switching and associated factors among adolescent girls and young women participating in HPV vaccine trial; **Imeldah Wakhungu**
	154.	Incident and recurrent sexually transmitted infections in adolescents and young women in southwestern Kenya; **Maricianah Onono**
	155.	Adverse pregnancy outcomes and associated risk factors among adolescents and young women aged 15-20 years in Kenya; **Charlene Jepkoech**
Time (EAT) 0830-1000hrs	**Abstract No**	**Scientific Session 20: HIV** **VENUE: Mt. Kenya D** **Session Chair: Dr. Samoel Khamadi** **Rapporteur: Hellen Koka**
	156.	Factors associated with severe psychological stress among adults living with HIV in western Kenya; **Judy Mwai**
	157.	Assessing user preferences for design characteristics of oral dissolvable strips for pediatric HIV medication: a qualitative study; **Catherine Wexler**

	158.	Assessing challenges to pediatric ART provision: a qualitative study; **Michala Sliefert**
	159.	Factors associated with ART retention among adults (>15yrs) living with HIV enrolled in JM Kariuki Hospital, Nyandarua County, 2017-2021; **Margaret Wanjiku**
	160.	Utility of hair samples in monitoring antiretroviral therapy adherence of persons living with HIV in Kenya; **Philomena Chepkirui**
	161.	We tested together": Experiences of PLHIV Delivering HIVST to Partners of Unknown HIV Status in Kenya; **Catherine Kiptinness**
1000-1045HRS: TEA BREAK		
1045-1245hrs	**PARALLEL SCIENTIFIC SESSIONS 21- 24**	
Time (EAT) 1045-1245hrs	**Abstract No**	**Scientific Session 21: Health Systems 3 VENUE: Amboseli Session Chair: Dr Richard Mutisya Rapporteur: Ishmael Ahamed**
	162.	Quality assessment of clinical practice guidelines in Kenya using the Appraisal of Guidelines for Research and Evaluation (AGREE) II tool. A Methodological Review; **Sagam Caleb**
	163.	Evaluating the effectiveness of the National Health Insurance Fund in providing financial risk protection to households with hypertension and diabetes patients in Kenya; **Robinson Oyando**
	164.	Examination of sub-national capacities for health workforce governance in Kenya: A qualitative case study of two county governments; **Joshua Munywoki**
	165.	Seasonal Influenza Vaccination in Kenya: What Determines Healthcare Workers' Willingness to Accept and Recommend Vaccination?; **Nancy Otieno**
	166.	Evaluation of Cholera Surveillance System in Kenya between 2019-2021; **Oscar Adidi**
	167.	Community Engagement and Co-Development in Designing Non-Communicable Disease Interventions: Case study of HEKIMA; **Mbuka Schiller**
	168.	Targeting the 'missing middle,' Do free healthcare policies improve health insurance coverage among informal sector workers? A case of the Afya Care pilot program in Kenya; **Phidelis Wamalwa**
Time (EAT) 1045-1245hrs	**Abstract No**	**Scientific Session 22: MCH-2 VENUE: Tsavo Session Chair: Dr. Benson Singa Rapporteur: Lillian Mayieka**
	169.	Caring for providers to improve patient experience: mentorship needs of maternal healthcare providers in Migori County, Kenya; **Joyceline Gaceri**
	170.	Characterizing Aspiration Pneumonia among Under Five deaths enrolled in the Child Health and Mortality Prevention Surveillance (CHAMPS) Network in Western Kenya; **Joyce Akinyi**
	171.	Non-Communicable Diseases research: Trends and priorities in KEMRI's past 5 years; **Timothy Kipkosgei**
	172.	The difficult situation in maternity care: triggers and strategies from provider perspective in Migori County, Kenya; **Edwina Ndhine**
	173.	Quantitative culture of the probiotic microorganisms contained in the supplements administered to infants in the PROSYNK (PRObiotics and SYNbiotics in infants in KENYA) study; **Micah June**
	174.	Group care for antenatal care services: Experiences of women in rural Ghana; **Jedidia Ayoka**
Time (EAT) 1045-1245hrs	**Abstract No**	**Scientific Session 23: Malaria VENUE: Samburu Session Chair: Francis Kimani Rapporteur: Rukia Haji**
	175.	Four years of antimalarial Resistance Marker Surveillance using School Surveys in Kenya; **Victor Osoti**
	176.	Variability of Plasmodium falciparum asexual and sexual parasite carriage amongst individuals with symptomatic and asymptomatic infections in Kombewa, Kisumu county Kenya; **Gladys Chemwor**
	177.	Influence of landscape heterogeneity on entomological and parasitological indices of malaria in Kisumu, Western Kenya; **Wilfred Ouma**

	178.	Impact of Malaria Rapid Diagnostic Tests on Patient-Important Outcomes in sub-Saharan Africa: A systematic Review of Study Methods; **Jenifer Otieno**
	179.	Low frequency of Plasmodium falciparum hrp 2/3 deletions from symptomatic infections at a primary healthcare facility in Kilifi, Kenya; **Dorcas Okanda**
	180.	Antimalarial Susceptibility of Plasmodium falciparum field isolates from Busia county in Kenya; **Farid Abdi**
	181.	Identification of malaria hotspots in a highland site in western Kenya; **Benyl Ondeto**
	182.	Limited genetic variations of the Rh5-CyRPA-Ripr invasion complex in Plasmodium falciparum parasite population in selected malaria-endemic regions, Kenya; **Harrison Waweru**
Time (EAT) 1045-1245hrs	**Abstract No**	**Scientific Session 24: AMR-2 VENUE: Bogoria Session Chair: Dr. John Mwaniki Rapporteur: Kelvin Kering**
	183.	Most common resistant phenotypes, genotypes and prevalence of multidrug resistant (MDR) Salmonella Typhi in acute disease and chronic carriage in endemic setting in Nairobi County, Kenya; **Susan Kavai**
	184.	Genomic characterization of two community-acquired methicillin-resistant staphylococcus aureus with novel sequence types in Kenya; **John Njenga**
	185.	Extended spectrum beta lactamase producing Gram negative bacteria colonizing neonates admitted in the neonatology units at Bugando Medical Centre, Mwanza, Tanzania; **Jacobo Machimu**
	186.	Typhoidal Salmonella disease, carriage, diversity and antimicrobial resistant genes in Mukuru informal settlement, Nairobi Kenya; **Purity Nakhayo**
	187.	Multidrug resistant bacterial infections in severely ill COVID-19 patients admitted in a national referral and teaching hospital, Kenya; **Jeniffer Mutua**
	188.	Comparative Evaluation of The Automated Vitek 2 And Microbroth Dilution Methods On Colistin Antibiotic Susceptibility Test Results; **Michelle Atieno**
	189.	Gastrointestinal Carriage of Vancomycin-Resistant Enterococci and Carbapenem-Resistant Gram-Negative Bacteria among Inpatients and Outpatients at Kiambu County Referral Hospital, Kenya; **Anthony Maina**

1300-1400HRS: LUNCH BREAK

CLOSING CEREMONY

	Master of Ceremony: **Dr. Sophie Uyoga**
1400-1600hrs	Conference outcomes & resolutions Chief Rapporteur: **Dr. Steve Wandiga**
	Awarding Ceremony: **Dr. Vera Manduku**
	Sponsors and Exhibitors: **Prof. Charles Mbogo**
	Official Closing remarks KASH Chair: Dr. Cecilia Mbae Ag. Director General & CEO, KEMRI Chair KEMRI Board of Directors
	Vote of thanks- **Dr. Damaris Matoke-Muhia**

POSTERS

SUB THEME	Abstract No	Poster Title
Antimicrobial Resistance	1.	Point prevalence survey to assess antibiotic prescribing pattern among hospitalized patients in a county referral hospital in Kenya; **Racheal Wanjiku**
Antimicrobial Resistance	2.	Antimicrobial Resistance in ESKAPE Pathogens from Inpatients at Nairobi West Hospital, June-December 2021; **Mercy Cheptoo**
COVID-19	3.	COVID-19 symptoms prevalence and associated outcomes in COVID-19 patients admitted at two major isolation centers in Kisumu County, Western Kenya; **Josephine Awino**
COVID-19	4.	Multidisease testing of covid-19 and tb in Kenya; **Solomon Bundi**
Genomics	5.	Analysis of the metagenomic virome of Aedes aegypti mosquitoes from Coastal Kenya; **Solomon Langat**
Genomics	6.	Dengue serotype dynamics at the Kenyan Coast, 2019-2022; **Josphat Nyataya**
Genomics	7.	An integrated analysis of host transcriptome and metagenome to elucidate etiology of acute non-traumatic coma of unknown cause in Kilifi, Kenya; **Brenda Karumbo**
Health Systems	8.	Population Health Needs, Health Systems Readiness, and Client Satisfaction in the Context of Implementation of Universal Health Coverage in Bomet County, Kenya; **Priscah Otambo**
Health Systems	9.	Implementation of the caring for providers to improve patients experience (cpipe) intervention in Kenya: challenges,success and lessons; **Beryl Akinyi**
Health Systems	10.	External validation of a pediatric triage model for use in resource limited facilities to guide frontline health workers; **Joyce Kigo**
Health Systems	11.	The Evaluation of Human Brucellosis Surveillance System in Uasin Gishu County-Kenya 2022; **Stephen Olubulyera**
Health Systems	12.	Overcoming Barriers to Clinical Trial Enrollment in Sub-Saharan Africa by Addressing Financial Burdens of Cancer Patients: A Case of International Cancer Institute, Kenya; **Gloria Kitur**
Health Systems	13.	Laboratory safety audits a game changer in infection prevention and control; **Duncan Odhiambo**
Health Systems	14.	Lessons from a unique system to promote child and youth health; **Symone Detmar**
Health Systems	15.	Developing a digital health Intervention to promote uptake and use of PrEP and contraception among adolescent girls and young women in Kenya :Insights from a qualitative study; **Joan Ongere**
Health Systems	16.	Case Report: β-thalassemia major on the East African coast (Kilifi); **Johnstone Makale**
HIV	17.	Linkages of HIV exposed, and HIV positive children aged 0-24 months between PMTCT and nutrition clinics in 3 facilities in Western Kenya; **Damaris Odhiambo**
HIV	18.	Retension strategies for cross-border hiv clients during COVID-19 pandemic a case of olasi dispensary ,Migori County; **Eugene Ariya**
Malaria	19.	Macrophage responses in Placental malaria; **Fred Owuor**
Malaria	20.	The Role of Plasmodium falciparum HSP90 in Antimalarial Drug Treatment Outcome in a 3 Malaria Endemic Region, Kisumu County; **Lewis Karani**
Maternal and Child Health	21.	Midwifery-Led Research For Evidence-Based Practice: Clinical Midwife's Engagement In Research In Ethiopia, 2021; **Keflie Yohannes**
Mental Health	22.	Utilization of Patient Health Questionnaire-9 depression screening tool at Care and Treatment Centers in Mbeya, Tanzania; **Amani Kway**
Mental Health	23.	Acceptability of using Friendship Bench as an Intervention for addressing trauma among Adolescent Girls and Young Women experiencing Gender-based violence in Kisumu County, Kenya; **Eucabeth Awuonda**
Neglected Tropical Diseases (NTDs) and One Health	24.	An outbreak investigation: The burden and factors associated with occurrence of Visceral Leishmaniasis in Tharaka Nithi County, Kenya; **Joanne Yego**

Non-Communicable Diseases	25.	Ochratoxins and deoxynivalenol contamination of cereals in Kibra; **Evageline Gatumwa**
Non-Communicable Diseases	26.	The adaptation of therapeutic carbohydrate restriction diet for the reversal/remission of type 2 Diabetes mellitus in Kenya; **Evaline Onyango**
Non-Communicable Diseases	27.	Community health workers' awareness regarding oral health in kigali, rwanda; **Niyigena Fabrice**
Public Health	28.	Hepatitis B vaccination status among healthcare workers at Nyahera Sub-county hospital; **Duncan Odhiambo**
Public Health	29.	Modelling heat stress in conjunction with other stressors: identification of vulnerable; **Bernice Scholten**
Public Health	30.	Understanding U=U informs HIV prevention decisions in Kenya; **Njeri Wairimu**
Public Health	31.	Perspectives of healthcare workers on pre-treatment loss to follow-up in adults with pulmonary TB in Western Kenya: an exploratory qualitative study; **Mercy Mulaku**
Public Health	32.	Phylogenetic diversity of fungi isolated from indoor urban environments in Nairobi Kenya; **Olga Mashedi**
SRH	33.	Factors Associated with Research knowledge and Attitude among Clinical Midwives Working at Public Health Facilities of Northwest Ethiopia, 2021: A Cross-Sectional Study; **Keflie Yohannes**
SRH	34.	Prevalence of selected sexually transmitted infections among men who have sex with men on pre-exposure prophylaxis in Kiambu County, Kenya; **Caleb Ombati**
Tuberculosis	35.	Localization of tuberculosis patients' determinants: Patterns for presumptive cases from a coastal health facility in Kenya; **Fred Orina**
Tuberculosis	36.	Association between the latent TB infection and body mass index of patients from clinical sites in Nairobi, Kenya; **Robi Chacha**
Tuberculosis	37.	Integration of Quality Improvement (QI) approach in intensified TB active case finding (ACF), a case of Awendo Sub County; **Nelly Okwiri**
Tuberculosis	38.	Clinical and Social Demographic characteristics of TB/HIV cohort in Nairobi, Kenya; **Paul Waiganjo**
Vector Biology	39.	Detection of Insecticide Resistance by Culex pipiens complex to several insecticides in Kenya; **Santos Yalwala**
Vector Biology	40.	Microsporidia MB is associated with Anopheles mosquitoes in different agro-ecological conditions; **Oscar Mbare**
Vector Biology	41.	Comparison of different trapping methods to collect malaria vectors indoors and outdoors in western kenya; **Jackline Jeruto**

Scientific Session 1: TB-1

Abstract No. 001

Title: Isolation of Non-Tuberculous Mycobacterial Infections among Tuberculosis presumptive cases at the National Tuberculosis Reference Laboratory Kenya, 2018 –2019

Authors: George G kamau (Graduate school)*; Raphael Lihana (KEMRI); Maurice O Owiny (Kenya FELTP); Nellie Mukiri (NTRL); Nduku Kisia (NTLD-P); BEATRICE NASIMIYU KHAMALA (NPHL); Richard kiplimo (AMREF); Nassoro J Mwanyalu (Kenya FELTP); Joel Bargul (JKUAT)

Introduction: Mycobacterial pathogens are among the top causes of diseases in humans. In Kenya, the Incidence of Non-Tuberculous Mycobacteria (NTM) species was 35.7% in 2016 and, in 2019, 2.6% in infants. Most NTMs are resistant to first-line treatment of tuberculosis (TB) and have a challenge with a timely and accurate diagnosis. Misdiagnosis has led to prescribing of anti-TB regimens to patients suffering from NTM. We aimed to determine the most prevalent Non-Tuberculous Mycobacterium in Kenya.

Methodology: We reviewed records from the NTRL Laboratory information management system (LIMS) from January 2018 – December 2019 for the patients on surveillance. All isolates were cultured in Mycobacterial Growth Indicator Tubes (MGIT) and incubated for detection using the BACTEC™ MGIT™ system. Those with negative acid-fast bacilli (AFB) growth and negative for Mycobacterium Tuberculosis Complex Species (MTBC) protein-MPT64 were suggestive of non-tuberculous mycobacterial infections (NTM), which were sub-cultured in MGIT and characterized using Line Probe Assay (LPA) GenoType® MTBDR CM/AS.

Results: of the 24,549 records reviewed, 0.7% (167) were NTM isolates. Male was 74.3% (124), and the mean age was 42 years (SD±16), with the age group 35-44 years more at 28% (46/167). The NTMs were from 31/47 counties; Nairobi had 12.6% (21/167), Mombasa 10.8% (18/167), Kilifi and Meru each had 7.8% (13/167). Of the eleven NTM species isolated, the majority were Mycobacterium intracellulare at 37% (65/167), M. fortuitum at 27% (48/167), and M. scrofulaceum at 10% (17/167). Most NTMS were isolated from previously treated patients 63.5% (106/167) and Drug-resistant follow-up patients 24.6% (41/167). NTMs and HIV coinfection was at 27.5% (46/167).

Conclusion: Previously treated patients should have an additional screening of NTMS and should do drug susceptibility testing before initiation of treatment. Keywords: Non-tuberculous Mycobacteria, Kenya, Information Management, Mycobacterium tuberculosis, Incidence

Keywords: Nontuberculous Mycobacteria, Kenya, Information Management, Mycobacterium tuberculosis, Incidence

Abstract 002

Title: Distribution of Mtb genotypes/strains among presumptive multidrug resistant tuberculosis patients in western Kenya

Authors: ALBERT O OKUMU (KEMRI)*; Steve Wandiga (KEMRI); George Oballa (MOH- National TB program, DNLTP); Jeremiah Ogoro (MOH- National TB program, DNLTP); Collins Ouma (Department of Biomedical Sciences, Maseno, University); Benjamin Ochieng (KEMRI); James Orwa (School of Health Sciences, The Aga Khan University); Kennedy Muimi (Centres for Health Solutions, Kenya); Edgar Kigozi (Dept of Immunology & Molecular Biology, School of Biomedical Sciences, College of Health Sciences, Makerere University); Fred Katabazi (Dept of Immunology & Molecular Biology, School of Biomedical Sciences, College of Health Sciences, Makerere University)

Background: Tuberculosis (TB) is a critical health crisis in the world with attention directed toward profiling of global lineages of Mycobacterium tuberculosis (Mtb). of Mtb lineages is important for the analysis of phenotypic associations, informing the possible origins and predicting any potential future outbreaks. Genotyping of Mtb strains is important in understanding the dynamics of Mtb population, tuberculosis (TB) surveillance, and control programs.

Methods: Fifty-seven Mtb isolates from sputum culture samples of presumptive Mtb patients were processed for DNA extractions (heat-killed at 90℃ for 60 minutes), followed by conventional PCR. Gel electrophoresis to distinguish the DNA fragments (lengths and sizes), and finally, MIRU VNTR was performed to determine Mtb lineages, allele calling, phylogenetic analysis, and calculated the allelic diversity (h) and discriminatory power of each VNTR locus.

Results: Out of the 57 sputum isolates analysed, 42 (73.7%) males and 15 (26.3%) females with a median age of IQR 36 (26-45) were processed. Further, 26 (45.6%) HIV-infected, 30 (52.6%) HIV-uninfected and 1 (1.8%) unknown HIV status. Isolates from previously treated individuals were the majority at 48 (84.2%). Identified genotypes/strains were, Delhi/CAS (23/57), Beijing (15/57), Harlem (3/57), LAM (5/57), S (4/57), TUR (3/57), Uganda II (3/57) and, one Uganda I genotype. Among the HIV-infected, the prevalence of both genotypes Delhi/CAS and Beijing was 17/26 as compared to 20/30 among HIV-uninfected, respectively. Beijing genotype was present in all counties except Kakamega, however, most of the strains were predominant in 12 (21.1%) Homabay and 11(19.3%) Kisii.

Conclusion: While both Beijing and Delhi/CAS (both from the 4th lineage) strains were predominant, Beijing genotype was more prevalent in all the counties. There was an equal distribution of these genotypes amongst the individuals of either HIV status, gender, and age, in addition to RIF and INH for either resistance or susceptibility.

Keywords: Tuberculosis, Genotypes, Mtb Lineages, DNA, MIRU-VNTR, Distributions, Prevalence

Abstract 003

Title: Assessing impact of pre-analytical challenges experienced in samples received for TB diagnosis in an MDR surveillance in Western Kenya and North Rift

Authors: JOSEPH J.O ORURE (KEMRICGHR)*; RUTH SITATI (KEMRICGHR); LAURENE NYONGESA (KEMRICGHR); JOAN TONUI (KEMRICGHR); CAROLINE DANDE (KEMRICGHR); ALBERT O OKUMU (KEMRI)

Background: Pre-analytical phase in a diagnostic laboratory is crucial for service delivery to clients. It involves sample collection, labelling, packaging as well as transportation. Among the three phases of laboratory testing, pre-analytical phase has been considered more prone to errors (Alavi N, 2020). This is despite being a lesser identified area, when it comes to accurate diagnosis of tuberculosis, caution during the pre-analytical phase cannot be over-emphasized. We sought to assess pre analytical challenges for samples received at KEMRI CGHR TB laboratory.

Methods: This cross-sectional study evaluated sputum specimen received at the KEMRICGHR TB laboratory between January 2017 to December 2021 from Health facilities in western Kenya and North rift for tuberculosis multi drug resistance surveillance. The sample rejection status, or reason for testing delay and name of the affected facilities were accessed from the request forms, sample problem log and the KEMRI TB laboratory data management system.

Result: A total number of samples collected were 5989 of which 160(2.67%) were either rejected or delayed processing as follows; 59(36.88%) had no request forms, 40(25%) had missing identities, 28(17.5%) had leakage, 24(15%) had no samples, 6(3.8%) had insufficient volume and 3(1.9%) were wrong samples. The most affected counties were Kisii (80), Homabay (12), Kisumu (16), Siaya (15), Kakamega (14), Rift Valley (12) and Migori (11).

Conclusion /Recommendation: Compliance with good practices can significantly reduce the frequency of preanalytical challenges. Frequent training on specimen collection and management should be done on staff to enhance quality patient management and treatment, minimize TB spread, reduce turnaround time and maintain patient trust.

Keywords: TB diagnosis

Abstract 004

Title: Assessment of TB cases tested using GeneXpert in Ndaragwa Sub county,2021

Authors: Lucy Njoki Munyeki (County Government of Nyandarua)*

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Background: Tuberculosis (TB) diagnosis is essential for disease identification and elimination. In 2016, Kenya listed GeneXpert as the preferred first test for TB diagnosis and identification of Rifampicin resistance. This was informed by the need for a fast and efficient diagnosis of presumptive TB cases, especially in children and those living with HIV. This study sought to assess the socio-demographic and clinical characteristics of TB cases tested using GeneXpert.

Methods: A retrospective cross-sectional study design was used. A case was defined as any suspected Tuberculosis case screened using GeneXpert® technology in Ndaragwa in 2021. Sociodemographic and clinical variables were collected onto an MS-Excel® database. Descriptive statistics were used to analyze the data.

Results: A total of 363 records were analyzed. Female cases were 191 (53%) and 172 (47%) were male. 189 (52%) were aged 30–59 years while those <9 years accounted for 2.5% of all cases. New presumptive cases were 325 (91%) and 165/363(45.4%) were not tested for HIV. Of the suspected cases assessed, 21 (5.8%) were positive for Tuberculosis of which 17 (81%) were male and 4(19%) were female. No rifampicin resistance was detected in any of the positive cases.

Conclusion: While more females than males sought the test using GeneXpert® technology, the positivity rate was higher among male cases. HIV testing for all suspects was not prioritized with some HIV positive being classified as new presumptive. We recommend public health education among health care workers on importance of active case finding for TB.

Keywords: GeneXpert, presumptive, TAT, type of patient

Word count 298 (excluding heading)

Abstract 005

Title: Spectrum of Fungi Isolated from Sputum of Patients Attending Tuberculosis Reference Facilities in Kenya

Authors: Abdi Mohamed (KEMRI)*; Sally N Loronyokie (KEMRI); Hannah Kariuki (KEMRI); Richard R.K Korir (KEMRI); Christine Bii (KEMRI)

Background: Fungal infections represent a significant cause of morbidity and mortality among pulmonary tuberculosis (PTB) patients. Inhaled infective fungal spores colonize preexisting Tuberculosis (TB) lung lesions resulting in disease. Lack of clinical suspicion and diagnosis of fungal infection in PTB patients may complicate PTB management in patients with fungal co-infections. This study reports the spectrum of fungi isolates in PTB patients in four TB treatment health facilities in Kenya.

Methods: This was a cross sectional laboratory based study. Patients with PTB like symptoms were recruited following an informed consent. Sputum samples were subjected to microscopy and standard fungal culture. The isolated fungi were subjected to macro and micro morphological identifications and confirmed by sequence analysis of calmadulin, betatubilin and ITS genes.

Results: Out of 234 sputum samples analysed, 88(38%) were positive for fungal culture. Aspergillus spp. accounted for 25(28%) of which A. fumigatus was 13(14.8%), A. niger 8(9.1%), A. terreus, A. flavus, A. candidus and A. clavatus 1 (1.1%) each. This was followed by Penicillium spp. 10 (11.4%), Scedosporium spp. 5 (5.7%) and Rhizopus spp. 3 (3.4%). Among the yeasts; Candida albicans accounted for 18(20.5%) followed by C. glabrata 5(5.7%). Cryptococcus spp. was isolated from 3(3.4%) of the samples while 13(14.8%) were other yeasts.

Conclusion: Pulmonary fungal infection is a significant co-morbidity in PTB patients in Kenya. Fungal co-infection could be misdiagnosed as PTB relapses or treatment failures in the absence of a reliable diagnosis in patients with persistent clinical symptoms. The isolation of Aspergillus species in this population is of clinical significance due to its intrinsic resistant to azole drugs. We recommend sputum samples from PTB patients be subjected to fungal investigations for early diagnosis and treatment important to lower morbidity and reduce the apparent high mortality for PTB patients in the country.

Keywords: Pulmonary Tuberculosis, Fungal infections, Kenya

Abstract 006

Abstract Title: Active Community Transmission for Drug-Resistant Tuberculosis: Are We Safe?

Authors: James M Maragia (Turkana County Governmennt-MOH)*

Background: Drug-resistant tuberculosis (DRTB) remains a major public health crisis. WHO has categorised it as a significant contributor to antimicrobial resistance (AMR), contributing to about half a million people falling ill globally. In Kenya, the 2021 tuberculosis annual report shows that most affected patients are new, a group that has never taken anti-tuberculosis drugs, an indication of active community transmission of the resistant strains. Previous reports have also shown that DRTB is on an upward trend of 40% despite the global picture showing a downward trend with a fall of 22%. Therefore, the objective of this study was to share the characteristics and epidemiology of this vulnerable and forgotten group (New patients) from the data spanning 2019-2021.

Methods: This was a cross-sectional study. DRTB data was obtained from National Tuberculosis Program from across 47 counties. Clinical and social-demographic factors were extracted from the Treatment Information from Basic Unit (TIBU) system for further analysis.

Results: A total of 2578 records were obtained from the TIBU system. Of this, 1317 (51.1%) were from the new patient category. Males (66.8%) aged 24-44 accounted for most DRTB cases. 68.7% of the DRTB cases were HIV-negative. Nutritionally, patients with a BMI of less than 18.5 accounted for most of the cases, with a proportion of 46.0%, closely followed by people with normal BMI, recording 44.1%. The data also shows increased Rifampicin resistance (57.5%) and Isoniazid Mono resistance (29.0%) over time. Poor outcomes were recorded where the death rate stood at 9.1%, the cure rate at 27.5% and loss to follow-up at 3.1%. The country adopted three DRTB care delivery models, where most patients are on community ambulatory (70%). All counties recorded new cases except Lamu. Nairobi accounted for 14.8%, with the Embakasi sub-county leading with 5.1%. This is closely followed by Meru (7.9%), Mombasa (7.1%), Embu (7.1%) and Nakuru (5.4%). Most cases are identified at public facilities (83.6%), a few in private facilities (9.7%) and least at prisons (1.8%). Generally, 2020 contributed the highest number of new DRTB cases (39.4%), while 2019 accounted for the lowest number proportion (25.1%).

Conclusion: It is crystal clear that the DRTB is now a menace than it was thought before. Patients who have never taken anti-TBs, have normal BMI, HIV negative are vulnerable to DRTB. In the same vein, poor outcomes are recorded with a resistance pattern showing an exponential increase in both RR and INH resistance. Nairobi leads with the highest of DRTB cases emanating from public facilities.

Recommendation: Robust ongoing surveillance for DRTB is critical to mounting an effective response, especially in high-risk areas and populations. Equally, accurate diagnosis and treatment should be available and accessible to all legible clients regardless of their previous anti-TB drug interaction and interruption.

Keywords: Anti-microbial resistance, Transimission, Tuberculosis,

Abstract 007

Title: Sputum Smear Conversion rates in relation to HIV status after 6 months of Tuberculosis treatment in Nairobi Kenya

Authors: Dorcas W Ihuthia (Kenya Medical Research Institute)*; ROBI CHACHA (KEMRI); Jeremiah K. Ndeto (Kenya Medical Reseaerch Institute); Pascah Bulia (KEMRI); Geoffrey Okallo (KEMRI); Paul Mwangi (KEMRI); Evans Amukoye (KEMRI); Asiko Ongaya (KEMRI)

Background: Tuberculosis (TB) remains one of the world's deadliest communicable diseases. In 2021, an estimated 9.0 million people developed TB and 1.5 million died from the disease. The management of TB is a great challenge in developing countries such as Kenya due to limited resources, weak health-care systems and high HIV infection rates. According to the World Health Organization (WHO), it is recommended that TB patients be monitored through sputum smear examination during treatment to assess their response to therapy. The proportion of smear-positive patients with sputum smear conversion at the end of the intensive phase is an indicator of TB program performance as well as response to treatment. The objective of this study was to determine sputum smear conversion rates in relation to HIV status after intensive phase of TB treatment.

Methods: A total of 214 sputum samples from positive TB cases were obtained from three health facilities in Nairobi; AIDS Healthcare Foundation, Rhodes TB clinic and Mbagathi hospital were collected, processed and stained with Auramine-rhodamine stain. Fluorescence microscopy was performed on the smears.

Results: of the 214 patients, 192(89.7%) were HIV non-infected, 22(10.3%) were HIV infected. Of the 192 patients, 184(95.8%) had a negative sputum smear result and 8(4.2%) had a positive smear result after the intensive phase of TB treatment. Of the 22 patients, 21(95.6%) had a negative sputum smear and 1(4.4%) had a positive smear result after the intensive TB treatment. The conversion rate of sputum smear for HIV non-infected was 95.8% and 95.6% for the HIV infected. There was no significant difference in the sputum smear conversion rates.

Conclusion: Studies show that sputum smear conversion is strongly influenced by adherence to TB treatment. Patients' demographics should be analyzed to support the above findings.

Keywords: Sputum smear conversation rates, Tuberculosis, HIV status

Scientific Session 2: Vector Biology-1

Abstract 008

Title: Mosquitocidal Effect and Pharmacokinetics of Different Ivermectin Dose Regimens in Preparation for Bohemia Cluster Randomized Controlled Trial

Authors: Yvonne N Kamau (KEMRI-CGMRC)*; Mercy J Tuwei (Kemri-Wellcome Trust Research Programme); Kelly Ominde (KEMRI-Wellcome Trust Research Programme); Jonathan Kazungu Karisa (KEMRI-Wellcome Trust Research Programme); Mwanajuma Ngama (KEMRI-Wellcome Trust Research Programme); Martha Muturi (KEMRI-Wellcome Trust Research Programme); Festus Mure (KEMRI-Wellcome Trust Research Programme); Lawrence Babu (KEMRI-Wellcome Trust Research Programme); Frida Lewa (KEMRI-Wellcome Trust Research Programme); Jane Adetifa (KEMRI-Wellcome Trust Research Programme); Felix Hamman (University Hospital of Bern); Urs Duthaler (University Hospital of Basel); Carlos Chaccour (Is Global, Barcelona Institute for Global Health, Barcelona, Spain); Regina Rabinovich (Is Global, Barcelona Institute for Global Health, Barcelona, Spain); Marta F Maia (KEMRI)

Background and Objectives: Malaria is preventable and treatable, and yet it remains a significant public health problem around the world, particularly in Africa. Despite reductions in the burden of malaria over the past 20 years, recently these gains have stalled. To halt and overturn this trend current control methods need to be augmented with additional tools that are effective at reducing transmission, particularly in Africa where there is rising insecticide resistance and where outdoor biting vectors are becoming an increasing problem. A novel method that is currently being explored in clinical trials as a potential tool for malaria control is mass drug administration (MDA) with ivermectin at the start of the malaria transmission season. Ivermectin (IVM) is an endectocide drug which addresses the problems of behavioural adaptation and residual malaria transmission. Based on available pharmacokinetic (PK) data and mathematical modelling of plasma levels expected to kill mosquitoes, we aimed to compare a single dose of 400mcg/Kg to proposed 300mcg/Kgx3 regimen with entomological and PK outcomes while investigating the mosquitocidal activity of albendazole as a potential comparator.

Methods: Healthy individuals from Ngerenya subcounty, Kilifi county in Kenya were randomized to receive either 1) Single dose oral IVM 400 mcg/Kg (12 participants), 2) Single dose oral IVM 300 mcg/Kg given on three consecutive days (6 participants) 3)single dose oral 400mg albendazole (6 participants) or 4) no treatment (6 participants). Participants were followed-up up to 28 days with blood samples drawn hourly and two hourly for PK measurement and the mosquitocidal effect assessed on D0+4h, D7, D10, D14, D21, D28

Results: Mosquito survival up to 28 days post treatment was assessed by measuring the daily proportion of knocked-down mosquitoes after feeding on blood from participants. Cumulative mortality was estimated by quantifying number of dead mosquitoes in the treatment and control groups and then correcting for percentage mortality. Plasma PK parameters of IVM were derived either directly from observed data (Cmax, Tmax) or by non-compartmental analysis of the concentration-time profiles.

Conclusion: Albendazole has no impact on mosquito survival thus adequate as a comparator for trials evaluating IVM as an endectocide for malaria vector control

Ivermectin 400mcg/Kg x1 has slightly higher mosquitocidal effect than 300mcg/kg x3. Mosquito survival below extrinsic incubation period (EIP) is only assured up to 7 days post treatment. DBS technique is a good field-friendly sampling method for PK evaluations. Plasma drug concentrations for the two regimens are comparable. Ivermectin 400mcg/Kg single dose strategy can be more attractive than 300mcg/Kg x3 as it presents higher feasibility of MDA, more affordable and likely to yield higher compliance at the community level.

Keywords: Endectocides, ivermectin, malaria,

Abstract 009

Title: UDP-Glucuronosyltransferase plays a key role in Insecticide Resistance: A study using bioinformatics approaches.

Authors: Cynthia CAO Odhiambo (Kenya Medical Research Institute)*

Background: Vector control is a vital malaria prevention strategy that involves two core intervention strategies:; indoor residual spraying (IRS) and insecticide treated nets (ITN). Currently, efficacy of these interventions is limited by vector resistance to insecticide, posing new challenges to malaria control measures. Phenotypic bioassays and extensive geographic IR mapping are the conventional methods utilized for evaluating Insecticide Resistance (IR) status of the population . There is need to identify molecular markers that can enhance IR surveillance and improve understanding on the molecular mechanisms associated with IR. The purpose of this study was to use Weighted Gene Co-Expression Network Analysis (WGNCA) algorithm to identify similar co-expression patterns and hub genes, for use as molecular markers for insecticide resistance surveillance.

Methodology: Anopheles arabiensis samples were collected from western Kenya. The F1 generations of the field samples were exposed to alphacypermethrin, permethrin and deltamethrin insecticides). RNA was extracted from unexposed, susceptible and resistant samples and sequenced using Illumina sequencing platform. Downstream analyses were performed using fastqc, trimmomatic, hisat, and htSEQ tools. EdgeR was used to explore differentially expressed genes (DEGs). Co-expression analysis was then performed based on the DEGs using WGCNA in R to identify modules, hub genes and a gene co-expression network was generated. KEGG analysis was performed using DAVID's annotation tools to evaluated the molecular mechanisms associated with IR.

Results: A total of 141,172, and 239 DEGs ($P<0.05$, FC=1) were identified from groups SU vs SA, SU vs SP and SU vs SD, respectively. The DEGs with similar expression patterns were identified as modules using WGCNA package in R . We identified 12 modules from all the groups. KEGG analysis showed that the DEGs were associated with significant enrichment of metabolic pathways, protein processing, glycolysis/gluconeogenesis and glutathione metabolism pathways. UDP Glucuronosyltransferase (n=156, K-core=2) was identified as the seed, which refers to the highest scoring node commonly known as the top hub gene. Genes coding for CYP91M, MAP-K, CP-RR and Opsin were also among the top five hub genes with the highest connections.

Conclusion: The findings of study showed for the first time the role of UDP Glucuronosyltransferase(AARA005133) as a potential marker for IR and demonstrated the role of metabolic proteins such as carboxylases, esterase, cytochrome P450s and structural proteins including cuticular proteins, opsin, chitin-like proteins and dynein in insecticide resistance in A. arabiensis . The identified hub genes can be used as molecular markers for insecticide resistance surveillance.

Keywords: RNAseq; Hub genes ; Malaria Control; Molecular markers;WGNCA

Abstract 010

Title: Age grading of Afrotropical malaria vectors using MALDI TOF MS

Authors: Mercy J Tuwei (Kemri-Wellcome Trust Research Programme)*; Jonathan Kazungu Karisa (KEMRI-Wellcome Trust Research Programme); Martha Muturi (KEMRI-Wellcome Trust Research Programme); Kelly Ominde (KEMRI-Wellcome Trust Research Programme); Marta F Maia (KEMRI)

Background: Assessing the age structure of mosquito populations could help in evaluating the impact of control methods. MALDI-TOF MS is a technique that uses laser technology for protein profiling and identification.This technique is commonly used in the clinical diagnostic laboratories for microorganisms identification. Recently, it has been presented as an innovative tool for mosquito species identification and their blood meal. This study aimed to determine if MALDI-TOF MS is capable of distinguishing different age groups (physiological and chronological) of Anopheles gambiae sensu stricto based on their protein profiles as they undergo proteomic changes during aging.

Methods: Anopheles gambiae sensu stricto mosquitoes (Kilifi strain) were reared in a laboratory controlled environment at KEMRI-Wellcome Trust insectary. Mosquito were reared to different physiological and chronological ages. The individual life history of each mosquito was recorded including mating, blood-feeding and oviposition. Approximately 100 mosquitoes per group of distinct physiological and chronological age were processed using MALDI TOF MS. Few spectra from each category of mosquito age were used for database creation (training set) and the remaining were used for validation (testing set).

Results: For the physiological age grading, a total of 394 mosquitoes were subjected to MALDI-TOF MS. Out of the total, 57/394 were used in the data base creation and validation. The overall accuracy of identification was 85.1% (2 days old blood naïve-90.5%, 4 days old blood fed-74.6%, pregravid-82.5, Parous-88.36%). For the chronological work, out of 119 mosquitoes subjected only 31 were used for data base creation. Overall accuracy was 92.3% (<7 days old-85.29%, >7 days old-97.7%).

Conclusion and discussion: Using insectary reared mosquitoes, MALDI TOF MS was able to distinguish and differentiate mosquitoes based on their age. Therefore studies should be conducted using wild mosquitoes. MALDI-TOF MS is a promising tool for routine vector surveillance.

Keywords: MALDI-TOF MS, Age grading, Anopheles gambiae s.s.

Abstract 011

Title: Resting behaviour of African malaria mosquitoes in an era of high indoor insecticide use

Authors: Kevin O Owuor (KEMRI)*; Maxwel Machani (Kenya Medical Research institute); Richard Mukabana (University of Nairobi); Yaw Afrane (University of Ghana); Eric O Ochomo (Kenya Medical Research institute)

Background: Malaria morbidity and mortality are still of global concern with more emphasis on the Sub-Saharan Africa regions. Management has been through drug therapies and integrated vector management strategies. The backbone of vector control is insecticide use in Long Lasting Insecticidal Nets (LLINs) and indoor residual spraying (IRS) which are representations of powerful tools for controlling malaria vectors in sub-Saharan Africa. The success of these interventions relies on their ability to inhibit indoor feeding and the resting of malaria mosquitoes. This study sought to understand the resting behavioural responses in this era of high indoor insecticide use.

Methods: Anopheles mosquitoes were sampled from Kisumu (Kisian) and Bungoma (Kimaeti) counties in Western Kenya. Sampling of resting mosquitoes was carried out indoors and outdoors. The physiological ages of the mosquitoes from respective resting locations were examined using ovarian dissections for parity and the number of egg-laying cycles. Mark-release-recapture experiments were conducted to investigate the plasticity of resting behavior in indoor and outdoor resting malaria mosquitoes in a typical LLIN use scenario within a semi-field set-up (malariasphere). The status and intensity of insecticide resistance were evaluated together with the Plasmodium sporozoite infectivity in indoor and outdoor-resting mosquito populations.

Results: The study found out that the majority of younger mosquitoes preferred to rest indoors while older mosquitoes preferred to rest outdoors ($p=0.001$) in a typical insecticide (LLIN) use scenario. The level of phenotypic, genotypic and biochemical insecticide resistance was higher in the indoor resting vector populations compared to outdoor populations ($p<0.05$) with moderate intensity resistance as classified by WHO guidelines. The plasmodium sporozoite infectivity rate was also higher in the indoor-resting malaria vectors compared to the outdoor-resting counterparts ($p<0.05$).

Conclusion: It was apparent that these vectors exhibited plasticity in their resting behavior regardless of having an intervention (LLIN) in place. The study recorded high physiological (phenotypic, metabolic and genotypic) insecticide resistance and sporozoite rate in indoor resting populations of malaria vectors compared to their outdoor resting counterparts. The indication of moderate insecticide resistance intensity by indoor resting mosquitoes could have an operational impact on the efficacy of the existing indoor insecticide-based vector control tools. The use of insecticides indoors, besides impacting biting phenology and host-seeking behaviour, also alters the resting behaviour and therefore, sustenance in malaria transmissions. This information bridges the gap between resting behaviour and indoor insecticide control which now opens up an important front for further exploitation through monitoring and research.

Keywords: Insecticide resistance, Resting behaviour, Malaria transmission

Abstract 012

Title: A field bioassay for assessing ivermectin bio-efficacy in malaria vectors

Authors: Kelly Ominde (KEMRI-Wellcome Trust Research Programme)*; Yvonne N Kamau (KEMRI-CGMRC); Jonathan Kazungu Karisa (KEMRI-Wellcome Trust Research Programme); Martha Muturi (KEMRI-Wellcome Trust Research Programme); Caroline Kiuru (IS Global, Barcelona, Spain); Caroline Wanjiku (KEMRI-Wellcome Trust Research Programme); Lawrence Babu (KEMRI-Wellcome Trust Research Programme); Festus Yaah (KEMRI-Wellcome Trust Research Programme); Mercy J Tuwei (Kemri-Wellcome Trust Research Programme); Haron Musani (KEMRI-Wellcome Trust Research Programme); Zedekiah Ondieki (KEMRI-Wellcome Trust Research Programme); Joseph Mwangangi (KEMRI); Carlos Chaccour (Faculty of Medicine, Universidad de Navarra, Pamplona, Spain); Marta F Maia (KEMRI)

Background: Ivermectin (IVM) mass drug administration is currently under evaluation as a complementary malaria vector control tool. Mosquitoes that ingest blood from treated hosts suffer reduction in survival. Estimating the bio-efficacy of IVM on wild-caught mosquitoes requires they ingest the drug in a bloodmeal either through a membrane or directly feeding on a treated host. The latter, has ethical implications, and the former results in very low feeding rates. Therefore, there is a need to develop a safe and effective method for monitoring IVM bio-efficacy in wild mosquitoes.

Methods: Insectary-reared Anopheles gambiae s.s. mosquitoes were exposed to five IVM doses: 85, 64, 43, 21, 11 and 0 ng/ml (control) in three different types of solutions: i) blood, ii) 10% glucose, and iii) blood mixed with 10% glucose in four ratios: 1:1, 1:2, 1:4, and 1:8 fed through a filter paper. Similarly, wild-caught An. gambiae s.l. were exposed to 0 ng/ml (control) and three IVM doses: 85, 43 and 21 ng/ml (highest, intermediate, low dose respectively) in blood mixed with 10% glucose in ratio 1:4 fed through filter paper in the insectary. Following treatment, mosquito survival was monitored for 28-days. Shortly after ingesting the meal a pool of mosquitoes was sacrificed and weighed to determine the mean weight of each meal type.

Results: The mosquitocidal effect of IVM when administered in sugar solution is not comparable to the observed effects when same concentrations are administered in blood. Equal concentrations of IVM administered in blood resulted in more pronounced reductions in the probability of mosquito survival compared to when administered in sugar solution. However, by adding small amounts of blood to a sugar solution mosquito mortality rates can be increased and result in effects closer to what is observed when blood feeding. A field bio-assay was developed in the insectary to test bio-efficacy of IVM by using sugar solution containing a small amount of blood and administering it through a filter paper. Finally, the feasibility of the bio-assay was tested using wild-caught mosquitoes in Kwale, Kenya.

Conclusion: Bio-efficacy of ivermectin is strongly dependent on how the drug is ingested by the mosquito and is likely influenced by digestive processes. The assay developed is a good candidate for field-based bio-efficacy monitoring: wild mosquitoes readily feed on the solution, the assay can be standardized using pre-selected doses and by not involving a treated blood host (human or animal) it avoids variation due to individual pharmacokinetic profiles as well as ethical issues. Meal volumes did not explain the difference between the lethality of IVM compared across the different meal types, further research is needed to understand the underlying mechanism.

Keywords: Ivermectin, monitoring, vector control, bio-efficacy assay, Anopheles gambiae s.s.

Abstract 013

Title: Ivermectin mass drug administration for malaria control (BOHEMIA): updates on trial progress

Authors: Marta F Maia (KEMRI)*; Joseph Mwangangi (KEMRI); Yvonne N Kamau (KEMRI-CGMRC); Isabella Ocholla (KEMRI); Caroline Wanjiku (KEMRI); Mary Mael (ISGlobal); Lawrence Babu (KEMRI); athuman chiguzo (KEMRI); Almudena Sanz (ISGlobal); Joanna Furnival-Adams (ISGlobal); Urs Duthaler (University of Basel); Aina Casellas (ISGlobal); Felix Hammann (University of Bern); Carlos Chaccour (ISGlobal); Regina Rabinovich (ISGlobal)

Background: The world is currently not on-track to achieve the goals proposed by the WHO in the Global Technical Strategy for Malaria 2016-2030. Vector control has been central to the control of malaria; however, it is increasingly challenged by spread of insecticide resistance and mosquito behavioral adaptations that allow them to elude long-lasting insecticide-treated nets (LLINs) and indoor residual spraying (IRS). Ivermectin mass drug administration (MDA) could potentially complement the malaria toolbox as it provides an approach that can target vectors irrespective of feeding behavior; and has a different mode-of-action compared to insecticides.

Methods: The BOHEMIA consortium (Broad One Health Endectocide-base Malaria Intervention in Africa) proposes to evaluate the epidemiological and entomological impact of ivermectin MDA to humans and livestock in Kwale, Kenya with the aim of developing a complementary strategy for malaria elimination. The BOHEMIA clinical trial is an open label, cluster randomized controlled trial (cRCT) consisting of three study arms (Ivermectin to humans and livestock; Ivermectin to humans alone; and control arm (albendazole)). Participants randomized to clusters assigned to receive ivermectin will receive single dose 400mcg/Kg and participants in the control arm will receive single dose of albendazole 400mg. MDA rounds will be done once a month for three months during the long rains. The trial will assess the efficacy and safety of the intervention. A pediatric cohort of 35 children (5-15 years old) per cluster will be randomly selected and followed up monthly for 6 months (3 MDA months and 3 months post MDA) to assess malaria infection incidence by mRDT. The trial will also assess safety by recording incidence of adverse events in all treated population up to one month post last MDA round. The trial will be supported by entomological monitoring of malaria vectors.

Discussion: The trial is in preparation and results are expected late 2023. Detailed trial design, updates on progress, challenges and ongoing activities will be shared.

Keywords: malaria, ivermectin, endectocide, cRCT, clinical trial, mass drug administration, Kwale

Abstract 014

Title: Upscaling integrated vector management in the control of malaria and schistosomiasis in Mwea, Kirinyaga County. Baseline Epidemiological and Entomological results.

Authors: Paul PMG Gichuki (KEMRI)*; CASSIAN Mwatele (KEMRI); Lydiah Kibe (KEMRI); Charles Mbogo (KEMRI)

Background: Vector control has been instrumental in the control and elimination of most vectorborne diseases including malaria, and schistosomiasis. The distribution of these infections often overlaps. In such areas it's economically viable to employ an integrated approach in the control for the vectors which largely shares the same breeding ecosystem. We carried out a baseline epidemiological and entomological surveys for malaria and schistosomiasis in Mwea, Kirinyaga County, in preparation for the upscaling of integrated vector management. Methods: A repeated cross sectional survey, where mosquito and snail vectors were sampled during the dry and wet seasons in three different ecological zones (Kiamaciri, Thiba and Murinduko). Mosquito larvae were collected using standard dippers, while adults were collected using light traps. Snail vectors were sampled using standard snail scoops. School going children were examined for malaria and intestinal schistosomiasis. Malaria was examined using malaria rapid diagnostic tests, while stool samples were processed using the kato katz technique. Results: The overall prevalence of intestinal schistosomiasis was 9.08%, with Kiamaciri recording highest prevalence at 19% (95%CI: 0.15-0.23) and Murinduko the least prevalence at 0.17% (95%CI: 0.00-0.01). The majority of infections were of light intensity, 78.9%. There was no positive malaria case among 1200 children examined. A total of 3,208 adult mosquitoes were sampled during the dry season. Of these, 20.6% (95% CI: 19.25-22.08) were Anopheles gambiae s.l while 79.4% (95% CI: 77.92-80.75) were culicines. During the wet season, 3,378 adult mosquitoes were collected. Of these 14.7% (95% CI: 13.56-15.98) were Anopheles gambiae s.l and 85.3% (95% CI: 84.02-86.44) culicines. Overall, 4,085 mosquito larvae were collected during the two seasons, with 14.9% (95%CI: 0.14-0.16) being collected during the dry season and 85.1% (95%CI: 0.84-0.86) during the wet season. Culex quinquefaciatus was dominant in the area. A total of 2,292 fresh water vector snails were collected. Majority of the snails 69.6% (95%CI: 0.68-0.71) were Biomphalaria pffeiferi responsible for transmission of intestinal schistosomiasis. Conclusion: Schistosomiasis was prevalent in Kiamaciri and Thiba zones. In Murinduko zone the presence of infected vector snails was an indication of active transmission. Malaria vector Anopheles gambiae s.l. was predominantly observed in all sites, Anopheles funestus, were also observed as well as Culex quinquefaciatus responsible for the spread of several arboviruses. In conclusion, three important disease vectors were found in all the study sites, and this could lead to future disease outbreaks if concerted control initiatives are not undertaken. All these disease vectors shared the same breeding sites and thus its economical and feasible to adopt an integrated vector management approach for disease control in the study area.

Keywords: Schistosomiasis, malaria, disease vectors, integrated, control

Abstract 015

Title: Over-expression of CYP6M2, CYP6P3, CYP4H15 and a cuticular protein is associated with transfluthrin response in Anopheles gambiae ss from Bungoma, Western Kenya.

Authors: Stephen O Okeyo (Kenya Medical Research Institute)*; Derilus Dieunel (Centers for Disease Control and Prevention); Lucy Impoinvil (Centers for Disease Control and Prevention); Diana Omoke (Kenya Medical Research Institute); Helga Saizonou (Tropical Infectious Diseases Research Centre(TIDRC), University of Abomey-Calavi(UAC), Benin); Cynthia CAO Odhiambo (Kenya Medical Research Institute); Nsa Dada (School of Life Sciences, Arizona State University, Tempe, AZ, USA); Nicola Mulder (Human, Heredity and Health in Africa H3ABionet network, Cape Town, South Africa); Benard Kulohoma (Department of Biochemistry, University of Nairobi, Kenya); John Gimnig (Centers for Disease Control and Prevention); Luc Djogbénou (Regional Institute of Public Health (IRSP), Ouidah, Benin ; Department of Vector Biology, Liverpool School of Tropical Medicine, Liverpool, United Kingdom); Eric O Ochomo (Kenya Medical Research institute); Audrey Lenhart (Centers for Disease Control and Prevention)

Background: Insecticide resistance (IR) is a major threat to malaria vector control in endemic areas. Alternative or complementary methods to address resistance to traditional vector control tools are therefore essential. Spatial repellents (SRs) can prevent human-vector contact, potentially improving epidemiological outcomes. However, the molecular basis of insecticide repellency in mosquitoes is poorly understood. Investigating gene expression patterns related to insecticide exposure can offer greater insights into the molecular basis of the behavioral response to spatial repellents in malaria vectors.

Methods: In this study, RNA-Seq was performed to characterize gene expression patterns following exposure to transfluthrin, a highly volatile pyrethroid with a low insecticide resistance profile, due to its poly-fluorinated benzyl-ring backbone structure. Larvae of Anopheles gambiae s.s. were collected from Bungoma in Western Kenya and reared to adults. Three-to-five-day-old female mosquitoes were analyzed using a high throughput screening system (HITSS) to measure their spatial activity index (SAI) to transfluthrin exposure.

Results: The results showed that the mosquitoes from Bungoma responded at a dose of 10.215µg/ml to the spatial repellency activity of transfluthrin (SAI = 0.3804 (0.27, 0.5). In comparison, the Pimperena-resistant strain responded at a dose of 102.15µg/ml (SAI = 0.8206 (0.73, 0.91) while the Kisumu susceptible strain responded at a dose of 0.84µg/ml (SAI = 0.572 (0.48, 0.66). RNA-Seq was performed on mosquitoes that either responded, did not respond, or was not exposed to transfluthrin. The susceptible Kisumu and resistant Pimperena laboratory strains were included as controls. RNA-Seq pairwise comparisons analysis between non-responders and responders showed an over-expression of detoxification genes, including cytochrome P450s (CYP6M2, CYP6P3, and CYP4H15). A gene encoding a cuticular protein (CPR30) was also overexpressed in all the non-responder-responder pairwise comparisons, indicating its potential role in the behavioral responses of An. gambiae ss to transfluthrin.

Conclusion: The observed behavioral response could be associated with the activity of cytochrome P450 monooxygenase encoding genes, thus, need further investigation to validate their functional role in An. gambiae ss repellency and possibly the development of insecticide resistance.

Keywords: Insecticide resistance, spatial repellency, Anopheles gambiae ss, RNA-seq, gene expression, cytochrome P450 monooxygenases

Abstract 016

Title: Controlling malaria from within: Using microbial symbionts to decrease vector competence

Authors: Thomas O Onchuru (Icipe)*

Malaria is a major health problem across sub-Saharan Africa. High numbers of malaria cases and deaths are being reported despite the large-scale implementation of malaria control programmes. This suggests that the current malaria control strategies are limited and therefore a need for novel approaches to fight this disease. One promising strategy is the use of microbial symbionts that reduce vector competence. Recently, it was demonstrated that malaria vectors, Anopheles mosquitoes, harbor a natural symbiont, Microsporidia MB, that completely blocks the transmission of Plasmodium falciparum, the causative agent for malaria. Importantly, Microsporidia MB is vertically transmitted and therefore it can be applied sustainably to control malaria. However, the mechanism through which vertical transmission occurs is not yet known. In this study, we used advanced microscopic techniques to describe the vertical transmission of the symbiont in Anopheles gambiae mosquitoes. Our results show that Microsporidia MB infects the germline stem cells at a very early stage. The symbiont is subsequently transferred into developing eggs following germline cell division and differentiation. In early stages of egg development, Microsporidia MB is randomly present in the oocyte and the nurse cells as large multinucleated cells which later divide and migrate into the oocyte in the late stages of egg development. These results on transovarial transmission of the symbiont via germline stem cell infections reveal an intimate and long-term symbiotic relationship between Anopheles gambiae mosquitoes and Microsporidia MB. This suggests that the association may be a result of millions of years of host and symbiont co-evolution. Understanding the mechanisms of vertical transmission of Microsporidia MB is critical to the longer-term goal of sustainably using this microbe for malaria control.

Keywords: Symbionts, Malaria control

Scientific Session 3: NTDS and One Health

Abstract 017

Title: Epidemiological profile of Leprosy cases and the Treatment Outcomes, Kenya January 2011-To December 2021

Authors: vallerian karani (Kenya Field Epidemiology and Laboratory Training Programme(FELTP))*

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Background: Leprosy is a chronic bacterial disease that mainly affects the nerves. If untreated, it may cause progressive and permanent damage to the skin, nerves, limbs, and eyes, leading to physical disability. Nationally, Kenya has maintained a global target of leprosy elimination. However, there are still pockets of leprosy cases reported across the Country where physical disability persists, mainly due to late diagnosis. we evaluated the surveillance system to characterize the leprosy cases and the treatment outcomes of leprosy from 2011-2021.

Methodology: The study utilized retrospective secondary data extraction from the TIBU system from 2011- 2021 to characterize the leprosy cases. The critical patient variables collected in the TIBU system for evaluation include sex (male/female), age in years, patient classification Multibacillary (MB) and paucibacillary (PB) type of patient, treatment outcome, and disability grading at diagnosis. The case-based data was downloaded as an excel file; the database was anonymized and analyzed using Epi info version 7.

Results: Out of 1162 cases 59.5% were males and 40.5% were females. Of all the cases notified, 49.7% were between 30-60 years of age, and 6.01% were below 15 years of age. Generally, 80% of all counties have at least notified an active case of leprosy over 10 years, with Kilifi and Kwale notified 26% and 20.3% of all the cases in the Country. Disability Grade 1 and II accounted for 25.3% and 17.3%, respectively. Among notified cases, the proportion of MB and PB types of leprosy was 86.7% and 13.3%, respectively.

Conclusion: Kilifi and Kwale are high-risk Counties where targeted interventions like early diagnosis of patients and active community case finding, contact tracing and screening household contacts of children below 15 years.

Keywords: Leprosy, Treatment Outcomes, Contact tracing, and early diagnosis

Abstract 018

Title: PRODUCTION AND USE OF POLYCLONAL ANTIBODIES FOR THE DIAGNOSIS OF HUMAN AFRICAN TRYPANOSOMIASIS

Authors: Dawala Koromtili Oumar (Pan African University)*; Matthew Mutinda Munyao (Kenya Medical Research Institute); Anne Wanjiru Mwangi (Kenya Medical Research Institute); Prof. Rebecca Waihenya (Jomo Kenyatta University for Agriculture and Technology); Peter Kipkemboi (KEMRI); Robinson M Irekwa (Kenya Medical Research Institute); Tonny T Nyandwaro (KEMRI); Njoroge Carol Wangui (Kenya Medical Research Institute); Joanne J Yego (Kenya Medical Research Institute); Primrose Muthoni (University of Nairobi); Sharlene Mageto (Pan African University); Damaris Mutethya Kilei (Jomo Kenyatta University for Agriculture and Technology); Otimoil Poul Stephen (Pan African University); Nicole Sian Tanchu (Nagasaki University Institute of Tropical Medicine); Grace Ngendo Kanyita (Kenyatta University); Lucy Nungari (Kenya Medical Research Institute); Prof. Shingo Inoue (Nagasaki University Institute of Tropical Medicine); Prof. Samson Muuo Nzou (Kenya Medical Research Institute)

Background: Human African trypanosomiasis (HAT), commonly known as sleeping sickness is one of the neglected tropical diseases (NTDs), which is fatal if left untreated. Its diagnosis is a challenge since the signs and symptoms of the primary phase are not specific and the existing diagnostic methods have low sensitivity and specificity, and available drugs have some toxicity. New, robust, and cost-effective techniques are needed for the early identification of parasites.

The present invention relates to the field of diagnostics in which polyclonal antibodies were used for the detection of a pathogen. The invention also relates to methods of preparing the products and their use in diagnosis.

Methods: Two (2) New Zealand white rabbits (3 months old) were immunized with purified Tbg I2 and Tbg I17 expressed proteins, and one (1) rabbit was used as negative control. Indirect ELISA was done to check the antibody titers as well as the sensitivity and specificity of the novel polyclonal antibodies.

Results: The antibody titer measured was greater than 32 g/L after the 3rd immunization for the expressed protein Tbg I2. For the expressed protein Tbg I17 the antibody titer measured was greater than 32 g/L after the 4th immunization. The sensitivity and specificity of the Tbg I2 polyclonal antibody confirmed with Polymerase Chain Reaction (PCR) as gold standard were respectively 89.5% and 80.6%, while for the Tbg I17 polyclonal antibody, the sensitivity and specificity were respectively 92.1% and 88.9%. The area under the curve for the Tbg I2 polyclonal antibody was 0.90 ± 0.032, while for the Tbg I17 polyclonal antibody, the area under the curve was 0.92 ± 0.0. The Tbg I17 polyclonal antibody produced in New Zealand white rabbits has good sensitivity and good specificity, it can be successfully used in the diagnosis of HAT.

Conclusion: Diagnosing HAT in the field presents many challenges, including diagnosis, and logistical problems for testing teams to reach communities in rural areas. According to the sensitivity and specificity of the novel polyclonal antibodies, they can be successfully used in the diagnosis of HAT.

Keywords: Human African Trypanosomiasis, Tbg I2 expressed protein, Tbg I17 expressed protein, diagnostic

Abstract 019

Title: Exploring Service Provider Related Determinants of Surgery Non-acceptance Among Women with Trachoma Trichiasis in North Pokot Sub County

Authors: Victoria Akoth Ochwal (St. Paul's University Limuru)*

Background: Despite the World Health Organization recommending surgical sessions to be conducted at fixed sites and periodic outreach stations in North Pokot, 72.5% of surgery declines were recorded among women. This was amid some men and women with trachoma trichiasis accepting the surgery.

Methods: A cross-sectional study was conducted in October 2020 to explore the service provider related determinants of surgery non-acceptance among women with trachoma trichiasis (TT) in the 6 wards of North Pokot Sub County. Qualitative methods were used for data collection whereby 27 women who declined TT surgery were sampled purposively for In-depth interviews. Key informant interviews were conducted among National and County Health Workers (4), local administrators (3) and Development actors (2). Separate Focus Group Discussions were conducted among women who underwent TT surgeries (1), and trachoma case finders (1). Data was audio recorded, transcribed, coded, and analyzed thematically based on the themes of accessibility, service provider competencies and service experience

Results: While most participants reported knowledge of trachoma and its transmission including the importance of the surgical intervention, the perception of the use of epilation forceps as less painful triggered non-acceptance among majority (n=18) of the women. Accessibility to the surgical sites was impeded by long distances to the outreach sites or static facilities, poor road networks and unavailability of TT surgeons or inconsistent closing hours of clinics which demotivated the women. Sporadic intercommunity conflicts characterized by cattle raiding further curtailed access to TT surgical camps. Service provider competencies were linked to unsatisfactory surgical outcomes including complications, unsightly looks, and some cases of recurrence. Some women therefore reported to cross the border to Uganda for services. However, some informants indicated the challenge of inadequate surgical consumables like absorbable sutures which promised better outcomes. Some women felt they did not get timely information about the TT camps while others had misconceptions about TT surgery as sight restoring. Furthermore, presence of direct and indirect costs, mistrust of the motivation for surgery referrals by health workers , presence of ocular co-morbidity such as cataract exacerbated the fear of surgery. Some women also decried absence of postoperative follow-up, which they perceive contributed to TT recurrence.

Conclusion: There is need to improve on the programmatic organization and coordination to ensure service integration via targeted multi-sectoral collaboration which would increase service accessibility. Furthermore, increased financial allocation for eye health will enable routine trainings for eye health workers, timely post-operative follow ups and surgical quality audits thereby enhancing competencies and service experience.

Keywords: "Trachoma" "Service Provider" "Trichiasis" "TT Surgery" "Community engagement"

Abstract 020

Title: Presence of an invasive exotic freshwater snail, Pomacea canaliculata (Gastropoda: Ampullaridae) in Mwea Irrigation Scheme, Kirinyaga County: Potential implications for public health and wetlands biodiversity

Authors: Mutuku, M.W., Mwangi, I.N, Kinuthia, J. M , Maina, G.M, Lelo, E.A, and Mkoji, G.M.

Centre for Biotechnology Research and Development, Kenya Medical Research Institute (KEMRI).

Background: The apple snail, Pomacea canaliculata (Gastropoda: Ampullaridae), a native of South America, was recently reported to be present in Kenya. This invasive freshwater snail is considered a devastating agricultural and ecological pest, likely to be a threat to rice farming and wetlands biodiversity in Kenya, and a potential public health threat. P. canaliculata serves as intermediate host of the rat lungworm, Angiostrongylus cantonensis, which causes human eosinophilic meningitis, an emerging disease. Long term impact of this snail in Kenya, remains unknown. A survey was recently done in Mwea in February and October 2022 to assess the spread of this snail in the area

Methods: Sampling was done using a standard snail scoop in 15 streams, 4 ponds and 4 canals within the Mwea rice irrigation scheme. The snails and snail egg masses collected were transferred into plastic containers, and identified using snail taxonomic keys based on morphological features, with the aid of a dissecting microscope.

Results: The presence of a thriving population of P. canaliculata in the Mwea irrigation canals, ponds and rice paddies was confirmed, and numerous Pomacea egg masses also, observed. Only 2 canals located on the upper periphery side of the irrigation scheme were found to be having Biomphalaria Pfeifferi snails

Conclusions: The presence of P. canaliculata in Kenya is a cause for great concern, given the invasive nature of this snail species and its likely, long-term impact on public health, rice farming, and freshwater biodiversity in the country. This calls for intentional efforts to closely and continuously monitor the situation in Mwea and other parts of the country, for intervention.

Keywords: Pomacea canaliculata, Biopmphalaria pfeifferi, Schistososma mansoni, Angiostrongylus cantonensis

Abstract 021

Title: Severe dengue in Mandera : a case for event based surveillance

Authors: Albert O Nyunja (KEMRI)*

Background: Dengue fever is an emerging public health problem in Africa. The virus is endemic in thirty four African countries and the main mosquito vector, Aedes aegypti, inhabits all African countries except five. Data from Africa has been insufficient to estimate the level of susceptibility to Dengue virus compared to Asia and the Americas. Factors such as vector competence and vulnerability of the population influence disease transmission. Traditionally, prevention strategies rely heavily on vector control efforts and coupling these to enhanced surveillance methods using modern technological tools may be what is needed to contain Dengue outbreaks.

Methods: Ten blood samples were obtained from patients with no immunization history who had presented with body pains, fever, difficulty in walking and swelling of both knees and legs. All were males with an age range of 10-15 years. Serum was obtained for screening purposes. Dengue Rapid Diagnostic Test (RDT) and blood slides for malaria was performed at the referral facility in Mandera. Samples were then shipped to the Viral Hemorrhagic Fever laboratory facility in KEMRI and screened using Dengue IgM ELISA and reverse transcriptase PCR using primers targeting the Dengue capsid gene.

Results: At the local referral facility, only two samples tested positive for Dengue IgM by Dengue RDT and all ten blood slides were negative for Plasmodium parasites. At KEMRI , all samples tested positive for anti Dengue virus IgM using IgM ELISA and negative for Dengue by reverse transcriptase PCR. The ten patients were admitted on the 29th September 2022, blood collected on 30th October which were received at KEMRI on 31st October. The patients recovered and were released on 3rd November 2022 and resumed schooling.

Conclusion: Clinical symptoms can be used to form case definition to trigger further investigation as exhibited in these cases. Despite RDT tests at the local level detecting only two Dengue cases, the clinical manifestation prompted the sub-county disease surveillance officer to seek for further investigation. Severe dengue may present with unorthodox symptoms that clinicians may be primed to be on the lookout for. Enhancing the flow of information from schools, communities and hospitals to the disease surveillance infrastructure will enhance the existing surveillance system. This will entail creating or updating traditional structures and performing training of healthcare providers and other stakeholders to detect and promptly report signals to appropriate public health units.

Keywords: severe dengue infectious public health surveillance

Scientific Session 4: Natural Products

Abstract 022

Title: LC-MS/MS method for simultaneous determination of selected antidiabetic adulterants in formulated herbal remedies being sold in Nairobi and Uasin Gishu Counties, Kenya

Authors: Caroline N Maina (Jomo Kenyatta University of Agriculture & Technology)*; Anthony Gachanja (Jomo Kenyatta University of Agriculture & Technology); Elizabeth Kigondu (KEMRI); Ruth Nyangacha (KEMRI); Pius Kinoti (University of Jyvaskyla); Josephine Ouma (Jomo Kenyatta University of Agriculture & Technology)

Background: Herbal products are usually marketed as natural products with multiple beneficial health claims. However, several studies have established that these products are usually adulterated with pharmaceuticals, which undermines their safety because of potential adverse herb-drug interactions. Therefore, it is important to routinely analyse herbal drugs for adulteration using pharmaceuticals to ensure their safety, as the number of people relying on herbal drugs for treatment of chronic illnesses like diabetes is on the rise. One analytical technique commonly used to analyse for this adulteration is liquid chromatography coupled with mass spectroscopy (LC-MS/MS) because of its high selectivity and sensitivity. As such, this study was designed to develop a rapid, simple, selective, and sensitive LC-MS/MS method to identify and quantify antidiabetic adulterants present in herbal products being marketed in Nairobi and Uasin Gishu Counties in Kenya.

Methods: A Waters alliance 2975 LC system (LC, Milford, MA, USA) coupled to a Waters Quattro Micro quadrupole mass spectrometer was used. An LC-MS/MS method was developed and validated according to the guidelines of the International Council for Harmonization (ICH) regarding validation of analytical techniques involving pharmaceuticals for human consumption. The validated method was then applied to 24 samples that were randomly purchased from herbal clinics, herbal product manufacturers, herbalists, local retailers, and hawkers/ street vendors in both Uasin Gishu and Nairobi Counties, Kenya.

Results: Chromatographic separation of these analytes was done using a C-18 column and a gradient elution program consisting of 0.1% of formic acid in acetonitrile. The developed method showed detection limits and quantification limits ranging from 2.86 to 7.67 ng/mL and 8.64 to 23.24 ng/mL respectively. The precision of the developed method ranged from 8.5% to 18.1%, while the accuracy was above 80% for all analytes except metformin (52%). This method was then applied to analyse 24 powdered herbal drugs available in the Kenyan market to ascertain if they were adulterated using the mainstream antidiabetic medication. Metformin was detected in four of the samples. However, the concentration levels were below the quantification limit in all the samples. Neither glibenclamide, glimepiride, nor gliclazide were identified in any of the samples.

Conclusion: A rapid LC-MS/MS method was developed, validated, and applied to simultaneously detect four common antidiabetics medications present as adulterants in herbal products. This method showed high precision, accuracy, selectivity, linearity, and sensitivity. Additionally, metformin was detected in 16.67% of the herbal samples, evidence that adulteration is occurring without the knowledge of regulatory bodies. Therefore, this study recommends using the validated method to routinely test herbal products in the country for possible adulteration using pharmaceuticals.

Keywords: LC-MS/MS; Adulteration of herbal products; Antidiabetic pharmaceuticals

Abstract 023

Title: Antimicrobial activities and phytochemical content of honey and pollen of Meliponula beccarii and Plebeina hildebrandti from Baringo County

Authors: Chepkemoi Christine (Masinde Muliro University of Science and Technology)*; Sabella Kiprono (Masinde Muliro University of Science and Technology); Jared M Onyancha (Mount Kenya University); Sammy Kimoloi (Masinde Muliro University of Science and Technology)

Background: The antimicrobial activity of stingless bee products is attributed to their chemical content and physicochemical properties which are greatly dependent on species, geographical regions, botanical sources, harvesting season, processing and storage conditions. As such stingless bee products from geographic or ecological distinct regions and species represent a rich source of novel compounds, which can potentially be developed into novel antimicrobial agents. In Baringo County, honey from stingless bees are traditionally used to treat various ailments commonly associated with bacterial and fungal infections with the top most being respiratory disorders, stomach disorders and oral thrush. However, these acclaimed traditional uses and the putative antimicrobial activities of stingless bee products from Baringo County have not been validated.

Objective: This study aimed at determining the antimicrobial activities and phytochemical content of honey and pollen from Meliponula Beccarii and Plebeina hildebrandti stingless bees from Baringo County against three selected pure bacterial strains (MRSA, Escherichia coli and Haemophilus influenza) and a fungal strain (Candida albicans).

Methods: Ten honey and pollen samples conveniently sampled from ten stingless bee nests in different ecological zones of Baringo County were analysed. The study adopted a factorial experimental design, whereby different concentrations of honey and pollen samples were prepared and tested against the microorganisms. Agar well diffusion method and broth microdilution susceptibility technique tests were used to determine the antimicrobial activities and to measure MIC, MBC and MFC of the samples. Phytochemical analysis of the samples was done qualitatively. Data was analysed by Two-way Analysis of Variance and Tukey's post-hoc tests using Graphpad Prism software version 9.1.1.

Results: All samples of honey demonstrated significant antimicrobial activities against Haemophilus influenzae, Escherichia coli and methicillin-resistant staphylococcus aureus at 100% (v/v). Remarkably, the honey and pollen sample extracts exhibit a diverse phytochemical profile.

Conclusion: Honey of Plebeina hildebrandti and Meliponula beccarii from Baringo have potent in vitro antimicrobial activity and may be an attractive source of lead compounds that can be developed into new drugs and research tools.

Keywords: antimicrobial activities, phytochemical content

Abstract 024

Title: In silico evaluation and prediction of novel pyrazoline, pyrazole and isoxazoline derivatives of Polygonum senegalense chalcones as anti-cancer agents

Authors: DR. EVANS OKEMWA KENANDA (KISII UNIVERSITY)*; Fidelis T Ndombera (Covance Labs); Prof. Leonidah Kerubo (University of Nairobi)

Polygonum senegalense is very rich in chalcones (1,3-diphenyl-2-propen-1-ones) imbedded in its surface exudates. Chalcones are reactive a, b-unsaturated cyclic aromatic compounds that can be isolated from plants but can also be synthesized. They are active lead molecules in medicinal chemistry for the discovery of new drugs. In the present study, heterocycles with vicinal heteroatomic nitrogen and / oxygen in five- membered ring systems were synthesized from P. senegalense chalcones. Previous work indicates that compounds with this type of structural pattern have anti-cancer properties. We performed Cell line cytotoxicity prediction based on PASS technology (http://www.way2drug.com/PASSonline) and the training set created based on data on cytotoxicity retrieved from ChEMBLdb (version 23) (https://www.ebi.ac.uk/chembldb/). The highest cytotoxicity of the molecules revealed Pa values of about 0.7 in targeted cell lines that include ovarian adenocarcinoma, breast carcinoma, renal carcinoma, and glioblastoma, underscoring the therapeutic potential of the chalcones in our library. In addition, we used SWISSADME in silico tools in estimation of ADME, physicochemical, drug-likeness, pharmacokinetics, and medicinal chemistry properties. Our data, revealed that most of our molecules obey the Lipinskis rule of five, are moderately soluble to be absorbed by the GI tract, do not penetrate the blood-brain barrier, and possess physicochemical properties of druglike molecules. Furthermore, the molecules are easily synthetically accessible. In this presentation we will present data to demonstrate synthesis, in silico drug properties evaluation as well as cytotoxicity data in various cancer lines. The goal of the presentation also includes equipping African scholars and participants with vital tools for early drug development.

Keywords: pyrazoline, pyrazole, isoxazoline

Abstract 025

Title: Evaluation of Effects of Spirulina Extracts on Immunologic Dysfunction and Inflammation Associated with Aflatoxin B1 Induced Toxicity in Mice

Authors: Gilbert Kipkoech (KEMRI)*; Charles Mutai (Masinde Muliro University of Science and Technology); Susan Musembi (Kenyatta University); Johnson Masese (Masinde Muliro University of Science and Technology); Peter G Mwitari (KEMRI); Mercy Jepkorir (KEMRI); James Kuria (KEMRI)

Background: Mycotoxin contamination of food is a serious public health concern across the world. The most common type of mycotoxins are aflatoxins which are produced by certain strains of molds that inhabit agricultural produce. The main aflatoxin producing strains are Aspergillus flavus and Aspergillus parasiticus which infect food crops in the field and after harvesting. Out of all the types of aflatoxins, the most potent type is aflatoxin B1. The use of natural products as a remedy to health effects of aflatoxins in humans and animals is gaining popularity. Owing to its anti-inflammatory effects, Spirulina plantesis has been studied for protective effects. This study aimed at evaluating the effects of spirulina extract against aflatoxin B1 (AFB1) induced immune dysfunction and inflammation.

Methods: Male BALB/c mice weighing 28-34g were randomly placed into six groups and orally treated as follows: Group 1 was not treated but received food and water for entire experimental period. Group 2 received 200 μg/kg b.w of aflatoxin B1 orally. Group 3 received 1g/kg b.w of activated charcoal and an hour later 200 μg/kg b.w of aflatoxin B1 orally. Group 4, 5 and 6 received 50mg/kg, 100 mg/kg and 150 mg/kg b.w of Spirulina plantesis respectively then an hour later each group received 200 μg/kg b.w of aflatoxin B1 orally. Treatments were repeated daily for a total of 14 consecutive days. At the end of the last day of the experiment, all the mice were deprived of food and water for 12 hours, thereafter sacrificed and samples processed for immunological studies.

Results: The results indicated that there is a significant increase in body weight in 100mg/kg+AFB1 and 150mg/kg+AFB1 groups compared to AFB1 treated group ($p<0.05$). AFB1 was shown to increase serum levels of IFN- γ and IL-2 and decrease levels of IL-4. Treatment with spirulina extract did not have significant effect on the serum levels of IL-4 and IL-2 ($p>0.05$). Compared to AFB1 treated group, there was significant reduction in the serum levels of IFN- γ and IL-2 ($p<0.05$). Treatment with spirulina extract at different doses had no significant effect on serum levels of IgA, IgG and IgM ($p<0.05$). The mRNA expression of IL-4 was downregulated while that of TNF-α, and IFN-γ were upregulated. The results indicated that increasing mRNA expressions of TNF-α, and IFN-γ as a result of AFB1was prevented ($p\leq0.01$) by administration of spirulina extract.

Conclusion: These findings suggests that spirulina extract could be used as a remedy to AFB1 induced immune dysfunction and inflammation.

Keywords: Spirulina plantesis, Aflatoxin B1, immune dysfunction, inflammation, liver necrosis

Abstract 026

Title: Antimycobacterial Activity of Albizia zygia (Dc.) J.F. Macrb Root Bark Extracts tested singly and in Combination, their Cytotoxicity, and Phytochemicals Profiles.

Authors: Kehongo KM Moses (PAULESI-University of Ibadan)*

Tuberculosis (TB) is the most prevalent infectious disease after COVID-19. This has been accelerated due to the emergence of Multidrug-resistant TB (MDR-TB) and Extensively Drug-Resistant TB (XDR-TB). Medicinal plants have reportedly been used to treat TB and MDR-TB in East Africa. However, few have been evaluated for antimycobacterial activity. The present study examines cytotoxicity, antimycobacterial activity, synergistic interactions, and phytochemical profiles of the root bark of Albizia zygia (Dc.) J.F. Macrb. The plant materials were subjected to serial successive (sequential) extraction by a simple maceration method with organic solvents of increasing polarity as well as water. The extracts were tested for cytotoxicity against monkey Vero cells P18 using the MTT assay and for antimycobacterial activity against Mycobacterium smegmatis (Msm) using Microplate Alamar Blue Assay (MABA). The bioactive extracts were evaluated for synergistic interactions with rifampicin using the checkerboard assay and for phytochemical profiles and

characterization using FT-IR and GC-MS. The cytotoxicity concentration (CC50) of the tested extracts was >1000 µg/mL (non-cytotoxic) except for dichloromethane extract with 82.59±00 µg/mL (moderately cytotoxic). The MIC99 of methanolic and aqueous extracts was 625±0 µg/mL and 2500±0 µg/mL, respectively. Hexane, dichloromethane, and ethyl acetate extracts were inactive. The methanolic and aqueous extracts exhibited synergistic (FICI of 0.5) and additive (FICI of 0.75) interactions, respectively. GC-MS revealed 21 phytochemicals each in the methanolic and aqueous extracts. 7-ethyl-quinoline and acetyl-hydroquinone with reported antimycobacterial activity and numerous phytochemicals with reported antibacterial activity were identified in A. zygia. The findings in this study provide scientific evidence for the ethnomedicinal knowledge and use of A. zygia for the treatment of TB and its associated symptoms by Kenyan practitioners of traditional medicine.

Keywords: Albizia zygia, Antimycobacterial activity, Cytotoxicity and Synergy

Abstract 027

Title: PHYTOCHEMICAL AND ANTI-INFLAMMATION ACTIVITY OF Fagaropsis angolensis AND Fagaropsis hildebrandtii USING ANIMAL MODEL.

Authors: MALOBA MUKHUNYA PETER (MASINDE MULIRO UNIVERSITY)*

Indigenous plants of genus Fagaropsis have been widely used in traditional medicine to treat various illnesses, particularly those associated with pain and inflammation. However, scientific data to validate the use of Fagaropsis angolensis and Fagaropsis hildebrandtii in the treatment and management of inflammation is limited. Therefore, the objectives of this study were to determine the phytochemical composition and anti-inflammatory effects of F. angolensis and F. hildebrandtii aqueous and methanol extracts. Extraction of the leaves of F. angolensis and stem bark of F. hildebrandtii was done through cold and hot maceration processes to obtain methanol and aqueous extracts respectively. Qualitative phytochemical screening was conducted using standard methods while quantitative screening to determine total phenolic and total flavonoid content was done by Folin-Ciocalteu and aluminum chloride calorimetric methods respectively. To obtain the total phenolic content and flavonoid content, garlic acid and catechin were used as standards respectively. Carrageenan-induced hind paw edema in vivo model using swiss albino mice was adopted to determine the anti-inflammatory activities of the plant extracts. Both extracts were evaluated at four different doses; 250 mg/kg bw, 50 mg/kg bw, 10 mg/kg bw and 2 mg/kg bw while dexamethasone at dose of 10 mg/kg bw was used as the standard. The progressive reduction in the paw size was monitored for a period of five hours in all the treatment groups. Data analysis was conducted using graph pad prism and the significant differences between control and treatment groups determined at $p \leq 0.05$. Phytochemical screening revealed presence of steroids, phenols, saponins, alkaloids, flavonoids and coumarins in both F. angolensis and F. hildebrandtii extracts while fatty acid, essential oil and fixed oils were absent. F. angolensis methanol extracts had total phenolic content of 55.523±3.050mg GAE/g and total flavonoid content of 172.53±7.095mg CE/g. F. hildebrandtii and F. angpolensis extracts exhibited anti-inflammatory activity by inhibiting the increase in paw size after administration of carrageenan over the five hours monitored period. A significant progressive decrease in the paw size from one hour to the fifth hour was witnessed in the treatment groups administered with the plant extract and the positive control group (dexamethasone 10 mg/kg bw) $p=0.0001$, ($p<0.05$). Similarly, positive control exhibited more inhibition of the increase in the paw edema as compared to both the extracts at $p=0.0001$, ($p<0.05$). In the negative control, increase in the paw edema was observed over the five hours monitoring period. The study revealed that these two plant species have anti-inflammatory activity which can be attributed to the various phytochemicals present in these extracts. The finding validates the use of F. angolensis and F. hildebrandtii extracts by Embu and Kamba communities in management of inflammatory diseases.

Keywords: New frontier in natural products in management of inflammatory conditions.

Abstract 028

Title: ANTI-INFLAMMATORY MECHANISMS OF ACTION OF A HERBAL COMBINATION REMEDY FOR THE MANAGEMENT OF COVID-19 AND OTHER INFLAMMATORY DISEASES INCUDING ARTHRITIS.

Authors: Peter G Mwitari (KEMRI)*; Mercy Jepkorir (KEMRI); Elizabeth Kigondu (KEMRI); Sospeter Njeru (KEMRI); James Kuria (KEMRI)

Background: Growing evidence shows that coronavirus disease 2019 (COVID-19) can lead to a dysfunctional regulation of the immune system with the development of autoimmunity. The consequence of this immune dysfunctional regulation ranges from the production of auto-antibodies to the onset of rheumatic autoimmune disease. The onset of autoimmunity could most likely be due to Interleukin-6 overproduction among other markers of inflammation including C reactive protein, lactate dehydrogenase, ferritin, and creatinine.

Interleukin 6 (IL-6) is immediately and momentarily produced in response to infections and tissue injuries, it contributes to host defense mechanisms through the stimulation of acute phase responses, and immune reactions. Although its expression is strictly controlled by transcriptional and post-transcriptional mechanisms, dysfunctional regulation leads to continued synthesis of IL-6 which leads to pathological chronic inflammation and autoimmunity.

Cytokine interleukin (IL)-4 orchestrate type 2 immunity to infections and toxins. IL-4 induces differentiation of naïve T cells to type 2 T helper and T follicular helper cells and B cell antibody production. IL-4 also inhibits macrophage production of pro-inflammatory cytokines, including TNF-α, IL-1, and IL-6, in part via transcriptional repression.

Methods: The regulatory effects of the herbal remedy on the expression of IL-4, IL-6 and TNFα genes was evaluated by employing carrageenan-induced paw edema test in Swiss Albino mice. The expression of IL-4, IL-6 and TNFα in the paw tissue was determined by RT-PCR method. GAPDH was used as the house keeping gene while Diclofenac was used as the positive control.

Results: TNF-α and IL-6 genes were observed to be heavily down regulated to below 0.5 times while IL-4 was up-regulated up to 3 times.

Conclusion: The herbal remedy has been confirmed in previous computer docking and current in vivo studies to have superb anti-inflammatory potential and is a potential treatment to inflammatory and autoimmune diseases.

Keywords: Inflammation, Anti-inflammation,Autoimmunity,Interleukin-6, Interleukin-4, TNFα, COVID-19, Arthritis

Abstract 029

Title: IN VIVO ANTI-INFLAMMATORY POTENTIAL, SYNERGY, GENE EXPRESSION PROFILES AND SAFETY OF SELECTED MEDICINAL PLANTS ON RHEUMATOID ARTHRITIS

Authors: Mercy Jepkorir (KEMRI)*; Peter G Mwitari (KEMRI); Steven Ger Nyanjom (JKUAT); Gilbert Kipkoech (KEMRI); jean chepngetich (Pan African University Institute for Basic Sciences, Technology, and Innovation (PAUSTI)); Sally Kamau (Kenyatta University)

Background: Our body's immune system plays a critical role. An overactive immune system may lead to certain fatal diseases because of various hypersensitive or allergic reactions causing autoimmune diseases. Rheumatoid arthritis (RA) is a chronic, inflammatory, and systemic autoimmune disease. The primary symptoms of RA include pain, swelling, and destruction of cartilage and bone as a result of which permanent disability occurs. In Kenya, rheumatic diseases are still a poorly understood field, with infectious diseases dominating. Due to the lack of required population studies, the prevalence of rheumatoid arthritis in Kenya is still unknown hence no specific figures are available. The goal of treatment for rheumatoid arthritis patients is to eliminate symptoms, slow disease progression, and optimize quality of life. However, drugs available for treatment are associated with adverse side effects, which include: immune deficiency, gastrointestinal tract disorders, hormonal disturbances, and complications in the cardiovascular system. Therefore, the search for treatment is ongoing and, focus in this study is directed towards the traditional herbal plants owing to the fewer side effects and more compatibility with long-term usage compared to the conventional drugs. This study was done to establish the safety and effectiveness of the selected medicinal plants in the management and treatment of rheumatoid arthritis.

Method: Carrageenan was used to induce inflammation on the paw of each experimental mouse. After an hour, treatment was done using freshly prepared water extracts of the selected medicinal plants and paw edema observed for five hours. Extracts potential on pro-inflammatory cytokines (IL-6 and TNF-α) and anti-inflammatory cytokine (IL-4) expression was evaluated using Real Time Polymerase Chain Reaction with GAPDH as the endogenous control. Acute oral and sub-acute toxicity was evaluated in female Albino Swiss mice.

Results: Carissa edulis, Withania somnifera, Prunus africana and Rhamnus prinoides downregulated TNF-α at 50mg/kg with n-fold changes of 0.3, 0.23, 0.28 and 0.13 respectively. All extracts also down regulated the expression of 1L-6 at 50mg/kg with n-fold changes of 0.4, 0.3, 0.54 and 0.25 respectively. A combination of the four extracts had the highest regulation of the pro-inflammatory cytokines at both 50 and 100mg/kg concentrations. The four plant extracts conversely up-regulated IL-4. For the acute toxicity, no mortality and no significant changes were observed in body weight and wellness parameters at 500, 1000 and 2000mg/kg body weight doses of the plants' extracts compared to the untreated control group. The sub-acute toxicity studies also demonstrated no toxic effects.

Conclusion: This study confirms the potential application of these plant extracts in rheumatoid arthritis management and as leads to RA drug development.

Keywords: Rheumatoid arthritis,autoimmune diseases,carrageenan,cytokines

Abstract 030

Title: Formulation, Characterization, and Efficacy Evaluation of Moringa oleifera Leaf Polyphenols-Loaded Phytosome Delivery System

Authors: Jecinta Wanjiru Ndung'u (KEMRI)*; Jeremiah Gathirwa (KEMRI); Elingarami Sauli (The Nelson Mandela African Institute of Science and Technology (NM-AIST)); Hulda Swai (The Nelson Mandela African Institute of Science and Technology (NM-AIST))

Background: Herbal medication efficiency is mainly dependent on the delivery of effective level of therapeutically bioactive compounds. Severe limitation exists in polyphenols due to their bioavailability when administered by topical or orally applications thus decreased efficacy. This is attributed by their poor lipid miscibility and their large molecular size or both. Phytosomes are recently novel delivery system introduced herbal formulations that addresses limitations of traditional drug delivery systems. They have improved solubility, controlled drug release, protection of compounds, stability profile, and superior bioavailability than the conformist phyto molecules. As a result, phytosomes produce a better bioavailability due to higher absorption rate thus lower dosage. This study therefore aims at improving the bioavailability of Moringa oleifera leaf polyphenols (Mopp) through phytosomes encapsulation to enhance their bioavailability, safety and efficacy.

Methods: The Mopp were characterized using Fourier transform infrared spectroscopy and the dialysis membrane techniques. The Acute toxicity was assessed using Swiss albino mice.

Results: A significant amount of polyphenols were successfully extracted. Infrared (IR) spectra showed fatty acids' long-chain bands of the phospholipid molecule at 2958, 2923, and 2855 cm-1 confirming successful phytosomes synthesis. The drug release profiles demonstrated biphasic and prolonged subsequent sustained release. A fast polyphenol release (43.43%) was observed at 8th hour, followed by a sustained drug release (53.49%) over the remaining 72 hours for MoP. Korsmeyer peppas model release kinetics with linear regression R2 = 0.9306 was best fit. This shows that the diffusion and erosion is the drug release mechanism. The oral administration of Mopp and the MoP at doses below 2000 mg/kg doses resulted in no clinical signs of acute toxicity. The oral administration of free Mopp and Moringa oleifera phytosomes at a dose upto 2000 mg/kg did not influence the body weight of the Swiss albino mice during 5 h and in a prolonged period of 14-day of observation. There was no mortality in both control and treated groups across the different doses. Additionally, there were no abnormalities in the autopsy organs.

Conclusion: MoP drug delivery system complex was successfully developed. The results indicate the potential of Moringa oleifera phytosomes to improve the bioavailability of polyphenols by increasing stability, control of drug release and absorption as compared to conventional herbal extracts. The in vivo investigation showed the safety of MoP at a dose below 2000 mg/kg. The present findings also reveals that Moringa oleifera polyphenols loaded phytosomes have potential in exhibiting better pharmacokinetic profile than the conventional polyphenol herbal extracts.

Keywords: Phytosomes; Moringa oleifera; Bioavailability; Release kinetics; Characterization

Scientific Session 5: Public Health-1

Abstract 032

Title: Preliminary findings from a photovoice study of community members' choice, experiences and perceptions around fuel use and cooking practices in Mukuru (Kenya) and Ndirande (Malawi)

Authors: fred orina (kemri)*; Mary Nyikuri (KEMRI)

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Background: Worldwide, 2.4 billion people rely on solid fuels for cooking. About 3.2 million deaths from illnesses attributable to the household air pollution, is caused by incomplete combustion of solid fuels and kerosene used for cooking. Inhaling of particulate matter is responsible to almost half of all lower respiratory infection deaths among children under 5 years, this is mainly experienced by poor urban and peri-urban dwellers who have limited access to affordable clean energy in low- and middle-income countries. We aimed to understand the choice and utilization of fuels for cooking in the informal settlements in Kenya (Mukuru) and Malawi (Ndirande).

Methods: This was a qualitative study in which photovoice method was used in data collection. Recruited participants were trained and asked to take photographs around the topic of the study over a period of 2 weeks. Facilitated by the research teams, a series of sorting and analysis meetings of the photos, were held to contextualize data collected.

Results: In Kenya, 10 participants (7 females) participated in the study while in Malawi 9 Participants (6 females) took part in the study. In both study sites, firewood, charcoal, and briquettes were the main fuels utilized for cooking. However, additional sources included liquid petroleum gas, ethanol, and paraffin in Mukuru, while plastic waste bottles, maize stalks and Cobs were used in Ndirande. The type of food being prepared, availability of cash to purchase fuels, and availability of the fuel, including seasonality were determinants of fuel choice. Men, women and young people were involved in fuel procurement and food preparation in both countries. Contrastingly, in Mukuru, most families preferred purchase of precooked foods for reheating or frying, while in Ndirande according to availability, families prepared meals themselves at home. Participants in both countries were cognizant of the dangers of using firewood due to the smoke emitted.

Conclusion: This study offers an in-depth exploration of fuel procurement and use in informal settlements through utilization of novel and participatory methods. Interventions to address the issues of household air pollution related harms must consider the economic, social, and cultural context of local communities.

Keywords: Food preparation, photovoice, Fuel, Air pollution

Abstract 033

Title: Individual and social level factors influencing repeated pregnancy among unmarried adolescent mothers in Katavi Region—Tanzania: A qualitative study

Authors: Minyahil Tadesse Boltena (1. Institute of Health, Jimma University, 2. Armauer Hansen Research Institute, Ministry of Health)*; Salim Juma Mpimbi (Ifakara Health Institute (IHI), Dar es Salaam, Tanzania)

Background: Adolescents' pregnancy rates are still high in Tanzania, despite the efforts made by the national campaign. Within two years after the first pregnancy, adolescent mothers are more at risk of repeat conception. Repeated pregnancies are associated with increased maternal and perinatal outcomes. Katavi is a leading region in the country, with 45% adolescent pregnancy. Studies are scarce on factors influencing repeated pregnancy among unmarried adolescent mothers in the region. Therefore, this study explored the individual and social level factors influencing repeated pregnancy among unmarried adolescent mothers in the Katavi Region.

Method: An exploratory qualitative study, using key informant interviews (KIIs) was adopted for 16 participants. The study participants were unmarried adolescent mothers, aged 15–19 years, who were purposively sampled. Thematic analysis was used to analyze qualitative data. QSR Nvivo version 14 was used to analyze these data.

Result: The study established the individual factors influencing repeated pregnancy, which were inadequate sexuality knowledge, individually perceived barriers to contraceptive use, and the guarantee for marriage. Furthermore, the social factors identified were the power of decision-making, peer pressure, and the parent–child relationship.

Conclusion: Inadequate education on sexuality is observed as a crucial factor influencing repeated pregnancy. Parents as primary educators should be encouraged to talk with their children, especially adolescent girls about sexual education.

Keywords: Adolescents; Individual; Repeated pregnancy; Social Tanzania; Unmarried

Abstract 034

Title: Population, Climate Change, and Sustainable Development in Africa

Authors: Ndirangu Ngunjiri (University of Nairobi)*

This study examines population, climate change, and sustainable development within and around the African forests. The encroachment has led to extreme and considerable land fragmentation, deforestation of the headwater catchments, and destruction of wetlands previously existing within the fertile upstream parts. The increase in environmental degradation has led to the escalation of structural and violent conflict. In this regard, forests in African countries have undergone severe destruction as a result of the growing population. However, the complex faces many threats mainly due to large-scale anthropogenic activities leading to climatic changes. The main objective of the study is to critically examine the relationship between the population, climate change, and sustainable development. Both secondary and primary data were employed to study the links between population growth and climate changes around the forest. The study findings reveal that climate changes are led by human actions such as population pressure, political motives influencing occupation of the forest land, growth of subsistence agriculture, logging, charcoal making, and rural-urban development. The study concludes that the areas around the forests are experiencing rapid climate changes, including recurrent and persistent drought periods and rainfall variability. These changes in the local climate pose unprecedented implications for the sustainable development of the country and the region that depends on the forest complex. The study recommends that while dealing with climate change issues, national policies are guided by taking into consideration of addressing population growth dimensions as a major threat to forest lands.

Keywords

climate change; resource; human; Forest; conservation; sustainable development

Abstract 035

Title: Host transcriptional RNA signatures as predictive markers of outcome in children with severe lung infection

Authors: Angela W Maina (KWTRP)*; Charles Sande (KWTRP)

Background: Children with severe acute infection often present with symptoms that are poorly predictive of the likely survival outcome, making it difficult to distinguish between children with a higher risk of death from those with a better clinical outlook using clinical data alone. In addition to the paucity of early prognostic markers of survival, the biological mechanisms that precede inpatient death in African children are not fully understood. A detailed understanding of these mechanisms is imperative in devising potential interventions to reverse the clinical trajectory of at-risk children. Here, we profiled the gene expression patterns of acutely ill children who (i) recovered and were discharged from hospital or (ii) who succumbed to infection prior to discharge. These data were used to identify biological mechanisms and markers that highly correlated with the likelihood of death.

Methods: Total RNA from the peripheral blood mononuclear cells of 19 survivors and 22 non-survivors was extracted and used for generation of Illumina exome sequencing libraries. Paired end sequencing was performed on the HiSeq4000 75bp platform, generating a raw read count of >19.7 million reads per sample. A custom bioinformatics analysis pipeline was created to perform pre-processing of raw RNA sequencing reads, quality control and analysis of gene expression levels. Cell phenotype composition of peripheral blood was inferred using the CIBERSORTx method. Gene set enrichment analysis (GSEA) was used to identify functional blood transcription modules that were statistically over-represented by survival outcome. Weighted gene co-expression network analysis (WGCNA) was used to perform unsupervised clustering of genes that enabled the description of correlation relationships between genes and samples. All analyses were performed in the R programming environment.

Results: Results of GSEA analysis showed an upregulation of T-Cell receptor and type 1 interferon signaling pathways in survivors compared to non-survivors. The unfolded protein response was among the most significantly upregulated biological pathways in non-survivors. Analysis of the expression profile of 22 molecular chaperones, that are known to be upregulated during endoplasmic reticulum (ER) stress showed that 82% of these genes were significantly overexpressed in non-survivors compared to survivors. The expression levels of genes encoding for two of the three major ER stress sensing proteins, and the main molecular triggers of unfolded protein response (UPR), were significantly elevated in non-survivors compared to survivors.

Conclusion: These data provide the first important clues of the biological mechanisms that are associated with inpatient death in African children. Further work is ongoing to unravel more mechanistic links with fatal outcomes and to validate them in independent cohorts.

Keywords: Gene expression, transcriptomics, biological pathway

Abstract 036

Title: Association of household food insecurity and malnutrition among caregivers of children attending mother child clinics in western Kenya.

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Background: Food insecurity is a serious public health concern in low and middle-income countries where agriculture is the main source of livelihood. Maternal nutritional status and mental health may be affected by household food insecurity. We sought to determine the correlation between food insecurity and malnutrition in mothers who were enrolled in the Maternal Administered Malnutrition Monitoring System (The MAMMS Trial).

Methodology: This is a secondary analysis of a randomized controlled trial conducted in western Kenya which enrolled caregivers of children aged 5 and 12 months with a mid-upper arm circumference (MUAC) of 12.5 to 14.0 cm. A structured questionnaire was administered and anthropometric measurements (MUAC, weight, and height) were taken from the primary caregivers of enrolled children. Maternal nutritional status was measured using body mass index (BMI) and were categorized as underweight, normal, overweight and obese. Food insecurity was analyzed using the Household Food Insecurity Access Scale. A linear regression model assessed associations between maternal nutrition, household food insecurity, maternal depression (PHQ-9) and household Income.

Results: We assessed 1170 caregivers out of which 742 (63%) lived in food secure households while 428(37%) lived in food insecure households. Of all mothers assessed 674 (58%) had normal BMI, 145 (12%) were obese, 290 (25%) were overweight and 61(5%) were underweight out of which 36 (59%) lived in food secure households. Food insecurity and household income were predictors of caregiver BMI. Caregivers who lived in food insecure households had a lower-than-normal BMI making them more likely to get malnutrition compared to those who lived in food-secure households(p=0.003). Households that had higher income were less likely to be malnourished compared to those who had less income(p=0.000)

Conclusion: Income was a determinant of food security among the caregivers in this study, and both these factors were associated with lower maternal BMI. Interventions such as cash or food transfers may promote maternal health among undernourished households. However, there is also a need to review the nutritional knowledge among caregivers, as the data shows some caregivers lived in food-secure households but were still underweight.

Keywords: Household food insecurity,

Abstract 037

Title: EVALUATION OF COMMUNITY EVENT-BASED SURVEILLANCE (CEBS)in SIAYA, KENYA 2021

Authors: Cynthia A Musumba (Field Epidemiology and Laboratory Training Programme)*; Ahmed Abade (Field Epidemiology and Laboratory Training Programme); Phillip Ngere (Division of Disease Surveillance and Response); Nzisa Liku (Washington State University)

Authors: Cynthia Musumba1* Ahmed Abade1 Phillip Ngere2 Liku Nzisa3

1Field Epidemiology and Laboratory Training Program 2Disease Surveillance and Response Unit, Ministry of Health 3Washington State University

Background: In a world that is increasingly vulnerable to high impact Outbreaks, a sensitive early warning system is imperative, that would rapidly detect public health events before they become large and uncontrollable. Event-based surveillance (EBS) is a key component of an effective early warning system enabling countries to be prepared for outbreaks. This evaluation aimed at establishing whether the system met its intended objective as per the EBS guideline.

Methods: We conducted a retrospective data review and key informant interview. The CDC MMWR guideline was used for surveillance system evaluation. Purposive sampling was used to select 49 stakeholders who were interviewed using a structured questionnaire. EBS data was reviewed for the period between October 2021 to May 2022. Data was cleaned and analysed using Ms Excel, Epi info and Stata. Frequencies and proportions for qualitative variables and measures of central tendency and dispersion for quantitative variables were calculated.

Results: A total of 2079 signals were reported out of which 1320(63%) were verified, verified true were 526(40%), 284(54%) were investigated,273(96%) responded to and signal completeness was 51%. Rarieda Sub-county reported most of the signals, 29% (595). The highest number of signals was reported in October (637), and signal reporting dropped to 118 in April 2022. The median time from signals reporting to detection in CEBS was one (1) day with a range of 0– 85 days, thus able to detect signals in real-time. Users interviewed reported the system as simple, flexible, and useful since covid 19 signals were added and the system was able to detect events including covid 19 cases; they also reported lack of refresher training and support supervision as factors contributing to decline in performance in CEBs.

Conclusion: Signal Completeness was low from the evaluation, with an evident decline in reporting rates, triaging, verification and investigation of signals. We recommend further studies to determine factors associated with performance in CEBS, refresher training and support supervision to CEBs actors.

Keywords: Public Health Surveillance, Event-based surveillance, CDC, Completeness

Abstract 038

Title: ASSESSING THE TRANSITION OF CAMPAIGN DELIVERY OF VITAMIN A SUPPLEMENTATION TO ROUTINE DELIVERY IN CÔTE D'IVOIRE AND SENEGAL

Authors: Melissa M Baker (Helen Keller International)*; Fatou Ndiaye (Helen Keller International); David Doledec (Helen Keller International)

Background/Objectives: Vitamin A supplementation (VAS) health campaigns are costly, intermittent events that ensure sustainable VAS coverage among children aged 6–59 months who are at risk of vitamin A deficiency. Disruptions to these campaigns due to funding constraints, the eradication of diseases, and global health crises have postponed, cancelled, suspended and even ended some health campaigns. Countries across Sub-Saharan Africa have started to rethink the planning and implementation of VAS to ensure no at-risk child is left without supplementation. The government of Côte d'Ivoire is currently transitioning, and the government of Senegal has fully transitioned from campaign to a routine VAS delivery model. The objective of this study is to assess the VAS coverage through the routine health system, and to identify factors that hinder or help routine VAS at the household, community and health facility levels.

Methods: This baseline assessment employed qualitative and quantitative methods, utilizing the WHO (2015) randomized cluster design with areas selected using probability proportional to size sampling methodology. In Senegal, 1305 household surveys were administered and eight focus group discussions among caregivers of children aged 6 to 59 months, and interviews with 60 health actors from four health districts. In Côte d'Ivoire, 1703 surveys were administered and six focus group discussions among caregivers of children aged 6 to 59 months, surveys among 207 community health workers, 164 health workers, and 47 interviews among caregivers of children aged 6 to 59 months and key community and health actors in 28 health districts.

Results: VAS coverage in Senegal in first semester 2019 was 42%, and was 66.8% in the second semester 2020 (July-December) and 73.2% in semester one 2021 (January-June) in Côte d'Ivoire. Several challenges were noted as hindering VAS coverage from reaching >80% through routine delivery in Côte d'Ivoire and Senegal. At the individual level there is an overall lack of awareness among caregivers of the importance of VAS and the need for continued supplementation after infant immunization schedules are completed, and among community health workers there is a high workload with little renumeration, which affects motivation to distribute VAS. At the health facility level there is poor estimation of the number of target children eligible for VAS each month, which results in insufficient stock of vitamin A capsules to fulfill demand. The incomplete reporting of capsules distributed each month also contributes to poor stock planning and results in stockouts.

Conclusion: The VAS coverage through routine delivery is lower than the target coverage of >80%, which highlights the need to reflect on dysfunctions in the quality of reporting and stockage of vitamin A, appropriate motivation of community health workers, and caregiver knowledge on the importance of VAS that need to be corrected to improve coverage.

Keywords: Vitamin A Supplementation, Children, Vitamin A, Health System Strengthening, Campaign, Routine Health Care

Abstract 039

Title: ASSESSMENT OF HEALTH CARE WASTE MANAGEMENT (HCWM) IN CONTEXT OF ENVIRONMENTAL SAFEGUARDS IN UNIVERSAL HEALTH COVERAGE,KISUMU WEST SUB COUNTY,NYAHERA SUB COUNTY HOSPITAL

Authors: duncan odhiambo ongayi (ministry of health)*

Author; Duncan Ong'ayi

Background: The government of Kenya has prioritized Universal Health Coverage (UHC) in its big 4 agenda. Kisumu County is one of the first four piloting counties in UHC together with Nyeri, Isiolo, and Machakos. Poor management oh health care waste (HCW) may expose health workers and the community to infection/hazards from health care establishments.

Objective: Environmental safeguards are key to UHC implementations hence it is therefore important to review and analyze the adopted practices in waste management.

Methods: This was across sectional study done to assess the availability of functional incinerators, burning chambers, well protected ash pits, well protected placenta pits, and having colour coded bins and waste segregation in Kisumu west sub county.one county hospital, four sub county hospitals, ten health centers and seven dispensaries public, faith based and private were surveyed by collecting data by using infection prevention and control (IPCAT) questionnaire/observation checklist. This was carried out between May and july2021. Data collected was later analyzed using Excel data analysis tool to determine the percentages.

Findings: The study reveled that 60% of the hospitals had a functional incinerator, 20% of health centers and 11% of the dispensaries had burning chambers. On availability of color coded bins 90% of hospitals, 78% of health centers and 100% of dispensaries had them. 50% of hospitals had proper waste segregation . 75% of hospitals, 45% of health centers and 40% of dispensaries had well protected ash pits. 78% of hospitals, 52% of health centers had well protected placenta pits.

Conclusion: More resources needed to be allocated by the County Government to be spent on provision of basic commodities/amenities and training of staff on health care management.

Keywords: UHC

Abstract 040

Title: Health-seeking behavior for child illnesses in western Kenya: Qualitative findings from the Child Health and Mortality Prevention Surveillance (CHAMPS) Study

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Introduction: Health care seeking behavior by caregivers for childhood illnesses is an important determinant of child survival, and delayed healthcare is associated with high child mortality. Acquiring health information and making use of the information can moderate inaccurate assessment and response to childhood diseases.

Methods: The Child Health and Mortality Prevention Surveillance (CHAMPS) Kenya team assessed factors affecting caregivers' Health care seeking behavior for childhood illness in western Kenya by conducting a qualitative study of 88 community members between April 2017 and February 2018 using purposive sampling in an informal urban settlement in Kisumu County, and in rural Siaya County. Key informant interviews, semi-structured interviews and focus group discussions were audio-recorded and transcribed. All participants provided verbal consent. Data management was completed on Nvivo 11. Iterative analysis process was utilized and themes were identified and collated.

Results: Our findings reveal three broad thematic areas: cultural beliefs, religious beliefs and economic factors. Often, caregivers prefer not to take children with measles symptoms to the hospital because of a belief that the child will die upon medical intervention. In other instances, caregivers would take their children to traditional healers for illness believed to be caused by witchcraft. Caregivers would seek prayers for their children illness and wellbeing because of the belief in the healing power of prayers. Caregivers low income and perception of prohibitive cost of clinical care attributes to seeking over the counter medication first, which further delays care. Pain relievers were the most commonly reported medication purchased by caregivers to relieve symptoms of illness in children.

Conclusion: To improve timely health care seeking behavior, it is important to increase health literacy in caregivers and improve their ability to accurately assess the timing and importance of clinical health care. Education should include a focus on danger signals in childhood illness which should prompt immediate clinical healthcare-seeking.

Keywords: Healthcare seeking behavior, health literacy, public health

Abstract 041

Title: Over-The-Counter Antimicrobial Sale in Kenya: A mystery client survey

Authors: John Ndemi Maina (Kenya Medical Research Institute)*; John Mwaniki (Kenya Medical Research Institute (KEMRI)); Annette Aduda (Kenya Medical Research Institute (KEMRI)); Beatrice Ongadi (Kenya Medical Research Institute (KEMRI)); Susan W Kiiru (KEMRI); Franklin Mwiti (Kenya Medical Research Institute (KEMRI)); japhet jk katana (kenya medical research institute); Terry Judah (KEMRI-CMR); John Kiiru (KEMRI-CMR)

Background: Irrational usage and overuse are among the key contributors to the increasing antimicrobial resistance globally. The contemporary argument for self-medication in poor resource settings, especially in Low and Middle-income countries, has been poverty and limited rapid diagnostic points of healthcare. In Kenya, "out of hospital" antimicrobial dispensing supersedes the hospital-based. While it is not always possible to administer antimicrobials based on the results of an antibiogram, therapeutic decisions may be influenced by diagnostic test results, patient demographic information, and judgments made by a qualified doctor. As a result, a prescription is a necessity for antimicrobial sales. Despite Kenya's regulation on prescription-only sales, weak legislation enforcement and ignorance by key stakeholders risks perpetuating none-adherence leading to antimicrobial misuse and over-use.

Objective: The present study aimed to assess the antimicrobial sale practices of community drug sellers in Kenya.

Methods: A cross-sectional study design was used to conduct mystery client surveys in community drug sellers between 2020 and February 2022. A total of 462 mystery surveys were conducted in Nairobi (313), Makueni (116), and the Central Kenya region (33), using urinary tract infections as the select disease.

Results: From the 462 surveys, 404 (87.4%) drug sellers did not ask for a prescription. Despite 58 drug sellers asking for a prescription, only 7 (12%) refused to sell antibiotics without a prescription. In addition, only 228 (49%) engaged the buyer, where 181 (39.2%) asked about the disease history, 25 (5.4%) asked whether a female client was pregnant, and 127 (27.5%) asked about medication history. Furthermore, only 43 (9.3%) recommended the patient see a doctor, while 10 (2.2%) said there was no need for medication. Most drug sellers lacked awareness of antimicrobial resistance (84.8%).

A wide variety of antibacterial and antifungal medications were sold over the counter, including Amoxil (19%), fluconazole (16%), ciprofloxacin (13%), azithromycin, doxycycline, and nitrofurantoin (each at 9%), cefixime, levofloxacin, and metronidazole (all at 4%), among others. In addition, 129 (23.9%) sold a half dose; nevertheless, the majority (94, 72.9%) advised the customer to purchase the whole medication later.

Conclusion: Over-the-counter sales continue to derail antimicrobial stewardship efforts. Notably, the sale of vital antimicrobials, some of which are on the World Health Organization and the national watch list, risk stretching the already elevated resistances, narrowing treatment options readily available. Therefore, there is a dire need to strengthen enforcement and adherence to prescription-only sales to alleviate the risk of antimicrobial resistance emergence.

Keywords: Drug sellers, Antimicrobial, Prescription

Abstract 042

Title: Respiratory Syncytial Virus and Vaccination in Kenya; What are the Healthcare Workers' Preference?

Authors: VICTOR A OPERE (KEMRI)*; RAPHAEL O ATITO (KEMRI-CGHR); Bryan BN Nyawanda (KEMRI); Nancy Otieno (KEMRI); James Ougo (KEMRI); Joyce U Nyiro (KEMRI-Wellcome Trust Research Programme)

Background: Respiratory syncytial virus (RSV) remains a major cause of childhood pneumonia, especially among infants under 6 months of age who bare the biggest burden of RSV disease. Little is known about healthcare workers' (HCWs) knowledge, attitudes and beliefs around RSV and RSV vaccination; this study investigated the general and RSV- specific knowledge and attitudes of HCWs towards RSV and RSV immunization in two Kenyan counties.

Methods: Between September and October 2021, the Kenya Medical Research Institute (KEMRI) conducted a cross-sectional survey among HCWs in five health facilities in Siaya county, three health facilities in Nairobi county and Ministry of Health (MoH) officials in the two counties. This study was a follow up to a larger cross-sectional survey examining factors that shape acceptance of maternal vaccines in Kenya. We enrolled HCWs delivering services directly to mothers at the maternal and child health departments in the selected health facilities and MoH officials in-charge of vaccine distribution, policy and management.

Results: We interviewed 104 HCWs, 60 from Siaya and 44 from Nairobi Counties. Of the 104, 94 (90.4%) were HCWs while 10 were MoH officials. 64 (61.5%) were female, 65 (62.5%) were nurses, 67 (64.4%) had diploma certificates and 49 (47.1%) had 5-10 years of experience. The respondents noted that most women attended ANC for the first time while in the second trimester of pregnancy and that they made ≥4 ANC visits, 78 (83.0%) and 78 (83.0%), respectively. In general, most respondents would recommend maternal immunization to protect the mother 91 (88.4%) and the baby 76 (73.8). and would recommend a single dose vaccine schedule 62 (59.6%) for maximal adherence and compliance 38/62 (61.3%). Considering vaccine vial size, most respondents recommended single dose/device vaccines 50/86 (58.1%) mainly to prevent wastage and contamination. Of the 104, only 41 (39.4%) had heard about RSV and 38/41 (92.7%) thought that pregnant women should be vaccinated against RSV. Nearly all (39/41) respondents were not aware of RSV vaccination products in the market but would recommend the vaccine if available

Conclusion: This study found that there is a huge gap in knowledge around RSV and RSV vaccination among Kenyan HCWs. It also found that most HCWs would recommend maternal immunizations, preferring single dose scheduling and single-dose vials/devices should the vaccines be available. Given the knowledge gap, we recommend creation of RSV awareness among the HCWs.

Keywords: Respiratory Syncytial Virus , healthcare workers

Scientific Session 6: MCH-1

Abstract ID: 043

Title: Dental Visits and Perceived Benefits of Oral Health during Pregnancy Are Associated with Preterm Birth Outcome: Retrospective Analysis of US PRAMS data from 2009 to 2020

Authors: Hyewon Lee (Seoul National University)*

Background: Previous research on the maternal population has shown a positive association between expecting mothers' periodontal disease and adverse birth outcomes, such as pre-eclampsia, low birth weight, and preterm birth. Periodontitis can induce systematic inflammation responses when uncontrolled and untreated. Studies showed that systematic inflammation due to untreated periodontitis might lead to premature rupture of membranes and myometrial contraction. The current study examines the association of preterm birth with oral health variables, including dental visits before and during pregnancy and the perceived benefit of oral health during pregnancy among a representative sample of women with a recent history of birth in the United States.

Methods: This retrospective cross-sectional study utilized the US CDC's Pregnancy Risk Assessment Monitoring System (PRAMS) datasets from 2009 to 2020. All the demographic and prenatal care information was obtained from the birth certificate data, and respondents reported dental visits and perceived oral health benefits through a survey form. Descriptive and multivariate logistic regression analyses were performed to examine the association between oral health variables and preterm birth outcomes.

Results: 365,788 women with a recent single live birth were included in the study, representing 19,418,308 women in 35 states in the U.S. Among these women, 7.9% had preterm birth based on the birth certificate data. More than half of women (56.5%) reported that they had their teeth cleaned by dentists prior to pregnancy, and 46.1% of women reported that they had their teeth cleaned by dentists during pregnancy. When adjusted for mother's age, marital status, insurance type, mother's educational level, adequacy of prenatal care (Kotelchuck index), previous preterm birth, and other medical conditions associated with preterm birth, women who had dental visits for cleaning during pregnancy (OR=0.87, 95% CI [0.83, 0.91], $p<0.001$) had lower odds of having preterm birth compared to women who did not have dental visits for cleaning. Women who perceived oral health benefits during pregnancy had 12% lower odds of having preterm birth outcomes than women who did not perceive the benefits of oral health during pregnancy (OR=0.88, 95% CI [0.82, 0.95] $p=0.001$).

Conclusion: This study showed a significant association between dental visits for cleaning during pregnancy and the preterm birth outcome when controlled for prenatal care visits and other socio-demographic variables and medical conditions related to preterm birth. The significant association of perceived oral health benefits during pregnancy with preterm birth outcomes highlights the importance of women's oral health beliefs related to their overall health. Future research with a prospective study design in both developed and developing countries will provide the temporal relationship between perceived oral health benefits, dental care, and preterm birth outcome.

Keywords: Prenatal Oral Health, Pregnancy, Oral Health, Preterm Birth

Abstract 044

Title: Religious Factors Affecting Utilization of Maternal Health Services in Siaya County, Kenya: A Qualitative Study.

Authors: Evans O Dzenis (Maseno University)*; Louisa Ndunyu (Maseno University); Charles Olan'go (Maseno University)

Background: Approximately 99% of all maternal deaths occur in developing countries. Siaya County had a maternal mortality ratio of 691 deaths to Kenya's 362 deaths per 100,000 live births. Previous studies on maternal morbidity and mortality have been quantitatively oriented. This has resulted in limited explanations of religious factors, a component of maternal morbidity and mortality framework factors. Pregnancy care is conventional and locally by TBAs, FP use is linked to promiscuity, maternal vaccination to sterilization, and birth done by church TBA. Religious factors are difficult to measure using statistical tools. So far, qualitative studies are yet to give explanations of how religious factors affect utilization of maternal health services.

Methods: This exploratory phenomenological study was conducted in Siaya County. 22 women of reproductive age were interviewed by snowballing technique. Triangulating IDI's findings was done with KII's and FGD's harmonized themes and sub-themes. Analysis and report guided by Andersen's model of healthcare utilization.

Results: Mothers sought health services from both skilled and alternative service providers, but, mostly utilized alternative care services. Hesitance to visit the hospitals was because of long waiting time for services. Late ANC visits are due to fear of many re-visit trips demanded. Instead, mother's sought services of 'madha' (church-ordained female birth attendant and health counselor) who they reported to have experienced hands in massaging pregnant women and conducting deliveries. Gender and unfriendly health providers make women shy away. These complicate the desire to utilize ANC and SBA services. Women avoid maternal vaccination and contraception services as the church teachings assert that such lead to sterility, abortions, cancers, and disgrace women. The church has own maternal caring norms and practices to observe. These not only complicate utilization of maternal health services but also complicates utilization of SRHR services. 'Madha' and mother's in-law believe and prefer women to deliver at home. Mothers believe in the cleansing power of herbal medicines. Held beliefs about delivering a 'dirty child' at the hospital further complicate the plans to gain on utilization of skilled birth services. Mothers did not have knowledge of PNC services.

Conclusion: The complex nature of maternal health demands that solutions to their problems need to be equally complex. One model approach to solutions can not suffice. To increase utilization of maternal health services, we need respectful and friendly health service providers conscious of the faithful's needs, beliefs and practices. There is need to engage stakeholders and implementing partners involved in maternal health initiatives to address internal (health facilities), external (community) environments, and personal (individual) factors to demystify the myths, misconceptions, and fears about maternal health services.

Keywords: Religious factors, beliefs, maternal morbidity and mortality, conventional care

Abstract 045

Title: Knowledge level and associated factors about sexual and reproductive health rights among University of Gondar students, Gondar Ethiopia

Authors: Keflie Yohannes Gebresilassie (University of Gondar)*

Background: Young people's knowledge of sexual and reproductive health rights (SRHRs) is essential in exercising these rights. Knowledge about SRHRs helps to tackle neglected issues, such as adolescent sexuality, gender-based violence, and unsafe abortion. But little is known about the level of knowledge and the important predictors in the study area, therefore this study was done to fill the gap.

Objective: This study aimed to assess knowledge about sexual and reproductive health rights and associated factors among undergraduate regular students at the University of Gondar, in 2018.

Methods: Institution-Based Cross-Sectional Study was conducted from March to April 201 at the University of Gondar. A simple random sampling technique was used to select participants from five randomly selected faculties after proportional allocation was done for each department in each faculty. A structured pre-tested self-administered questionnaire was given for the participants to collect data. Both bi-variable and multivariable logistic regression analysis were carried out to estimate association. Crude and Adjusted Odds Ratios with their 95% confidence intervals were estimated. A p-value less than 0.05 was taken as a cut-off point for significance.

Result: A total of 827 students were included making the response rate 98.8%. Four hundred twenty-two (51%) were male. The overall optimal knowledge level about SRHRs was 57.7% (95% CI 54.2-61.1) 60.5% (95% CI 55.5-65.3) for females and 54.9% (95% CI 49.9-59.8) for male students. Being Muslim (AOR=0.33; 95% 0.18, 0.63), Information and education faculty students (AOR=0.45 95% CI 0.32,0.65) had a negative, while Urban residents (AOR=1.49; 95% 1.10, 2.01), availability of reproductive health service in the campus clinic (AOR=1.40; 95% CI 1.04, 1.89) had a positive significant association with having optimal knowledge about SRHRs.

Conclusion: Large proportion of students didn't have optimal knowledge about SRHRs. Factors such as religion, residence, type of faculty, and availability of RH service in student clinics had statistically significant associations with knowledge of SRHRs. To bridge the knowledge gap, we recommend the provision of sexuality and rights education, and also availing reproductive health services for students, giving emphasis to Muslims and students from rural areas.

Keywords: Sexual and Reproductive rights; University students; Cross-sectional; Ethiopia

Abstract 046

Title: Prevalence and factors associated with anaemia in pregnancy among women attending first ante-natal care clinic between January 2021 and April 2022 at Doldol Subcounty Hospital, Laikipia County: A cross-sectional study

Authors: David M Kariuki (County government of Laikipia)*

Background: Anaemia in pregnancy causes adverse maternal-fetal morbidity and mortality outcomes. Kenya's prevalence of anaemia in pregnancy in 2019 was 40.7%, a severe public health problem. Our study aimed to: determine the prevalence of anaemia in pregnancy, characterize its associated sociodemographic and clinical factors, and to assess data quality at Doldol Subcounty Hospital Antenatal Care Clinic (ANCC).

Methods: We performed a retrospective cross-sectional study, reviewing data from 425 pregnant women who attended their first ANCC at Doldol Subcounty Hospital from January 2021 to April 2022. Data on sociodemographic and clinical factors were abstracted from ANC (MOH405) and laboratory registers (MOH204). We defined anaemia in pregnancy as haemoglobin concentration <11g/dl at first ANC. We included 393 (92.5%) eligible women whose haemoglobin level at first ANC was recorded, and excluded those without. We cleaned and analyzed the data using Microsoft Excel and Epi Info7, and a data quality audit was performed with the standardized Centre for Disease Control (CDC) tool. We used mean with standard deviation (SD), median with interquartile range (IQR) for continuous variables and frequencies and proportions for categorical variables. We conducted bivariate analysis to determine factors associated with anaemia in pregnancy using odds ratios (OR) with 95% confidence intervals (CI).

Results: The median age was 22 years (IQR=9 years). The mean haemoglobin level was 10.9±1.8g/dl. Prevalence of anaemia in pregnancy was 48.6%; 26.7% had moderate anaemia, 20.4% had mild anaemia and 1.5% had severe anaemia. Of the anaemic women 28.3% were in second trimester, 15.0% were in third trimester while 5.3% were in the first trimester of pregnancy. Women in their second and third trimesters of pregnancy were 61.1% and 23.4% respectively. Early childhood and teenage pregnancies were 27.3% and 6.7% had advanced maternal age. The proportion of nulliparous women was 29% and 11.5% were grand-multiparous. Women who had undergone FGM were 17.3% and 17.8% had bacteriuria in pregnancy. The factors associated with anaemia in pregnancy were: late initiation of ANC [OR 1.99, CI (1.13-3.54)], non-residents of Doldol [OR 1.42 CI (0.75-2.68)], being unmarried [OR 1.33 CI (0.74-2.37], grand-multiparity [OR 1.31 CI (0.88-2.12)] and advanced maternal age [OR 1.06 CI (0.48-2.35)]. All variables achieved a threshold of >80% in the DQA.

Conclusion: Anaemia in pregnancy, though preventable, is a severe public health problem at Doldol subcounty hospital ANCC. Late initiation of ANC was associated with anaemia in pregnancy likely due to delayed supplementation with iron and folate. Other factors were associated but not statistically significant. We recommend enhanced emphasis and education on early initiation of ANC with iron and folate supplementation, routine surveillance for anaemia in pregnancy with early interventions. Multivariate analysis was not conducted in this study.

Keywords: Anaemia, pregnancy, Kenya, prevalence, cross-sectional studies, dietary supplements

Abstract 047

Title: Developing and Implementing A Vital Signs And Feeds And Fluids Monitoring Chart For Neonatal Hospital Care In LMIC: A Human-Centered Design.

Authors: Naomi Muinga (KEMRI/Wellcome Research Programme)*; Mike English (KEMRI Wellcome Trust)

Background: Care for sick newborns is provided by multi-professional teams that are required to adhere to best practices. Therefore, documentation of patient progress plays an important role in the provision of quality care and team communication. Little attention has been paid to paper charts for documenting repeated observations during the inpatient stay for newborns. Current newborn unit charts for monitoring in Kenya vary from one facility to another and are poorly designed. These challenges might explain the poor quality of information in hospitals' records on vital signs and the ability to determine whether interventions are delivered accurately.

Methods: To address this issue, we developed a structured chart for monitoring admitted newborns using a human-centred design (HCD) approach. This approach is designed to identify problems and user needs and then design products that meet those needs. We present the results of design workshops and initial implementation experience at the Clinical Information Network in Kenya. We conducted interviews with 12 nurses and paediatricians and a focus group discussion with data clerks.

Results: Chart reviews and discussions with nurses and paediatricians revealed that there were diverse and sub-optimally designed monitoring charts (vital signs, feed and fluid prescription and monitoring) in use. We designed a monitoring chart together with participants between March and May 2019, that can be used to record the feed and fluid prescription as well as monitor the baby's progress during the admission episode. The chart was piloted in 4 hospitals and modified based on feedback from hospital-based staff. In July 2020, we launched the chart virtually in the clinical information network and trained the senior nurses who in turn, together with paediatricians trained the staff in the newborn ward on how to use the chart. Health workers appreciated that the chart made their work easier by consolidating monitoring information on one sheet of paper. There were challenges in adopting the chart such inadequate supply of charts, a high workload and work environment, and inappropriate equipment. Chart adoption was facilitated by training and complementary projects that encouraged chart uptake. Participants suggested that future implementations should include training, peer experience sharing and mentorship as part of a facilitated implementation process that should be contextually adapted

Conclusions: We successfully used a HCD approach to develop a monitoring chart that meets the users' need and overcome existing challenges while involving the end user. We implemented the chart in the clinical information network and identify opportunities to improve the chart implementation process for a wider scale-up that is contextually adapted.

Keywords: newborn,nursing,documentation,HCD,

Abstract 048

Title: NEONATAL SEPSIS INCIDENCE AT JM KARIUKI MEMORIAL COUNTY REFERAL HOSPITAL, NYANDARUA COUNTY. Michael Ruitururi1, Emma Wanjenga2,Josphine Imera3 1.JM Memorial County Referral Hospital Deputy Nursing Officer in Charge and IPC Coordinator 2.JM Kariuki Memoria

Authors: MICHAEL CHEGE RUITURURI (JM HOSPITAL OLKALOU)*

Background and objectives: Neonatal sepsis is a major threat to lives of newborn babies. It possesses adverse health and economic effects, as the mother and the baby will be admitted to hospital leaving their families unattended. Long hospital stay can also lead to nosocomial infections to the immune compromised neonate. It is therefore important to ensure a safe delivery process, sterility in handling the babies' cord and overall cord care and baby hygiene.

The overall objective of the study was to determine the possible causes of increased incidence of neonatal sepsis in JM Hospital, Pediatric Ward.

Methodology: A survey was done on 18th March to 20th March 2022. A structured checklist was used in collecting quantitative data i.e. mother's age, parity, number of hospital deliveries and number of admissions with newborn babies. Only mothers of babies with neonatal sepsis were interviewed. Nurses in the MCH, Newborn Units, Maternity and Pediatric Wards were interviewed on knowledge, skills and practice of cord care. A researcher administered questionnaire was used. Purposive sampling was used to select nurses in maternity, MCH and pediatric ward,while Convenient Sampling used to select respondents.Swabs for culture were taken from specific surfaces in labor ward, (delivery bed, neonate baby warmer, and neonate weighing scale) infected cords, sterile delivery packs and decontamination buckets. Descriptive analysis was done using MS excel and presentation done in tables and figures.

Results: A total of 6 mothers with neonates were interviewed: neonates ages range of 2-21 days.66.6% were delivered in JM hospital, one at a health center and one was home delivery.

100 % had no skills on cord care and thus, didn't perform correct cord care practices. 33.3% had knowledge on correct cord care. 66.6% didn't perform good practices of washing the baby,16.6% had correct practice and 16.6% didn't wash the baby at all.

A total 10 nurses were interviewed on cord care practices:ages ranging from 30 to 51 years, with an average working experience of 14.2 years.20% applied nothing on the cord,20% used surgical spirit, 20 % were not aware of the current updates while 40% were not ready to give their responses.

No growth was identified on surfaces and instruments. E Coli was identified on theatre decontamination bucket,33.3% of the cords had staphylococcus aureus,33.3% had streptococci while 16.6% had pseudomonas growth.

Conclusion: Lack of knowledge and skills on proper cord care contributes to neonatal sepsis. There's no uniform way of cord care among nurses. Staphylococcus aureus is a hospital acquired infections; enhancing IPC practices is very essential to curb infections.

We recommend that the pediatrician assists in formulation of SOP for cord care and sensitization of the best practice of cord care should also be done to all health care workers. All mothers should be shown how to clean babies' cords before discharge.

Keywords: nosocomial:neonatal sepsis:newborn baby:pseudomonas

Scientific Session 7: Young Investigators

Additional Abstract

Title: The Role of *Plasmodium falciparum* HSP-90 in Antimalarial Drug Treatment Outcome in a Malaria Endemic Region, Kisumu County

Authors: Lewis Karani(Kenya Medical Research Institute); Rukiya M. Haji(KEMRI); Dorcas Wachira(KEMRI), Dr.Nancy Kinyatta(KEMRI), Francis Kimani(KEMRI), Japheth Lusweti(KEMRI), Rosemary Githae(KEMRI), Christine Ichugu(KEMRI)

Introduction: *Plasmodium falciparum* nuclear genome consists of 14 chromosomes which encode about 5,300 genes with a large proportion of the genes devoted to immune evasion and host–parasite interactions. In the host, especially during febrile episodes observed in clinical malaria, *P. falciparum* adapts to the environment by translocating heat shock proteins 90 (HSP-90) for its survival. These proteins assist the parasite to adapt and adjust to repeated temperature fluctuations in the form of periodic fever in the patient. Limited studies have been conducted to determine the role of *Pf*HSP-90 on treatment outcomes in clinical malaria isolates from high prevalence *P. falciparum* zones of Kenya. This study was designed to characterize the plasmodial heat shock proteins 90 and determine their role in the treatment outcome of Plasmodium falciparum malaria infections.

Objective: To determine the expression levels of *P. falciparum* HSP90 gene that are associated with acute febrile malaria and at the remission phase in malaria isolates

Methodology: This was a cross sectional study that focused on *Plasmodium falciparum* positive blood samples collected from Nyando, Kisumu County. cDNA was obtained for day 0 and day 2 samples, for a total of 45 participants and real time PCR used to amplify the HSP90 gene in the samples. Each sample was amplified in triplicate with housekeeping control genes 18S and beta-actin and a control 3D7 strain included in each run. NF54 *Plasmodium falciparum* strain was included as a parallel one copy control. Average Ct was calculated and the fold change between *Pf*HSP-90 expression at day 0 and day 2 computed using the 2^-(ΔΔCt) method.

Results: Of the 45 blood samples included in the study, HSP-90 gene expression was compared between day 0 and day 2 samples from the same patients. A fold change of >1.6 was used as an indication of a two-fold increase in the gene expression levels. 33%(n=15) of the samples showed an increase in *Pf*HSP-90 gene expression level while 67%(n=30) had the same expression for both malaria and treated samples. From the samples with increased expression(N=15) 53.3% (n=8) of the samples had a twofold increased expression level, 20%(n=3) had a three-fold increase while 6.7%(n=1) of the samples had a 4X, 5X, 7X, and 9X fold increase respectively. Correlation of HSP-90 expression and temperature at a *p-value* of 0.5 gave a correlation co-efficient value of -0.0146.

Conclusion: Correlation of *Pf*HSP-90 expression and temperature, $r^2 = 0.0146$, shows that temperature value is not a confident predictor for the expression of *Pf*HSP-90 in malaria parasites. This is further bolstered by the majority of the sample population; 67%(n=30) showing similar expression of *pf*HSP-90 for both febrile and treated samples. All samples at day 2 were non-febrile and had cleared parasitemia. This concludes that *Pf*HSP-90 expression, as a standalone, is not a reliable indicator of the treatment outcome of *P. falciparum* malaria infections. Further analysis needs to be done to define *pf*HSP-90 *de novo* mutations and epigenetic effects on gene regulation, and if there is differential expression of *pf*HSP-90 at the different stages of the malaria parasite life cycle**.**

Abstract:049

Title: EPIDEMIOLOGICAL ANALYSIS AND DIVERSITY OF EXTENDED SPECTRUM β-LACTAMASES FROM ESCHERICHIA COLI AND KLEBSIELLA SPECIES FEACAL ISOLATES IN NAIROBI, KENYA

Authors: Sophia A Kuve (KEMRI Graduate School)*; John Njeru (KEMRI); Jacob Ochieng Ouko (UNICEF); Susan W Kiiru (KEMRI); Dan waithiru (KENYA MEDICAL RESEARCH INSTITUTE); Ben Brian Owino (KEMRI Graduate School); John Ndemi Maina (Kenya Medical Research Institute)

Introduction: In 2021, World Health Organization declared Antimicrobial Resistance (AMR) a global health threat. Bacterial strains especially Escherichia coli and Klebsiella species are known for their ability to confer resistance against various antimicrobial agents. Despite the rising threat to the public, there is still limited epidemiological data on both species among the general public. This study investigated epidemiological data of E. coli and Klebsiella species and determined presence of resistance genes.

Methods: The study was conducted in Kibera areas in Nairobi County. We targeted outpatients visiting Mbagathi hospital presenting with gastritis-like symptoms. Follow-up visits were also done to recruit contacts (household level). Stool samples were collected and subjected to basic microbiology procedures including Antimicrobial Sensitivity testing. Molecular analysis using PCR was done to determine the presence of AMR genes.

Results: From a total of 328 (100%), 221 (67.4%) tested positive for either E. coli or Klebsiella. However, E. coli was predominant (91.5%). Infection was noted in 70% of contacts and 85% of patients. 72% of infections were attributed to lack of proper water and sanitation (WASH) services. AMR was reported in 67% of the samples (148 of 221). Significant resistance was observed against Imipenem (15%) and Ceftazidime (20%). Forty-four isolates were confirmed by PCR to harbor ESBL genes such as OXA genes (65%) while 28% had KPC genes.

Conclusion: The high prevalence of infection noted may be attributed to overcrowding and socio-economic factors including WASH services. Data from the study will be used for reference by policy makers and by health practitioners. This will help in control of treatment prescription and ensure proper diagnosis of infections mitigating AMR. Awareness and educational programs are to be rolled out to the general public. More data to determine and confirm risk factors attributed to infection will be critical in the fight against AMR.

Keywords: Antimicrobial Resistance, Escherichia coli, Kkebsiella species, Blagenes,

Abstract 050

Title: Red Blood Cell Parameters and Associated Factors among Infants Attending Sangabuye and Makongoro Health Centres, Mwanza,Tanzania

Authors: ROTGEN ARNOLD ELICHILIA (Catholic University of Health and Allied Sciences)*; Mariam M Mirambo (CATHOLIC UNIVERSITY OF HEALTH AND ALLIED SCIENCES); Delfina R Msanga (CATHOLIC UNIVERSITY OF HEALTH AND ALLIED SCIENCES)

Abstract: Authors: Rotgen A Elichilia1, Caroline A Minja2, Delfina R Msanga3, Mariam M Mirambo4

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Background: Red cell parameters are useful anaemic and inflammatory markers in diagnosis and monitoring of diseases. Result interpretation for these parameters is population and ethnic specific. However, among infants, establishment of normal values is difficult due to recruitment difficulties, together with the dynamic growth and development patterns.This study aimed to assess and highlight the significance of locally derived RBC parameters reference intervals and associated factors among infants attending Sangabuye and Makongoro Health Centres in Mwanza Tanzania.

Methods: A cross sectional hospital-based study involving 300 infants attending post-natal clinics was conducted. Using a structured questionnaire, demographic and other study related data was collected and tested in the auto analyzer (Dymind DH-76). Data was analyzed using STATA version 13.

Results: Majority of study participants were female 164/300 (54.7%) with a mean(SD) age of6 (±3)months. The mean Hb, MCV, and Erythrocyte count was10.3(±1.25) g/dl, 73.1(±9.3)mm3 and 4.47 (± 0.87)x106/mm3 respectively.By two sample t-test, only infants 'current breast-feeding status had an effect on erythrocyte count (p=0.0009). On univariate analysis age (p=0.001) and body temperature (p=0.001)had effects on erythrocyte count while body temperature alone had effect on both erythrocyte count (p=0.009) and haemoglobin (p=0.026).

Conclusion: This study reports lower RBC value compared to parameters specific reference intervals routinely used in our setting. This has highlighted the relevance of currently used reference intervals and serves as a baseline information for future studies.This study has observed variations in the normal value of red blood cell parameters attributed to several factors such as age and infants on breastfeeding with combination with other feeds current feeding status. We recommend further locally derived age-specific studies, with large sample size and wide range assessment of disease screening to guide monitoring and management of patients.

Keywords: RBC Parameters, Reference intervals, infants

Abstract 051

Title: Behaviors and Sexual Patterns leading to HIV risk among young transgender women in Coastal Kenya; a qualitative Study

Authors: MELANIE AWINO ABONGO (KNH)*

Background: Transgender women are globally ranked as a high-risk population for their high HIV prevalence compared to other key populations and 49 times higher than cisgender populations. Recent Studies have cited characteristics of key populations that contribute to high HIV risks including stigmatization and discrimination and access to universal health care. This study however aims to access the behavioral and sexual tendencies of transgender women that predispose them to HIV risk. This paper informs on the sexual and behavioral risk factors predisposing transgender women to a high HIV prevalence.

Methods: This was a cross-sectional study done in 2021. The study enrolled 200 transgender women aged between 18-24 years. An interviewer-administered questionnaire was used to capture the sociodemographic, behavioral, and sexual characteristics of young transgender women.

Results: 74% of the young transgender women are introduced into sex work at an average age of 17 years, over 70% of the young transgender women prefer to hang out in physical hotspots as opposed to online hotspots,80% reported marital status to be single and 50% have attained secondary school level of education. 68% of transgender sex workers (TGSW) have an average of 3 sex acts daily and have multiple sex partners ranging from 2-5 partners per individual. Up to 50% of TGSW report being under the influence of drugs during sex, and up to 49% report consistent condom-less, non-lubricant anal sex (49%).

Conclusion: The main behavioral characteristics and sexual tendencies that render young transgender women vulnerable and at risk of HIV are; Early initiation into sex work, engaging in sex under the influence of drugs, having multiple partners, and condom-less and/or non-lubricant anal sex.

Recommendation: Programs aimed at HIV prevention among key populations should focus more on behavioral patterns and motivational skills aimed at reforming the attitudes and knowledge of HIV and other STIs.

Keywords: HIV/AIDS; Young Transgender women : 18-24 years

Abstract 052

Title: Dengue fever outbreak at the Kenyan south coast involving serotype 3, genotypes III and V

Authors: Eric M Muthanje (KEMRI/Walter Reed Project); Kimita Gathii (KEMRI/Walter Reed Project); Josphat N Nyataya (Kenya Medical Research Institute); Beth Mutai (KEMRI/Walter Reed Project); Sarah Kituyi (University of Embu); John N Waitumbi (KEMRI/Walter Reed Project)*

Background: The etiological agent of Dengue Fever (DF) is Dengue virus (DENV) of the Flaviviridae family that is transmitted by the Aedes aegypti mosquito. The virus is classified into four distinct serotypes (DENV 1-4). There have been increasing reports of DF outbreaks in Africa, including Kenya, yet very little information is available on the virus, for instance its genome structure and diversity of circulating genotypes. This study aimed at characterizing DENV-3 strains obtained from the March 2019 DF outbreak at the Kenyan south Coast.

Methods: Total RNA was isolated from 37 human plasma samples and screened for the presence of the four DENV serotypes using the EasyScreen Flavivirus typing kit by real time quantitative PCR. RNA from DENV-3 positive samples was used for cDNA synthesis using sequence-independent single-primer amplification (SISPA). SISPA products were used to prepare libraries using the NexteraXT kit, and the libraries sequenced on the Miseq. Quality filtering, sequence assembly and annotation was done using CLC Genomics v.8.5, while phylogenetic analysis of DENV-3 from this study and global isolates was conducted in MEGA v10. A targeted sequencing approach was used on samples that failed to yield complete genomes using in-house designed primers.

Results: 21/37 samples tested positive for DENV-3 with Ct values ranging between 15 and 40. On sequencing, 4 samples produced complete polyprotein-coding sequences (10,173 bp) and 3 had partial sequences with complete envelop (env) genes (1479 bp). Partial sequences with incomplete env gene were generated from 14 samples which were re-sequenced by amplifying the env gene. This approach produced ten complete env genes (1439-1479 bp). Maximum likelihood analysis of the 4 complete genomes and the 17 env genes confirmed DENV-3 as the cause of the March 2019 outbreak, with majority of strains belonging to genotype III (n=15) and V (n=2). The estimated time-to-most-common recent ancestor for the two genotypes was in 2015 and that both had been introduced independently. Genotype III's origin was estimated to have been from pointed to Pakistan. The origin of genotype V could not be ascertained due to rarity of these sequences globally but was related to 2006 Brazilian isolate. Unlike genotype III that has been described in East and West Africa multiple times, this was the second description of genotype V in Kenya.

Conclusion: DF outbreak experienced at the Kenyan coast in 2019 was confirmed to have been caused by DENV-3, and was closely related to other DENV-3 isolated in Pakistan and Asia. One of the pitfall of this study is the limited number of samples analyzed may not provide a true representation of the circulation of DENV-3 in 2019, thus introducing bias in the reported data. It is however the current data provides a useful reference for the design of local diagnostics and for studies aimed at understanding DENV-3 evolution and transmission in Kenya.

Keywords: Dengue virus, RT-PCR, Whole genome Sequencing, Targeted sequencing, Origin, phylogenetic

Abstract 053

Title: A comparative analysis of Portable Microbiological Lab (10ml colilert, 1ml pertrifilm) and the Colilert Quanti - tray 2000.

Authors: Nancy N Chebichii (Kenya Medical Research Institute)*

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Background: Water quality testing is dominated by operational monitoring of urban piped systems, while surveillance monitoring of non-piped sources is limited. This is a significant public health concern since surveillance testing is the only form of oversight applied to the informal water supplies and other point sources not piped to the premises that serve a vast majority of people. The study verified the field test method, Portable Microbiology Lab (PML) Kit under different water source conditions by comparing it to a laboratory standard method Quanti-Tray 2000.

Methods: Water samples were collected from 7 different locations n=27. The samples were tested using both test kits to determine P/A and risk level for drinking water sources according to WHO, and the accuracy of PML in reducing error relative to improved/unimproved water source designation. PML reliability for point source surveillance testing was determined using the coefficient of determination.

Results: PML and Quanti-Tray yielded matching risk level results for 26 samples of the 27 samples analysed, 4 of the 27 samples presence/absence test of the 10ml and 100ml colilert tests was not congruent with each other. Thus error for the test with 10ml colilert of PML resulted in a percentage variation of 14.81%, with the addition of Petrifilm to identify risk levels the proportional reduction in error relative to water source designation, for improved water source the highest percentage variation was noted for moderate levels at 61.54%. The proportional reduction in error relative to unimproved water source, very high-risk level was noted at 66.54% with high risk at 33.45%. The exact match for PML to improve predictions of risk levels with unimproved water sources was 99.99%. To determine the degree of association of the Petri film count and MPN, a correlation statistic resulted in a coefficient of 0.874, with a 0.7623 proportion in variance.

Conclusion: The PML provides accurate results that correspond to the WHO disease-risk categories. PML can be used to improve community understanding of the safety of drinking water and provide a baseline to set national policies and strategies. This could be integrated into current water supply surveillance practices under universal health coverage to improve public health.

Keywords: PML, Quanti tray, water testing

Abstract 054

Title: Bacterial Etiologies of Diarrhea in Children Under 5 Years from Mukuru Informal Settlement and their Antimicrobial Sensitivity Profiles.

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Background: In Kenya, diarrhoeal disease is the third leading cause of child mortality after malaria and tuberculosis, accounting for nearly 100 deaths daily. Children in informal settlements are more prone to diarrhoea due to more exposure risks associated with insufficient toilet facilities, lack of or poor sewage drainage infrastructure,and poor sanitation practices. Therefore, routine surveillance in these high-risk areas is crucial to determine circulating diarrheal bacterial etiologies, evaluate the effectiveness of commonly available antibiotics for disease outbreak preparedness, and support prevention and control strategies.

Objectives: To determine the enteric bacterial pathogens associated with diarrhea in children (<= 5 years) attending Mukuru clinics in Nairobi and their corresponding antibiotic susceptibility patterns.

Methods: In this cross-sectional study, 218 diarrheagenic children(<= 5 years) were recruited from outpatient clinics in Municipal City Council, Mukuru Kwa Reuben, Medical Missionaries of Mary, and Mama Lucy Kibaki Hospital, Nairobi. Through the guardians, stool samples were collected from May 2021 to August 2021. Bacterial recovery was done on Mac and Salmonella Shigella Agar, while identification was done using VITEK®2GNID and ASTs using VITEK®2AST-GN83.

Results: At least one bacterial organism was recovered from 207 (95%) participants. The normal intestinal flora(E.coli (36%), Enterobacter sp (27.8%), Klebsiella sp (11%), and Citrobacter sp(4.7%)) were the dominant isolates. Of 109/307 E.coli isolates recovered, 2 (1%) were EHEC, 6 (3%) were EAEC, and 8 (4%) were EPEC. Potentially pathogenic isolates like Salmonella 7 (2%), Proteus mirabilis 16 (6%), Providencia alcalifaciens 1 (0.3 %), and Shigella 16 (4.7%) were also detected. Pantoea spp 0.67%(2), Raoultella planticola 0.33%(1), and Kluyvera 2%(5), rarely reported but implicated with diarrhea diseases, were also recovered. Overall, AMP, CFZ, and SXT were the most resisted antimicrobials at 64%, 57% & 55%, respectively. Resistance towards expanded spectrum cephalosporins such as CAZ, CRO, and FEP ranged between 5 – 14%. Two (4%) E. coli isolates were resistant to MEM. E.coli, Enterobacter spp & Klebsiella spp were the most resistant to broad-spectrum antimicrobials such as CAZ, CRO, CIP, GEN, and FEP, ranging between 6 – 33%. The resistance profile for commonly used antibiotic diarrhea treatment was; AMC(31%), CRO (14%), and CIP (11%). About 33(21%) of 307 enterics were multidrug-resistant (MDR), while 22(14%) were ESBLs, 4(2%) carbapenemases, and 8(5%) had Beta-lactam, Fluoro/ Quinolones, Aminoglycosides(BFQA) phenotype.

Conclusion: There is a risk of severe diarrhea from known pathogenic strains like Enterohemorrhagic E.coli. Additionally, the detection of Meropenem-resistant strains suggests the possible emergence of carbapenem-resistant strains in Mukuru slums. Increasing resistance towards AMC means narrowed treatment options for diarrhea.

Keywords: Bacteria, Diarrhea, Children under 5 years of age, Antiimicrobial Susceptibility Patterns, Informal Settlement

Abstract 055

Title: Characterization of Aeromonas species From Dhaka, Bangladesh through whole genome sequencing and phylogeny

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Background: Aeromonas are gram-negative, rod-shaped facultative anaerobic bacteria that are widely distributed in aquatic environments, and are responsible for causing gastroenteritis, septicemia, and wound infections. A major cause of concern is that Aeromonas are frequently cultured from water and stool of patients in cholera-endemic regions and are biochemically indistinguishable from Vibrio cholerae. Therefore, understanding the dynamics of Aeromonas spp. associated with gastro-intestinal infections in Bangladesh is important to gain insights into the mechanisms associated with the endemicity of the disease in the country, the epidemicity at local and regional level, and to understand sources of infection.

Methods: The Aeromonas isolates sequenced using Illumina-B Hiseq platform, and analyzed in this study were fortuitously isolated, after being mistakenly classified as for V. cholerae during a 2013 cholera study in Bangladesh. We aimed to define the local and global population structure of Aeromonas by comparing the diversity and species composition between the Aeromonas isolated from Dhaka and a global genome collection obtained from the European nucleotide archive (ENA). We used whole genome sequencing data to determine the presence of shared clonal lineages, antibiotic resistance, virulence genes, and phylogenetic relatedness of 814 Aeromonas genomes (681 from the ENA, 133 from Dhaka). The genetic relatedness of Bangladesh isolates to those from other countries was examined, as well as connection of certain resistance and virulence genes with phylogenetic lineages.

Results: We identified at least 5 main significant species of Aeromonas both in the global population and Dhaka population. Phylogenetically, the results of population structure determination revealed that Aeromonas species had a high degree of genetic variation. Most multilocus sequence types (MLST) were novel to public databases, and BAPS clustering grouped samples into 20 clusters. We observed high levels of antimicrobial resistance towards Oxacillin, represented by blaOXA-504 gene (44%), and Chlorampenicol (40%). Mobile colistin resistance genes (mcr-3.1 and mcr-3.2.7) were detected only in A. salmonicida at high abundance (n=104/176; 59%). Also, ten types of virulence genes were identified with A. caviae and A. salmonicida having the highest proportion of alt (n=176/176; 100%), ela (n=176/176, 100%), and lip (n=175/176, 99.4%).

Conclusion: This study redefines our understanding of the Aeromonas global genetic diversity and population structure. The results of this study have the potential to offer useful information that will help with the proper identification of Aeromonas, particularly in cholera endemic areas, as well as with prevention measures.

Keywords: Genomics, Phylogeny, AMR, Diversity

Abstract 056

Title: Vectorial capacity and TEP1 genotypes of Anopheles gambiae sensu lato mosquitoes on the Kenyan coast

Authors: Brian K Bartilol (KEMRI-WELLCOME TRUST)*; Donwilliams Omuoyo (KEMRI-Wellcome Trust); Kelly Ominde (KEMRI-Wellcome Trust Research Programme); Jonathan Karisa (KEMRI-Wellcome Trust); Charles Mbogo (KEMRI); Joseph Mwangangi (KEMRI); Marta F Maia (KEMRI); Martin Rono (KEMRI - Wellcome Trust Research Programme)

Background: Malaria remains one of the most important infectious diseases in sub-Saharan Africa, responsible for approximately 228 million cases and 602,000 deaths in 2020. In this region, malaria transmission is driven mainly by mosquitoes of the Anopheles gambiae and, more recently, Anopheles funestus complex. The gains made in malaria control are threatened by insecticide resistance and behavioural plasticity among these vectors. This, therefore, calls for the development of alternative approaches such as malaria transmission-blocking vaccines or gene drive systems. The thioester-containing protein 1 (TEP1) gene, which mediates the killing of Plasmodium falciparum in the mosquito midgut, has recently been identified as a promising target for gene drive systems. Here we investigated the frequency and distribution of TEP1 alleles in wild-caught malaria vectors on the Kenyan coast.

Methods: Mosquitoes were collected using CDC light traps both indoors and outdoors from 20 houses in Garithe village, along the Kenyan coast. The mosquitoes were dissected, and the different parts were used to determine their species, blood meal source, and sporozoite status. The data were analysed and visualised using the R (v 4.0.1) and STATA (v 17.0).

Results: A total of 18,802 mosquitoes were collected, consisting of 77.8% (n=14,631) Culex spp., 21.4% (n=4026) An. gambiae s.l, 0.4% (n=67) An. funestus, and 0.4% (n=78) other Anopheles (An. coustani, An. pharoensis, and An. pretoriensis). Mosquitoes collected were predominantly exophilic, with the outdoor catches being higher across all the species: Culex spp. 93% (IRR=11.6, 95% Cl [5.9–22.9] P<0.001), An. gambiae s.l. 92% (IRR=7.2, 95% Cl [3.6–14.5]; P<0.001), An. funestus 91% (IRR=10.3, 95% Cl [3.3–32.3]; P<0.001). A subset of randomly selected An. gambiae s.l. (n=518) was identified by polymerase chain reaction (PCR), among which 77.2% were An. merus, 22% were An. arabiensis, and the rest were not identified. We were also keen on identifying and describing the TEP1 genotypes of these mosquitoes, especially the *R3/R3 allele that was identified recently in the study area. We identified the following genotypes among An. merus: *R2/R2, *R3/R3, *R3/S2, *S1/S1, and *S2/S2. Among An. arabiensis, we identified *R2/R2, *S1/S1, and *S2/S2. Tests on haplotype diversity showed that the most diverse allele was TEP1*S1, followed by TEP1*R2. Tajima's D values were positive for TEP1*S1, indicating that there is a balancing selection, negative for TEP1*R2, indicating there is a recent selective sweep, and as for TEP1*R3, there was no evidence of selection.

Conclusion: We find the malaria vectors An. gambiae and An. funestus are predominantly exophilic. TEP1 genotyping for An. merus revealed five allelic combinations namely R2/R2, *R3/R3, *R3/S2, *S1/S1 and *S2/S2, while in An. arabiensis we only identified three allelic combinations: *R2/R2, *S1/S1, and *S2/S2. The TEP1*R3 was restricted to An. merus.

Keywords: Anopheles merus, Thioester-containing protein 1, Allele, Kenya

Abstract 057

Title: Genetic Diversity of Nontuberculous Mycobacteria among Symptomatic Tuberculosis Negative Patients from Kenya

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Background: Non-Tuberculous Mycobacteria (NTM) transmission to humans occurs through inhalation of dust particles or vaporized water containing NTM leading to pulmonary manifestations. NTM infections are often misdiagnosed for tuberculosis (TB) due to their similar clinical and radiological manifestations.

Aims and Objectives: We, therefore, performed a species-level identification of NTM in symptomatic TB negative patients through sequencing of the hsp65 gene. The hsp65 gene belongs to the heat shock protein family that is involved in intracellular protein folding, assembly and transport thus being highly immunogenic. The hsp65 gene sequence has more genetic variability, and has a stronger ability to discriminate between NTM species.This property enables it to produce a more robust phylogenetic tree with most nodes having bootstrap value above 80%

Materials and Methods: We conducted a cross-sectional study at the National Tuberculosis Reference Laboratory in the period between January to November 2020. One hundred and sixty-six mycobacterial culture-positive samples that tested negative for TB using capilia underwent Polymerase Chain Reaction targeting the hsp65 gene. Isolates showing a band with gel electrophoresis at 441 bp position were sequenced using Sanger technology. Geneious software was used to analyze the obtained sequences, and the National Center for Biotechnology Information gene database identified NTM species for each isolate. A phylogenetic tree was constructed from the DNA sequences and evolutionary distances computed using the general time-reversible method. Pearson chi-square was used to determine the association between NTM infection and participants' characteristics.

Results: Our study identified 43 different NTM species. The dominant NTM belonged to Mycobacterium avium complex 37 (31%). Slow-growing NTM were the majority at 86 (71%) while rapid-growing NTM were 36 (29%). A significant association (P<0.05) was observed for regions and age, while patient type had a weak likelihood of NTM infection. Conclusion: Our study characterized the diversity of NTM in Kenya for the first time and showed that species belonging to M. Avium Complex are the most prevalent in the country.

Keywords: Nontuberculous mycobacteria, slow growing mycobacteria, rapid growing mycobacteria, hsp65

Abstract 058

Title: Entomological surveillance of main malaria vectors on the Kenyan coast using MALDI-TOF MS

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Background: Protein analysis using matrix-assisted laser desorption/ionization time-of-flight mass-spectrometry (MALDI-TOF MS) represents a promising tool for entomological surveillance. In this study we tested the discriminative power of this tool for measuring species and blood meal source of main Afrotropical malaria vectors on the Kenyan coast.

Methods: Mosquito collections were conducted along the coastal region of Kenya. MALDI-TOF spectra were obtained from each individual mosquito's cephalothorax as well as the abdomens of blood-engorged mosquitoes. The same mosquitoes were also processed using gold standard tests: polymerase chain reaction (PCR) for species identification and enzyme linked immunosorbent assay (ELISA) for blood meal source identification and detection of malaria parasites.

Results: Of the 2,332 mosquitoes subjected to MALDI-TOF MS, 85% (1,971/2,332) were considered for database creation and validation. There was an overall accuracy of 97.5% in the identification of members An. gambiae (An. gambiae - 100%, An. arabiensis; 91.9%, An. merus; 97.5% and An. quadriannulatus; 90.2%) and An. funestus (An. funestus – 94.2%, An. rivulorum – 99.4% and An. leesoni – 94.1%) complexes. Furthermore MALDI-TOF MS also provided accurate (94.5% accuracy) identification of blood host sources across all species.

Conclusion: This study provides further evidence of the discriminative power of MALDI-TOF MS to identify sibling species, and blood meal source of Afrotropical malaria vectors further supporting its utility in entomological surveillance. The low cost per sample (<0.2USD) and high throughput nature of the method represents a cost-effective alternative to molecular methods and could enable programs to increase the number of samples analyzed and therewith improve the data generated from surveillance activities.

Keywords

MALDI-TOF, entomological surveillance, Anopheles, high-throughput, mass spectrometry, Kenya, Coast

Abstract 059

Title: Therapeutic response to artemisinin combination therapies among individuals with Plasmodium falciparum single infection versus mixed Plasmodium species infections in Kisumu County, western Kenya

Authors: Gladys Chemwor (Department of Emerging Infectious Diseases (DEID), United States Army Medical Research Directorate-Kenya (USAMRD-K), Kenya Medical Research Institute (KEMRI))*; Hoseah Akala (KEMRI/USAMRD-A/K)

Background: As studies continue to confirm the rising frequency of mixed Plasmodium species infections, there is little data on the response of non-falciparum species to the Artemisinin Combination Therapies (ACTs) which is a critical tool for malaria elimination. This study was based on a retrospective cross-sectional design that reanalyzed samples collected in Kombewa for ACT clinical efficacy assessment and DOT was used to ensure the patients completed the full antimalarial dosage. We sought to compare the therapeutic response of P. falciparum single infection versus mixed Plasmodium species to ACT's specifically artemether-lumefantrine, artesunate-mefloquine and dihydroartemisinin-piperaquine.

Methods: A total of 1211 blood samples collected on days 0, 7, 14, 21, 28, 35, and day 42 from 173 individuals out of 236 enrolled in an ACT efficacy study between 2013 and 2015 were diagnosed for malaria using the 18s rRNA-based real-time PCR. All recurrent parasitaemia were also characterized for species composition; Plasmodium falciparum (Pf), Plasmodium malariae (Pm), Plasmodium ovale curtisi (Poc), and Plasmodium ovale wallikeri (Pow). ACTs treatment outcome was monitored during the 42-day follow-up period. MSP1 and MSP2 assays were done to identify recrudescence and reinfection.

Results: Overall, 71•1% (116/163) of the day zero samples were single Pf infections while 28•2% (46/163) were co-infections. 54.0% (88/163) of individuals tested positive for infection at least once between days 7 - 42 after treatment. 19•3% (17/88) of individuals with recurrent infections were infected with a different Plasmodium species than observed at day 0, with 76•5% (13/17) of these "hidden" infections appearing after clearing P. falciparum present at day 0. Artesunate-mefloquine (16•4) and dihydroartemisinin-piperaquine (17•6) had the increased clearance rates over artemether-lumefantrine (21•0) with exhibiting the longest duration of reinfection prophylaxis based on day 28 positivity.

Conclusion: Analysis based on species composition revealed minor difference in clearance rates depending on whether the infection contained other species other than P. falciparum.

Keywords: Therapeutic efficacy, non-falciparum, ACT, Treatment outcome, Parasite clearance rate

Abstract: 060

Title: Examining the influence of actor interactions and power dynamics on health system responsiveness in Kilifi County, Kenya

Authors: Nancy N Kagwanja (KEMRI Wellcome Trust Research Programme)*; Sassy Molyneux (KEMRI Wellcome Trust Research Programme); Benjamin Tsofa (KEMRI-Welcome); Lucy Gilson (University of Cape Town)

Background: Responsiveness was introduced as a health system goal alongside service outcomes and equity in financing by the World Health Report (WHR), 2000. It has intrinsic value and is considered important for building accountable and inclusive health systems. However, responsiveness has been under-researched. Specifically, there is little evidence on how health facility committees (HFCs) and Sub-county Health Management Teams (SCHMTs), which play critical governance roles within health systems, enhance responsiveness. Power dynamics are, further, an acknowledged but under-researched feature of health systems that could impact responsiveness. We conducted this research to understand how SCHMTs and HFCs receive and respond to public feedback, and how power dynamics influence these processes. An improved understanding of responsiveness practice and the influence of power over it can generate ideas to strengthen responsiveness and improve performance.

Methods: We adopted a qualitative case study approach involving two SCHMTs and four HFCs. We conducted in-depth interviews with county, sub-county health managers, facility-in-charges and Members of County Assembly, focus group discussions with HFC community members, observation of SCHMT meetings and document review. We applied a conceptual framework developed from literature to analyse the practice of responsiveness, and Gaventa's power cube and Long's actor interface analysis to synthesise insights about power.

Results: We found limited responsiveness across the case study SCHMTs and HFCs, largely as a result of actor interactions and power dynamics. Invisible power undermined responsiveness from the health system side (manifesting in organisational norms and culture) and public engagement (manifesting in low awareness, and fear of victimisation). Hidden power limited inclusion of public feedback for health sector planning. While some SCHMT and HFC members exercised visible power to support responsiveness, power practices by higher-level system actors undermined responsiveness overall. These power practices were rooted in social and organisational power relationships, personal characteristics (such as interests, attitudes, and previous experiences) and worldviews (such as values and beliefs).

Conclusion: Our findings illustrate the social and political nature of health systems, and can be drawn upon to strengthen responsiveness. For example, considering the lifeworlds of the public could offset invisible and hidden power and work to strengthen the public's capacity to provide feedback. This might include increasing public awareness about their rights and mechanisms for providing feedback, as well as by reducing participation costs. Higher-level health system managers could formally endorse processes that encourage sub-county and facility-level managers to engage positively with public feedback and feedback mechanisms, leveraging the hierarchical power of the system.

Keywords: responsiveness, public, feedback, Health Facility Committee, Sub-county Health Management Team

Abstract 061

Title: County governments' capacity of human resources for health in the implementation of Universal Health Coverage in Kenya

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Introduction: Kenya currently faces significant challenges in overcoming health worker shortages and low retention, as well as difficulty in attaining equitable distribution of human resources for health (HRH), particularly in hard-to-reach areas. Ministry of Health has set HRH norms and standards which refer to the minimum and appropriate mix of human resources for health and infrastructure that is required to serve the expected populations at the different levels of the health system. The study assessed HRH capacity in twelve counties in Kenya.

Methods: The study applied a Convergent-Parallel-Mixed-Methods-study-design utilizing both quantitative and qualitative methods. The study targeted health care providers. The study sites were Nyeri, Machakos, Isiolo, Kisumu, Nyandarua, Meru, Kitui, Homabay, Bomet, West Pokot, Taita Taveta and Bungoma. Health facilities were stratified by ownership and KEPH level and the required number of facilities, both public and non-public per strata determined using square root allocation method. The study employed a customized Service Availability and Readiness Assessment Mapping (SARAM) data collection tool. HRH general service availability index was measured using the five tracer items namely clinical officers, nutritionists, pharmacists, nurses and laboratory personnel. Data cleaning and validation were done prior to statistical analysis using IBM SPSS version 27. Qualitative data was collected using FGD and In-depth interviews guides and analyzed thematically. Ethical approval was obtained from KEMRI IRB and research permit from NACOSTI and county governments.

Results: A total of 746 Health facilities were assessed giving a response rate of 94.3 (N=791). Public health facilities accounted for 75.0 %. The overall HRH availability index score was 17.2%. Public health facilities had lower index score of 14.7% compared to Non-public facilities with 27.0%. Only three counties of Kisumu, Bungoma and Kitui had more than 20% HRH index scores of 21.2%, 23.3% and 21.0%, respectively. The Counties of Bomet and Isiolo had lowest percentage of HRH index scores at 9.7% and 10.3%, respectively. Kitui County had the highest index score of health workers norms meet in public facilities at 21.2% and Isiolo with the lowest at 4.5%. The availability of health workers increased with advancement in the KEPH Levels where the Level 2 across all counties except Taita Taveta (8.3%) didn't meet HRH norms and standards. Nursing profession had the availability index of 93.2%, followed by clinical Officer and laboratory professions at 52.3% and 55.2% respectively. The least available professions were nutrition at 21.6% and pharmacy personnel 33.0% respectively.

Conclusion: The study established that all selected counties did not meet MOH minimum staffing norms. Investment in HRH for the health facilities is an urgent need, therefore recommends progressive recruitment of HRH in order to enhance health service delivery.

Keywords: Human resource for health, MoH staffing norms, SARAM; Convergent-Parallel-Mixed, Counties, Index score, UHC

Abstract 062

Title: Patterns and determinants of antibiotic prescription among children admitted to 12 public hospitals in Kenya: A cross-sectional observational study

Authors: Rachel A. Otuko (KEMRI-Wellcome Trust)*; Michuki J Maina (KEMRI Wellcome Trust); Paul Mwaniki (KEMRI-Wellcome Trust); Marshal Mweu (University of Nairobi, Department of Public and Global Health); Samuel Akech (KEMRI-Wellcome Trust)

Background: Antibiotic prescription rates are high among children and the use of broad-spectrum penicillins is common worldwide. Injudicious antibiotic use can lead to antibiotic resistance resulting in negative consequences due to treatment failure. This study describes the patterns and identifies the factors influencing antibiotic prescription among admitted children, which has not been previously examined.

Methods: Routine inpatient data for children aged ≥ 2 months collected prospectively between 2014 and 2020 in 12 hospitals which are part of a Clinical Information Network (CIN) were used in this study. Multivariable mixed effects logistic regression was used to assess the determinants of antibiotic prescription.

Results: A total of 107,500 participants were included in the study. About 81.1% (87,183/107,500) of the study participants had an antibiotic prescription. The commonly prescribed antibiotics were the combination of benzylpenicillin and gentamicin (37,939/127,984 - 29.6%), ceftriaxone (31,172/127,984 - 24.6%) and oral amoxicillin (12,593 /127,984 - 9.8%). The factors found to be associated with higher odds of antibiotic prescription were cough (aOR 2.06), bloody diarrhoea (aOR 5.6), diagnoses of pneumonia (aOR 27.66), malnutrition (aOR 6.3) and meningitis (aOR 11.85) while older age groups; 13-24months (aOR 0.88) and 25-59 months (aOR (0.87), signs of severe anaemia (aOR 0.8), diagnoses of malaria (aOR 0.22), diarrhoea (aOR 0.36) and dehydration (aOR 0.4) were significantly associated with lower odds of antibiotic prescription.

Conclusion and recommendation: The proportion of children on antibiotics was high, reflecting a high usage of antibiotics in paediatric wards in Kenyan public hospitals. Age, cough, bloody diarrhoea, signs of severe anaemia and diagnosis were found to be significantly associated with antibiotic prescription among admitted children. There is need to improve diagnostic support in these hospitals in order to inform rational prescription of antibiotics.

Keywords: Antibiotic use, antibiotic resistance, determinants

Abstract 063

Title: Profiling Genome-wide Recombination in Epstein Barr Virus reveals Type-Specific Patterns and associations with Endemic-Burkitt Lymphoma

Authors: Eddy O Agwati (KEMRI-CGHR)*

Background: Endemic Burkitt lymphoma (eBL) is potentiated through the interplay of Epstein Barr Virus (EBV) and holoendemic Plasmodium falciparum (Pf) malaria. To better understand EBV's biology and role in eBL, we characterized genome-wide recombination sites and patterns as a source of genetic diversity in EBV genomes in our well-defined population of eBL cases and controls from Western Kenya.

Methods: EBV genomes representing 54 eBL cases and 32 healthy children from the same geographic region in Western Kenya that we previously sequenced were analyzed. Whole-genome multiple sequence alignment, recombination analyses, and phylogenetic inference were made using Multiple Alignment with Fast Fourier Transform (MAFFT), Recombination Detection Program 4 (RDP4), and Molecular Evolutionary Genetics Analysis 7 (MEGA 7).

Results: We identified 28 different recombination events and of the 86 EBV genomes analyzed, 71 (82.6%) contained evidence of one or more recombinant segments. Associated recombination breakpoints were found to occur in a total of 42 different genes, with only 7 (16.67%) being latent genes. Recombination events were major drivers of clustering within genome-wide phylogenetic trees. The occurrence of recombination segments was comparable between genomes from male and female participants and across age groups. More recombinant segments were found in EBV type 1 genomes (p=6.4e-06) and the genomes from the eBLs (p=0.037). Two recombination events were enriched in the eBLs; event 47 (OR=4.07, p=0.038) and event 50 (OR=14.24, p=0.012).

Conclusions: EBV genomes have extensive evidence of recombination likely acquired progressively and cumulatively over time. Recombination patterns display a heterogeneous occurrence rate across the genome with enrichment in lytic genes. Overall, recombination appears to be a major evolutionary force impacting EBV diversity and genome structure with evidence of the association of specific recombinants with eBL.

Keywords: Epstein - Barr virus, Genome-wide Recombination, Endemic-Burkitt Lymphoma

Abstract 064

Title: Cytokine profile of a TB and TB/HIV co-infected cohort in Kenya

Authors: Asiko Ongaya (KEMRI)*; Pascah Bulia (KEMRI); Paul Mwangi (KEMRI); Robi Chacha (KEMRI); Jeremiah Kyalo (KEMRI); Yazmin Martinez-Martinez (University of Texas Medical Branch, Galveston, Texas); Megan Files (University of washington); Dorcas Wanjiru (KEMRI); Matthew Huante (University of Texas Medical Branch, Galveston, Texas); Kubra Navqi (University of Texas Southwestern Medical Center, Dallas, Texas); Geoffrey Okallo (KEMRI); Evans Amukoye (KEMRI); Janice Endsley (University of Texas Medical Branch, Galveston, Texas)

Background: Tuberculosis (TB) and HIV remain a top global public health concern. Complexities associated with TB/HIV co-infections, including in those virally suppressed with anti-retroviral therapy (ART), present significant challenges to efforts to reduce both infections. Pattern of cytokines produced by T helper (Th) lymphocytes likely play a central role in susceptibility, relapse and reinfection to TB. Purpose of this study was to understand how HIV and ART status in TB patients affects recovery of Th cell effector function and cytokine profile during TB treatment.

Objective: To determine the cytokine profile of a TB and TB/HIV cohort at the beginning of TB treatment and at the end of TB treatment.

Methodology: A prospective study of TB participants who are either HIV-infected or HIV-uninfected from 3 clinical sites [Mbagathi Hospital, Rhodes Chest Clinic and AIDS healthcare Foundation (AHF) Mathare clinic] in Nairobi. Blood samples were taken at start of and on completion of TB treatment between October 2019 and November 2022 from 6 groups of adult participants; Group A (TB-HIV-), B (TB-HIV+ART+), C (TB-HIV+ART-), D (TB+HIV-), E (TB+HIV+ART+), F (TB+HIV+ART-). Cytokine bead array (CBA) was used to assess human Th cell-derived cytokines isolated from plasma from Nil, TB1 and Mitogen QuantiFERON tubes, including; IL-5, IL-2, IL-6, IL-13, IL-4, IL-9, IL-10, IL-17A, IL-17F, IL-22, IFN-γ and TNF-α. CBA BioLegend kits is a bead-based immunoassays used to quantify multiple soluble analytes simultaneously in biological samples using a FACSCanto II cytometer. A total of 380 samples were analyzed according to the manufacturer's instructions.

Results: Between no TB and TB groups; There was significant changes seen in TNF-α, IL-5, IL-2, IL-13, IL-4, IL-17A and IL-17F. Slight significant changes was seen in IL-6, IL-22 and IFN-γ. No significant change was seen in IL-9. Results show reduced plasma IL-9, IFN-γ and IL-22 activation by mitogen in TB+HIV+ subjects that is independent of ART status, while IL-17A is moderately reduced in TB+HIV+ART- participants. Cytokine recall to TB1 antigen was observed to be similar across all TB groups, with the exception that a moderate reduction of IFN-γ and IL-17A was observed in the TB-HIV+ group.

Conclusion: Results identify defects in effector cytokines produced by Th cells that may persist after ART and contribute to poorer TB treatment outcomes in subjects with HIV. By contributing to an increase in T-lymphocyte activation already found in HIV patients, TB disease can have an impact on viral replication. Functional cytokine status of Th cell populations, including Th17 and Th22 cells, may differ at time of TB drug treatment, increased and decreased levels of some cytokines were found between samples collected on start of TB treatment and samples collected after completion of TB treatment. To understand these complexities, the profile of immune activation markers in TB patients needs to be continuously explored.

Abstract 065

Title: Entomological and epidemiological drivers of visceral and cutaneous leishmaniasis outbreak in Kajiado County, Kenya

Authors: Barrack Omondi (ICIPE)*; Damaris Matoke (KEMRI); Steve Kiplagat (ICIPE); Hannah Njiriku (KEMRI); Johnstone Ingonga (KEMRI); Daniel Njenga (KEMRI); Charles Magiri (FIND); Mwatela Kitondo (ACCIH); Daniel Mwiti (MOH, Vector-Borne & NTDS); Hellen Nyakundi (ACCIH); Richard Wamai (Northeastern University, Boston); Jandouwe Villinger (ICIPE); Tobias Landmann (ICIPE); Abhay Satoskar (College of Medicine, The Ohio State University); Daniel Masiga (ICIPE)

Background: The Kajiado-West sub-county emerged in 2021 as a new transmission focus for visceral (VL) and cutaneous leishmaniasis (CL). We investigated entomological and epidemiological factors contributing to VL and CL occurrence to establish transmission hotspots and inform targeted disease control strategies.

Methods: We conducted a cross-sectional survey in September 2021 in Esonorua, Oldonyo Nyokie, Musenke, and Shompole. Suspected VL and CL cases were diagnosed by trained clinicians using the rK39 rapid antibody test and microscopy. We subjected positive samples to parasite speciation by ITS1 PCR and sequencing. For the entomological surveys, we sampled sandflies in November 2021 and February 2022 using CDC miniature and Silver bullet 2.0 light traps. We identified the sandfly species using morphological keys and COX1 PCR. We determined the sources of sandfly bloodmeals by cyt-b PCR and sequencing.

Results: We examined 100 cases (males:56; females:44) of VL infections. Overall, VL seroprevalence in the sub-county was 10%. 80% (n=8) of the infected VL patients were below 15 years old, with more infections in males (75%; n=6) than females (25%; n=2). There was no significant association between VL seropositivity and the age group or gender of the cases. We estimated the overall CL prevalence in the sub-county at 36.4% (8/22), with L. tropica as the causative agent. We sampled 4,781 sandflies and identified 1,624 (males: 422; females: 1202) samples comprising four Phlebotomus spp. and eight Sergentomyia spp. Ph. martini was the most abundant Phlebotomus species in the sub-county (8.4%; n=136), while S. clydei was the most abundant sandfly species (39.2%; n= 637) overall. We detected L. donovani in S. clydei (n= 13), S. adleri (n= 4), S. antennatus (n= 2), and Ph. saevus (n= 1), while L. tropica was detected exclusively in Ph. saevus (n=1). L. donovani and L. tropica infection rates were 4.4% (20/450) and 0.2% (1/450), respectively. Humans were the primary sandfly hosts in Kajiado County. Ph. saevus, S. clydei, and S. squamipleuris exhibited a broad host range from humans to livestock and wildlife.

Conclusion: L. donovani and L. tropica are the main Leishmania species in the sub-county. The presence of the parasites in humans and high human blood indices may indicate increased transmissions in the area. The detection of L. donovani in S. clydei and S. antennatus suggests their potential involvement in VL transmissions in Kajiado County, a finding which requires further investigation. Factors behind the recent outbreak after long dormancy need further exploration.

Keywords: Leishmaniasis, visceral leishmaniasis, cutaneous leishmaniasis, sandflies

Abstract 066

Title: ASSOCIATION BETWEEN FIVE-MINUTE APGAR SCORES AND ADVERSE SHORT-TERM OUTCOMES IN NEONATES IN THE CLINICAL INFORMATION NETWORK HOSPITALS IN KENYA, 2018-2022

Authors: Pauline N Karing'u (University of Nairobi)*

Background: The Apgar score is a good indicator of the quality of obstetric and newborn care. More than two-thirds of neonates with a low Apgar score will die in the perinatal period. There is therefore a need to determine the association between the Apgar score at five minutes and mortality, encephalopathy, and hospital stay among neonates admitted to the Clinical Information Network (CIN) hospitals in Kenya.

Methodology: This is a retrospective cohort study carried out in 22 neonatal units that are part of the CIN across 14 counties in Kenya. Singleton-born neonates admitted to the neonatal unit on day one of life between the years 2018-2022 were included. Those with major congenital defects, those born in multiple gestation and those with a recorded score of less than zero or greater than ten were excluded. Data was abstracted from the Neonatal Admission Record and Newborn Unit Exit Form and captured into the REDCap tool and analysed using R software version 4.1.2. Descriptive statistics were summarized as means, medians and proportions while inferential analysis were done using the Cox proportional hazards model and logistic regression.

Results: This study found that 77% of neonates inborn in the CIN-N facilities had normal Apgar scores while 3% had low score at five minutes. For every additional increase in the Apgar score, the hazard of death was 0.63(CI 0.61-0.64) times lower regardless of other covariates included. At 28 days, the probability of survival for babies with normal, intermediate, and low Apgar score at five minutes were 80%, 51% and 26% respectively. The odds of developing encephalopathy when a baby has intermediate and low Apgar score at five minutes are 5.73 (CI 5.37-6.12) and 15.87(CI 13.9-17.6) times higher respectively compared to the normal Apgar score. Length of hospital stay was longer in the neonates with low and intermediate score than in those with a normal score.

Conclusion The Apgar score remains a useful tool in assessing the newborn status and planning for newborn care needs at birth especially in our low resource settings where biochemical markers and other important investigative modalities may be unavailable.

It is equally an informative tool for the clinician/health worker for risk stratification for the neonates with regards to outcomes such as death, hospital stay and the development of encephalopathy. It is therefore useful to ensure that it is assigned correctly by staff working in maternity and newborn units.

Additionally, there is need for proper resource planning in terms of health workers numbers, skill set and competence, newborn unit resuscitation equipment to improve outcomes for neonates who may score a low or intermediate score and for pregnant women who may be a risk of delivering a neonate who may score less than normal Apgar score.

Keywords: Apgar score, neonate, neonatal mortality, encephalopathy, hospital stay

Abstract 067

Title: Advances in The Ambulatory Management of Pneumothorax: A systematic Review and Meta-Analysis.

Authors: Vincent Kipkorir (University of Nairobi, College of Health Sciences)*; Wongi Woo (2. Department of Thoracic and Cardiovascular Surgery, Gangnam Severance Hospital, Yonsei University College of Medicine, Seoul 03722, Republic of Korea); Bahadar Srichawla (3. Department of Neurology, University of Massachusetts Chan Medical School 55 Lake Ave N Worcester MA 01655 U.S.A.)

Abstract

Background: Pneumothorax continually remains as one of the most common clinical pathologies, with observed significant burden on global health. Despite several advancements, there still remains a lack of consensus in the management of pneumothorax, with the ambulatory alternative gaining wide traction owing to its associated low morbidity, mortality and enhanced mobility of patients. The present study reviews available literature and compares the clinical benefits and complications between ambulatory and conventional managements.

Methods: A search of literature was performed through PubMed, SCOPUS and ScienceDirect in order to identify eligible studies. Primary outcomes included the overall success rates of ambulatory management of pneumothorax and in comparison, with conventional treatment. Secondary outcomes included success rates according to pneumothorax types and according to geographical areas. A pooled analysis of 24 studies was conducted to calculate the pooled success rates and the pooled relative risks. Head-to-head comparison and subgroup analysis was done comparing ambulatory vs. conventional treatment of pneumothorax. To assess risk of bias among the included studies, risk of bias assessment was conducted using Version 2 of the Cochrane risk-of-bias tool for randomized trials (ROB 2) and the risk of bias for non randomized interventional studies (RoBANS) tool for the respective study designs.

Results: A total of 1,211 records were identified, with only 26 studies meeting the criteria for inclusion. The overall pooled success rate was approximately 84% (95% confidence interval (CI) of 79-88%). Five studies included in the treatment failure rate observed a pooled relative risk (RR) of 0.75 (95% CI 0.47-1.20). Ambulatory treatment carried an increased relative risk of pneumothorax enlargement (RR 4.84, CI 1.10-21.29). Four studies identified an iatrogenic (post-biopsy) pneumothorax and had a pooled success rate of 90% (CI 78-96%). Overall, the risk of bias for non-randomized trial was low. The domain with the highest risk of bias was in the blinding of outcome assessment. No RCT showed a low risk of bias in all domains. The greatest risk of bias was seen in the selection of reported results.

Conclusion: Ambulatory treatment of pneumothorax demonstrates favorable and non-inferior success rates, especially in iatrogenic pneumothorax, with comparable outcomes to standard care. Despite the noted enlargement of pneumothorax, negative clinical outcomes such as severe morbidity, mortality or tension pneumothorax have not been observed due to the enlargement. With proper stratification of pneumothorax and application of tailored treatment according to patients' risk, ambulatory management holds a promising role especially in the treatment of iatrogenic pneumothorax.

Keywords: Ambulatory Management, Pneumothorax

Abstract 068

Title: The Effect of climate change on Biomphalaria pfeifferi populations in Asao stream, Western Kenya..

Authors: Noel Oduor1*, Eric Lelo1, Daniel Kariuki2, Gerald mkoji1, and Sam Locker3 1. Center for Biotechnology Research and Development- Kenya Medical Research Institute. 2. Jomo Kenyatta University of Agriculture and Technology. 3. University of New Mexico.

Background: Schistosoma mansoni is endemic in Kenya and widely distributed within the Lake Victoria basin. About 16 million people are at risk of the infection, and more than 9.1 million are infected. The most at-risk population are poor communities without access to safe drinking water and adequate sanitation near waterbodies, habourouring the intermediate host. Schistosomiasis is transmitted through contact with water infected with cercaria, the infective stage of the disease. Among the three Biomphalaria snail species that transmit S. mansoni in Kenya, B. pfeifferi is the most prominent and widespread. Snail populations respond to temperature fluctuations in the aquatic environment; Studies have shown that B. pfeifferi abundance remains constant in temperatures 20–27°C. Outside this range, snail numbers drop sharply. Heavy rainfall and severe flooding wash snails downstream, reducing their quantity in transmission sites. The Asao stream experiences periodic flooding and drought. Following these adverse weather conditions, the snails are cleared out in the process, causing an interruption in the transmission of S. mansoni.

Method: 206 B. pfeifferi snail samples were collected bimonthly across the Asao stream from November 2018 to September 2019. DNA was extracted from the snail's soft tissues by the HOTSHOT method. Amplification was performed in a multiplex PCR format using the QIAGEN Multiplex PCR Kit; and 14 microsatellite markers in two panels. The PCR products were diluted in N, N'-dimethyl formamide with Genescan® – 500 [LIZ 500] as an internal size standard and genotyped using an ABI3500XL automated sequencer and scored with GeneMaker® software. Micro-Checker Version 2.2.3 was used in data cleaning and statistical analysis performed in GenAIEx 6.51.

Results: Analysis of Molecular Variance (AMOVA) showed a genetic differentiation of 52% among individuals, 39% within individuals, and 9% among the snail populations. The values of the matrix of genetic divergence of the isolates were above 0.05, implying that the genetic variation among the B, pfeifferi snails collected in the Asao stream is increased. Also, genetic variation compared to weather conditions during and before collection time indicates that temperatures and rainfall are the major causes of genetic variation in the Asao Stream.

Conclusion: This study confirms that increased temperatures and Intense rainfall are causes of genetic variation in B. pfeifferi habiting the Asao stream.

Environmental factors are serious candidates for driving genetic variation and should be considered in studies involving B. pfeifferi snails.

Keywords: Schistosoma mansoni.

SYMPOSIUM 1: KNOWLEDGE MANAGEMENT

Institution: Kenya Medical Research Institute (KEMRI)

Title: Promoting Systematic Use of Research Evidence to Inform Health Policy And Practice: Lessons From Knowledge Translation During COVID-19 Pandemic.

Abstract: Public health emergencies open a policy window in which policy actors become more receptive to research evidence. As an example, the COVID-19 pandemic set the stage for researchers and policymakers to work together and identify the best interventions in response to the public health emergency. Researchers provided evidence on effective treatment strategies for treating coronaviruses that informed the development of COVID-19 treatment protocol, vaccine development and vaccine efficacy modelling that informed acceptance and distribution of vaccines in the country, and analysis of COVID-19 surveillance results that regularly informed pandemic containment measures. We propose a symposium to discuss Kenya's experience with the role and use of research evidence to inform pandemic responses for the health system. Specifically, the symposium will provide the opportunity to discuss the role of evidence in informing the strategies employed to respond to the pandemic and the emerging capacities in the system that can be leveraged to ensure health system function post-public health emergencies. We shall use the knowledge cafe format that allows symposium participants to break into small groups and discuss. The panel discussion will end with discussions on how the knowledge translation process can be systematically integrated into MoH (Ministry of Health) decision-making processes to build a more resilient health system. At the end of the knowledge 3 cafes, facilitators shall present a summary of discussions of each round table discussion.

SYMPOSIUM 2: PAMCA

Institution: PAMCA Kenya Chapter

Title: Surveillance and control of vector borne diseases in Kenya

PAMCA - Kenya Chapter, a professional body of vector control practitioners in Kenya, and registered as a society by the Registrar of Societies in Kenya. The Chapter has a membership of over 65 members comprising of entomologists, vector control specialists, social scientists, students, academicians, institution/companies among other stakeholders. The vison of PAMCA Kenya chapter is a country free of mosquitoes and vector-borne diseases. One of the mandates for the society is to promote general awareness to the public and any other relevant groups about mosquito-borne diseases, control, and related subjects. Additionally, the chapter aims at promoting activities of research, evaluation, and expertise in vector borne disease control. An upsurge of mosquito borne diseases and invasive mosquitoes have been reported in the country. Their surveillance and control are hampered by insufficient information and tools coupled with other threats including COVID 19 pandemic. The pandemic interfered with the control efforts against mosquitoes and associated diseases. This symposium aims to highlight the identified threats, progress made in vector borne disease surveillance as well as innovative interventions being developed and implemented.

SYMPOSIUM 3: FAMILY HEALTH UNIT (FHU)

Institution: KEMRI-CGHR, Family Health Unit (FHU)

Title: Neglected/Undiagnosed causes of under 5 deaths; case reports from CHAMPS

There is a notable gap in comprehensive data on causes of death among under-five children. The problem is exacerbated among neonates, who make up a big portion of the U5. Obtaining quality data in low- and middle-income countries is hampered by insufficient diagnostics, reporting, resources, and infrastructure. These limitations pose particular challenges in investigating the causes of early childhood deaths. The Child Health and Mortality Prevention Surveillance (CHAMPS) platform in Western Kenya has in the last 4 years elicited data on a myriad of undiagnosed causes of deaths. Data from this study can help us understand trends and real change in under-5 mortality which can eventually be used to guide policymakers in their efforts to prevent childhood diseases and mortality. We present a few case studies on diseases/conditions that would have been undiagnosed through the routine health system and suggest ways in which these shortcomings can be addressed.

SYMPOSIUM 4: SERU

Institution: Kenya Medical Research Institute

Title: BIOETHICS AND RESEARCH REGULATION

Bioethics is a multidisciplinary field that addresses concerns from diverse fields of study including life sciences, biotechnology, public health, medicine, public policy, law, philosophy and theology.

The discipline is crucial as there is a need to balance the advancement of knowledge and innovations through science with the protection of human participants. This led to the establishment of research ethics committees which are accredited by NACOSTI in Kenya to review research proposals for ethical clearance before the proposal is considered by NACOSTI for issuance of research license.

The KEMRI Scientific and Ethics Review Unit Symposium on Bioethics and Research Regulation will seek to:

- Create awareness on research ethics
- Share research findings on bioethics related studies
- Explore the research regulation landscape in Kenya including; peer review, scientific and ethics review, expert clinical trials review, implementation and approval by the Pharmacy and Poisons Board, issuance of research permits by NACOSTI and accessing the community through County authorities
- Address researcher concerns relating to research regulation.

The symposium will facilitate conversations among researchers and members of ethics committees, health care professionals, bioethicists, research administrators and others who are interested in Bioethics.

SYMPOSIUM 5: TUNGIASIS

Institution: KEMRI-Wellcome Trust, University of Oxford with International Centre for Insect Physiology and Ecology (icipe) and University of Berlin, Germany Funded by Wellcome Trust UK and DFG, Germany.

Title: Frontiers in Tungiasis Research in Kenya

Tungiasis is an extremely Neglected Tropical Skin Disease, common in the Americas and Sub-Saharan Africa. It is caused by the sand flea Tunga penetrans, the female of which burrows into the skin, where it remains for the rest of its life. Morbidity results from the intense inflammatory response around growing embedded sand fleas. The inflammation is further intensified by frequent bacterial superinfection of the lesions. The inflammatory response causes immense pain and itching, difficulty walking, sleeping and concentrating on any task. There is no safe, effective and affordable treatment available and in their desperation, people extract the fleas with non-sterile sharp instruments such as thorns, needles or safety pins. Children under 15 years carry the highest disease burden with prevalence in schools previously reported to range between 15% and 60% in endemic areas. Tunga penetrans also infects domestic and sylvatic animals which may act as important reservoirs for human infection. There has been very limited research conducted on tungiasis globally compared to other parasitic diseases, hampering the development of effective disease prevention and control measures. Little is known of the actual disease burden and distribution in Kenya or globally, nor the ecology of off-host stages and transmission dynamics, including the physical, social and economic environment, linking the human, the domestic animal and the sylvatic animal cycle. The partners organizing this symposium lead current entomological, parasitological, molecular, veterinary and medical research on tungiasis. This symposium aims to create awareness and generate interest in this debilitating zoonotic disease and to present most recent findings from three ground-breaking research projects in Kenya.

Scientific Session 8: TB-2

Abstract 069

Title: Identification of Mycobacterium species causing pulmonary tuberculosis in sputum samples from three heath facilities in Nairobi county, Kenya.

Authors: Jeremiah Ndeto1, Robi Chacha1, Pascah Bulia1, Geoffrey Okallo1, Paul Mwangi1, Janice Endsley2, Evans Amukoye1, Asiko Ongaya1

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Background: Tuberculosis is the leading cause of death in the world especially in the sub-Saharan Africa. Pulmonary tuberculosis is caused by Mycobacterium tuberculosis(TB). Laboratory diagnosis is necessary for identifying Mycobacterium tuberculosis. Non-Tuberculous Mycobacterium species are known to cause disease with similar characteristics to pulmonary tuberculosis. This study aimed to identify Mycobacterium species causing Pulmonary tuberculosis in sputum samples to enhance improved treatment and management of tuberculosis.

Methodology: Sputum samples were collected from the three sites in Nairobi county; Mbagathi hospital, Rhodes TB clinic and Aids Healthcare Foundation for 3 years and transported to KEMRI laboratories for analysis. Samples were analyzed using Fluorescent microscopy, Lowenstein Jensen culture and MGIT TBc identification test. Samples that had no growth after 120 days of incubation at 370c were reported as negative. All culture positive samples were identified for Mycobacterium tuberculosis using MGIT TBc identification test. Those that were MGIT TBc identification test negative were presumptively identified as Non-Tuberculous Mycobacterium.

Results: Out of 287 samples which were culture positive, 277(96.5%) were identified Mycobacterium tuberculosis complex positive and 9(3.1%) were suspected to be Non-Tuberculous Mycobacterium.

Discussion and Conclusion: Studies have shown that diagnostic tools have been designed to identify Mycobacterium tuberculosis complex only which causes majority of infections and not identifying the Non-Tuberculous Mycobacterium. According to the above study,96.5% of the total samples analyzed had Mycobacterium tuberculosis complex and 3.1% where identified as Non-Tuberculous Mycobacterium which is statistically significant.

Emphasis on precision on laboratory diagnosis and identification of Mycobacterium strains causing pulmonary tuberculosis is key. Characterization is necessary for epidemiological and treatment of patients. Identification of Non-Tuberculous Mycobacterium species averts misdiagnosis and misuse of anti-TB drugs. Treatment for Non-Tuberculous Mycobacterium disease varies despite use of multiple antibiotics. A national wide survey to characterize all mycobacterium species causing pulmonary tuberculosis for better understanding of the circulating species is needed

Keywords: Tuberculosis

Abstract 070

Title: Novel Approaches for Developing a Highly Sensitive Molecular Assay for the Diagnosis of Tuberculosis

Authors: Clement Likhovole (Mount Kenya University)*; Jesse Gitaka (Mount Kenya University); Asiko Ongaya (KEMRI); Bernard Kanoi (Mount Kenya University)

Introduction: Globally in 2020, approximately 1.3 million deaths occurred among HIV-negative people as a result of Tuberculosis (TB) infection. The COVID-19 pandemic has reversed years of progress in reducing number of notified TB cases. To effectively manage TB cases, rapid, affordable, and accurate diagnostic approaches are required. Nucleic acid amplification methods such as polymerase chain reaction (PCR) offer high specificity and sensitivity for smear-positive TB but poorer sensitivity and specificity for smear-negative TB. These assays require specialized laboratory infrastructure and expertise. While being open systems, they are also at risk of contamination particularly in set-ups with sub-optimal laboratory infrastructure. Therefore, uptake of these assays in high-burden settings with resource scarcity is limited.

Methods: We used genome-mining approaches to identify identical multi repeat sequences (IMRS) distributed throughout the Mycobacterium tuberculosis (MTB) genome to design a primer pair that target 32 repeat sequences. Genomic H37Rv DNA was 10-fold serially diluted (100pg/μl to 1×10-3 pg/μl) and used as DNA template for PCR reactions using the MTB IMRS primers. The gold standard PCR with 16s rRNA primers was also run as a comparative test, and both assay products were resolved on agarose gel. Further, we cultured 20 sputum samples on Mycobacteria Growth Indicator Tubes (MGIT) and incubation was done in a BACTEC MGIT 960 instrument. Extracted DNA from instrument positive cultures was used as template for the MTB–IMRS and the gold standard 16s rRNA PCR assays, thereafter, amplicons were resolved on 1% gel.

Results: The MTB IMRS-PCR assay had an analytical sensitivity of 0.1259 pg/μl (2.6×101 genome copies per μl), representing >200 times better sensitivity. We further showed that MTB-IMRS PCR is both sensitive for detecting MTB cultured isolates.

Conclusion: De novo genome mining of MTB IMRS as amplification primers can serve as a platform for developing ultrasensitive diagnostics for TB and potentially a wide range of infectious pathogens. The cost of the novel assay is comparable to conventional PCR tests but it offers higher pathogen sensitivity.

Keywords: Mycobacterium tuberculosis, IMRS

Abstract 071

Title: Implementing and Improving the Quality of Tuberculosis Diagnosis in Kenya in 2021

Authors: Solomon C Bundi (National Tuberculosis Lab)*; Nelly Mukiri (National Tuberculosis Lab); samson Ireri (National Tuberculosis Lab); mary w mbugua (ministry of health); BEATRICE NASIMIYU KHAMALA (NPHL); Laura Onzere (National Tuberculosis Lab); Sila Omondi (AMREF)

Background: Kenya has a tiered network of tuberculosis (TB) diagnostic laboratories and National TB Reference Laboratory (NTRL) serves as the main TB Reference Laboratory. There are approximately over 2,700 identified TB diagnostic facilities in Kenya across all counties in the country. A proficiency testing program is used to review the performance of these facilities to give a good indication on staff competency, equipment functionality, adherence to testing standard operating procedures, implementation of quality controls and overall quality of services.

Method: The NTRL as part of its mandate initiated the microscopy proficiency testing program whereby all county referral facilities were enrolled and supplied with five unstained AFB microscopy smears for analysis. They were required to stain smears using either Ziehl Nielsen or florescence microscopy and return the results to the NTRL for evaluation. The results were sent back to the facilities by mail and courier for their consumption.

Results: Fifty (50) facilities across the country in the 47 counties were enrolled. These were mainly the County Referral facility laboratories with Nairobi County having more facilities due its large number of diagnostic facilities in the country. Out of the 50 enrolled facilities 41(80%) responded while 9(20%) did not respond due to various reasons. Overall pass mark was at 80% in which 34(82.9%) facilities passed with Nairobi, Siaya, Meru among others leading while seven (17.1%) Performed below pass mark like Busia, Makueni, Nyandarua among others 26 (64.4%) facilities used the Florescence Microscopy method while 15(36.6%) used Ziehl Nielsen method. From the analysis, facilities with FM are many and emerge overall winner due to the quality of the method.

Conclusion:

- There is need for training and mentorship in smear microscopy to enhance the competency of the laboratory personnel.
- There is need to enroll all TB diagnostic facilities into the External Quality Assurance program in order to identify the existing gaps in smear microscopy.

Keywords: Implementing, Quality, Tuberculosis, Ziehl Nielsen, florescence, competency

Abstract 072

Title: SCALING UP ACTIVE CASE FINDING THROUGH INTEGRATING QUALITY IMPROVEMENT IN TB SETTINGS THE CASE OF SUNA WEST SUB COUNTY

Authors: Peter P.O.O Omware (Ministry of health)*; Stella Omulo (Centre for health solution); David Nyamohanga (Ministry of health)

Background: Suna west is third in terms of contribution to tuberculosis(TB) case finding amongst the eight sub counties in Migori County .The main economic activity is mining and has the largest slum which contribute greatly to increased TB transmission. In 2021 the sub county experienced a drop in TB case finding by 6.7% against an expected national target of 20%. Increase annually.

PLAN

The sub county health management identified this problem and started a quality improvement (Q)I project. The following root causes were identified using a fish bone analysis i.e. late diagnosis, clinician knowledge gap on TB case finding, Inadequate assessment of contacts of bacteriologically confirmed TB cases and Inadequate access to commodities e.g. x-rays, nasogastric tubes, inadequate access to gene expert due to commodity stock out, poor laboratory staff attitude towards microscopy

Objective (goal setting): To improve TB case finding by 20% through use of the PDSA cycle in Suna West Sub County, Migori County

Methodology: This is a mixed method study design with a retrospective review of records from the online TB platform (TIBU) comparing data in the year 2021 before interventions and 2022 after interventions.

Strategies employed (activity planning) DO

1.Training of facility staffs on integrated TB and pediatric TB (7)

2. Continous medical education to sensitize facility staffs on active case finding and contact management register.

3. Regular on job training, mentorship and support supervision on screening and TB management.

3. Increased engagement of private facilities in TB agenda

4. Monthly tracking of indicators on the TB dash boards after QI meetings.

5. Training community health volunteers on screening, contact tracing and community facility referrals of suspects.

6. Quarterly acid alcohol fast bacilli (AAFB) refreshers for laboratory technicians in both private and public facilities.

7. Weekly and monthly sub county TB data review meeting on the sub county TB What Sapp plat form

RESULTS (STUDY): In 2021 the cases dropped from 222 to 208(6.7%) i.e public facilities 139 (67%) and private facilities 69 (33%).

In 2022 with quality improvement interventions the sub county increased significantly number of TB cases notified to 377 (81.3%) i.e public facilities 218(58%) and private facilities 158 (42%).

Conclusion (ACT): The study made it evident that through the PDSA cycle (quality improvement approach) facilities and Sub Counties can be able to improve their performance especially TB indicators such as TB case finding.

RECOMMENDATION (ACT): The National TB program and Counties should adopt the CQI strategy as a way of improving TB indicators' performance for facilities with unsatisfactory performance. This should be achieved through the introduction of policies/ guidelines that incorporate quality improvement in the implementation of TB activities especially active case finding (ACF)

Keywords: TB

Abstract 073

Title: Treatment outcomes among cases with Drug Resistant TB, Nairobi County TB Treatment Centers, 2016 - 2022

Authors: Selina N Marwa (FELTP)*

Introduction: Drug Resistant Tuberculosis (DR-TB) strains threaten global progress towards the targets set by the End TB Strategy by 2030 of the World Health Organization (WHO). Kenya is among the three global lists of high-burden countries for TB, HIV-associated TB and MDR/RR-TB. The national treatment success rate (TSR) for DRTB is 90%. Nairobi County has the highest burden of DR-TB in Kenya. We sought to describe the outcomes of DR-TB cases in Nairobi County. Method: We conducted a retrospective analysis of routine program data for cases managed for DR-TB from 2016-2022 in Nairobi County. We identified DR-TB cases from the Nairobi County TIBU® (Treatment Information from Basic Unit) data base. Treatment outcomes were classified as poor (death, lost to follow up or failure) or successful (cured or treatment complete). Treatment outcomes were assessed at the end of treatment. We calculated descriptive statistics and odds ratios to measure the strength of association between variables and a p-value of <0.05 was considered statistically significant. Results: We analyzed 504 records. The mean age was 34 (±12) years and age group 30-44 years were 239 (47%). Males were 352 (70%) and 267 (53%) were new DR-TB patients. DR-TB cases who were people living with HIV (PLHIV) were 189(38%), 178(39%) were on injection regimens and 217(48%) had a recorded BMI <18.5 g/dl. Poor outcomes were 151 (30%); of these, 67% (101) were males. Odds of having a poor outcome were higher among cases who were PLHIV, OR 2.5 (95% CI 1.4-3.1), body mass index (BMI) <18.5g/dl 1.9 (95%CI 1.2-2.9) and were managed on injection regimens OR 1.6(95%CI 1.1-2.4). Conclusions: Majority of cases with DR-TB were young and male. Low BMI, being human immunodeficiency virus (HIV) positive and management on injection regimens were associated with having poor outcomes. Low BMI also requires nutritional support with supplements to decrease poor outcomes among DR-TB cases.

Key words: Kenya, Drug resistant tuberculosis, treatment outcomes, lost to follow-up, nutritional support, BMI, HIV

Keywords: Key words: Kenya, Drug resistant tuberculosis, treatment outcomes, lost to follow-up, nutritional support, BMI, HIV

Abstract 074

Title: Characterization of first line drug resistance for mycobacterium tuberculosis complex by MTBDRplus™ for specimens received at the National Tuberculosis Reference Laboratory Kenya, 2021

Authors: BEATRICE NASIMIYU KHAMALA (NPHL)*; Nellie Mukiri (NPHL/NTRL); Solomon C Bundi (National Tuberculosis Lab); Laura Onzere (NPHL/NTRL); Ronald Odero (AMREF); Charity Maina (NPHL); Jack k Irungu (Field epidemiology and laboratory training program (FELTP))

Introduction: Drug resistant tuberculosis (DR-TB) has been increasing globally. Kenya reported 589 MDR/RR cases in 2020. The prevalence of rifampicin resistance and isoniazid resistance among new TB cases is 1.3% and 5.5% respectively and 5.2% and 6.8% among previously treated TB cases respectively. Line Probe Assay provides for a rapid modality in the detection of mycobacterial tuberculosis complex (MTBc) and drug susceptibility testing (DST) to TB medicines compared to phenotypic DST. We reviewed data for specimens tested using first line probe assay (FL LPA) in 2021

Methods: We collected test data from the laboratory management system at the National Tuberculosis Reference Laboratory (NTRL) in a spreadsheet. The data was cleaned and analyzed in MS Excel 2013. We calculated measures of central tendency for continuous variables and frequencies and proportions for categorical variables. We obtained administrative approval from the Head NTRL.

Results: We analyzed 3,692 specimens where 3190(86.4%) were male and human immunodeficiency virus (HIV) infected were 422(11.4%). The median age was 36 years IQR1-28, IQR3-45 what Central region had 1516(41.0%) specimens. Specimens resistant to rifampicin and isoniazid were 53(1.4%), 92 (2.4%) to rifampicin and 244(6.6%) to isoniazid only. North-Eastern region reported 2/430(0.9%) resistance to both rifampicin and isoniazid, 16/430(7.2%) rifampicin and 49/430(22.2%) Isoniazid only. There is a gap in data quality for the HIV as 573/3692(15.5%) status is unknown. The lab turnaround time (TAT) was 15 days Q1-10, Q3-24 and transit TAT 3 days Q1-2, Q3-6.

Conclusion: The highest proportion of the resistance was seen in North-Eastern region. The resistance pattern of the study was similar to 2015 Drug Resistance Survey (DRS) done in Kenya.

Keywords: Drug resistant TB is a global issue and has been on an increase in kenya

Scientific Session 9: COVID-19

Abstract 075

Title: Severe Covid-19 cases in the county hospitals in rural central Kenya, a case study of JM Kariuki hospital, Nyandarua county

Authors: Angelica N Kabue (Nyandarua County, Department of Health)*; Rachel Kinuthia (Nyandarua County, Department of Health)

Background: Understanding the clinical presentation of COVID-19 is key to inform the process of formulating guidelines and testing. The aim of this study was to characterize the severe cases of COVID-19 patients admitted in the Isolation ward to understand the different manifestations of the disease in an African setting.

Methods: We conducted a retrospective study. Data for patients admitted in the Isolation ward at the JM Kariuki hospital as from July 2020 to May 2021 was extracted from the patients file and entered in the excel sheet for analysis. The data extracted included age, sex, duration of symptoms before admission, symptoms on admission, presence of comorbidities and the type of comorbidity, presence of fever during admission and the average temperature during hospital stay, average oxygen saturation levels, average respiratory rates, duration of admission and the outcome. We gave each patient a unique code for confidentiality and analysis purposes. During analysis, variables were analyzed in terms of sex as males have been shown to be more vulnerable to the disease. Mean and median were reported for continuous variables. Pearson Chi-squared test and t-test were used for categorical variables and continuous variables respectively. All the analyses were conducted in STATA version 14, A two-side p-value < 0.05 was considered statistically significant.

Results: There were 82 patients admitted in the Isolation ward between July 2020 and May 2021 . The mean age of the patients was 60.7(± 15.6) years with 55% being males. Median days of signs and symptoms before admission was 7(3-8) for males and 4.5 (3-7) for females. The median hospital stay was 5(3-9) and 5(3-7) days for males and females respectively. There was no statistical difference observed for the mean age ($p = 0.6652$), median days of signs and symptoms before admission ($p = 0.1803$), median hospital stay ($p = 0.6099$) and mean SPO2 ($p = 0.5988$) between males and females Dyspnea was most prevalent sign at 78% seconded by cough at 62.2%. Hypertension was most prevalent comorbidity at 25.6% followed by diabetes 15.9%. The mortality of the group was 28.1%. .

Conclusion: This study shows that majority of the characteristics and presentations among COVID-19 patients with severe disease is consistent with what has been observed globally emphasizing the need for multinationals collaboration not only during pandemics but also for other conditions. Although the differences noted among males and females were not statistically significant, further studies are required to determine if indeed there is a difference between males and females among Covid-19 patients as this will guide on prevention and treatment of the disease.

Keywords: COVID-19, Severe cases, Rural Kenya, Retrospective Study

Abstract 076

Title: Application of isothermal amplification and detection methods for clinical diagnostics

Authors: bart keijser (TNO)*; Michel Ossendrijver (TNO); Kim Vermeulen (TNO); Hans van Leeuwen (TNO); Jasper Kieboom (TNO)

Background: Infectious disease diagnostics is dominated by PCR-based methodologies, offering robust and sensitive detection of molecular targets in clinical samples. Despite its widespread use, the method is demanding regarding laboratory infrastructure, and laboratory consumable. Isothermal amplification and detection techniques, such as LAMP (Loop mediAted IsotherMal amplification) offer an attractive and versatile alternative to diagnostic testing. The single reaction temperature and robustness towards impurities in the reaction mixtures enabling more simple laboratory workflows while remaining speed and sensitivity. Here, we explored the application of LAMP-based testing for detection of SARS CoV-2 for both high throughput routine diagnostics as well as instrument-free point of care diagnostics.

Methods: To enable efficient LAMP-based detection for SARS CoV-2, different primer sets were evaluated for their performance and assay conditions were optimized. Once established, the protocol was validated using diagnostic panels. Validation was performed in two sepearate studies using either nasopharyngeal (npx) samples or mouth rinses, in comparison to routine detection by RT-qPCR (Seegene Allplex) in npx swabs. To further simplify the method, we developed a container with phase change material that ensures instrument-free maintenance of the appropriate reaction temperature for the LAMP reaction to take place.

Results: In our prospective validation, involving 900 volunteers, we determined for our LAMP-based analysis of npx swabs a sensitivity of 97.9%, specificity of 99.1% and concordance in test results of 99.0%, as compared to the RT-qPCR. LAMP analysis of 776 mouth rinse samples showed an overall sensitivity of 75.98% and a specificity of 99.81%. The LAMP protocol ensured rapid and quantitative detection with 20 minutes of sample pre-treatment and 18 minutes assay time. We further showed that instrument-free molecular diagnostic detection using LAMP is possible. Incubating samples in a holder of phase change material ensuring the appropriate reaction condition for the duration of the assay. Using either pH indicators, of magnesium specific dyes, the test result can be detected by eye, of by mobile phone camera, effective detection in resource deprived conditions.

Conclusion: The LAMP assay was found to provide a robust, rapid and versatile alternative for PCR based testing. With the lessons learned during the COVOD pandemic, we established additional LAMP-based protocols for detection of common respiratory pathogens. Given the speed, sensitivity and cost efficiency of the LAMP method is a valuable methodology of molecular diagnostics that can be operated under conditions with limited resources.

Keywords: isothermal diagnostics LAMP

Abstract 077

Title: Influenza and SARS-CoV-2 co-circulation in Kenya, Apr 2020 – Mar 2022

Authors: Daniel Owusu (US-CDC); Linus Ndegwa (US-CDC); Jorim Mr Ayugi (KEMRI-CGHR)*; Peter Muturi (HJFMRI); Rosalia Kalani (MOH KENYA); Mary Okeyo (MOH KENYA); Nancy Otieno (KEMRI-CGHR); Gilbert Kikwai (KEMRI-CGHR); Bonventure Juma (CDC); Peninah Munyua (CDC); Fracis Kuria (MOH KENYA); Ann Moen (US-CDC); Gideon Emukule (US-CDC)

Background: Little is known about levels of influenza activity during the SARS-CoV-2 pandemic in tropical low- and middle-income countries. We aimed to describe influenza and SARS-CoV-2 co-circulation and factors associated with detection and severity of both infections individually and co-infection with the two viruses. We also describe how the SARS-CoV-2 data from the influenza sentinel surveillance align with that of the Kenya national SARS-CoV-2 data.

Methods: Influenza sentinel surveillance data were collected from 8 sites in Kenya. The national SARS-CoV-2 surveillance data were obtained from the Kenya Ministry of Health. We conducted univariate and multivariable logistic regression to assess factors associated with detection and severe clinical illness among participants who tested positive for influenza only, SARS-CoV-2 only, and influenza and SARS-CoV-2 co-infection. We defined severe clinical illness as any of oxygen saturation <90%, in-hospital death, admission to intensive care unit (ICU)/ High Dependance Unit (HDU), mechanical ventilation, or a report of any danger sign among children <5 years among patients with severe acute respiratory illness.

Results: Among 7,349 patients enrolled from sentinel sites during April 2020 through Mar 2022, 76.3% were aged <5years, 45.3% were female, and 12.2% had at least one underlying medical condition. We detected influenza A in 4.2% (306/7224), Influenza B in 4.7% (337/7224), SAR-CoV-2 in 10.7% (768/7,199), and co-infection in 0.9% (63/7,165) samples tested. The odds of clinical severe illness among participants with co-infection were similar to those of patients with influenza only (aOR: 1.06; 95% CI: 0.72–1.39, p=0.795) and SARS-CoV-2 only (aOR: 1.00; 95% CI: 0.54–2.10, p=0.814), however, malnourished patients who had co-infection had increased odds of clinical severe illness. Although the number of samples tested from the sentinel surveillance was only 0.2% of the number tested in the national data (60/week vs 36,000/week), peak positivity in the sentinel surveillance data aligned with that of the national data.

Conclusion: Influenza co-circulated with SARS-CoV-2 in Kenya and peaks in SARS-CoV-2 positivity from the influenza sentinel surveillances data were comparable to that of the national surveillance system. These findings demonstrate the need for all countries to implement or strengthen national influenza sentinel surveillance system as a sustainable platform to monitor respiratory pathogens of public health importance.

Keywords: Influenza, SARS-CoV-2, co-circulation, disease severity

Abstract 078

Title: Occupational correlates for Covid19 disease among Staff at Kenyatta National Hospital

Authors: John Macharia Kiragu (University of Nairobi)*; Richard Ayah (University of Nairobi)

Background: A worsening shortage of health workers (HWs) and overwhelmed health systems have been attributed to the growing spread of Covid19 disease among HWs in health settings that have had a preexisting chronic shortage of HWs such as the sub-Saharan African region. In Kenya, disruption in health service delivery has been reported to have arisen from the isolation and quarantine of Covid19 infected and exposed HWs. Therefore, sustaining safe hospital staffing has been a public health challenge. Despite the growing evidence on the risk factors for the spread of Covid19 among HWs, contextual evidence in the Kenyan hospital setup remains scarce. This study sought to identify occupational correlates for Covid19 disease among Staff in a Kenyatta National Hospital (KNH) to inform optimal infection prevention and control (IPC) measures for HWs.

Study Objective: Our objective was to identify occupational characteristics predicting Covid19 disease among HWs in a tertiary hospital in Kenya.

Methods: This study was a hospital-based case-control study design that assessed for occupational exposure differences between the Polymerase Chain reaction (PCR) test positive for Covid19 infected HWs and Covid19 PCR-negative and asymptomatic HWs between November and December 2021 at Kenyatta National Hospital. A sample of 39 randomly sampled cases and 108 conveniently sampled controls were virtually interviewed using a structured questionnaire adapted from the WHO Tool for Covid-19 Exposure Risk assessment, to determine occupational characteristics. At 80% study power, a minimum Odds Ratio (OR) of 3 and an alpha (p-value) of less than 0.05 were selected for statistical significance, and a multivariable logistic regression with the Akaike information criteria (AIC) for model selection was applied. Confounding was controlled for and the overall effect size was estimated by McFadden pseudo R squared. Funding was provided by KNH, Informed Consent from the participants, and Ethical approval was given by KNH-UON Ethics and Research Committee.

Results: The predictors for Covid19 disease included non-adherence to infection prevention protocols while in tea and dining rooms (OR,7.65;p<0.05), working in medium-risk departments e.g the outpatient medical clinics (OR,4.38;p<0.05), and suboptimal adherence to face shield/protective gears (OR,3.88;p<0.05) in the last 2 weeks before PCR Covid19 testing, after controlling for confounders.

Conclusion: Reinforcing adherence to personal protective equipment (PPE) and IPC protocols for hospital staff is critical in areas with a lower perception of risk of Covid19 exposure such as in tea and dining rooms and medium-risk departments. Reinforcing adherence to face protective gear in addition to other PPE is vital for the safety of the hospital staff from Covid19 disease.

Keywords: Covid19 , occupational risk factors, Health Workers, Hospital

Abstract 079

Title: Incidence of SARS-CoV-2 and Influenza Viruses among Pregnant and Postpartum Women and their Infants, Siaya County, Kenya 2020–2021

Authors: Nancy Otieno (KEMRI-CGHR); Eduardo Azziz-Baumgartner (US-CDC); Bryan BN Nyawanda (KEMRI); MICHAEL O OTIENO (kemri cghr)*; Eunice Oreri (MOH KENYA); Sascha Ellington (US-CDC); Clayton Onyango (CDC-Kenya); Gideon Emukule (US-CDC)

Background: Little is known about the incidence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) among pregnant women in Sub-Saharan Africa. We quantify the incidence of symptomatic laboratory-confirmed SARS-CoV-2 and influenza infections among pregnant and postpartum women and their infants in one county in western Kenya to assess the value of prioritizing vaccination for this population.

Methods: We enrolled pregnant women seeking prenatal care at Siaya County Referral and Bondo Sub-County hospitals and then called or visited them at home once a week until six months postpartum to identify respiratory illness. We similarly followed their infants for six months. Staff obtained nasopharyngeal and oropharyngeal (NP/OP) swabs within 10 days of illness onset from patients presenting with COVID-like illness (CLI) and Acute Respiratory Illness (ARI) and tested these by real-time reverse transcription polymerase chain reaction for SARS-CoV-2 and influenza A and B viruses at the Kenya Medical Research Laboratory in Kisumu.

Results: During May 2020–August 2021, we enrolled 1,329 pregnant (<31 weeks of gestation) women. Overall, 342/1192 (29%) pregnant women, 206/1,015 (20%) postpartum women, and 415/1,015 (41%) infants developed at least one CLI episode. Among CLI episodes that had a swab collected, 37/354 (10%) pregnant women, 26/218 (12%) postpartum women, and 14/407 (3%) infants tested positive for SARS-CoV-2. The incidence rate (per 1000 person-months) of SARS-CoV-2 increased from 4.8 May-December 2020 to 9.3 January-August 2021 among pregnant women; 2.4 to 6.4 among postpartum women; and 1.2 to 3.4 among infants. We did not detect any influenza in 2020; the incidence rate of influenza during January-August 2021 was 2.8, 0.4 and 1.6 among pregnant women, postpartum women, and infants, respectively.

Conclusions: The incidence of SARS-CoV-2 in pregnant and postpartum women and their infants increased during the study period. These findings highlight the need to prioritize COVID-19 vaccination for pregnant and postpartum women.

Keywords: Pregnancy, Infants,SARS-CoV-2, Influenza

Abstract 080

Title: Wastewater Surveillance of SARS-CoV-2 in Kisumu City, Kenya

Authors: Eric M Muthanje (KEMRI/Walter Reed Project); Kimita Gathii (KEMRI/Walter Reed Project); Beth Mutai (KEMRI/Walter Reed Project); John N Waitumbi (KEMRI/Walter Reed Project)*

Background: To date, COVID-19 pandemic has infected 542 million people and killed >6 million worldwide. Kenya has not been spared, but the reported morbidity/mortality has been lower than published models. This study illustrates the use of wastewater as a “dipstick” for COVID-19 in the community.

Methods: The study was conducted at 17 wastewater sites in Kisumu. Samples were collected twice weekly, processed by filtration and centrifugation to concentrate the virus. Following RNA extraction, qPCR was used to detect SARS-CoV-2. RNA of positive samples at Ct <33 was used to prepare libraries for whole genome sequencing.

Results: Between December 2021 to November 2022, 65/421 (15.4%) wastewater samples tested positive SARS-CoV-2. In December, when the country was going through the 5th wave caused by the Omicron VOC, 4/7 wastewater samples tested positive for SARS-CoV-2, and thereafter positivity rate declined to 1/36 samples in January, 1/19 in February and 2/37 in March. On sequencing, 3/8 had SARS-CoV-2 genome lengths >70% and were reliably classified as Omicron where two were BA.1 and one was BA.1.1 variants. The other 5 positive samples had partial sequences and could not be reliably assigned to a particular lineage. After a lapse in positive samples in April, there was a sudden surge in positivity rate in samples collected in May (7/46) and June (28/80) which coincided with the beginning of wave-6. Only one sample was successfully sequenced and was identified as Omicron, BA.4.1 lineage. Thereafter, none of the waste water samples tested positive until November 2022, when there was another surge in positivity (13/41), which correlated with an increase in the number of increased clinical cases in the country. Genetic analysis for November samples (n=5) indicated presence of BQ.1 that corroborated sequences data from clinical samples submitted to GISAID.

Conclusion: Beyond SARS-CoV-2, this study helped the laboratory to build local capacity for infectious disease surveillance in sewage. Given the high dilution of pathogens in sewer samples, we are optimizing methodologies that concentrate the sewer sample so as to maximize on pathogen recovery.

Keywords: COVID-19, SARS-CoV-2, Wastewater, RT-qPCR, whole-genome sequencing, VOC

Abstract 081

Title: Xpert xpress SARSCOV -2 Testing in Kenya.

Authors: mary w mbugua (ministry of health)*

Affiliations :National tuberculosis reference laboratory.

Background: Emerging of COVID 19 Virus affected provision of essential health services in Kenya. Much effort and time was put on COVID testing and results reporting which was a must for patient care.

Prolonged Turn Around Time (TAT) was witnessed due it's to unavailability of a faster testing platform. To ensure there is a faster diagnostic method, the government through the MOH adopted the real time polymerase chain reaction (RT PCR) where the gene Xpert machine played a big roll due to its sensitivity as compared to other rapid tests, and shorter its turnaround time (TAT)as compared to other platforms.

Methodology: Type of samples used; nasopharyngeal swabs, oropharyngeal.

Media used; Viral transport media(VTM)

The analysis was done using xpert xpress SARSCOV -2 .Which is an automated molecular invitro diagnostic test based on nucleic acid amplification technology .

Response: Online sensitization, commodities distribution, site visit and training was done on respective regions. In total,39 facilities from14 counties benefited on the same

The training involved hands on training on COVID testing using gene Xpert, results interpretation and online submission to the National server. This adoption on gene Xpert testing reduced the overall Turn Around Time (TAT)of 72hrs to 24hrs.

Results: Of the 3787 samples 90.47% (3419) was tested using Gene Xpert while 368 was tested on other plat forms.56.3% were male while 43.68% were female.

There was low infection in children 0-9(27.34%) and >80 (0.85%) years while we had higher infection rate among age 30-39(8.29%) – study of clinical infection 4% to 16.3%

May 2021 tested Low samples 7.13% and July tested 84.39% due to Stock outs.

Conclusions:

- Social life style may have contributed to higher male infection, need for sensitization
- The Ministry to consider use of Gene Xpert for testing COVID 19 across all the counties as a confirmation method
- Gene Xpert has the shortest COVID-19 testing time, and can be recommended for testing of COVID 19 by relevant authorities.

Keywords: Covid-19,VTM,Genexpert,Facilities

Abstract 082

Title: Determinants of COVID-19 vaccine uptake among eligible residents of two populations in Siaya and Nairobi County, Kenya, July 2021 to August 2022

Authors: GEORGE AOL OTIENO (KEMRI)*; Patrick K Munywoki (CDC, Nairobi, Kenya); GODFREY BIGOGO (KEMRI); Terrence Q LO (CDC, Nairobi, Kenya); George O. Agogo (CDC); Richard O. Onyando (KEMRI-CGHR); Amy Herman-Roloff (CDC); Peninah Munyua (CDC); Victor Akelo (KEMRICGHR); David Obor (KEMRI); Joshua Auko (KEMRI); Terry Komo (KEMRI); Carolyne Nasimiyu (WASHINGTON STATES UNIVERSITY); Ratwar Okoth (KEMRI)

Background: Vaccines have been the most effective intervention against infectious diseases. Globally, as of 30th November 2022, 64.34 persons per 100 population were fully vaccinated compared to Kenya where 19.91 persons per 100 population were fully vaccinated. Understanding factors influencing uptake of COVID-19 vaccines among those aged ≥ 15 years in Kenya may help increase coverage.

Methods: We used data from the Population-Based Infectious Disease Surveillance (PBIDS) platform, which monitors the health of ~35,000 individuals in rural western Kenya (Asembo, Siaya County) and ~24,000 in Kibera, an urban informal settlement in Nairobi County, from July 2021 to August 2022. PBIDS-enrolled households are visited every four months to collect key demographic, socio-economic, clinical, and vaccination information. During household and health facility visits, a COVID-19 vaccine uptake questionnaire, and additional questions for not getting vaccinated among the unvaccinated were administered. Vaccine coverage was defined as the proportion of those aged ≥15 years who reported receiving any COVID-19 vaccine. Multivariable logistic regression was used to determine demographic, socioeconomic, and clinical factors associated with the receipt of the COVID-19 vaccine.

Results: A total of 17,626 interviews were reported from households and health facilities in Asembo, with 7,232 (41.0%) indicating receipt of at least one dose of the COVID-19 vaccine, while 3,814 (21.6%) were fully vaccinated. Among 10,394 unvaccinated, fear of negative side effects after vaccination (38.0%), 'did not know where to get the vaccine' (23.5%), and the vaccine was offered far away (20.0%) were commonly reported reasons. In Kibera, 9,044 interviews were reported, with 4,052 (44.8%) indicating receipt of at least one dose of the COVID-19 vaccine while 2,750 (30.4%) were fully vaccinated. Among 4,992 unvaccinated, fear of negative side effects after vaccination (46.0%) and being busy (19.1%) were commonly reported reasons.

Factors that were positively associated with the uptake of the COVID-19 vaccine in Asembo and Kibera were age and women who were not pregnant, while unskilled household heads were negatively associated. In Asembo, those with secondary schooling or higher, married/

widowed, having a prior positive test of COVID-19, and hypertension was positively associated. In Kibera, sharing a household with a COVID-19 positive person, having cancer and asthma, were positively associated, while married/widowed was negatively associated with the uptake of the COVID-19 vaccine.

Conclusion: Our study found a low uptake of the COVID-19 vaccine in Asembo and Kibera but comparable to the national coverage. Our findings demonstrate the similarities and disparities in the uptake of the COVID-19 vaccine in rural and urban areas. These findings highlight the need for tailored approaches during planning and communication strategies for increased uptake of the COVID-19 vaccine.

Keywords: uptake, COVID-19, Vaccine, Asembo, Kibera

Abstract 083

Title: Characteristics of COVID-19 vaccine defaulters in Busia County, 2021

Authors: Jude T.B Oduor (Ministry of Health)*; Melsa Lutomia (Ministry of Health- Busia); Bridget Wesonga (Kenya FELTP); Maurice O Owiny (Kenya FELTP); Maria Nunga (Kenya FELTP)

Background: The daily COVID-19 report generated from the Chanjo-ke system indicated an upsurge of COVID-19 vaccine defaulters in Busia County. There had been no assessment of COVID-19 vaccine defaulters in Busia County. We sought to describe the socio-demographic and clinical characteristics of COVID-19 vaccine defaulters.

Methods: We conducted a cross-sectional study; data was abstracted retrospectively from the Chanjo-ke system from May to December 2021. We used a cased definition of anyone who has not completed the prescribed COVID-19 vaccine doses within the specified period. Sociodemographic and clinical information was measured and analysed for the cases. Data was analysed using Microsoft Excel. Continuous variables were summarized using central tendency and dispersion measures, whereas proportions and frequencies were used for categorical variables. We performed Data Quality Audit (DQA) using a standardized Centre for Disease Control (CDC) tool, cleaned the data, and corded it in MS Excel.

Results: We reviewed 1298 defaulter cases, with the mean age 43.6 ±15.3 years. Males were 742 (57.2%), Busia County residents 1113 (86%) and 549 (42.3%) reportedly permanently employed. Cases who reportedly received 1st doses within Matayos Sub-County were 795 (61.25%), those presenting with Co-morbidity 70 (5.4%), and those having Adverse Effects Following Immunization (AEFI) were 28 (2.2%). December had 413 (32%) defaulters. After the assessment, those confirmed not having received 2nd doses were 814 (63%) while those fully vaccinated but 2nd dose data not updated to the Chanjo-ke system were 484 (37%). The DQA showed that 9/11(82%) variables met the lower data quality threshold.

Conclusion: We found out that most clients had not received their 2nd vaccine doses, however, some received but their vaccination status was not updated in the chanjo-ke system. We recommend repeat training for Chanjo-ke system data entry clerks.

Keywords: Morbidity, COVID-19 vaccine, Cross-sectional study, retrospectively, Data Quality, software

Abstract 084

Title: Assessment of the Quality of Alcohol-Based Hand Sanitizers, Pre and Peri - COVID-19 Pandemic Outbreak in Kenya

Authors: Samuel O Wafula (Kenya Medical Research Institute)*; Florence Ng'onga (Jomo Kenyatta University of Agriculture and Technology); James Kimotho (Kenya Medical Research Institute)

Background: In the wake of the Coronavirus disease 2019 (COVID-19) pandemic, the World Health Organization recommended the use of alcohol-based hand sanitizers (ABHRs) to curb transmission of the disease. This led to an upsurge in their production and use that posed a danger of production and use of poor-quality ABHRs as well as increased availability of counterfeit products. This study assessed the quality of alcohol-based hand sanitizers in the Kenyan market that were produced before and after outbreak of the COVID-19 pandemic.

Methods: Between March 2020 and August 2021, thirty-five ABHRs brands were collected from retail outlets, while Fifty-five unexpired ABHRs that had been collected and archived before March 2020 were retrieved, these constituted the pre and peri- COVID-19 samples respectively. Efficacy was tested using European Standard EN 1500:2013 protocol. Alcohol content was analyzed using Gas Chromatography. Visual inspection was done to assess compliance with labeling and packaging requirements as per Kenyan Standard EAS 789:2013.

Results: It was observed that 27.8% of the peri-pandemic sanitizers had less than 90% bactericidal reduction activity as compared to 12.5% manufactured pre-pandemic. None of the samples manufactured during the pandemic period had efficacy performance above 3 log reduction. Of the peri-pandemic ABHRs, only 25% met the EAS 789:2013 acceptable limit of over 60% alcohol content. Product adulteration was also detected with 20 % of the samples having methanol substitution. Only 5% complied with FDA approval of <0.063% v/v methanol content. Study found no correlation between the total alcohol content and the efficacy of ABHRs.

Conclusion: The study found significant variation in quality between pre- and peri- pandemic alcohol-based hand sanitizers with more substandard products reported in the peri-pandemic samples. This raises a concern about possible emergence of alcohol resistant strains of microorganisms. The study therefore recommends an adequate quality monitoring system to curb against substandard products.

Keywords: Coronavirus, COVID-19, Pandemic, Alcohol-based hand sanitizers, hand

Scientific Session 10: HEALTH SYSTEMS 1

Abstract 085

Title: INCORPORATING MHEALTH INTERVENTIONS INTO KENYA'S HEALTH INFRASTRUCTURE TO AUGMENT UNIVERSAL HEALTH COVERAGE, SERVICE DELIVERY IMPROVEMENT APPROACH

Authors: Oduor K Otieno (Stowelink)*; Stephen Ogweno (Stowelink)

Background: The National Institute of Health defines mHealth as the use of mobile and wireless devices to improve health outcomes, healthcare services, and health research. Globally, over 68% of the world's population owns mobile phones with Kenya alone having an estimated 80% mobile phone penetration.

The purpose of this study was to examine 1) the various forms of mHealth interventions that have been incorporated into Kenya's health infrastructure, 2) their effectiveness in improving health services delivery in Kenya, and 3) the barriers to the uptake of mHealth interventions.

Method: This review followed the Preferred Reporting Items for Systematic Reviews checklist. The search criterion was derived from the review's objectives and the search done on CINAHL and PubMed. To ensure the search was contextual, exhaustive terms including mHealth, text messaging, Kenya, and low-middle income countries were used. The initial search generated 41, 047 results. After filtering these studies by location (Kenya), time period (2010-2020), and relevance, the search yielded 29 citations which were included in the final review. The search strategy was not limited to any particular study design.

Results:

1. Forms of mHealth Interventions

Call centers, SMS, and Mobile Apps are the most common forms of implementing mHealth interventions in the country with SMS being used most predominantly. mHealth interventions in the form of mobile Apps are mostly found in cities where there is access to good internet connectivity and higher phone penetration while SMS and call centers generally are found in both cities and rural areas

2. Effectiveness of mHealth interventions in service delivery

A systematic review of peer-reviewed articles, policy briefs, and credible materials published on mHealth showed that mHealth has succeeded in the health infrastructure such as in collecting and transferring health and patient data, remote diagnosis, treatment, patient follow-up, behavior and cultural change and adaptation of new health-friendly behavior.

3. Challenges Facing mHealth Interventions

Some of the challenges identified in this review included long bureaucratic approval processes causing considerable timeline challenges, security concerns surrounding data safety, language barriers in the user interface, and interoperability challenges.

Conclusion and Recommendations

The review affirmed that there have been, indeed, a lot of mHealth interventions in Kenya. However, for mHealth interventions to be fully optimized in Kenya to augment UHC, the different forms of mHealth interventions must ensure efficiency which is a component of usability. Similarly, an effective regulatory framework must be developed to inform the implementation of mHealth solutions Governments should also develop an mHealth strategy and forge partnerships with NGOs implementing mHealth solutions. It is also important that the government focus on increasing investment in technology and infrastructure.

Keywords: mHealth, Universal Health Coverage, Low and Middle Income countries

Abstract 086

Title: Examining the Responsiveness of the National Health Insurance Fund (NHIF) to People Living with Hypertension and Diabetes in Kenya: A qualitative study

Authors: Robinson RO Oyando (KEMRI-Wellcome Trust Research Programme)*; Vincent Were (KEMRI-Wellcome Trust Research Programme); Ruth Willis (London School of Hygiene and Tropical Medicine); Hillary Koros (AMPATH); Jemima Kamano (AMPATH); Violet Naanyu (AMPATH); Anthony Etyang (KEMRI-Wellcome Trust Research Programme); Richard Mugo (AMPATH); Adriana Murphy (London School of Hygiene and Tropical Medicine); Ellen Nolte (London School of Hygiene and Tropical Medicine); Pablo Perel (London School of Hygiene and Tropical Medicine); Edwine Barasa (KEMRI Wellcome Trust)

Background: Non-communicable diseases (NCDs) account for 50% of hospitalisations among adults in Kenya. Pre-payment mechanisms such as health insurance have been considered to enable financial access and financial risk protection to healthcare services for NCDs. This study assessed the responsiveness of the National Health Insurance Fund (NHIF) Supa Cover benefit package to the needs of individuals with diabetes and hypertension in Kenya.

Methods: We carried out a qualitative study and collected data using key informant interviews (n = 39) and focus group discussions (n = 4) in two purposively selected counties in Western Kenya. Study participants were drawn from NHIF officials, county government officials, health facility managers, healthcare workers and individuals living with diabetes and hypertension who were enrolled in NHIF. We analysed data using thematic analysis.

Results: Healthcare workers and NCD patients reported that the NHIF Supa Cover benefit package expanded access to services for people living with NCDs. However, the NHIF members and healthcare workers had inadequate awareness of the NHIF service entitlements. Healthcare workers reported that the NHIF benefit package inadequately covered the range of services needed by people living with hypertension and diabetes and that the benefits package did not prioritise preventive and promotive services. NCD patients with NHIF also reported that they were sometimes discriminated against by healthcare providers who preferred cash-paying patients, and some NHIF-empanelled health facilities had inadequate structural inputs essential for quality of care. NCD patients were enrolled in NHIF felt that the NHIF premium for the general scheme was unaffordable, and NHIF members faced additional out-of-pocket costs because of administration charges, input supply shortages, balance billing, and payments for services not covered.

Conclusion: NHIF has reduced financial barriers for NCD patients. To enhance its responsiveness to the needs of people living with hypertension and diabetes, NHIF should include preventive and promotive services in the benefit package and strengthen its monitoring and accountability mechanisms for contracted providers.

Keywords: Non-communicable diseases, health system reforms, universal health coverage, Kenya

Abstract 087

Title: Experiences of Pilot Rollout of Web Laboratory Information Management System Remote Sample Login in Western Kenya

Authors: BEN ODHIAMBO OKOTH (KEMRI)*

Background: Timely clinical decision is crucial in management of all forms of TB. The conventional sample referral system has been a major reason for laps in sample reception and relaying of results from referral laboratories to clinicians in TB screening facilities. This affects timely clinical intervention for patient management. Here, we report a pilot study on an application called TB Remote Login system conducted at KEMRI- TB Reference Laboratory in selected routine TB facilities within Kisumu County. The main objective was to improve data quality, reduce turnaround time and empowering facilities to track their samples real time.

Methodology: A total of 10 facilities were assessed for feasibility for this study. Inclusion criteria for site selection were; facilities within Kisumu County, availability of TB laboratory personnel, desktop/laptop, printer and working internet connection as the system is web based. Nine facilities met inclusion criteria while one was excluded due to poor internet connection. The system was installed in the selected facilities. Four facilities were used as sample referral hubs where sputa samples would be pooled. Facility personnel were trained on sample login in the System, tracking samples, generating patient reports and viewing historical patient results. Kemri personnel/ system administrators provided emergency contacts to facilities for system support.

Results: 9 facilities,(100%) reported successful referral of samples using the system, and accessed patient results immediately testing was concluded at TB lab. Kisumu county hospital sent 2 samples, Ahero 2, Muhoroni 3 and Chulaimbo 3.Of the 10 samples, there was zero rejection compared to a 2-5% sample rejection experienced on samples received conventionally. Sample rejection criteria includes incorrectly filled forms, incomplete forms, insufficient sample volume, no request form accompanying a sample, missing sample and specimen-request form mismatch. There was high data quality as most parameters of the samples were captured at facility level. Sample reception time improved by approximately 90% as Kisian TB lab staff captured sample quality details and volumes.

Conclusion: The National TB Program/MOH should implement the Remote Login system in TB screening facilities to ensure improved TB Patient Management. The facilities should also be provided with robust internet access to support this system. The earlier practice of writing emails to Kisian TB Lab or sending text messages asking for results will be eliminated by this system. The only shortcoming of this system is it relies heavily on robust internet connection to work effectively. Facilities without internet access will therefore miss out on the benefits accrued from adoption of this system.

Keywords: web laboratory information remote system

Abstract 088

Title: The Experience of rolling out a Mobile Van for conducting Minimally Invasive Autopsy for Community Deaths as part of Child Health and Mortality Prevention Surveillance in Siaya, western Kenya

Authors: Peter N Onyango (KEMRI-CGHR)*; Richard Oliech (KEMRI-CGHR); Peter Onyango (KEMRI -CGHR); Humphrey KIzito (KEMRI-CGHR); Dickens Onyango (MOH); Richard Omore (KEMRI-CGHR); Victor Akelo (KEMRICGHR); Sammy Khagayi (KEMRI-CGHR)

Background: Credible, accurate and timely mortality data on leading causes of childhood mortality are crucial in guiding intervention strategies. Minimally Invasive tissue sampling (MITS) procedure, developed as an option to reduce uncertainty around cause of death determination in high mortality settings with unreliable data. The Child health and mortality prevention surveillance (CHAMPS) Kenya site introduced a new innovation where MITS is done in a mobile van within the community. The rationale for introduction of a mobile MITS van emanated from the challenges encountered in the process of enrolling community deaths.

Methods: We conducted a feasibility study on the acceptability of the mobile van and its community engagement. 3 pathologists were interviewed as key Informants and 5 FGDs with Chiefs, Assistant Chiefs, CHVs and Health-care workers were conducted in Kisumu and Siaya counties in western Kenya. A qualitative rapid assessment of preparedness to conduct MITS procedures in the mobile van was done. The van was then taken to the community before roll out to help get initial community responses and views regarding its planned use.

Results: The stakeholders who gave us their views on the rollout of the mobile MITS van in the community were in agreement that the mobile MITS van was a good idea given the reasons and challenges concerning the missed opportunities in regards to cases that were supposed to be recruited but were missed. The MITS procedure therefore does not need a morgue set up for it to be carried out. The KII and FGDs helped the study to measure Community acceptability of the Van

Conclusions: The MITs van has proven most helpful in conducting MITs within the shortest time possible and allow the family to proceed and bury eliminating the need of inconveniencing the family by taking the body to the mortuary

Keywords: CHAMPS

Abstract 089

Title: Relationship between caregivers engagement through a 2-way mHealth platform and depressive symptoms in Western Kenya.

Authors: Catherine A Otieno (KEMRI)*; Kirk Tickell (UW); Mary Masheti (KEMRI); Emily Yoshioka (University of Washington); Sean Galagan (University of Washington); Marline MMS Serede (Kemri); Maureen Okello (KEMRI); Emanuel Odhiambo (KEMRI); Lorine Odero (KEMRI); David Mukiria (KEMRI); Phlona Amam (KEMRI); Olieng'o Okoth Geoffrey (KEMRI); George Owuor (KEMRI); Danish Oyuga (KEMRI); Margaret Oluoch (KEMRI); Carolyne Onyango (KEMRI); Susan Oongo (KEMRI); Agnes Ndirangu (KEMRI); Julius Onyango Nyaoke (KEMRI/UNIVERSITY OF WASHINGTON); Agnes Ndirangu (KEMRI); Eric O. Ochola (KEMRI/ UNIVERSITY OF WASHINGTON); Benson Singa (KEMRI); Christine Mcgrathc@uw.edu (University of Washington)

Background: The association between depressive disorders among caregivers and their engagement with two-way SMS programs has not been adequately studied. We hypothesized that caregivers' mental health status may have an impact on the probability of engaging with mHealth text messaging systems.

Methodology: We analyzed data from participants enrolled in the intervention arm of the Mama Aweza trial. These were caregivers and their children who were aged 5 to 12 months attending routine appointments in maternal child health clinics assigned to receive weekly SMS with key health messages, and a request to measure their child's mid-upper arm circumference and return the measured value to the SMS platform. A linear regression model was used to determine whether there was a relationship between the caregivers' PHQ-9 depressive symptoms score at enrollment and their probability of responding to the SMS sent by the mHealth platform. The primary outcome of this secondary analysis was the caregiver's probability of responding to the SMS sent.

Results: Among 599 Caregivers engaged on the mHealth platform, 366 (61%) had no depressive symptoms, 216 (36%) had mild to moderate depression, 13 (2%) had severe depression and 4 (1%) had missing phq-9 scores. There was no significant relationship between phq-9 scores and responding to SMS texts, (OR 1.039, 99%CI (0.96 -1.12) p-value 0.302). However, sharing phones with a friend or partner was associated with a lower response rate to the mHealth platform. (b -0.0506698, p-value 0.02). Of the 229 caregivers that had depressive symptoms, 138 (60%) were aged $\geq$ 25 years, 91 (40%) were <25 years,181 (79%) were married, 13 (5%) were divorced, 37(16%) were never married, 153 (67%) were not living with HIV, 68 (30%) were living with HIV, 124 (54%) had up to primary education, 99 (43%) had up to secondary education and 7(3%) had post-secondary education.

Conclusion: Caregiver depression did not hinder them from engaging with a two-way SMS mHealth system. This suggests that some mHealth interventions may be helpful in reducing the inequalities in health care access associated with mental health challenges.

Keywords: Mental Health

Abstract 090

Title: The Impact of an Integrated Health System Approach in improving access to services for persons with Lymphoedema in Coastal Kenya

Authors: Stella Kepha (KEMRI)*; Wyckliff Omondi (Division of Vector Borne and Neglected Tropical Diseases); Lydiah Kibe (Kenya Medical Research Institute); Bridget Kimani (KEMRI); Vincent Were (KEMRI); Collins Okoyo (KEMRI); Sultani Hadley Matendechero (Public Health Institute (Kenya CDC)); Doris Njomo (KEMRI)

Background: Kenya has been conducting successful rounds of mass drug administration for lymphatic filariasis (LF) elimination since 2015. To be able to apply for certification of LF elimination, the World Health Organization requires countries to institute a Morbidity Management and Disability Prevention program for person with lymphoedema and hydrocele. While there has been progress made in hydrocele management very little has been done to manage lymphoedema due to LF. The current study sought to demonstrate the use of an integrated health systems approach, in improving access to morbidity management and disability prevention services for person with lymphoedema due to LF and provide the evidence needed for scaling activities for other endemic communities.

Method: We conducted a mixed methods study using an experimental design without control groups in two wards of Lunga Lunga sub-county, Kwale county. The study was divided in three phases: pre-intervention phase in which quantitative and qualitative data was collected to assess knowledge of utilization of lymphoedema management services, barriers and facilitators of access to the services; intervention phase, a lymphoedema management care package developed using participatory approaches followed by training of health care workers, patients and caregivers how to use the care package. In the post-intervention phase qualitative data was collected to assess perceptions of the impact of the intervention on patients' knowledge of utilization and access to lymphoedema management services.

Results: Results from the pre-intervention phase show that the patients faced challenges such as distance to health facilities, inability to work optimally, lack of finances to afford lymphoedema management commodities and stigma from the community. In the post-intervention phase the participants indicated that the lymphoedema management programme had improved the health of the enrolled patients The patients, their care givers and health care providers felt they were more informed about the LF disease and lymphoedema management. Most participants also reported that the involvement of community health volunteers (CHVs) in awareness creation, identification, referal and accompanying the patients to health facilities improved health-seeking behaviour thus increasing service utilization.

Conclusion: Training of health care providers, caregivers and patients using the developed intervention care package contributed to improved knowledge on cause and management of lymphoedema. The CHVs played a critical role in the identification and referral of patients, which contributed to improved health-care seeking behaviour and increased service utilization. Collaboration with the county health authorities contributed to improved quality of health care services provided for lymphoedema management

Keywords: Lymphatic filariasis, Lymphoedema management, Kwale

Abstract 091

Title: Strategies to Reduce Informal Payments at Public Health Facilities in Kenya: Patients and Health Workers Perspectives

Authors: Evelyn Kagure Kabia (KEMRI Wellcome Trust Research Programme)*; Dina Balabanova (London School of Hygiene and Tropical Medicine, London); Eleanor Hutchinson (London School of Hygiene and Tropical Medicine, London); Edwine Barasa (KEMRI Wellcome Trust)

Background: Informal payments are payments made by a patient to a provider in addition to the officially determined service fees. In 2019, 16.9% of Kenyans reported having paid a bribe to access health services at public health facilities. Patients pay informally to access services, receive drugs, get higher-quality care, and skip queues. Informal payments limit access to care, especially for vulnerable groups such as the poor, and expose individuals and households to financial hardship. Despite being a common phenomenon in many low and middle-income countries, there is limited evidence on measures to curb informal payments and their effectiveness. We examined strategies to reduce informal payments in Kenya from patients' and health workers' perspectives. Addressing informal payments is crucial in enhancing financial protection as Kenya progresses toward attaining universal health coverage by 2030.

Methods: We conducted a qualitative cross-sectional study in 2022 at four public health facilities (two hospitals and two health centers) in an urban county in Kenya. We conducted focus group discussions with patients (18 male and 20 female) seeking care at various departments at the study facilities and 17 in-depth interviews with health workers and non-clinical staff of various cadres (8 male and 9 female). We analyzed data using a framework approach.

Results: Some of the crosscutting strategies reported by patients and health workers were increasing and timely payment of health workers' salaries, ensuring adequate numbers of health workers, and availability of drugs and supplies. Other measures include the use of cashless payment systems, enhancing awareness of patients right to refuse to pay informally, enhanced internal and external supervision of health facilities, and taking disciplinary action against individuals found engaging in informal payment practices, with the latter reported as key in building trust and confidence in the health system. Some notable strategies reported by patients included digitizing queue management systems, enhancing public awareness of avenues to report demands for informal payments, and collective action by the public to decline engaging in informal payment practices. Key measures reported by providers included timely promotions, ensuring job security, adherence to working hours, and providing staff with incentives for engaging in the provision of extra/non-routine services.

Conclusion: Strategies to reduce informal payments are linked to addressing inadequacies within the health system. Most measures point to the need for increased government spending on health, especially to enable better remuneration of health workers and ensure adequacy of the health workforce and health commodities. Strengthening governance structures is also crucial, with routine monitoring of health facilities and availing effective patient feedback mechanisms being some of the potentially effective measures.

Keywords: Informal payments, patients, health workers, perspectives, Kenya

Scientific Session 11: NCDS

Abstract 092

Title: METABOLIC SYNDROME AND ITS ASSOCIATED FACTORS AMONG WOMEN USING HORMONAL CONTRACEPTIVES IN REFERRAL HOSPITAL, NEKEMTE, ETHIOPIA.

Authors: Endalo Asefa Guluma (Arba Minch Univesrity)*

Background: Metabolic syndrome is a health issue that is associated with several medical disorders, including hypertension, hyperglycemia, low HDL cholesterol, and central obesity. According to some research evidence, the hormonal contraceptive user has been linked to an increased risk of metabolic syndrome. Therefore, this study aimed to see how common metabolic syndrome and its associated characteristics were among contraceptive users at Nekemte Referral Hospital.

Methods: Facility-based cross-sectional study design that was conducted from March to April 2021 on 342 women who use hormonal contraceptives. The data were collected by questionnaires and laboratory tests. Bivariate and multivariable binary logistic regression analysis was used to investigate the factors associated with metabolic syndrome. The odds ratio with 95% CI was calculated as the measure of association and a p-value of less than 0.05 was considered statistically significant.

Result: The prevalence of metabolic syndrome was 22.8%. Triglycerides > 150 mg/dl (AOR = 4.77, 95% CI; 2.50-9.09), fasting blood sugar level >125mg/dl (AOR = 5.57, 95%CI; 2.13 – 14.56), duration of hormonal contraceptives use > 42months (AOR= 5.86, 95%CI; 1.87-18.39), consuming meat >4 times per week (AOR= 2.75, 95%CI; 1.02-7.38, not consuming vegetables (AOR= 2.09, 95%CI; 1.06-4.14) were factors significantly associated with metabolic syndrome.

Conclusion: Almost one out of four women who used hormonal contraceptives had metabolic syndrome. Factors that are associated with metabolic syndrome were having high triglycerides, high fasting blood sugar, using hormonal contraceptives more than three, having eaten meat four times a week, and people who do not use vegetables. We recommended that the health care system in the country should focus on setting strategies that help for the delivery of information on the concept of metabolic syndrome and get adequate education related to metabolic syndrome.

Keywords: Metabolic syndrome, reproductive-age women, hormonal family planning, Nekemte, Ethiopia

Abstract 093

Title: The Diagnostic Accuracy of Diabetes Retinopathy Screening by Ophthalmic Clinical Officers, Ophthalmic Nurses and County Ophthalmologists against a Retina Specialist in 2 Selected County Referral Hospitals, Kenya

Authors: Jane R Ong'ang'o (KEMRI)*; Olga Mashedi (KEMRI); Micheal Gichangi (Ministry of Health); Richard Kiplimo (KEMRI); Kennedy Alwenya (Fred Hollows Foundation, Kenya)

Background: Diabetes is rapidly becoming a major cause of blindness among Kenyans, with the prevalence of any form of diabetes retinopathy (DR) ranging from 36% to 41%. Globally DR is currently the leading cause of vision loss in working age adults. In Kenya, specialized examinations are only available at national and some county referral hospitals through retina specialists, ophthalmologists or trained technicians. This has resulted in low coverage of retinal assessment and inadequate access to this service. An innovative service run by ophthalmic nurses (ONs), ophthalmic clinical officers (OCOs) and county ophthalmologists was established since 2018.

Study Objectives: The purpose of this study was to investigate the diagnostic accuracy of DR screening by ONs, OCOs and county ophthalmologist against that of a retina specialist measured by sensitivity and specificity as the primary outcomes.

Methods: Cross sectional study conducted at two referral hospitals in Kenya. Patients with diabetes underwent a complete ophthalmic examination and graded for DR using the Early Treatment Diabetic Retinopathy Study (ETDRS) classification system. All photos taken by the first grader (ON and OCO) were later assessed by the county hospital ophthalmologist who was blinded to the reading of the first grader. The third grader (retina specialist) similarly was blinded to the readings of the first and second graders and assessed all the images from the 2 hospitals also using ETDRS

Results: A total of 308 patients with diabetes (median age 58 IQR 56-60, 53% female) were enrolled in the study. Sensitivity to identify any DR was acceptable (81.3%, 80.6%, and 81.54% for the OCO, ON and county ophthalmologist respectively). The corresponding specificities were 92.7%, 92.8% and 92.59%. Analysis of diagnostic accuracy of non-sight threatening DR against sight threatening DR revealed lower sensitivity for the three cadre groups although specificity remained high.

Conclusions and Recommendations: Despite fewer years of training and skills levels, ON and OCO can perform screening with sufficiently high level of specificity. However, the sensitivity to detect sight threatening DR was generally low by all the cadres which may leave severe forms of DR undetected. Re-training of all the cadres in detection of specific stages of DR is warranted.

Keywords: Diabetes Retinopathy, sensitivity, specificity, ophthalmic nurse, ophthalmic clinical officer, county ophthamologist

Abstract 094

Title: FACTORS ASSOCIATED WITH ORAL HEALTHCARE UTILIZATION AMONG PREGNANT WOMEN ATTENDING ANTENATAL CARE CLINICS IN KIAMBU LEVEL V HOSPITAL, KIAMBU COUNTY, KENYA

Authors: Salome W Kinyita (Smile Art)*

Background: Oral health care in pregnancy is crucial for the health of the mother and the unborn child. Pregnancy is associated with hormonal and behavioural changes that lead to dental problems, including gingivitis, periodontitis, and dental caries. Untreated oral diseases can lead to poor pregnancy outcomes and poor pregnancy-related quality of life. A regular dental check-up is recommended during pregnancy.

This study's main objective was to determine the factors associated with oral healthcare utilization among pregnant women at Kiambu level v hospital.

Methodology: This was a cross-sectional study design targeting 308 pregnant women attending antenatal care clinics. Participants were selected through systematic random sampling, and data was collected through a structured questionnaire. Data collected was on the utilization of oral health services during pregnancy and factors affecting the utilization. Binary logistic regression was used to analyze data.

Results: The study response rate was 99.3%. The age distribution of the pregnant women ranged between 18 and 45 years. Only 7.84% of the pregnant women had seen a dentist in their current pregnancy. The two key reasons for such a visit were routine check-ups and bleeding gums. Among patient-related factors, only education (p=0.008) had a statistically significant association with oral health care utilization. Among the health system-related factors, only access to oral health counselling (p = 0.010) was statistically significantly associated with oral health care utilization. None of the sociocultural factors was found to be statistically significant.

Conclusion: The undermentioned conclusions were made on the basis of this study's findings: (a) Very few pregnant women attending Kiambu level 4 hospital antenatal care clinics utilized oral health care; (b) There was a significant association between access to antenatal oral health counselling and oral health utilization; (c) There was a significant association between the women's level of education and oral healthcare usage. Higher utilization was observed among those with a secondary level of education.

Recommendation:

1). There is a need to incorporate oral health promotion as part of Focused Antenatal Care (FANC) through a collaboration of all the stakeholders. This initiative will lead to better pregnancy and maternal outcomes, promoting economic development due to increased productivity by women of reproductive age. 2). The study was conducted during the Covid-19 Pandemic, a follow-up study to show if there will be any significant difference in numbers utilizing oral health care in pregnancy post-Covid is recommended. 3). A larger sample size study and an additional qualitative method like focus group discussion are highly recommended.

Keywords: Oral health, oral health care utilization , Pregnant women, Pregnancy outcome

Abstract 095

Title: Adaptive immune receptor features related to breast cancer in Kenyan patients: High immunoglobulin gene expression and BC-resident gamma-delta T-cells

Authors: Kennedy Mwangi (Mount Kenya University)*; Francis Makokha (Mount Kenya University); Moses Kamita (Mount Kenya University); Jacqueline Waweru (ICIPE); Shahin Sayed (Aga Khan University Hospital); Jonine Figueroa (The University of Edinburgh); Stefan Ambs (National Cancer Institute, National Institutes of Health); Konrad Cios (Morsani College of Medicine); George Blanck (Morsani College of Medicine)

Abstract: The adaptive immune response recognize and clear foreign cells in the body. The infiltration of the immune cells in the breast cancer (BC) tumor enables prediction and prognosis during the course of the disease. Therefore, additional characterization of the BC immune response may provide information for a point of intervention, such as application of immunotherapeutic treatments. In this case study, we sought to recover and characterize the adaptive immune receptor (IRs) recombination reads from genomics files representing 44 Kenyan patients, to better understand the immune response specifically related to those patients. The patients who consented for the inclusion of their breast tumor and non-tumor tissue in the genetic analysis had malignant breast cancer and were undergoing surgery. We used a previously scripted algorithm to obtain productive IR recombination reads from cancer and adjacent normal tissue samples representing 22 Kenyan BC patients. From both the RNAseq and exome (WXS) files, there were significantly more T-cell receptor (TCR) recombination reads recovered from tumor samples compared to marginal tissue samples. Also, the immunoglobulin (IG) genes were expressed at a much higher level than the TCR genes (p-value = 0.0183) in the tumor samples. In addition, certain physicochemical features of the IG CDR3s were associated with the tumor samples. For Kenyan patients, a high level of IG expression, representing specific CDR3 chemistries, was associated with BC compared to the expression of other adaptive immune receptor genes. These results lay the foundation for studies that could support immunotherapeutic interventions for Kenyan BC patients.

Keywords: RNAseq, exome, Kenya, adaptive immune receptor recombinations, breast cancer, gamma-delta cells

Abstract 096

Title: ASSOCIATION BETWEEN MATERNAL PERIODONTAL DISEASE AND PRETERM BIRTH AMONG WOMEN IN KISUMU COUNTY, KENYA

Authors: Linus Dr Ndegwa (KEMRI)*; Veronica Wangari (University of Nairobi)

Background: Preterm birth (PTB), defined as birth before the gestational age of 37 completed weeks, is the most frequent cause of neonatal death and the second leading cause of under-five mortality worldwide. According to the WHO 2010 report, it was estimated that of the 135 million live births globally that occurred in that year, about 15 million babies were born preterm, representing a preterm birth rate of 11.1%. Periodontal disease is a chronic, low-grade, gram negative bacterial infection of the periodontal tissues. Periodontal pathogens or by-products may reach the placenta and spread to the foetal circulation and amniotic fluid. Their presence in the foeto-placental compartment can stimulate a foetal immune/inflammatory response characterized by the production of IgM antibodies against the pathogens and the secretion of elevated levels of inflammatory mediators, which in turn may cause miscarriage or premature birth. Based on reported studies, periodontitis is associated with PTB. Furthermore, some studies have shown that successful routine periodontal treatment is associated with a decreased incidence of spontaneous preterm birth. The objective of this study was to evaluate the association between periodontal status in pregnancy and preterm birth.

Methods: A longitudinal study design was conducted at Kisumu County Hospital. Pregnant women of between 18-49 years of age were recruited at an estimated 22-24 weeks of gestational age. Confirmation of gestational dating was done via ultrasound. At baseline recruitment, an oral exam was performed. Follow-up was conducted at delivery with a subsequent oral exam. Known risk factors like smoking, alcohol, drug consumption and socio-economic status were recorded.

Results: A total of 429 pregnant women were recruited into the study. Those followed up with postpartum information were 342 (80.3%). The median age was 25 years. Over three-quarters of study participants had no or mild periodontitis, both antepartum (79.4%) and postpartum (80.4%). The median gestational age at birth was 38 weeks (Interquartile range (IQR): 38 – 39 weeks) and ranged from 29 to 43 weeks. Using a cut-off of 37 weeks, 44 (13.0%) were preterm, and 294 (87.9%) were term deliveries.

Conclusion: Data show an association between the presence of periodontitis at 22-24 week gestation and subsequent preterm birth. The maternal age group of the participants showed a decreased likelihood of the presentation of mild or severe periodontitis. Preterm birth in this population remains a threat, and more interventions must be implemented to prevent such outcomes. The findings highlight the need to strengthen collaboration between the antenatal and dental departments to improve the uptake of oral health check-ups before and during pregnancy.

Keywords: Periodontitis, Preterm birth

Abstract 097

Title: Complications among Hypertensive cases, Kitui County Referral Hospital, January 2019- March 2022.

Authors: Diana Rose W Mwaura (FELTP)*; Caren Ndeta (FELTP); Juliet Akoth (Ministry of Heath- Kitui County); Vincent Ithuku (Ministry of Health- Kitui County); Maria Thuita (FELTP)

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Background: Hypertension is the leading cause of cardiovascular disease and premature deaths worldwide but its control remains a major challenge. Sub-optimal BP control leads to microvascular and macrovascular complications. There is limited data on complications associated with hypertension in Kitui County. We sought to evaluate the prevalence of hypertension-related complications and demonstrate their association with sociodemographic and clinical characteristics in patients admitted to KCRH medical wards.

Methods: We conducted a retrospective records review of the inpatient registers and files from January 2019 - March 2022 to retrieve socio-demographic and clinical information of hypertensive patients admitted to the medical wards at KCRH. We used a case definition of any person admitted with a file diagnosis of known or newly diagnosed hypertension. Data were abstracted into an MS Excel database and exported into Epi info for analysis. We calculated proportions and frequencies for categorical variables, central tendency, and dispersion measures for continuous variables. The prevalence odds ratio was used to measure the strength of the association between variables and a p-value of <0.05 was considered statistically significant.

Results: We obtained 533 records. The mean age was 63(±18) years, 285 (53%) were females, 209(39.2%) resided in Kitui Central sub-county and 447 (84%) were unemployed. One hundred and fifty-four (29%) took tobacco and 170 (32%) took alcohol, among them 117(76%) and 130(76%) respectively had a complication. Three hundred and fifty-one (66%) had a systolic blood pressure of >130mmHg while 300 (56%) had a diastolic blood pressure of >80mmHg. The cases with underlying diabetes mellitus were 120 (22%). Those who had a macrovascular and/or a microvascular complication were 382 (72%) with stroke 198(51.8%) being the most common. The odds of developing a complication in men were higher (OR 2.14, 95% CI 1.44-3.17) compared to women and in those aged 65 and above (OR- 1.67 CI-1.44-2.44) and lower in those with diabetes mellitus (OR- 0.25 CI 0.17-0.38).

Conclusion: More than half of the patients admitted had a complication. We recommend public health messaging targeting those aged 65 and above, males, and those who smoke and take alcohol on the importance of regular screening. Future studies should include additional patient behavioural characteristics, health care workers, and health care system characteristics to better understand more factors associated with complications to be used for targeted and tailored interventions.

Keywords: Cardiovascular diseases, Public health, Hypertension, Retrospective studies

Abstract 098

Title: Association between nutrition knowledge and practise and cardiovascular disease risk factors among community members in Vihiga County

Authors: Doreen Mitaru (KEMRI)*; Lydia Kaduka (KEMRI); MIRIAM BOSIRE (KEMRI); Melvine Obuya (KEMRI); Schiller Mbuka (KEMRI); Joseph Mutai (KEMRI); Erastus Muniu (KEMRI); Esther A Shiraho (Kenya Medical Research Institute); Rodgers Ochieng (KEMRI)

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Background: Non-communicable diseases (NCDs) are currently responsible for 74% of deaths globally, 86% occurring in low-and middle income countries. Cardiovascular diseases (CVDs) account for a majority of NCD related deaths (14% in Kenya), yet, knowledge about CVDs and their risk factors remains low in a majority of the population. Knowledge in nutrition and practise is a key factor in preventing CVDs. This study sought to determine the association between nutrition knowledge and practice and occurrence of CVD risk factors among community members in Vihiga County

Methods: This was a mixed method feasibility study. Data on socio-demographic factors and nutrition knowledge, practise and CVD risk factors knowledge were collected using semi-structured questionnaires, In depth Interviews and Focus Group Discussions. Quantitative data was analyzed using SPSS version 22.0. Data treatment incorporated calculation of frequencies, mean, percentages of nutrition knowledge and dietary scores. Chi square test were used to assess relationships between nutrition knowledge and practise and socio-demographics. Qualitative data were processed and analyzed using the framework method.

Results: Of the 2224 respondents: 65.1% were within the prime working age 25-50 (M-28.9%; F-71.1%). The overall score for nutrition knowledge and practise was found to be significant with age, wealth index and education level ($p<0.05$). A majority of the participants had general knowledge about CVD risk factors. Lack of physical activity, and poor dietary habits were the 2 most cited potential risk factors, while consuming a diet with insufficient fruits and vegetables, and high salt intake were the least cited risk factors.

Conclusion: Knowledge of risk factor did not correlate with good dietary practices and nutrition knowledge. The observed gap between knowledge and practice call for further research to understand drivers of behaviour and practice to inform tailored interventions.

Keywords: NCDs, Cardiovascular Diseases

Scientific Session 12: VECTOR BIOLOGY 2

Abstract 099

Title: Whole transcriptomic gene profile of Anopheles arabiensis resistant to pyrethroid and organophosphate from western Kenya reveals overexpression of salivary gland and cuticular proteins

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Background: Effective vector control is key to malaria prevention. However, this is now compromised by increased insecticide resistance in malaria vectors due to continued reliance on insecticide-based control interventions, thus posing a global challenge. In Kenya, resistance to pyrethroids and organophosphates has been shown to occur at varying levels in Anopheles arabiensis which is one of the major malaria vectors. We investigated the gene expression profiles of insecticide resistant An. arabiensis populations from Migori and Siaya counties in Western Kenya using RNA-Seq.

Methods: CDC bottle assays were conducted using deltamethrin (DELTA), alphacypermethrin (ACYP) and pirimiphos-methyl (PMM) to determine the resistance status in both sites. RNA-Seq analysis was done on pools of mosquitoes which were resistant or non-exposed, alongside the susceptible An. arabiensis Dongola strain.

Results: Gene expression profiles of mosquitoes from Migori resistant to DELTA (average mortality of 91%), ACYP (92%), and PMM (58%); and mosquitoes from Siaya resistant to DELTA (85%), ACYP (86%), and PMM (30%), showed overexpression of mainly salivary gland proteins belonging to both the short and long form D7 genes, and cuticular proteins (including CPR9, CPR10, CPR15, CPR16). Additionally, the overexpression of detoxification genes including cytochrome P450s (CYP9M1, CYP325H1, CYP4C27, CYP9L1 and CYP307A1), 2 carboxylesterases and a glutathione-s-transferase (GSTE4) were also found to be shared between DELTA, ACYP, and PMM survivors, reflecting their association with both pyrethroid and organophosphate resistance.

Conclusion: This study provides preliminary results of the molecular basis of resistance in An. arabiensis in Western Kenya, further adding to the evidence base that suggests that salivary gland proteins and cuticular proteins may play an important role in conferring resistance across insecticide classes.

Keywords: Insecticide resistance, malaria, Anopheles arabiensis, RNAseq, whole transcriptomic sequencing

Abstract 100

Title: Plausibility of skin bacteria as a source of attractive olfactory ecology for Anopheles mosquitoes

Authors: David M Mburu (Pwani University Biosciences Research Cetre)*

Plausibility of skin bacteria as a source of attractive olfactory ecology for Anopheles mosquitoes

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Background: Malaria is a mosquito borne disease caused by parasitic Plasmodium spp which is debilitating African population particularly in sub-Saharan Africa. Transmission of the parasitic disease is through piercing and sucking of blood from human hosts by parasite infected female Anopheles mosquitoes. Volatile olfactory cues from microbiome in foot mediate attraction of the Anopheline to human hosts for contacts. Some of the olfactory cues may be used in mosquito-mass trapping, but the presence of skin bacterial flora as a plausible source of the odour plume remains unclear.

Methods: The hypothesis underlying the study was that the presence of differential bacteria species could play a synergistic role in odour plume emission from human niche between the toes important in attracting mosquitoes. Thus, the presence of bacteria between the toes in human feet were investigated. Six student volunteers from Pwani University were consented and given pairs of black cotton socks that they wore for 24 hrs on left and right foot and this replicated three times per participants. From these pairs of socks differential attraction experiments of female Anopheles towards these socks were done using a modified olfactometer. Additionally, pure cultures of bacteria in the socks were isolated on nutrient agar. The bacteria were identified through microscopy and Gram staining.

Results and conclusion: gram positive coccus, gram positive Streptococcus, gram positive Staphylococcus and both gram positive and negative Bacillus bacterial phenotypes were present in the sock parts worn from the toes of the participants which were all absent in controls. The results suggest plausibility of volatile cues from the varying bacterial flora phenotype in attraction of female Anopheles mosquitoes among the different participants. These may explain preference of blood-meals by mosquitoes for different humans.

Key word: Anopheles mosquitoes, Bacteria, olfaction, odour plume, mass-trapping

Abstract 101

Title: THE EFFECT OF HIGH AND LOW LARVAL GROWTH TEMPERATURE ON MICROSPORIDIA MB in Anopheles gambiae sl.,

Authors: OTIENO GABRIEL FIDEL (INTERNATIONAL CENTER OF INSECT PHYSIOLOGY AND ECOLOGY)*

Microsporidia MB is a vertically transmitted endosymbiont of Anopheles mosquitoes. It has been shown to interfere with the development of Plasmodium in the insect vector and therefore is a good candidate for symbiont-based malaria control strategies. To successfully deploy the symbiont as a control tool, there is a need to efficiently spread the symbiont through the insect populations and maintain a high prevalence of the infection. Abiotic factors such as temperature are known to affect the vector host and thus may have a direct/ indirect effect on the symbiont as well. Knowing how abiotic factors affect Microsporidia MB could be instrumental in determining regions that are likely to maintain higher levels of Microsporidia MB and therefore be more suitable for Microsporidia MB-based malaria control. In addition, it will be important to establish what temperature is more suitable for rearing Microsporidia MB-infected mosquitoes for experimentation. Our study is aimed at determining the effect of different constant larval rearing temperatures on the survival, development time and Microsporidia MB prevalence, and Microsporidia MB density in An arabiensis. At the L1 larval stage, F1 larvae from Microsporidia MB+ iso female lines were split into four groups and reared in incubators set at constant temperatures of 220C, 270C, 320C, and 370C until pupation. Microsporidia MB density was highest in larvae reared at 220C; however, the prevalence of infection was highest at 270C. Microsporidia density was determined through relative qPCR analysis of the 18s MB gene in correspondence to the s7 host gene. The prevalence of microsporidia MB infection was determined through total counts of all the positive infections at each treatment temperature. These suggest that Microsporidia MB growth is compromised at higher temperatures, temperature 270C confers the best growth for the development of Microsporidia infected mosquito colony. Lastly, tropical areas experiencing 270C temperatures are good for Microsporidia field experimentation.

Keywords: Microsporidia MB

Abstract 102

Title: Vectors of malaria An. arabiensis and An. funestus sampled in Kisumu and Siaya, Kenya, show resistance to permethrin and other insecticides

Authors: Richard O Ochieng (USAMRD-AK)*; Gladys Kerich (USAMRD-AK); Stephanie Cinkovich (WRAIR); Jaree Johnson (WRAIR); Janet Ambale (USAMRD-AK); David Oullo (USAMRD-AK); Eunice Achieng (USAMRD-AK); Francis Ngere (USAMRD-AK); Charles Waga (USAMRD-AK); David Abuom (USAMRD-AK); Nicholas Odemba (USAMRD-AK); Santos J Yalwala (KEMRI/ USAMRD-AK); Eric Garges (USAMRD-AK); Elly Ojwang (USAMRD-AK); Fredrick Eyase (US Army Medical Research Directorate-Africa)

Malaria remains the top public health threat in select regions of Kenya including the Lake basin Counties of Kisumu and Siaya. Children under the age of 5 years bear the larger part of the malaria burden owing to their yet to develop immunity against the disease. An. arabiensis a member of the An.gambiae s.l complex and An.funestus are two major vectors of malaria in Kisumu and Siaya, respectively. Although effective drugs are available, and hopes of a vaccine coming to the market are high, vector control using insecticides including ITNs has been an effective first-line intervention. However, insecticide resistance by these malaria vectors threaten to derail malaria control efforts.

Methods: Mosquito immatures of Anopheles arabiensis were collected from larval habitats around rice paddies in Ahero while female blood-fed and gravid Anopheles funestus were collected from Siaya through aspiration techniques. An.arabiensis immatures and An. funestus adults were transported to the KEMRI-CGHR Walter Reed insectary where the immatures were reared to adults, at the same time blood-fed/gravid adults given laying tray pads to oviposit eggs that were allowed to hatched and emerged larvae reared to adults according to standard mosquito rearing procedures. Standard WHO tube bioassays were conducted on the emerging 3–5-day old adults to detect phenotypic insecticide resistance. The mosquitoes were subjected to public-health-employed pyrethroids, carbamates, organophosphates and an organochloride.

Results: The An.arabiensis from Ahero in Kisumu, showed the following average mortality results; Permethrin-46.9%, Deltamethrin-30.9%, Alpha-cypermethrin-23%, Lambdacyhalothrin-28.7%, Malathion-100%, P-methyl-35.7%, Dieldrin-100%, DDT-94%, Propoxur-83%, Bendiocarb-100%. On the other hand, An. funestus showed the following average mortality results; Permethrin-65.9%, Deltamethrin-45%, P-methyl-100%, Dieldrin-100%, Propoxur-86.7%, Malathion-100%, DDT-96%, Bendiocarb-100%.

Discussion: High levels of resistance against all pyrethroids by the two vectors of malaria is worrisome, as pyrethroids are the most preferred class of Insecticides due to low toxicity levels. This data provides alternatives for vector control in these areas as the two malaria vectors are susceptible to some of the tested insecticides.

Conclusion: More data from other areas within the lake basin region and with the other Anopheles species will give a full picture of the nature of insecticide resistance (IR) and thus help with policy formulation for control.

Keywords: Malaria, Insecticide resistance, Anopheles arabiensis and Anopheles funestus

Abstract 103

Title: Environmental factors modulate symbiont-host dynamics: Microsporidia MB in Anopheles arabiensis, at the Ahero Irrigation Scheme, Kenya

Authors: Joseph N Gichuhi (icipe)*; Syeda Tullu Bukhari (International Center of Insect Ecology and Physiology); Oscar Mbare (International Centre of Insect Physiology and Ecology); Jeremy Herren (icipe)

Background: In the rice-growing Ahero Irrigation Scheme in western Kenya, the tropical warm and humid climate as well as massive irrigation water bodies provide an ideal breeding ground for malaria-transmitting mosquitoes. It was against this backdrop that a <i>Plasmodium</i> transmission-blocking endosymbiont, <i>Microsporidia MB</i> was recently discovered in the <i>Anopheles arabiensis</i> mosquito species. This study aimed at understanding the environmental factors at the Scheme that influence the relatively high prevalence of <i>An. arabiensis</i> with the symbiont in the region.

Method: We conducted a correlational analysis using data recorded by an on-site weather station against the prevalence of the symbiont as well as on mosquito catches during a consistent sampling period of 14 months.

Result: The relative humidity and rainfall in the sampling zone were found to have a significant positive correlation with <i>Microsporidia MB</i> prevalence, whereas the ambient air temperatures had a negative correlation with the same. In addition, the average numbers of <i>An. arabiensis</i> mosquitoes collected in each house were not influenced by the ambient air temperatures but were negatively affected by increases in rainfall and relative humidity. The proportion of caught mosquitoes that oviposited increased with rises in relative humidity and reducing ambient air temperatures but did not respond to changes in rainfall. All correlations recorded were subtle and indicate an interplay of multiple environmental factors influencing the host-symbiont interactions.

Conclusion: These findings provide insights relevant to the optimization of conditions and strategies for proliferating <i>Microsporidia MB</i> in mosquito populations.

Keywords: environment, Microsporidia MB, malaria

Abstract 104

Title: Community engagement to understand the challenges and opportunities for a Microsporidia MB-based vector control strategy.

Authors: Syeda Tullu Bukhari (International Center of Insect Ecology and Physiology)*; Oscar Mbare (International Centre of Insect Physiology and Ecology); Joseph N Gichuhi (icipe); Jeremy Herren (International Center of Insect Ecology and Physiology)

Introduction: Microsporidia MB is a naturally occurring symbiont in Anopheles arabiensis that inhibits the development of Plasmodium without causing any fitness consequences. These characteristics provide Microsporidia MB advantage over other transmission blocking strategies such as sterile insect techniques and genetically modified mosquitoes.

Method: Currently, experimentation with Microsporidia MB relies on field collected infected females and their progeny which makes interaction with community in the field sites inevitable. This together with mapping and enumeration exercise aimed at understanding the correlation between ecological factors and Microsporidia MB prevalence over time provided an opportunity for rapid assessment of public health concerns, awareness to malaria, malaria control practices and attitude towards novel control methods in local communities of Ahero, western Kenya. The rapid assessment was not formative, but enabled us to establish a digital data collection, management, and storage system. To carry out the rapid assessment, we conducted an enumeration and mapping exercise through administration of an enumeration and mapping tool with both structured and semi structured questions. This tool was administered by a total of 40 community health volunteers to 3582 household representatives from 20 villages of Kakola location and also to 3695 household representatives from 22 villages of Ombeyi location in Kisumu County.

Result: This rapid assessment indicated that malaria is recognized as an important issue in communities in Ahero and that there is a high level of support for novel malaria control tools if concerns are addressed well.

Conclusion: This information will be used to design formative research involving “naïve” communities and national stakeholders. The result of this as well as follow up work will be imperative for conducting field trials.

Keywords: Microsporidia Symbiont Malaria

Abstract 105

Title: Isolation of tick-borne viruses in ticks collected from domestic animals in selected Counties Kenya

Authors: Hellen Koka1, Joel Lutomiah1, Solomon Langat1, Francis Mulwa1, James Mutisya1, Samuel Owaka1, Faith Cherop2, Millicent Sifuna1, Gilbert Rotich2, Edith Chepkorir1, Samuel Oyola3, Samson Limbaso1, Juliette R. Ongus4, Rosemary Sang2

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Background: Tick-borne viral infections are mainly asymptomatic or cause a mild transient fever with malaise and myalgia or a rash. However, severe viral infections result in hemorrhage, meningitis, encephalitis, paralysis or death. Humans get infected through the bite of an infected tick, or on contact with contaminated fluids. Entomological surveillance is a critical component that can be used to avert outbreaks of vector-borne diseases. The main objective of the study, was to understand the diversity of tick-borne viruses in ticks and the risk they pose to humans in pastoralist communities.

Methods: Ticks were collected from different animal hosts in six Counties: Isiolo, Baringo, Turkana, Marsabit, West Pokot and Kwale. All the ticks collected from a particular animal per site were stored in cryogenic tubes and preserved in a liquid nitrogen shipper, transported to the laboratory and stored in an ultra low temperature freezer until processed. The ticks were identified, pooled (1-8) and homogenized; the homogenate was centrifuged. The tick supernatant obtained were inoculated in Vero cells and those that showed virus cytopathic effect (CPE) were harvested. The virus isolates obtained were sequenced and phylogenetic analysis was performed.

Results: A total of 15773 ticks were collected, identified and pooled to 2259 tick pools. A majority of the ticks tested were from Turkana 35.6% (n=806), Isiolo 18.1% (n=409), Baringo 17.8% (n=403), Marsabit (n=253), Kwale 10.2 % (n=232) and Kacheliba 6.9% (n=156) respectively. Most of the ticks were collected from Camel (32.98%), Cattle (26.6%), Sheep (22.3%) and Goat (17.9%) respectively. Fourteen virus isolates were obtained. Ten (10) from Isiolo County, two (2) each from Baringo and Kwale County. Thogoto virus and a virus closely related to Guertu virus from ticks collected in Isiolo County were identified by Whole Genome Sequencing, the rest of the samples will be sequenced.

Conclusion: We report the isolation of a virus closely related to Guertu virus and Severe Fever thrombocytopenia virus (Bandavirus) from a tick collected in Isiolo County. This novel-tick-borne virus like other emerging life threatening Bunyaviruses may pose a risk to public health in Isiolo County. In addition, Thogoto virus, that has been reported before in Kenya was also isolated. This study provides more data on the viruses endemic in pastoral communities that will inform the choice of appropriate control measures in the event of outbreaks.

Keywords: Tick-borne viruses

Abstract 106

Title: Natural sugar feeding rates of Anopheles mosquitoes collected by different methods in western kenya

Authors: Seline Omondi (Kenya Medical Research Institute)*; Jackline Jeruto Kosgei (KEMRI); Silas Agumba (KEMRI); Brian Polo (KEMRI); Nick Yallah (KEMRI); VINCENT MOSHI (PTBiKenya); Bernard Abong'o (KEMRI); Maurice Ombok (KEMRI); Daniel McDermott (LSTM); Julian Entwistle (IVCC); Aaron Samuels (CDC); Feiko Ter Kuile (LSTM); John Gimnig (CDC); Eric O Ochomo (Kenya Medical Research institute)

Background: Attractive targeted sugar baits (ATSBs) are a potential vector control tool that exploits the sugar-feeding behaviour of mosquitoes. We evaluated the sugar-feeding behaviour of Anopheles mosquitoes as part of baseline studies for cluster randomised controlled trial to evaluate the impact of ATSBs on malaria transmission.

Methods: Anopheles mosquitoes were collected from two villages in Siaya County in western Kenya. Three trapping methods were compared, UV light traps placed indoors, outdoors within 10 meters from the structure, and outdoors 10 meters from the compound, prokopack aspirations (conducted indoors and outdoors), and malaise traps (set outside the compound). Individual mosquitoes were subjected to the cold anthrone test to assess the presence of sugar.

Results: Overall, 15.7% of collected mosquitoes had fed on natural sugar sources. By species and sex, the proportion sugar-fed was 41.3% and 27.7% in male and female Anopheles funestus, 27.2% and 12.8% in male and female An. arabiensis, and 9.7% and 8.3% in male and female An. coustani, respectively. Sugar-feeding was higher in unfed than blood-fed mosquitoes and higher in male than gravid mosquitoes.

Conclusion: Anopheles mosquitoes obtained sugar meals from natural sources during all physiological stages, whether they rest indoors or outdoors. These findings offer a potential avenue to exploit for the control of mosquitoes, particularly with the advent of ATSBs, which have been shown to reduce mosquito densities in other regions.

Keywords: Entomology

Scientific Session 13: Sexual Reproductive Health-1

Abstract 107

Title: HYBRID RDT FOR DIAGONISING GONORRHOEA AND SYPHILLIS

Authors: Mathenge julius mutiso (N.A)*

Background of study Rapid Diagnostic Test (RDT) is the fastest method in diagnosing diseases which aids in medications. Some diseases tend to have similar. Sexually transmitted infections (STIs) are one of the major health care problems worldwide, especially in resource-poor settings.

Like most STIs, HIV and syphilis are often asymptomatic, which makes sensitive diagnostic testing particularly crucial for early detection and diagnosis, and for guidance of treatment and prevention of onward transmission.

Problem Statement – hybrid RDTmentioned leads to efficient testing just when patient has a co-infection of the two bacterias involved.

global burden For gonorrhea, the global estimate was 0.9% in women and 0.7% in men, with regional values in women ranging from 0.3 to 1.9% and from 0.3 to 1.6% in men.

In 2020, some 7.5 million people in Africa had gonorrhea. The prevalence was higher among females, with about 4.3 million people infected, whereas the number of infections among males was 3.2 million.

justification of study Innovation is key to revolution of new pathogens which are emerging. Reconstitution of buffers is helpful in making the kit work for multiple pathogen identification.

Methodology Antigens and antibody extraction extraction

Sandwich nitrocellulose membrane in antigen and antibodies extracted, preparation of buffer, centrifugation of samples e.g serum and urine to form uniform samples since sample types are different except swab from sores/genital areas having sores, fitting absorbent pad, sample pad and conjugate pad. Dye labelled antibody for specific target antigen and vice versa.

Use of ready-made separate kits to validate on accuracy of new kit

Before commencement of kit hybrid kit design, sample mixing should be tested on its accuracy and to show that Ag-Abs of different samples don't interfere with the possible result.

study design Cross-sectional study design will be used in this study

Sample type can be urine, blood and swab on sores from genitals area for testing.

Target population Archived samples of gonorrhea and syphilis.

Conclusion WHO, CDC and KEMRI has goals in health care in innovation and research is key in addressing health cases. This study is useful in achieving WHO, CDC and KEMRI goals in health.

Keywords: RDT

Abstract 108

Title: EFFECTIVE MANAGEMENT OF ADOLESCENT HEALTH THROUGH MULTISECTORAL APPROACH

Authors: Onchari Mr Micah (Ciheb)*

Background: Adolescent health has been a major challenge worldwide with Ndiwa Dispensary serving 1200 aged10-19years. There has been a myriad of challenges ranging from adolescent pregnancies, SGBv issues, HIV/AIDS, STIs, school drop outs, mental health among others. By 2021 September, Ndiwa had a higher pregnancy rate among adolescents with 136 reported cases out of the 518 cases reported in north Kadem ward and 1818 reported in the subcounty, 8 reported cases of defilement and 7 were HIV positive. Though data review we actioned a quality improvement plan to establish the cause and consequently implement an improvement strategy.

Objective: Improve quality of ASRH within the catchment of Ndiwa dispensary through reduced pregnancies,Sgbv cases, HIV/AIDS and other STIs, improved mental health and reduced school dropouts.

Methods/ Approaches: By use of simple open ended questionnaires among adolescents visiting Ndiwa Dispensary, 60 adolescents were enrolled into a clinical review within a period of six months.36 (60%)of them were pregnant at first contact with 16 (44%) having dropped out of school, 6 (10%) had SGBV, 4 (6.6%) were newly enrolled HIV positive and the rest(14%) had been treated for other STIs.Among the issues discovered included lack of access to family planning services, lack of awareness of family planning services,HIV/AIDS prevention strategies including PrEp and PEP and Poor multi-sectoral linkage at Ndiwa Dispensary.

Results: Through increased engagement and impactful support from Ps Kenya on family planning service provision through bintishupavu stories,clinics and outreaches which has lead to increased access to FP services,STIs prevention and treatment to adolescents through increased awareness of FP services and other ASRH activities.CIHEB has greatly helped in supporting HIV services for the adolescents. from October 2021,there has been an increase in adolescent enrolled for fp services with an average number of 15 per month,this has enhanced reduction of adolescent pregnancies with 42 cases of pregnancies reported between October 2021 – September 2022 at Ndiwa dispensary. Through multisectoral linkage –education department, legal department, police department, children department and support from CIHEB and Nuru ya mtoto, cases of SGBV (2 reported cases from October 2021 and September 2022) have been reported, Out of the 42 cases of adolescents pregnancies, 30 have reported back to school. There have been little reported cases of STIs and only 1 case of HIV positive adolescent enrolled into care within the period of October 2021 – September 2022 through increased uptake of PrEP and PEP services with 17 adolescents currently on PrEP 54 documented having used PEP within the review period.

Conclusion: Quality improvement projects is a key intervention strategy through support programmes and Implementations through continuous sensitization through a community level approach with multisectoral involvement

Keywords: adolescent health

Abstract 109

Title: Syndromic Verses Laboratory diagnosis of Chlamydia trachomatis and Neisseria gonorrhoea among Adolescent girls and young women aged 15-20 years in South Western Kenya.

Authors: Samya Said Rashid (KEMRI-CMR)*; Maricianah Onono (KEMRI); George Omondi Otieno (KEMRI); Imeldah N Wakhungu (Kenya Medical Research Institute (KEMRI)- Research Care and Training Programme (RCTP)); Lizzie N Kabete (KEMRI); Elizabeth Anne Bukusi (KEMRI); Betty Njoroge (KEMRI); Ruanne V Barnabas (Harvard University); Nelly R. Mugo (KEMRI)

Background: Syndromic diagnosis of sexually transmitted infections (STIs) is based on the identification of a group of symptoms and signs that characterize a clinical condition. It is simple, cost effective, and capable of yielding rapid diagnosis for immediate treatment. Despite these advantages, syndromic diagnosis relies on subjective judgment, cannot detect asymptomatic infections, and may result in over- diagnosis, overtreatment, and potential drug resistance. The main objective of the study was to compare syndromic verses laboratory diagnosis of Chlamydia trachomatis (CT) and Neisseria gonorrhoea (GC), in a cohort of AGYW enrolled in a single dose HPV vaccine trial in South Western Kenya.

Method: The study utilizes data collected from a blinded, prospective randomized clinical trial of evaluating efficacy of a single dose HPV vaccination which enrolled adolescent girls and young women aged 15-20 years and were followed for 36 months. STIs symptoms were recorded on the sexual reproductive health form and were used to define syndromic cases for treatment. Endocervical samples were collected using Aptima swabs and transported to the laboratory for analysis. The Aptima Combo 2 Assay was used to detects CT and/or GC rRNA in clinician-collected endocervical. For analysis, we use diagnostic test with laboratory results as the gold standard, calculate sensitivity, specificity, false positives and false negatives.

Results: Out of 920 syndromic cases, 464 were confirmed and treated for GC & CT with 85% sensitivity [95% CI: 81.7% - 88.4%], specificity of 26% [95% CI: 22.3% - 30.5%], positive predictive value 53% [49.5% - 56.9%], while negative predictive value was 64% [57.3% - 71.4%]. Sixty-seven (15%) turned out to be false positive (15% vs. 26%, p-value <0.001), whereas 342 (74%) came out as false negatives. Area under the receiver operating characteristic (ROC) curve was 0.558 [95% CI: 0.53 – 0.58].

Conclusion: Our study findings add to the growing evidence for the need to augment syndromic management of STIs with more objective tests. Within a setting of high STI incidence, there is a need for a rapid, accurate, affordable, and easy-to-use point-of-care testing kit to provide better care to patients and address the growing threat of multidrug-resistant organisms.

Keywords: Syndromic diagnosis, Chlamydia trachomatis, Neisseria gonorrhoea, Adolescent girls and young women

Abstract 110

Title: Pre-exposure prophylaxis (PrEP) uptake & associated factors among adolescent girls and young women (15-20) participating in HPV vaccine trial

Authors: Mildred L Obare (-Kenya Medical research Institute)*; Maricianah Onono (Kenya Medical research Institute); George O Otieno (KEMRI); Elizabeth Bukusi (Kenya Medical research Institute); Betty Njoroge (Kenya Medical research Institute); Nelly R. Mugo (KEMRI); Ruanne Barnabas (University Of Washington)

Background: When combined with other methods, PrEP is highly effective and a vital HIV prevention tool for Adolescent girls and young women (AGYW). However, uptake, adherence and persistence are challenging in this cohort. We sought to evaluate the factors associated with PrEP uptake, continuation and discontinuation among AGYW participating in HPV vaccine trial.

Methods: Data from a blinded, prospective randomized study of a single dose efficacy HPV vaccination trial were used to evaluate uptake, continuation and associated factors over 36 months. Participants who were eligible and interested in taking PrEP were initiated, with refills being done every three months. Prep continuation was evaluated with the number of participants who refilled PrEP at least once within the period of initiation regardless of any gaps in pill coverage. Gaps in PreP refill was defined as any PrEP stop, restart or refill more than fifteen days after their expected refill date. Within the generalized linear regression framework, Poisson regression was used to analyze factors associated with PrEP uptake and continuation.

Results: At 36 months of study follow-up, 523 (46%) AGYWs out of 1148 PrEP eligible sexually active AGYW were initiated on PrEP, with a median age17 years IQR [15-23]. Of whom 472 (90%), continued on PreP. Participants reporting two or more sexual partners were 32% more likely to initiate PrEP(RR=1.32,95%CI:1.0-1.65), those who had sex in the last six months had 30% increased likelihood of initiation (RR=1.30,95%CI:1.10-1.54). AGYW who reported condom use during last sexual intercourse were less likely to initiate PrEP (P=0.002). Participants who attained post-secondary level of education or were divorced/separated/widowed were more likely to continue (RR 1.18,95%CI:1.05-1.31,RR=1.15,95%CI:1.0-1.24 respectively). Low perceived HIV risk(35%) and pill burden(29%)were common reasons for declining or discontinuing PrEP. Among those ever initiated on PrEP, eleven seroconverted including eight who reported ongoing PrEP use with gaps, and three who had discontinued PrEP prior to HIV diagnosis.

Conclusion: AGYW with high sexual behavioural risk factors and increased perceived HIV risk initiated on PreP, but had persistent gaps in refills. Targeted strategies are needed to improve persistence and adherence in this cohort.

Keywords: HIV PrEP AGYW

Abstract 111

Title: Repeat pregnancy, incidence & associated risk factors among adolescent girls and young women in Southwestern Kenya

Authors: Erick O Aol (KEMRI)*; Maricianah Onono (KEMRI); George Omondi Otieno (KEMRI); Imeldah N Wakhungu (Kenya Medical Research Institute (KEMRI)- Research Care and Training Programme (RCTP)); Barnabas Ruanne (Harvard); Elizabeth Bukusi (KEMRI); Nelly R. Mugo (KEMRI); Betty Njoroge (KEMRI)

Background: Pregnancy among adolescent girls and young women (AGYW) remains a major social and public health issue in developing countries. The adolescent birth rate in eastern and Southern Africa Region is twice the global rate at 92 births per 1,000 girls. In Kenya, AGYW pregnancies and repeat pregnancies continue to expose this group to higher risk of HIV infection, unwanted pregnancies and unsafe abortions.

Objectives: To determine incidence rate of repeat pregnancy and identification association of the correlates among AGYW in Southwestern Kenya.

Methods: Data is drawn from a blinded, prospective randomized trial assessing efficacy of single dose HPV vaccination among AGYM age 15-20 years trend. Pregnancy testing was done at enrolment and at every 3 months. We defined our closed cohort as participants with more than one pregnancy during the study. Data on Pregnancy repeat trends were also determined, pre-and post-COVID-19 lockdown period. Within the generalized estimating equations (GEE), we used Poisson regression, assuming a common correlation, we modelled predictors of repeat pregnancies.

Results: Over a median of 22 months follow-up, 459 girls were pregnant, of whom 61 (13.3%) had repeat pregnancies. Of the repeat pregnancies outcome, 52% ended in therapeutic or elective abortions. The overall repeat pregnancy incidence rate of 9 per 100 person-years of observation (PYOs) (95% CI: 7.11 – 11.76). All the repeat cases of pregnancies happened post-COVID-19 lockdown, with 64% being unintended. Median time to repeat pregnancy was 1.6 months IQR (0.7-2.2). A steady increase in trend of repeat pregnancy was observed across the study period, peaking in 2021 and 2022 ($p<0.001$). Repeat pregnancy rate was similar between minors (<18 years) and adults (>18 years), 9 per 100 PYOs versus 10 per 100 PYOs, (95% CI: 6.10 – 11.96) and (95% CI: 6.88 – 14.64), respectively. Married participants had nearly two-fold risk of repeat pregnancy (IRR= 1.70, 95% CI: 1.04 - 2.78, p= 0.001). Participants who reported having used contraceptive methods had 62% less risk of repeat pregnancy (IRR= 0.38, 95% CI: 0.23 - 0.64, p <0.001). 53(87%). Level of education or income level had no significant influence on repeat pregnancies.

Conclusion: The prevalence of repeated adolescent pregnancies and subsequent abortions remains unacceptably high. There is a critical need for interventions, programs, and policies to target this highly vulnerable group.

Keywords: Repeat pregnancies, adolescent girls and young women, abortion

Abstract ID:112

Title: HIV incidence, trend and associated risk factors among a cohort of adolescents and young women (15-20 years) participating in HPV vaccine study in Kisumu

Authors: George O Otieno (KEMRI)*; Maricianah Onono (KEMRI); Mildred L Obare (-Kenya Medical research Institute); Samya Rashid (Kemri); Barnabas Ruanne (Havard); Nelly R. Mugo (KEMRI)

Background: Kenya HIV 2018 report indicates that young women ages 15-24 years account for third of new HIV adult infections. Kisumu County is one of four Counties with the highest HIV prevalence in Kenya, however, specific data on HIV incidence among AGYW is lacking. This study aims to determine HIV incidence, trends, and associated risk factors among adolescents girls and young women (AGYW)

Methods: The primary study is a blinded prospective randomized study in Kenya evaluating ‘single dose HPV vaccine efficacy (KENSHE), it enrolled 2,275 sexually-active HIV-negative, AGYW aged 15-20 years in Thika, Kisumu, and Nairobi. HIV testing was done at enrolment and every three months. This analysis is restricted to Kisumu site. Person-time started at enrolment, and ended at the date of HIV sero-conversion, lost to follow-up or end of observation (30th September 2022). We computed incidence rates. Cox proportional hazards model was used to analyze risk of HIV incidence.

Results: Of 1,150 participants included in the analysis, the median age was 17 with IQR (16-18). At enrolment, most were not married 1,069 (94%), and 988 (88%) had secondary education. HIV incidence was 6.7 (4.54 – 10.11) per 1000 person-years from 2019 to 2022. Infection rate peaked in 2020 & 2022, 8.02 (4.17 – 15.41) and 12.14 (6.53 – 22.57) per 1000 person-years. Risk factors for HIV incidence included: STI at baseline (HR= 3.4 ,95% CI: 1.39 - 8.61), married compared to being single (HR= 3.03, 95% CI: 1.18 - 8.66), and AGYW who perceived their partners were having sex with other partners (HR= 12.2, 95% CI: 2.71 - 55.19).

Conclusion: HIC incidence in this cohort was higher than the 4.6/1000 person-years reported in 2012-2016 in Western Kenya 2018 HIV report among the same age group. Among AGYW, HIV incidence is still high and not close to the elimination target of one per 1000 person-years.

Keywords: HIV incidence, adolescents and young women

Abstract 113

Title: Prevalence of Chlamydia trachomatis and its associated factors among sexually active women in a high HIV-burden region, Western Kenya using Point-of-Care approach

Authors: Martha N Nyakambi (Pan African University)*; Anthony Waruru (CDC); Adesina Oladokun (University of Ibadan)

Background & Objective: Chlamydia trachomatis is a sexually transmitted infection (STI) that affects sexual and reproductive health. Chlamydia can also be perinatally transmitted from mother to child resulting in poor pregnancy outcomes. Women infected with Chlamydia are five times more likely to become infected with Human Immunodeficiency Virus (HIV) among other STIs. Syndromic approach results to under-reporting. The study investigates the prevalence, knowledge, awareness and predisposing factors associated with Chlamydia infection among sexually active women.

Methods: The study was cross-sectional, conducted among women aged 18 to 49 attending outpatient clinics at Kisumu County Referral Hospital, Western Kenya. The required sample size was 385 women. We approached a total of 400 women. Out of which 391 (97.75%) women fulfilled the eligibility criteria. Nearly all women 385/391(98.47%) participated in the study. They completed the electronic questionnaire after consenting. The 6 women who did not participate were either in a hurry or not ready. We collected socio-demographic and clinical data. Either the health providers or the women self-collected vaginal swab samples. Using rapid point-of-care (POC) diagnostic test kit, we tested the samples for Chlamydia trachomatis. Women who tested positive were treated with a single dose of azithromycin.

Results: Twenty-nine (29; 7.5%) participants tested Chlamydia-positive and were treated. Chlamydia positivity was highest (48.3%) among inconsistent condom users and lowest (10.3%) among users. Women in polygamous and low education had higher prevalence (7.3%). The age group 18-25 years had the highest positivity (79%; 5.7%). Factors associated with Chlamydia were multiple sexual partners, adjusted odds ratio (aOR) 15.7 (95% CI: 2.1, 120); being HIV-infected aOR 4.0 (95% CI: 1.3, 12.5); and having UTI aOR 4.3, (95% CI: 1.8,10.7). Nearly all participants (92%) had no explicit knowledge of the symptoms or effects of Chlamydia. Self-collection of vaginal swabs was highly acceptable (99.7%).

Conclusions: Chlamydia trachomatis infections are prevalent among women with multiple sexual partners, who have other STIs, or inconsistently use condoms. Most women had poor knowledge of symptoms and Chlamydia-associated risk factors; therefore, awareness may ease the STI burden. Using Chlamydia POC diagnostic tests, provision of same-day results and treatment is feasible.

Recommendations: There is a need for integration of Chlamydia trachomatis into routine health talks and STIs testing and treatment due to its asymptomatic nature to reduce the burden of the disease.

MoH should encourage use of Chlamydia RDT; non-invasive, can screen large numbers with the provision of a-same-day result and treatment if required

Keywords: Chlamydia trachomatis, Chlamydia rapid diagnostic test kit, sexually active women

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Abstract 114

Title: A multi-causal pathway to suicide, understanding suicide risk in coastal Kenya: A qualitative study.

Authors: Linnet Ongeri (Kenya Medical Research Institute)*; Miriam Nyawira (KEMRI-Wellcome Trust Research Programme); Symon Kariuki (KEMRI - Wellcome Trust Research Programme); Mary Bitta (KEMRI Wellcome Trust Research Programme Kilifi); Chris Schubart (Tergooi Hospital); Brenda Penninx (Amsterdam UMC, Vrije Universiteit); Charles Newton (KEMRI - Wellcome Trust Research Programme); Joeri Tijdink (Amsterdam UMC VUMC Site)

Background: Suicide is a major public health concern globally. In Kenya, media reporting of suicide has been on the rise, generating a growing interest in finding solutions to curb this problem. However, even with this recent escalation of suicide prevention efforts, data exploring reasons for suicidal behaviour in our communities and recommendations for suicide prevention is lacking. Understanding communities' perspectives on triggers for suicidal behaviour in specific populations is critical in prioritizing and designing targeted interventions and policies for suicide prevention. In this study we sought to explore perspectives, experiences and opinions on reasons for suicidal behaviour and recommendations for suicide prevention.

Methods: Using individual in-depth interviews, we conducted a qualitative study with a diverse group of key informants residing at the Coast region of Kenya. A region with a reported high prevalence of suicidal behaviour (20%) and where treatment gap for mental disorders is large. Study participants were purposively selected and included: health care providers, persons with a history of suicide attempt, bereaved family members, religious leaders, traditional healers, judiciary, and law enforcement officers. Interviews were audio recorded, transcribed, and translated prior to thematic inductive and deductive data analysis.

Results: Out of a total of 25 in-depth interviews, we identified four key themes as reasons for suicidal behaviour: i) interpersonal and relationship problems ii) financial and economic difficulties iii) mental health conditions; and iv) religious and cultural influences. In addition, six themes on recommendations for suicide prevention were identified: (i) increasing access to counselling and social support; (ii) improving mental health awareness and skills training; (iii) restriction of suicide means; (iv) decriminalization of suicide; (v) economic and education empowerment; and (vi) encouraging religion and spirituality. Reasons provided were interrelated and recommendations suggested aligned well with these reasons.

Conclusion: Based on the varied reasons suggested and the interrelatedness of these reasons, a multifaceted approach in preventing suicides in coastal Kenya is warranted. Community-based interventions will likely improve and increase access to suicide and self-harm prevention in this study area. Future research and interventions should prioritize vulnerable groups such as the youth and persons with substance use disorders.

Keywords: suicide; risk factors; suicide prevention; qualitative study

Abstract 115

Title: Visual arts as a tool to tackle mental health stigma: Findings from the Difu Simo Mental Health Awareness project in Kilifi County, Kenya

Authors: Mary Bitta (KEMRI Wellcome Trust Research Programme Kilifi)*; Judy Baariu (KEMRI Wellcome Trust Research Programme Kilifi); Simone Grassi (Documentary Institute of Eastern Africa); Symon Kariuki (KEMRI - Wellcome Trust Research Programme); Belinda Lennox (University of Oxford); Charles Newton (KEMRI - Wellcome Trust Research Programme)

Background: Globally, stigma associated with mental disorders is rampant and is a barrier to good health and overall well-being for people with lived mental health experience. Visual arts such as photography, videography and filmmaking are powerful tools to tackle stigma, but evidence on their effectiveness in persons with lived experience from Africa are conspicuously absent.

Methods: We evaluated the effectiveness of using participatory videos (PV), which is a visual arts method. In PV, people with lived experience in mental illness are involved in the process of concept development, filming, editing and dissemination of the videos, aimed at raising awareness against mental health stigma. To measure effectiveness of PV in lowering stigma, we evaluated changes in levels of knowledge, attitudes, and behaviour (KAB) among 420 members of the general population in Kilifi, Kenya. Using multivariable linear regression models, changes in scores from baseline were compared to scores immediately after watching the PV and at a four-month follow-up. Sociodemographic correlates of stigma scores were examined.

Results: Compared to baseline, KAB stigma scores significantly improved at both time points suggesting reduced stigma levels. At four months, the change in scores were: knowledge (β=0.20, 95% CI= 0.16-0.25, p=0.00), liberal attitude (β=1.08, 95% CI= 0.98-1.17, p=0.00), sympathetic attitude (β=0.52, 95% CI= 0.42-0.62, p=0.00), tolerant attitude (β=0.72, 95% CI= 0.61-0.83, p=0.00) and behavior (β=0.37, 95% CI= 0.31-0.43, p=0.00). Different sociodemographic variables were significantly correlated with KAB scores, but the correlations differed across the domains.

Conclusions: Visual arts such as PV are a feasible and effective strategy in lowering stigma against people with mental illnesses, especially if they are created and disseminated by people with lived experience. Further studies are required to understand the mechanisms through which PV bring change and to examine whether these findings are consistent when applied to other forms of visual arts such as photography and filmmaking.

Keywords: visual arts, stigma, mental health awareness, participatory approaches, service user involvement

Abstract 116

Title: Design and Evaluation by Action Research of the BoB-programme (Build your Own Buddy) in South Sudan: Mental Health & Psychosocial Support for young children.

Authors: Remy Vink (TNO Innovation for Life); Jacqueline Stam (TNO Innovation for Life); Yvette Fleming (TNO Innovation for Life)*

Background: Research shows the detrimental effects of Adverse Childhood Experiences (ACEs) on the development and well-being of children. Children growing up in hardship settings are at a greater risk for chronic stress, which in turn negatively influences brain development, behaviour, academic achievements, and in the long run may even contribute to physical disease. Young children are often overlooked in this respect and are even at greater risk. It is important to invest in the mental health of children (and parents) as early as possible, with evidence based methods, that are easy to apply and upscale. Build your Own Buddy (BoB), developed by TNO (Netherlands Organisation for Applied Scientific Research) in collaboration with the NGO Help a Child, is a generic mental health and psychosocial support (MHPSS) programme with elements of Cognitive Behavioural Therapy (CBT) and Emotion Focused Therapy (EFT). Based on recent scientific insights, the BoB-programme offers physical and mental strategies for children aged 5 to 7 years, to recognise emotions, to communicate about them and to actively influence their own stress levels. To enhance impact during and after the sessions, children also create their own 'buddy Bob' from local materials. Experience through activities, stories and metaphors are key. Storytelling is an element of many cultures, especially in Africa where the programme was first piloted. The BoB-programme consists of 12 sessions for kids and parallel sessions for parents, both facilitated by two trained lay counsellors.

Method: The BoB-programme was developed and piloted by action research with three cycles of development/adaption, action, reflection and learning. The research was conducted through a mixed method design: pre- and post-measurement using the Strengths and Difficulties Questionnaire (SDQ), focus group discussions and interviews, observations and systematic evaluation after each BoB-session.

Results: Build your Own Buddy was implemented in four communities around Wau in South Sudan. Lay facilitators were trained to run the programme. Based on the outcomes of the SDQ, children showed significant improvement between pre- and post-measurement (p<.001; n=380). Two third of the children improved their well-being and 82% of parents improved their parenting skills. Qualitative data too revealed an enormous impact of the BoB-programme on participants, and on the community as a whole.

Conclusions: Developing Build your Own Buddy through action research resulted in a feasible and appealing MHPSS group-programme, for emotion-regulation in young children (and parents). The programme proved easy to apply by trained lay facilitators. Quantitative and qualitative data showed that the well-being of participants improved. Next steps are to conduct further research by experimental design, and to upscale the implementation of the programme. Currently the BoB-programme is being digitalized and adapted to other languages.

Keywords: mental health and psychosocial support children - chronic stress - resilience

Abstract 117

Title: ASSOCIATION BETWEEN MATERNAL DEPRESSION AND CHILD GROWTH IN HOMA-BAY AND MIGORI COUNTIES, KENYA

Authors: Julius Onyango Nyaoke (KEMRI/UNIVERSITY OF WASHINGTON)*; Christine J. McGrath (UNIVERSITY OF WASHINGTON); Maureen Okello (KEMRI/UNIVERSITY OF WASHINGTON); Mame M Diakhate (UNIVERSITY OF WASHINGTON); Catherine A Otieno (KEMRI); Marline MMS Serede (Kemri); Mary Masheti (KEMRI/UNIVERSITY OF WASHINGTON); Olieng'o Okoth Geoffrey (KEMRI); Emily Yoshioka (UNIVERSITY OF WASHINGTON); George Owuor (KEMRI/UNIVERSITY OF WASHINGTON); Sean Galagan (UNIVERSITY OF WASHINGTON); Margaret Oluoch (KEMRI/UNIVERSITY OF WASHINGTON); Danish Oyuga (KEMRI/UNIVERSITY OF WASHINGTON); Lorine Odero (KEMRI/UNIVERSITY OF WASHINGTON); David Matinde (KEMRI/UNIVERSITY OF WASHINGTON); Phlona Amam (KEMRI/UNIVERSITY OF WASHINGTON); Emmanuel Odhiambo (KEMRI/UNIVERSITY OF WASHINGTON); Carolyne Onyango (KEMRI/UNIVERSITY OF WASHINGTON); Susan Kemunto (KEMRI/UNIVERSITY OF WASHINGTON); Kirk Tickell (UW); Benson Singa (KEMRI)

Background: Women are at particularly increased risk of depression during pregnancy and postpartum, and this depression when left undiagnosed and untreated, it may impact child growth. We examined the association between maternal depression and growth in children aged 5-12 months.

Methods: We conducted a cross-sectional analysis of mother-infant pairs at enrollment in the Mama Aweza Trial conducted in four facilities in Migori and Homabay counties between August 2019 to January 2022. Children were eligible if aged 5-12 months, attending clinic or community outreach day, and had a mid-upper arm circumference (MUAC) of 12.5–14.0 cm. WHO z-scores were used to calculate weight-for-age (WAZ), length-for-age (LAZ), and weight-for-length (WLZ). Primary outcomes were growth (WAZ, LAZ, WLZ) and growth faltering defined as underweight (WAZ<-2), stunting (LAZ<-2), and wasting (WLZ<-2). Maternal depression scores were calculated using the Patient Health Questionnaire-9 and categorized as none (≤4), mild (5-9), and moderate and above (≥10). Linear and Poisson regression were used to determine associations between maternal depression and child growth.

Results: Among 1,182 mothers assessed for depression, 745 (63%) had no depressive symptoms, 340 (29%) had mild depressive symptoms, and 97 (8%) had moderate and above depressive symptoms. Of the 437 mothers reporting depressive symptoms, 63% were ≥25 years, 82% were married, and 57% had completed primary education or below. Three-quarters (78%) of mothers with moderate or above depressive symptoms were married. Mean infant age was 7.9 months (standard deviation=1.9). Of the 1110 (94%) mothers who were breastfeeding, 37% had any depressive symptoms. Fifteen percent (n=179) of infants were stunted, 10% (n=114) underweight, and 5% (n=58) wasted. Higher maternal depression scores were associated with lower child WAZ (-0.01, 95%CI: -0.02, 0.00, p=0.057) and WLZ (-0.02, 95% CI: -0.03, -0.004, p=0.01). However, no significant association was found between maternal depression and child LAZ (0.00, CI: -0.02, 0.02, p=0.97). Mild depressive symptoms were associated with 40% higher stunting prevalence than no symptoms (PR=1.40, 95%CI: 1.02-1.91, p=0.04). Moderate and above depressive symptoms were associated with a higher underweight prevalence than no symptoms (PR=2.0, 95%CI:1.16-3.49, p=0.01). Maternal depressive symptoms were not associated with wasting.

Conclusion: Our results suggest an association between maternal depressive symptoms and child underweight and stunting and contribute to the limited evidence on postpartum depression and child growth in western Kenya. Longitudinal data are needed to understand the relationship between maternal depression and infant growth.

Keywords: Maternal Depression, Child growth, stunting, wasting, underweight, LAZ, WAZ, WLZ, ASSOCIATION

Abstract 118

Title: Where are the perpetrators? A situational analysis of the Sexual and gender based violence cases among women at Kendu Sub County Hospital, Homa Bay County, Kenya

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

Introduction: Sexual and gender-based violence (SGBV) refers to any act that is perpetrated against a person's will and is based on gender norms and unequal power relationships.

Globally, more than a third of women have experienced sexual and/or physical violence at some point in their lives. Women in Kenya suffer even higher rates of violence compared to the global rate (35%) with 38% experiencing violence in their lifetime, rising to 60% in western Kenya, where the risk factors of poverty and low education are prevalent. With the increase of teenage pregnancy due to defilements, we sought to find out whether the perpetrators were identified and reported to the authorities for legal action.

Method: We conducted a cross sectional retrospective study by review of the SGBV records at the out-patient, laboratory and ante-natal care clinics in Kendu Sub County Hospital between October 2021 and October 2022.The case definition was any record of defilement including any pregnancy of a girl below 18 years, rape, attempted rape, sexual assault or physical assault. We abstracted data into a Microsoft Excel tool and collected information on demographics, SGBV cases reported, and cases referred for legal action. Descriptive analysis was done using measures of central tendency for continuous variables and frequencies and proportions for categorical variable

Result: We collected data on 97 cases, 50 (52%) from outpatient and 47 (48%) from ante-natal clinic. The median age was 16 years. Defilement cases were the highest at 84 (87%), rape 10 (10%), sexual assault 3 (3%), one person reported being defiled, physically abused and harassed. 47% (n=41) of the defilement cases were found to be pregnant and 6% (n=5) were already having children. The study revealed that, only 35 (36%) out of 97 cases were reported to the police for legal action and only 12 suspected perpetrators were accompanied with the survivors to the laboratory for sample collections and testing.

Conclusion: This data indicates that young girls are the most vulnerable to SGBV since they cannot defend themselves against the perpetrators or they are easily lured by the perpetrators. There is need to report all the cases of SGBV to the police for investigation and prosecution of the perpetrators in order to bring to an end the question of "Where are the perpetrators?"

Keywords: SGBV, Women, Perpetrator,

Abstract 119

Title: Factors associated with substance abuse among mentally ill outpatients seen in a psychiatric hospital in Nairobi, Kenya: A retrospective study.

Authors: JANE N MURIUKI (MINISTRY OF HEALTH- FELTP)*

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Introduction: Substance abuse is a social problem that has spread rapidly worldwide, leading to significant morbidity, mortality, and burden on the health care system. We sought to investigate socio-demographic and clinical factors associated with substance abuse among the mentally ill and conduct Data Quality Audit (DQA) at Mathari National Teaching and Referral Hospital (MNTRH) outpatient.

Methods: Substance abuse was defined as the harmful or hazardous use of psychoactive substances, including alcohol and illicit drugs We conducted a retrospective records review of 500 files of patients seen from February 2019 through January 2020, randomly sampled from an overall sample of 5700 new patients. We collected data using a preformed excel sheet. Continuous data analyzed using measures of central tendency and dispersion while categorical data were analyzed using frequencies and proportions. To measure the strength of association between variables, Epi info software was used to calculate the Odds ratio (OR) and Confidence Intervals (CI) at 95% confidence level. DQA for completeness was conducted on 30 randomly selected patients' files.

Results: We analyzed 500 patients' records. The mean age was 34 years (sd ± 14 years). Males were 338(68%). Unemployed were 286(57%). Youths in secondary and tertiary schools were 339(68%). Substance use-related disorders were 284 (57%) with 291(58%) having ever abused substances. Alcohol was used by 189(38%) of the patients, Cannabis 149(30%), cigarettes/ tobacco 102 (20%), and khat 77 (15%), 43(9%) had a family history of mental illness, 134(27%) reported history of stress while 15 (3%) had reported crime history. Of the 291 substance abusers, 134(46%) were admitted, 274(94%) received medication, 59(20%) received psychotherapy and 27(9%) were rehabilitated. When cross-tabulated against history of substance abuse, youths aged ≤ 34 years had an OR of 1.58(CI 1.1-2.27), males OR 5.83(CI 3.87-8.77), educated OR 2.07(CI 1.38-3.12), Family history of mental illnesses OR 0.51(CI 0.26-1.02), Stress history OR 1.47(CI 0.48-4.56), History of crime OR 5.3(1.06-26.7). DQA had a weighted average of 42.4% completeness

Conclusion: Age, sex, level of education, family history of mental illness, and history of crime were associated with substance abuse. Health Ministry to strengthen substance abuse prevention programs in learning institutions. MNTRH to develop standardized patient intake forms to improve documentation.

Key Words: Substance-Related Disorders, Hospitals, Psychiatric, Retrospective Studies

SYMPOSIUM 6: NUITM-KEMRI

Institution: NUITM-KEMRI project

Title: Cooperation from research projects to human resource development: KEMRI-NAGASAKI Symposium

KEMRI and Nagasaki University have a long history of research collaboration, mainly in tropical medicine. This year, a new SATREPS project (Science and Technology Research Partnership for Sustainable Development: a research and development and social implementation project by AMED and JICA) has been adopted with the theme of combating schistosomiasis. In addition, many other research areas have been developed, including developing biometric identification technology for newborns, epidemiological research based on maternal and child registration, malaria vector research, and virologic and bacteriological research. In terms of human resource development, the cooperative relationship between KEMRI and Nagasaki University is further developing, as evidenced by JICA's support for study in Japan and the adoption of the JSPS Inter-University exchange program. This symposium aims to share the status and discuss future developments.

SYMPOSIUM 7: NAPREDA

The role of Herbal and Traditional Medicine in primary health care in Kenya and the region can never be over emphasized, especially due to its wide use and availability. Inadequate provision of conventional health care to the population, more so, during this period of COVID-19, further rejuvenates this use. In these circumstances, an effective health agenda for the Country, especially in view of the Kenyan Vision 2030 and the Government's big four initiative that encompasses Universal Health Coverage (UHC), can never be adequately achieved unless complemented with Traditional and Herbal medicine. Therefore, the most workable health agenda for Kenya is the institutionalization of Herbal/Traditional Medicine, in parallel with conventional medicine, within the main stream national health care scheme. Our Country is blessed with a wealth of biodiversity in medicinal plants and our ancestors had a way of co-existing with this valuable resource without necessarily destroying it, harnessing it for use as medicine, food and timber and protecting it for prosperity. Presently, and most unfortunately, most of it is being lost with knowledge of its medicinal values eroding. This is despite the fact that advent of emerging and re-emerging new diseases and the difficulties being experienced in drug resistance, researchers in the region and indeed the whole world, still depends on this natural resource as a major raw material for identification of new management therapies. There is therefore a strong need for scientific validation and documentation of the potential of this natural product as medicine. The Centre for Traditional Medicine and Drug Research (CTMDR) of the Kenya Medical Research Institute (KEMRI) is a major player in this field and serves as reference hub for government on issues herbal/traditional medicine and collaborates in research, at local and international, with Universities and other like-minded Institutions. It has well established laboratories and expertise for evaluation of in vitro, in silico and in vivo aspects of any natural product against most common disease-causing agents. The Centre recognizes the support given by our Government in the delivery of this mandate and continues to welcome more support from all angles including our National Parliament who previously have been able to give valuable direct support.

SYMPOSIUM 8: IMPACT OF CLIMATE CHANGE

Institution: Kenya Medical Research Institute (KEMRI)-Kisumu Project: Climate change and health in sub-Saharan Africa

Title: Impacts of climate change on undernutrition, heat stress, and malaria and potential adaptation strategies for rural Kenya and Burkina Faso

This interdisciplinary Research Unit (RU) addresses the astonishingly big evidence gap on climate change and health in sub-Saharan Africa. In the first RU phase, we focused on studying the climate change impacts, evaluating potential adaptation strategies to lift those impacts, and projecting both, the health impacts and the potential health-benefits from adaptation strategies, to future climate scenarios. We work in rural Health and Demographic Surveillance Systems (HDSS) in south-western Kenya and north-western Burkina Faso, where undernutrition, cardiovascular heatstress, and malaria constitute major health problems. At both sites, we evolved the HDSS to climate-ready population observatories with demographic, health, climate, socio-economic, agriculture, and behaviour data of entire population cohorts. The existing models for future climate, climate impacts, and economic effects were tailored to the study locations through downscaling, biascorrection, and nation-wide economic and health data. Historical and prospective links between climate change and the three health outcomes were established, and will be advanced in the second RU phase. Importantly, we will introduce an additional research focus on adaptation measures, providing best-practice examples for designing, implementing and evaluating adaptation strategies that apply technological innovation, behaviour change or policy options. The overarching goal of the second RU phase is to gain in-depth understanding about the effectiveness of local adaptation strategies on health in sub-Saharan Africa – today and under future climate scenarios. We have four specific objectives: i) Identify and quantify potential impacts of future climate change on child undernutrition, malaria and heat stress; ii) Determine the effectiveness and potential socio-economic costs of specific adaptation policies and interventions with respect to reducing climate impacts on child undernutrition, malaria, and heat stress; iii) Quantify the economic effects of climate-related health impacts and adaptation strategies at the national level; and iv) Establish the importance of human mobility for climate change-related health impacts and adaptation strategies.

SYMPOSIUM 9: BOHEMIA

Institution: KEMRI/CGMRC/BOHEMIA Project

Title: Broad One-Health Endectocide-based Malaria Intervention in Africa (BOHEMIA) Forum

The BOHEMIA consortium (Broad One Health Endectocide-base Malaria Intervention in Africa) proposes to evaluate the epidemiological impact of ivermectin mass drug administration to humans and livestock in Kwale, Kenya with the aim of developing a complementary strategy for malaria elimination. Ivermectin is an endectocide, a drug with excellent safety profile that can kill ecto- and endo-parasites, as well as mosquitoes fed on treated humans or animals. MDA of ivermectin holds the potential to complement the malaria toolbox by tackling residual transmission and overcoming insecticide resistance. Two independently powered cluster-randomized clinical trials are underway in Kenya and Mozambique. The trials will generate efficacy and safety data and will be supported by entomological, social and health economic data collection on the intervention. Evidence will be generated to support a WHO policy recommendation, briefing and engagement of country and regional leaders and civil society in order to forge country ownership and create demand, as well as ensuring supply of quality product by working with well-positioned manufacturers to scale-up production and prequalify product for this new indication

SYMPOSIUM 10: Drug Delivery using Nanotechnology

Institution: KEMRI

Nanotechnology can be defined as the science and engineering involved in the design, synthesis, characterization, and application of materials and devices whose functional organization is on the nanometer scale. It is an exciting new area in science, experiencing rapid growth with many and diverse potential applications being explored in the biomedical field geared towards improvements to current approaches for diagnosis, immunization, drug design and delivery. The development of advanced nanomaterials has greatly enhanced drug discovery through improved pharmacotherapeutic effects and reduction of toxicity and side effects. One application of nanotechnology in medicine involves employing nanoparticles to deliver drugs or other substances to specific cell types. Particles are engineered so that they are attracted to diseased cells, which allows direct treatment of those cells. These materials and devices can be designed to interact with cells and tissues at a molecular (i.e., subcellular) level, for applications in medicine and physiology, with a high degree of functional specificity, thus allowing a degree of integration between technology and biological systems not previously attainable. The ability to control the release of therapeutic compounds is also achievable with nanotechnology. The technique thus reduces damage to healthy cells in the body and potentially enables safe use of otherwise highly toxic treatments like in the case of cancer chemotherapy. The promise that nanotechnology brings is multifaceted, offering not only improvements to the current techniques, but also providing entirely new tools and capabilities. By manipulating drugs and other materials at the nanometer scale, the fundamental properties and bioactivity of the materials can be altered. These tools can permit a control over the different characteristics of drugs or agents such as; a) alteration in solubility and blood pool retention time, b) controlled release over short or long durations, and c) environmentally triggered controlled release or highly specific site-targeted delivery. KEMRI in collaboration with other partners is in the forefront of championing nanotechnology research in medicine. The proposed symposium therefore seeks to provide a platform for discussion on the subject and stimulate interest in nanotechnology application in biomedical research.

Abstracts

Preclinical Drug Development: Considerations for Anti-Malarial Nano Drug Formulations

Rose Hayeshi (DSI/NWU Preclinical Drug Development Platform, Faculty of Health Sciences, North-West University, South Africa)*

The DSI/NWU Preclinical Drug Development Platform (PCDDP) is a national facility contributing to building a vibrant pharmaceutical industry in South Africa by functioning as a preclinical testing platform for local and international research institutions and companies involved in development of pharmaceutical drugs, vaccines, and phytomedicines. The PCDDP has qualified professionals and a state-of-the-art AAALAC accredited and GLP compliant, animal testing facility (Vivarium) equipped with environmental control and data capturing systems for conducting preclinical studies.

Preclinical studies for antimalaria drug development normally entail pharmacokinetics, safety and efficacy studies. Safety studies could include safety pharmacology, in addition to GLP toxicity studies. The use of humanized NOD/SCID/IL2Rγnull mouse, a model engrafted with human erythrocytes to support infection with *Plasmodium falciparum* is a useful model for efficacy studies.

The application of nanotechnology for anti-malarial drug development, brings with it further considerations for preclinical studies. These include endotoxin contamination, pharmacokinetics safety of the delivery system and interactions with the immune system. An additional consideration is mathematical modeling approaches or pharmacometrics for example PBPK and PD modeling, biomolecular corona formation and cellular internalization.

Nanotechnology in Delivery of Antimalarial Chemotherapeutic Agents

Jeremiah Gathirwa (Centre for Traditional Medicine and Drug Research, Kenya Medical Research Institute)*

Ever since malaria was discovered to be a threat to human existence; several attempts for eradication have been made. Key among these is use of antimalarial drugs to combats the disease. The efficacy of many antimalarial drugs and that of novel drug candidates have been compromised by their *intrinsic physicochemical properties and how they interact with biological systems.* Artemisinin and its derivatives for example have shown high efficacy but has the shortfalls of poor water-solubility and pharmacokinetic profile. Primaquine (PQ) is one of the most widely used antimalarial drugs and is the only available drug to date for combating relapsing form of malaria. PQ has a unique and powerful role in the prevention and cure of malaria. However, the drug has serious side effects including nausea, vomiting, stomach cramps, and hemolytic anemia. This prohibits its use in key groups, such as pregnant women. The PQ dose-limiting side effects is partly due to the nonspecific targeting and short half-life that necessitates frequent dosing. For instance, for *P. vivax*, the dosage is 30 mg daily for 14 days, while for *P. ovale*, the dosage is 15 mg daily for 14 days. The drug is also a casual prophylactic, especially for travelers to endemic areas, but the dose frequency is also relatively frequent. PQ oral bioavailability is limited due to pre-systemic metabolism and excretion.

The need to reformulate some of these drugs in order to enhance efficacy, reduce dose frequency, and subsequently reduce toxicity cannot be overemphasized. A promising strategy to overcome these challenges involves the development of a suitable drug-carrier system. Nanomedicine drug-delivery systems present the ability to enhance the therapeutic properties of current antimalarials and to overcome delivery barriers. Advantages includes maintaining drug therapeutic concentrations and circulatory time at target sites; protection from premature degradation in the gastrointestinal tract; improved pharmacokinetics, solubility, bioavailability, and stability; reduced toxicity; reduction in dose and dose frequency; enhancement of patient compliance; and prevention, reduction, or delay of onset of resistance. The main aim of using nanocarriers as drug-delivery systems is to promote drug protection against extracellular degradation, to improve selectivity in relation to the target, and to reduce dose frequency as well as duration of the treatment via enhancing the pharmacokinetic profile of the drug.

In our previous studies, Dihydroartemisinin (DHA) and PQ were reformulated into solid lipid nanoparticles (SLNs) as a nanomedicine drug delivery system. The drug loaded-SLNs were characterized for physical parameters and evaluated for *in vitro* and *in vivo* antimalarial efficacy. Drug loaded-SLNs showed desirable particle characteristics and enhanced antimalarial activity when subjected to pre-clinical evaluation.

Formulation and Pre-Clinical Testing of Novel Nanoparticle-Based Triple Combination Antimalarial Drug

Pesila Odera (Technical University of Kenya (TUK))*; Jeremiah Gathirwa (Kenya Medical Research Institute (KEMRI)); Geoffrey Otieno (TUK); Joab Onyango (TUK); Martin Ogas (Strathmore University); Florence Oloo (Strathmore University); James Owour (TUK); Lucy Ochola (Institute of Primate Research); Bernhards Ogutu (KEMRI)

Background; Malaria remains one of the killer diseases in sub-Saharan Africa, with high mortality and morbidity rates recorded annually. Previously, monotherapy drugs were used to treat malaria. The World Health Organization currently recommends the use of artemisinin-based drugs for the treatment of malaria. However, these drugs face a great delivery challenge, partly due to poor aqueous solubility in some and non-specific target approaches in others. Therefore, malaria treatment requires unnecessary high doses of drugs over an extended time to achieve therapeutic levels, which present toxic concerns. The superiority of solid lipid nanoparticle-based delivery over conventional delivery systems, as demonstrated in other disease management, will be a significant boost to the malaria fight.

Methodology; For the nano-formulation of drugs, the single solvent extraction approach was employed. The preferred method of drug delivery system used was solid lipid nanoparticles. Stearic acid, which served as the lipid matrix, polyvinyl alcohol, D-lactose monohydrate, which served as the binder and assisted in further reducing the particle size, and chitosan, which served as the adhesive and increased the stability of the nano-formulated drug, were the main reagents used in the process. Heparin was used to functionalize the nano-formulated medication, which increased its effectiveness. Using zetasizer equipment and double quadraple liquid chromatography, the average particle size, polydispersity index, zeta-potential, and encapsulation efficiency were assessed. The drug loading effectiveness of the nano-formulated medication was further assessed using Fourier transform infrared spectroscopy. *In vivo* assay and preliminary toxicity analysis of the drug were conducted using Swiss albino mice.

Results; Nanoparticles of 273.2±8.65 nm in size, zeta potential -17.8±0.361mV and polydisperity index of 0.212±0.02 was formed. The zeta potential and nano-particle sizes did not vary widely at different storage temperatures of between 4°C and 25°C. Encapsulation efficiencies of dihydroartemisinin, primaquine, and lumefantrine in the triple nano-formulated drug were 93.98±0.41, 42.03±9.46, and 87.60±0.64 respectively. The FTIR results showed that the nano-formulated drugs exhibited less pronounced peaks as compared to the free drugs. N-H peaks were evidenced at 2,853 and 2, 914 cm^{-1}. The C=N and C=C absorption peaks were also evidenced at 1,642 and 1,565 cm^{-1} respectively. The OH-absorption peak that was more pronounced in the three free drug samples at wavelength number 3,732 cm^{-1} was not present in the nano-formulated drug samples. The triple nano-formulated and free drugs exhibited antimalarial chemosuppression efficiencies of 91.34% and 62.29% respectively. A drug concentration of 2,000mg/kg did not exhibit any form of toxicity and no deaths were recorded from the toxicity study.

Conclusion; The *in-vivo* results showed that the nano-formulated drug samples exhibited better antimalarial results compared to the counterpart free drugs. Toxicity studies also indicated that the nano-formulated drugs were safe. Solid lipid nanoparticles was thus demonstrated to be a good nano-drug delivery system for the antimalarial drugs in a triple treatment regimen.

Formulation of Electrospun Poly-Methyl Methacrylate (PMMA) into Solid Lipid Nano-Particle as a Novel Long-Lasting Insecticidal Nets (LLINs)

James Owour (Department of Chemistry, Technical University of Kenya)*

Electrospinning is a very versatile technique used for many purposes, such as tissue engineering, textiles, air and water treatment filter, and solar cells. It is currently being introduced in drug delivery systems. This method is cheap, easy to handle, reproducible when ambient parameters are controlled and can be used for many formulations. With the fast-paced progress of nanotechnology, various Drug Delivery Systems (DDSs) have been developed to counter challenges such as discontinuous drug release, unsatisfactory drug loading efficiency, burst, low drug stability and utilization efficiency *in vivo*. Compared with DDSs based on liposomes, micelles, nanoparticles and

hydrogels, electrospun fibres have attracted increasing attention as promising drug carriers. DDSs based on electrospun fibres are being studied and explored due to the maneuverability of the electrospinning process and the subsequent customizable design of the fibre-based scaffolds. Electrospun fibre scaffolds include simple preparation, high material universality, and favorable surface chemical properties for drug adsorption. The importance of this research is to create new and innovative drug carriers with higher efficiency in transporting the bioactive agent to the target zone, avoiding secondary effects in the body. Nanofibers and nanoparticles have become an important strategy in pharmacology due to their physicochemical and biocompatible properties useful for this purpose among the techniques compared are blending coaxial, emulsion and surface modification electrospinning, followed by electrospray and coaxial electrospray. The current study seeks to explore the potential of electrospun Poly-Methyl Methacrylate into solid-lipid nanoparticle (SLNs) for target delivery of pyrethrin as a novel long-lasting insecticidal nets (LLINs).

Identification of Candidate Drugs and Targets using In Silico Chemogenomics Strategies

Reagan M. Mogire (Kenya Medical Research Institute -Wellcome Trust Research Programme); Silviane A. Miruka (KEMRI-Wellcome Trust Research Programme/Centre for Research in Therapeutic Sciences, Strathmore University); Dennis W. Juma (KEMRI-Wellcome Trust Research Programme); Ben Andagalu (KEMRI-Wellcome Trust Research Programme); Bernhards R. Ogutu (KEMRI), **Hoseah M. Akala** (KEMRI)*

Background; Identification, prioritization and optimization of compounds with antipathogenic activity is huge challenge in drug discovery and development. The classical methods that are reliant on dose-response based assays are time-consuming and costly. Further, most bioactive compounds discovered using the classical methods fail to progress to treatments due to safety concerns.

Methods; We used in-silico Chemogenomics in drug discovery strategies to identify new drug candidates, new drug targets, or repurposing of approved drugs for use against previously undiscovered purposes. This was attained by searching publicly available biomedical information on known targets of drugs, characteristics of predicted molecules and approved drugs databases. For malaria, all the *Plasmodium falciparum* proteins sequences available in NCBI RefSeq were mined and used to perform a similarity search against DrugBank, TTD and STITCH databases to identify similar putative drug targets. Essentiality and druggability indices of the *P. falciparum* protein analogs were obtained from the Tropical Disease Research (TDR) database. Candidate drugs or targets obtained from these strategies were validated using *in vitro / ex vivo* testing against reference clones plus clinical isolates as well as clinical efficacy studies. Association between the compounds', *in vitro* antiplasmodial activity and the percentage similarity were assessed between their known targets and similar Plasmodium proteins using regression analyses.

Results; Antiplasmodial activity was highest in compounds that were predicted to target *P. falciparum* proteins that were essential or had a druggability index of 1. The antiplasmodial *in vitro* activity of compounds was also positively correlated with the percentage similarity between its known target and the *Plasmodium* protein analogs.

Conclusions; Our findings suggest that the protein target-similarity approach can be used to identify and prioritize compounds with activity against *P. falciparum* or predict their potential targets. This approach may also be useful in repurposing compounds against other pathogens or other potential disease targets.

Nanoformulation, Characterization and Antidiabetic Activity of Metformin Hydrochloride

Mark Kimani (Kenyatta University (KU))*; Peter Mwitari (Kenya Medical Research Institute (KEMRI)); Eliud N. M. Njagi (KU); Susan Musembi (KU); Lucia Keter (KEMRI); Jeremiah Gathirwa (KEMRI)

Background; Despite metformin hydrochloride being accepted and widely used as first line monotherapy agent for the treatment of type 2 diabetes, pharmacokinetics profile studies have indicated that metformin has a low absolute bioavailability. This is due to decreased absorption. Furthermore, it has a short biological half-life. 90% of the absorbed drug is eliminated via the renal route within the first 24 hours. This necessitates repeated dose administration thus increasing risk of drug dependence and toxicity when used for a long period of time by patients. Formulating drugs into nanoparticulate delivery systems has demonstrated distinct advantages over traditional dosage forms. For oral drug delivery, encapsulation of drugs to Solid Lipid Nanoparticles (SLNPs) has been shown to significantly improves specificity and efficacy, stability, safety, absorption and able to control the release of the incorporated drug. The objective of this study was to encapsulate metformin into SLNPs and determine *in vivo* safety and hypoglycemic potential.

Methods; In this experimental study design, encapsulation was done by covering metformin hydrochloride with physiological lipid stearic acid dispersed in polyvinyl alcohol as the surfactant. This was then spray dried using Mini Bosch Spray drier into powder form. The SLNs were then characterized for average particle size, zeta potential, polydispersity index, encapsulation efficiency, stability and surface chemical composition. Hypoglycemic activity was determined in diabetes induced Swiss Albino mice. Hematological, biochemical and histological parameters were used to established safety.

Results; The size of nanoparticles was optimized against a benchmark of less than 500 nm as it is reported that smaller particles undergo passive diffusion through a thin simple columnar epithelial layer of the intestines. All particles showed a positive zeta potential ranging between +30.2 to +21.7 mV. The average size measured ranged between 267.5 to 335.3 nm. PDI was between 0.070 and 0.176 confirming a homogenous size distribution. Stability of the SLNPs was tested for a period of 3 months at both 4 °C and 25 °C. After this period SLNPs under 4 °C had a slight increase in size from 267.5 nm to 298 compared to 25 °C. pH remained between 5.6 and 6.5. The metformin content was quantified to be 0.4mg/ml. *In vivo* antidiabetic assay showed that at the highest concentration of metformin-loaded-SLNPs the blood glucose level was significantly lower compared to that of similar concentration for the free metformin within the first 2 to 3 hours suggesting an increase in absorption.

Conclusion; Metformin hydrochloride was successfully encapsulated into solid nanoparticles using the solvent emulsification evaporation method. The particle size was small enough to allow higher absorption into the gastrointestinal tract before elimination. Efficacy evaluation in Swiss Albino mice showed that the nanoformulated metformin was more effective as compared to the conventional oral dose.

Scientific Session 15: ANTIMICROBIAL RESISTANCE-1

Abstract 120

Title: Antimicrobial Resistance Profiles of Bacteria Recovered from Patients seeking COVID-19 PCR Testing in Nairobi

Authors: japhet jk katana (kenya medical research institute)*; kenneth malombe (kenya medical research institute); Susan W Kiiru (KEMRI); John Njeru (KEMRI); dr. caroline ngugi (JKUAT); John Kiiru (KEMRI-CMR)

Antimicrobial Resistance Profiles of Bacteria Recovered from Patients Seeking Covid-19 Testing in Nairobi

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Background: Bacterial co-infections are common with COVID-19 infection and increase the disease outcomes among individuals. Resistant bacterial synergy with the SARS-CoV-2 virus increases the risk of intensive care unit hospitalization among patients with underlying conditions. There is no data in Kenya and Africa showing the impact prevalence of AMR in the COVID-19 pandemic. Antimicrobial surveillance among individuals seeking COVID-19 PCR tests was crucial in determining the prevalence of bacterial antimicrobial resistance.

Objectives: To determine the common bacterial co-infections and the resistance phenotypes of bacteria recovered from individuals seeking COVID-19 PCR testing services at KEMRI and Mbagathi County hospital.

Methods: A cross-sectional study design was used; 385 oral pharyngeal swabs samples were collected from individuals seeking COVID-19 PCR testing services at KEMRI and Mbagathi County hospital between March and October 2022. A structured questionnaire was used to collect clinical, antibiotics usage patterns, and social demographics data Bacterial isolation was done on Blood Agar, Chocolate Agar, MacConkey Agar, and mannitol Agar in aerobic and anaerobic conditions, while identification was made using biochemical media. Additionally, ASTs were done using the disk diffusion method.

Results: A total of 389 patients were sampled and at least one bacteria was isolated from 50.13% (194) of the samples analyzed. Bacteria isolated: 30.9% (60) were Streptococcus spp, 0.5% (1) was Acinetobacter spp, 2.1% (4) were Escherichia coli,10.3% (20) were Klebsiella, 0.5% (1) was Serratia spp and 47.4% (820) were Staphylococcus. Gram-positive bacteria were 82.5% (160) and 17.5% (34) were gram-negative. Most of the bacteria isolated were resistant to Ceftazidime, Sulfamethoxazole Trimethoprim, and Nalidixic acid at 75%,72%&71%, respectively. In contrast, Amikacin (90%), chloramphenicol (84%), gentamicin (80%) & Cefoxitin (68%), were the most susceptible. Resistance to expanded spectrum cephalosporins such as Ceftriaxone, cefepime, and Ceftazidime, ranged between 30–75%. Acinetobacter spp, E. coli, streptococci spp & Klebsiella spp were the most resistant to broad-spectrum antimicrobials such as Ceftazidime, Ceftriaxone, and Ciprofloxacin, ranging between 24 – 33%. About 53(27%) of all upper respiratory isolated were MDR, while 15(7.7%) were ESBLs.

Conclusion: The study findings highlighted bacterial phenotypes and how viral respiratory infections predispose patients to upper respiratory-resistant bacterial infections thus the need for management and control of bacterial co-infection.

Keywords: antimicrobial serveilance of upper respiratory bacteria using patients seeking COVID-19 PCR testing services.

Abstract 121

Title: Bacteriophages for the treatment and bio control of multidrug resistant Acinetobacter baumannii

Authors: Felix Mwai (KEMRI)*; Ivy J. Mutai (Institute of Primate Research/USAMRD-A); Martin MG Omondi (walter reed); Lillian Musila (USAMRD-A, Kenya/KEMRI)

Background: Acinetobacter baumannii is a common nosocomial infection on the WHO priority pathogen list with increased reports of multiple-drug resistance (MDR) globally and in Kenya. Their resistance to the last-line antibiotics and the occurrence on hospital surfaces increase their transmission of untreatable extensively-drug resistant strains. This study aimed to identify environmental bacteriophages as alternative to antibiotics for human therapy and surface decontamination.

Methods: Endemic clinical MDR A. baumannii isolates with different strain types (STs), geographical distribution, resistant to last-line drugs carbapenem were selected to screen for phages. Samples from soil, and sewerage water around Nairobi County were enriched with the host bacteria to screen for phages with lytic activity towards A. baumannii through spot test. Plaque assay was used to quantify and purify the phages. Phage host range was conducted through direct spot test (DST) and efficiency of plating (EOP) to analyze the cross reactivity and the efficiency of the isolated phages against 23 A. baumannii isolates. Phages with the broadest host range were also subjected to EOP.

For stability studies, the selected phages were subjected to the pH of 2, 4, 6, 8, 10, 12, and 14 and temperature range of 4ºC, 20ºC, 37ºC, 49ºC, 60ºC, 70ºC, and 80ºC environments. The ability of phages to degrade biofilms was also tested by allowing the bacteria to form adhesions on the microtitre plate followed by phage treatment. The phage effect was tested through absorbance.

Results: 15 phages targeting six A. baumannii strain types were isolated from sewerage systems: ST1137 (7), ST1 (2), ST2 (3) and 1 each against STs 22, 374, 164. Six out of the fifteen phages exhibited a broad host-range among the 23 isolates: AB04ST0201RS1 (12/23), AB15ST37401RS1 (10/23), AB05ST2201PS1 (9/23), AB12ST113701CHK (9/23), AB04ST0201RUAII (7/23) and AB04ST0201CHK (6/23).

In EOP, phages AB04ST0201RS1 and AB04ST0201RUAII were the most efficient with the highest progeny production.

The six phages had lytic activity at 4ºC, 20ºC, 37ºC, 49ºC with reducing activity at 60ºC and 70ºC and no activity at 80ºC. Optimal activity was observed at 20ºC and 37ºC. There was optimal lytic activity at pH 6 and 8 with reduced activity in pH 4, 10, 12 and no activity at pH 2,14.

On biofilm action, the phages were able to eliminate biofilm evidenced by the decrease in absorbance readings in the phage treated wells.

Conclusion: The study confirms that our environment harbors lytic phages against the endemic MDR strain types of A. baumannii in Kenya. The lytic activity of the phages in broad pH and temperature, and biofilm digestion indicates their potential in therapeutic and bio control purposes.

Keywords: Bacteriophages for treatment and bio control of Acinetobacter baumannii

Abstract 122

Title: Low Microbiology Diagnostic Capacity in Kenya Public Hospitals: findings from a cross-sectional survey for 20 facilities

Authors: Brian M Nyamwaya (KEMRI/Wellcome Trust Research Programme)*; Joyce W Kigo (KEMRI-Wellcome Trust); Felix Bahati (KEMRI-Wellcome Trust); Morris Ogero (KEMRI-Wellcome Trust); Jackline Gachoki (KEMRI-Wellcome Trust); Salim Mwarumba (KEMRI-Wellcome Trust); Samuel Akech (KEMRI-Wellcome Trust)

Background: Antimicrobial resistance (AMR) is an emerging public health problem that is challenging to tackle owing to its complex nature. Infection with resistant microorganisms result in adverse clinical outcomes making their timely detection very important. Laboratory surveillance plays a crucial part in establishing the burden of AMR however this depends on microbiology diagnostic capacity. We aimed to establish microbiology laboratory capacity across 20 Kenyan hospitals.

Methods: An online questionnaire adopted from the WHO laboratory assessment tool was used to gather the data.

Results: Thirteen of the 20 hospital laboratories reported having a microbiology department. Ten of these 13 laboratories reported that they performed blood cultures but the utilisation varied markedly (0 to 720 cultures in 2020), while 3 laboratories only performed other types of cultures. Majority (8/10) of the laboratories that performed blood cultures reported using an automated blood culturing system; all these 10 reported utilising gram staining and manual biochemical testing for pathogen identification and half of these used additional methods including analytic profile index (API). These 10 laboratories also reported carrying out antibiotic susceptibility testing (AST) for blood culture samples with all but 1 using manual disc diffusion methods. Majority (7/10) of these laboratories reporting performing internal quality control (IQC) for media, reagents, antibiotic discs and AST on control strains. All 20 laboratories reported having an aspect of a quality management system with more than three-quarters being accredited nationally and participating in internal and/or external quality control programmes. Lastly, all the laboratories that performed blood cultures were set up through external donor funding.

Conclusion: There is need for microbiology laboratories in Kenya to be supported to optimally conduct these tests. Alternatively, given the high cost of operating microbiology laboratories, other approaches to setting up and operating microbiology laboratories need to be explored. Lastly, future research can look into the reason for the varied uptake in blood culture samples and sustainability of services for short-term externally funded laboratories.

Keywords: antimicrobial resistance, surveillance, microbiology capacity, laboratory, diagnostic

Abstract 123

Title: First report of colistin resistance gene mcr-10 in Kenya

Authors: Collins K Kigen (KEMRI/USAMRD-A)*; Lillian Musila (KEMRI/USAMRD-A); Angela Muraya (JKUAT)

Background: The emergence and spread of mobile colistin resistance (mcr) genes has exacerbated colistin resistance, a last-line drug used in treatment of multi-drug resistant gram-negative infections. Ten mcr variants have been reported globally since its discovery in China in 2015.

Methods: This study reports the first mcr-10 gene identified in Kenya from a clinical isolate obtained in April 2015 from a consenting male patient presenting with an infected leg wound in a hospital in Nairobi, Kenya. VITEK2 was used for identification and Antimicrobial Susceptibility Testing (AST). Colistin resistance was confirmed using the broth microdilution method and interpreted in accordance with the CLSI 2022 guidelines. Whole Genome Sequencing was performed on both Illumina and Nanopore, and the hybrid assembly queried against ResFinder database using ABRicate tool, to identify antimicrobial resistance (AMR) genes.

Findings: The isolate was identified as a sequence type 1 (ST1) Enterobacter cloacae. AST revealed it was resistant to cefuroxime, colistin, cefixime and displayed intermediate susceptibility to chloramphenicol. The broth microdilution test confirmed Colistin resistance with MIC ≥ 4 µg/mL. The AMR genes detected were mcr-10.1 harbored on a plasmid pECC59-2 and four chromosomally encoded genes, blaCMH-3.1 (AmpC β-lactamase), OqxA-1, OqxB-1 (efflux pumps) and fosA-7 (fosfomycin thiol transferase).

Conclusion: The discovery of mcr-10 gene in this study as well as the previously identified mcr-8 in Kenya highlights the risk of spread of highly mobile genes and the risk of losing the utility of this critical last-line drug for clinical care unless appropriate control measures, such as antimicrobial stewardship, are implemented.

Keywords: colistin, antimicrobial resistance, mcr

Abstract 124

Title: Antibiotic Resistant Vibrio cholerae O1 and its SXT elements associated with cholera outbreaks in Kenya between 2007 and 2016

Authors: Mohammad Shah (Nagasaki University); Martin Bundi (Kenya Medical Resarch Institute)*; Cyrus Kathiiko (Nagasaki University - KEMRI (NUITM-KEMRI)); Sora Guyo (Kenya Medical Research Institute); Amina Galata (Nagasaki University - KEMRI (NUITM-KEMRI)); Gabriel Miringu (Nagasaki University - KEMRI (NUITM-KEMRI)); Yoshio Ichinose (Nagasaki University - KEMRI (NUITM-KEMRI)); Lay-Myint Yoshida (Nagasaki University)

Background: Multidrug-resistant Vibrio cholerae O1 strains have long been observed in Africa, and strains exhibiting new resistance phenotypes have emerged during recent epidemics in Kenya. This study aimed to assess the epidemiological aspects, drug resistance patterns, and genetic determinants of V. cholerae O1 strains isolated from cholera outbreaks in Kenya during 2007-2010 and 2015-2016.

Methods: A total of 228 V. cholerae O1 strains, including 226 clinical isolates from 2007-2010 and 2015-2016 cholera outbreaks, and two environmental strains isolated from thirteen counties in Kenya were subjected to biotyping, serotyping, and antimicrobial susceptibility testing, including the detection of antibiotic-resistance genes and mobile genetic elements.

Results: All V. cholerae isolates were identified as El Tor biotypes and susceptible to ceftriaxone, gentamycin, and ciprofloxacin. Concurrently, the majority of isolates were resistant to trimethoprim-sulfamethoxazole (94.6%), streptomycin (92.8%), and nalidixic acid (64.5%), while lower resistance was observed against ampicillin (3.6%), amoxicillin (4.2%), chloramphenicol (3.0%), and doxycycline (1.8%). On the other hand, the 2015-2016 outbreak strains were found only to be resistant to nalidixic acid (100%). SXT element was found in 95.5% of the V. cholerae isolates; conversely, class 1, 2, and 3 integrons were absent. Additionally, 64.5% of the isolates exhibited multidrug resistance patterns. We identified that outbreak cholera strains were primarily resistant due to chromosomal mutation and SXT element-oriented antibiotics.

Conclusion: Antibiotic-resistant gene clusters suggest that environmental bacteria may act as cassette reservoirs that favour the emergence of resistant pathogens.

Keywords: V. cholerae O1, Cholera outbreaks, Multidrug-resistant strain, Antibiotic-resistant mechanisms

Abstract 125

Title: Mutations in MtrR and 23S rRNA genes associated with macrolide resistance in Neisseria gonorrhoeae, Chlamydia trachomatis, and Mycoplasma genitalium among symptomatic women in Busia County, Kenya

Authors: Primrose M Ndungu (MoH)*; James Kimotho (Kenya Medical Research Institute); Robinson M Irekwa (Kenya Medical Research Institute); Tonny T Nyandwaro (KEMRI); George Osanjo (University of Nairobi); Peter Kemboi (Kenya Medical Research Institute); Caroline Njoroge (Kenya medical Research Institute); Anne Mwangi (Kenya medical Research Institute); Matthew Mutinda (Kenya medical Research Institute); Nicole Tanchu (Kenya medical Research Institute); Joanne J Yego (Kenya Medical Research Institute); Grace Ng'endo (Kenyatta University); Dawala Koromtili Oumar (Pan African University); Poul Otilmoi (Pan African University); Samson Muuo (Kenya Medical Research Institute)

Background: Chlamydia trachomatis, Neisseria gonorrhoeae, and Mycoplasma genitalium are among the most commonly reported organisms that cause urogenital tract infections in women. Mutations in the 23s rRNA gene which is the drug binding site, is a significant cause of resistance in C. trachomatis and M. genitalium. In N. gonorrhoeae, mutations in the mtrR gene responsible for drug efflux can lead to macrolide resistance. This study aimed to determine the presence mutations in mtrR and 23SrRNA genes associated with macrolide resistance as well as establish the mechanisms of resistance and determine evolutionary relationships among the isolates.

Methods: Using consecutive sampling, endocervical swabs were collected from 424 women who presented with symptoms of sexually transmitted infections in two hospitals in Busia County. C. trachomatis, N. gonorrhoeae, and M. genitalium were detected using multiplex polymerase chain reaction (PCR). Amplification and sanger sequencing for the macrolide-resistant genes of interest were subsequently done. The sequence data were analyzed for point mutations and evolutionary relationships.

Results: None of the most commonly reported mutations were found for the 23SrRNA gene (A2058G and A2059G) or the mtrR gene (H105Y, A39T and G45D). The most prevalent mutations were; P101A, H102Yand S110N for N. gonorrhoeae, G1987T (Escherichia. coli numbering) for C. trachomatis and G2010T (E. coli numbering) for M. genitalium. Phylogenetic analysis indicated that each organism had distinct clades with similar resistance profiles and evolutionary relationships.

Conclusion: The most commonly reported mutations responsible for macrolide resistance were not found in any of the isolates for this population. New resistant markers for resistance were however present and most of them were responsible for amino acid changes. This study reinforces the importance of continuous surveillance to detect the spread and evolution of resistant strains against macrolides.

Keywords: Antimicrobial resistance, Sexually transmitted infections, Mutations, MtrR gene, 23S rRNA gene, symptomatic women, Busia

Scientific Session 16: Health Systems-2

Abstract 126

Title: PLAN DO STUDY ACT (PDSA) CYCLE APPROACH TO INCREASE YIELD FROM CONTACT MANAGEMENT THE CASE OF SUNA WEST

Authors: Peter P.O.O Omware (Ministry of health)*; Stella Omulo (Centre for health solution); Nelson Mandela (Impact RDO site coordinator); David Nyamohanga (Ministry of health)

Background: Suna west is third in terms of contribution to tuberculosis (TB) case finding amongst the eight sub counties in Migori county .The main economic activity is mining and it has the largest slum which contribute greatly to increased TB transmission but from 2020 began experiencing a drop in yield from TB contact management to 1.2%.

PLAN: In 2021 the sub county TB work improvement team identified this problem and started a quality improvement (Q)I project. The following root causes were identified using a fish borne analysis i.e clinician knowledge gap on pediatric TB diagnosis, Inadequate assessment and evaluation of contacts of bacteriologically confirmed TB cases, poor documentation of TB contact management register.

Objective (goal setting): To increase TB case yield from community referrals of presumptive TB cases from 1.2% to 10% by December 2022.

Methodology: This was a mixed method study comparing data collected from the facility TB patient registers and contact management from 2019 to 2020 before integrating quality improvement and 2021 after the number of TB cases diagnosed was then analyzed.

Strategies employed were (DO)

1. Training of facility staffs on integrated TB and pediatric TB (7)

2. Continuous medical education to sensitize facility staff on contact management register.

3. Regular on job training, mentorship and support supervision on screening and TB management.

4. Training community health volunteers on screening, contact tracing and community facility referrals of suspects.

5. Training of community health volunteers on infection prevention, proper sample handling and providing them with cooler boxes to ferry samples from the field.

6. Weekly and monthly sub county TB data review meeting on the sub county TB What Sapp plat form.

RESULTS (STUDY)

In 2019 out of 352 contacts 142 (40.34%) were referred to the facility for evaluation and 11 (7.7%) cases of TB were diagnosed.

In 2020 out of 585 contacts 322 were referred to the facility for evaluation and 4 (1.2%) cases of TB were diagnosed.

In 2021 out of 530 contacts 275 (51.9) were referred to the facility for evaluation and 16 (5.8%) cases of TB were diagnosed

In 2022 out of 614 contacts 728(66.3%) were referred to the facility for evaluation and 51 (10.6%) cases of TB were diagnosed

CONCLUSION: The higher the proportion of contacts of bacteriologically confirmed TB cases reffered the higher the yield (training of CHVs to improve refferals and facilty staff to better evaluate contacts was key)

Integrating quality improvement (PDSA cycle) in contact management helps in improving TB yield by identifying problems, solutions and tracking progress.

RECOMMENDATION (ACT): Interventions to increase number of contacts of bacteriologically confirmed TB cases reaching and assessed at the facility are needed to increase yield from contact management..

Integrate quality improvement in TB contact management to increase TB case finding yield.

Keyword: TB

Abstract 127

Title: ASSESSING THE RECEPTION AND APPLICATION OF COVID-19 COMMUNITY HEALTH MESSAGING IN TWO LARGE DIVERSE URBAN SETTLEMENTS IN NAIROBI: A CASE OF KIBRA AND NYAYO ESTATE EMBAKASI.

Authors: James M Wodera (Kenya Medical Research Institute)*; Davis Mkoji (Kenya Medical Research Institute); Veronica Manduku (KEMRI); VINCENT MOSHI (PTBiKenya); Tervil Okoko (Numbers Afrika)

Introduction: The WHO declared COVID-19 a pandemic in March 2020. The government devised strategies to mitigate its impact including Advocacy, Social Mobilization & Behavior Change Communication. Despite efforts by the MOH to control its spread, congested urban communities continued to register rise in cases. This study sought to assess how communities living in two large diverse urban settings, Kibra and Nyayo Estate Embakasi, received & applied the COVID-19 health messages for mitigation.Methodology: A mixed methods approach; qualitative and quantitative data collection was used after consenting. Semi-Structured Questionnaire, In-depth Interviews, desk review, and direct observation checklist were used to assess behaviour in response to the COVID-19 health messages. Eight IDIs were done, 4 each in Kibra & Nyayo, while a SSQs involving 397 (Kibra) and 147 (Nyayo) participants was done. At least 4 Observations were made at each sites to assess the behaviour of the two communities in response to COVID-19 messages. Thematic analysis was applied using relevant computer software and Quantitative data presented using tables while qualitative information was presented in a descriptive format. Results: Majority (98.71%) of study participants had access to at least one of the mainstream media used to transmit COVID-19 information. Television (TV) was most accessed (78.68%) followed by Radio (78.13%). TV was accessed more (88.75%) by those in formal employment. Respondents from Nyayo reported having more (97.28%) access to TV compared to (71.79%) in Kibra. Participants in Nyayo reported more (97.96%) access to Android mobile phone than those in Kibra (63.73%). More males than females had access to radio and Android mobile phone. Access to Newspaper in Nyayo was higher (61.90%) compared to Kibra (21.16%). On average 86.68% respondents reported to adhere to the five key messages (wash hands, wear mask, keep distance, stay at home, sanitize) on Covid -19 mitigation. The use of simple, precise language, guidelines translation to various local languages, and use of popular media outlets like TV, radio and SMS positively influenced message uptake. Inaccessibility to media outlets, constant electricity outages, especially in Kibra, poverty and living in congested households negatively impacted the reception and application of the guidelines. In terms of adherence, more females adhered to the guidelines than males. Conclusions: Despite majority of residents of Kibra and Nyayo, having access to the Covid-19 messages, guidelines adherence was affected by various barriers including economic conditions and peer influence. More females adhered to the guidelines than males, and females were more persuadable with respect to the influence of the health strategies on their behaviour. While TV was most preferred medium of information in urban settings, TV, radio and Android mobile phone remained most suitable media for disseminating behavior change messages among women

Keywords: health messages, assessing, communities COVID-19

Abstract 128

Title: PREVALENCE OF HIV DRUG RESISTANCE MUTATIONS IN HIV PATIENTS RECEIVING ANTIRETROVIRAL THERAPY IN WESTERN AND COASTAL REGIONS IN KENYA

Authors: Juster Mungiria (Chuka University)*; John Njeru (KEMRI)

The increase in HIV infection and drug-resistant strains is an important public health concern, especially in resource-limited settings. HIV drug-resistance threaten the gains of the HIV infection control programs and have continued to have an effect on the response to antiretrovirals (ART). There is therefore a need for a sustainable surveillance for the emergence and spread of HIV drug resistance mutations. This study aimed at determining the occurrence of drug resistance mutations in patients receiving ART in Western and Coastal regions in Kenya. Blood samples were collected from consenting 114 cases (viral load >1000RNA copies/mL) and 263 control participants (viral load <1000 RNA copies/mL) receiving first line ART regimen namely Zidovudine, Lamuvidine, Stavudine, Tenofovir and Nevirapine from Kisumu (n = 272) and Malindi (n = 105). A detailed social demographic questionnaire was administered to gather information on ART adherence, health and health care, HIV testing and sexual behaviour and nutritional status. The HIV drug resistance mutations were detected using an in-house conventional PCR assay. A total of thirty-one participants (8.2%) were infected with a drug resistant virus strain. Out of the 31participants 26 were from cases group and 5 were from the control group. Sixteen mutations were detected against nucleoside reverse transcriptase inhibitors (NRTI) including; 14 nucleotide analogue mutations (NAMs) 1(M184V, Y), 2(M184V, G),1(M184V, A),2(M184V, K), 2(M184M, V), 2(M184V),2(M184V,T), 2(M184V,V) and 2 thymidine analogue mutations (TAMs)1(T215TN),1(Y115YF). Eleven out of the sixteen NRTI mutations detected were from Kisumu while remaining five were from Malindi. Fifteen mutations were found against Non nucleotide reverse transcriptase inhibitors (NNRTI) including; 3(K103),3(V106),1(Y1 81),6(G190),1(A98),1(V108). Out of these, eleven were from Kisumu and four from Malindi. Significant associations were found between cases and controls (p=0.001), gender (p=0.016), meal preparation (p=0.030) and drug resistant mutations. For the first time, G190A and NAMS mutations were found to be most frequent drug resistant mutations in the study sites. Emergence of HIV drug resistance and virologic failure are major challenges for ART. Investigations on emergence of HIV Drug resistance mutations among patients on ART as well as virologic failure in the absence of HIV Drug resistance mutations might help in better understanding the HIV drug resistance dynamics and planning appropriate clinical management for patients with HIV. Moreover, HIV drug resistance testing should be encouraged especially among those on ARVs with low genetic barriers like NNRTIs in that HIVDRMs are known to jeopardize clinical outcome of ARV treatment.

Keywords: Drug Resistance Mutations

Abstract 129

Title: Influence of Strategic Leadership Style on Partnerships Implementation in a Medical Research Organisation in Kenya: A Case Study

Authors: George Kirigi (kemri)*

Background: Partnership in leadership is a phenomenon that has received little attention in the field of strategic management research. The study sought to investigate the use of partnership styles in a Kenyan medical research institute. The overarching goal was to gain a better understanding of the role of partnership style in fostering organisational leadership.

Methods and Materials: Methods and Materials: This was a case study based on the collection and analysis of primary data. The sample was drawn from a single public medical research institution in Nairobi County. In this context, a purposeful sampling for units of inquiry included three key informants, strategic leaders with direct involvement in KEMRI's partnerships who were the study's only source of information. After ensuring confidentiality and anonymity, willing potential respondents were given verbal consent. The main data collection instrument was a modified self-reported questionnaire that included separate pertinent themes such as leadership, financial and non-financial aspects, communication, interpersonal relationships, agreements, conflict resolution, interpersonal relationships, agreements, conflict resolution, power bases, existing mechanisms, identity, opinion, sharing information, and so forth. Every questionnaire was completed and returned- A 100% response rate. Data were analysed using the content analysis technique.

Findings: The study's data reveal descriptive baseline information about partnerships and leadership in a medical research organisation, which could aid in the future use of larger samples and research designs that include not only quantitative but also qualitative methodologies and statistical analysis.

Conclusion: The strategy used to bring together multiple partnerships is not well understood, it should be examined. As a result, it appears that a knowledge gap exists, particularly in the party's roles and recognition of leadership to reduce inequalities. The aspects of the power base leave inadequacies. However, the sample might be considered small.

Keywords: partnership, leadership, medical research organisation, case study

Abstract 130

Title: Are stories-of-significant change technique useful as a source of capturing experiential evidence for informing policy and practice? Lessons learnt from Kenya

Authors: JAMES N. KARIUKI (KENYA MEDICAL RESEARCH INSTITUTE)*; Tiner J Ouma (KEMRI); LILIAN MAYIEKA (KEMRI); WAMBUI NJONGE (KEMRI); JENNIFER ORWA (KEMRI); LEYLA ABDULLAHI (AFIDEP); CAROL MUKIIRA (AFIDEP); ROSE ORONJE (AFIDEP)

Introduction: It is postulated that health managers require contextualized evidence for better health systems outcomes. Research communicators are exploring tools that facilitate evidence uptake. Experiential stories-of-significant-change written by healthcare workers can provide contextualized evidence. These stories potentially increase the likelihood of developing evidence-informed policies. Objective - to explore usefulness of stories-of-significant change tool to document experiential and localized interventions that have potential to inform health systems strengthening initiatives in Kenya.

Methodology: A participatory-action research approach was used. During capacity-building workshop, 14 research officers drawn from six pilot counties (Bungoma, Isiolo, Kitui, Makueni, Nyandarua, and Taita-Taveta) health departments, were encouraged to write stories of what they thought were significant changes arising from service processes improvements or innovations in English language. The stories were collected between September- November 2020. These stories were then verified by research scientists to ascertain their authenticity. A template outlining sections of stories-of-significant change was used. This methodology provided an inductive, indicator-free, participatory evaluation method that complements deductive research methods.

Findings: A total of 14 stories were received. The team classified them into 6 broad domains. The domain included community attitude/ behavior change -4 stories; awareness creation -4 stories; healthcare personnel behavior -3 stories; technology adaption -2 stories; health care provision -1 story; and innovations in laboratory processes had one story. Implications - personnel willingness, cooperation and teamwork among healthcare workers produces positive health outcomes; listening to clients is critical for service improvement; experiential learning leads to improvements in service delivery; community participation and ownership is crucial for sustainability of interventions; internal innovations by healthcare workers produced significant outcomes and are low-cost to implement; and sustained follow-up of post-training among healthcare workers leads to early adoption and adaption of the new skills learnt.

Conclusion: Stories-of-significant change tool was a useful methodology for documenting staff experiences. These documented experiences were codified and re-packaged (infographics) so as to provide useful lessons for implementing contextualized low-cost health services or interventions in a resource-constrained setting. Local experience and process innovations present valuable evidence that should supplement county and national health guidelines if national universal-health-coverage aspirations are to be realized.

Implication for Practice: For research communicators, the stories-of-change technique could be potential source of innovative ideas that could revolutionize knowledge brokerage targeting policy actors.

Keywords: Knowledge, Evidence, Context, Experiential, Stories-of-significant change,

Scientific Session 17: Genomics

Abstract 131

Title: Comprehensive profiling of antibodies against infectious diseases using the protein microarrays

Authors: Elijah Gicheru (Kemri Wellcome Trust)*

Background: In the first two decades of this century there have been numerous reports of newly emergent infectious disease pathogens that have caused major human outbreaks. While some of these outbreaks such as the pandemic corona and influenza viruses have attracted global investment in vaccine research and development, many others with localized transmission phenotypes in low income countries have attracted less interest. These pathogens continue to exert a considerable and often covert morbidity and mortality burden among the world's poorest populations. To identify local priorities for vaccine research and Development, we used an inhouse protein microarray to reconstruct the paediatric infectious disease landscape in Kenyan children and estimated seroprevalence to forty-two distinct infectious disease pathogens over a 15-year period.

Methods: Pathogen-specific antibodies against 42 infectious disease pathogens were simultaneously assayed in 956 serum samples collected from one hundred and twenty four children who were part of a longitudinal birth cohort that was recruited repeatedly sampled between February 2002 and November 2005. To estimate changes in seroprevalence that occurred in the second decade of the century serum samples from 176 paediatric inpatients admitted to Kilifi County Hospital were collected between December 2006 and June 2017 and assayed for antibodies against the same set of infectious disease antigens printed on the in-house microarray chip.

Results: Respiratory syncytial virus, Cytomegalovirus, Norovirus, Coxsackie B1, Mumps virus and H3N2 influenza ranked top in order of seroprevalence, ranging from 53% for RSV to 37% for H3N2 Influenza in the first year of life. These patterns were consistent throughout the 15-year study period. There was limited serological evidence of exposure to pathogens such as the Yellow Fever Virus, Ebola Virus, Zika Virus and Chikungunya Virus, all with estimated seroprevalence below 1%. Serological analysis of antigen targets that are currently part of the Kenyan Expanded Programme on Immunization showed synchronized rises in antibody level that were consistent with immunization at prescribed age-points, although the population-level seroprevalence estimates for targets such as Diphtheria (71%) in the first year of life suggested relatively low vaccine coverage.

Conclusion: We report the successful development and validation of a locally-designed protein microarray chip for high throughput assessments of population-level exposure to a range of common and emerging infections The data suggest high transmission levels for a number of vaccine preventable infections in the vulnerable first year of life and provide an objective, data-driven approach for prioritizing candidates for vaccine development or rollout.

Keywords: Micro array

Abstract 132

Title: Whole genome sequencing-based surveillance of rotaviruses in Kenya reveals interspecies transmission, evolution and reassortment events

Authors: Ernest A Wandera (Kenya Medical Research Institute)*; Natsuki Kurokawa (Mitsubishi Tanabe Pharma Corporation); Maurine M Mutua (Nagasaki University-KEMRI); Mary N Wachira (NUITM-KEMRI, Kenyatta University); James Nyangao (Kenya Medical Research Institute); Samoel Khamadi (Kenya Medical Research Institute); Koki Taniguchi (Fujita Health University); Jesse Gitaka (Mount Kenya University); Satoshi Kaneko (Nagasaki University); Naohisa Tsutsui (Mitsubishi Tanabe Pharma Corporation); Satoshi Komoto (Fujita Health University); Yoshio Ichinose (Nagasaki University)

Background: Rotaviruses are the leading cause of severe gastroenteritis in the young of both humans and animals worldwide. A whole genome-based genotyping system, which assigns genotypes to all the 11 gene segments of rotavirus, was recently adopted. Using the next-generation sequencing, we have characterized the full genomes of rotavirus strains identified in fecal specimen from diarrheic children in Kenya between 2009 and 2020 in order to gain insights into their origin, evolutionary patterns and transmission dynamics.

Methods: Genomic dsRNA of selected Kenyan rotavirus strains was 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. The nucleotide sequences were translated into amino acid sequences using GENETYX v11 (GENETYX).

Results: Whole genomic analysis of the globally emerging G12 rotaviruses detected in Kenya during the study period revealed a Wa-like genetic backbone: G12-P[6]/P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1. Of note is that the NSP4 genes of the Kenyan G12 strains appeared to be of porcine origin, suggesting the occurrence of reassortment between human and porcine strains. On the other hand, full genome analysis of the unconventional Kenyan G4P[6] strain revealed a unique Wa-like genogroup constellation: G4-P[6]-I1-R1-C1-M1-A1-N1-T7-E1-H1. Phylogenetic analysis showed that 10 of 11 genes of Kenyan G4P[6] strain were of porcine origin, while the remaining NSP2 gene was of human origin. Thus, the Kenyan G4P[6] strain had a porcine rotavirus backbone, hence is likely to be of porcine origin. Moreover, genomic characterization of uncommon G3P[6] rotavirus strains that have emerged in Kenya after rotavirus vaccine introduction revealed an uncommon DS-1-like genotype constellation: G3-P[6]-I2-R2-C2-M2-A2-N2-T2-E2-H2. These Kenyan G3P[6] strains showed numerous amino acid changes in the VP4 and VP7 antigenic epitopes compared to the current rotavirus vaccine strains, which could potentially result in reduced antibody binding and thus reduced neutralization of these strains.

Conclusion: The full genome-based characterization of Kenyan rotavirus strains reveals interspecies transmission and reassortment events involving porcine and human rotavirus strains and high number of consistent amino acid differences in the antigenic epitopes between some Kenyan strains and those of the current rotavirus vaccine strains. Our observations provide important insights into the origin, evolutionary patterns and transmission dynamics of these zoonotic and uncommon rotavirus strains and underscore the need for vaccine effectiveness against these strains to be closely monitored.

Keywords: Rotavirus; Full genome analysis; Evolution; Transmission; Reassortment; Kenya

Abstract 133

Title: Proteomics an agnostic approach to detect emerging viruses

Authors: Armand Paauw (TNO); Jelle de Koning (TNO); Hans van Leeuwen (TNO); Jasper Kieboom (TNO); bart keijser (TNO)*

Background: Identification of novel pandemic threats is a technological challenge. Efficient and rapid detection of novel pathogens and variants is of key importance to effectively institute counter measure and establish diagnostic protocols. In this project, we aimed to develop a proteomics-based workflow for efficient virus and strain variant identification.

Methods Heat inactivated viral samples, derived by cell cultivation (36) as well as fecal samples of children with a known gastrointestinal virus infection were subjected to proteolytic cleavage, using trypsin, to produce smaller peptide sequences. These peptides were then subjected to liquid chromatography-tandem mass spectrometry (LC-MS/MS) on a Orbitrap instrument coupled to a nano-LC, in which the masses of the peptides and fragments thereof were measured. The obtained data was processed in PEAKS X using a combination of de novo sequencing and database searching. Human contaminants were removed from the peptide mass spec data prior to virus identification. To enable virus species and strain variant identification, we set-up a proteome web-database with >1809 viruses including strain variants. (proteome4pandemic preparedness.com). Performance is the methodology was evaluated using viral panels, spanning diverse viral species.

Results Our proteome-based identification pipeline has been applied to analyze 36 samples derived by cell cultivation as well as 8 fecal samples of children with a known gastrointestinal virus infection . All 18 different viral species (Betacoronavirus OC43, Enterovirus A, Human coronavirus 229E, Human mastadenovirus F, Human metapneumovirus, Human orthopneumovirus (RSV A and RSV B), Human rubulavirus 4, Influenza A virus (H1N1 and H3N2), Influenza B virus, Mamastrovirus 1, Measles morbillivirus, Norwalk virus, Parechovirus A, Rhinovirus A, Rotavirus A, SARS-CoV-2, Vaccinia virus and West Nile virus) were correctly identified.

Conclusion The presented proteomics-based approach demonstrates that a variety of clinically relevant viral species can be identified within eight hours through single shotgun proteomic analysis. Implementation of this platform will enable rapid identification of novel pandemic threats.

Keywords

proteome virus agnostics diagnostics

Abstract 134

Title: Characterization of URST7 as a novel prognostic biomarker and therapeutic target for breast cancer

Authors: Regina Wachuka Mbugua (Kenya Medical Research Institute)*; Yataro Daigo (Shiga University of Medical Science)

Background: Breast cancer is one of the highly frequent cancers in women and causes the greatest number of cancer-related deaths worldwide. Despite a sustained decline in mortality rates and significant improvement in clinical outcome for patients, the efficacy of the current standard therapies is limited and prognosis of the disease is still poor. Therefore, new biomarkers and therapeutic targets for breast cancer are eagerly awaited. URST7 is an RNA modifying protein that has been reported to be upregulated in breast cancer cells and tissues compared to normal cells and tissues, therefore our study aims to evaluate the role of URST7 (Up-regulated in solid tumor 7) as a prognostic biomarker and therapeutic target for breast cancer.

Methods: We screened molecular targets by following methods: 1) Identification of candidate genes by gene expression profile database. 2) Examination of the candidate gene expression in breast cancer cells and clinical tissues by qPCR and western blotting. 3) Immunohistochemical validation of clinicopathologic significance of their protein expression by tissue microarray. 4) Examination of their functional effect on cell growth by siRNAs and plasmid transfection. 5) Identification of downstream targets by microarray. During this process, we selected up-regulated in solid tumor 7 (URST7) as a prognostic biomarker and therapeutic target for breast cancer.

Results: URST7 mRNA and its gene product were highly elevated in the majority of breast cancer cell lines and clinical breast cancer tissues, but barely detected in normal breast epithelial cells and tissues. Immunocytochemical staining showed that URST7 protein was mainly localized in nucleus and cytoplasm of cancer cells. Tissue microarray analysis revealed that URST7 was expressed in 204 of 252 (80.9%) breast cancers. High levels of URST7 expression were significantly associated with poorer prognosis for breast cancer patients ($P = 0.0102$ by log-rank test) and it was an independent prognostic factor for breast cancer. Suppression of URST7 expression by siRNAs significantly inhibited breast cancer cell growth. Intriguingly, enhanced URST7 expression led to a significant increase in cancer cell proliferation.

Conclusion: These results suggest that URST7 could be a potential biomarker and therapeutic target for breast cancer.

Keywords: Breast cancer, biomarker, therapeutic, cell proliferation

Abstract 135

Title: Genomic Analysis of Dengue virus 1 Associated with an Epidemic in Eritrea, 2011

Authors: Victor Mr Ofula (KEMRI)*; Solomon K Langat (Kenya Medical Research Institute (KEMRI)); Edith C Koskei (KEMRI); Hellen S Koka (Kenya Medical Research Institute); Samuel Owaka (KEMRI); Konogoi Limbaso (KEMRI); Rosemary Sang (ICIPE)

Dengue viruses (DENVs) are mosquito-borne viruses which can cause disease ranging from mild fever to severe dengue infection. These viruses are endemic in several tropical and subtropical regions. In Africa, there is paucity of data on the extent of the epidemiology and public health impact of the disease. Several major epidemics have been reported in several countries in Africa, which have caused outbreaks with increasing frequency. Between 2011 and 2014, an outbreak of Dengue swept through East Africa, with cases being reported in Kenya, Tanzania, Somalia and Eritrea. Prior to this, Eritrea had reported cases of Dengue since 2005. Despite the numerous cases of dengue being reported in Eritrea and Africa at large, there is limited number of genomic data on the isolates obtained. Consequently, this has contributed to lack of information on the circulating strains as well as the genotypes associated with outbreaks in the region. In this study, we report 3 genomes of Dengue virus 1 isolates obtained from Eritrea during the outbreak in East Africa between 2010 and 2014. The isolates were obtained from archived samples at Arbovirus/Viral Haemorrhagic Fever laboratory at the Centre for Virus Research, KEMRI.

The samples were processed for high-throughput sequencing, which was achieved with Illumina miseq sequencer. Sequence and phylogenetic analysis was carried out on the generated sequences, together with sequences obtained from Genbank.

In our analysis, we obtained two whole genome sequences and one partial sequence. Genome annotation on the whole genome sequences identified the expected polyprotein which was 10129 nt (3392 aa) in length, flanked by 5' and 3' untranslated regions (UTRs) of 73 nt and 125 nt, respectively. Pairwise similarity showed high similarity between the sequenced isolates, with 99.8% nucleotide similarity. BLASTN analysis showed a similarity of the isolates to DENV1-2522 (GenBank accession number KU509258.1), which was an imported strain to Germany by a traveller from Eritrea. Phylogenetic analysis placed the isolates from this study under the Genotype 1, and these isolates formed a clade with other strains from East Africa specifically Somalia, Kenya and Djibouti.

The findings in this study reveals that the virus strain that caused the dengue outbreak in East Africa in 2014, spread to multiple countries in the region, including Eritrea. This necessitates multi-country efforts to halt the spread of the virus during a dengue outbreak. The genomes made available in this study will add to the currently available genomes from the horn of Africa region, which will allow for better assessment of evolutionary and epidemiological history of Dengue 1 in the region as well as assist in vaccine development efforts. Furthermore, sequencing of dengue strains from other countries in the region is required in order to understand the patterns of spread of this virus across the different countries in the region.

Keywords: Dengue virus, Full genome, Phylogenetic analysis, Eritrea

Abstract 136

Title: The use of unbiased whole genome sequencing for pathogen discovery: A case of Rift Valley Fever in Marigat, Baringo County, Kenya

Authors: Allan P Lemtudo (KEMRI/USAMRD-K)*; Kimita Gathii (KEMRI/USAMRD-K); George Awinda (KEMRI/USAMRD-K); Beth Mutai (KEMRI/USAMRD-K); John N Waitumbi (KEMRI/Walter Reed Project)

Background: Rift Valley Fever (RVF) outbreaks occur following abnormal heavy rains, such as the May to June 2018 outbreak in Wajir County, north-eastern Kenya. In December 2019, one sample that was collected in June 2018 from a febrile child attending a hospital in Baringo county, inadvertently produced sequence hits homologous to RVFV by unbiased whole genome sequencing (WGS). This study describes the utility of WGS for the discovery of emergent or novel pathogens.

Methodology: The serum sample tested in this study was negative for multiple endemic pathogens that are tested routinely. Such pathogen-negative samples are further tested by sequence-independent, single-primer amplification (SISPA), a pathogen diagnostic approach for pathogen discovery. Following SISPA, products were used for library preparation, and the libraries were sequenced on Illumina's MiSeq platform. Genome assembly was performed using the NGS mapper pipeline, while lineage classification and phylogeny were performed using rvfv typing tool v1 (https://www.genomedetective.com/) and phyml v3 respectively.

Results: Retrospective qPCR in 44 samples collected between June and September 2018 detected 2 RVFV samples. The whole genome of RVFV comprising the large (L), medium (M), and small (S) segments were obtained from the index sample. The RVFV genome obtained was lineage C. Phylogeny showed similar tree topologies that clustered in a clade consisting of sequences obtained from human samples during the 2017 RVFV outbreak in Uganda, and sequences obtained from cattle samples in the 2021 outbreak in northern Kenya.

Conclusion: Unbiased pathogen detection has the potential to revolutionize disease surveillance, especially for emergent or novel pathogens that are not in routine diagnostic radar. Because WGS is expensive, the choice of samples to be used for pathogen discovery need to be thought out carefully in order to maximize the possibility of identifying emergent pathogens that would otherwise be missed in routine diagnosis that tend to be biased towards endemic pathogens.

Keywords: Rift Valley Fever Virus

Abstract137

Title: Genetic diversity and antigenic variation at vaccine target sites in Rabies Virus collected from different host species in Makueni and Siaya counties, Kenya

Authors: Evalyne N Wambugu (US Army Medical Research Directorate- Kenya)*; Kimita Gathii (US Army Medical Research Directorate- Kenya); Clement Masakhwe (US Army Medical Research Directorate- Kenya); Lucy Mutunga (Institute of Tropical and Infectious Diseases, University of Nairobi, Nairobi, Kenya); Gurdeep Jaswant (Institute of Tropical and Infectious Diseases, University of Nairobi, Nairobi, Kenya); Dr. Thumbi mwangi (Institute of Tropical and Infectious Diseases, University of Nairobi, Nairobi, Kenya); John N Waitumbi (KEMRI/Walter Reed Project); Sarah Kituyi (University of Embu)

Background: Rabies, a viral disease that causes lethal encephalitis is endemic in Kenya and is transmitted to humans mainly by domestic dogs. Rabies kills an estimated 2000 people annually, despite there being effective vaccines for dogs and humans. This study characterized the genetic diversity of RABV obtained from brains of suspected rabid animals from Makueni county, Eastern region and Siaya county, Western Kenya and determined variances within the antigenic sites of RABV vaccines currently in use in Kenya.

Methods: Brain biopsies (165) confirmed positive for rabies with rapid kits were collected between July 2021 and August 2022 from dogs, cats, cows, sheep and goats and re-screened for RABV by qPCR. Whole genome sequences (WGS) and individual nucleoprotein

(N) and glycoprotein (G) genes were used for phylogeny. The amino acid variances in the N and G genes antigenic sites were compared to three RABV vaccine sequences: Pitman-Moore L503 (PM), Challenge Virus Standard (CVS) and the Pasteur vaccine (PV) strains.

Results: Of the 165 brain samples, 156 were positive by qPCR and 141 (74 from Makueni and 67 from Siaya) produced useable sequences. Phylogenetic lineages drawn from WGS or from individual N and G genes showed two geographical distinct lineages: The Eastern Kenya sequences overwhelmingly (n=72) clustered with the Africa 1b lineage, with only 2 in Africa 1a. In contrast, the Western Kenya sequences (n=64) clustered with Africa 1a with only 3 in Africa 1b. The nearest common ancestor of the Africa 1a traced to Ethiopia, while the Africa 1b traced to Tanzania. The percent amino acid homologies of the N gene to the RABV vaccines were at least 97.6% for PV, 97.8% for CVS and 98.5% for PM. The homology with the G gene were at least 93.0% for PV, 93.3% for CVS and 92.2% for PM.

Conclusion: Our data confirm geographical isolation of RABV in Eastern and Western Kenya. The data suggests limited migration, probably through wild carnivore movement or translocation of domestic dogs by humans. The observed amino acid variances RABV vaccines antigenic sites would predict good vaccine efficacy, indicating that the RABV endemicity in Kenya is due limited programmatic vaccine coverage.

Keywords: Rabies Virus, Genetic diversity, Antigenic variation, Makueni county, Siaya county

Abstract 138

Title: Development of Thermostable Moloney Murine Leukemia Virus Reverse Transcriptase (MMLV-RT) Enzyme Prototype in Kenya, Utilizing Codon Optimization Strategy

Authors: Abdiaziz A Gosar (KEMRI)*

Development of Thermostable Moloney Murine Leukemia Virus Reverse Transcriptase (MMLV-RT) Enzyme Prototype in Kenya, Utilizing Codon Optimization Strategy

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ABSTRACT

Background: Viruses contain genomes either in form of Ribonucleic Acid (RNA) or Deoxyribonucleic Acid (DNA). Molecular detection of RNA viruses utilizes the action of the Reverse Transcriptase enzyme that does cDNA synthesis. The cDNA then undergoes amplification in Polymerase Chain Reaction (PCR). Developing countries such as Kenya are dependent on imported reagents. Owing to the high cost of molecular analysis of viruses' there is a need to bring the cost down by promoting the local production of diagnostic reagents. In this regard, the production of a thermostable Reverse Transcriptase locally will bring Kenya one step closer to achieving affordable diagnosis and prognosis of viral diseases. In this study codon optimization strategy was utilized in locally developing a Reverse Transcriptase enzyme prototype using gene sequence for Moloney Murine Leukemia Virus Reverse Transcriptase (MMLV-RT) Enzyme.

Methodology: Gene encoding thermostable MMLV-Reverse Transcriptase was identified in NCBI https://www.ncbi.nlm.nih.gov/ and analyzed. Codon optimization was done using Genscript https://www.genscript.com/. The MMLV-RT gene which was cloned in the pET28a (-) vector was over-expressed in the E.coli expression system. The enzyme obtained was purified using metal affinity chromatography using Talon accept resin. The purified protein was then analyzed using SDS-PAGE and Western Blotting for quality. Assessment of RT activity was done using Reverse Transcriptase PCR (RT-PCR). Complementary DNA (cDNA) synthesis assay of the developed enzyme was done using RNA extracted from both Dengue Hemorrhagic Fever viral RNA and SARS-CoV-2. The RNA first underwent cDNA synthesis using both concentrated and diluted purified RT enzyme against a commercial RT, PCR was then done to ascertain the enzyme activity.

Results: The SDS-PAGE and western Blotting assays showed that the enzyme was successfully expressed in the E. coli expression system. The concentration of MMLV-RT was 0.313mg/mL which is a good yield. The cDNA assay of both purified MMLV-RT and the commercial RT showed the presence of both SARS-CoV-2 and Dengue DNA. The concentrated enzyme detected 98% of Dengue RNA and 97% of SARS-CoV-2 RNA while the diluted RT enzyme detected 93% of Dengue RNA and 92% of SARS-CoV-2 RNA. The produced MMLV-RT prototype showed that it can be used in PCR amplification.

Conclusion: We successfully produced a recombinant Moloney Murine Leukemia Virus Reverse Transcriptase enzyme prototype. Codon Optimization resulted in enhanced expression of MMLV-RT.

Scientific Session 18: Public Health-2

Abstract 139

Title: Community members knowledge and perceptions of lung diseases in an urban informal settlement in Nairobi, Kenya

Authors: Cynthia W Kairu (University of Glasgow)*

Background: Africa bears the greatest burden of lung diseases globally, which disproportionately affects the poor. Evidence shows that growing prevalence may be due to lack of knowledge and low perceptions of risk factors for lung diseases. This study aims to find out what people in Mukuru, an informal settlement in Nairobi, know about lung diseases and how they perceive risk factors. Treatment-seeking strategies were also investigated to identify any challenges in pursuing care.

Methods: Qualitative in-depth WhatsApp interviews with sixteen residents from Mukuru Informal Settlements, Nairobi. Data was analysed using thematic analysis on NVivo 12. The Coding was broadly informed by two theories; theory of Health and Illness Perception and the PASS model for health seeking behaviour.

Results: Seven themes were identified and categorized under three domains. The knowledge of lung diseases domain revealed that residents have some knowledge, but gaps were evident in their knowledge of symptoms of specific lung diseases. The residents' main source of information about lung diseases was derived mainly from their personal and contextual experiences. In the perceptions of environmental risk factors domain residents perceived air pollution as a major issue and showed awareness of air pollution sources in Mukuru. However poor environmental practices persist due to systematic barriers such as corruption and poor waste management systems. The treatment-seeking strategies domain found that multiple treatment options are pursued during care-seeking including use of over-the counter drugs, herbal remedies and bio-medical treatment. Social support is an important prompt or facilitator for seeking treatment, while symptom perception, affordability, availability and access to healthcare services are potential barriers for seeking treatment.

Conclusion: Potential recommendations based on the findings include: an upscale of community-based interventions to educate residents on lung health, symptom recognition of prevalent lung diseases and environmental management. There is a need for policy interventions to restrict toxic emissions from industries. Collaborations between national/municipal governments and local residents is also recommended to improve waste management in Mukuru. Further research into health system in Mukuru is recommended to better understand Mukuru's medically pluralistic environment that allows residents to negotiate between various treatment options.

Keywords: lung health, qualitative study

Abstract 140

Title: A mixed-methods study on residents' treatment-seeking behaviour of tungiasis in Homa Bay County, Kenya

Authors: Kana Suzuki (Nagasaki University)*; Asiko Ongaya (KEMRI); Evans Amukoye (KEMRI); Gordon Okomo (Ministry of Health Homa Bay County); Muuo Nzou (KEMRI); Yasuhiko Kamiya (Nagasaki University)

Background: Tungiasis, an ectoparasitosis caused by sand fleas, causes suffering to millions of people in the tropics yet has been neglected. Although the Kenyan tungiasis guideline was made in 2014, insufficient knowledge and economic challenges in individuals may lead to neglect and inappropriate self-treatment. If not appropriately managed, infestation by jiggers can result in health and socio-economic effects. The surgical extraction of embedded sand fleas is widespread but has several shortcomings. Therefore, we studied the residents' treatment-seeking behaviour against tungiasis in Homa Bay County, Kenya.

Methods: The study was a cross-sectional study design involving a quantitative survey (N=421) followed by a qualitative phase with a sub-sample of the survey participants (N=20) among residents over 60 years old who have experience with tungiasis. This was done in Suba-south and Ndhiwa sub-counties, which reported higher prevalence, but no studies about tungiasis were done in this region. A purposive sampling method was used in this study. For the analysis of quantitative data, SPSS Statistics ver. 25 was used. Univariate and multivariate analyses were used, and the statistically significant factors at $p<0.05$ were considered independently associated with choosing guideline tungiasis treatments. Qualitative data were analyzed by themes and used to triangulate the qualitative data. The method of connecting was used to explain the results.

Results: From the quantitative study, the barriers to choosing guideline treatments for tungiasis were 'Not knowing fleas as a cause of tungiasis', 'Not sweeping the house at least twice a day', 'Not seeking treatment to health facilities' and 'traditional healer', and 'Wait and see to prevent for other non-affected members'. In the qualitative study, all participants used treatments not listed in the guideline. In the communities, 19 tungiasis treatment options were found, and 40% of participants used self-removal using pins, fish bone, hen's feather, and local plants. Paraffin, organophosphorus insecticides, herbs and natural plants were used as a treatment in 6, 5, and 5 participants, respectively. Three participants used cow dung, urine, and waste. The most frequently mentioned reason for using the treatment was 'Other's suggestion', 'Availability and accessibility' and 'Own experience'. The most frequent reason for choosing the best treatment was 'Effectiveness'.

Conclusion: There are varieties of local practices, whether guideline-listed or not. It is necessary to review the guidelines, and urgently search for treatments that are available and accessible to local people. Instead of choosing skin-friendly treatments, many residents use treatments that can harm the human body. This study will contribute to further investigations in establishing an effective and safe topical treatment that is suitable and sustainable for the local population in Western Kenya.

Keywords Tungiasis, treatment, seeking behaviour, western Kenya

Abstract 141

Title: Exploring Gender Based Violence service provision for Adolescent Girls and Young Women during the COVID-19 pandemic in Kisumu County: A qualitative study among service providers.

Authors: Isdorah IAO Odero (KEMRI-CDC)*; Hellen Barsosio (KEMRI/CGHR); Mevis Omollo (KEMRI/CGHR); Eucabeth A Awuonda (KEMRI-CGHR); Peter Ochere (KEMRI/CGHR); Clea Sarnquist (Stanford University); Jennifer Kang (Stanford University); Ruby Reed (Stanford University)

Introduction: One of the largest populations in Low and Middle-Income Countries (LMIC) that has been affected by Gender-Based Violence (GBV) is Adolescent Girls and Young Women (AGYW). Kisumu is among the three counties that recorded the highest cases of GBV during the COVID-19 pandemic. There are several service providers, offering many services, to combat GBV in Kisumu, but there were many barriers to providing and accessing services during the early phase of the COVID-19 pandemic. Our objective was to explore the gaps in, and potential opportunities, in GBV service provision during this time.

Methods: Community partnered participatory approach was used to generate 49 in-depth interviews (IDIs) with GBV service providers. The selection criteria involved the GBV service providers within Kisumu East and Central sub-counties. Data was collected using a semi-structured interview guide in either English, Swahili or Dholuo by two trained research assistants. The interviews were audio recorded, transcribed and analyzed thematically using Nvivo 12.

Results: Two themes were identified; types of services provided and the effects of COVID-19 on service provision. There were about twenty different GBV service providers targeting the AGYW. Their services varied from provision of psycho-social support, referrals, and linkages, economic empowerment, and reproductive health services. Most of these GBV services were interrupted due to the COVID-19 challenges. Services being closed entirely, fear of accessing services, higher travel costs, and reduced hours of operations were some of the challenges. Furthermore, majority of these GBV service providers operated independently offering the same GBV services to their own cohort of AGYW even though they were in the same location. The Sexual and Gender-Based Violence Alliance acted as an umbrella for all these service providers and its main role was to capacity build the various GBV service providers.

Conclusion: Despite the existence of numerous GBV service providers, there were evident gaps in the service provision due to COVID-19. This could be as a result of lack of interoperability among the GBV services as the majority were operating independently.

Keywords: Violence, Services, Adolescent Girls and Young Women

Abstract 142

Title: Evaluation of Diabetes and Hypertension Surveillance through the Community Empower Health System in Makueni County, Kenya, 2021.

Authors: Dominic Ongaki (FELTP)*; Maurice O Owiny (Kenya FELTP); Gladwell Gathecha (MOH - DNCD); Oren Ombiro (Medtronic LABS); Mary Murugami (Medtronic LABS)

Background: Diabetes and hypertension are among the top ten causes of death globally and in Kenya. The burden of the two conditions has been on the rise in Kenya. In 2018, the Ministry of Health and Medtronic LABS rolled out the Community Empower Health System to strengthen the surveillance of the two conditions. Periodic surveillance system evaluation enhances the efficient utilization of data and optimizes the system's operation. We conducted this evaluation to determine if the surveillance system was meeting objectives.

Methods: We conducted a retrospective data review and interviewed six key informants. We abstracted data from the system on hypertensive and diabetic clients attending six select facilities in Makueni County in 2021. We abstracted data on demographic and clinical variables and assessed system attributes based on CDC MMWR guidelines. Data were cleaned and analyzed using MS Excel 2019. We calculated frequencies and proportions for categorical variables.

Results: A total of 1,812 records were reviewed; [1,254 (69.2%)] were females. Most females were diagnosed with hypertension [782 (68%)] and diabetes [396 (70.5%)]. Only [104 (5.7%)] clients were enrolled on national health insurance. The system had 100% timeliness but with gaps in data completeness, followed clear case definitions and managed data in real-time without fail. It was first designed for hypertension and diabetes, but currently, haemophilia is being incorporated. It is representative of both genders. Donor partners majorly fund the system.

Conclusion: This evaluation indicates that the system is well structured with standardized tools and a clear flow of information. It can characterize cases based on demographic and clinical features. It was generally useful, stable, timely, representative, and flexible. It was relatively acceptable and simple to use. Its Performance on data quality was low. We recommend regular data audits and capacity building of healthcare providers on data quality.

Keywords: Diabetes Mellitus, Hypertension, Surveillance, Kenya

Abstract143

Title: Using community assets to improve access to cardiovascular disease prevention services: Case study of Health Kiosks in Markets

Authors: MIRIAM BOSIRE (KEMRI)*; Lydia Kaduka (KEMRI); Schiller Mbuka (KEMRI); Joseph Mutai (KEMRI); Erastus Muniu (KEMRI); Melvine Obuya (KEMRI); Doreen Mitaru (KEMRI); Esther A Shiraho (Kenya Medical Research Institute); Rodgers Ochieng (KEMRI)

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Background: The increasing burden of cardiovascular diseases (CVDs) in Kenya threatens its healthcare system. There is growing demand for initiatives to improve access to CVDs prevention services. Community markets are social establishments with untapped potential to promote public health. HEKIMA is a multi-phased feasibility study exploring the potential of market-based health kiosks in improving access to CVDs prevention and health promotion services. This study sought to assess enablers and barriers to developing this system interface for CVDs prevention and health promotion.

Methods: Health kiosks were set up in two markets, each staffed with 2 trained community health volunteers supervised by a nurse with primary care experience. Services offered included screening for high blood pressure, overweight and obesity; health education, referrals, and follow-up for pre-hypertensive and overweight participants. Each kiosk operated for 3 days a week. In-depth interviews with kiosk staff, healthcare workers and community members revealed factors influencing acceptability of the intervention.

Results: 2224 participants (f: 71%; primary school education level: 60%) were served in the kiosks from November 2021 to June 2022. Incident hypertension was 18%, obesity 17%. Key enablers included political goodwill, market and primary healthcare governance structures, strong stakeholder commitment, partnerships and networks, and communication. Challenges included political environment, seasonality, erratic commodity supply and lack of patient psychosocial support.

Conclusions: HEKIMA demonstrates the potential community assets have in improving detection and prevention of CVDs in an accessible manner, and the utility of this approach in promoting wide range preventive services at community level.

Keywords: Community markets , cardiovascular disease prevention, market-based health kiosks Enablers, Challenges

Abstract 144

Title: Burden and Perception of Overweight and Obesity as a Risk Factor to Cardiovascular Diseases in Vihiga County, Kenya

Authors: Melvine Obuya (KEMRI)*; Lydia Kaduka (KEMRI); Schiller Mbuka (KEMRI); MIRIAM BOSIRE (KEMRI); Doreen Mitaru (KEMRI); Rodgers Ochieng (KEMRI); Esther A Shiraho (Kenya Medical Research Institute); Joseph Mutai (KEMRI); Joanna Olale (KEMRI); Erastus Muniu (KEMRI)

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Background: Overweight and obesity are a major risk factor for cardiovascular diseases such as hypertension, stroke, diabetes, and some cancers. They are associated with increased morbidity and mortality globally, with Sub-Saharan Africa recording an average annual increasing rate of 5%. The national prevalence of overweight and obesity in Kenya is at 52% in women and 22% in men. There is a paucity of data on burden and perception of obesity in Vihiga County, which has hypertension as the leading cause of morbidity among adults.

Methodology: The Health Kiosk In Markets (HEKIMA) is a multi-phased feasibility study exploring the potential of market-based health kiosks in improving access to CVD prevention and health promotion services. Services offered in HEKIMA include screening for CVD risk factors including overweight and obesity. Data on socio-demographic and behavioral factors was collected using a semi-structured questionnaire. BMI was calculated for community members above the age of 15 years. Associations between BMI and other categorical variables was analyzed using chi-square tests. Overweight and obesity was categorized using WHO categories (normal weight, 18.5 to <24.9; overweight, 25.0 to <29.9; and obese, ≥30.0). Focus group discussions were conducted using interview guides, to understand community's perceptions of obesity as a risk factor to CVDs. Transcription/translation was done verbatim and analysis done thematically.

Findings: Overall, 2224 community members were screened (m:29%; f:71%). There was a significant association between obesity and sex, marital status and employment status ($p<0.0001$). 31.4% of males and 67.4% of females were overweight and obese. 62.5% of the participants were married, out of which 58.6% had high BMIs. Although 75.1% reported engaging in physical activity, 56.2% had high BMIs. Additionally, 63.9% of the self-employed and 62% of small scale farmers exceeded normal BMIs. Majority of FGD participants were married women (82%), mean age =43yrs, mainly traders (70%) and had primary level education (60%). The major factors that influenced perceptions were cultural beliefs, Iack of nutrition literacy, not prioritizing obesity as a health issue and financial constraints.

Conclusions: Preponderance of overweight and obese women, socio-cultural factors and knowledge gaps point to the need of targeted and culturally appropriate interventions to address overweight and obesity as a key NCD risk factor, for effective prevention and control of CVDs in Vihiga County.

Keywords: overweight, obesity, Basic Metabolic Index, Cardiovascular Diseases

Abstract 145

Title: My neighbor my buddy: A strategy to reaching the hard-to-reach defaulters in the HIV Stigma burdened Ntimaru area of Kuria Community in Kenya

Authors: NANCY B MWITA (MOH)*; BENSON ONYANGO OKOME OKOME (CMMB); EVANS OTIENO (CMMB)

Background: Successful treatment of human immunodeficiency virus infection/acquired immunodeficiency syndrome (HIV/AIDS) with highly active antiretroviral therapy (HAART) requires that patients more so pregnant and lactating women maintain nearly perfect adherence to the prescribed regimen. Given the critical role of adherence in successful antiretroviral therapy, it is essential that providers of care for patients with HIV infection have a strategy that proactively assists and supports their patients' efforts to adhere to medication regimens. Ntimaru Sub County sits in the deep end of Kuria community in Migori county. Kuria practices Female Genital Mutilation (FGM) and is a highly male chauvinist community. These are predisposing factors not only to teenage pregnancies, and early marriage but also new HIV infection. Access to mobile phones is still a luxury to many. This is a precursor to missing clinic appointments, defaulting, and ultimately leading to low retention and viral suppression. CMMB therefore came up with an innovative approach to reaching these needy and hard to reach clients. The strategy took a buddying system that ensured clients conscientiously support their needy neighbors.

Methodology: 5 Pregnant and 12 lactating mothers who are on HART, 15 newly initiated clients, clients who do not know how to read & write and clients with no telephone contacts were profiled (they were 132 which is 50% of the total clients on treatment). They were then grouped per area of residence. On the other end, 33 clients with good treatment outcomes (good adherence and virally suppressed) were profiled. They were linked to the needy clients who had earlier consented to the process during the one-on-one sessions with the service providers on their clinic days. Linkage of clients was done on a ratio of 1 : 4. The buddy's main role was to reach out to these needy clients on one-on-one basis. This included reminding the peers on clinic appointments, accompanying the clients to the facilities, getting refills for the client and tracing. A review of the health facility over a period of six months between March and September 2022 shows significant improvement in defaulter management at Ntimaru sub-county hospital.

Results: The number of missed appointments moved from a high of 11 clients in the month of March 2022 to no miss in September 2022. In the same month zero defaulters were reported. Ntimaru now boasts of clients keeping their clinic appointments, supporting each other to get refills, reduced expenses on calls and SMS used to send clinic appointment reminders, improved retention to care.

Conclusion: Proper mapping, identification and Peer/buddy pairing reduces defaulter rates thereby improving treatment outcomes and ultimately reduced stigma and discrimination. This strategy is cost-free and is replicable in any community setting.

Keywords: REATMENT BUDDIES,HARD TO REACH DEFAULTERS,STIGMA AND DISCRIMINATION, NEWLY DIAGNOSED,GOOD TREATMENT OUTCOMES

Abstract 146

Title: Integrated Approaches to empower adolescent girls and young women in Muhuru Ward, Migori County

Authors: Seth Midenyo Obura (MOH)*; Dorice Akinyi Ochieng (Dorice); Linet Ochieng (CIHEB); Nancy Yienya (CIHEB); Ann Odongo (Ciheb); Mary Ann (CIHEB); Lilian Njoki (Moh)

Background: Muhuru is one of the seven wards in Nyatike Subcounty, located along the banks of Lake Victoria. Research has shown evidence of vulnerable Adolescent girls and young women brought about by the environmental, cultural and socio-economic effects. Fishing being the main economic activity in the region, Young girls are exposed to early sexual debut at a tender age hence increasing their vulnerability.Muhuru Ward January –june Data of 2021 showed teenage pregnancy of 27.8%.Therefore DREAMS is being implemented in Muhuru to curb these vulnerabilities and empower the Adolescent girls and Young Women (AGYW)

Objective: To nurture young girls into Determined, Resilient, Empowered, Aids Free, Mentored and Safe Women

Methods: Offering integrated age appropriate services including age appropriate sexuality Education in schools while assessing their needs.1.Using combined social Economic Approaches (CSEAs) to provide economic strengthening Business Startup kit, Vocational training, Entrepreneurship training, Entrepreneurship support, Financial capability training, Linkages to employment, paid and unpaid internships, linkage to income generating activities (VSLA)2.Enhancing social protection by providing school fees, school uniforms and stationery to the school going AGYW.3Offering parental caregiver programs ie Family Matters Program FMP I and II to the parents of AGYW

Result: The number of young women attending vocational training increased by 40% from 36 in 2020 to 77 in 2022.Out of this,16 enrolled in male dominated courses that were previously neglected. Also cases of teenage pregnancies dropped by about 8% from 27.8% between January to June 2021 to 19.5% between January to June 2022.(KHIS).Effective partnership with MOH has been a driving force towards realization of objectives of the county's multisectoral Action Plan for implementation of youths and adolescents well being(2018-2022)

Conclusion: DREAMS Program uses an integrated service delivery model that has been curtailed to four core elements, to empower adolescent girls and young women and reduce their HIV risk, Strengthening families, mobilize communities for norm change and reduce the risk of sexual partners of AGYW.

Aknowledgement: CIHEB, MOH-Migori County

Keywords: Empower adolescent and young women ,Prevent new HIV infection and teenage pregnancy

Abstract 147

Title: Lessons from a Ghanaian model of care that addresses antenatal care holistically, focusing on quality, health promotion, and patients' needs

Authors: Jedidia Ayoka (Presbyterian Church of Ghana Health Service); Rudolf Abugnaba-Abanga (Presbyterian Church of Ghana Health Service); Maurits van der Heiden (TNO Innovation for Life); Loan Liem (Simavi); Eline Vlasbom (TNO Innovation for Life); Yvette Fleming (TNO Innovation for Life)*

Background: In the Binduri District of the Upper East Region of Ghana, a largely rural area, only 37.4% of women utilized ANC services in 2019. GC_1000 project aims to break the vicious cycle by offering group care (GC) with the Check2gether kit (screening instruments for pre-eclampsia, anemia, diabetes, and urinary tract infection), a model of care that addresses health holistically, focusing on quality, health promotion, and patients' needs. Evidence collected from November 2021 onwards shows that women receiving prenatal GC may have fewer preterm births, better mental health outcomes, fewer low birth weight babies, increased breastfeeding rates, longer pregnancy spacing and increased satisfaction with care. The GC model has three components: 1. health care, 2. interactive learning, and 3. peer support/community building.

Methodology: The GC_1000 project is an implementation research project (ethical approval from the Navrongo Health Research center, IRB. Ethics approval ID: NHRCIRB413) focuses on knowledge generation and dissemination of successful and sustainable scale-up of facilitated antenatal and postnatal groups in the first 1000 days. Midwives are leading the recruiting process by one on one sensitization of all first ANC registrants. Participation in group care is voluntary. Participants who agreed to participate sign a consent form.

This project aims to develop a systematic and in-depth understanding of feasible and sustainable ways to integrate evidence-based GC into health systems in the Binduri District of the Upper East Region of Ghana. To enhance the efficiency of GC, Check2gether, a non–invasive diagnostic tool for HB, Urine, and B/P, has been integrated into the GC sessions.

Results: A Rapid Appraisal (RA) was conducted with eighty-four respondents participating. The respondents comprised health providers, community stakeholders, and pregnant women, followed by a readiness assessment of the six sites. Based on RA, the GC model was adapted into 8 ANC sessions in line with national standards and context-specific needs of women. 24 staff from the implementation sites were trained on the use of Check2gether and GC. A total of 23 groups with membership of 213 women and a total of 142 sessions , are currently running across all six sites, with ten women dropping out (7%). All settings have had at least one group formed. Steering Committees at various levels (Site, District, and National) have met half-yearly.

Conclusion: Pregnant women and partners are pleased with the model as abundant opportunities exist for discussion, questions, and answers. Health providers have reported a reduced workload, as they see several women at a time, reducing the time that would have been spent focused on ANC. Improved access to HB Urine, protein & UTI tests which have resulted in the early detection and management of complications.

Keywords: rural holistic antenatal care - group care - diagnostic sreening pregnant women

Abstract 148

Title: The effect of Corn Soy Blend plus Vegetable Oil Enhanced with Fish Oil on Immunological Patterns and Clinical Outcomes Among Children Aged 9 to 24 months with Moderate Acute Malnutrition (MAM): A Randomized Clinical Trial

Authors: PHELGONA OTIENO (KEMRI)*; Peter Melby (UTMB); BEATRICE OLACK (KEMRI); Mary Inziani (KEMRI); Mark Muchina (KEMRI); Margaret Mbuchi (KEMRI); Chris Melby (CSU); Finnley Osuna (KEMRI); Linet Ouma (KEMRI); Thaddaeus Egondi (KEMRI); Rukia Kibaya (KEMRI); Mary Muriu (KEMRI)

Background: Undernutrition is a major public health problem contributing >45% of all deaths among children < 5 years of age. The Kenyan Ministry of Health guidelines specify a 14-day treatment with Corn Soy Blend (CSB) mixed with vegetable oil (VO) for treatment of moderate acute malnutrition (MAM). There is still great need to explore more effective treatments of undernutrition as cases of relapse and or deterioration are not uncommon. Previous research document dietary omega-3 long chain polyunsaturated fatty acids (PUFA)/Fish Oil (FO) as important for optimal health throughout the lifespan, especially in children. More explorations to determine the relationship between immunity and malnutrition and the effect of different nutritional interventions help to guide treatment policy. In this study, we assessed the effect of CSB-VO-FO compared to standard-of-care CSB-VO on changes in inflammatory markers, episodes of common infectious diseases, recovery from MAM, as well PUFA levels in children with MAM.

Methods: A double blind randomized control trial was conducted among children ages 9 to 24 months with MAM with random allocation of 40 in each arm to receive either CSB-VO or CSB-VO-FO. For background comparisons a total of 20 healthy controls were also recruited and examined once. Study procedures included, medical history, anthropometric measurements, blood for inflammatory markers and hematology, urinalysis and a full physical examination conducted at baseline, and during the 6-month follow-up.

Results: Among the two treatment arms, male to female ratio was similar (FO, 1:2 versus V.O, 1:1.5). Majority of the caregivers were mothers (> 97.0%) with a mean age of 27 years, majority married and most unemployed (>74.4%). In terms of common childhood infections, the two treatment arms hard similar experiences with >97% having at least one episode during follow-up. Nutritional recovery by 12 weeks was similar in the two study arms (VO, 92.5% versus FO 95%). Before treatment the pattern of inflammatory markers was similar among the healthy controls compared to children with MAM. At the end of follow-up there were very close similarities in the two treatment arms with majority of markers such as CRP, IL-6 and Ferritin remaining at the same level, while Liposaccharide binding protein and chemokine for neutrophils declining, and TNF and FA binding protein increasing. Investigations into levels of Omega-3 FA revealed that healthy controls had higher levels compared to MAM patients (0.048 versus 0.029 and 0.032 ug/uL) at baseline. During follow-up the two study arms had fully and equally recovered with no superiority of the FO arm (VO: 0.046 versus 0.047 ug/uL).

Conclusion: Enhancing treatment of MAM in children with FO was similar to using CSB with VO in terms of inflammatory markers, recovery rates, clinical parameters as well as omega-3 levels.

Keywords: Immunology, Malnutrition, Children, Omega-3, Inflammatory markers, Clinical trial, Randomized, Infections

Abstract 149

Title: Diversity and distribution of fungi in urban and peri-urban residences in Kenya

Authors: Olga M. Mashedi (Kenya Medical Research Institute (KEMRI) (420))*; Olga Mashedi (KEMRI)

Introduction: Rural-urban migration, poverty, unemployment, and social inequalities capped by Post Covid Pandemic are major problems facing most African cities. Poor sanitation and pollution often lead to an increase in respiratory tract infections (RTIs).RTIs are globally responsible for one-third of infectious diseases–accounting for 4.3 million annual deaths. Although fungi are known RTI pathogens, their contribution and true infection burden remain unknown in Africa but it is known that invasive fungal infections are associated with high mortality rates for diseases. Fungi are however unknown to cause allergies that affect the upper and lower respiratory tract, eyes, intestinal tract, and skin. However, there is limited public awareness and information on indoor fungi contamination and potential health indoor health issues associated with exposure to fungi in Kenya's urban residential homes. Furthermore, no studies have been steered to determine the biodiversity of fungi mycoflora and their distribution in those locations. This study was designed to provide clarity and address those gaps.

Methods: This was a cross-sectional study conducted from 2018-2020, whereby a total of 220 residential Units from Nairobi and Busia Counties were sampled. Questionnaires were administered with key components on Demographic characteristics, House and Environmental Assessments. Fungal exposure assessments was conducted using sedimentary and air sampling methods. Fungal identification was done by direct microscopy and morphological features.

Results: A total of 740 fungal species were isolated from the indoor households and their prevalence is as followed Actinomycetes 47/740 (6.4%), Rhodotorula 80/740(10.8%), Mucor 38/740(5.1%), Aspergillus flavus 48/740 (6.5%), Aspergillus fumigatus 14/740(1.9%), Aspergillus niger 45/740 (6.1%), white fungi 30 /740 (4.1%), Penicillium137/740(18.5%), Trichoderma 16/740(2.2%), Alternaria spp 33/740 (4.5%), Fusarium 63/740(8.5%), fungi 67/740, (9.1%) and white yeasts 94/740 (12.7%) respectively. (121; 55.0%) of the households revealed that they had between>5 occupants, mean age of 39 years. Ninety (40.9%) respondents have a member in their household who has allergies, asthma, and bronchitis. (185; 84.9%) of the homes that were infested with rats, 192 (87.3%) had cockroaches, and ants, whereas, 104 (47.3%) homes had either furry and/or feathered pets. The use of Biomass fuel was observed in (143; 66.8%), Poor ventilation and dampness were reported in 67% of the homes.

Conclusions: Kenya still faces a high disease burden in HIV/AIDS, Respiratory Diseases, Malnutrition and Rapid urban migration that contribute to high mortality and morbidity among its vulnerable populations .Fungi isolated from indoor environments are emerging pathogens associated with upper, lower, and opportunistic infections in urban populations

Keywords: Fungi

SCIENTIFIC SESSION 19: SEXUAL REPRODUCTIVE HEALTH-2

Abstract 150

Title: Prevalence, Progression, and Risk Factors for Abnormal Pap Smear In adolescents and young girls aged 15-20 years in Kenya

Authors: Lizzie N Kabete (KEMRI)*; Maricianah Onono (KEMRI); George Omondi Otieno (KEMRI); Simon Muthusi (KEMRI-RCTP); Annette Opondo (KEMRI-RCTP); Moses Siaji (KEMRI-RCTP); Elizabeth Bukusi (KEMRI); Betty Njoroge (KEMRI); Nelly R. Mugo (KEMRI); Ruanne Barnabas (Harvard)

Prevalence, Progression, and Risk Factors for Abnormal Pap Smear In adolescents and young girls aged 15-20 years in Kenya

Lizzie Kabete, Maricianah Onono, George Otieno, Simon Muthusi, Annette Opondo, Moses Siaji, Elizabeth Anne Bukusi, Betty Njoroge, Nelly Mugo, Ruanne Barnabas for the KEN SHE team

Background: The majority of genital human papillomavirus (HPV) occur within 3 occurs of sexual debut and peak at ages 25 years. Kenya HPV Single Dose (KEN SHE) enrolled adolescent girls and young women ages 15 -20 years and were assessed for HPV infection and abnormal cytology.

This study will assess the prevalence, progression, and risk factors for abnormal Pap smear in a cohort of AGYW.

Methods: The KENSHE study enrolled 2275 AGYW ages 15-20 years from Thika, Kisumu, and Nairobi. PAP smear tests were done at enrollment and exit visits. AGYW with an abnormal pap smear were managed in alignment with the Kenya Cervical cancer prevention guidelines (https://www.health.go.ke/wp-content/uploads/2019/02/National-Cancer-Screening-Guidelines-2018.pdf). Repeat Pap smears were repeated after six months for Low Grade Lesions after treatment for High Grade Lesion and Logistic regression was used to analyze factors associated with abnormal pap smear.

Results: At enrolment, 60 (3%) AGYW had an abnormal pap smear, 37 (1.63%) low grade lesions and 2(0.09%) high grade lesions. Higher proportion of abnormal pap smear was noted among participants reporting vaginal intercourse in the last six months (3% vs.1%, p-value=0.004), presence of a sexually transmitted infection (OR=13.12,95%CI:1.16–120.67) were associated with increased risk for abnormal Pap smear and condom use at last sex was protective (OR=0.18, 95%CI:0.05–0.71). All repeat Pap smears after six months were normal.

Conclusion: Condom use as protection against HPV infection and abnormal cervical lesions should be promoted as part of the benefits of condom use beyond HIV prevention.

A higher proportion of abnormal pap smears was noted among participants reporting vaginal intercourse in the last six months compared to those reporting none

Keywords: Adolescent girls and young women, HPV, low grade lesions, high grade lesions

Abstract 151

Title: Prevalence, persistence, clearance and associated risk factors of Bacterial Vaginosis in adolescents and young girls aged 15-20 years in South Western Kenya

Authors: Caren Awinja Wemali (Kenya Medical Research Institute)*

Caren Awinja, Maricianah Onono, George Olilo, Imeldah Wakhungu, Elizabeth Anne Bukusi, Betty Njoroge, Ruanne V Barnabas, Nelly R Mugo, for the KEN SHE Study Team

Background: Bacterial vaginosis (BV) is the most common genital tract infection in women of reproductive age. BV infection increases the risk of contracting other genital tract infections. We evaluated the prevalence, persistence, clearance and associated risk factors of BV among adolescent girls and young women (AGYWs) aged 15-20years in South Western Kenya over a 36-month period.

Methods: Data from a blinded, prospective randomized study on the efficacy of a single dose HPV vaccine among AGYW aged 15-20 years was used. Data on BV and associated risk factors were abstracted from sexual and reproductive health questionnaires and laboratory test results over a 36-month period. Persistence was defined as having at least two consecutive episodes of Nugent score of seven and above for samples six months apart. Clearance was defined as a Nugent score of six or less in the subsequent visit after a score of seven and above. Multivariable poison regression was used to estimate the relative risk (RR) for persistence, clearance, and associated risk factors of BV.

Result: Of the 1164 girls included in the analysis, the mean age was 17 years (SD±1.3). 744(63.9%) had at least one episode of BV over 36 months. BV cleared in 140 (19%) and persisted in 402 (54%). Participants diagnosed with Neisseria Gonorrhea and Chlamydia Trachomatis were 20% (RR=1.20 95%CI:1.01-1.42) and 24% (RR=1.24 95%CI:1.10-1.39) more likely to have BV respectively. Protective risk factors from BV infection included: having at least secondary education (RR=0.81 95%CI:0.66-0.99), use of combined oral contraceptives (RR=0.67,95%CI:0.50-0.91), and use of condom during the last sexual intercourse (RR=0.83 95%CI:0.74-0.94). AGYW who thought their partners were having sex with other partner/s had an increased risk of BV persistence (RR=1.27 95%CI:1.03-1.58), while participants in secondary school had a lower risk compared to those in primary school (RR=0.84 95%CI:0.72-0.99). BV clearance in those treated (90%) was similar to those asymptomatic (89%). Similar results were in those treated with persisted BV and those asymptomatic (90% versus 88%, respectively).

Conclusion: BV prevalence and persistence in AGYW with or without treatment was high. There is a need to reinforce education, combined oral contraceptives and condom use as these were protective. Future research to focus on prevention and sustainable treatment strategies in order to reduce the burden of BV.

Keywords: Bacterial vaginosis, prevalence, persistence, clearance, associated risk factors.

Abstract 152

Title: Partner Notification Practice among Kenyan Adolescent Girls and Young women aged 15-20 years diagnosed with sexually transmitted infections

Authors: Teresia A Otieno (KEMRI-RCTP)*; Maricianah Onono (KEMRI); George Omondi Otieno (KEMRI); Imeldah N Wakhungu (Kenya Medical Research Institute (KEMRI)- Research Care and Training Programme (RCTP)); Elizabeth Anne Bukusi (KEMRI); Betty Njoroge (KEMRI); Ruanne V Barnabas (Harvard University); Nelly R. Mugo (KEMRI)

Abstract: Background: Partner notification is essential in the management of sexually transmitted infections (STI). Partner notification can provide timely treatment of partners exposed to STI, interrupt chains of STI transmission and prevent re-infection. The objective of this study is to determine the acceptance rate and factors associated with partner notification practices in the management of STIs among AGYW 15-20 years in Western Kenya.

Methods: Data from a blinded, prospective, randomized study of a single dose HPV vaccination was used. Those with positive STI results were offered treatment and asked if they were willing to notify their partners and deliver the treatment package. Management of STIs followed local guidelines for treatment and repeat screening. Data was abstracted from a sexual and reproductive health and demographics questionnaire. We used bivariable Poisson regression to model factors associated with partner notification

Results: Of the 1,164 AGYW included in the analyses 523 (44.9%) had a positive STI diagnosis; HSV-2 (34%), CT (11%), TV (6%), NG (2%), and Syphilis (2%). Partner notification acceptance rate was N (52.9%). AGYW were less likely to initiate partner notification if: 1) they had recurrent STIs compared to those with one episode of infection (RR=0.75,95% CI:0.65-0.89); 2), ages 17 and 18 years compared to those aged 15-16 years, (RR=0.66,95% CI:0.50 -0.87) and (RR=0.72,95% CI:0.54 -0.96) respectively; 3) pregnant (RR= 0.83, 95% CI: 0.70 - 0.98) or in secondary school (RR=0.42,95% CI:0.20 -0.89). Marital status, condom use and number of sexual partners had no significant influence on participants decision to notify their partners. Being away from partner, not being sexually active and fear of disclosure were some of the reported barriers to partner notification.

Conclusion: Partner notification practice was moderately well accepted in this cohort. However, there is need to strengthen counselling approaches towards AGYW to enable participants overcome perceived barriers.

Keywords: STI Diagnosis,Partner notification

Abstract 153

Title: Contraceptive uptake, method switching and associated factors among adolescent girls and young women participating in HPV vaccine trial

Authors: Imeldah N Wakhungu (Kenya Medical Research Institute (KEMRI)- Research Care and Training Programme (RCTP))*; Maricianah Onono (KEMRI); George Omondi Otieno (KEMRI); Elizabeth Anne Bukusi (KEMRI); Betty Njoroge (KEMRI); Ruanne V Barnabas (Harvard University); Nelly R. Mugo (KEMRI)

Background: Approximately half of pregnancies in girls aged 15 to 19 years are unintended globally. Meeting the unmet need for effective contraception in adolescents would reduce unintended 6.0 million pregnancies annually. We explored adolescent girls and young women's (AGYW) contraceptive method (CM) use pattern and factors influencing continuation and method switch.

Method: Data for this analysis was drawn from an ongoing randomized clinical trial testing the efficacy of single-dose HPV vaccine as a catch-up strategy among AGYWs in Kenya aged 15-20 years. We described contraceptive uptake as CM use; method continuation as consisted use of a CM for a year; discontinuation as CM stopping; method switch as discontinuing and initiating a different CM during the study period. The average time between a switch was computed. Poisson regression was used to analyze factors associated with uptake, continuation, and switch.

Results: Of the 1,164 AGYW included in the analyses, 817 (69%) had ever initiated contraceptives. DMPA was the most preferred method (40%). A total of 261 (34%) consistently used contraceptives, 337 (41%) stopped using contraceptives, while 219 (27%) had at least one CM switch. Among those switching, 14% switched from OCP to DMPA, 18% from Jadelle to DMPA, and 21% from DMPA to Jadelle. Average time between- switch was 1.8 years with a range of (0.07-3.5). AGYW on PrEP, those having any income source, and those reporting alcohol intake were more likely to use contraceptives (RR=1.19, 95% CI: 1.10 - 1.27), (RR= 1.11, 9% CI: 1.01 - 1.23) and (RR=1.28, 95% CI: 1.19 - 1.38). AGYW in secondary school and those having any income source had more likelihood of contraceptive continuation (RR= 3.12, 95% CI: 1.17 – 8.33) & (RR= 1.39, 95% CI: 1.06 - 1.83). Married AGYW had increased risk of method switch (RR=1.69, 95% CI: 1.14 - 2.51).

Conclusion: Integration of contraception in the study was successful in promoting uptake among AGYW. Notably, consistent use was limited as contraception switching and discontinuing were common. There is a need for targeted strategies by providers for AGYWs to enhance effective use of contraceptive methods.

Keywords: Contraceptives, uptake, switching, discontinuation, Adolescents, consistency

Abstract 154

Title: Incident and recurrent sexually transmitted infections in adolescents and young women in southwestern Kenya

Authors: Maricianah Onono (KEMRI)*; George Omondi Otieno (KEMRI); Elizabeth Bukusi (KEMRI); Betty Njoroge (KEMRI); Nelly R. Mugo (KEMRI); Ruanne Barnabas (Havard University)

Background: Sexually transmitted infections (STIs) are associated with increased transmission of HIV, poor reproductive health outcomes, and reduced sexual health. People with recurrent STIs are at risk for these sequelae of STIs. The objective of this study was to determine the prevalence of STIs, recurrent STIs, and associated risk factors among adolescent girls and young women (AGYW).

Methods: The primary study enrolled sexually-active AGYW age 15-20 years into a blinded, prospective randomized study of a single dose HPV vaccine efficacy. This analysis was restricted to participants enrolled in Kisumu. AGYW provided genital swabs every six months for nucleic acid testing for Neisseria gonorrhea (NG), Chlamydia trachomatis (CT), and blood which was tested for syphilis. Participants with STI were treated based on local guidelines. Incidence of STI infection was defined as the first case of STI for those who were STI uninfected at enrolment, whereas we considered recurrent STI infection as the repeated event, measured as any second infection. Semi-parametric Cox proportional hazards model regression was used to explore association between participants characteristics at baseline and STI incidence as well as recurrent incident STI during the follow-up.

Results: Baseline prevalence of any STI was 12%, while for NG, CT, and syphilis were 2%, 11%, and 0,2% respectively. Over a median follow-up of 18 months, STI incidence was 63.4, 54.8, and 45.7 per 100 person-years for NG, CT, and syphilis respectively. Being married (HR 0.37, 95% CI: 0.14 – 0.91), aged ≥ 18 years and having sex in the last 6 months (HR=0.40, 95% CI: 0.20 – 0.79), having secondary and post-secondary education conferred protection from STI infection. Participants reporting sexual intercourse in the last 6 months (HR 2.75, 95% CI: 1.74 – 4.34), and those using PrEP had increased risk of infection (HR 1.62, 95% CI: 1.24 – 2.12). The recurrent incidence rate was 24.07 per person-years (95% CI; 20.74 – 27.92). CT had the highest incidence rate at 32.3 per 100 person-years (95% CI; 27.24 - 38.32). Having lower level education, (HR 1.57, 95% CI: 1.00 - 2.05); using PrEP (HR 1.52, 95% CI: 1.11 - 2.06) increased risk of recurrent STI. Although, there was no association between recurrent STI and HIV, there was a strong association between incident STI and HIV (HR 3.68, 95% CI: 1.27 – 2.19)

Conclusion: The high incidence rates along with its strong association of HIV and high rates of recurrent STIs among AGYW, warrant clinical practice guidelines related to: 1) HIV prevention after incident STI as well as 2) retesting after treatment of initial infection. Novel intervention approaches are needed to help recurrent STI patients reduce their risk for HIV infection and the risk of onward transmission.

Keywords: Sexually transmitted Infections, Adolescents, HIV, Recurrent, Kenya

Abstract 155

Title: Adverse pregnancy outcomes and associated risk factors among adolescents and young women aged 15-20 years in Kenya.

Authors: Charlene Jepkoech Biwott (Kenya Medical Research Institute)*; Maricianah Onono (KEMRI); George O Otieno (KEMRI); Lynda Oluoch (KEMRI); Stephen Gakuo (KEMRI); Elizabeth Bukusi (KEMRI); Betty Njoroge (KEMRI); Ruanne Barnabas (Harvard University); Nelly R. Mugo (KEMRI)

Background: Pregnancy among adolescents remains a public health issue, with research showing that pregnancy in adolescence is associated with an increased risk of adverse pregnancy outcomes such as preterm birth, low birth weight, perinatal death, obstructed labor, and maternal deaths. We analyzed pregnancy adverse outcomes and its associated factors among a cohort of AGYWs enrolled in an HPV vaccine trial in Kenya.

Method: We evaluated secondary data from the Kenya Single Dose HPV (KENSHE) trial which enrolled AGYW age 15-20 years in Thika, Kisumu, and Nairobi. Pregnancy tests were done at enrollment and every 3 months, and pregnancy outcome assessed. Pregnancy outcome indicators evaluated were abortion, stillbirth, preterm live birth<37 weeks and ectopic pregnancy. Access was provided to pregnancy and HIV prevention counselling and access to both PrEP and contraceptives. Proportion of adverse pregnancy outcome was defined as number of adverse events divided by the number of pregnancies. Mixed effect logistic regression was used to examine factors associated with adverse pregnancy outcome.

Results: Of 2,262 enrolled AGYW, 958 (42%) had a confirmed pregnancy during 36 months period of follow-up. There were 310 (32%) pregnancy related infant adverse outcomes; abortion 268 (84%), stillbirth 24 (8%), preterm live birth <37 weeks 14(5%), and ectopic pregnancy at 4(1 %). Across the study sites; incidence of abortion, still birth, preterm birth, and ectopic pregnancy had no statistically significant difference. Therapeutic /elective abortion occurred in higher proportions in Nairobi (18%) and Kisumu (18%), among AGYW compared to Thika (5%, p <0.001). Married, trying to get pregnant, age ≥18 years were associated with lower odds of an adverse pregnancy outcome (OR=0.37, 95% CI: 0.19-0.72), (OR= 0.33, 95% CI: 0.14-0.75) (OR= 0.24, 95% CI: 0.07-0.84) respectively. Alcohol use (OR= 1.80, 95% CI: 1.01 – 2.23); secondary education was associated with more than 5-fold likelihood of an adverse pregnancy outcome (OR=5.80, 95% CI: 1.61-20.94) compared to those in primary.

Conclusion: Though the trial provided access to contraceptive and counselling, pregnancy rates were high in this cohort of AGYW, with high occurrence of elective abortion in some regions. Adverse pregnancy outcomes were common, with high rates of pregnancy loss, more so among the younger women.

Keywords: adverse pregnancy outcome,adolescents,young women,abortion,preterm live birth<37 weeks,stillbirth,ectopic pregnancy

SCIENTIFIC SESSION 20: HIV

Abstract 156

Title: Factors associated with severe psychological stress among adults living with HIV in western Kenya

Authors: Juddy Wachira (Moi University)*; Catherine Kafu (AMPATH); Ben Mosong (AMPATH); Marta Wilson (Brown University); Omar Galarraga (Brown University); Becky Genberg (Johns Hopkins University)

Background: Psychological distress among persons living with HIV (PLWH) has been shown to have a negative impact on their behavioral and clinical outcomes. This study aimed to identify factors associated with psychological distress among PLWH in western Kenya during the COVID pandemic.

Methods: A cross-sectional survey was conducted (May-November 2021) among 1040 PLWH receiving care through the Academic Model Providing Access to Healthcare program (AMPATH) and enrolled in a cluster randomized control trial [NCT04417127] in western Kenya. The trial is testing the effect, mechanisms, and cost-effectiveness of integrating community-based HIV and non-communicable disease care within microfinance groups (MF) on HIV treatment outcomes. Participants were drawn from Busia and Trans-Nzoia counties. Eligibility included: consenting adults (≥ 18 years); initiated antiretroviral therapy (ART) at least 6 months prior to study enrollment. Logistic regression analysis was conducted to determine factors associated with psychological distress.

Results: The mean age of participants was 51 years [standard deviation (SD): 11]. The majority were from Busia County (63%), female (75%), and participated in MF (69%). Above average (53%) reported mild/high social support. The average wealth index was 0.00 (1.91) with only 19.1% earning an income of ≥ 5000 KES. Overall, 24% reported severe psychological distress. Compared to participants earning < 1000 KES, those with an income of ≥ 5000 KES (AOR 0.50; 95% CI, 0.27-0.93) and those receiving non-monetary gifts (AOR 0.55; 95% CI, 0.32-0.92) were less likely to report severe psychological distress. Similarly, participants at the highest wealth index (Quintile 5) compared to those at the lowest (quintile 1) (AOR 0.36; 95% CI, 0.18-0.70) and those receiving mild/high social support compared to those with low support (AOR 0.46; 95% CI, 0.46-0.98) were less likely to report severe psychological distress.

Conclusion: Findings showed that severe psychological distress was low among PLWH in western Kenya. Having a higher economic status and receiving mild/high social support was protective against psychological distress. Efforts to ensure PLWH are economical empowered and continue to receiving social support is therefore fundamental.

Keywords: Psychological distress; HIV; Economic; Kenya

Abstract 157

Title: Assessing user preferences for design characteristics of oral dissolvable strips for pediatric HIV medication: a qualitative study

Authors: Catherine M Wexler (University of Kansas Medical Center)*; May Maloba (Global Health Innovations); Michala Sliefert (University of Kansas Medical Center); Frederick Were (University of Nairobi); Yvonne Mbiithi (University of Nairobi); George Mugendi (University of Nairobi); Gregory Thomas (University of Kansas); Edward Maliski (Oak Therapeutics); Zachary Nicolay (Oak Therapeuticsq); Ithar Hassaballa (University of Kansas Medical Center); Sarah Finocchario-Kessler (University of Kansas Medical Center)

Background: Current infant antiretroviral therapy (ART) formulations pose barriers to daily adherence due to complex weight-based dosing, conspicuous preparation to reconstitute crushed or dispersible tables, and poor palatability, jeopardizing infant ART adherence. Our team has previously established proof-of-principal for multi-drug oral dissolvable strips (ODS) as alternative pediatric ART formulations with the potential to overcome these challenges and improve pediatric ART adherence and outcomes. The objective of this study was to assess user (caregiver and provider) preferences for ODS and its packaging to inform ODS development.

Methods: Guided by concepts of user-centered design, we conducted key informant interviews with 30 HIV care providers and 9 focus group discussions with 72 caregivers of children living with HIV at 3 Kenyan hospitals (Bondo Referral, Port Reitz, and Ambira). All KII and FGD were audio recorded and translated/transcribed verbatim and hand coded for a-priori and emergent themes.

Results: The 72 caregivers interviewed cared for a total of 83 children living with HIV. Mean caregiver age at the time of the interview was 37.2 (range: 18-74) years old and their children ranged in age from 5 months to 18 years (mean child age: 4.7 years). A total of 83.3% were females and most (60%) were the child's parents; however, grandparents (20%), aunts (11%) siblings, stepparents, and other types of caregivers were also represented. The 30 providers interviewed had a mean age of 37.7 years and had worked in the healthcare sector for a mean time of 9.6 years. Mentor mothers, pharm techs, community health volunteers, nurses, clinical officers, and administrators were among the providers represented in interviews. Caregivers and providers expressed a strong desire for an easier way to administer medication, especially among children too young to swallow tablets whole, and expressed enthusiasm around the idea of ODS. Key preferences for ODS included a pleasant taste; one strip per dose with no need to measure or cut; small size with rapid dissolution; clear markings and instructions; and no special storage requirements. For packaging, stakeholders seemed to prefer individually wrapped strips within a dispenser. The individual packaging should be durable, waterproof, and easy to dispose of in communal spaces. They should also be easy to open, with clear serration and markings on where to open. The dispenser holding the strips should be durable, re-usable, accommodating of various refill frequencies, and easy to use for children as young as 6.

Discussion: The concept of ODS was highly acceptable to caregivers of children living with HIV and HIV care providers. By engaging stakeholders in an iterative design process starting from the early phases of design and development, we will maximize the likelihood of developing a product that is acceptable to the caregiver and infant, therefore leading to sustainable adherence.

Keywords: PMTCT, HIV, Pediatric ART

Abstract 158

Title: Assessing challenges to pediatric ART provision: a qualitative study

Authors: Michala J Sliefert (University of Kansas Medical Center)*; May Maloba (Global Health Innovations); Catherine M Wexler (University of Kansas Medical Center); Frederick Were (University of Nairobi); Yvonne Mbiithi (University of Nairobi); George Mugendi (University of Nairobi); Gregory Thomas (University of Kansas); Edward Maliski (Oak Therapeutics); Zachary Nicolay (Oak Therapeutics); Ithar Hassaballa (University of Kansas Medical Center); Sarah Finocchario-Kessler (University of Kansas Medical Center)

Background: Current formulations of pediatric antiretroviral therapy (ART) for patients with HIV present significant barriers to adherence, leading to drug resistance, ART ineffectiveness, and preventable child morbidity and mortality. Understanding these challenges and how they contribute to suboptimal adherence is an important step in improving outcomes. The objective of this study was to identify regimen-related challenges to pediatric ART and describe how they create barriers to adherence, in order to inform the development of more user-friendly formulations.

Methods: We conducted key informant interviews (KIIs) with 30 healthcare providers and 9 focus group discussions (FGDs) with a total of 72 caregivers, across three hospitals in Kenya. The KIIs and FGDs were audio recorded, translated, and transcribed verbatim. The transcripts were hand coded based on emergent and a-priori themes.

Results: Major regimen-related challenges to adherence included poor palatability of current formulations, complex preparation, and administration process (including measuring, crushing, dissolving, mixing), complex drug storage, and frequent refill appointments. These regimen-related challenges contributed to individual barriers to adherence. Providers and caregivers discussed how poor taste leads to child anxiety, refusal of medications, and the need for caregivers to add bribes or threats during administration. Complex preparation led to concerns and challenges about maintaining privacy and confidentiality, especially during times of travel. The frequency of refills (ranging from every 2 weeks to every 3 months) interrupted work and school schedules, risked unwanted disclosure to peers, required use of financial resources for travel, and ultimately added unnecessary burden to families with HIV.

Discussion: The findings highlight the need for newer and improved formulations for pediatric ART to ease the daily burden on caregivers and children to increase adherence, improve child health, and overall quality of life of families.

Keywords: HIV, pediatric ART, qualitative, barriers to ART

Abstract 159

Title: Factors associated with ART retention among adults (>15yrs) living with HIV enrolled in JM Kariuki Hospital, Nyandarua County, 2017-2021

Authors: Margaret Wanjiku Gatungu (Ministry of health)*

Background: Retention is continuous engagement of PLHIV with health care provider for a good health outcome. The country targets to retain 95% of PLHIV in care. There is need to describe treatment outcomes that include transfer out, interruptions of treatment, defaulters, Lost to Follow Up (LTFU) and deaths in order to come up with targeted interventions to improve patient retention. The study sought to characterize cases retained on ART care in JM Kariuki Hospital.

Method: We conducted a retrospective analysis of records of all cases enrolled into Anti-retroviral Therapy (ART) in JM Kariuki Hospital from 2017- 2021. We used a case definition of any person living with HIV enrolled into ART care in JM Kariuki Hospital from 2017-2021.Following the revision of ART treatment guidelines in 2016 that required clients testing positive to be started on ART irrespective of their CD4 counts (test and treat), 2017 was the initial year after the revision. We collected sociodemographic and clinical variables into a prepared MS Excel from clinical encounter card (MOH257). Continuous variables were summarized using measures of central tendency and dispersion, whereas proportions and frequencies were used for categorical variables.

Results: We analyzed a total of 589 cases. The mean age was 44.4 (±13.5) years and 385 (66%) were female cases and 18.6% (109) had no recorded viral load. Cases on ART were 511 (85%) of these 65% (338) were females, 96% (567) had no recorded opportunistic infection, 59% (298) were reported to be in WHO stage 2. Poor clinic appointment was reported in 65 (11%) cases. Cases not on ART were 87 (15%); of these 65% (57) were females where15-49yrs 33(38%) were at their reproductive age had dropped from care,96% (83) of client not on ART had no recorded opportunistic infection, 65% (57) were reported to be in WHO stage 2. Poor clinic appointment adherence was reported in 65 (74 %) cases.

Conclusion: Majority of cases with poor ART adherence were recorded to have poor adherence to clinic visits. This probably was either they might have self-transferred to other facilities of choice or were known positives from other facilities or were still in denial. We recommend closer monitoring of clients with poor appointment adherence by staff at JM Kariuki Hospital.

Limitation of the study was that was not able to assess the viral suppression for some of the clients since a proportion of them did not have viral load result documented and also did not include clients who had been initiated ART in JM Kariuki Hospital in the same period but had documented transfer out or death

Keywords: Retrospective, lost to follow-up, treatment outcome, hiv, ART

Abstract 160

Title: UTILITY OF HAIR SAMPLES IN MONITORING ANTIRETROVIRAL THERAPY ADHERENCE OF PERSONS LIVING WITH HIV IN KENYA

Authors: Philomena Chepkirui (Kenyatta University)*; Beatrice N Irungu (Kenya Medical Research Institute); Elizabeth Kigondu (Kenya Medical Research Institute); Margaret Nganga (Kenyatta University); Musa Otieno (Kenya Medical Research Institute); Bhavna Chohan (Kenya Medical Research Institute); Josephine Ouma (Jomo Kenyatta University of Agriculture and Technology)

Background of the study: Antiretroviral therapy (ART) is critical in reducing the human immunodeficiency virus (HIV) epidemic by preventing vertical transmission. Routine monitoring of of patient adherence in receiving antiretroviral therapy (ART) is essential as it guides in tracking response to ARVs treatment and assesses treatment failures. Measurement of ARVs drug concentration in biological matrices such as blood and urine has been used previously for monitoring adherence. Unfortunately, they only reflect ARV doses taken within 1 to 2 days of sampling. Hair testing has become the most preferred tool to determine chronic exposure to some drugs, especially drugs of abuse, due to its long detection window. This study, , evaluated the utility of hair samples in therapeutic drug monitoring (TDM) as an indicator of ART adherence t as an alternative method to ARVs analysis in blood. This study used nevirapine (NVP), an ARV integral component of the first-line ART in Kenya, for many years.

Methods Matched hair and blood samples were obtained from 234 and 328 consenting HIV patients with virologic failure (viral load >1000copies/ml) and suppressed viral load (VL<1000 copies/ml) first-line antiretroviral therapy (ART), respectively. The ARV plasma concentration was measured by liquid chromatography-tandem mass spectrometry (LC-MS/MS).

Results: The calculated median (IQR) of NVP levels in hair and blood samples was 36.80 ng/ml and 19.32 ng/ml respectively. Wilcoxon signed-rank test was used to test the hypothesis; there is no significant difference between the level of NVP in hair and matched plasma samples. The Wilcoxon signed-rank test statistical result was, ($Z = -0.93$, $p > 0.05$) meaning there was no significant difference between the NVP hair concentration and the plasma.

Conclusion: Since there was no significant difference between the levels of NVP in hair and matched plasma samples, this study has demonstrated that analysis of ARV drugs in the hair can determine drug exposure as an alternative to conventional plasma drug analysis, especially in our settings where laboratory facilities and skilled personnel to do phlebotomy are few or lacking. However, it is not implied that the results support replacing plasma testing with hair testing as a research measure in all cases since the analysis of ARVs in hair and plasma samples can be taken as different tools that can also be used in combination to predict adherence to antiretroviral therapy.

Keywords: NVP concentration; hair samples; plasma samples

Abstract 161

Title: “We tested together”: Experiences of PLHIV Delivering HIVST to Partners of Unknown HIV Status in Kenya.

Authors: Catherine Kiptinness (KEMRI)*; Njeri Wairimu (KEMRI-CCR-PHRD); Kenneth Ngure (Jomo Kenyatta University of Agriculture and Technology); Faith Ambiyo (KEMRI-CCR-PHRD); Nicholas Kipkurui (KEMRI-CCR-PHRD); Nelly R. Mugo (KEMRI); Kenneth Mugwanya (UW)

Background: HIV testing for partners of persons living with HIV (PLHIV) is an important starting point for HIV prevention and treatment, for those unaware of their HIV status or their partners’ HIV positive status. PLHIV find it difficult to negotiate for partner HIV testing. HIV self-tests (HIVST) provide a unique opportunity for partners to test in privacy and could encourage PLHIV to disclose their HIV status. We explored the experiences of PLHIV delivering HIVST to their partners.

Methods: The Partner HIVST Study evaluated the impact of HIVST distribution by PLHIV with partners of unknown status on identifying individuals who could benefit from HIV prevention services at two comprehensive care clinics in Central Kenya. We interviewed 21 PLHIV, 12 who successfully delivered HIVST, and nine who did not. We analyzed data thematically using inductive and deductive approaches to capture concepts related to HIVST delivery and partners’ HIV testing experiences.

Results: Participants’ median antiretroviral therapy (ART) use was 18 months (IQR 8-108), 15 were female, and 13 had previously disclosed their HIV status. Participants who delivered HIVST reported that they were happy as it was more convenient and offered privacy compared to clinic-based testing. Many PLHIV reported that they either assisted their partners to test or partners tested in their presence. Participants who had previously disclosed their HIV status reported that it was easy for them to deliver HIVST because they had been to the clinic together and received regular counselling. Whereas some participants reported that HIVST helped them disclose their HIV status which made it easier to take their medication, some reported conflict, and relationship dissolution. Participants who had not disclosed their HIV status reported that they were worried about delivering HIVST for fear of potential conflict or separation.

Conclusion: Secondary delivery of HIVST by PLHIV to partners was acceptable, promoted partner testing, and helped PHLIV adhere to their medication, but success was majorly influenced by HIV status disclosure. These data suggest that integrating HIVST has potential to synergize treatment and prevention programs but must be paired with effective strategies to support PLHIV with status disclosure to fully realize its impact.

Keywords: HIV self-test kits

SCIENTIFIC SESSION 21: HEALTH SYSTEMS-3

Abstract 162

Title: Quality assessment of clinical practice guidelines in Kenya using the Appraisal of Guidelines for Research and Evaluation (AGREE) II tool. A Methodological Review

Authors: SAGAM CALEB KIMUTAI (KENYA MEDICAL RESEARCH INSTITUTE CENTER FOR GLOBAL HEALTH RESEARCH)*; Lisa Were (KENYA MEDICAL RESEARCH INSTITUTE CENTER); Jenifer A. Otieno (Kenya Medical Research Institute); Mercy N Mulaku (Kenya Medical Research Institute/stellenbosch University); Simon Kariuki (KEMRI); Eleanor Ochodo (KENYA MEDICAL RESEARCH INSTITUTE)

Background: Clinical practice guidelines (CPGs) play a significant role in informing clinical decision-making and improving the quality of health care. Kenya, a lower-middle income country, is faced with a high disease burden amidst a shortage of health workers. Well-developed and implemented CPGs are essential in enhancing quality healthcare. The objective of this study was to assess the quality of available and accessible national CPGs in Kenya using the Appraisal of Guidelines for Research and Evaluation II (AGREE II) tool.

Methods: In this methodological review, we searched websites of the Kenyan Ministry of Health, professional associations and contacted the relevant experts in these organizations. Our focus was guidelines on maternal, neonatal, nutritional disorders, injuries, communicable and non-communicable diseases in Kenya published in the last 5 years as at 2022. Three reviewers independently conducted study selection and data extraction. We conducted quality assessment using online English version of AGREE II tool. The primary outcome of this study was the quality of the CPGs assessed by a score. We resolved discrepancies on inclusion through consensus or discussion with a senior reviewer. Descriptive statistics (scaled domain percentages) were analyzed using STATA software version 17 (Stata Corp LLC, College TX).

Results: We retrieved a total of 95 CPGs however after screening 24 were included in the analysis. The appraisal scores (mean and CI) per domain were as follows: Scope and purpose 61.75% (95% CI 54.19-69.31) with seven guidelines scoring less than 50%; stakeholder involvement 45.25% (95% CI 40.01-50.49) with 16 CPGs scoring less than 50%; Rigour of development 3% (95% CI 0.61-5.39) with no CPG scoring at least 50%; Clarity of presentation 82.96% (95% CI 78.35-87.57) with all guidelines scoring above 50%: Applicability domain 19.88% (95% CI 13.32-26.43) with only one CPG scoring above 50%; Editorial independence 6.92% (95% CI 3.47-10.37) with no CPG scoring above 50%.

Conclusion: Our findings suggest that the quality of CPGs in Kenya is relatively low. Training initiatives to improve guideline development process involving Stakeholder involvement, rigor of development, applicability, and editorial independence is needed in Kenya.

Keywords: Clinical Practice Guidelines, Quality, AGREE II, Kenya.

Abstract 163

Title: Evaluating the effectiveness of the National Health Insurance Fund in providing financial risk protection to households with hypertension and diabetes patients in Kenya

Authors: Robinson RO Oyando (KEMRI-Wellcome Trust Research Programme)*; Vincent Were (KEMRI-Wellcome Trust Research Programme); Hillary Koros (AMPATH); Richard Mugo (AMPATH); Anthony Etyang (KEMRI-Wellcome Trust Research Programme); Jemima Kamano (AMPATH); Adrianna Murphy (London School of Hygiene and Tropical Medicine); Kara Hanson (London School of Hygiene and Tropical Medicine); Pablo Perel (London School of Hygiene and Tropical Medicine); Edwine Barasa (KEMRI Wellcome Trust)

Background: The rising burden of non-communicable diseases (NCDs) presents a huge economic burden to households due to high out-of-pocket payments (OOP) that lead to catastrophic health expenditures (CHE). We assessed the effectiveness of the national health insurance fund (NHIF) national scheme to provide financial protection to households with NCD patients in Kenya.

Methods: We employed a one-year cohort study design to collect data quarterly from 888 households, in which at least one member had hypertension and/or diabetes, in two counties in Western Kenya. Households were classified by NHIF enrolment status. Two outcome measures were assessed: 1) OOP as a share of total household expenditure and 2) the incidence of CHE. CHE was defined as annual healthcare expenditure exceeding 40% of annual household non-food expenditure. We assessed the depth of NHIF cover (i.e., the proportion of healthcare costs paid by NHIF) for outpatient and inpatient services as well as the NHIF attrition rate after one year. We used the coarsened exact matching approach to assess the difference in experiencing CHE between NHIF-enrolled households and those not enrolled. Socioeconomic inequality in incurring CHE was examined using concentration indices.

Results: Almost half (46.3%) of households reported active NHIF enrolment at baseline but this reduced to 9.3% after one year. A higher share of households with no NHIF coverage (19.6%) incurred CHE compared to households with active NHIF coverage (14.3%) ($p = 0.283$). A similar trend was observed across the wealth quintiles, with 35.8% of the poorest households incurring CHE compared to the richest households (10%) ($p < 0.001$). The concentration index (CI) for CHE showed a significant pro-poor distribution (CI: -0.190, $p < 0.001$). The depth of NHIF cover among households with active NHIF coverage was more than double (31.8%) for inpatient compared to outpatient costs (13%). Also, NHIF covered 29.6% of total healthcare costs among households with active NHIF. However, the NHIF attrition rate during the one-year follow-up was 76.7%. After matching, households that were enrolled in NHIF across the four waves were less likely to incur CHE, but the difference was not statistically significant (OR = 0.67; $p = 0.47$).

Conclusion: Households with NCDs patients and are enrolled in NHIF national scheme incur lower OOP compared to households without NHIF. However, the NHIF scheme's depth of cover is inadequate for outpatient and inpatient costs. Consequently, we did not find strong evidence that NHIF protects these households from CHE. NHIF should review its benefits package and provider payment rates to enhance the depth of cover and provide financial protection to households with NCDs. National and county governments should consider providing insurance subsidies for informal sector NHIF members given that the current voluntary contributions lead to high attrition.

Keywords: Health insurance, out-of-pocket payments, non-communicable diseases, Kenya

Abstract 164

Title: Examination of sub-national capacities for health workforce governance in Kenya: A qualitative case study of two county governments

Authors: Joshua M Munywoki (Kemri-Wellcome Trust Research Programme)*; Yingxi Zhao (Oxford University); Zeinab Gura (Ministry of Health); Lizah Nyawira (Kemri-Wellcome Trust Research Programme); Jacinta Nzinga (Kemri-Wellcome Trust Research Programme); Benjamin Tsofa (KEMRI-Welcome)

Background: Achieving Sustainable Development Goal 3 on health and and well-being for all requires investment in health workers (HWs). Developing countries face chronic HW shortages and sub-Saharan Africa countries are most affected. In Kenya, despite an increase in HW recruitment after 2013 devolution, HW shortages, maldistribution challenges, poor working conditions & weak HW management systems persist. There is a knowledge gap on Kenya's county-level capacity for HW management and this study sought to address this knowledge gap.

Methods: We used a qualitative case study design with HW management practices as our phenomenon of interest. We purposively selected two study counties to tease out how context shapes processes & outcomes of HW management practices. County A had a high gross county product (GCP), relatively high health system efficiency but low HW density while county B had low GCP, relatively low health system efficiency but high HW density. We used a data abstraction tool to review 9 relevant policy document and a guide to interview 35 county government officials with a formal HW management role. 14 and 21 key informants were interviewed in Counties A and B respectively. We managed data using NVIVO12 & used a thematic content analysis approach to analyze the data.

Results: We examined the policy and practice of five human resource management functions: recruitment, deployment, remuneration, in-service training & disciplinary processes. Both counties had clear recruitment guidelines though recruitment processes were not fully adhered to. Recruitment was used as a political tool; County A recruited some HWs without advertising for respective positions while County B recruited less of required HW professionals and more of support staff. Lack of policy guidelines on HW deployment seems to have created room for misuse of HW deployment so that those in good terms with senior county government officials would be posted to more favorable workstations. Even though county-level HW remuneration terms needed Salaries and Remuneration Commission approval, both county governments didn't seek approval of their HW remuneration terms and they paid non-specialized HWs less than the recommended pay. Finally, both counties had inadequate resources to support both short and long-term in-service training. They thus relied on development partners to support short-term training, and HWs released for long-term training were often self-sponsored.

Conclusion: Whereas decentralization of HW management aimed to have the national level regulating county-level autonomy over health workforce management, county governments have been operating without adequate oversight and guidance from the national government. This has created room for HW management malpractices that affect the quality of HWs recruited or serving in county governments. There is need to improve county-level HW management capacity and also improve oversight and regulation by the national government.

Keywords: health systems management, human resources for health, decentralization, Kenya

Abstract 165

Title: Seasonal Influenza Vaccination in Kenya: What Determines Healthcare Workers' Willingness to Accept and Recommend Vaccination?

Authors: NANCY OTIENO (KEMRI-CGHR); Rosalia Kalani (MOH- KENYA); Jorim Mr Ayugi (KEMRI-CGHR); RAPHAEL O ATITO (KEMRI-CGHR)*; ERIC OSORO (WSU - NAIROBI); PETER MUTURI (HJFMRI); LINUS NDEGWA (US-CDC); MALEMBE EBAMA (TSGH); Joseph Bresee (TSGH); Sandra Chaves (US-CDC); Eduardo Azziz-Baumgartner (US-CDC); GIDEON EMUKULE (US-CDC)

Background: Influenza contributes to significant morbidity and mortality worldwide. Influenza vaccination remains the most effective way to prevent influenza virus infection and its complications, and vaccinating healthcare workers (HCWs) is required in many hospitals globally, to reduce infection among the HCWs and protect patients who are at higher risk for influenza-related complications. Data on HCW's willingness to accept or recommend seasonal influenza vaccination in countries without influenza vaccination programs are limited. Kenya has been trying to introduce influenza vaccines for key target groups for the past decade. Such data will be critical in guiding introduction of- and increase uptake of seasonal influenza vaccination.

Methods: We conducted a cross-sectional survey in 7 of the 47 counties in Kenya, where we conduct sentinel surveillance for influenza, to examine knowledge and perceptions of HCWs towards seasonal influenza disease and vaccination. We enrolled a convenient sample of HCWs (professionals delivering clinical services directly/peripherally to patients) from 5 health facilities in each county: a county referral hospital, health center, dispensary, private facility and a faith-based health facility. We used chi-square tests and logistic regression models to identify variables that were associated with HCW's willingness to accept or recommend seasonal influenza vaccination. In our adjustments, we made a priori selection of age, sex and the county of study site.

Results: During May-June 2018, we enrolled 2,035 HCWs from 35 facilities. Most of the HCWs (82%) were from public health facilities and 64% were female. Of the HCWs who had heard of seasonal influenza (1,671/2,012, 83%), 87% believed that it could cause severe illness. Most (1,076/1,209, 89%) of the HCWs were willing to receive the seasonal influenza vaccine if it was recommended for HCWs and provided for free, and 91% (1,441/1,576,) would vaccinate their patients or recommend vaccination if the vaccine was available. Only 18% (213/1212) had received the vaccine before. HCWs who believed that influenza could cause severe illness (adjusted odds ratio [aOR] 2.2; 95% CI 1.3-3.5) and that people around them were better protected if they were vaccinated (aOR 3.1; 95% CI 2.0-4.6) were more willing to get vaccinated. Willingness to recommend seasonal influenza vaccination to patients was higher among HCWs who had seen patients with influenza (aOR 1.7; 95% CI 1.2-2.5), believed it could cause severe illness (aOR 2.0; 95% CI 1.3-3.2) and HCWs who believed that people around them are better protected if the HCW is vaccinated (aOR 3.6; 95% CI 2.3-5.7).

Conclusion: Our findings suggest favorable attitudes among HCWs towards a free-of-charge seasonal influenza vaccination, many of whom are motivated by the desire to protect others around them. These findings may inform future influenza vaccine rollout strategies targeting HCWs in Africa and other low-middle-income settings.

Keywords: Influenza, Vaccination, Healthcare worker

Abstract 166

Title: Evaluation of Cholera Surveillance System in Kenya between 2019-2021

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Background: Cholera remains a disease of significant public health importance and one of the 36 priority diseases under Kenya's updated Integrated Disease Surveillance and Response (IDSR) strategy 2021. A functional disease surveillance system is essential for defining health problems and informing appropriate action.

Methodology: The evaluation was guided by the updated CDC MMWR guideline for evaluating public health surveillance. The evaluation involved stakeholders' engagement where different stakeholders were identified and interviewed using a questionnaire to evaluate the surveillance system to ascertain its effectiveness.A review of records data reported to the Kenya Ministry of Public Health and Sanitation (Division of Disease Surveillance and Response) between 2019 and 2021 was analyzed to describe cases by Person, Place and Time. We interviewed key Informants both at the National (DDSR) and County levels on the effectiveness of the surveillance system. The roles of Key Informants at the National level were to; Provide technical advice on cholera surveillance-related issues, Capacity build counties on cholera and other infectious diseases, assist in the development of cholera technical guidelines & finally provide data management tools (Reporting tools) Whereas the roles of Key Informants were to; Coordinate cholera surveillance at the county, respond to cholera outbreaks at the county, Spearhead training at the county and Sub-county levels, cascade cholera prevention & control key messages & ensure data management tools are available and ensure timely reporting at the county.

Results: A total of 5945 cholera surveillance data were reviewed. The mean age was 22.3, and the most affected age group were between 0-9 years representing (30%). Nairobi City County had the highest cholera cases (26.2%)1555. 2019 recorded the greatest number of cholera-suspected cases (87.4%)5196. A total of 14 Counties reported outbreaks during the 3 years of evaluation. However, Garissa and Turkana Counties feature throughout the evaluation period. Finally, most cases were reported during EPI weeks 5,17 and 37 in 2019, Epi week 19 in 2020 and Epi week 25, in 2022. Ninety per cent (90%) of the stakeholders agreed that the Surveillance system was acceptable, useful and flexible.

Conclusion: There is the existence of a Cholera surveillance system to enable the detection of outbreaks, monitor morbidity and mortality, and also help institute Cholera Prevention and Control measures. However, there is a need to address the gaps within the system to strengthen sensitivity and effectiveness in surveillance.

Keywords: cholera Surveillance, Cholera, Descriptive analysis

Abstract 167

Title: Community Engagement and Co-Development in Designing Non-Communicable Disease Interventions: Case study of HEKIMA

Authors: Schiller Mbuka (KEMRI)*; Lydia Kaduka (KEMRI); Joseph Mutai (KEMRI); Erastus Muniu (KEMRI); Joanna Olale (KEMRI); Melvine Obuya (KEMRI); MIRIAM BOSIRE (KEMRI); Doreen Mitaru (KEMRI)

Abstract: Mbuka Schiller1, Obuya Melvine1, Mitaru Doreen1, Bosire Miriam1, Olale Joanna2, Muniu Erastus1, Mutai Joseph1, Kaduka Lydia1 Harding Seeromanie3

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Background: Co-production of research and generation of knowledge with local stakeholders is a widely acknowledged best practice. Community-based participatory research methods foster collective action for mutual long-term benefits. Guided by the UK Medical Research Council (MRC) guidance on complex interventions, and principles of community engagement, this study sought to identify contextual factors likely to influence the creation and use of health kiosks in markets (HEKIMA) as a system interface between the community and primary healthcare system, to improve access to cardiovascular disease preventive services.

Methods: This was a multi-phased mixed methods feasibility study in Vihiga County. Phase one (July 2019 to Feb 2020) involved partnership building through consent mapping workshops and consensus building with 35 stakeholders including primary healthcare practitioners (n=22), market and business community representatives (n=10), and NGO and patient representatives. Training of healthcare workers, kiosk development and provision of CVD screening and health promotion services in the kiosks was done in phase two (October 2021 to June 2022). Findings from concept mapping and consensus building were analyzed using the Group Concept Mapping (GCM) App. A locally constituted implementation team provided supervisory support and oversight.

Results: Stakeholders identified important and feasible action necessary for creation and use of HEKIMA. They included equipment and drug supply, efficient referral mechanisms, communication, competent manpower, and multi-sectoral partnerships. Findings informed a bespoke implementation model, which saw 2,224 participants served in 2 health kiosks over a 6-month period. Power sharing with locally constituted implementation team promoted political buy-in, ensured quality in processes and outcomes, impacted organization culture and working relationships among stakeholders.

Conclusion: Community engagement and co-development of health interventions enhances ownership, power, decision and knowledge sharing, reciprocity and partnership building. This process enhances acceptability, utilization of research findings and potential sustainability of health interventions.

Keywords: Community engagement and Co-development, NCD's ,Stakeholder engagement, Building Consensus

Abstract 168

Title: Targeting the ‘missing middle,’ Do free healthcare policies improve health insurance coverage among informal sector workers? A case of the Afya Care pilot program in Kenya

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Background: The informal sector workers (ISWs), the so-called “Missing Middle,” characterized by low, unpredictable, and fluctuating incomes, are excluded from health insurance (HI) programs leading to high out-of-pocket health expenditures. While most Low and Middle-Income Countries (LMICS) have identified HI as a reliable vehicle to achieve Universal Health Coverage (UHC), they have a characteristic approach of mandatory enrolment for the formal sector and tax subsidies for the vulnerable. The ISWs accounting for over two-thirds of the employment globally and 89% in Kenya, is often neglected for inclusion in HI schemes and has to enrol voluntarily, irrespective of their capacity to pay premiums. Following the implementation of the Afya Care UHC pilot, a free health policy project in 2019, the Kenyan Government opted for contributory HI to finance health towards achieving UHC. The informal sector workers remain a hard-to-reach population for HI targeting due to a lack of structures and coordination units for enrolment, yet their inclusion is critical to achieving UHC. This study aims to examine the effect of the free health policy pilot on HI coverage among ISWs and the factors to be considered to ensure inclusion.

Methods: The analysis utilized secondary data from two Kenyan nationally representative household-level repeat cross-sectional surveys on social protection, including HI. Data were collected before (Dec2018) and after (Dec2020) the pilot implementation under a blanket NACOSTI approval obtained by the UoN Institute of development. No additional ethical approval is required when using anonymized secondary data. The pilot was implemented in 4 purposively selected counties. Multistage random sampling methods were used to identify the household. Interviews were conducted with the household head using a standardized questionnaire. Our analytical model relied on a quasi-experimental approach with the pilot counties as the treatment group and the remaining 43 counties as the control group. We used bivariate analysis to describe sample characteristics and a difference-in-differences logistic regression to estimate the effect of the pilot on HI coverage.

Results: 5042 and 9682 respondents were surveyed in December 2018 and 2020, respectively. Our findings showed low overall HI coverage (23.1%) in ISWs. HI coverage between the pilot and control counties was significantly different after the intervention (29.8% & 20.8% respectively, P-value <0.001). Regression model showed 55% increase in the probability of enrollment in pilot counties compared to control counties (OR 1.55; CI 1.14-2.11; P<0.001) at 95% confidence level.

Conclusion: UHC pilot project positively influenced the HI coverage among the ISWs. However, the HI coverage remains low. The ISWs in Kenya are heterogeneous; hence the Kenyan Government ad other LMICs facing similar challenges of ISWs inclusion in HI schemes should adopt policy strategies to their varying needs.

Keywords: UHC, Health insurance, Informal sector workers, Missing middle

SCIENTIFIC SESSION 22: MATERNAL AND CHILD HEALTH-2

Abstract 169

Title: CARING FOR PROVIDERS TO IMPROVE PATIENT EXPERIENCE: MENTORSHIP NEEDS OF MATERNAL HEALTHCARE PROVIDERS IN MIGORI COUNTY, KENYA.

Authors: Joyceline Gaceri Kinyua (Kenya Medical Research Institute)*; Monica Getahun (UCSF); Linnet Ongeri (Kenya Medical Research Institute); Edwina Ndhine (Global Program &Research Training); BERYL AKINYI OGOLLA (GLOBAL PROGRAMS&RESEARCH TRAINING); Patience Afulani (UCSF)

Introduction: Mentoring is a system of hands-on training and consultation that can promote professional development and health care outcomes when implemented among clinical providers. Clinical mentoring can be achieved through utilization of experienced, practicing clinicians with strong teaching abilities. Further, provider-focused behavior change, including supportive supervision and mentorship interventions, can be used to powerfully influence provider attitudes and practices. However, mentorship programs in low and middle income settings such as Kenya are not well researched and collated to inform policy and practice. Hence, we sought to explore providers' perspectives about mentorship to inform a mentorship program as part of the Caring for Providers to Improve Patient Experience (CPIPE) study.

Methods: We conducted 31 In-depth interviews with maternal health care providers drawn from selected facilities in Migori County to identify mentoring capacity, needs, and preferences. Respondents included both clinical and non-clinical maternity providers tasked with care provision in the unit. Interviews conducted by two field researchers, trained in qualitative research methods were audio recorded. The audios were then transcribed and transcripts uploaded into Dedoose software for coding. Codes were developed prior based on interview guides and iteratively refined based on review of initial transcripts. Coded text were analyzed thematically.

Results: We highlighted five main themes: 1) Benefits mentorship, 2) Interest in participating in a mentorship program, 3) Expectations for mentorship, 4) Selection of mentor-mentee pairs, and 5) Sustaining the mentorship relationship. Providers cited knowledge sharing as a benefit of mentorship and expressed a desire to participate. They expected a supportive mentor system opposed to a supervision model and recommended that Mentor-Mentee pairs be selected based on expertise and competency level. Both non-financial and financial incentives were mentioned as essentials for motivating mentors to sustain the program.

Conclusion: The findings highlight mentorship as an essential component of knowledge sharing and capacity building in the dynamic maternity work environment. Strategies to support the roll-out and sustainability of mentorship programs within the maternal healthcare environment are needed.

Keywords: Maternal healthcare, Mentorship,

Abstract 170

Title: Characterizing Aspiration Pneumonia among Under Five deaths enrolled in the Child Health and Mortality Prevention Surveillance (CHAMPS) Network in Western Kenya

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Background: Aspiration pneumonia (AP) results from passage of secretions from the oropharyngeal, esophageal or stomach contents into the lower respiratory tract. AP is common among children with deglutition abnormality, congenital malformations, gastroesophageal reflux and preterm births. Children with AP have longer hospitalizations, higher ICU admission and readmission rates compared to children with non-aspiration pneumonia, but data characterizing AP deaths in Africa are lacking. We describe AP among decedent children aged under-five years enrolled in the Child Health and Mortality Prevention Surveillance (CHAMPS) platform in Western Kenya.

Methods: Under-five decedents underwent minimally invasive tissue sampling (MITS) autopsy. Specimen were subjected to PCR, culture, histopathological and immunohistochemical testing. Causes of death (CODs) in the causal chain (immediate, antecedent and underlying), and other contributory/significant conditions were determined by an expert panel. We calculated proportions of child deaths with AP anywhere in the causal chain or as a contributing factor. We also characterized other conditions diagnosed in AP-associated deaths and related etiologies. Stata MP 16 was used for analysis.

Results: Between May 2017 and March 2022, 43/474 (9.1%) deceased children aged 0-59 months had AP either in the causal chain or as other contributing factor. Twenty-three (53.5%) had AP as immediate or morbid COD, 7 (16.3%) as underlying COD and 13 (30.2%) as other significant condition. Ten (23.3%) of the AP deaths were in neonates 0-27 days, 21 (48.8%) in infants 28 days to <12 months and 12 (27.9%) in children 12 to <60 months. Overall, AP accounted for up to 13.9% of deaths among infants. Prevalence in children and neonates were 9.6% and 5.1% respectively. Fifteen (34.9%) of AP-associated deaths happened in the community.

Thirty-eight (88.4%) of the deaths had a condition that likely increased aspiration risk or resulted in a poor outcome, including pneumonia (bacterial or viral), HIV, gastroenteritis, sepsis, malnutrition, low birth weight, intestinal obstruction, down syndrome, cleft palate and lip, cerebral palsy and convulsive disorder. Only 4 (9.3%) children had AP diagnosis ante-mortem.

The commonest etiologies of pneumonia and gastroenteritis preceding AP were Klebsiella Pneumoniae, Streptococcus Pneumoniae and E. coli.

Conclusion: CHAMPS revealed AP-associated pediatric deaths that would have otherwise been unreported. Aspiration pneumonia cases were mostly diagnosed post mortem, indicating a complexity in accurate diagnosis and management. A high index of clinical suspicion and routine clinical audits of child deaths should therefore be encouraged to identify and manage aspiration pneumonia cases

Keywords: Aspiration, pneumonia, mortality, pediatric

Abstract 171

Title: Non-Communicable Diseases research: Trends and priorities in KEMRI's past 5 years

Authors Timothy Kipkosgei Kiplagat (KEMRI)*; Evans Tanui (KEMRI)

Background: Non-communicable diseases (NCDs) are a significant public health challenge. In Kenya, cardiovascular disease is the leading cause of mortality followed by cancer in third place. The burden of NCDs in developing countries is expected to rise due to the aging population, urban migration, and lifestyle changes. There is a need for evidence-based strategies in the treatment and prevention of NCDs. Although KEMRI conducts a significant number of research studies, little is known about the proportion and priority areas of NCD research conducted by KEMRI and its collaborators.

The study sought to determine the proportion of NCD research done in KEMRI within the last five years and the focus areas.

Methods: Data was abstracted retrospectively from the KEMRI SERU committee meeting agendas from October 2017 to November 2022. All the studies reviewed during this period were included. The study title and the objectives were used to obtain information on the area of focus.

Results: A total of 1165 research proposals were submitted to the SERU committee for review during this period, with 14% (165) studies focusing on Non-Communicable Diseases. Out of 165, studies on cancer accounted for 22% (36), Sickle Cell Disease 21% (35), Mental health 11% (18), Malnutrition 6% (10), Food and health 5% (8), and other NCDs accounting for less than 5% each and cumulatively accounting for approximately 35% (n=58 proposals). Over the last five years, data shows a steady increase in research focusing on NCDs. There were 5 (3%) proposals submitted in the last quarter of 2017, 37 (22%) in 2018, 24 (15%) in 2019, 17 (10%) in 2020, 41 (25%) in 2021, and 41 (25%) in 2022.

Most of the proposals were from CCR 36 (22%), CGMR-C 21 (13%), CRDR 16 (10%), CPHR 15 (9%), ICI 14 (8%), and 63 (38%) from other KEMRI Centres and other partners/collaborating institutions. Disaggregating NCDs areas of focus per Centres shows; CCR submitted the biggest number of both Cancer 11 (7%) and SCD 18 (10.9%) proposals, followed by CRDR 9 (5.5%) SCD proposals, ICI 8 (4.8%) Cancer proposals and CGMR-C 6 (3.6%) had the highest number of Mental health proposals.

Conclusion: Non-Communicable disease research constitutes less than a quarter of all research studies approved for implementation in KEMRI. Cancer, sickle cell disease, and mental health are the top three NCD areas of focus by researchers in the last 5 years.

Keywords: NCD, Cancer, Diabetes, Mental Health

Abstract 172

Title: The difficult situation in maternity care: triggers and strategies from provider perspective in Migori County, Kenya.

Authors: Edwina Ndhine Oboke (UCSF global program for research & training)*; BERYL AKINYI OGOLLA (GLOBAL PROGRAMS&RESEARCH TRAINING); Joyceline Gaceri Kinyua (Kenya Medical Research Institute); Monica Getahun (UCSF Institute for Global Health Sciences); Linnet Ongeri (Kenya Medical Research Institute); Patience Afulani (Epidemiology and Biostatistics Department, University of California, San Francisco (UCSF))

Background: One of the primary reasons for justifying patient disrespect and abuse during childbirth is that the woman was "difficult." While a confluence of circumstances including the provider, the patient, and others in the maternity ward all contribute to creating difficult environments, the labeling of patients remains pervasive. Few studies have explored both patient and providers perspectives, in an effort to improve difficult situations and promote respectful patient centered care. This study sought to examine the contributors to difficult situations from the perspective of providers.

Methods: Data are from 31 in-depth interviews (IDIs) with maternity providers (doctors, nurses, clinical officers, and support staff) in Migori county in western Kenya and Upper East region (UER) of Ghana (20). Interviews conducted in the local languages, were recorded, transcribed into English, and coded using a collaboratively developed deductive and inductive framework, by a team of seven researchers using Dedoose software. Data were analyzed using a thematic analysis approach.

Results: We identified 5 themes which were perceived to contribute to and create difficult situations: (1) patient's behavior, (2)patient condition, (3) patient background; (4) provider characteristics and behavior; and (5)inadequate resources to manage the situation. Providers' responses to difficult situations included 4 themes: (1) asking for help from others, (2) communicating effectively, (3) avoidance and enforcement, and (4) planning for potential repercussions .

Conclusions: The patient, the provider, and the environment all contribute to difficult situations, which ultimately shape patient-provider interactions. To improve person-centered care and reduce mistreatment of women during childbirth, a nuanced understanding of the contributors to these difficult situations is important. Future interventions can leverage current management strategies and promote positive coping.

Keywords: Maternal healthcare, Difficult situation

Abstract 173

Title: Quantitative culture of the probiotic microorganisms contained in the supplements administered to infants in the PROSYNK (PRObiotics and SYNbiotics in infants in KENYA) study.

Authors: Micah June June (KEMRI-LSTM)*

Background: Probiotics are live microorganisms which, when administered in adequate amounts, confer health benefits on the host. When presented for therapeutic use should contain enough live microorganisms to confer expected health benefits. In the PROSYNK trial, probiotics used alone or in combination with prebiotics (synbiotic) were evaluated for the prevention of environmental enteric dysfunction (EED). The purpose of assessing probiotic viability was two fold: (1) to determine if products contained viable micro-organisms shipped and stored at manufacturers' recommended temperatures at point of use and (2) to assess effect of storage at ambient temperature for different time periods on probiotic viability to inform design of a larger study and further upscaling of administration of the intervention.

Methods: We performed viability testing by quantitative culture for investigational products used in the PROSYNK trial. At point of use, we drew 24 and 7 capsules from the two shipments received from the manufacturers that were shipped and stored in recommended temperatures of 2-80C. Testing was done on same day of draw for capsules. Additionally, we stored some capsules at ambient temperature and tested over durations of 1, 3, 6 and 11.5 months. During the storage period, temperatures were monitored using digital temperature loggers. Quantification of micro-organisms was achieved by counting the total number of colony forming units (CFU) per capsule. Using Miles and Misra method, working from highest dilution to lowest (i.e 10-5 to 10-1), plating out 10 x 10 µl drops onto the surface of the agar (MRS agar for Lactobacillus Spp. and MRS-X agar for Bifidobacterium Spp.). Plates were allowed to dry and then were incubated anaerobically at 370C for 72 hour. Plates with 30-300 colonies were selected, description by type: Size (e.g. L= large, M= medium, S= small) and Color of colony (e.g. W= white, G= grey, C= cream, Y= yellow).

Results: All capsules tested within a day of draw and stored under manufacturers recommended temperatures of 2-80C had viable microorganisms. Labinic synbiotic had no growth from cultures of capsules stored under ambient temperature for periods exceeding one month. The Lab4b capsules (both probiotic and synbiotic) manufactured by Cultech, had colony forming units decline over time but organisms were viable over the entire period.

Conclusion: All products were viable at point of use when shipped and stored using a cold chain. The Lab4b probiotics and synbiotics retained viable microorganisms up to 11 months, though declining in number of CFU when stored in ambient temperatures (between 24.0C and 25.50C). Studies on effective dose and performance in reducing EED, resilience of Lab4b probiotics to stirgare at ambient temperature should inform selection for upscaling of the intervention where access to refrigeration is a challenge.

Keywords: Quantitative culture of the probiotic microorganisms

Abstract 174

Title: Group care for antenatal care services: Experiences of women in rural Ghana.

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Abstract

Background: The World Health Organization (WHO) estimates that about 94% of preventable deaths from pregnancy and childbirth complications occur in low-resource settings, reflecting inequalities in access to quality health services. In the Binduri District of the Upper East Region of Ghana, a largely rural area, only 37.4% of women utilized antenatal care services in 2019. The GC-1000 project is implementing group care across seven countries globally across seven countries with funding from the EU Horizon 2020 research grant. Group care utilizes strategies to break the vicious cycle of care. In Ghana, group care sessions integrate Check2gether (C2G) (a non-invasive diagnostic tool kit), which screens for risk factors (pre-eclampsia, anemia, diabetes and urinary tract infections) in pregnancy. This model of care seeks to holistically provide health care through its three components: healthcare, interactive learning and community building.

Methods: Stakeholder engagements at all levels of the Ghana healthcare system were held (community, district and national levels) to get them to understand and appreciate the concept of group care. A situational analysis was then carried out involving local and international researchers (LUMC, Netherlands and VUB Belgium), and adaptations were made to suit the local context. Healthcare professionals comprising midwives and community health workers with midwifery skills were trained to use C2G and group care.

Results: Twenty-three (23) groups have been formed, with about 128 group sessions held as of October 2022 with a dropout rate of 7%. Healthcare providers reported an increased antenatal care attendance by women, a better understanding of their blood pressure reading and other diagnostic results like Hemoglobin and Urine tests due to the support they received with measurements and interpretation using the C2G toolkit and all increase in knowledge regarding their pregnancies. There has also been an improvement to access to services as women noted that they no more had to travel long distances to access care, translating to saving on cost and time on their part.

Conclusion: Women accessing health services under the group care model are very optimistic about the model. They demonstrate a high understanding and appreciation of the care received at group care sessions. Antenatal group care has the potential to bridge the gap in access to quality health care in low-resource settings.

Keywords: rural holistic antenatal care - group care - diagnostic sreening pregnant women

SCIENTIFIC SESSION 23: MALARIA

Abstract 175

Title: Four years of antimalarial Resistance Marker Surveillance using School Surveys in Kenya

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Background: Globally, Plasmodium falciparum malaria continues to be a leading cause of mortality and morbidity, particularly in sub–Saharan Africa. Control measures such as insecticide-treated nets (ITNs), use of artemisinin combination therapy (ACT) and increased donor funding has led to a decline in malaria incidences and prevalence in sub-Saharan Africa and Southeast Asia. The emergence of drug resistance to artemisinin and its derivatives in Southeast Asia and recent reports from Rwanda and Uganda pose a significant threat to malaria control and elimination. Therefore, the rise and spread of parasites not responding to artemisinin and its derivatives will create a challenge in controlling and eliminating malaria. In this study, we use dried blood spot (DBS) samples collected from Primary school children in Kenya between 2019 - 2022 to analyze P. falciparum drug resistance markers.

Method: DBS samples collected from primary school children in select counties (Migori, Homabay, Kisumu, Siaya, Vihiga, Bungoma, Busia, Kakamega, Kisii, Kirinyaga, Taita Taveta, Kwale, Kilifi, Tana River, Turkana and West Pokot) whose aim was to evaluate the incidences of malaria infection among school children were analysed. A rapid diagnostic test (RDT) was used to determine malaria positivity. DNA was extracted from RDT positive samples using the Chelex saponin method and a P. falciparum quantitative polymerase chain reaction (Pf qPCR) assay was used to quantify parasitemia in the samples. The DNA from P. falciparum positive samples by qPCR Ct<31 was used to generate amplicons for Pfdhfr, Pfk13, Pfdhps, and Pfmdr1 genes and sequenced using a targeted amplicon deep sequencing (TADs) assay on the Illumina MiSeq platform.

Results: None of the Kelch 13 validated (Y493H, R539T, I543T, R561H, C580Y) genetic changes associated with artemisinin resistance were found in this population. However, changes in mutant allele numbers were seen in Sulphadoxine-Pyrimethamine (SP), Pfdhfr N51I(98%), C59R(89%), S108N(98%), including a rise in the Pfdhps S436H(67%), A437G(100%), A540E(100%) resistance alleles. This data also describes novel mutant alleles such as Pfmdr1 codon T199 and Pfdhfr codons 85I and 164L mutations in the Kenyan population.

Conclusion: The findings show that there were no mutations linked to parasite resistance to ACTs currently. However, the data presented here suggest that ongoing evaluation of antimalarial drug efficacy, particularly for artemisinin-based combinations, is required in Kenya and other malaria-endemic regions to implement timely evidence-based malaria treatment policies. This study proposes the inclusion of molecular monitoring of Pfdhfr/Pfdhps mutations in SP-based effectiveness studies. We also present a robust molecular surveillance tool that the national malaria control program can adapt.

Keywords: Antimalarial drug resistance markers surveillance

Abstract 176

Title: Variability of Plasmodium falciparum asexual and sexual parasite carriage amongst individuals with symptomatic and asymptomatic infections in Kombewa, Kisumu county Kenya

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Background: Malaria prevalence continues to decline across sub-Saharan Africa because of various intervention strategies but still poses a public health concern in the region. The burden is based on convenient screening of symptomatic cases only. Asymptomatic infections are becoming highly prevalent hence increasingly an important target for interrupting transmission. This study aimed at describing P. falciparum asexual and sexual parasite carriage as well as P. falciparum multidrug resistance (Pfmdr1) and P. falciparum chloroquine resistance transporter (Pfcrt) genotypes associated with antimalarial drug resistance among individuals with symptomatic and asymptomatic infections.

Methods: 739 samples obtained from 339 symptomatic and 400 asymptomatic individuals in Kombewa Western Kenya between 2018 and 2021 were characterized for P. falciparum prevalence and gametocyte carriage by using reverse transcription-quantitative PCR (RT-qPCR). Genotyping of Pfcrt and Pfmdr1 was carried out on the iPLEX MassARRAY platform.

Results: Plasmodium falciparum prevalence was 71% and 56% in symptomatic and asymptomatic cases respectively ($p=0.002$). Gametocyte prevalence was higher in symptomatic 78% than in asymptomatic individuals 33%, $p<0.001$. A total of 4.4% ($n=206$) symptomatic infections harbored Pfmdr1 86Y mutations while none of the asymptomatic cases were observed with this allele ($p=0.037$).

The prevalence of Pfmdr1 184F mutation in symptomatic individuals was 38% compared to 54% among asymptomatic. In addition, Pfmdr 1246Y mutations present in symptomatic was 7% and asymptomatic had 3% p=0.8. For Pfcrt 76, both symptomatic and asymptomatic did not have any mutations. Correlation of gametocyte carriage with the SNPs indicated 88% having both Pf16 and Pf25 lifecycle stage had mutant Pfmdr1 184F, p=0.025.

Conclusion: The marginally high Pfmdr1 184F mutation observed in asymptomatic individuals and the differences in the asexual and sexual parasite carriage may suggest an association with pathogenicity and virulence since studies have shown some Pfmdr1 and Pfcrt genotypes have a distinct prevalence according to clinical status, therefore the need to monitor and treat the asymptomatic cases. In addition, an increase in gametocyte carriage with resistant infections must be an important factor driving resistance of P. falciparum.

Key words; Asymptomatic malaria, drug resistance markers, single nucleotide polymorphisms

Abstract 177

Title: Influence of landscape heterogeneity on entomological and parasitological indices of malaria in Kisumu, Western Kenya

Authors: Wilfred Ouma Otambo (PhD scholar)*

Background: Identification and characterization of larval habitats, documentation of Anopheles spp. composition and abundance, and Plasmodium spp. infection burden, are critical components of integrated vector management. The present study aimed to investigate the effect of landscape heterogeneity on entomological and parasitological indices of malaria in western Kenya.

Methods: A cross-sectional entomological and parasitological survey was conducted along an altitudinal transect in three eco-epidemiological zones: Lakeshore along the lakeside, hillside, and highland plateau during the wet and dry seasons in 2020 in Kisumu County, Kenya. Larval habitats for Anopheles mosquitoes were identified and characterized. Adult mosquitoes were sampled using Pyrethrum Spray Catches (PSC). Finger prick blood samples were taken from residents and examined for malaria parasites by real time-PCR (RT-PCR).

Results: Increased risk of Plasmodium falciparum infection was associated with residency in the lakeshore zone, school-going age children, rainy season, and no ITNs ($\chi2 = 41.201$, df = 9, $P < 0.0001$. Similarly, lakeshore zone and the rainy season significantly increased Anopheles spp. abundance. However, house structures such as wall type and whether the eave spaces were closed or open, as well as the use of ITNs did not affect Anopheles spp. densities in the homes ($\chi2 = 38.695$, df = 7, $P < 0.0001$). An. funestus (41.8%) and An. arabiensis (29.1%) were the most abundant vectors in all zones. Sporozoite prevalence was 5.6% and 3.2% in the two species respectively. The lakeshore zone had the highest sporozoite prevalence (4.4%, 7/160) and inoculation rates (135.2 infective bites/person/year). High larval densities were significantly associated with lakeshore zone and hillside zones animal hoof prints and tire truck larval habitats, wetland and pastureland, and the wet season. The larval habitat types differed significantly across the landscape zones and seasonality ($\chi2 = 1453.044$, df = 298, $P < 0.0001$).

Conclusion: The empirical evidence on the impact of landscape heterogeneity and seasonality on vector densities, parasite transmission, and Plasmodium infections in humans emphasizes the importance of tailoring specific adaptive environmental management interventions to specific landscape attributes to have a significant impact on transmission reduction.

Keywords: Anopheles density, Plasmodium infection prevalence, landscape, risk factors

Abstract ID:178

Title: Impact of Malaria Rapid Diagnostic Tests on Patient-Important Outcomes in sub-Saharan Africa: A systematic Review of Study Methods

Authors: Jenifer A. Otieno (Kenya Medical Research Institute)*; Lisa Were (Kenya Medical Research Institute); SAGAM CALEB KIMUTAI (KENYA MEDICAL RESEARCH INSTITUTE CENTER FOR GLOBAL HEALTH RESEARCH); Simon Kariuki (Kenya Medical Research Institute); Eleanor Ochodo (Kenya Medical Research Institute)

Background: Malaria is among the leading causes of death in sub-Saharan Africa. According to the World Health Organization (WHO) (2021), in 2020, 93% of global malaria deaths were reported within sub-Saharan Africa. As a result, the scale-up of malaria interventions have been reinforced, e.g., pre-treatment parasitological confirmation using malaria rapid diagnostic tests (mRDTs). Consequently, mRDT impact evaluations have been conducted. However, impact evaluations require guidance about execution as poorly designed evaluations often misguide health policy. We, therefore, aimed to assess the study designs, patient-important outcome measures, methodological quality, and implementation challenges of studies that evaluate the impact of mRDTs on patient-important outcomes.

Methods: We included primary studies done in sub-Saharan Africa assessing the impact of RDTs compared to other malaria diagnostic methods, i.e., microscopy, PCR, or clinical diagnosis, among persons suspected of malaria on patient-important outcomes. We excluded descriptive cross-sectional designs, modelling, secondary and qualitative designs, and studies that did not assess patient-important outcomes. We searched MEDLINE, EMBASE, Cochrane Library & African Index Medicus from inception until 2 May 2022. Two independent reviewers screened studies against the eligibility criteria & extracted data using the Covidence platform. We assessed study quality using the National Institutes of Health (NIH) tool. Data were analysed using descriptive statistics & thematic content analysis using STATA version 17 and presented using tables & graphs & narratively.

Results: Our search yielded 4,717 studies 24 studies were included. Of all studies included, 62.5% (n=15) were randomised, 20.8% (n=5) were quasi-experimental and 16.7% (n=4) were observational. A total of 48 patient-important outcomes were reported; 30 measures of therapeutic impact (62.5%), 17 measures of direct patient impact (35.4%) and one measure of diagnostic impact (2.1%). Implementation challenges were mainly reported in the domain: of health system constraints, whereby the predominant theme was human resources. Methodological quality ratings were as follows; 11/15 (73.3%) experimental, 3/5 (60%) quasi-experimental and 2/4 (50%) observational studies were rated good, while all the remaining studies qualified for a fair rating.

Conclusion: Generating evidence on malaria RDT impact is challenging since an idealistic choice for outcomes or designs does not exist. In addition, other factors, such as test unacceptability and low confidence in test results, often dictate options. Although randomised studies are the most adopted designs, they come with trade-offs concerning the non-implementation of essential safeguards like blinding. Future research on other techniques may be employed to assess the impact of mRDTs. As mRDTs aim at improving overall patient health, including patient-centred outcomes during evaluations, is advisable.

Keywords: Malaria, Rapid Diagnostic Tests, Diagnosis, Impact, Patient outcomes, sub-Saharan Africa.

Abstract 179

Title: Low frequency of Plasmodium falciparum hrp 2/3 deletions from symptomatic infections at a primary healthcare facility in Kilifi, Kenya

Authors Dorcas Okanda (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi); Leonard Ndwiga (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi)*; Victor Osoti (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi); Nicole Achieng (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi); Juliana Wambua (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi); Caroline Ngetsa (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi); Peter Lubell-Doughtie (Ona); Anuraj Shankar (Nuffield Department of Medicine); Philip Bejon (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi); Lynette Ochola-Oyier (KEMRI-Wellcome Trust Research Programme, CGMRC, Kilifi)

There is a growing concern for malaria control in the Horn of Africa region due to the spread and rise in the frequency of Plasmodium falciparum Histidine-rich Protein (hrp) 2 and 3 deletions. Parasites containing these gene deletions escape detection by the major PfHRP2-based rapid diagnostic test. In this study, the presence of Pfhrp2/3 deletions was examined in uncomplicated malaria patients in Kilifi County, from a region of moderate-high malaria transmission.

A total of 345 samples were collected from the Pingilikani dispensary, Kilifi county, in 2019/2020 during routine malaria care from patients below the age of 14 years. The CarestartTM RDT and microscopy were used to test for malaria. In addition, qPCR was used to confirm the presence of parasites. In total, 249 individuals tested positive for malaria by RDT, 242 by qPCR, and 170 by microscopy. 11 samples that were RDT-negative and microscopy positive and 25 samples that were qPCR-positive and RDT-negative were considered false negative tests and were examined further for Pfhrp2/3 deletions. Pfhrp2/3-negative PCR samples were further genotyped at the dihydrofolate reductase (Pfdhfr) gene which served to further confirm that parasite DNA was present in the samples. The 242 qPCR-positive samples (confirmed the presence of DNA) were also selected for Pfhrp2/3 genotyping. To determine the frequency of false negative results in low parasitemia samples, the RDT- and qPCR-negative samples were genotyped for Pfdhfr before testing for Pfhrp2/3.

There were no Pfhrp2 and Pfhrp3 double deleted samples but positive for dhfr parasites in the: 11 (RDT negative and microscopy positive) and 25 samples (qPCR-positive and RDT-negative). Of the 11, 4 had had more than 1000 parasites/µl, suggesting true hrp2/3 deletions. In the larger qPCR-positive sample set, only 5 samples (2.1%) were negative for both hrp2 and hrp3, but positive for dhfr.

These findings revealed that there is currently a low prevalence of Pfhrp2 and Pfhrp3 deletions in the health facility in Kilifi. However, routine monitoring in other primary health care facilities across the different malaria endemicities in Kenya is urgently required to ensure appropriate use of malaria RDTs

Keywords: hrp2, hrp3, deletions, Malaria RDTs, Plasmodium falciparum

Abstract 180

Title: Antimalarial Susceptibility of Plasmodium falciparum field isolates from Busia county in Kenya

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Plasmodium falciparum Kelch 13-propeller gene (PfK13) mutations in A578S, A568G, and D584Y loci have been shown to confer resistance to artemisinin-based combination therapies (ACTs) in Southeast Asia. Though these polymorphisms have not yet been detected in Africa, more than a decade since they were first reported, studies associated artemisinin resistance with parasites that harbor PfK13-propeller gene mutations in loci R561H for Rwanda and Uganda (C469Y and A675V). These parallel findings warrant intensified surveillance to map the dispersion of these mutations or new ones causing impaired response to ACTs in Africa. Busia county in western Kenya, is an entry point for travelers from both Rwanda and Uganda where resistance has been reported. The objective of this study was to find out the response of P. falciparum field isolates from Busia to a panel of antimalarial drugs.

A total of 30 P. falciparum positive clinical samples obtained from individuals presenting to Busia county Hospital with uncomplicated malaria between year 2020 - 2022 were tested for in vitro susceptibility to chloroquine (CQ), quinine (QN), atovaquone (AV), primaquine (PQ) and artemisinin (ART), dihydroartemisinin (DHA), artemether (AR) and amodiaquine (AMQ). Response to each drug was estimated using a dose response curve generated by relative fluorescence units of 2-fold dilution dose range across 11-wells. Each isolate was also genotyped for PfK13-propeller gene polymorphisms.

The median drug concentration that inhibits parasite growth by 50% (IC50s) for 30 isolates were 18.68 ng/ml (12.31 to 28.57) for chloroquine, 19.43 ng/ml (12.3 8 to 33.42) for quinine, 7.170ng/ml (3.071 to 12.04) for atovaquone, 38.86 ng/ml (95%Cl,26.32 to 81.48) for piperaquine and 0.8535 ng/ml (0.4478 to 1.597) for amodiaquine.

The median IC50s for artemisinin derivatives including artemisinin, artesunic acid, dihydroartemisinin and artemether were 2.384 ng/ml (1.385 to 4.072), 4.169 ng/ml (1.748 to 5.912), 0.4047 ng/ml (95%Cl,0.3192 to 0.6633) and 2.926 ng/ml (1.957 to 3.942), respectively.

The median IC50s for the 8-aminoquinolines were 893.0 ng/ml (619.5 to 1210) for primaquine and 933.3 ng/ml (95% Cl,577.9 to 1213) for tafenoquine.

The antibiotic antimalarial doxycycline had a median IC50 of 2418 ng/ml (723.0 to 5662). The IC50s for chloroquine and quinine were below the resistance threshold while those of the artemisinin derivatives and partner drugs were comparable to those from other regions.

Mutations in PfK13-propeller gene loci A578S, A568G, and D584Y found in Southeast Asia, R561H Rwanda and C469Y and A675V in Uganda and R561H found in Rwanda were absent, suggesting that field isolates from Busia County were susceptible to the artemisinin derivatives bases on phenotypic and genotypic assessment. Owing to existing evidence of both dispersion and sporadic emergence of resistance to ACTs, continued surveillance is important for early detection of changing response antimalarials.

Keywords: Antimalarial,Kelch-13 propeller gene(k13),polymorphism,Plasmodium falciparum,gene loci,,susceptibility,malaria field isolates

Abstract 181

Title: Identification of malaria hotspots in a highland site in western Kenya

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Background: The transmission of malaria often shows spatial heterogeneity. This heterogeneity reduces the effectiveness of control strategies, however targeting control strategies on hotspots of transmission may represent a highly effective strategy for reducing transmission and could be essential for malaria elimination. This study aims to identify and map hotspots and cold spots of malaria transmission in a low endemic area that is prone to epidemics in the western Kenyan highland.

Methods: Cross-sectional survey was conducted in the community from 575 individuals (children and adults) and entomological survey in 300 households. Getis-Ord Gi* statistic was used to detect hotspots of malaria transmission based on asymptomatic malaria detected by quantitative polymerase chain reaction (qPCR), aquatic habitats, and densities of Anopheles mosquitoes in pyrethrum spray catches (PSC).

Results: Cold spots and hotspots of spatially clustered asymptomatic malaria, elevated vector abundance, and aquatic larval habitats were detected. Proximity to larval habitats was correlated to high asymptomatic parasitaemia and increased vector abundance. We observed hotspots of asymptomatic parasitaemia detected by PCR only partially overlapped with clusters of vector abundance and larval habitats.

Conclusion: Geospatial technology is essential for analysis of spatial and temporal data and the tool is particularly important in targeted control interventions that may effectively reduce malaria burden and eventually eliminating. Further studies are required to understand the environmental, socio-demographic, and behavioural determining factors of malaria risk.

Keywords: Hotspots, Malaria, Asymptomatic parasitemia, Mosquito

Abstract 182

Title: Limited genetic variations of the Rh5-CyRPA-Ripr invasion complex in Plasmodium falciparum parasite population in selected malaria-endemic regions, Kenya.

Authors: HARRISON K WAWERU (MOUNT KENYA UNIVERSITY)*; Bernard Kanoi (MOUNT KENYA UNIVERSITY); Josiah Kuja (University of Copenhagen, Copenhagen, Denmark); Mary Maranga (Malopolska Centre of Biotechnology, Jagiellonian University); James Kongere (Centre for Research in Tropical Medicine and Community Development); Michael Maina (MOUNT KENYA UNIVERSITY); Johnson Kinyua (Jomo Kenyatta University of Agriculture and Technology); Jesse Gitaka (Mount Kenya University)

Background: The invasion of human erythrocytes by Plasmodium falciparum merozoites requires interaction between parasite ligands and host receptors. Interaction of PfRh5-CyRPA-Ripr protein complex with basigin, an erythrocyte surface receptor, via PfRh5 is essential for erythrocyte invasion. Antibodies raised against each antigen component of the complex have demonstrated erythrocyte invasion inhibition, making these proteins potential blood-stage vaccine candidates. Genetic polymorphisms present a significant challenge in developing efficacious vaccines, leading to variant-specific immune responses. This study investigated the genetic variations of the PfRh5 complex proteins in P. falciparum isolates from Lake Victoria islands, Western Kenya.

Methods: Twenty-nine microscopically confirmed P. falciparum field samples collected from islands in Lake Victoria between July 2014 and July 2016, and sixty eighty samples collected from a dihydroartemisinin, piperaquine and artemether-lumefantrine drugs resistance trial study conducted in Kilifi, coastal Kenya between 2005 and 2008 were genotyped by whole genome sequencing. We analyzed the frequency of polymorphisms in the PfRh5 protein complex proteins, PfRh5, PfCyRPA, PfRipr, and PfP113, and their location mapped on the 3D protein complex structure.

Results: We identified a total of 58 variants in the PfRh5 protein complex. PfRh5 protein was the most polymorphic with 30 SNPs, while PfCyRPA was relatively conserved with 3 SNPs. The minor allele frequency of the SNPs ranged between 1.9% and 21.2%. Ten high-frequency alleles (>5%) were observed in PfRh5 at codons 147, 148, 277, 410, and 429 and in PfRipr at codons 190, 255, 259, and 1003. A SNP was located in protein-protein interaction region C203Y and F292V of PfRh5 and PfCyRPA, respectively.

Conclusion: This study revealed low polymorphisms in the PfRh5 invasion complex in the Lake Victoria parasite population. However, the two mutations identified on the protein interaction regions prompts for investigation on their impacts on parasite invasion process to support the consideration of PfRh5 components as potential malaria vaccine candidates.

Keywords: Genetic variations, Rh5-CyRPA-Ripr invasion complex, malaria, vaccines

SCIENTIFIC SESSION 24: ANTIMICROBIAL RESISTANCE-2

Abstract 183

Title: Most common resistant phenotypes, genotypes and prevalence of multidrug resistant (MDR) Salmonella Typhi in acute disease and chronic carriage in endemic setting in Nairobi County, Kenya

Authors: SUSAN M KAVAI (KENYA MEDICAL RESEARCH INSTITUTE)*; Samuel Kariuki (Kenya Medical Research Institute); Cecilia Mbae (KEMRI); Kelvin kering (Kenya Medical Research Institute); Peter muturi (Kenya Medical Research Institute)

Background: The emergence and persistence of multidrug-resistant Salmonella Typhi infections is a major challenge globally affecting countries where typhoid fever is endemic. In Kenya, multidrug-resistant Salmonella Typhi remains a big public health problem with an incidence rate of 263 per 100,000 persons time across all age groups (95% CI: 199–347). The burden of typhoid infections has increased in limited resource settings within low- and middle-income countries. In tandem, S. Typhi carriage, which occurs in 3 to 5% of S. Typhi infected individuals, has also become more common in these settings. Nevertheless, the role of carriers in the transmission of S. Typhi in low-income communities, including Kenya, remains poorly understood. These gaps hamper the design of effective control interventions for typhoid infections. This study used archived and prospectively collected S. Typhi isolates from Mukuru informal settlement settings. The study sought to identify the most prevalent antimicrobial resistance phenotypes and genotypes and prevalence of multidrug-resistant (MDR) Salmonella Typhi in acute illness and chronic carriage in Mukuru settlement.

Methods: Our study utilized both archived Salmonella Typhi isolates (collected from 2013-2018) and those isolated from prospectively collected blood and stool samples (2020-2022). We subjected a total of 427 positively confirmed Salmonella Typhi to antibiotics sensitivity testing using Kirby Bauer disc diffusion (archived and prospectively collected). We also subjected 221 of the archived isolates (collected from 2013-2016) to whole genome sequencing to check for presence of antimicrobial resistance (AMR) genes.

Results: Of the archived S. Typhi isolates, (156/338, 42%) were found to be multi drug resistant (MDR) (they all had the resistance phenotypes against ampicillin, sulfamethoxazole trimethoprim and chloramphenicol). For the prospectively isolated S. Typhi (31/89, 34.8%) were reported to have similar resistance phenotypes (resistance to ampicillin, sulfamethoxazole trimethoprim and chloramphenicol). Of all 221 MDR isolates sequenced, we reported the presence of bla Tem,137/221(62.0%), Sul1,123/221(55.7%), Acc-6,104/221(47.1%) and Cat 1,91/221(41.2%) as the most common resistance genotypes.

Conclusion: This study reported ampicillin, sulfamethoxazole trimethoprim and chloramphenicol (AMP, SXT & CHL) as the most common resistant phenotypes across Salmonella Typhi isolates collected within a period of 10 years. Resistance genotypes for ampicillin, sulfamethoxazole trimethoprim and chloramphenicol were also the most reported. MDR prevalence of 43.8% was reported for all S. Typhi isolated within the period of 10 years (2013-2022).

Keywords: Key words: Multidrug resistance, Salmonella Typhi, Typhoid fever, Resistant Phenotypes, Prevalence, Genotypes

Abstract 184

Title: Genomic characterization of two community-acquired methicillin-resistant staphylococcus aureus with novel sequence types in Kenya

Authors: John Njenga (Kenya Medical Research Institute)*; Justin T Nyasinga (Aga Khan University); Zubair Munshi (Aga Khan University); Angela Muraya (JKUAT); Geoffrey Omuse (Aga Khan University); Caroline Ngugi (JKUAT); Revathi Gunturu (Aga Khan University)

Background: Staphylococcus aureus is a clinically important bacteria with high antimicrobial resistance (AMR) challenge globally. The emergence of methicillin-resistant Staphylococcus aureus (MRSA) clones with unique sequence types have been identified in the community showing evidence that the epidemiology of MRSA globally is changing and requires continual surveillance.

Methods: We utilized whole genome sequencing to characterize two community acquired-MRSA (CA-MRSA) strains isolated from wound swabs from community-onset infections in two health facilities in Kenya.

Results: The two strains belonged to sequence type (ST) 7460 and 7635. The resistance genes detected showed that the novel STs are carriers of clinically relevant resistance genes. Linezolid and mupirocin resistance was observed, yet mupirocin is not commonly used in the country. Mutations within resistance genes were also detected and the pathogenicity toward the human host matched various pathogenic global S. aureus families, e.g., S. aureus subsp. aureus USA300. Multidrug efflux transporters, important in antimicrobial resistance including restriction enzymes type I and type IV were detected. Plasmids identified showed similarities with the plasmids in other clinically significant non-staphylococcal species, such as Pseudomonas aeruginosa, Escherichia coli, Morganella morganii, and Enterococcus faecium. Both STs belong to clonal complex 8 (CC8) which is the most successful MRSA clone in Kenya. Spa type t30 to which ST 7635 belongs has not been reported in the country.

Conclusion: This study further highlight the need for epidemiological studies to reveal circulating strains and antimicrobial resistance spread between hospitals and the community. The genomic research highlights resistance to anti-staphylococcal broad-spectrum antimicrobials not used frequently in the country, jeopardizing successful MRSA treatment since most health facilities do not perform genotypic resistance tests for routine patient management. Preliminary insights into unidentified STs of CA-MRSA in Kenya show the need for molecular epidemiological surveillance studies to further understand the diversity of S. aureus in Africa.

Keywords: CA-MRSA, Sequence typing, AMR, Kenya

Abstract 185

Title: Extended spectrum beta lactamase producing Gram negative bacteria colonizing neonates admitted in the neonatology units at Bugando Medical Centre, Mwanza, Tanzania.

Authors: Jacobo E Machimu (Muhimbili National Hospital)*; Vitus Silago (Catholic University of Health and Allied Sciences); Delfina Msanga (Catholic University of Health and Allied Sciences)

Background: Recent studies at Bugando medical center (BMC) have shown evidences of increased neonatal rectal colonization by Extended-spectrum β-lactamases producing Gram negative bacteria (ESBL-GNB). Reports were shared to the neonatology units where by interventions to minimize and control colonization were initiated and are currently on going. This study investigated the prevalence, antibiotic susceptibility patterns and factors associated with neonatal rectal colonization by ESBL-GNB at BMC, Mwanza-Tanzania so as to assess the impact of initiated interventions.

Methods: This cross-sectional hospital-based study was conducted among 259 neonates admitted in neonatology units at BMC between February and August 2021. Participants' data were collected using structured questionnaires. A total of 476 neonatal rectal swabs were collected during study period. Rectal swabs were directly inoculated on MacConkey agar (MCA) plates supplemented with cefotaxime 2μg/ml for screening of ESBL-GNB. Conventional biochemical identification tests, Kirby-Bauer technique and Combination disks technique were used for species identification, antibiotic susceptibility testing and phenotypic confirmation of ESBL-GNB production, respectively.

Results: Out of 476 rectal swabs, 182 (38.2%) had positive growth on MCA-C of which 19 samples had poly-microbial growth resulting to 201 bacteria isolates. The prevalence of neonatal rectal colonization by ESBL-GNB among neonates was 20.08% (54/259). Majority of the isolates were highly resistant to trimethoprim-sulfamethoxazole, gentamycin and tetracycline, while they were highly sensitive to amikacin and meropenem. Significantly, the use of nasogastric tubes in situ (OR [95%CI] 1.891 [1 – 3.55], p = 0.048) was associated with ESBL-GNB neonatal rectal colonization.

Conclusion: This study found that prevalence of neonatal colonization with ESBL-GNB at BMC is relatively lower than recent studies. Continuous implementation of the initiated interventions to reduce neonatal colonization such as frequent decontamination protocols, awareness campaign for mothers on potential spread of bacteria and antimicrobial stewardship are recommended. Further studies are also suggested to explore the other sources and associated risk factors for neonatal rectal colonization.

Keywords: Extended spectrum beta lactamase, ESBL, Gram negative bacteria, Neonatal rectal colonization and Bugando medical center.

Abstract 186

Title: Typhoidal Salmonella disease, carriage, diversity and antimicrobial resistant genes in Mukuru informal settlement, Nairobi Kenya

Authors: Purity Nakhayo Kasiano (KEMRI)*; Samuel Kariuki (KENYA MEDICAL RESEARCH INSTITUTE); SUSAN M KAVAI (KENYA MEDICAL RESEARCH INSTITUTE); Andrew Nyerere (3Department of Medical Microbiology, Jomo Kenyatta University of Agriculture and Technology, P.O. Box 62000-00200 Nairobi, Kenya)

Background: Typhoid fever (enteric fever) is a global public health challenge, especially in low and middle-income countries such as Kenya. It is associated with poor hygiene and sanitation. Enteric fever is contracted through the fecal-oral route. Isolation of S.Typhi can been done from blood, stool, urine, and bone marrow samples. Asymptomatic carriage has been implicated with endemicity of the disease in an area. In 2018, a study done in Nairobi highlighted the emergence of multi-drug resistant (MDR) Salmonella Typhi pathogen. MDR Salmonella Typhi strains are characterized with resistance to ampicillin, sulfamethoxazole-trimethoprim, and chloramphenicol drugs, commonly used in the treatment of typhoid fever. This study aimed at determining the prevalence of S.Typhi in Mukuru settlement and identifying and characterizing antibiotic resistance genes within the same population.

Methods: This was a cross-sectional study in which 400 blood and stool samples were collected for isolation of S.Typhi from both adults and children within 6 months from patients presenting with typhoid-like symptoms such as fever above 37.5oC in outpatient clinics namely Municipal City Council, Mukuru Kwa Reuben, Medical Missionaries of Mary, and Mama Lucy Kibaki Hospital, Nairobi. 8-10ml and 1-3ml of whole blood was collected from adults and children respectively. From each positive typhoid case, one individual from the household of the case was requested to give a stool sample to check for carriage. The Kirby-Bauer disc diffusion was used to test the antimicrobial susceptibility of isolates from both stool and blood samples on Mueller-Hinton agar (Oxoid) using selected antibiotic disks. MDR S.Typhi isolates were characterized for antibiotic resistance genes using conventional PCR.

Results: From the 400 samples collected, 59 tested positive for S.Typhi indicating a prevalence of 14%. Thirty-nine (70%) of the isolated were from stool samples and 20 isolates were from blood meaning a high S.Typhi isolation rate from stool than blood samples. Only 2 (3%) of the isolates were from asymptomatic carriers. Of the 59 isolates, 20 (34%) were found to be MDR. Ciprofloxacin and nalidixic acid had a resistance of 37% and 47 % respectively. Azithromycin showed a resistance of 8% while tetracycline had 3%. Amoxicillin clavulanic acid (beta-lactam inhibitor showed 1% resistance. BlaTEM genes were found to be present in 95% (19) of the MDR isolates.

Conclusion: This study reports that MDR is still prevalent in Mukuru. Apart from poor sanitation practices in the area, asymptomatic carriers remain a risk factor in the transmission of typhoid. Circulation of these MDR isolates is worrying as this compromise the efficiency of the current treatment regimen. The presence of Typhoid disease carriers in the community should prompt the availing of vaccine strategies in these settings and initiation of evidence-based policies by policy makers to minimize typhoid burden in the area.

Keywords: Antimicrobial Resistance, Informal settlement, Typhoid fever

Abstract 187

Title: Multidrug resistant bacterial infections in severely ill COVID-19 patients admitted in a national referral and teaching hospital, Kenya

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

Background: Bacterial infections are a common complication in patients with seasonal viral respiratory tract infections and are associated with poor prognosis, increased risk of intensive care unit admission and 29-55% mortality. Yet, there is limited data on the burden of bacterial infections among COVID-19 patients in Africa, where underdeveloped healthcare systems are likely to play a pertinent role in the epidemiology of the COVID-19 pandemic. Here, we evaluated the etiologies, antimicrobial resistance profiles, risk factors, and outcomes of bacterial infections in severely ill COVID-19 patients.

Methods: A descriptive cross-sectional study design was adopted in severely ill COVID-19 patients at Kenyatta National Hospital, Kenya, from October to December 2021. We used a structured questionnaire and case report forms to collect sociodemographics, clinical presentation, and hospitalization outcome data. Blood, nasal/oropharyngeal swabs and tracheal aspirate samples were collected based on the patient's clinical presentation and transported to the Kenyatta National Hospital microbiology laboratory for immediate processing following the standard bacteriological procedures.

Results: We found at least one bacterial infection in 44.2% (53/120) of the patients sampled, with a 31.7% mortality rate. Pathogens were mainly from the upper respiratory tract (62.7%, 42/67), with gram-negative bacteria dominating (73.1%, 49/67). Males were about three times more likely to acquire bacterial infection ($p = 0.015$). Those aged 25 to 44 years ($p=0.009$), immunized against SARS-CoV-2 ($p = 0.027$), and admitted to the infectious disease unit ward ($p=0.031$) for a short length of stay (0 -5 days, $p<0.001$) were more likely to have a positive outcome. Multidrug-resistant isolates were the majority (64.3%, 46/67), mainly gram-negative bacteria (69.6%, 32/46). The predominant multidrug-resistant phenotypes were in Enterococcus cloacae (42.9%, 3/7), Klebsiella pneumonia (25%, 4/16), and Escherichia coli (40%, 2/5).

Conclusion: Our findings highlight a high prevalence of multidrug-resistant bacterial infections in severely ill COVID-19 patients, with male gender as a risk factor for bacterial infection. Elderly Patients, non-SARS-CoV-2 vaccination, intensive care unit admission, and long length of hospital stay were associated with poor outcomes. There is a need to emphasize strict adherence to infection and prevention at KNH-IDU and antimicrobial stewardship in line with local and global AMR control action plans.

Keywords: COVID-19, SARS-CoV-2, bacterial infections, multidrug resistant, severely ill patients

Abstract 188

Title: COMPARATIVE EVALUATION OF THE AUTOMATED VITEK 2 AND MICROBROTH DILUTION METHODS ON COLISTIN ANTIBIOTIC SUSCEPTIBILITY TEST RESULTS

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Background: Colistin is a critical last-resort antibiotic used to treat multi-drug resistant (MDR) Gram-negative bacterial infections. Given the global rise in colistin resistance, it is important to monitor its antibiotic resistance trends to evaluate its clinical utility. In Kenya, colistin is not routinely tested for but is included in automated platforms such as the VITEK 2 and could be reported for clinical use. However, VITEK 2 is not the Clinical and Laboratory Standards Institute (CLSI) recommended method for colistin tests, and CLSI breakpoints for colistin have changed significantly in the past three years but are not updated regularly on automated platforms. Misreporting results could lead to treatment failures and even unnecessary mortality among 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 42 Gram-negative clinical bacterial isolates that were colistin-resistant on the VITEK 2 GN AST Card. The isolates were 30 Pseudomonas aeruginosa, 5 Acinetobacter baumannii, 3 Enterobacter cloacae, 1 Enterobacter kobei, 1 Myroides sp., 1 Aeromonas hydrophila/caviae, and 1 Sphingomonas paucimobilis. We included P. aeruginosa ATCC strain 29853 as the negative control and Proteus mirabilis 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 VITEK 2 colistin-susceptibility results.

Results: On VITEK 2, all 42 (100%) isolates were colistin-resistant. By the microbroth dilution assay, 32/42 (76.2%) isolates were classified as intermediate, including 26 P. aeruginosa, 4 A. baumanii isolates, 1 Myroides sp. and 1 Sphingomonas paucimobilis. In comparison, 10/42 (23.8%) isolates were consistently classified as colistin-resistant, including 4 P. aeruginosa isolates, 1 A. baumanii, 3 Enterobacter cloacae, 1 Enterobacter kobei, 1 Aeromonas hydrophila/caviae.

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. Therefore, the Microbroth dilution assay should be part of routine microbiology tests in hospitals with high MDR levels despite it being tedious and time-consuming as critical last-line drugs like colistin are reliably tested only by this method.

Keywords: Colistin Antibiotic Susceptibility Test

Abstract 189

Title: Gastrointestinal Carriage of Vancomycin-Resistant Enterococci and Carbapenem-Resistant Gram-Negative Bacteria among Inpatients and Outpatients at Kiambu County Referral Hospital, Kenya.

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Background: Vancomycin-resistant Enterococci (VRE) and Carbapenem-Resistant Gram-Negative Bacteria (CRGNB) are growing public health concerns globally. Gastrointestinal carriage of these microorganisms increases the risk of endogenous infection,disease outbreaks and can serve as reservoirs for antimicrobial resistance determinants. Because of limited treatment options for CRGNB and VRE infections, prevention and control programs based on locally available epidemiological data are indispensable. However, information on the epidemiology of CRGNB and VRE in Kenya are scanty. The aim of the study was to investigate gastrointestinal carriage and risk factors associated with CRGNB and VRE among patients aged 18 years and above at Kiambu County Referral Hospital(KCRH).

Objective: To determine gastrointestinal carriage, assess their antimicrobial susceptibilities and risk factors associated with carriage of VRE and CRGNB among inpatients and outpatients treated at KCRH, Kenya.

Methods: Stool samples were obtained with consent,both inpatients and outpatients who presented with or without GIT symptoms and were selectively cultured on Vancomycin and Meropenem-potentiated media for VRE and CRGNB, respectively. Identification and antimicrobial susceptibility profiles were then performed on Vitek®2. Risk factors for VRE and CRGNB carriage were determined using filled structured questionnaires.

Results: A total of34(10.9%)positive isolates were recovered from 310 samples analysed. Enterococcus spp. 16(47.0%),Enterobacter spp. 8(23.5%), Acinetobacterbaumannii 6(17.6%) and E. coli 4(11.8%)were main pathogens isolated. All CRGN isolates were resistant to Penicillin,Cephalosporins, and Monobactam. Additionally, E. coli 4(100%) and A.baumannii 6(100%) showed resistance to ciprofloxacin and trimethoprim/sulfamethoxazole. Amikacin and Gentamicin were effective against all CRGNB. All VRE isolates exhibited resistance to Erythromycin and Tetracycline. More than 12% of Enterococcus faecalis and Enterococcus faecium showed resistance to Teicoplanin, (43.8%) of Enterococcus faecium were resistant to Levofloxacin. All CRGN and VRE were sensitive to Nitrofurantoin (100%). All CRGN and VRE isolates were MDR (resisted≥3antibiotic classes with atleast one drug per class).

Conclusion: Our findings highlighted high prevalence of MDR among patients. Faecal carriage of MDR pathogens have emerged at KCRH, posing public health challenge; hence, need for regular AMR surveillance, CRGN and VRE regular screening and continuous monitoring to mitigate the further spread of AMR pathogens at KCRH and beyond. Healthcare providers, attention should be paid to the old drugs (i.e. Amikacin, Gentamycin) to replace use of most resisted antibiotics

Keywords: Vancomycin-Resistant Enterococci, Carbapenem-Resistant Gram-Negative Bacteria, Multi-Drug Resistan

POSTER SESSION

Antimicrobial Resistance

Abstract ID: 01

Abstract Title

Point prevalence survey to assess antibiotic prescribing pattern among hospitalized patients in a county referral hospital in Kenya

Authors

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Abstract

Antibiotic resistance causes higher morbidity and mortality and higher healthcare costs. One of the factors influencing the emergence of antibiotic resistance is the inappropriate use of antibiotics. Clinical practitioners' incorrect prescription patterns and a disregard for antibiotic usage recommendations are the leading causes of this resistance. This study examined the antibiotic prescription patterns among hospitalized patients at the Kiambu Level 5 hospital (KL5) to find potential for hospital quality improvement. This study was conducted in July 2021, and all patients hospitalized on the study day were included. The information was extracted from patient medical records using a World Health Organization Point Prevalence Survey (PPS) instrument. Anonymized data was gathered, entered, and then SPSS version 26 was used for analysis. Among the 308 surveyed patients, 191 (62%) received antibiotic medication, and 60.1% of the total were female. The pediatric ward, which had an antibiotic prescription rate of 94.1%, had the highest rate of antibiotic usage, followed by the medical ward (69.2%) and gynecological ward (65.6%). Over 40% of antibiotic prescriptions had a prophylactic medical indication. Penicillin G was the most prescribed antibiotic for community-acquired infections (32.2%), followed by 3rd generation cephalosporins (27.6%) and aminoglycosides (17.2%). Based on the AWaRe classification, 57% of the prescribed antibiotics were in the Access class while 42% were in the Watch class. Incomplete site of indication, lack of a method of administration, and length of administration are some of the conformities that were missing in the medical records. This study shows that antibiotic prescription rates are high, particularly for young patients, and there is a higher risk of antibiotic misuse. The data makes a compelling justification for using antibiotic stewardship practices in Kenyan hospitals.

Keywords

point prevalence, antibiotic use, Kenya, antibiotic stewardship (ABS), referral hospital

Antimicrobial Resistance

Abstract ID:02

Abstract Title

Antimicrobial Resistance in ESKAPE Pathogens from Inpatients at Nairobi West Hospital, June-December 2021

Authors

Mercy Cheptoo (Ministry of Health)*

Abstract

Background: Antimicrobial Resistance (AMR) is a global public health threat. ESKAPE pathogens (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp.) have been associated with rapid antibiotic resistance development. ESKAPE pathogens are composed of both gram positive and gram negative bacteria with mechanisms that allows them to withstand antibiotics exposure. These include enzyme production like β-lactamases, efflux pumps, biofilm production, and antibiotic target site modification. The aim of this study was to describe AMR patterns in ESKAPE pathogens isolated from inpatients at Nairobi West Hospital, Kenya.

Methods: A retrospective review of laboratory data for positive bacterial cultures and their susceptibilities from the Hospital Information System (HIS) was conducted from June to December 2021. A case was defined as an inpatient whose susceptibility test was performed using BD Phoenix M50 instrument. Socio-demographic and clinical information was collected onto MS- Excel® 2016 database. Descriptive statistics were calculated.

Results: We retrieved 1703 records, from which 153 were positive bacteria culture isolates obtained from urine, pus swabs, tracheal aspirates and blood specimens, and 79 categorized as ESKAPE pathogens. Klebsiella pneumoniae were the main isolates at 33% (26/79) followed by Staphylococcus aureus at 27% (21/79). Multidrug resistance was observed with Acinetobacter baumanni showing 0% sensitivity to cephalosporins and fluoroquinolones, and 90% resistance to carbapenems. Pseudomonas aeruginosa had 82% resistance to carbapenems, 80% to cephalosporins and fluoroquinolones, and 35% sensitivity to aminoglycosides. Klebsiella pneumoniae had 87% resistance to cephalosporins and 65% to carbapenems. Methicillin-resistant Staphylococcus aureus at 24% (5/21) was detected. One Enterococcus faecium was isolated and was resistant to vancomycin.

Conclusion: The burden of AMR in ESKAPE pathogens is high. Antibiotics that are considered "last resort", including carbapenems and third generation cephalosporins have high resistance. We recommend further surveillance of ESKAPE pathogens and their resistant

patterns, both phenotypic and genotypic to guide antimicrobial stewardship practices.

Keywords

ESKAPE, AMR

COVID-19

Abstract ID:03

Abstract Title

COVID-19 symptoms prevalence and associated outcomes in COVID-19 patients admitted at two major isolation centers in Kisumu County, Western Kenya

Authors

Josephine L Awino (KEMRI/CGHR)*; Sarah H Ngere (KEMRICGHR); Fredrick Onduru (KEMRICGHR); Douglas Okelloh (KEMRI/CGHR); Broline Sagini (KEMRI/CGHR); Peter Ogutu (MINISTRY OF HEALTH); Steve O Wandiga (KEMRI)

Abstract

Introduction: Corona Virus Disease 19 (COVID-19) infection is associated with clinically significant symptoms which can vary from moderate to severe illness which may lead to hospitalization and even death. There is need to establish the prevalence of COVID-19 symptoms and associated outcomes to inform future management of corona virus disease 2019 (COVID-19) patients. This study sought to quantify the proportion of symptoms and associated outcomes with the pandemic.

Methods: A retrospective cross-sectional study was conducted between May to July at Jaramogi Oginga Odinga Teaching and Referral Hospital and Kisumu County Referral Hospital COVID-19 isolation centers within Kisumu County. A total of 534 COVID-19 patients' records was abstracted for the period Mar 2020 to July 2022. Vital signs at time of admission and history of COVID-19 associated symptoms were recorded. Data was entered into REDCap and saved in MS Excel. Data analysis was conducted using R version 4.2.1. Descriptive statistics was conducted to quantify proportions of COVID-19 associated symptoms and their outcome. A Poisson model was used to determine the association between the symptoms and COVID-19 outcome adjusting other confounders/effect modifiers.

Results: A total of 523 COVID-19 patients were included in the analysis of which 125(23.9%) died. We enrolled 301(57.6%) males and 222(42.4%) females. A total of 66(21.9%) males and 87(39.2%) above 60 years of age died. Those with dyspnea reported the highest mortality 98(78.4%) followed by cough symptoms 88(70.4%) while chest pain reported the least number of deaths 25(20.0%). Patients who had a wet cough, age category [greater than 60years] were more likely to die (IRR= 2.35, 95% CI [1.33,4.27], p = 0.004), (IRR =2.48, 95% CI [1.33,4.95], p=0.006) respectively. Patients who had chest pains had 53% reduction in the risk of death (IRR = 0.47, 95% CI [0.22,0.92], p = 0.037).

Conclusion: Wet cough and being over 60 years old were significant determinants of mortality hence a need to more targeted care to groups exhibiting both or either of these characteristics.

Keywords

COVID-19,PREVALENCE,ASSOCIATED OUTCOMES

COVID-19

Abstract ID:04

Abstract Title

MULTIDISEASE TESTING OF COVID-19 AND TB IN KENYA.

Authors

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Abstract

Introduction:

Emerging of coronavirus disease of 2019 (COVID-19) affected provision of essential health services worldwide including Kenya. Africa reported its first case in February 2020 while Kenya confirmed its first case in March 2020.Effort and time was put on COVID-19 testing and results reporting which was mandatory in-patient identification, Contact tracing, treatment and care. Prolonged turnaround time (TAT) was witnessed due to unavailability of a rapid testing platform. To ensure there is a faster diagnostic method, the government through the MOH adopted the realtime polymerase chain reaction (RT PCR) where the Gene Xpert machine played a big roll due to its shorter TAT of one hours as compared to other PCR platforms.

Methodology:

Gene Xpert was endorsed by the WHO to diagnose Covid which Kenya also adopted in 2020. Availability of the machine across all counties made it possible to select highly burden regions and do multidisease of TB/Covid diagnosis on Gene Xpert platform.

By May 2021, Kenyan through GF introduced the Covid testing to public facilities. Online sensitization, commodities distribution, Onsite training was done to 39 facilities across 14 counties.

Training involved hands on training on Covid testing using Gene Xpert, results interpretation and online submission to the National server. This adoption on Gene Xpert testing reduced the overall TAT of 72hrs to 24hrs.

Results:

In 3787 samples 90.47% (3419) was tested using Gene Xpert while 368 was tested on other plat forms. On the 3419 tested 56.3% were male and 43.68% female Overall TAT of 72 hours was experienced using other platforms while GeneXpert was 24 hours during the March and May 2021. There was low infection in children and elderly 0-9(27.34%) and >80 (0.85%) respectively. Age 30-39 had 8.29% infection. May 2021 tested 7.13% and July tested higher of 83.39%.

Conclusions :

There was higher male infection as compared to female

- High positivity rate using Gene-Xpert was noted.
- Gene-Xpert has the shortest Covid-19 testing time, and can be recommended for testing of COVID-19

Keywords

MULTIDISEASE, OF COVID-19, GENE-XPERTGene-Xpert PCR, DIAGNOSTIC, diagnosticTuberculosis ,

Genomics

Abstract ID:05

Abstract Title

Analysis of the metagenomic virome of Aedes aegypti mosquitoes from Coastal Kenya

Authors

Solomon K Langat (Kenya Medical Research Institute (KEMRI))*; Gladys Kerich (US Army Medical Research Directorate - Africa); Stephanie Cinkovich (Walter Reed Army Institute of Research (WRAIR)); Jaree Johnson (Walter Reed Army Institute of Research (WRAIR)); Janet Ambale (US Army Medical Research Directorate - Africa); Benjamin H Opot (United States Army Medical Research Directorate - Africa/Kenya); Eric Garges (US Army Medical Research Directorate - Africa); Elly Ojwang (US Army Medical Research Directorate - Africa); Fredrick Eyase (US Army Medical Research Directorate-Africa)

Abstract

Background

Mosquito-borne viruses such as Zika, West Nile, Dengue (DENV), Yellow Fever (YFV), Rift Valley Fever, Chikungunya, and Sindbis, pose a serious risk to public health globally. Majority of these pathogens are transmitted by Aedes aegypti mosquito vectors. These viruses affect both human and livestock, particularly in the tropical regions. To better understand and mitigate the infections caused by these viruses, early detection of the causative pathogens and epidemic forecasting is essential. Current knowledge on arbovirus diversity is heavily biased toward pathogens that have had significant health and economic impacts, with little knowledge on the potentially emergent arboviruses.

Methods

In the current study, we carried out metagenomics analysis among Ae. aegypti vectors from Kwale and Malindi regions in Coastal Kenya. Insect vectors were processed and sequenced using the Illumina iSeq 100 sequencer. The sequence data were analyzed to determine the diversity of viruses as well as determine the whole genomes of these viruses among Ae. aegypti vectors.

Results

The diversity of viruses detected among these vectors was quite variable. The viruses detected belong to different families including Bunyaviridae, Dicistroviridae, Rhabdoviridae, Iflaviridae and a Negevirus. Specifically, the viruses detected among these vectors include phasivirus, Cripavirus, and unclassified viruses belonging to negevirus group, and Rhabdoviridae family.

Conclusion

In conclusion, the study has characterized a number of viruses some of which belong to families known to be pathogenic. Nonetheless, majority of the viruses detected are insect-specific viruses (ISVS). These can be quite useful for purposes of control of pathogenic viruses, considering they play an important role in regards to competence of insect vectors for transmission of viral pathogens.

Keywords: metagenomics, Aedes aegypti, virome, viruses

Keywords

metagenomics; Aedes aegypti; virome; viruses

Genomics

Abstract ID:06

Abstract Title

Dengue serotype dynamics at the Kenyan Coast, 2019-2022

Authors

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Abstract

Background: Dengue fever (DF), caused by four distinct serotypes of dengue virus (DENV-1-4) is transmitted majorly by the mosquito vector Aedes Aegypti and Aedes albopictus. DF is responsible for more than 390 million infections globally of which 96 million have clinical manifestations. In Kenya, DENV is an emerging public health concern, especially at the Kenyan coast where DF is a common occurrence.

Methods: In this study, we determined the heterotypic infections of DENV serotypes from November 2019 to September 2022 from study subjects presenting with febrile illness at Mtongwe Naval Base hospital in south coast and Lamu County Hospital in the north coast. DENV serotypes were identified by qPCR.

Results: Our data shows cyclical transmission of DENV-1-3. Overall, we detected three dengue serotypes (DENV1, DENV2, and DENV3) over the study period. DENV1 was the most dominant serotype with positive cases being detected across the entire period except in July to September 2020, April 2021, and October 2022 where no DENV1 cases were detected. Cases of DENV1 were highest in January-April 2020 (lowest=13 cases, highest=41cases) and September 2021 to May 2022 (lowest=10 cases, highest=70cases). DENV2 was reported between December 2019 to April 2020 (lowest=4 cases, highest=12 cases) after which no cases were reported again except a single case in November 2020. For DENV3, only few cases were reported in December 2019 to March 2020(highest=2 cases), followed by a period of no cases of DENV3 until July 2022 to October 2022 (lowest=1 case, highest=3 cases) where we started reporting cases of DENV3 again. The burden of infection was highest in males (67%) between ages 19-39 years (52%) and the most common clinical symptoms of infection included headache 85.8% (218/254), chills 79.1% (201/254), joint ache 78.3% (199/254), muscle pain 77.6% (197/254) and eye pain 54.7% (139/254). Of the 251 DENV1 positive samples (Mtongwe Naval Base=122 and Lamu County Hospital=129) that were sequenced, we obtained complete sequences for 135 samples. On phylogenetic analysis, all the 135 genomes belonged to DENV-1, genotype V and all clustered with genotype V isolates from China.

Conclusion: Our findings provide data on the transmission dynamics of DENV serotypes observed over a 3-year study period. Such data is useful in bridging the science gaps necessary for development of more effective vaccines, and also reinforces the importance of surveillance in the management of the infection to mitigate public health disruptions associated with outbreaks of dengue.

Keywords

Dengue, Dengue Fever, Febrile

Genomics

Abstract ID:07

Abstract Title

An integrated analysis of host transcriptome and metagenome to elucidate etiology of acute non-traumatic coma of unknown cause in Kilifi, Kenya

Authors

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Abstract

Background: Acute non-traumatic coma (aNTC) is a common paediatric presentation to hospitals in sub-Saharan Africa and is associated with a high risk of death and neurological sequelae. Acute bacterial meningitis (ABM) and cerebral malaria (CM) are often the common causes of aNTC. However, the cause for a considerable proportion of aNTC admissions remains unknown and is referred to as a coma of unknown cause (CUC). These groups of children have a higher risk of morbidity and mortality. Therefore, identifying the underlying

causes, including infectious aetiology, is of great public health importance. Omics approaches have revolutionized diagnosis and circumvent challenges associated with clinical and laboratory diagnosis. This study aimed to classify patients clinically categorised as CUC and identify infectious aetiologies among children admitted to Kilifi County Hospital located on the Kenyan Coast using transcriptomics and RNA-based metagenomic next-generation sequencing (mNGS) approaches.

Materials and methods: This study used RNA sequencing to analyze cerebrospinal fluid samples from children classified as CUC (n= 72), ABM (n=15), and CM (n= 13). A transcript signature of differentially expressed genes (DEGs) between CM and ABM was used to identify ABM and CM cases within CUC that might have missed by conventional diagnostic methods. RNA-based mNGS approach was used to identify any pathogens present among CUC cases that could not be classified using the transcript signature.

Results: 534 DEGs between ABM and CM grouped the CUC into CM-like CUC and non-CM like CUC. This showed that 55% (40/72) of the children clinically classified as CUC had a transcriptome profile like that of children with CM. Notably, the genes upregulated in non-CM-like CUC were associated with T cell function suggesting possible viral infection while those of CM-like CUC was associated with neurological function. Hemoglobin was significantly different between CM-like CUC patients and non-CM-like CUC. The mNGS approach identified infectious pathogens among children categorized as CUC (48/72), 31 in the CM-like CUC group and 17 in the non-CM-like CUC grou The most common viral infections were Cytomegalovirus (n=6), Herpes simplex virus (n=7) and Lymphocryptovirus (n=9), while P. falciparum (n=14) and Aspergillus spp (n=18) were commonly identified eukaryotic pathogens.

Conclusion: This study has demonstrated that a large proportion of children diagnosed with CUC likely do not have bacterial etiology. Further, the study has shown that CUC cases likely have coinfections between viral infections, Plasmodium falciparum, or Aspergillus spp. , highlighting that RNA sequencing can potentially improve disease diagnosis. This is a small single-site study, and the results need to be verified in a larger cohort.

Keywords

Acute non-traumatic coma, cerebral malaria, acute bacterial meningitis, coma of unknown cause

Health Systems

Abstract ID:08

Abstract Title

Population Health Needs, Health Systems Readiness, and Client Satisfaction in the Context of Implementation of Universal Health Coverage in Bomet County, Kenya

Authors

Priscah C Otambo (KEMRI)*; Zipporah Bukania (KEMRI); JAMES N. KARIUKI (KENYA MEDICAL RESEARCH INSTITUTE); sarah karanja (KEMRI); Lilian Nyandieka (KEMRI); Mathu Mingu (KEMRI); Elizabeth Echoka (KEMRI); Ismail Adaw (KEMRI); Schillar Mbuka (KEMRI); Violet Wanjiha (KEMRI); Erastus Muniu (KEMRI)

Abstract

Introduction: Implementation of Universal Health Coverage(UHC) has its challenges and one of these being to ensure that services reach those most in need and the hardest to reach (Sustainable Development Goal, 2016). Kenya needs to build sustainable financing systems to reduce the barriers of access to care, while protecting people against the financial risks of accessing this care in order to achieve success in UHC. This study sought to understand the critical elements needed even as Kenya rolls out UHC implementation nationwide.

Methodology: This was a mixed method study. A health facilities assessment tool was administered to selected facility in-charges and client exit tool to patients on exit while qualitative data was collected using FGD guides administered to elderly men and women, youth and women-of-reproductive age. Descriptive and thematic analysis was employed. Ethical approvals were adhered to and all participants consented to participate.

Findings: Health systems capacity and readiness: The service readiness index was 68.8%, meaning nearly 7 in 10 health facilities were ready to provide health services in the context of UHC. Availability of standard precautions for infection prevention was 91.7%, diagnostic capacity at 68.4%, and basic equipment scored 63.2%, Availability of essential medicines was 51.3% while shortage of human resources scored 8.8%. Population needs included: sanitary pads, gender issues, leaders of integrity, counselling services (to all groups) adequate drugs, ramps, assistive devices for people-living-with-disability (pwd),and additional maternity units.

Conclusion: A significant number of health facilities were ready to offer UHC services. However, there is need for more investments in terms of basic equipment, diagnostic capacity, essential drugs and human resource.

Recommendation: County and national governments to focus in maximizing on delivery of patient centered services while optimizing on available resources.

Keywords

UHC, health systems, population needs

Health Systems

Abstract ID:09

Abstract Title

IMPLEMENTATION OF THE CARING FOR PROVIDERS TO IMPROVE PATIENTS EXPERIENCE(CPIPE)INTERVENTION IN KENYA:CHALLENGES,SUCCESS AND LESSONS

Authors

BERYL AKINYI OGOLLA (GLOBAL PROGRAMS&RESEARCH TRAINING)*; Patience Afulani (UCSF); Monica Getahun (UCSF); Linnet Ongeri (Kenya Medical Research Institute); Joyceline Gaceri Kinyua (Kenya Medical Research Institute); Edwina Ndhine (GPRT)

Abstract

Implementation of the Caring for Providers to Improve Patient Experience (CPIPE) Intervention in Kenya: Challenges, Successes, and Lessons

Abstract

Background: Key drivers of Person-Centered Maternal Care (PCMC)—care that is respectful and responsive to women's preferences, needs, and values—include provider stress and unconscious bias. Yet they remain unincluded in interventions to improve PCMC. We describe the piloting of the Caring for Providers to Improve Patient Experience (CPIPE) intervention to address provider stress and unconscious bias, as well as the challenges, successes, and lessons learned.

Program Implementation: CPIPE, which has 5 components including provider training, peer support, mentorship, embedded champions, and leadership engagement, was successfully piloted over 6-months (October 2021 to April 2022) in two health facilities in Migori County, Kenya. The training, which included didactic and interactive content on PCMC, stress, burnout, dealing with difficult situations, and bias, was delivered in an an initial 2 day training, with subsequent monthly refreshers led by the embedded champions. The embedded champions also facilitated formation of peer support groups in each facility which met monthly over the project period. We identified 24 mentors who provided mentorship in various areas to their mentees. We engaged facility and county leadership and key stakeholders early and throughout the process through a community advisory board.

Challenges and Successes: Challenges included inadequate time for training, hierarchical system that hindered cross-cadre activities, varying levels of engagement of intervention sites, and balancing competing demands. Successes included increased advocacy among providers and facility and county leadership to address their sources of stress, provide mental health support to providers, and greater among to provide PCMC, especially to the most disadvantaged women.

Conclusions: CPIPE is an innovative but practical intervention to improve PCMC, that centers the experiences of the providers and the needs of vulnerable groups. The successful piloting underscores the timeliness, relevance, and feasibility of a similar interventions in resource-constrained settings. This intervention has great potential to advance the evidence base for interventions to improve patient and provider experience. The lessons learnt from this pilot will inform future iterations of the intervention and are key for any health systems intervention that requires wide-spread culture change to better advance patient outcomes. Given the current climate of high stress and burnout among providers in Kenya, and the related high prevalence of poor patient reported experiences, interventions such as CPIPE are urgently needed in Kenya. Uptake of such interventions by the Kenya Ministry of health is key to sustainability.

Keywords

Caring for Providers to Improve Patients Experience Intervention in Kenya

Health Systems

Abstract ID:10

Abstract Title

External validation of a pediatric triage model for use in resource limited facilities to guide frontline health workers.

Authors

Joyce W Kigo (KEMRI-Wellcome Trust)*

Abstract

Authors: Joyce Kigo*, Stephen Kamau,Alishah Mawji, Paul Mwaniki ,Dustin Dunsmuir, Yashodani Pillay, Katija Pallot, Morris Ogero, David Kimutai, Mary Ouma ,Ismael Mohamed, Mary Chege, Lydia Thuranira, Niranjan Kissoon, J Mark Ansermino, Samuel Akech.

Introduction: Automated algorithms developed from readily available clinical data offer an opportunity to improve prioritization and outcomes of clinical care. Prior to widespread adoption of these algorithms external validation must be performed to ensure generalizability and robustness using a different patient population.

Methods: We externally validated a previously published 9- predictor pediatric triage model (Smart Triage) developed in Jinja, Uganda,

using prospectively collected data from two hospitals in Kenya both individually and from both hospitals combined. We assessed the discriminative ability of the model using the C index (area under the receiver-operator curve-AUC) and the calibration graphically by estimating the slope of a calibration plot of predicted versus observed outcome rates in each decile of predicted probability. We performed recalibration by optimizing the calibration intercept and evaluated the pre/post calibration models accuracy in classifying patients into 3 triage categories: emergency, priority or non-urgent based on selection of risk thresholds with low-risk threshold selected to maximize sensitivity and high-risk threshold to maximize specificity.

Results A total 2539 patients were eligible at Hospital and 1, 2464 at Hospital 2 (5003 for both hospitals); the admission rates were 8.9%, 4.5% and 6.8%, respectively. The model showed good discrimination with an AUC 0.826 for Hospital 1, 0.784 for Hospital 2 and 0.821for both hospitals combined. The pre-calibrated model at respective at low-risk threshold of 8% achieved sensitivity of 92.5% (88.9%, 95.6%) ,81.3% (74.1%, 88.4%) ,88.8% (85.2%, 92%), and at high-risk threshold of 40%, the model achieved specificity (95% CI) of 85.9% (84.4%, 87.3%), 96% (95.2%, 96.8%) and 91% (90.2%, 91.8%), respectively. Recalibration improved the graphical fit but new unique risk thresholds were selected to optimize sensitivity and specificity.

Conclusion: Discrimination was good at all sites, but recalibration was necessary to improve the graphical fit of the model. There was no significant change in order of prioritization which alleviates concerns about model updating for prediction if prioritization based on rank is all that is required. The drift in the graphical calibration plot however supports the need for researchers to consider adjusting the existing predictive model to new patient populations by assessing the statistical and clinical validity of the models.

Keywords

prediction model, triage, external validation

Health Systems

Abstract ID:11

Abstract Title

The Evaluation of Human Brucellosis Surveillance System in Uasin Gishu County-Kenya 2022

Authors

Stephen J.O. Olubulyera (Ministry of Health, Kenya-FELTP)*; Maurice O Owiny (Kenya FELTP); Athman Mwatondo (Zoonotic Disease Unit); Hillary Limo (The Public Health Emergency Operations Centres)

Abstract

Background: The lack of national estimates of the burden of brucellosis in human and livestock populations in Kenya reveals uncertainty in establishing the true prevalence and socioeconomic impacts of brucellosis. This is contributed by the inadequate human capacity for research, poor surveillance systems and lack of standardized diagnostics. The study aims to evaluate the brucellosis surveillance system.

Methods: We conducted a retrospective review of the cases for all brucellosis cases from 2017 to 2021 in Uasin Gishu County in Kenya. We assessed the surveillance system attributes using the CDC standard checklist tool for surveillance system evaluation. We interviewed system users using a structured questionnaire in a few health facilities. We presented the findings in charts and graphs.

Results: We reviewed human brucellosis cases in forty health facilities across six sub-counties. The annual positivity rate for human brucellosis was between 21% and 33%, with an observed increase in infection burden from 2013 to 2018. The brucellosis surveillance system is simple and user-friendly. Its design allows users to mine, explore and understand data with little to no teaching; the great data visualization generated by the system is convenient and understandable. However, the surveillance system is not flexible to change and is insensitive to acute outbreaks since reporting cases are relatively passive rather than active. There was no structured funding mechanism for the brucellosis surveillance system in Uasin Gishu County.

Conclusion: The evaluation determined that the brucellosis surveillance system is useful in passive surveillance of trends of changes in brucellosis cases in Uasin Gishu County. The high brucellosis prevalent in sub-counties lacked control and prevention intervention programs. The resources and funding for running the brucellosis surveillance system were not outlined. Additional research is required to establish the reasons behind the high cases of brucellosis in Uasin Gishu County.

Keywords

Brucellosis, Evaluation, Surveillance, Outbreak, Retrospective Review

Health Systems

Abstract ID:12

Abstract Title

Overcoming Barriers to Clinical Trial Enrollment in Sub-Saharan Africa by Addressing Financial Burdens of Cancer Patients: A Case of International Cancer Institute, Kenya

Authors

Gloria Kitur (International Cancer Institute)*; Lilian Ouma (International Cancer Institute)

Abstract

Background

Clinical trials are essential for advancing cancer care thus enhancing patient outcomes. However, there exists barriers to clinical trial enrollment which contribute to low participation in clinical trials more especially in low-and-middle-income countries and Sub-Saharan Africa. Some of these include financial barriers, logistical concerns and lack of resources among patients.

Methodology

International Cancer Institute (ICI) is an approved clinical trials site based in Eldoret, Kenya and is currently conducting clinical trials in breast cancer, esophageal cancer and sickle cell disease. Partnering with its outreach sites, ICI seeks to recruit participants from the outreach clinics. This means patients have to travel to the ICI care and research clinic to undergo screening and recruitment processes. To counter the distance and logistical barriers, the potential clinical trials participants are given transport refund as well as accommodation and meals for their entire stay in Eldoret which can take up to 3 days.

Results

In the period between February and September 2022 (8 months), a total of 162 patients were hosted at the ICI Child and Family Wellness Center with 40% of them being clinical trials patients. Of these, 92% were from 9 different counties in Kenya some located up to 12 hours away from Eldoret with a unique case of patient traveling from outside Kenya. Patients would be provided with three meals in day at the center.

Conclusion

In order to address the persistent low participation of cancer and other non-communicable diseases patients in clinical trials, it is necessary to provide practical solutions to the patients' immediate challenges. As a result, clinical trial recruitment, enrollment and retention will be ensured.

Keywords

Clinical Trials, Sub-Saharan Africa, Cancer

Health Systems

Abstract ID:13

Abstract Title

LABORATORY SAFETY AUDITS A GAME CHANGER IN INFECTION PREVENTION AND CONTROL

Authors

duncan odhiambo ongayi (ministry of health)*; alfred ojwaka (moh)

Abstract

Background

Facility and Biosafety is one of the quality system essentials envisaged in the Kenya Quality Manual for medical laboratories. ISO 15189-2012 Management clause 4.12(continual improvement) stipulates that a laboratory shall participate in improvement project activities and laboratory shall conduct internal audits at planned intervals to identify nonconforming activities and institute corrective/preventive actions. Safety requirements are also highlighted in Section 12(Facility and Biosafety) of WHO SLIPTA assessment checklist for clinical and health laboratories undergoing through ISO Accreditation. Chulaimbo County Hospital Laboratory in Kisumu west sub County, Kisumu County begun the journey of ISO Accreditation in October 2016 through mentorship by Global Health Solutions (GIS).

Problem Statement

Baseline safety audit conducted in October 2016 while exit audit was in April 2019, baseline audit indicated low scores (18%) . In view of this, Chulaimbo County Hospital laboratory embarked on this project to ensure compliance with this section requirement with the ultimate goal of improving safety, infection prevention and control and finally ISO Accreditation.

Methods

Baseline safety Laboratory audits was conducted using section 12 of the WHO SLIPTA observational assessment checklist. Action plan with strict timelines were developed with the primary goal being closing the gaps identified during the audits. Laboratory management appointed a safety focal person whose primary role was to spearhead closure of the nonconformities. Three follow up audits were thereafter conducted at an interval of one, three and four months respectively.

Results

The key findings identified were:18% score at baseline with poor waste management, no annual medical surveillance and Hepatitis B vaccination to staff, no first aid/spill kits and emergency eye wash/showers, no safety audits conducted, no incidences and occurrences investigated, laboratory staffs not all trained on biosafety/biosecurity, no safety sops developed, sample transporters not trained on biosafety and no clear policies on PEP among others. 58% score in

audit one, 95% score in audit two and 98% score at third audit.

Key Findings

Baseline (18%), First Audit (58%) ,Second Audit(95%),Exit Audit(98%).

Conclusion

There was a tremendous progress noted from 2016(18%) to 2019(98%) with regards to SLIPTA scores and ultimately the laboratory safety.

Laboratory safety audit is an essential component of IPC in clinical and public health laboratories.

Keywords

lab audits

Health Systems

Abstract ID:14

Abstract Title

Lessons from a unique system to promote child and youth health

Authors

Symone Detmar (TNO Innovation for Life); Remy Vink (TNO Innovation for Life); Yvette Fleming (TNO Innovation for Life)*

Abstract

Background

The Netherlands has a unique system to promote child and youth health (up to age of 18) called the preventive child and youth healthcare (CYH). CYH has an important contribution to our children and young people thriving by offering information, immunization and screening, identifying care needs and providing preventive support to children and their families. The CYH is a national programme implemented through 38 regional CYH organizations funded by the municipalities.

Methods

CYH is guided by three basic principles: the bio psychological-ecological perspective on health and development, a joint assessment, and shared decision-making by professionals, children and their parents. CHY services offers screening and basic preventive care supported by 35 evidence-based guidelines and special preventive care to children who grow up in a disadvantaged situation.

Results

The coverage rate of our CYH is with 95% among all young children very high. In 2020, over 164 thousand children were born in the Netherlands. Life expectancy at birth is steadily increasing. Meanwhile, one in six children (15%) are born prematurely (<37 weeks of gestation) and/or small for gestational age and are thus at risk of serious short- and long-term health problems. Moreover, one in six Dutch children and young adults (15%) are overweight or obese. Nowadays, 26% of children and young adults (0–25 years) living in the Netherlands suffer from a chronic disease. One of these chronic diseases is depression. Depression, together with anxiety, makes up about one-third (28.3%) of all causes of chronic disease among children and young adults. Despite the above figures literature shows that Dutch children and young adults are among the tallest, the happiest, and the healthiest in the world.

Conclusion

According to increasing insight, early intervention during childhood is an effective strategy to prevent problems later on in life as well as inter-generational inequality. The earlier the needs for preventive and curative care is identified and interventions are implemented, the higher are the expected returns. Lessons learned during the Covid-19 epidemic showed that the Dutch CYH is a solid public health system. However, the coverage rate could be further improved by giving more attention to effective strategies to reach and support extra vulnerable children. Outreach programs, digitization of care and E-health are important strategies in this respect. In addition, the generation of nationwide data can help to show the impact of CYH and will direct and prioritize the necessary care. By continuously developing care on the basis of new (scientific) insights and societal issues, the CYH will continue to offer all children the best preventive healthcare in the Netherlands and can serve as a model to learn from for other countries as well.

Keywords

child and youth health promotion - preventive child and youth healthcare -

Health Systems

Abstract ID:15

Abstract Title

Developing a digital health Intervention to promote uptake and use of PrEP and contraception among adolescent girls and young women in Kenya :Insights from a qualitative study.

Authors

JOAN A ONGERE (KEMRI)*; Kenneth Ondeng'é (KEMRI); Maurine Ochieng (KEMRI); Lilian Odunga (KEMRI); Felix Omondi (KEMRI); Caren Awinja (KEMRI); Nelly R. Mugo (KEMRI); Elizabeth Bukusi (KEMRI); Ruanne Barnabas (Havard University); Maricianah Onono (KEMRI)

Abstract

Background: HIV and pregnancy-related complications are the leading causes of death among adolescent girls and young women (AGYW) ages 15-24. Combining digital health information and clinical assessment with online ordering and integrated-product delivery (e.g. by courier) of HIV self-testing (HIVST), PrEP, and contraceptives supplies could increase uptake and thereby prevent unplanned pregnancies and HIV. We aimed to co-develop, tailor and refine a digital health service model known as ConceptPrEP-on-demand for AGYW in Kisumu, Kenya using participatory methods.

Methods: We applied human centered design (HCD) methods to co-develop and tailor the ConceptPrEP-on-demand intervention for AGYW. The Discover phase conducted 1 Focus group discussion (FGD) with AGYW and male partners and 8 In-depth interviews with AGYW, to get a clear recognition of the contents (PrEP, oral contraceptives, emergency pills, condoms, self-injectable contraception, pregnancy and HIV self-testing kits), delivery strategies and health information. The Define phase refined the intervention through participatory client journey mapping and by posing 'How might we…?' questions to potential intervention users and influencers (1 FGD with AGYW male partners, 3 with AGYW, 1 with health providers). Finally in the Develop phase we collaboratively adapted the define phase solutions addressing modifiable content, delivery strategies, and the optimal ConceptPrep-on-demand delivery format with intervention users (1 workshop with AGYW, health providers, community members and sexual reproductive health (SRH) experts).

Results: Insights from AGYW and their partners revealed preference for ConceptPrep-on-demand because it's discrete, convenient, less stigmatizing, affordable, and enhances their sense of autonomy and control. Participants expressed overall satisfaction with the package of interventions but suggested the inclusion of sanitary towels. Participants expressed concerns regarding: self-efficacy of AGYW administering self-injectable contraception and limitations of counseling and linkage to care for the HIVST kit. Adequate training and toll-free lines were suggested as potential mitigation measures. Preference for unknown, non-branded, blinded and professional delivery riders was expressed. There were tensions regarding preference for cute, girlish and appealing packaging but ensuring it cannot attract attention. Sentiments by male partners on the SRH products revealed misinformation and fears regarding contraceptives, harmful gender norms and patriarchal notions of control on the woman's body.

Conclusions: Applying an HCD approach to designing content, packaging, and delivery of integrated SRH and HIV interventions was effective, acceptable, and insightful. This approach could help answer "why" and "how" digital methods may be a useful tool to support pregnancy, STI and HIV prevention.

Keywords

PrEP,Contraception,Digital Health Intervention,Adolescent Girls and Young Women,Kenya,Human Centred design

Health Systems

Abstract ID:16

Abstract Title

Case Report: β-thalassemia major on the East African coast (Kilifi).

Authors

Johnstone O Makale (Kemri/Wellcome Trust)*

Abstract

Abstract

Background: β-thalassemia is rare in sub-Saharan Africa and to our knowledge there has been no case of homozygous β-thalassemia major reported from this region. In a recent cohort study, we identified four β-thalassemia mutations among 83 heterozygous carriers in Kilifi, Kenya. One of the mutations identified was a rare β-globin gene initiation codon mutation (ATG□ACG) (rs33941849). Here we present a patient with β-thalassemia major resulting from this

mutation, only the second homozygous patient to have been reported.

Methods: The female patient presented to Kilifi County Hospital aged two years with a one week left sided abdominal swelling. Clinical, hematological and genetic information were collected at admission

and follow-up.

Results: Admission bloods revealed marked anemia, with a hemoglobin (Hb) value of 6.6 g/dL and a low mean corpuscular volume of 64 fL. High performance liquid chromatography (HPLC) revealed the absence of HbA0 and elevated levels of HbF, suggesting a diagnosis of β-thalassemia major. Sequencing revealed that the child was homozygous for the rs33941849 initiation codon mutation.

Conclusions: We hope that this study will create awareness regarding the presence of β-thalassemia as a potential public health problem in Kilifi, and this can lead to further studies in the East Africa region that can prompt the development of local guidelines regarding the diagnosis and management of this condition.

Keywords

β-thalassemia major, rs33941849, East Africa, HbA2, sequencing.

HIV

Abstract ID:17

Abstract Title

Linkages of HIV exposed, and HIV positive children aged 0-24 months between PMTCT and nutrition clinics in 3 facilities in Western Kenya

Authors

Damaris Odhiambo (KEMRI/UNIVERSITY OF WASHINGTON); Benson Singa (KEMRI); Julius Onyango Nyaoke (KEMRI/UNIVERSITY OF WASHINGTON)*; Marline MMS Serede (Kemri); Eric O. Ochola (KEMRI/UNIVERSITY OF WASHINGTON); Emmanuel Oduor (KEMRI/UW); Emoly Yoshioka (University of washington); Arianna Means (University of Washington); Megan Coe (University of Washington)

Abstract

Background:

Malnutrition and HIV interact in a vicious cycle and almost half of the HIV-exposed infants (HEIs) are malnourished. This highlights the importance of routine nutritional screening for children receiving HIV services as well as HIV testing for children with acute malnutrition. However, a small proportion of malnourished children receive guideline-adherent treatment. This study aims to quantify the proportion of HIV exposed children who are managed according to national paediatric HIV-nutrition guidelines.

Methodology:

This study included data abstraction both retrospectively and prospectively utilizing the HEI register, HEI follow-up card, and outpatient nutrition program register to identify HEIs aged 0-24 months between 1st January 2019 and 15th November 2022 in 3 facilities in Western Kenya. To trace children across registers, data was linked using the child's HEI number, parent's clinic ID number, child's name, child gender, child age and/or guardian's telephone number. We present data on the proportion of successfully documented linkages across HIV and nutrition clinics for children with indication based on HIV and nutrition status.

Results:

Overall, 4,614 records were abstracted from the HIV register, nutrition register and HEI follow-up card. Of the total records abstracted, 720(16%) records were from Migori County referral hospital, 2458(53%) records from Homabay County referral hospital and 1436(31%) records from Awendo Sub-County referral. Out of the 1743 records abstracted from the HEI register, 16 were found to be HIV positive with 31.25% of them needing nutritional support. In total, only 378(8%) children were linked across the nutrition register, HIV register and HEI follow-up card. Out of the total number of child records linked, 32(9%), 330(87%) and 16(4%) was from Migori County referral hospital, Homabay County referral and Awendo Sub-County hospital respectively.

Conclusion:

Overall, there was low linkage between HIV and nutritional clinics for the HIV exposed children with indication for nutritional support. This could be due to dual stigma of HIV and malnutrition preventing caregivers from timely attendance to the various linked clinics, skilled staff shortages (nutritionists) and low promotion of task shifting at the facilities and low active screening for children for malnutrition.

Recommendations:

As HIV services tend towards being paperless, facilities should encourage the adoption of EMR in the nutritional clinic for proper linkages of services with the dedicated staff at triage, to improve linkage to other services. Facilities should also ensure availability and encouragement.

Limitations:

The study did not have comparison data thus could not conclusively assess the impact of covid-19 on clinic attendance. The study focused only on linkage and rather not the severity of malnutrition among the linked cases.

Keywords

Malnutrition, nutritional screening, abstraction,

HIV

Abstract ID:18

Abstract Title

RETENSION STRATEGIES FOR CROSS-BORDER HIV CLIENTS DURING COVID 19 PANDEMIC A CASE OF OLASI DISPENSARY ,MIGORI COUNTY

Authors

Eugene E,A. Ariya (Ministry of health)*; Benson Okome (CMMB); John kiruo (Ministry of health); Martin Ogolla (CIHEB-Kenya)

Abstract

INTRODUCTION

Management of cross-border HIV clients presents unique challenges in health seeking behavior and access to service delivery.COVID 19 pandemic led to decreased access to quality HIV services for this cohort population, increased missed appointments and inability of health workers to reach clients. Employing both provider and client oriented interventions increased access to treatment and retention to care and ensured continuity of HIV services among people living with HIV(PLHIV) in cross-border territories.

BACKGROUND

Olasi Dispensary is one of the facilities in Nyatike Sub county in Migori County bordering Tanzania with 821 patients who are currently on Care with 292 (36%)residing in Tanzania.The facility reported lots of missed appointments due to Kenyan border homesteads were not receptive to Tanzanians .

Objective

To improve medication access and retention to care among cross-border HIV clients attending Olasi Dispensary duringCOVID-19 pandemic period

Methodology

290 clients used to for this strategy were divided in 5 groups each having 58 members from different locations where the peer educator would take the drugs every two weeks to the identified group leaders.

identifying individual challenges , Individualized health education, and joint strategy development with clients was adopted.Some of these ways included

1.Buddy system-willing clients were introduced to those living near them to trace clients in case they miss clinic,

2.Appointments for cross-border clients was scheduled on one day

3.Implementing community refill groups.

4.Clients started Community ART refill groups,which involved having medication delivered at client's homes by a buddy or at border points by facility staff. .

5.Staff identified as suitable spot near the border to meet cross-border client.

RESULTS

Retention rates for cross-border clients and facility in general improved from 53% to 72%, this strategy also improved general clients viral suppression of clients, at 94% Missed appointment from cross border clients reduced from a high of 35%to less than7% according the the monthly report submitted by the identified focal persons to the peer educator in the month of July 2020 to December 2020 and also the facility register .

CONCLUSIONS/RECOMMENDATION AND IMPLICATIONS

Differentiated Care Model is a sustainable way of supporting clients on Care but requires some of the following.

·Utilize existing government and intergovernmental structures like East African Community (EAC) and Intergovernmental Authority on Development (IGAD) to access border points.

·Same sociopolitical understanding between different countries

·Prior engagement with clients on implications of cross border seeking of HIV care & treatment services

·Ease cross-border communication e.g.facility operating communication lines of both nations

Keywords

PUBLIC HEALTH

Malaria

Abstract ID:19

Abstract Title

Macrophage responses in Placental malaria

Authors

FRED OWUOR OWINO (KEMRI)*

Abstract

Background: Malaria in pregnancy poses a great health challenge to both mother and fetus, particularly for primigravid mothers living in malaria-endemic areas. Successful pregnancy depends on the appropriate regulation of pro-inflammatory and anti-inflammatory cytokines to avoid rejection of the fetus and achieve equilibrium between immunity and the risk of inflammation associated with severe malaria. During pregnancy, macrophages reside in the maternal-fetal interface and their polarization is essential for successful pregnancy. Polarization of macrophages into either of the phenotypes (Classically activated, M1-like and alternatively activated, M2-like macrophage phenotypes) can be skewed during an infection resulting into poor pregnancy and/or infection outcomes.

Methods: In this cross-sectional study, 60 women of age between 18 and 45 years attending antenatal clinic at Webuye County Hospital were enrolled in the study. At delivery, only placentas from singleton births from women with or without malaria who had consented were collected. These were then used to analyze maternal macrophage polarization and responses to malaria infection. Placental tissues were digested using collagenase type 2 to obtain immune cells. These cells were analyzed for flow cytometry and gene expression. Macrophages were obtained from the isolated immune cells by use anti CD 14 beads. Gene expression levels of angiogenic factors ANG-1, ANG-2, VEGF, and STAT-1, IRF-5 for M1-like macrophages and STAT-6, cMAF for M2-like macrophages were analyzed using qRT-PCR. Flow cytometry was used to analyze the surface markers including CD 68, CD80, CD 86, CD 163, and CD 209. Histopathologic examination was used to identify malaria and non-malaria in placental tissues.

Results: There were observed high levels of M2 macrophages as compared to M1 macrophages in both malaria positive and non-malaria. This is seen in both the double positive (M1-CD80+CD86+, M2-CD163+CD209+) and single markers cell counts and frequency. Although 50% of the participants were malaria positive during pregnancy, placental histological examination showed 11% of placental malaria at term. This can be attributed to malaria treatment or use of IPTp during pregnancy.

Conclusion: Malaria positive samples showed a higher level of M2 macrophage expression while the same was observed in non-malaria but in low levels. This indicates an influence malaria has on macrophage immune status activation.

Keywords

Macrophages, Placental malaria, polarization,primigravid

Abstract ID: 20

Abstract Title

The Role of *Plasmodium falciparum* HSP-90 in Antimalarial Drug Treatment Outcome in a Malaria Endemic Region, Kisumu County

Authors

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Introduction: *Plasmodium falciparum* nuclear genome consists of 14 chromosomes which encode about 5,300 genes with a large proportion of the genes devoted to immune evasion and host–parasite interactions. In the host, especially during febrile episodes observed in clinical malaria, *P. falciparum* adapts to the environment by translocating heat shock proteins 90 (HSP-90) for its survival. These proteins assist the parasite to adapt and adjust to repeated temperature fluctuations in the form of periodic fever in the patient. Limited studies have been conducted to determine the role of *Pf*HSP-90 on treatment outcomes in clinical malaria isolates from high prevalence *P. falciparum* zones of Kenya. This study was designed to characterize the plasmodial heat shock proteins 90 and determine their role in the treatment outcome of Plasmodium falciparum malaria infections.

Objective: To determine the expression levels of *P. falciparum* HSP90 gene that are associated with acute febrile malaria and at the remission phase in malaria isolates

Methodology: This was a cross sectional study that focused on *Plasmodium falciparum* positive blood samples collected from Nyando, Kisumu County. cDNA was obtained for day 0 and day 2 samples, for a total of 45 participants and real time PCR used to amplify the HSP90 gene in the samples. Each sample was amplified in triplicate with housekeeping control genes 18S and beta-actin and a control 3D7 strain included in each run. NF54 *Plasmodium falciparum* strain was included as a parallel one copy control. Average Ct was calculated and the fold change between *Pf*HSP-90 expression at day 0 and day 2 computed using the 2^-(ΔΔCt) method.

Results: Of the 45 blood samples included in the study, HSP-90 gene expression was compared between day 0 and day 2 samples from the same patients. A fold change of >1.6 was used as an indication of a two-fold increase in the gene expression levels. 33%(n=15) of the samples showed an increase in *Pf*HSP-90 gene expression level while 67%(n=30) had the same expression for both malaria and treated samples. From the samples with increased expression(N=15) 53.3% (n=8) of the samples had a twofold increased expression level, 20%(n=3) had a three-fold increase while 6.7%(n=1) of the samples had a 4X, 5X, 7X, and 9X fold increase respectively. Correlation of HSP-90 expression and temperature at a *p-value* of 0.5 gave a correlation co-efficient value of -0.0146.

Conclusion: Correlation of *Pf*HSP-90 expression and temperature, $r^2 = 0.0146$, shows that temperature value is not a confident predictor for the expression of *Pf*HSP-90 in malaria parasites. This is further bolstered by the majority of the sample population; 67%(n=30) showing similar expression of *pf*HSP-90 for both febrile and treated samples. All samples at day 2 were non-febrile and had cleared parasitemia. This concludes that *Pf*HSP-90 expression, as a standalone, is not a reliable indicator of the treatment outcome of *P. falciparum* malaria infections. Further analysis needs to be done to define *pf*HSP-90 *de novo* mutations and epigenetic effects on gene regulation, and if there is differential expression of *pf*HSP-90 at the different stages of the malaria parasite life cycle**.**

Maternal and Child Health

Abstract ID:21

Abstract Title

Midwifery-Led Research For Evidence-Based Practice: Clinical Midwife's Engagement In Research In Ethiopia, 2021

Authors

Keflie Yohannes Gebresilassie (University of Gondar)*

Abstract

Background: Health workers' involvement in research impacted studies and the whole system. They could influence clinical practice and help to implement evidence. Although the International Confederation of Midwives put research as one of the midwifery competencies, clinical midwives are poorly involved in research.

Study aim: To assess clinical midwives' engagement in research and associated factors at public health facilities of Northwest Ethiopia, 2021.

Method: Institution-based cross-sectional study conducted among all clinical midwives working at public health facilities (at health centers, primary, general, and specialized hospitals) of Gondar Zones in Northwest Ethiopia from September to October 2021. A structured and pre-tested self-administered questionnaire was used to collect data. We operationalized good research skills if a participant scores 50% and above on skill assessment questions (12). We checked the collected data for completeness and entered using Epi-info V7 software. Descriptive statistics were used to describe the study population. For identifying factors, bi-variable and multi-variable logistic regression analysis was performed using STATA - V14. We declare a statistical significance level at a 95% confidence interval, p-value ≤ 0.05, and

respective odds ratios.

Results: Out of 335 participants, 314 took part and make the response rate 93.7%. One hundred seventy-two (54.8%) have good skills in conducting research. Clinical Midwives with mothers having a formal education, currently work in referral hospitals, and have good knowledge of research have a significant association with having good research skills. Among all, forty-eight (15.2%) ever participated in research activities during their clinical services. Clinical Midwives who have good research knowledge had a reduced (by 30%) participation in research than those who have poor knowledge.

Conclusion: Although more than half have good research skills, only a small proportion of midwives are involved in research. We also noted that having the knowledge was not enough and creating opportunities for research activities and provision of capacity-building activities could strengthen midwives' research skills, involvement, and generation of context-specific evidence for quality maternal and child health services.

Keywords

Research, Midwives, Skill, Capacity Building, Ethiopia

Mental Health

Abstract ID:22

Abstract Title

Utilization of Patient Health Questionnaire-9 depression screening tool at Care and Treatment Centers in Mbeya, Tanzania

Authors

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Abstract

Background

Depression is one of the commonest mental health disorders among People Living with HIV (PLHIV) but it is neglected in Sub-Saharan Africa. Being 2-3 times more prevalent in PLHIV than in the general population with prevalence ranging between 14-32% in PLHIV on Highly Active Antiretroviral Therapy (HAART).

In Tanzania PLHIV on HAART attending Care and Treatment Center (CTC); moderate-severe depression assessed using Patient Health Questionnaire-9 (PHQ-9, score $\geq$10) was 10%.

Method

Management of PLHIV at CTCs level is provided by HIV trained Health Care Providers (HCPs). However, the lack of locally validated screening tools at their disposal has perhaps hampered routine screening for depression in PLHIV.

The recently validated PHQ-9 in an outpatient primary care population provides opportunity to test the feasibility of depression screening.

This study aimed to pilot the routine utilization of the PHQ-9 depression screening tool by HCPs at CTC of Mbeya Zonal Referral Hospital (MZRH).

Results

5 interviews were conducted at MZRH to a total of 22 CTC Health Care Providers, obtaining their perception on the routine utilization of PHQ-9 screening tool to attending PLHIV.

On job training was conducted in blocks to a total of 31 CTC Health Care Providers, on how to screen for depression in PLHIV using PHQ-9, assessment of PHQ-9 positive PLHIV for depression diagnosis and treatment.

Conclusion

Early depression screening and treatment may have the potential of reducing HIV disease progression, HAART non-adherence and decreased immune function as well as decreasing viral load in PLHIV attending CTC. This study lay better understanding on structural and personal factors that are hindering utilization of PHQ-9 and other validated tools.

Keywords

Patient Health Questionnaire-9 (PHQ-9), Depression, Care and Treatment Centers (CTCs)

Mental Health

Abstract ID:23

Abstract Title

Acceptability of using Friendship Bench as an Intervention for addressing trauma among Adolescent Girls and Young Women experiencing Gender-based violence in Kisumu County, Kenya

Authors

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Abstract

Introduction

Friendship bench (FB) is an intervention that is currently used by trained lay workers to improve the mental well-being of girls experiencing mild mental health disorders. It has been shown to have significant decrease in depressive symptoms. There are currently existing interventions for addressing Gender-Based Violence (GBV) related trauma which is one of the causes of mental health disorders. There is need to seek the end users‘ opinion on the use of the FB as an intervention for trauma caused by GBV. This paper aims at understanding the acceptability of implementing the Friendship Bench as a mental health care intervention for the AGYWs who have experienced GBV-related trauma.

Methods

The research design was a qualitative, community-partnered participatory approach. 5 Focus Group Discussions (FGDs) with AGYWs and 49 In-Depth Interviews (IDIs) with service providers were used to collect data within Kisumu East and Central Sub-counties using semi-structured interview guides in either English, Swahili or Dholuo. The interviews were conducted by two trained research assistants where data was audio recorded, transcribed and analyzed thematically using Nvivo 12.

Results

The Friendship Bench (FB) is a mental health intervention that has potential to be an effective way of creating an appropriate environment for the AGYW to open up on their experiences with violence and a platform where these experiences could be addressed on an individual basis. Two themes were identified that cut across both FGDs and IDIs; ownership by the community and preference of service providers at the FB. FB as an intervention would be acceptable if the community members are sensitized about it, and take ownership. The AGYW being able to identify with the providers, and provision of services that were integrated and tailor-made to fit the needs of the AGYW experiencing violence were additional aspects that would make the FB acceptable. Furthermore, the FB was said to be acceptable if it could be structured in a sustainable manner and could be implemented over a longer period that could bring effective change over time. Concerns around privacy and confidentiality, and the attributes of the service providers were raised about the FB.

Conclusion

Developing an intervention that is tailor-made to the needs of the AGYW can create a different approach for addressing GBV-related trauma. Prior understanding of the acceptability of the FB would help in limiting the implementation gaps that could hinder its success.

Keywords

Friendship Bench, violence, trauma, intervention

Neglected Tropical Diseases (NTDs) and One health

Abstract ID:24

Abstract Title

An outbreak investigation: The burden and factors associated with occurrence of Visceral Leishmaniasis in Tharaka Nithi County, Kenya.

Authors

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Abstract

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Background: Visceral leishmaniasis (VL) is spread by a bite of an infected sandfly. If left untreated, the disease is fatal. Tharaka Nithi County has previously experienced sporadic cases of the disease where the present study conducted during an outbreak, revealed a significantly high prevalence of the disease. Preventive and control measures for both the vector and population are key in reducing this burden.

Methods: A cross-sectional study design was used where participants were randomly selected from Tharaka North and South sub-counties. A sample size of 720 participants was arrived at over a period of two weeks. A questionnaire on demographic data, risk factors, clinical features, and health-seeking behaviors was administered. Samples of whole blood, a buffy coat smear, and plasma were collected and transported to NUITM-KEMRI laboratories for analysis. Whole blood was extracted and analyzed using PCR to detect active cases whereas microscopic analysis was performed for the buffy coats. Prior to data collection, necessary approvals were sought including the participants' informed consent.

Results: Out of 720 samples analyzed, 174 were positive for VL giving a prevalence of 24.4% which was equally distributed among all ages. Not all cases exhibited clinical symptoms of VL. 31% had a fever, 28% had a rash, and 15% had swelling of lower limbs. Considering other clinical features of VL, 12% of the cases had increased abdominal volume, bleeding in 6%, and 8% had splenomegaly. 2% had previously been diagnosed with VL indicating recurrence of the disease. There were population risks that contributed to this positivity. 30% lived in a mud-walled house with 78% of all cases living in houses with cracks on the walls. Generally, 80.9% of the population sampled lived in a mud-walled house with 78.5% having cracks on the wall showing a risk for spread. 15% of the bites from the cases occurred in the evening most of whom (57%) were outside the house. (61%) of the cases did not use a sandfly control measure such as repellents. Other risks identified included not sleeping under a treated mosquito net at 41% despite 53% of them sleeping under a net. The state of the nets was however questionable in relation to the number of bites that occur inside the house which stood at 40%.

Conclusion: There are a number of risks that the population exposes itself to leading to the occurrence and spread of VL in Tharaka Nithi which might lead to subsequent occurrences of outbreaks in the region. Community education and prevention and control measures should be put in place.

Keywords

Visceral Leishmaniasis

Non-Communicable Diseases

Abstract ID:25

Abstract Title

TITLE: OCHRATOXINS AND DEOXYNIVALENOL CONTAMINATION OF CEREALS IN KIBRA.

Authors

Evage.ine Gatumwa Mathiu (KEMRI)*

Abstract

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Format: poster

Category: 1-E

Background; Mycotoxins are secondary metabolites of fungi affecting agricultural products in the food value chain. Among mycotoxins,Ochratoxin (OTA) and Deoxynivalenol (DON) are widely distributed in cereals and grains products. They are of public health importance due to their nephrotoxic, hepatotoxic, and genotoxic effects in humans.Poor pre-harvest

and post-harvest handling practices leads to the formation of OTA and DON in various

food commodities due to fungal infestations.

Objectives; To characterize the OTA and DON producing fungi and determine the

contamination levels in cereals stores in Kibra.

Methodology;Thecross- sectional lab based study was conducted in kibra targeting cereal vendors. A total of 20 cereal samples consisting of; muthokoi 40.0%, njahi 15.0 %, beans 15.0 % maize 25 .0% and millet 5.0%)were collected and subjected to fungal culture and ELISA test for OTA and DON using standard laboratory procedures.

Results; The Ochratoxin contamination was 52.0% and fungal contamination with;Aspergillus niger, Aspergillus flavus,Rhizopusspp and Penicillium spp. Detection of Deoxynivalenol was 48.0% with Fusarium spp. infestations.

Conclusion; Mould and mycotoxin (OTA and DON) contamination of cereals is a significant public health concern with potential health consequences. Mycotoxins have been associated with stunting, malnutrition, acute mycotoxicoses, cancer, immune modulatory and infectious disease severity. We recommend more studies and interventions to reduce the effects of mycotoxin exposure.

•Poster

Keywords

OCHRATOXINS AND DEOXYNIVALENOL CONTAMINATION OF CEREALS IN KIBRA.

Non-Communicable Diseases

Abstract ID:26

Abstract Title

THE ADAPTATION OF THERAPEUTIC CARBOHYDRATE RESTRICTION DIET FOR THE REVERSAL/REMISSION OF TYPE 2 DIABETES MELLITUS IN KENYA.

Authors

Evaline A Onyango (Kenyatta University Teaching Research and Referral Hospital)*

Abstract

BACKGROUND

One death occurs every 5 seconds because of diabetes and its complications. According to the International Diabetes Federation (IDF), 537 million people were living with diabetes worldwide in 2021. This number is projected to reach 643 million by 2030 and 783 million by 2045 with Africa having the highest increase i.e., 129% compared to other continents. In Kenya, the total diabetes-related health expenditure in 2021 was KSH 44 billion and is projected to be KSH 91 billion by 2045.

Furthermore, normal medical interventions have proven unsuccessful in promoting remission during diabetes management. However, numerous studies including the Virta Health study, an open-label, non-randomized control study, offered definitive evidence that incorporating a carbohydrate-restricted diet contributes to better blood sugar level management and reduced insulin resistance providing a more effective way of creating remission.

METHODS

The study design is literature reviews of Randomized Control Trials that focused on in cooperation of therapeutic carbohydrate restriction to show the differential results between an entirely focused medication regimen and diet interventions with medicative care.

RESULTS

In the Virta Health Study from a case group of 349 adults with type 2 diabetes,60% of patients reversed their Type 2 Diabetes, 94%of patients reduced or eliminated insulin resistance and there was a 1.3 % average HBA1c reduction at 1 year.

The American Diabetes Association's (ADA) October 2018 joint position statement with the European Association for the Study of Diabetes (EASD) approved the use of a low-carbohydrate diet as Medical Nutrition Therapy (MNT) for adults with T2DM. The ADA's recently released Standards of Medical Care in Diabetes-2019 includes using low-carbohydrate diets as nutrition therapy in its lifestyle management guidance.

There is no observed significant difference in the variability of the study populace to other considered populations in Asia, Africa, and Europe hence the results of the study can be used to formulate policy interventions for T2DM management in various national health practices.

CONCLUSION

Despite evidence that proves the effectiveness of a carbohydrate-restricted diet in diabetes remission, the primary focus of type 2 diabetes management in Kenya is medication. Currently, no documented policy guideline exists on the safe implementation of the intervention. Such a document would prove useful for clinicians and patients who opt in incorporating the intervention. Ultimately, the success of carbohydrate restriction in diabetes remission in the health ecosystem will reduce both the health and financial burden the world is currently experiencing.

Keywords

Remission, Diet, T2DM

Public Health

Abstract ID:28

Abstract Title

HEPATITIS B VACCINATION STATUS AMONG HEALTHCARE WORKERS AT NYAHERA SUB COUNTY HOSPITAL.

Authors

duncan odhiambo ongayi (ministry of health)*

Abstract

Author; Duncan Ongayi 1, Michael Onyango2

Background

Health care workers are exposed to constant risk of Hepatitis B due to their occupational contact with blood, blood products and other body fluids as well as needle stick injuries.

Objective

To determine overall Hepatitis B vaccination coverage among HCWs per carder at Nyahera sub County Hospital.

Methods

Retrospective study was done involving extrapolation of data from 240 staff Personnel files as well as direct interviews of departmental heads to determine staff Hepatitis B(HBV)vaccination status at Nyahera sub County Hospital by cadre and department. Data was collected, analyzed by Microsoft Excel Sheet and represented in form of tables and graphs

Findings

The vaccination status of HCWs against HBV at Nyahera sub county hospital was at 15 %(n=36) out of total 240 staffs. This denotes Healthcare workers who had received at least one dosage of Hepatitis B vaccine while 5% (n=12) reported to have been fully vaccinated (3doses). In regards to HBV vaccination status by cadre; 18% (n=43) of the Lab Technologists had received 3 booster doses and were fully vaccinated, 11%(n=26) of the clinical officers, Nurses 10%(n=24) had received at least one dose and none had completed the 3 booster doses, 0% (n=1) of the physiotherapist none had received any dose and this applies to 0%(n=1)Radiographers .0%(n=2) of the Nutritionists, 0%(n=8) support staffs,46%(n=11) HIV counselors were fully vaccinated, 42% (n=1) Health Records Officer received only 1 dose. The rest of the cadres/departments did not comply at all.

Conclusion

Hepatitis B vaccination uptake was low and due to the rising number of cases of HBV in the region, Healthcare workers remain at risk. All cadres and more efforts and emphasis must be made to ensure vaccine availability and completeness of the dose regime among health care workers

Keywords

HBV

Public Health

Abstract ID: 29

Abstract Title

Modelling heat stress in conjunction with other stressors: identification of vulnerable populations

Authors

Bernice Scholten (TNO)*

Abstract

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 . High air temperatures, in combination with humidity, activity level and clothing level, may lead to heat stress. Besides the negative health effects of heat stress, high temperatures can also aggravate the effects of other stressors. For example there is evidence that high temperature could modify the effects of air pollution on daily mortality . Air pollution, in turn, can increase the permeability of the respiratory tract and facilitate the penetration of allergens, thereby causing negative health effects . Because multiple stressors interact and can have a combined effect on human health, it is important to consider them jointly.

Methods

The presentation consists of ongoing work to model heat stress in conjunction with other stressors, subdivided for several vulnerable groups. Heat stress is calculated for eight categories of people (healthy adults, workers, elderly (>65 years) and adults with asthma; all divided in male and female subgroups) using meteorological data from the ECMWF database to predict heat stress (wet bulb global temperature (WBGT) effective) using ISO-7243.

Results

The analyses identified subgroups groups that were more vulnerable to heat stress as a result of variation in personal conditions. In addition we visualised co-exposure to air pollutants (including ozone, volatile organic compounds and particular matter) and allergens.

Conclusions

We present a map that indicates where people are living that are vulnerable to heat stress based on the meteorological data and their personal characteristics, and in addition might be exposed to other stressors that can also negatively affect their health. This approach can be used as decision support for governments, local communities and businesses, and facilitate targeted measures to protect vulnerable groups.

Key words: heat, multiple stressors, air pollution, vulnerable populations

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Keywords

heat, multiple stressors, air pollution, vulnerable populations

Public Health

Abstract ID:30

Abstract Title

Understanding U=U informs HIV prevention decisions in Kenya

Authors

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Abstract

Background

Sustained viral suppression from antiretroviral therapy (ART) use has been proven to eliminate the risk of HIV transmission described as Undetectable = Untransmittable (U=U). We explored how persons living with HIV (PLWH) and their HIV-uninfected partners perceived U=U as an HIV prevention choice.

Methods

The Partner HIV Self-Testing Study is providing HIV self-testing kits to PLWH to catalyze HIV testing of partners of unknown status at two HIV clinics in Central Kenya. We purposively sampled participants among PLWH and their HIV-uninfected partners. Transcripts were analyzed using inductive and deductive approaches.

Results

We enrolled 32 participants; 21 PLWH and 11 HIV uninfected partners, with a median age of 35 years (IQR 31- 42) and ART use 18 months (IQR 8-108). All PLWH confirmed receiving counseling on the importance of ART adherence to achieve HIV viral suppression and prevent HIV transmission. HIV-uninfected partners also reported being counseled on use of HIV prevention interventions until their partners achieved viral suppression. Trust in U=U was demonstrated by some HIV-uninfected partners who ceased using HIV prevention interventions once their partners achieved viral suppression and the experience of having condomless sex with their partners without getting infected. They reported supporting their partners to achieve viral suppression and using condoms and/or PrEP when viral load was high or were unsure about it. Among HIV-uninfected partners expressing doubt of U=U, they reported not trusting health providers' advice and stated they would continue using condoms and/or PrEP even after their partners achieved viral suppression for fear of acquiring HIV. They felt it was better for HIV-uninfected partners in serodifferent relationships to use PrEP as long they were together and engaging in condomless sex as there was 'no guarantee' that viral suppression meant that HIV could not be transmitted. Similarly, some PLWH reported that they prefer their serodifferent partners to continue PrEP to prevent HIV as the viral load could rebound even after suppression.

Conclusion

Our study suggests that U=U is broadly acceptable but there are still many persons in serodifferent relationships that are not convinced that U=U. Therefore, there is a need to innovatively target these individuals to address their concerns.

Keywords

HIV prevention, #U=U

Public Health

Abstract ID:31

Abstract Title

Perspectives of healthcare workers on pre-treatment loss to follow-up in adults with pulmonary TB in Western Kenya: an exploratory qualitative study

Authors

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Abstract

Background

According to the World Health Organization (WHO) tuberculosis (TB) Global Report 2022, Kenya is one of the few countries globally to achieve the WHO End TB 2020 milestone. However, it is still among the top 30 countries globally with a high TB burden, yet TB disease is preventable and curable. The continued high TB burden indicates that there remain, unaddressed and unidentified gaps in the continuum of care. Pre-treatment loss to follow-up (PTLFU) has been shown to cause continuous transmission of TB to the community and subsequently cause mortality. Patient and healthcare system-related factors have been identified as factors contributing to PTLFU. There is limited data on factors leading to PTLFU from healthcare workers' (HCWs) perspectives. Therefore, we set out to explore factors contributing to PTLFU and propose solutions from the healthcare workers' point of view.

Methods

We conducted key informant interviews at one of the county referral hospitals in Western Kenya. The participants were purposively selected and were taken through written informed consent. The interviews were recorded and stored in a password-protected database. We transcribed the audio records and remove any identifying information. The transcripts were exported to QRS NVivo© (Version 20) for data management and coding. We gave the participants unique codes, and the codes were used to report their verbal quotes. We developed a codebook using the interview guide and existing literature. We used thematic analysis for our findings.

Results

We interviewed 19 participants in this study. The participants were between 26 and 62 years of age and 14 (74%) were females. Experience in TB care ranged from 7 months to 18 years. Key factors contributing to PTLFU reported by HCWs include patient-related: alcohol and drug use, stigma, misconceptions about TB; HCW-related: not wanting to work in the TB clinic, not offering psychosocial support, lack of health education to patients, attitude; healthcare system-related: having unclear linkage between the laboratory and the clinician, lack of financial support to community health volunteers, long turnaround time for the results and challenges in the infrastructure. HCWs suggested pragmatic solutions such as: offering health education to the patients before the clinic starts, offering psychosocial counseling, providing clear linkage between the laboratory and the clinician, and having regular data review meetings.

Conclusion

Our findings show that factors contributing to PTLFU relate to the patients, HCWs, and the healthcare system. Various suggestions have been put forth by the HCWs to address PTLFU although there is limited evidence to assess their impact on PTLFU. A qualitative study on patient perspectives on PTLFU in western Kenya should be done to complement these findings. Moreover, implementation studies should be done to evaluate the effect of the solutions proposed by the HCWs to inform policymaking.

Keywords

Tuberculosis, pre-treatment loss to follow-up, qualitative study, key informant interviews, healthcare workers

Public Health

Abstract ID:32

Abstract Title

Phylogenetic diversity of fungi isolated from indoor urban environments in Nairobi Kenya.

Authors

olga m mashedi (Kenya Medical Research Institute (KEMRI) (420))*; Olga Mashedi (KEMRI)

Abstract

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BACKGROUND: Anthropogenic indoor air pollution continues to be an environmental and public health problem. Exposure to fungi can trigger allergic reactions, hypersensitivity pneumonitis, allergic rhinitis, and fungal asthma. Fungi are ubiquitous in nature and contribute to 10% of bio-aerosols diversity. Identification of fungi is based on phenotypic methods whereas genotypic identification is seldom applied. This study sought to characterize indoor fungi by molecular methods.

METHODS: One hundred and fifty fungal strains isolated from indoor environments in urban settings in Kenya were used. Molecular characterization was performed with Polymerase chain reaction and Sequencing of the β-tubulin, Fum6, and Calmodulin genes. Immuno-chromatography, High-performance liquid chromatography (HPLC) were employed for detection of fungal metabolites.

RESULTS: The most frequently isolated indoor fungi were; Penicillium spp. [63%(81/127)], Fusarium spp. [19%(25/127)] and Aspergillus spp. [11%(15/127)]. Five percent (7/127) of the strains were mycotoxin producer in-vitro. The fum6 and fum8 genes responsible for fumonisin-production were detected among Fusarium spp. The idh gene for patulin-production was detected in Penicillium spp. while citrinin producing gene cluster was not detected.

CONCLUSION: The use of molecular tools provides reliable taxonomic identification and detection of mycotoxin potential of indoor fungi associated with severe asthma with fungi sensitization (SAFs), fungal sensitization and fungal allergies and Diseases.

Keywords

Taxonomy, Indoor fungi, Molecular techniques,Mycotoxins

SRH

Abstract ID:33

Abstract Title

Factors Associated with Research knowledge and Attitude among Clinical Midwives Working at Public Health Facilities of Northwest Ethiopia, 2021: A Cross-Sectional Study

Authors

Keflie Yohannes Gebresilassie (University of Gondar)*

Abstract

Introduction: Evidence-based care is pivotal in health and needs experience and scientific evidence. Clinical midwives are busy with patient care and not involved in research, so their research knowledge and attitudes are not scientifically assessed well. Our study aimed to address this gap and help to set interventions to provide evidence-based midwifery care.

Methods: An institution-based cross-sectional study was conducted from September to October 2021 among clinical midwives working at public health facilities in Ethiopia. A structured and pretested self-administered questionnaire was used to collect data. We define good research skills as if the participants score 50% and above on skills assessment questions (12). We entered the collected data into Epi-Info software. Descriptive statistics explained the variables. To identify factors, bivariate and multivariate (for knowledge) and ordinal logistic regression and correlations (for attitude) were computed with STATA Version 14 software. P-value ≤ 0.05 was taken as a cut-off point for significance. Odds Ratios and Spearman correlation coefficients are also reported.

Results: Of 335 originally selected, 314 participated, with a response rate of 93.7%. In sum, 154 (49%, 95% CI 43.5%–54.6%) had good knowledge of research. Having taken a research-methods course (AOR 6.93, 95% CI 3.37–14.24), having research skills (AOR 2.25, 95% CI 1.30, 3.91), and having taken part in research (AOR 3.08, 95% CI 1.37–6.90) showed significant associations with good knowledge on research. Of all, 252 (80.3%, 95% CI 84.8%–92.1%) had positive attitudes towards research. Age and having a positive attitude in the independent variables were significant predictors of a positive attitude toward research. There was a significant positive correlation (ρ=0.183, P=0.001) between knowledge and attitudes toward research.

Conclusion: Although a majority had a positive attitude, a significant proportion had poor knowledge of research. Provision of capacity-building activities (training and opportunities) and allocated time for research are important for the provision of evidence-based midwifery care.

Keywords

clinical midwives, capacity, research, knowledge, attitude, Ethiopia

SRH

Abstract ID:34

Abstract Title

Prevalence of selected sexually transmitted infections among men who have sex with men on pre-exposure prophylaxis in Kiambu County, Kenya

Authors

Caleb M Ombati (Kenyatta University)*; Prof. Alloys Orago (Kenyatta University); Dr. Rosebella Iseme (Aga Khan University)

Abstract

BACKGROUND:

Globally, men having sex with men (MSM) brace a high burden of STIs, hence they are a vital target population for public health response (CDC, 2018). Chlamydia trachomatis (CT), Naisseria gonorrhoeae (NG), Hepatitis B, syphilis and herpes are the most prevalent sexually transmitted infections (STIs) among the MSM (Okal, et al., 2017; Dudareva et al., 2017). The use of pre-exposure prophylaxis (PrEP) is recommended among high risk populations (WHO, 2015). The convergence of PrEP, has seen an increase in STIs (Beymer et al., 2018). 35% of the MSM on PrEP have acquired an STI and this is a 21% increase at a national level, (NASCOP 2018). STIs contribute to 41% of morbidity among the MSM (CDC, 2018). 29% of population on PrEP in Kiambu are MSM and there is an increment of STIs by 14% in Kiambu County (KHIS, 2020). The study aimed at assessing the prevalence of selected STIs (CT, NG and syphilis) and pre-disposing factors among current users of PrEP in MSM in Mamboleo Peers Empowerment Programme (MPEG) Progam in Kiambu County.

METHODS:

The study used a descriptive cross-sectional study, involving quantitative and qualitative methods targeting the MSM enrolled on PrEP at MPEG program. This was a community-based study and Venue-based and snowballing sampling was adopted to identify participants. Quantitative data was collected from 129 participants, while qualitative data was collected from 4 key informants (program coordinator and officers) and 3 focused group discussions. Quantitative data was analyzed using SPSS and qualitative using NVIVO software. All the

logical and ethical considerations from the Kenyatta University ethics committee, NACOSTI, MPEG programme and consent obtained from participants.

RESULTS:

The findings indicated the prevalence rate of STIs was 37.5% in the past three months. The more prevalent STIs as highlighted in the study were co-morbidities of Chlamydia & Gonorrhoeae, and genital warts at 47.9% and 31.3% respectively. The regression analysis results indicated that, there were significant associations between STI prevalence and the type of sexual typologies i.e combined anal, oral and bisexual sex, [OR=25.565; 95%CI=0.144-25.328; P=0.022]. Partner notification to testing positive for an STI had a strong significance effect on STI prevalence at [OR=0.447; 95%CI=0.862-1.393; P=0.013]. On the other hand, the number of sexual acts per week has no significant relationship with STI prevalence (28.6%) [OR=0.584; 95%CI=0.000; P=1.000].

CONCLUSION:

STI prevalence among MSM on PrEP was associated with sexual behavioural patterns such as lack of use of condoms especially with paying clients, not using condoms during anal sex, and different sexual typologies and the clinical characteristics such as and failing to notify their partners when they turned positive of any STI.

Keywords

Men who have sex with men, sexually transmitted infections, pre-exposure prophylaxis, condom use, adherence

Tuberculosis

Abstract ID:35

Abstract Title

Localization of tuberculosis patients’ determinants: Patterns for presumptive cases from a coastal health facility in Kenya

Authors

fred orina (kemri)*

Abstract

Orina F1*•., Mwangi M2•., Kitole B3., Amukoye E1., Meme H1. 1.Center for Respiratory Diseases Research, Kenya Medical Research Institute, 2. Center for Public Health Research, Kenya Medical Research Institute, 3. Malindi Sub-county hospital •These authors contributed equally to this work *corresponding author *orinafred@gmail.com

Background Most National Tuberculosis Programs in high tuberculosis (TB) incidence countries routinely collect data on patients’ characteristics but rarely utilize it in targeted approaches in TB control strategies. The aim of this study was to uniquely demonstrate factors associated with tuberculosis sputum positivity for patients attending a Coastal health facility in Kenya and how the results could be utilized in policy formulation for regional control programs.

Methods This was a cross-sectional study in which consenting of presumed tuberculosis patients was done prior to recruitment and enrollment. Participants were requested to give their clinical history, demographic information, environmental and behavioral characteristics and thereafter subjected to medical and laboratory examinations. Information was collected using a structured questionnaire subsequently, all participants were instructed on how to collect spot and morning sputum specimens for TB diagnosis. Binary logistic regression analysis was performed on the culture positivity using multiple endogenous and exogenous factors.

Results A total of 202 patients were randomly enrolled. Sex distribution was even with 50.5% being male. Of all specimens presented 15.4% were culture positive. Multivariate analysis indicated that culture positivity was significantly associated with the male sex, ages between 18 – 30 years, being underweight, not currently married, reduced air entry, dull percussion note and production of purulent specimen.

Conclusions The interaction between endogenic and exogenic factors of the patients from the coastal health facility in Kenya showed a predilection of some disease determinants for pulmonary tuberculosis unique. Routine localized analysis of determinants can be utilized as a solution base for effective TB control strategies

Keywords

tuberculosis, localisation, diagnosis of TB

Tuberculosis

Abstract ID:36

Abstract Title

Association between the latent TB infection and body mass index of patients from clinical sites in Nairobi, Kenya

Authors

ROBI CHACHA (KEMRI)*

Abstract

Robi Chacha1, Asiko Ongaya1, Paul Mwangi1, Jeremiah Ndeto1, Pascah Bulia1, Geoffrey Okallo1, Janice Endsley2, Evans Amukoye1

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Format: Poster

Category: 1- G. LTBI/TB Preventive Therapy

Introduction:

Globally tuberculosis is a major public health problem and among the leading causes of death from a single infectious pathogen. Individuals exposed to Mycobacterium tuberculosis infection develop a state of persistent immune response to the pathogen and remain clinically asymptomatic (LTBI) and may progress to active tuberculosis disease, particularly in immunosuppressed individuals. Decrease in body weight is a known risk factor that increases the burden of active tuberculosis (TB). However, conflicting evidence exists on the effect of body weight and the risk of latent tuberculosis infection (LTBI).

Methodology

We conducted a pilot study to estimate the relationship between BMI and LTBI. Purposive selection of three health facilities in Nairobi county was done; Mbagathi hospital, Rhodes TB clinic and AIDs Health Foundation-Mathare. Blood samples were collected from consented participants and subjected to the Interferon gamma release assay (IGRA) using Quantiferon Gold Plus according to the manufacturer's instructions. The Weight and height of the participants was also obtained.

Results

Among the 67 participants 34 (50.7%) were latent TB positive,17 (25.4%) male, 17 (25.4%) female, 25 (37.3%) were negative, 10 (14.9%) male, 15 (22.4%) female and 8 (11.9%) indeterminate 5 (4.5%) male, 5 (7.5%) female. Among the LTBI positive cases 5 (7.5%) were underweight, 19 (28.4%) healthy, 6 (9.0%) overweight and 4 (6.0%) obese. Of the LTBI negatives none were underweight, 18 (26.9%) healthy, 4 (6.0%) overweight and 3 (4.5%) obese. When adjusted for age and sex BMI was not significantly correlated with the status of LTBI ($r=0.302$, $P>.001$).

Conclusion

High BMI was not significantly associated with lower risk of LTBI, however these results are limited to a small sample size. Recruitment of more participants is ongoing to obtain reminiscent inference based on the findings to establish whether lower BMI is a risk factor in LTBI, the reservoir for active TB cases.

Keywords

Tuberculosis

Tuberculosis

Abstract ID:37

Abstract Title

Integration of Quality Improvement (QI) approach in intensified TB active case finding (ACF), a case of Awendo Sub County

Authors

Nelly A Okwiri (MOH)*

Abstract

INTRODUCTION:

During the Awendo sub county/facility performance review meeting in the year 2020, it was observed that TB case detection had been declining over the last 3 years and none of the facilities had achieved their target in case detection. A total of 183 cases were notified in 2018, 114 cases notified in 2019 and 110 cases notified in 2020, against the target of 20% increase in TB case notification.

A number of innovative and effective strategies to find missing people with TB and enhancing treatment outcomes were proposed, based on their possibility as evidenced from best practices and experiences over time. The aim of study was to increase TB case detection from 110 cases notified in 2020 to at least 132 cases in 2021.

METHODS:

This study adopted mixed research design, where I used retrospective data from TIBU platform and TB registers, comparing data from 2018 to 2020 before putting QI strategies in place and for 2021 after putting the QI strategies in place.

RESULTS

The strategies worked well and in 2021, we were able to increase case detection by 33%. We notified 146 TB cases in 2021 from 110 cases notified in 2020. Out of the 146 cases notified, CHVs referred 28 cases translating to 19% of the total cases notified.

The private facilities notified 87 cases out of the total 146 cases notified in 2021, translating to 60% of the total cases notified. In 2018, 2019 and 2020 private facilities contribution was at 35%, 30% and 42% respectively.

CONCLUSION

From this study, it was concluded that Quality improvement approach was quite appropriate for TB indicators, that the public private partnership in TB active case finding and management was also critical and that the CHVs play a critical role in TB active case finding and management.

Keywords

Quality improvement approach is the way to go not only in TB indicators but in all indicators of interest

Tuberculosis

Abstract ID:38

Abstract Title

Clinical and Social Demographic characteristics of TB/HIV cohort in Nairobi, Kenya.

Authors

paul m waiganjo (kemri)*; Asiko Ongaya (KEMRI); geoffrey okallo (kemri); janice endsley (utmb); evans amukoye (kemri)

Abstract

Background

Tuberculosis (TB) and (HIV/AIDS) constitute the main burden of infectious diseases in resource-limited countries. In Kenya the current co-infection ratio among the notified TB cases is 25.2%. This study evaluated the socio-demographic and clinical factors of a TB/HIV co-infected cohort at initiation of TB treatment and at five months in Nairobi, Kenya to inform clinical management and patient monitoring of TB.

Methodology

A prospective cohort study was carried out in three TB treatment Clinics in Nairobi. A structured questionnaire was used to extract demographic and clinical characteristics of TB/HIV co-infected patients. The findings were analysed using SPSS version 20.0, T-test was performed to compare the initial and follow-up (at 5 months) datasets.

Results

A total of 142 TB HIV coinfected patients were recruited at the initiation of treatment (n=85) and followed up at five months of treatment (n=57)

Men 81(57% were more than females,134(94%) were between 18-50 years, 8(6%) were over 50years. Most participants 100(70%, p=0.002) lived in semi-permanent houses. Source of income(p=1.4), level of education(p=0.12) and marital status(p=0.5) were not statistically significance. Majority 86(61%) had normal BMI while 21(15%) and 32(23%) had a history of smoking (p=0.36) and alcohol (p=0.89) use respectively. During the course of TB treatment 135(95%,p=0.009) were not on concomitant medication other than ARVs. Less than 1% reported to have used herbal preparations. At initiation of treatment most participants reported productive cough 82(96%), chest pains 66(78%), fever 61(72%), weight loss 78(92%) and body weakness 75(88%) but reduced at month five productive cough 1(2%), chest pains 2(4%), fever 2(4%), weight loss 4(7%) and body weakness 4(7%)). Majority140(99%) had no underlying medical condition.

Conclusion

Most HIV/TB coinfected patients were found to be living in semi-permanent structure. This could be indication of poor living conditions that can negatively impact TB control and management. Further studies on TB/HIV patients need to be conducted in order to understand their health seeking behavior for improved TB/HIV treatment outcome.

Keywords

Tuberculosis,HIV, coinfection, Clinical,Dermographic,Cohort,Visits

Vector Biology

Abstract ID:39

Abstract Title

Detection of Insecticide Resistance by Culex pipiens complex to several insecticides in Kenya

Authors

Santos J Yalwala (KEMRI/USAMRD-AK)*; Stephanie Cinkovich (WRAIR); Jaree Johnson (WRAIR); Richard O Ochieng (USAMRD-AK); Gladys Kerich (USAMRD-K); David Oullo (USAMRD-AK); Eunice Achieng (USAMRD-AK); Janet Ambale (USAMRD-AK); Francis Ngere (USAMRD-AK); Charles Waga (USAMRD-AK); Nicholas Odemba (USAMRD-AK); David Abuom (USAMRD-AK); Eric Garges (USAMRD-AK); Elly Ojwang (USAMRD-AK); Fredrick Eyase (US Army Medical Research Directorate-Africa)

Abstract

Mosquitoes transmit a variety of arboviruses that are responsible for disease in humans, livestock and pets. Culex pipiens species complex is crucial in maintenance of a number of these arboviruses that are a threat to both public and veterinary health. Some of the viruses transmitted by Cx. pipiens include Usutu virus, West Nile Virus and Sindbis virus. These viruses have no treatment or vaccine for human and animal protection. Thus, vector control remains the main public health intervention to protect against these mosquito borne viruses. Development of Insecticide Resistance (IR) by mosquito vectors complicates control measures and endangers public health.

Methods:

Culex pipiens larvae were collected from larval habitats in Nyalenda village, Kisumu County, Msambweni village, Kwale county and Isiolo town, Isiolo County using a standard larval dipping method. Collected larvae were transported to the KEMRI-CGHR USAMRD-K insectary and reared to adults at temperatures of 27 ± 2 °C and relative humidity of 70–80%. Emergent adults were separated by sex and species, and provided with 10% glucose solution. Emerged 3–5-day old Cx.pipiens were exposed to different classes of insecticides using the WHO tube bioassay protocols to detect phenotypic insecticide resistance. We tested for resistance of Cx.pipiens against permethrin, p-methyl, deltamethrin, dieldrin and malathion in Kisumu, Kenya. Additionally, samples from Isiolo and Kwale were tested for resistance against permethrin.

Results:

Cx.pipiens from Nyalenda, Kisumu showed confirmed resistance with average mortality as follows: permethrin-81.7%, p-methyl-73.9%, deltamethrin-40%, dieldrin-35.4% and mortality of 96.9% to malathion. Cx.pipiens from Isiolo and Kwale showed confirmed resistance against permethrin with an average mortality of 22.5% and 51.1% respectively.

Conclusion:

The present data is an indicator that there may be wide spread resistance by Cx. pipiens against current insecticides. More studies will reveal the nature and form of resistance and therefore provide policy makers with the necessary information for public health protection intervention.

Keywords

Insecticide Resistance, Culex pipiens, insecticides, Arboviruses

Vector Biology

Abstract ID:40

Abstract Title

Microsporidia MB is associated with Anopheles mosquitoes in different agro-ecological conditions

Authors

Oscar Mbare (International Centre of Insect Physiology and Ecology)*; Joseph N Gichuhi (icipe); Syeda Tullu Bukhari (International Center of Insect Ecology and Physiology); Jeremy Herren (International Centre of Insect Physiology and Ecology)

Abstract

Background: Recent studies have identified Microsporidia MB in field-collected Anopheles arabiensis, An. gambiae sensu stricto and An. coluzzii, the major vectors of malaria in sub-Saharan Africa, and that the microsporidian completely inhibits the transmission of Plasmodium falciparum. However, different Anopheles species in a range of ecological settings are involved in malaria transmission.

Methods: Here, we investigated whether Microsporidia MB is found in Anopheles species collected in different agro-ecological zones in Kenya. Anopheles mosquitoes sampled in the arid zone in Turkana county, semi-arid zone in west Pokot county and humid zones in Busia and Bungoma counties were tested for presence of Microsporidia MB.

Results: The prevalence of Microsporidia MB in An. gambiae sl and An. funestus sl was 1-2% in the arid zone in Turkana county, 8-9% in semi-arid zone in West Pokot county, and 0.7-3% in humid zones in Busia and Bungoma counties respectively. Microsporidia MB was also found in one An. pharoensis sampled in the humid zone in Bungoma county.

Conclusion: These findings show that Microsporidia MB is naturally found in different Anopheles species involved in malaria transmission. In addition, the results indicate that the microsporidian is found in Anopheles species that inhabit areas with diverse climatic conditions

Keywords

Microsporidia, malaria, Anopheles, agro-ecological zones

Vector Biology

Abstract ID:41

Abstract Title

COMPARISON OF DIFFERENT TRAPPING METHODS TO COLLECT MALARIA VECTORS INDOORS AND OUTDOORS IN WESTERN KENYA

Authors

Jackline Jeruto Kosgei (KEMRI)*; Seline Omondi (Kenya Medical Research Institute); VINCENT MOSHI (PTBiKenya); Daniel McDermott (Liverpool School of Tropical Medicine); Martin Donnelly (Liverpool School of Tropical Medicine); Daniel McDermott (Liverpool School of Tropical Medicine); John Gimnig (CDC); Bernard Abongo (KEMRI); Eric O Ochomo (Kenya Medical Research institute)

Abstract

Background: Entomological surveillance is essential for monitoring the impact of control tools and is mostly conducted using human landing catches (HLCs) or CDC-light traps (CDC-LT). HLCs may expose collectors to infectious mosquitoes. Other surveillance tools like light traps, pyrethrum spray catches and aspiration do not give adequate information on time and location of mosquito bites. This study evaluated a number of mosquito surveillance trapping methods with a modification to enable hourly collection of mosquitoes when assessing malaria vector control tools, especially novel ones.

Methods: Five mosquito sampling methods—Centre for disease control light traps (CDC-LT), UV light traps (UV-LT), aspiration, human landing catches (HLC), and malaise trapping were evaluated in villages of Asembo, in Siaya County, western Kenya between July and September 2020. CDC-LTs, UV-LTs, and HLCs were conducted in three locations of the same compound (inside houses; outside 10 meters from the house; and outside 10 meters from the compound boundary). Collections were rotated through houses following a five-by-five Latin-square design. Mosquito densities, species abundance, and sporozoite infectivity rates were compared across all sampling methods. Data analysis was performed using R statistics software version 4.1.2.

Results: 5483 Anopheles mosquitoes were sampled from 868 trapping efforts. Anopheles funestus constituted 3824, (69.74%) of the sampled Anopheles mosquitoes. Compared to HLC, indoor aspiration captured highest number of An. funestus, mean=8.82 (RR =12.74, 95% CI 6.02-24.58, P <0.001) followed by indoor UV-LT, mean=4.26, (RR= 5.13, 95% CI 2.80-9.39, P <0.001) and indoor CDC-LT mean=2.30 (RR= 3.00, 95% CI 1.63-5.53, P <0.001). Similarly, outdoor UV-LT and CDC-LT collected higher number of Anopheles mosquitoes across all species when compared to outdoor HLC. Hourly biting in UV-LT and CDC-LT indicated different peaks compared to HLC.

Conclusion: Anopheles funestus were primarily caught indoors. An. arabiensis and An. coustani were mostly collected outdoors with UV-LTs. The UV-LT and CDC-LT were superior to HLC both indoors and outdoors. Differences in hourly biting by different collection methods indicate the need to further investigate the behaviour of An. funestus.

Keywords

UV light trap, Human landing catches, Anopheles, malaria, vector, surveillance

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