



In Search of Better Health

KEMRI PUBLICATIONS (2019)

1. Li HK, Rombach I, Zambellas R, Walker AS, McNally MA, Atkins BL, Lipsky BA, Hughes HC, Bose D, Kumin M, Scarborough C, Matthews PC, Brent AJ, Lomas J, Gundle R, Rogers M, Taylor A, Angus B, Byren I, Berendt AR, Warren S, Fitzgerald FE, Mack DJF, Hopkins S, Folb J, Reynolds HE, Moore E, Marshall J, Jenkins N, Moran CE, Woodhouse AF, Stafford S, Seaton RA, Vallance C, Hemsley CJ, Bisnauthsing K, Sandoe JAT, Aggarwal I, Ellis SC, Bunn DJ, Sutherland RK, Barlow G, Cooper C, Geue C, McMeekin N, Briggs AH, Sendi P, Khatamzas E, Wangrangsimakul T, Wong T HN, Barrett LK, Alvand A, Old CF, Bostock J, Paul J, Cooke G, Thwaites GE, Bejon P, Scarborough M; OVIVA Trial Collaborators. Oral versus Intravenous Antibiotics for Bone and Joint Infection. *N Engl J Med.* 2019 Jan 31;380(5):425-436.

Abstract

Background: The management of complex orthopedic infections usually includes a prolonged course of intravenous antibiotic agents. We investigated whether oral antibiotic therapy is noninferior to intravenous antibiotic therapy for this indication.

Methods: We enrolled adults who were being treated for bone or joint infection at 26 U.K. centers. Within 7 days after surgery (or, if the infection was being managed without surgery, within 7 days after the start of antibiotic treatment), participants were randomly assigned to receive either intravenous or oral antibiotics to complete the first 6 weeks of therapy. Follow-on oral antibiotics were permitted in both groups. The primary end point was definitive treatment failure within 1 year after randomization. In the analysis of the risk of the primary end point, the noninferiority margin was 7.5 percentage points.

Results: Among the 1054 participants (527 in each group), end-point data were available for 1015 (96.3%). Treatment failure occurred in 74 of 506 participants (14.6%) in the intravenous group and 67 of 509 participants (13.2%) in the oral group. Missing end-point data (39 participants, 3.7%) were imputed. The intention-to-treat analysis showed a difference in the risk of definitive treatment failure (oral group vs. intravenous group) of -1.4 percentage points (90% confidence interval [CI], -4.9 to 2.2; 95% CI, -5.6 to 2.9), indicating noninferiority. Complete-case, per-protocol, and sensitivity analyses supported this result. The between-group difference in the incidence of serious adverse events was not significant (146 of 527 participants [27.7%] in the intravenous group and 138 of 527 [26.2%] in the oral group; $P=0.58$). Catheter complications, analyzed as a secondary end point, were more common in the intravenous group (9.4% vs. 1.0%).

Conclusions: Oral antibiotic therapy was noninferior to intravenous antibiotic therapy when used during the first 6 weeks for complex orthopedic infection, as assessed by treatment failure at 1 year. (Funded by the National Institute for Health Research; OVIVA Current Controlled Trials number, ISRCTN91566927).

Pubmed link- <https://pubmed.ncbi.nlm.nih.gov/30699315/>



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2.	<p>Wright D, Kortekaas J, Bowden TA, Warimwe GM. Rift Valley fever: biology and epidemiology. <i>J Gen Virol.</i> 2019 Aug;100(8):1187-1199.</p> <p>Abstract</p> <p>Rift Valley fever (RVF) is a mosquito-borne viral zoonosis that was first discovered in Kenya in 1930 and is now endemic throughout multiple African countries and the Arabian Peninsula. RVF virus primarily infects domestic livestock (sheep, goats, cattle) causing high rates of neonatal mortality and abortion, with human infection resulting in a wide variety of clinical outcomes, ranging from self-limiting febrile illness to life-threatening haemorrhagic diatheses, and miscarriage in pregnant women. Since its discovery, RVF has caused many outbreaks in Africa and the Arabian Peninsula with major impacts on human and animal health. However, options for the control of RVF outbreaks are limited by the lack of licensed human vaccines or therapeutics. For this reason, RVF is prioritized by the World Health Organization for urgent research and development of countermeasures for the prevention and control of future outbreaks. In this review, we highlight the current understanding of RVF, including its epidemiology, pathogenesis, clinical manifestations and status of vaccine development.⁹⁸</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31310198/</p>
3.	<p>Hay K, McDougal L, Percival V, Henry S, Klugman J, Wurie H, Raven J, Shabalala F, Fielding-Miller R, Dey A, Dehingia N, Morgan R, Atmavilas Y, Saggurti N, Yore J, Blokhina E, Huque R, Barasa E, Bhan N, Kharel C, Silverman JG, Raj A; Gender Equality, Norms, and Health Steering Committee. Disrupting gender norms in health systems: making the case for change. <i>Lancet.</i> 2019 Jun 22;393(10190):2535-2549.</p> <p>Abstract</p> <p>Restrictive gender norms and gender inequalities are replicated and reinforced in health systems, contributing to gender inequalities in health. In this Series paper, we explore how to address all three through recognition and then with disruptive solutions. We used intersectional feminist theory to guide our systematic reviews, qualitative case studies based on lived experiences, and quantitative analyses based on cross-sectional and evaluation research. We found that health systems reinforce patients' traditional gender roles and neglect gender inequalities in health, health system models and clinic-based programmes are rarely gender responsive, and women have less authority as health workers than men and are often devalued and abused. With regard to potential for disruption, we found that gender equality policies are associated with greater representation of female physicians, which in turn is associated with better health outcomes, but that gender parity is insufficient to achieve gender equality. We found that institutional support and respect of nurses improves quality of care, and that women's empowerment collectives can increase health-care access and provider responsiveness. We see promise from social movements in supporting women's reproductive rights and policies. Our findings suggest we must view gender as a fundamental factor that predetermines and shapes health systems and outcomes. Without addressing the role of</p>



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	<p>restrictive gender norms and gender inequalities within and outside health systems, we will not reach our collective ambitions of universal health coverage and the Sustainable Development Goals. We propose action to systematically identify and address restrictive gender norms and gender inequalities in health systems.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31155270/</p>
4.	<p>French JA, Brodie MJ, Caraballo R, Devinsky O, Ding D, Jehi L, Jette N, Kanner A, Modi AC, Newton CR, Patel AA, Pennell PB, Perucca E, Sander JW, Scheffer IE, Singh G, Williams E, Wilmschurst J, Cross JH. Keeping people with epilepsy safe during the COVID-19 pandemic. <i>Neurology</i>. 2020 Jun 9;94(23):1032-1037.</p> <p>Abstract</p> <p>Objectives: To provide information on the effect of the coronavirus disease of 2019 (COVID-19) pandemic on people with epilepsy and provide consensus recommendations on how to provide the best possible care for people with epilepsy while avoiding visits to urgent care facilities and hospitalizations during the novel coronavirus pandemic.</p> <p>Methods: The authors developed consensus statements in 2 sections. The first was "How should we/clinicians modify our clinical care pathway for people with epilepsy during the COVID-19 pandemic?" The second was "What general advice should we give to people with epilepsy during this crisis? The authors individually scored statements on a scale of -10 (strongly disagree) to +10 (strongly agree). Five of 11 recommendations for physicians and 3/5 recommendations for individuals/families were rated by all the authors as 7 or above (strongly agree) on the first round of rating. Subsequently, a teleconference was held where statements for which there was a lack of strong consensus were revised.</p> <p>Results: After revision, all consensus recommendations received a score of 7 or above. The recommendations focus on administration of as much care as possible at home to keep people with epilepsy out of health care facilities, where they are likely to encounter COVID-19 (including strategies for rescue therapy), as well as minimization of risk of seizure exacerbation through adherence, and through ensuring a regular supply of medication. We also provide helpful links to additional helpful information for people with epilepsy and health providers.</p> <p>Conclusion: These recommendations may help health care professionals provide optimal care to people with epilepsy during the coronavirus pandemic.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/32327490/</p>
4.	<p>Pérez-Mazliah D, Ndungu FM, Aye R, Langhorne J. B-cell memory in malaria: Myths and realities. <i>Immunol Rev</i>. 2020 Jan;293(1):57-69.</p> <p>Abstract</p> <p>B-cell and antibody responses to <i>Plasmodium</i> spp., the parasite that causes malaria, are critical for control of parasitemia and associated immunopathology. Antibodies also provide protection to reinfection. Long-lasting B-cell memory has been shown to occur in response to <i>Plasmodium</i> spp. in experimental model infections, and in human malaria. However, there are reports that antibody responses to several malaria antigens in young children living with malaria are not similarly long-lived, suggesting a dysfunction in the</p>



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	<p>maintenance of circulating antibodies. Some studies attribute this to the expansion of atypical memory B cells (AMB), which express multiple inhibitory receptors and activation markers, and are hyporesponsive to B-cell receptor (BCR) restimulation in vitro. AMB are also expanded in other chronic infections such as tuberculosis, hepatitis B and C, and HIV, as well as in autoimmunity and old age, highlighting the importance of understanding their role in immunity. Whether AMB are dysfunctional remains controversial, as there are also studies in other infections showing that AMB can produce isotype-switched antibodies and in mouse can contribute to protection against infection. In light of these controversies, we review the most recent literature on either side of the debate and challenge some of the currently held views regarding B-cell responses to Plasmodium infections.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31733075</p>
5.	<p>van Eijk AM, Zulaika G, Lenchner M, Mason L, Sivakami M, Nyothach E, Unger H, Laserson K, Phillips-Howard PA. Menstrual cup use, leakage, acceptability, safety, and availability: a systematic review and meta-analysis. <i>Lancet Public Health</i>. 2019 Aug;4(8):e376-e393.</p> <p>Abstract</p> <p>Background: Girls and women need effective, safe, and affordable menstrual products. Single-use products are regularly selected by agencies for resource-poor settings; the menstrual cup is a less known alternative. We reviewed international studies on menstrual cup leakage, acceptability, and safety and explored menstrual cup availability to inform programmes.</p> <p>Methods: In this systematic review and meta-analysis, we searched PubMed, Cochrane Library, Web of Science, Popline, Cinahl, Global Health database, Emerald, Google Scholar, Science.gov, and WorldWideScience from database inception to May 14, 2019, for quantitative or qualitative studies published in English on experiences and leakage associated with menstrual cups, and adverse event reports. We also screened the Manufacturer and User Facility Device Experience database from the US Food and Drug Administration for events related to menstrual cups. To be eligible for inclusion, the material needed to have information on leakage, acceptability, or safety of menstrual cups. The main outcome of interest was menstrual blood leakage when using a menstrual cup. Safety outcomes of interest included serious adverse events; vaginal abrasions and effects on vaginal microflora; effects on the reproductive, digestive, or urinary tract; and safety in poor sanitary conditions. Findings were tabulated or combined by use of forest plots (random-effects meta-analysis). We also did preliminary estimates on costs and environmental savings potentially associated with cups. This systematic review is registered on PROSPERO, number CRD42016047845.</p> <p>Findings: Of 436 records identified, 43 studies were eligible for analysis (3319 participants). Most studies reported on vaginal cups (27 [63%] vaginal cups, five [12%]</p>



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	<p>cervical cups, and 11 [25%] mixed types of cups or unknown) and 15 were from low-income and middle-income countries. 22 studies were included in qualitative or quantitative syntheses, of which only three were of moderate-to-high quality. Four studies made a direct comparison between menstrual cups and usual products for the main outcome of leakage and reported leakage was similar or lower for menstrual cups than for disposable pads or tampons (n=293). In all qualitative studies, the adoption of the menstrual cup required a familiarisation phase over several menstrual cycles and peer support improved uptake (two studies in developing countries). In 13 studies, 73% (pooled estimate: n=1144; 95% CI 59-84, I²=96%) of participants wished to continue use of the menstrual cup at study completion. Use of the menstrual cup showed no adverse effects on the vaginal flora (four studies, 507 women). We identified five women who reported severe pain or vaginal wounds, six reports of allergies or rashes, nine of urinary tract complaints (three with hydronephrosis), and five of toxic shock syndrome after use of the menstrual cup. Dislodgement of an intrauterine device was reported in 13 women who used the menstrual cup (eight in case reports, and five in one study) between 1 week and 13 months of insertion of the intrauterine device. Professional assistance to aid removal of menstrual cup was reported among 47 cervical cup users and two vaginal cup users. We identified 199 brands of menstrual cup, and availability in 99 countries with prices ranging US\$0.72-46.72 (median \$23.3, 145 brands).</p> <p>Interpretation: Our review indicates that menstrual cups are a safe option for menstruation management and are being used internationally. Good quality studies in this field are needed. Further studies are needed on cost-effectiveness and environmental effect comparing different menstrual products.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31324419/</p>
6.	<p>Tshilolo L, Tomlinson G, Williams TN, Santos B, Olupot-Olupot P, Lane A, Aygun B, Stuber SE, Latham TS, McGann PT, Ware RE; REACH Investigators. Hydroxyurea for Children with Sickle Cell Anemia in Sub-Saharan Africa. <i>N Engl J Med.</i> 2019 Jan 10;380(2):121-131.</p> <p>Abstract</p> <p>Background: Hydroxyurea is an effective treatment for sickle cell anemia, but few studies have been conducted in sub-Saharan Africa, where the burden is greatest. Coexisting conditions such as malnutrition and malaria may affect the feasibility, safety, and benefits of hydroxyurea in low-resource settings.</p> <p>Methods: We enrolled children 1 to 10 years of age with sickle cell anemia in four sub-Saharan countries. Children received hydroxyurea at a dose of 15 to 20 mg per kilogram of body weight per day for 6 months, followed by dose escalation. The end points assessed feasibility (enrollment, retention, and adherence), safety (dose levels, toxic effects, and malaria), and benefits (laboratory variables, sickle cell-related events, transfusions, and survival).</p>



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	<p>Results: A total of 635 children were fully enrolled; 606 children completed screening and began receiving hydroxyurea at a mean (\pmSD) dose of 17.5\pm1.8 mg per kilogram per day. The retention rate was 94.2% at 3 years of treatment. Hydroxyurea therapy led to significant increases in both the hemoglobin and fetal hemoglobin levels. Dose-limiting toxic events regarding laboratory variables occurred in 5.1% of the participants, which was below the protocol-specified threshold for safety. During the treatment phase, 20.6 dose-limiting toxic effects per 100 patient-years occurred, as compared with 20.7 events per 100 patient-years before treatment. As compared with the pretreatment period, the rates of clinical adverse events decreased with hydroxyurea use, including rates of vaso-occlusive pain (98.3 vs. 44.6 events per 100 patient-years; incidence rate ratio, 0.45; 95% confidence interval [CI], 0.37 to 0.56), nonmalaria infection (142.5 vs. 90.0 events per 100 patient-years; incidence rate ratio, 0.62; 95% CI, 0.53 to 0.72), malaria (46.9 vs. 22.9 events per 100 patient-years; incidence rate ratio, 0.49; 95% CI, 0.37 to 0.66), transfusion (43.3 vs. 14.2 events per 100 patient-years; incidence rate ratio, 0.33; 95% CI, 0.23 to 0.47), and death (3.6 vs. 1.1 deaths per 100 patient-years; incidence rate ratio, 0.30; 95% CI, 0.10 to 0.88).</p> <p>Conclusions: Hydroxyurea treatment was feasible and safe in children with sickle cell anemia living in sub-Saharan Africa. Hydroxyurea use reduced the incidence of vaso-occlusive events, infections, malaria, transfusions, and death, which supports the need for wider access to treatment. (Funded by the National Heart, Lung, and Blood Institute and others; REACH ClinicalTrials.gov number, NCT01966731).</p> <p>Puubmed link- https://pubmed.ncbi.nlm.nih.gov/30501550/</p>
7.	<p>Mogire RM, Mutua A, Kimita W, Kamau A, Bejon P, Pettifor JM, Adeyemo A, Williams TN, Atkinson SH. Prevalence of vitamin D deficiency in Africa: a systematic review and meta-analysis. <i>Lancet Glob Health</i>. 2020 Jan;8(1):e134-e142.</p> <p>Abstract</p> <p>Background: Vitamin D deficiency is associated with non-communicable and infectious diseases, but the vitamin D status of African populations is not well characterised. We aimed to estimate the prevalence of vitamin D deficiency in children and adults living in Africa.</p> <p>Methods: For this systematic review and meta-analysis, we searched PubMed, Web of Science, Embase, African Journals Online, and African Index Medicus for studies on vitamin D prevalence, published from database inception to Aug 6, 2019, without language restrictions. We included all studies with measured serum 25-hydroxyvitamin D (25[OH]D) concentrations from healthy participants residing in Africa. We excluded case reports and case series, studies that measured 25(OH)D only after a clinical intervention, and studies with only a meeting abstract or unpublished material available. We used a standardised data extraction form to collect information from eligible studies; if the required information was not available in the published report, we requested raw data</p>



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	<p>from the authors. We did a random-effects meta-analysis to obtain the pooled prevalence of vitamin D deficiency in African populations, with use of established cutoffs and mean 25(OH)D concentrations. We stratified meta-analyses by participant age group, geographical region, and residence in rural or urban areas. The study is registered with PROSPERO, number CRD42018112030.</p> <p>Findings: Our search identified 1692 studies, of which 129 studies with 21 474 participants from 23 African countries were included in the systematic review and 119 studies were included in the meta-analyses. The pooled prevalence of low vitamin D status was 18.46% (95% CI 10.66-27.78) with a cutoff of serum 25(OH)D concentration less than 30 nmol/L; 34.22% (26.22-43.68) for a cutoff of less than 50 nmol/L; and 59.54% (51.32-67.50) for a cutoff of less than 75 nmol/L. The overall mean 25(OH)D concentration was 67.78 nmol/L (95% CI 64.50-71.06). There was no evidence of publication bias, although heterogeneity was high (I² ranged from 98.26% to 99.82%). Mean serum 25(OH)D concentrations were lower in populations living in northern African countries or South Africa compared with sub-Saharan Africa, in urban areas compared with rural areas, in women compared with men, and in newborn babies compared with their mothers.</p> <p>Interpretation: The prevalence of vitamin D deficiency is high in African populations. Public health strategies in Africa should include efforts to prevent, detect, and treat vitamin D deficiency, especially in newborn babies, women, and urban populations.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31786117/</p>
8.	<p>Kariuki JN, Kaburi J, Musuva R, Njomo DW, Night D, Wandera C, Wodera J, Mwinzi PN. Research Dissemination Strategies Used by Kenya Medical Research Institute Scientists. <i>East Afr Health Res J.</i> 2019;3(1):70-78.</p> <p>Abstract</p> <p>Background: Dissemination of research findings is acknowledged as an important component of any research process. Implementation of research findings into practice or policy is necessary for improving outcomes in the targeted community. Given the context and dynamic environment in which researchers operate, there is need to find out existing gaps in terms of disseminating research findings to key stakeholders. The objective of this study was to investigate the health research dissemination strategies used by Kenya Medical Research Institute (KEMRI) researchers.</p> <p>Methods: This was a mixed-method study employing concurrent sequence (use of both qualitative and quantitative) methods of data collection. The study was conducted in KEMRI's 10 centres spread in 3 geographical areas: Kisumu, Kilifi, and Nairobi counties. Potential respondents were identified through purposive sampling. Three inter-related data collection methods were employed in this study. These methods included key informant interviews with: (a) MoH officials from county government; (b) KEMRI researchers; and (c) key KEMRI departments, namely Corporate Affairs and the library. Additionally, secondary sources of information, such as scientific reports, KEMRI annual reports, and financial statements, were also reviewed.</p>



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	<p>Results: Publication of papers in peer-reviewed journals was mentioned as the most common method of dissemination of research findings. Scientists published in 353 peer-reviewed journals (or publishing houses) between the years 2002 and 2015. Over 92.7% of these publications were in international peer-reviewed journals. Conferences and workshops were also mentioned. In the absence of a centralised electronic KEMRI publication database, the research team extracted and collated a publication lists from KEMRI annual reports and financial statements. This was limiting since it did not have an exhaustive list of all publications by KEMRI scientists. Only 3 respondents mentioned having written policy briefs or engaged the media as part of dissemination channels. The media representatives cited the use of social media (Facebook and Twitter) as another channel that KEMRI scientists could exploit. Challenges in dissemination included lack of knowledge on research translation leading to poor synthesis of research outputs as well as selective reporting by the media.</p> <p>Conclusion: Publications in peer-reviewed journals was the most preferred channel of communicating scientific outputs. Conferences and writing of policy briefs were the other sources of dissemination. We recommend that KEMRI dissemination channels should go well beyond simply making research available through the traditional vehicles of journal publications and scientific conference presentations but establish institutional mechanism which would facilitate extracting the main messages or key implications derived from research results and communicating them to stakeholders in attractive ways that would encourage them to factor the research implications into their work.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/34308198/</p>
9.	<p>Bandsma RHJ, Voskuil W, Chimwezi E, Fegan G, Briend A, Thitiri J, Ngari M, Mwalekwa L, Bandika V, Ali R, Hamid F, Owor B, Mturi N, Potani I, Allubha B, Muller Kobold AC, Bartels RH, Versloot CJ, Feenstra M, van den Brink DA, van Rheen PF, Kerac M, Bourdon C, Berkley JA. A reduced-carbohydrate and lactose- free formulation for stabilization among hospitalized children with severe acute malnutrition: A double-blind, randomized controlled trial. <i>PLoS Med.</i> 2019 Feb 26;16(2):e1002747.</p> <p>Abstract</p> <p>Background: Children with medically complicated severe acute malnutrition (SAM) have high risk of inpatient mortality. Diarrhea, carbohydrate malabsorption, and refeeding syndrome may contribute to early mortality and delayed recovery. We tested the hypothesis that a lactose-free, low-carbohydrate F75 milk would serve to limit these risks, thereby reducing the number of days in the stabilization phase.</p> <p>Methods and findings: In a multicenter double-blind trial, hospitalized severely malnourished children were randomized to receive standard formula (F75) or isocaloric modified F75 (mF75) without lactose and with reduced carbohydrate. The primary endpoint was time to stabilization, as defined by the World Health Organization (WHO), with intention-to-treat analysis. Secondary outcomes included in-hospital mortality, diarrhea, and biochemical features of malabsorption and refeeding syndrome. The trial was registered at clinicaltrials.gov (NCT02246296). Four hundred eighteen and 425</p>



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	<p>severely malnourished children were randomized to F75 and mF75, respectively, with 516 (61%) enrolled in Kenya and 327 (39%) in Malawi. Children with a median age of 16 months were enrolled between 4 December 2014 and 24 December 2015. One hundred ninety-four (46%) children assigned to F75 and 188 (44%) to mF75 had diarrhea at admission. Median time to stabilization was 3 days (IQR 2-5 days), which was similar between randomized groups (0.23 [95% CI -0.13 to 0.60], $P = 0.59$). There was no evidence of effect modification by diarrhea at admission, age, edema, or HIV status. Thirty-six and 39 children died before stabilization in the F75 and in mF75 arm, respectively ($P = 0.84$). Cumulative days with diarrhea ($P = 0.27$), enteral ($P = 0.42$) or intravenous fluids ($P = 0.19$), other serious adverse events before stabilization, and serum and stool biochemistry at day 3 did not differ between groups. The main limitation was that the primary outcome of clinical stabilization was based on WHO guidelines, comprising clinical evidence of recovery from acute illness as well as metabolic stabilization evidenced by recovery of appetite.</p> <p>Conclusions: Empirically treating hospitalized severely malnourished children during the stabilization phase with lactose-free, reduced-carbohydrate milk formula did not improve clinical outcomes. The biochemical analyses suggest that the lactose-free formulae may still exceed a carbohydrate load threshold for intestinal absorption, which may limit their usefulness in the context of complicated SAM.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30807589/</p>
10.	<p>Bandsma RHJ, Voskuil W, Chimwezi E, Fegan G, Briend A, Thitiri J, Ngari M, Mwalekwa L, Bandika V, Ali R, Hamid F, Owor B, Mturi N, Potani I, Allubha B, Muller Kobold AC, Bartels RH, Versloot CJ, Feenstra M, van den Brink DA, van Rheenen PF, Kerac M, Bourdon C, Berkley JA. A reduced-carbohydrate and lactose-free formulation for stabilization among hospitalized children with severe acute malnutrition: A double-blind, randomized controlled trial. <i>PLoS Med.</i> 2019 Feb 26;16(2):e1002747.</p> <p>Abstract</p> <p>Background: Children with medically complicated severe acute malnutrition (SAM) have high risk of inpatient mortality. Diarrhea, carbohydrate malabsorption, and refeeding syndrome may contribute to early mortality and delayed recovery. We tested the hypothesis that a lactose-free, low-carbohydrate F75 milk would serve to limit these risks, thereby reducing the number of days in the stabilization phase.</p> <p>Methods and findings: In a multicenter double-blind trial, hospitalized severely malnourished children were randomized to receive standard formula (F75) or isocaloric modified F75 (mF75) without lactose and with reduced carbohydrate. The primary endpoint was time to stabilization, as defined by the World Health Organization (WHO), with intention-to-treat analysis. Secondary outcomes included in-hospital mortality, diarrhea, and biochemical features of malabsorption and refeeding syndrome. The trial was registered at clinicaltrials.gov (NCT02246296). Four hundred eighteen and 425 severely malnourished children were randomized to F75 and mF75, respectively, with 516 (61%) enrolled in Kenya and 327 (39%) in Malawi. Children with a median age of 16</p>



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	<p>months were enrolled between 4 December 2014 and 24 December 2015. One hundred ninety-four (46%) children assigned to F75 and 188 (44%) to mF75 had diarrhea at admission. Median time to stabilization was 3 days (IQR 2-5 days), which was similar between randomized groups (0.23 [95% CI -0.13 to 0.60], $P = 0.59$). There was no evidence of effect modification by diarrhea at admission, age, edema, or HIV status. Thirty-six and 39 children died before stabilization in the F75 and in mF75 arm, respectively ($P = 0.84$). Cumulative days with diarrhea ($P = 0.27$), enteral ($P = 0.42$) or intravenous fluids ($P = 0.19$), other serious adverse events before stabilization, and serum and stool biochemistry at day 3 did not differ between groups. The main limitation was that the primary outcome of clinical stabilization was based on WHO guidelines, comprising clinical evidence of recovery from acute illness as well as metabolic stabilization evidenced by recovery of appetite.</p> <p>Conclusions: Empirically treating hospitalized severely malnourished children during the stabilization phase with lactose-free, reduced-carbohydrate milk formula did not improve clinical outcomes. The biochemical analyses suggest that the lactose-free formulae may still exceed a carbohydrate load threshold for intestinal absorption, which may limit their usefulness in the context of complicated SAM.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30807589/</p>
11.	<p>Gumba H, Waichungo J, Lowe B, Mwanzu A, Musyimi R, Thitiri J, Tigoi C, Kamui M, Berkley JA, Ngetich R, Kawai S, Kariuki S. Implementing a quality management system using good clinical laboratory practice guidelines at KEMRI-CMR to support medical research. Wellcome Open Res. 2019 Jun 25;3:137.</p> <p>Abstract</p> <p>Background: Good Clinical Laboratory Practice (GCLP) is a standard that helps ensure the quality and reliability of research data through principles of Good Laboratory Practice (GLP) and Good Clinical Practice (GCP). The implementation of GCLP includes careful documentation of procedures, competencies and safety measures. Implementation of GCLP is influenced by existing resources and quality systems, thus laboratories in low- and middle-income countries may face additional challenges. Methods: This paper describes implementation of GCLP at the Kenya Medical Research Institute-Center for Microbiology Research (KEMRI-CMR) as part of a quality system to support medical research. This study employed assessment, twinning (institutional mentorship) model, conducting relevant training workshops and Kaizen 5S approaches to implement an effective quality management system using GCLP standard. This was achieved through a collaboration between the KEMRI/Wellcome Trust Research Programme (KWTRP) and KEMRI-CMR. The aim was compliance and continuous monitoring to meet international GCLP standards in a way that could be replicated in other research organizations. Results: Following a baseline assessment in March 2017, training, mentorship and a cycle of quality audit and corrective action using a Kaizen 5S approach (sorting, setting in order, shining, standardizing and sustaining) was established. Laboratory personnel were trained in writing standard operating procedures and analytical plans, microbiological</p>



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	<p>techniques, and good documentation practice. Mid-term and exit assessments demonstrated significant declines in non-conformances across all GCLP elements. KEMRI-CMR achieved GCLP accreditation in May 2018 by Qualogy Ltd (UK). Conclusions: Involving all the laboratory personnel in implementation of quality management system processes is critical to success. An institutional mentorship (twinning) approach shows potential for future collaborations between accredited and non-accredited organizations to accelerate the implementation of high-quality management systems and continuous improvement.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30607370/</p>
12.	<p>Mwangome M, Prentice AM. Tackling the triple threats of childhood malnutrition. BMC Med. 2019 Nov 25;17(1):210.</p> <p>Abstract</p> <p>The term 'double burden of malnutrition' is usually interpreted in terms of the physical status of children: stunted and wasted children on the one hand and overweight/obese children on the other. There is a third category of malnutrition that can occur at either end of the anthropometric spectrum or, indeed, in children whose physical size may be close to ideal. This third type is most commonly articulated with the phrase 'hidden hunger' and is often illustrated by micronutrient deficiencies; thus, we refer to it here as 'undernutrition'. As understanding of such issues advances, we realise that there is a myriad of factors that may be influencing a child's road to nutritional health. In this BMC Medicine article collection we consider these influences and the impact they have, such as: the state of the child's environment; the effect this has on their risk of, and responses to, infection and on their gut; the consequences of poor nutrition on cognition and brain development; the key drivers of the obesity epidemic across the globe; and how undernourishment can affect a child's body composition. This collection showcases recent advances in the field, but likewise highlights ongoing challenges in the battle to achieve adequate nutrition for children across the globe.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31760952/</p>
13.	<p>Obonyo NG, Schlapbach LJ, Fraser JF. Corrigendum: Sepsis: Changing Definitions, Unchanging Treatment. Front Pediatr. 2020 Jan 23;7:538.</p> <p>Abstract</p> <p>The recently revised Sepsis-3 definitions were based on criteria that were derived and validated in adult patient databases from high income countries. Both sepsis and septic shock continue to account for a substantial proportion of mortality globally, especially amongst children in low-and-middle income country settings. It is therefore urgent to develop and validate standardized criteria for sepsis that can be applied to pediatric populations in different settings, including in- and outside intensive care, both in high- and low/middle- income countries. This will be a pre-requisite to evaluate the impact of sepsis treatment strategies to improve clinical outcomes.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30729101/</p>
14.	<p>Obonyo NG, Schlapbach LJ, Fraser JF. Sepsis: Changing Definitions,</p>



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	<p>Unchanging Treatment. <i>Front Pediatr.</i> 2019 Jan 23;6:425. Pubmed link-https://pubmed.ncbi.nlm.nih.gov/32039108/</p>
14.	<p>Gumba H, Musyoki J, Mosobo M, Lowe B. Implementation of Good Clinical Laboratory Practice in an Immunology Basic Research Laboratory: The KEMRI- Wellcome Trust Research Laboratories Experience. <i>Am J Clin Pathol.</i> 2019 Feb 4;151(3):270-274. Abstract Objectives: Good Clinical Laboratory Practice (GCLP) is a standard that ensures quality and reliability of research data by adopting the principles of Good Laboratory Practice and Good Clinical Practice. Even though implementing a quality system in a basic research laboratory is still a contentious issue, it ensures that the research data are accurate, valid, and reliable. GCLP implementation requires proper documented procedures and safety precautions to achieve this objective. Methods: This article describes the Kenya Medical Research Institute (KEMRI)-Wellcome Trust Research Laboratories experience in the implementation of GCLP guidelines in a laboratory conducting basic research. Results: The laboratory managed to implement GCLP elements that could be applied to a basic research laboratory, such as standard operating procedures, equipment management, laboratory analytical plans, organization, and personnel. The laboratory achieved GCLP accreditation in October 2015. Conclusions: The methodology, suggestions, and comments that arose from our experience in implementing GCLP guidelines can be used by other laboratories to develop a quality system using GCLP guidelines to support medical research conducted to ensure the research data are reliable and can be easily reconstructed in other research settings. Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30339188/</p>
15.	<p>Gildenhard M, Rono EK, Diarra A, Boissière A, Bascunan P, Carrillo- Bustamante P, Camara D, Krüger H, Mariko M, Mariko R, Mireji P, Nsango SE, Pompon J, Reis Y, Rono MK, Seda PB, Thailayil J, Traorè A, Yapto CV, Awono- Ambene P, Dabiré RK, Diabaté A, Masiga D, Catteruccia F, Morlais I, Diallo M, Sangare D, Levashina EA. Mosquito microevolution drives Plasmodium falciparum dynamics. <i>Nat Microbiol.</i> 2019 Jun;4(6):941-947. Abstract Malaria, a major cause of child mortality in Africa, is engendered by Plasmodium parasites that are transmitted by anopheline mosquitoes. Fitness of Plasmodium parasites is closely linked to the ecology and evolution of its anopheline vector. However, whether the genetic structure of vector populations impacts malaria transmission remains unknown. Here, we describe a partitioning of the African malaria vectors into generalists and specialists that evolve along ecological boundaries. We next identify the contribution of mosquito species to Plasmodium abundance using Granger causality tests for time-series data collected over two rainy seasons in Mali. We find that mosquito microevolution, defined by changes in the genetic structure of a population over short</p>



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	<p>ecological timescales, drives Plasmodium dynamics in nature, whereas vector abundance, infection prevalence, temperature and rain have low predictive values. Our study demonstrates the power of time-series approaches in vector biology and highlights the importance of focusing local vector control strategies on mosquito species that drive malaria dynamics.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30911126/</p>
16.	<p>de Menil V, Hoogenhout M, Kipkemoi P, Kamuya D, Eastman E, Galvin A, Mwangasha K, de Vries J, Kariuki SM, Murugasen S, Mwangi P, Singh I, Stein DJ, Abubakar A, Newton CR, Donald KA, Robinson E. The NeuroDev Study: Phenotypic and Genetic Characterization of Neurodevelopmental Disorders in Kenya and South Africa. <i>Neuron</i>. 2019 Jan 2;101(1):15-19.</p> <p>Abstract The NeuroDev study will deeply phenotype cognition, behavior, dysmorphias, and neuromedical traits on an expected cohort of 5,600 Africans (1,800 child cases, 1,800 child controls, and 1,900 parents) and will collect whole blood for exome sequencing and biobanking.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30605655/</p>
17.	<p>Gildenhard M, Rono EK, Diarra A, Boissière A, Bascunan P, Carrillo- Bustamante P, Camara D, Krüger H, Mariko M, Mariko R, Mireji P, Nsango SE, Pompon J, Reis Y, Rono MK, Seda PB, Thailayil J, Traorè A, Yapto CV, Awono- Ambene P, Dabiré RK, Diabaté A, Masiga D, Catteruccia F, Morlais I, Diallo M, Sangare D, Levashina EA. Mosquito microevolution drives Plasmodium falciparum dynamics. <i>Nat Microbiol</i>. 2019 Jun;4(6):941-947.</p> <p>Abstract Malaria, a major cause of child mortality in Africa, is engendered by Plasmodium parasites that are transmitted by anopheline mosquitoes. Fitness of Plasmodium parasites is closely linked to the ecology and evolution of its anopheline vector. However, whether the genetic structure of vector populations impacts malaria transmission remains unknown. Here, we describe a partitioning of the African malaria vectors into generalists and specialists that evolve along ecological boundaries. We next identify the contribution of mosquito species to Plasmodium abundance using Granger causality tests for time-series data collected over two rainy seasons in Mali. We find that mosquito microevolution, defined by changes in the genetic structure of a population over short ecological timescales, drives Plasmodium dynamics in nature, whereas vector abundance, infection prevalence, temperature and rain have low predictive values. Our study demonstrates the power of time-series approaches in vector biology and highlights the importance of focusing local vector control strategies on mosquito species that drive malaria dynamics.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30911126/</p>



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18.	<p>Kimenyi KM, Wamae K, Ochola-Oyier LI. Understanding <i>P. falciparum</i> Asymptomatic Infections: A Proposition for a Transcriptomic Approach. <i>Front Immunol.</i> 2019 Oct 15;10:2398.</p> <p>Abstract</p> <p>Malaria is still a significant public health burden in the tropics. Infection with malaria causing parasites results in a wide range of clinical disease presentations, from severe to uncomplicated or mild, and in the poorly understood asymptomatic infections. The complexity of asymptomatic infections is due to the intricate interplay between factors derived from the human host, parasite, and environment. Asymptomatic infections often go undetected and provide a silent natural reservoir that sustains malaria transmission. This creates a major obstacle for malaria control and elimination efforts. Numerous studies have tried to characterize asymptomatic infections, unanimously revealing that host immunity is the underlying factor in the maintenance of these infections and in the risk of developing febrile malaria infections. An in-depth understanding of how host immunity and parasite factors interact to cause malaria disease tolerance is thus required. This review primarily focuses on understanding anti-inflammatory and pro-inflammatory responses to asymptomatic infections in malaria endemic areas, to present the view that it is potentially the shift in host immunity toward an anti-inflammatory profile that maintains asymptomatic infections after multiple exposures to malaria. Conversely, symptomatic infections are skewed toward a pro-inflammatory immune profile. Moreover, we propose that these infections can be better interrogated using next generation sequencing technologies, in particular RNA sequencing (RNA-seq), to investigate the immune system using the transcriptome sampled during a clearly defined asymptomatic infection.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31681289/</p>
19.	<p>Miller Iii WA, Teye J, Achieng AO, Mogire RM, Akala H, Ong'echa JM, Rathi B, Durvasula R, Kempaiah P, Kwofie SK. Antimalarials: Review of Plasmepsins as Drug Targets and HIV Protease Inhibitors Interactions. <i>Curr Top Med Chem.</i> 2019;18(23):2022-2028.</p> <p>Abstract</p> <p>Malaria is a major global health concern with the majority of cases reported in regions of South-East Asia, Eastern Mediterranean, Western Pacific, the Americas, and Sub-Saharan Africa. The World Health Organization (WHO) estimated 216 million worldwide reported cases of malaria in 2016. It is an infection of the red blood cells by parasites of the genus <i>Plasmodium</i> with most severe and common forms caused by <i>Plasmodium falciparum</i> (<i>P. falciparum</i> or Pf) and <i>Plasmodium vivax</i> (<i>P. vivax</i> or Pv). Emerging parasite resistance to available antimalarial drugs poses great challenges to treatment. Currently, the first line of defense includes artemisinin combination therapies (ACTs), increasingly becoming less effective and challenging to combat new occurrences of drug-resistant parasites. This necessitates the urgent need for novel antimalarials that target</p>



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	<p>new molecular pathways with a different mechanism of action from the traditional antimalarials. Several new inhibitors and potential drug targets of the parasites have been reported over the years. This review focuses on the malarial aspartic proteases known as plasmepsins (Plms) as novel drug targets and antimalarials targeting Plms. It further discusses inhibitors of hemoglobin-degrading plasmepsins Plm I, Plm II, Plm IV and Histo-aspartic proteases (HAP), as well as HIV protease inhibitors of plasmepsins</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30499404/</p>
20.	<p>Murungi LM, Kimathi RK, Tuju J, Kamuyu G, Osier FHA. Serological Profiling for Malaria Surveillance Using a Standard ELISA Protocol. <i>Methods Mol Biol.</i> 2019;2013:83-90.</p> <p>Abstract</p> <p>The enzyme-linked immunosorbent assay (ELISA) is a reliable and relatively low-cost method for measuring soluble ligands such as antibodies and proteins in biological samples. For analysis of specific antibodies in serum, a capture antigen is immobilized onto a solid polystyrene surface from which it can capture the antibodies. The captured antibodies are subsequently detected using a secondary antibody conjugated to an enzyme. Detection is accomplished by addition of a colorimetric substrate, and the readout is absorbance (optical density). Here, we provide a detailed standardized ELISA protocol for the quantification of antibodies against malaria antigens.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31267495/</p>
21.	<p>Kaduka L, Muniu E, Mbui J, Oduor Owuor C, Gakunga R, Kwasa J, Wabwire S, Okerosi N, Korir A, Remick SC. Disability-Adjusted Life-Years Due to Stroke in Kenya. <i>Neuroepidemiology.</i> 2019;53(1-2):48-54.</p> <p>Abstract</p> <p>Background: There is little information on stroke morbidity in Kenya to inform health care planning. The disability-adjusted life-years (DALYs) are a time-based measure of health status that incorporates both disability and mortality.</p> <p>Methods: This was a multicenter prospective study in Kenya's public tertiary hospitals conducted in 2015-2017. Data on sex, age, and global disability outcome were collected and used to calculate the sum of years of life lost prematurely due to stroke (YLL), the years of healthy life lost due to disability (YLD), and the DALYs.</p> <p>Results: Up to 719 adult stroke patients participated in the study. The peak age group for stroke was 60-64 years, with ischemic stroke accounting for 56.1% of the stroke cases. After 1-year follow-up, the YLD were 2,402.50, YLL were 5,335.99, and the DALYs were 7,738.49. YLD contributed 31% of the total DALYs. The DALYs varied by sex (male: 2,835.79; female: 4,902.70 years) and by stroke type (ischemic stroke: 4,652.98; hemorrhagic stroke: 3,085.51). The young age group (< 45 years) bore a greater burden accounting for 35.6% of the total DALYs.</p> <p>Conclusion: The YLD, YLL, and DALYs observed reinforce the need for targeted prevention of risk factors and comprehensive stroke care initiatives in Kenya.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30986786/</p>



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22.	<p>Burmen B, Mogunde JO, Kwaro DP. Ethically providing Routine HIV testing services to bereaved populations. <i>Nurs Ethics</i>. 2019 Feb;26(1):195-200.</p> <p>Abstract</p> <p>Background:: The delivery of public health policies may be in conflict with individualism.</p> <p>Objectives:: To propose measures to ethically provide routine HIV testing services to persons visiting a funeral home.</p> <p>Research design:: A document analysis of study documents and presentations made to an institutional review board.</p> <p>Participants and research context:: Institutional review board members (both lay and professionals) and Study investigators attending an 'open session' where study investigators were invited to elaborate on some study procedures.</p> <p>Ethical considerations:: Identities of all parties were anonymized.</p> <p>Findings:: Opt-out approaches to HIV testing, grief counseling, relational ethics, and a modular consenting process were proposed to safeguard clients' autonomy. The golden-rule approach and protective empowering were suggested to protect clientele beneficence.</p> <p>Discussion and conclusion:: It is possible to ethically provide universal HIV testing and counseling services among grieving populations in this setting; elsewhere, this should be contextualized.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/29281932/</p>
23.	<p>Boyle MJ, Chan JA, Handayuni I, Reiling L, Feng G, Hilton A, Kurtovic L, Oyong D, Piera KA, Barber BE, William T, Eisen DP, Minigo G, Langer C, Drew DR, de Labastida Rivera F, Amante FH, Williams TN, Kinyanjui S, Marsh K, Doolan DL, Engwerda C, Fowkes FJI, Grigg MJ, Mueller I, McCarthy JS, Anstey NM, Beeson JG. IgM in human immunity to <i>Plasmodium falciparum</i> malaria. <i>Sci Adv</i>. 2019 Sep 25;5(9):eaax4489.</p> <p>Abstract</p> <p>Most studies on human immunity to malaria have focused on the roles of immunoglobulin G (IgG), whereas the roles of IgM remain undefined. Analyzing multiple human cohorts to assess the dynamics of malaria-specific IgM during experimentally induced and naturally acquired malaria, we identified IgM activity against blood-stage parasites. We found that merozoite-specific IgM appears rapidly in <i>Plasmodium falciparum</i> infection and is prominent during malaria in children and adults with lifetime exposure, together with IgG. Unexpectedly, IgM persisted for extended periods of time; we found no difference in decay of merozoite-specific IgM over time compared to that of IgG. IgM blocked merozoite invasion of red blood cells in a complement-dependent manner. IgM was also associated with significantly reduced risk of clinical malaria in a longitudinal cohort of children. These findings suggest that merozoite-specific IgM is an important functional and long-lived antibody response targeting blood-stage malaria parasites that contributes to malaria immunity.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31579826/</p>



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24.	<p>Strozzi F, Janssen R, Wurmus R, Crusoe MR, Githinji G, Di Tommaso P, Belhachemi D, Möller S, Smant G, de Ligt J, Prins P. Scalable Workflows and Reproducible Data Analysis for Genomics. <i>Methods Mol Biol.</i> 2019;1910:723-745.</p> <p>Abstract Biological, clinical, and pharmacological research now often involves analyses of genomes, transcriptomes, proteomes, and interactomes, within and between individuals and across species. Due to large volumes, the analysis and integration of data generated by such high-throughput technologies have become computationally intensive, and analysis can no longer happen on a typical desktop computer. In this chapter we show how to describe and execute the same analysis using a number of workflow systems and how these follow different approaches to tackle execution and reproducibility issues. We show how any researcher can create a reusable and reproducible bioinformatics pipeline that can be deployed and run anywhere. We show how to create a scalable, reusable, and shareable workflow using four different workflow engines: the Common Workflow Language (CWL), Guix Workflow Language (GWL), Snakemake, and Nextflow. Each of which can be run in parallel. We show how to bundle a number of tools used in evolutionary biology by using Debian, GNU Guix, and Bioconda software distributions, along with the use of container systems, such as Docker, GNU Guix, and Singularity. Together these distributions represent the overall majority of software packages relevant for biology, including PAML, Muscle, MAFFT, MrBayes, and BLAST. By bundling software in lightweight containers, they can be deployed on a desktop, in the cloud, and, increasingly, on compute clusters. By bundling software through these public software distributions, and by creating reproducible and shareable pipelines using these workflow engines, not only do bioinformaticians have to spend less time reinventing the wheel but also do we get closer to the ideal of making science reproducible. The examples in this chapter allow a quick comparison of different solutions.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31278683/</p>
25.	<p>Zeinali Z, Muraya K, Govender V, Molyneux S, Morgan R. Intersectionality and global health leadership: parity is not enough. <i>Hum Resour Health.</i> 2019 Apr 27;17(1):29.</p> <p>Abstract There has been a welcome emphasis on gender issues in global health in recent years in the discourse around human resources for health. Although it is estimated that up to 75% of health workers are female (World Health Organization, Global strategy on human resources for health: Workforce 2030, 2016), this gender ratio is not reflected in the top levels of leadership in international or national health systems and global health organizations (Global Health 50/50, The Global Health 50/50 report: how gender responsive are the world's leading global health organizations, 2018; Clark, <i>Lancet</i>, 391:918-20, 2018). This imbalance has led to a deeper exploration of the role of women in leadership and the barriers they face through initiatives such as the WHO Global Strategy on Human Resources for Health: Workforce 2030, the UN High Level</p>



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	<p>Commission on Health Employment and Economic Growth, the Global Health 50/50 Reports, Women in Global Health, and #LancetWomen. These movements focus on advocating for increasing women's participation in leadership. While efforts to reduce gender imbalance in global health leadership are critical and gaining momentum, it is imperative that we look beyond parity and recognize that women are a heterogeneous group and that the privileges and disadvantages that hinder and enable women's career progression cannot be reduced to a shared universal experience, explained only by gender. Hence, we must take into account the ways in which gender intersects with other social identities and stratifiers to create unique experiences of marginalization and disadvantage.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31029139/</p>
26.	<p>Hunsperger E, Juma B, Onyango C, Ochieng JB, Omballa V, Fields BS, Njenga MK, Mwangi J, Bigogo G, Omoro R, Otieno N, Chaves SS, Munyua P, Njau DM, Verani J, Lowther S, Breiman RF, Montgomery JM, De Cock KM, Widdowson MA; CDC and KEMRI laboratory and Epidemiology Team. Building laboratory capacity to detect and characterize pathogens of public and global health security concern in Kenya. <i>BMC Public Health</i>. 2019 May 10;19(Suppl 3):477.</p> <p>Abstract</p> <p>Since 1979, multiple CDC Kenya programs have supported the development of diagnostic expertise and laboratory capacity in Kenya. In 2004, CDC's Global Disease Detection (GDD) program within the Division of Global Health Protection in Kenya (DGHP-Kenya) initiated close collaboration with Kenya Medical Research Institute (KEMRI) and developed a laboratory partnership called the Diagnostic and Laboratory Systems Program (DLSP). DLSP built onto previous efforts by malaria, human immunodeficiency virus (HIV) and tuberculosis (TB) programs and supported the expansion of the diagnostic expertise and capacity in KEMRI and the Ministry of Health. First, DLSP developed laboratory capacity for surveillance of diarrheal, respiratory, zoonotic and febrile illnesses to understand the etiology burden of these common illnesses and support evidenced-based decisions on vaccine introductions and recommendations in Kenya. Second, we have evaluated and implemented new diagnostic technologies such as TaqMan Array Cards (TAC) to detect emerging or reemerging pathogens and have recently added a next generation sequencer (NGS). Third, DLSP provided rapid laboratory diagnostic support for outbreak investigation to Kenya and regional countries. Fourth, DLSP has been assisting the Kenya National Public Health laboratory-National Influenza Center and microbiology reference laboratory to obtain World Health Organization (WHO) certification and ISO15189 accreditation respectively. Fifth, we have supported biosafety and biosecurity curriculum development to help Kenyan laboratories safely and appropriately manage infectious pathogens. These achievements, highlight how in collaboration with existing CDC programs working on HIV, tuberculosis and malaria, the Global Health Security Agenda can have significantly improve public health in Kenya and the region. Moreover, Kenya provides an example as</p>



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	<p>to how laboratory science can help countries detect and control of infectious disease outbreaks and other public health threats more rapidly, thus enhancing global health security.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/32326916/</p>
27.	<p>Nyongesa MK, Ssewanyana D, Mutua AM, Chongwo E, Scerif G, Newton CRJC, Abubakar A. Assessing Executive Function in Adolescence: A Scoping Review of Existing Measures and Their Psychometric Robustness. <i>Front Psychol.</i> 2019 Mar 1;10:311.</p> <p>Abstract</p> <p>Background: There is much research examining adolescents' executive function (EF) but there is little information about tools that measure EF, in particular preference of use, their reliability and validity. This information is important as to help both researchers and practitioners select the most relevant and reliable measure of EF to use with adolescents in their context. Aims: We conducted a scoping review to: (a) identify the measures of EF that have been used in studies conducted among adolescents in the past 15 years; (b) identify the most frequently used measures of EF; and (c) establish the psychometric robustness of existing EF measures used with adolescents. Methods: We searched three bibliographic databases (PsycINFO, Ovid Medline, and Web of Science) using key terms "Adolescents," "Executive Functions," and "measures". The search covered research articles published between 1st January 2002 and 31st July 2017. Results: We identified a total of 338 individual measures of EF from 705 eligible studies. The vast majority of these studies (95%) were conducted in high income countries. Of the identified measures, 10 were the most used frequently, with a cumulative percent frequency accounting for nearly half (44%) the frequency of usage of all reported measures of EF. These are: Digit Span (count = 160), Trail Making Test (count = 158), Behavior Rating Inventory of Executive Function (count = 148), Wisconsin Card Sorting Test (count = 140), Verbal Fluency Tasks (count = 88), Stroop Color-Word Test (count = 78), Classical Stroop Task (count = 63), Color-Word Interference Test from Delis-Kaplan battery (count = 62), Rey-Osterrieth Complex Figure Test (count = 62), and Original Continuous Performance Test (count = 58). In terms of paradigms, tasks from Span (count = 235), Stroop (count = 216), Trails (count = 171), Card sorting (count = 166), Continuous performance (count = 99), and Tower (count = 94) paradigms were frequently used. Only 48 studies out of the included 705 reported the reliability and/or validity of measures of EF used with adolescents, but limited to studies in high income countries. Conclusion: We conclude that there is a wide array of measures for assessing EF among adolescents. Ten of these measures are frequently used. However, the evidence of psychometric robustness of measures of EF used with adolescents remains limited to support the validity of their usage across different contexts.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30881324/</p>



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28.	<p>Sande CJ, Njunge JM, Mwangeli Ngoi J, Mutunga MN, Chege T, Gicheru ET, Gardiner EM, Gwela A, Green CA, Drysdale SB, Berkley JA, Nokes DJ, Pollard AJ. Airway response to respiratory syncytial virus has incidental antibacterial effects. <i>Nat Commun.</i> 2019 May 17;10(1):2218.</p> <p>Abstract RSV infection is typically associated with secondary bacterial infection. We hypothesise that the local airway immune response to RSV has incidental antibacterial effects. Using coordinated proteomics and metagenomics analysis we simultaneously analysed the microbiota and proteomes of the upper airway and determined direct antibacterial activity in airway secretions of RSV-infected children. Here, we report that the airway abundance of <i>Streptococcus</i> was higher in samples collected at the time of RSV infection compared with samples collected one month later. RSV infection is associated with neutrophil influx into the airway and degranulation and is marked by overexpression of proteins with known antibacterial activity including BPI, EPX, MPO and AZU1. Airway secretions of children infected with RSV, have significantly greater antibacterial activity compared to RSV-negative controls. This RSV-associated, neutrophil-mediated antibacterial response in the airway appears to act as a regulatory mechanism that modulates bacterial growth in the airways of RSV-infected children.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31101811/</p>
29.	<p>Adhikari B, Vincent R, Wong G, Duddy C, Richardson E, Lavery JV, Molyneux S. A realist review of community engagement with health research. <i>Wellcome Open Res.</i> 2019 Aug 2;4:87.</p> <p>Abstract Introduction: Community engagement is increasingly recognized as a critical aspect of global health. Recent years have seen an expansion of community engagement activities linked to health research, but debates and inconsistencies remain about the aims of different types of engagement, mechanisms underpinning their implementation and impact, and influential contextual factors. Greater commitment to and consistency around community engagement by health research programs, implementers and funders requires a more coherent evidence base. This realist review is designed to improve our understanding of how and why community engagement contributes to intended and unintended outcomes (including research and ethical outcomes) in different contexts. Given the breadth and diversity of the literature on community engagement in health research, the review will initially focus on malaria research in low- and middle-income countries (LMICs) and draw on wider global health literature where needed. Methods and analysis: Community engagement in practice is often a complex set of interventions. We will conduct a realist review - a theory driven approach to evidence synthesis - to provide explanations for how and why community engagement with health research produces the pattern of outcomes observed across different contexts of application. We will consolidate evidence from a range of documents, including qualitative, quantitative and</p>



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	<p>mixed method studies. The review will follow several stages: devising an initial programme theory, searching evidence, selecting appropriate documents, extracting data, synthesizing and refining the programme theory, and reiteration of these steps as needed. Ethics and dissemination: A formal ethics review is not required for this literature review. Findings will be disseminated in a peer reviewed journal, through national and international conferences, and through a set of short briefings tailored for audiences with an interest in community engagement. Outputs and presentations will be informed by and feed into our network of community engagement experts.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31289754/</p>
30.	<p>Muriuki JM, Mentzer AJ, Kimita W, Ndungu FM, Macharia AW, Webb EL, Lule SA, Morovat A, Hill AVS, Bejon P, Elliott AM, Williams TN, Atkinson SH. Iron Status and Associated Malaria Risk Among African Children. Clin Infect Dis. 2019 May 17;68(11):1807-1814.</p> <p>Abstract</p> <p>Background: It remains unclear whether improving iron status increases malaria risk, and few studies have looked at the effect of host iron status on subsequent malaria infection. We therefore aimed to determine whether a child's iron status influences their subsequent risk of malaria infection in sub-Saharan Africa.</p> <p>Methods: We assayed iron and inflammatory biomarkers from community-based cohorts of 1309 Kenyan and 1374 Ugandan children aged 0-7 years and conducted prospective surveillance for episodes of malaria. Poisson regression models were fitted to determine the effect of iron status on the incidence rate ratio (IRR) of malaria using longitudinal data covering a period of 6 months. Models were adjusted for age, sex, parasitemia, inflammation, and study site.</p> <p>Results: At baseline, the prevalence of iron deficiency (ID) was 36.9% and 34.6% in Kenyan and Ugandan children, respectively. ID anemia (IDA) affected 23.6% of Kenyan and 17.6% of Ugandan children. Malaria risk was lower in children with ID (IRR, 0.7; 95% confidence interval [CI], 0.6, 0.8; P < .001) and IDA (IRR, 0.7; 95% CI, 0.6, 0.9; P = .006). Low transferrin saturation (<10%) was similarly associated with lower malaria risk (IRR, 0.8; 95% CI, 0.6, 0.9; P = .016). However, variation in hepcidin, soluble transferrin receptors (sTfR), and hemoglobin/anemia was not associated with altered malaria risk.</p> <p>Conclusions: ID appears to protect against malaria infection in African children when defined using ferritin and transferrin saturation, but not when defined by hepcidin, sTfR, or hemoglobin. Additional research is required to determine causality.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30219845/</p>
31.	<p>Obonyo NG, Byrne L, Tung JP, Simonova G, Diab SD, Dunster KR, Passmore MR, Boon AC, See Hoe L, Engkilde-Pedersen S, Esguerra-Lallen A, Fauzi MH, Pimenta LP, Millar JE, Fanning JP, Van Haren F, Anstey CM, Cullen L, Suen J, Shekar K, Maitland</p>



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	<p>K, Fraser JF. Pre-clinical study protocol: Blood transfusion in endotoxaemic shock. <i>MethodsX</i>. 2019 May 9;6:1124-1132.</p> <p>Abstract</p> <p>The Surviving Sepsis Campaign (SCC) and the American College of Critical Care Medicine (ACCM) guidelines recommend blood transfusion in sepsis when the haemoglobin concentration drops below 7.0 g/dL and 10.0 g/dL respectively, while the World Health Organisation (WHO) guideline recommends transfusion in septic shock 'if intravenous (IV) fluids do not maintain adequate circulation', as a supportive measure of last resort. Volume expansion using crystalloid and colloid fluid boluses for haemodynamic resuscitation in severe illness/sepsis, has been associated with adverse outcomes in recent literature. However, the volume expansion effect(s) following blood transfusion for haemodynamic circulatory support, in severe illness remain unclear with most previous studies having focused on evaluating effects of either different RBC storage durations (short versus long duration) or haemoglobin thresholds (low versus high threshold) pre-transfusion. •We describe the protocol for a pre-clinical randomised controlled trial designed to examine haemodynamic effect(s) of early volume expansion using packed RBCs (PRBCs) transfusion (before any crystalloids or colloids) in a validated ovine-model of hyperdynamic endotoxaemic shock. •Additional exploration of mechanisms underlying any physiological, haemodynamic, haematological, immunologic and tissue specific-effects of blood transfusion will be undertaken including comparison of effects of short (≤ 5 days) versus long (≥ 30 days) storage duration of PRBCs prior to transfusion.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31193460/</p>
32.	<p>Omondi WP, Owino EA, Odongo D, Mwangangi JM, Torto B, Tchouassi DP. Differential response to plant- and human-derived odorants in field surveillance of the dengue vector, <i>Aedes aegypti</i>. <i>Acta Trop</i>. 2019 Dec;200:105163.</p> <p>Abstract</p> <p>Linalool oxide (LO) and hexanoic acid (HA) represent plant- and human-derived odorants, respectively, previously found as attractants for the dengue vector <i>Aedes aegypti</i>. Here, we investigated if a blend of both compounds can improve captures of this mosquito species in field trials in two dengue endemic sites, Kilifi and Busia Counties in Kenya. <i>Ae. aegypti</i> captures were significantly higher in Kilifi than Busia ($\chi^2_{1,142} = 170.63, P < 0.0001$) and varied by treatments ($\chi^2_{25,137} = 151.19, P = 0.002$). We found that CO₂-baited BG Sentinel traps combined with a blend of both odorants decreased <i>Ae. aegypti</i> captures about 2- to 4-fold compared to captures with the individual compounds (LO or HA) used as positive controls. This was the case for all blends of LO and HA, irrespective of the doses tested. Our findings indicate that combining plant- and human-derived odors may elicit a masking effect in trapping <i>Ae. aegypti</i>. These results partly corroborate previous findings for malaria mosquitoes which showed that combining lures from both host sources either decreases or increases trap catches depending on the dose.</p>



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	<p>Further investigations in the usefulness of combining plant and animal odorants in mosquito trapping are therefore necessary. Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31494122/</p>
33.	<p>Barsosio HC, Gitonga JN, Karanja HK, Nyamwaya DK, Omuoyo DO, Kamau E, Hamaluba MM, Nyiro JU, Kitsao BS, Nyaguara A, Mwakio S, Newton CR, Sang R, Wright D, Sanders EJ, Seale AC, Agoti CN, Berkley JA, Bejon P, Warimwe GM. Congenital microcephaly unrelated to flavivirus exposure in coastal Kenya. <i>Wellcome Open Res.</i> 2019 Nov 15;4:179. Abstract Background: Zika virus (ZIKV) was first discovered in East Africa in 1947. ZIKV has caused microcephaly in the Americas, but it is not known whether ZIKV is a cause of microcephaly in East Africa. Methods: We used surveillance data from 11,061 live births at Kilifi County Hospital in coastal Kenya between January 2012 and October 2016 to identify microcephaly cases and conducted a nested case-control study to determine risk factors for microcephaly. Gestational age at birth was estimated based on antenatal ultrasound scanning ('Scanned cohort') or last menstrual period ('LMP cohort', including births ≥ 37 weeks' gestation only). Controls were newborns with head circumference Z scores between >-2 and ≤ 2 SD that were compared to microcephaly cases in relation to ZIKV exposure and other maternal and newborn factors. Results: Of the 11,061 newborns, 214 (1.9%, 95%CI 1.69, 2.21) had microcephaly. Microcephaly prevalence was 1.0% (95%CI 0.64, 1.70, n=1529) and 2.1% (95%CI 1.81, 2.38, n=9532) in the scanned and LMP cohorts, respectively. After excluding babies < 2500 g (n=1199) in the LMP cohort the prevalence was 1.1% (95%CI 0.93, 1.39). Microcephaly showed an association with being born small for gestational age ($p < 0.001$) but not with ZIKV neutralising antibodies ($p = 0.6$) or anti-ZIKV NS1 IgM response ($p = 0.9$). No samples had a ZIKV neutralising antibody titre that was at least fourfold higher than the corresponding dengue virus (DENV) titre. No ZIKV or other flavivirus RNA was detected in cord blood from cases or controls. Conclusions: Microcephaly was prevalent in coastal Kenya, but does not appear to be related to ZIKV exposure; the ZIKV response observed in our study population was largely due to cross-reactive responses to DENV or other related flaviviruses. Further research into potential causes and the clinical consequences of microcephaly in this population is urgently needed. Pubmed link- https://pubmed.ncbi.nlm.nih.gov/32175480/</p>
34.	<p>Emukule GO, Ndegwa LK, Washington ML, Paget JW, Duque J, Chaves SS, Otieno NA, Wamburu K, Ndigirigi IW, Muthoka PM, van der Velden K, Mott JA. The cost of influenza-associated hospitalizations and outpatient visits in Kenya. <i>BMC Public Health.</i> 2019 May 10;19(Suppl 3):471. Abstract Background: We estimated the cost-per-episode and the annual economic burden associated with influenza in Kenya.</p>



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	<p>Methods: From July 2013-August 2014, we recruited patients with severe acute respiratory illness (SARI) or influenza-like illness (ILI) associated with laboratory-confirmed influenza from 5 health facilities. A structured questionnaire was used to collect direct costs (medications, laboratory investigations, hospital bed fees, hospital management costs, transportation) and indirect costs (productivity losses) associated with an episode of influenza. We used published incidence of laboratory-confirmed influenza associated with SARI and ILI, and the national population census data from 2014, to estimate the annual national number of influenza-associated hospitalizations and outpatient visits and calculated the annual economic burden by multiplying cases by the mean cost.</p> <p>Results: We enrolled 275 patients (105 inpatients and 170 outpatients). The mean cost-per-episode of influenza was US\$117.86 (standard deviation [SD], 88.04) among inpatients; US\$114.25 (SD, 90.03) for children < 5 years, and US\$137.45 (SD, 76.24) for persons aged ≥ 5 years. Among outpatients, the mean cost-per-episode of influenza was US\$19.82 (SD, 27.29); US\$21.49 (SD, 31.42) for children < 5 years, and US\$16.79 (SD, 17.30) for persons aged ≥ 5 years. National annual influenza-associated cost estimates ranged from US\$2.96-5.37 million for inpatients and US\$5.96-26.35 million for outpatients.</p> <p>Conclusions: Our findings highlight influenza as causing substantial economic burden in Kenya. Further studies may be warranted to assess the potential benefit of targeted influenza vaccination strategies.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/32326937/</p>
35.	<p>Kombe IK, Munywoki PK, Baguelin M, Nokes DJ, Medley GF. Model-based estimates of transmission of respiratory syncytial virus within households. <i>Epidemics</i>. 2019 Jun;27:1-11.</p> <p>Abstract</p> <p>Introduction: Respiratory syncytial virus (RSV) causes a significant respiratory disease burden in the under 5 population. The transmission pathway to young children is not fully quantified in low-income settings, and this information is required to design interventions.</p> <p>Methods: We used an individual level transmission model to infer transmission parameters using data collected from 493 individuals distributed across 47 households over a period of 6 months spanning the 2009/2010 RSV season. A total of 208 episodes of RSV were observed from 179 individuals. We model competing transmission risk from within household exposure and community exposure while making a distinction between RSV groups A and B.</p> <p>Results: We find that 32-53% of all RSV transmissions are between members of the same household; the rate of pair-wise transmission is 58% (95% CrI: 30-74%) lower in larger households (≥ 8 occupants) than smaller households; symptomatic individuals are 2-7 times more infectious than asymptomatic individuals i.e. 2.48 (95% CrI: 1.22-5.57)</p>



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	<p>among symptomatic individuals with low viral load and 6.7(95% CrI: 2.56-16) among symptomatic individuals with high viral load; previous infection reduces susceptibility to re-infection within the same epidemic by 47% (95% CrI: 17%-68%) for homologous RSV group and 39% (95%CrI: -8%-69%) for heterologous group; RSV B is more frequently introduced into the household, and RSV A is more rapidly transmitted once in the household.</p> <p>Discussion: Our analysis presents the first transmission modelling of cohort data for RSV and we find that it is important to consider the household social structuring and household size when modelling transmission. The increased infectiousness of symptomatic individuals implies that a vaccine against RSV related disease would also have an impact on infection transmission. Together, the weak cross immunity between RSV groups and the possibility of different transmission niches could form part of the explanation for the group co-existence.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30591267/</p>
36.	<p>Seale AC, Baker CJ, Berkley JA, Madhi SA, Ordi J, Saha SK, Schrag SJ, Sobanjo-Ter Meulen A, Vekemans J. Vaccines for maternal immunization against Group B Streptococcus disease: WHO perspectives on case ascertainment and case definitions. <i>Vaccine</i>. 2019 Aug 14;37(35):4877-4885.</p> <p>Abstract</p> <p>Group B Streptococcus (GBS) is an important cause of disease in young infants, stillbirths, pregnant and post-partum women. GBS vaccines for maternal immunization are in development aiming to reduce this burden. Standardisation of case definitions and ascertainment methodologies for GBS disease is needed to support future trials of maternal GBS vaccines. Considerations presented here may also serve to promote consistency in observational studies and surveillance, to better establish disease burden. The World Health Organization convened a working group to provide consensus guidance for case ascertainment and case definitions of GBS disease in stillbirths, infants, pregnant and post-partum women, with feedback sought from external stakeholders. In intervention studies, case capture and case ascertainment for GBS disease should be based on antenatal recruitment of women, with active follow-up, systematic clinical assessment, standardised sampling strategies and optimised laboratory methods. Confirmed cases of invasive GBS disease in stillbirths or infants should be included in a primary composite endpoint for vaccine efficacy studies, with GBS cultured from a usually sterile body site (may be post-mortem). For additional endpoints, or observational studies, confirmed cases of GBS sepsis in pregnant and post-partum women should be assessed. Culture independent diagnostic tests (CIDTs) may detect additional presumed cases, however, the use of these diagnostics needs further evaluation. Efficacy of vaccination against maternal and neonatal GBS colonisation, and maternal GBS urinary tract infection could be included as additional, separate, endpoints and/or in observational studies. Whilst the focus here is on specific GBS disease outcomes, intervention studies</p>



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	<p>also present an opportunity to establish the contribution of GBS across adverse perinatal outcomes, including all-cause stillbirth, preterm birth and neonatal encephalopathy. Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31303524/</p>
37.	<p>Maia MF, Kapulu M, Muthui M, Wagah MG, Ferguson HM, Dowell FE, Baldini F, Ranford-Cartwright L. Detection of Plasmodium falciparum infected Anopheles gambiae using near-infrared spectroscopy. Malar J. 2019 Mar 19;18(1):85. Abstract Background: Large-scale surveillance of mosquito populations is crucial to assess the intensity of vector-borne disease transmission and the impact of control interventions. However, there is a lack of accurate, cost-effective and high-throughput tools for mass-screening of vectors. Methods: A total of 750 Anopheles gambiae (Keele strain) mosquitoes were fed Plasmodium falciparum NF54 gametocytes through standard membrane feeding assay (SMFA) and afterwards maintained in insectary conditions to allow for oocyst (8 days) and sporozoite development (14 days). Thereupon, each mosquito was scanned using near infra-red spectroscopy (NIRS) and processed by quantitative polymerase chain reaction (qPCR) to determine the presence of infection and infection load. The spectra collected were randomly assigned to either a training dataset, used to develop calibrations for predicting oocyst- or sporozoite-infection through partial least square regressions (PLS); or to a test dataset, used for validating the calibration's prediction accuracy. Results: NIRS detected oocyst- and sporozoite-stage P. falciparum infections with 88% and 95% accuracy, respectively. This study demonstrates proof-of-concept that NIRS is capable of rapidly identifying laboratory strains of human malaria infection in African mosquito vectors. Conclusions: Accurate, low-cost, reagent-free screening of mosquito populations enabled by NIRS could revolutionize surveillance and elimination strategies for the most important human malaria parasite in its primary African vector species. Further research is needed to evaluate how the method performs in the field following adjustments in the training datasets to include data from wild-caught infected and uninfected mosquitoes. Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30890179/</p>
38.	<p>Ogola EO, Odero JO, Mwangangi JM, Masiga DK, Tchouassi DP. Population genetics of Anopheles funestus, the African malaria vector, Kenya. Parasit Vectors. 2019 Jan 8;12(1):15. Abstract Background: Anopheles funestus is among the major malaria vectors in Kenya and sub-Saharan Africa and has been recently implicated in persistent malaria transmission. However, its ecology and genetic diversity remain poorly understood in Kenya. Methods: Using 16 microsatellite loci, we examined the genetic structure of An. funestus sampled from 11 locations (n = 426 individuals) across a wide geographical range in Kenya spanning coastal, western and Rift Valley areas.</p>



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	<p>Results: Kenyan <i>An. funestus</i> resolved as three genetically distinct clusters. The largest cluster (FUN1) broadly included samples from western and Rift Valley areas of Kenya with two clusters identified from coastal Kenya (FUN2 and FUN3), not previously reported. Geographical distance had no effect on population differentiation of <i>An. funestus</i>. We found a significant variation in the mean <i>Plasmodium</i> infectivity between the clusters ($\chi^2 = 12.1$, $df = 2$, $P = 0.002$) and proportional to the malaria prevalence in the different risk zones of Kenya. Notably, there was variation in estimated effective population sizes between the clusters, suggesting possible differential impact of anti-vector interventions in represented areas.</p> <p>Conclusions: Heterogeneity among Kenyan populations of <i>An. funestus</i> will impact malaria vector control with practical implications for the development of gene-drive technologies. The difference in <i>Plasmodium</i> infectivity and effective population size between the clusters could suggest potential variation in phenotypic characteristics relating to competence or insecticide resistance. This is worth examining in future studies.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30621756/</p>
39.	<p>Talbert A, Ngari M, Bauni E, Mwangome M, Mturi N, Otiende M, Maitland K, Walson J, Berkley JA. Mortality after inpatient treatment for diarrhea in children: a cohort study. <i>BMC Med.</i> 2019 Jan 28;17(1):20.</p> <p>Abstract</p> <p>Background: There is an increasing recognition that children remain at elevated risk of death following discharge from health facilities in resource-poor settings. Diarrhea has previously been highlighted as a risk factor for post-discharge mortality.</p> <p>Methods: A retrospective cohort study was conducted to estimate the incidence and demographic, clinical, and biochemical features associated with inpatient and 1-year post-discharge mortality amongst children aged 2-59 months admitted with diarrhea from 2007 to 2015 at Kilifi County Hospital and who were residents of Kilifi Health and Demographic Surveillance System (KHDSS). Log-binomial regression was used to identify risk factors for inpatient mortality. Time at risk was from the date of discharge to the date of death, out-migration, or 365 days later. Post-discharge mortality rate was computed per 1000 child-years of observation, and Cox proportion regression used to identify risk factors for mortality.</p> <p>Results: Two thousand six hundred twenty-six child KHDSS residents were admitted with diarrhea, median age 13 (IQR 8-21) months, of which 415 (16%) were severely malnourished and 130 (5.0%) had a positive HIV test. One hundred twenty-one (4.6%) died in the hospital, and of 2505 children discharged alive, 49 (2.1%) died after discharge: 21.4 (95% CI 16.1-28.3) deaths per 1000 child-years. Admission with signs of both diarrhea and severe pneumonia or severe pneumonia alone had a higher risk of both inpatient and post-discharge mortality than admission for diarrhea alone. There was no significant difference in inpatient and post-discharge mortality between children admitted with diarrhea alone and those with other diagnoses excluding severe pneumonia. HIV,</p>



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	<p>low mid-upper arm circumference (MUAC), and bacteremia were associated with both inpatient and post-discharge mortality. Signs of circulatory impairment, sepsis, and abnormal electrolytes were associated with inpatient but not post-discharge mortality. Prior admission and lower chest wall indrawing were associated with post-discharge mortality but not inpatient mortality. Age, stuntedness, and persistent or bloody diarrhea were not associated with mortality before or after discharge.</p> <p>Conclusions: Our results accentuate the need for research to improve the uptake and outcomes of services for malnutrition and HIV as well as to elucidate causal pathways and test interventions to mitigate these risks.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30686268/</p>
40.	<p>Njunge JM, Gwela A, Kibinge NK, Ngari M, Nyamako L, Nyatichi E, Thitiri J, Gonzales GB, Bandsma RHJ, Walson JL, Gitau EN, Berkley JA. Biomarkers of post- discharge mortality among children with complicated severe acute malnutrition. <i>Sci Rep.</i> 2019 Apr 12;9(1):5981.</p> <p>Abstract</p> <p>Background: There is an increasing recognition that children remain at elevated risk of death following discharge from health facilities in resource-poor settings. Diarrhea has previously been highlighted as a risk factor for post-discharge mortality.</p> <p>Methods: A retrospective cohort study was conducted to estimate the incidence and demographic, clinical, and biochemical features associated with inpatient and 1-year post-discharge mortality amongst children aged 2-59 months admitted with diarrhea from 2007 to 2015 at Kilifi County Hospital and who were residents of Kilifi Health and Demographic Surveillance System (KHDSS). Log-binomial regression was used to identify risk factors for inpatient mortality. Time at risk was from the date of discharge to the date of death, out-migration, or 365 days later. Post-discharge mortality rate was computed per 1000 child-years of observation, and Cox proportion regression used to identify risk factors for mortality.</p> <p>Results: Two thousand six hundred twenty-six child KHDSS residents were admitted with diarrhea, median age 13 (IQR 8-21) months, of which 415 (16%) were severely malnourished and 130 (5.0%) had a positive HIV test. One hundred twenty-one (4.6%) died in the hospital, and of 2505 children discharged alive, 49 (2.1%) died after discharge: 21.4 (95% CI 16.1-28.3) deaths per 1000 child-years. Admission with signs of both diarrhea and severe pneumonia or severe pneumonia alone had a higher risk of both inpatient and post-discharge mortality than admission for diarrhea alone. There was no significant difference in inpatient and post-discharge mortality between children admitted with diarrhea alone and those with other diagnoses excluding severe pneumonia. HIV, low mid-upper arm circumference (MUAC), and bacteremia were associated with both inpatient and post-discharge mortality. Signs of circulatory impairment, sepsis, and abnormal electrolytes were associated with inpatient but not post-discharge mortality. Prior admission and lower chest wall indrawing were associated with post-discharge</p>



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	<p>mortality but not inpatient mortality. Age, stuntedness, and persistent or bloody diarrhea were not associated with mortality before or after discharge.</p> <p>Conclusions: Our results accentuate the need for research to improve the uptake and outcomes of services for malnutrition and HIV as well as to elucidate causal pathways and test interventions to mitigate these risks.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30686268/</p>
41.	<p>Khayeka-Wandabwa C, Zhou G, Magak NG, Choge JK, Kemei WK, Makwali JA, Karani LW, Kisavi MP, Ndulu JV, Anjili CO. Combined chemotherapy manifest less severe immunopathology effects in helminth-protozoa comorbidity. <i>Exp Parasitol</i>. 2019 Sep;204:107728.</p> <p>Abstract</p> <p>Background: Co-infection with <i>Leishmania major</i> and <i>Schistosoma mansoni</i> may have significant consequences for disease progression, severity and subsequent transmission dynamics. Pentavalent antimonials and Praziquantel (PZQ) are used as first line of treatment for <i>Leishmania</i> and <i>Schistosoma</i> infections respectively. However, there is limited insight on how combined therapy with the standard drugs impacts the host in comorbidity. The study aimed to determine the efficacy of combined chemotherapy using Pentostam (P) and PZQ in murine model co-infected with <i>L. major</i> and <i>S. mansoni</i>.</p> <p>Methods: A 3 × 4 factorial design with three parasite infection groups (<i>Lm</i>, <i>Sm</i>, <i>Lm + Sm</i> to represent <i>L. major</i>, <i>S. mansoni</i> and <i>L. major + S. mansoni</i> respectively) and four treatment regimens [P, PZQ, P + PZQ, and PBS designating Pentostam (GlaxoSmithKline UK), Praziquantel (Biltricide®, Bayer Ag. Leverkusen, Germany), Pentostam + Praziquantel and Phosphate buffered saline] as factors was applied.</p> <p>Results: Significant changes were observed in the serum Interferon gamma (IFN-γ), and Macrophage inflammatory protein-one alpha (MIP-1α) levels among various treatment groups between week 8 and week 10 ($p < 0.05$). There was increased IFN-γ in the <i>L. major</i> infected mice subjected to PZQ and PBS, and in <i>L. major + S. mansoni</i> infected BALB/c mice treated with P + PZQ. Subsequently, MIP-1α levels increased significantly in both the <i>L. major</i> infected mice under PZQ and PBS and in <i>L. major + S. mansoni</i> infected BALB/c mice undergoing concurrent chemotherapy with P + PZQ between 8 and 10 weeks ($p < 0.05$). In the comorbidity, simultaneous chemotherapy resulted in less severe histopathological effects in the liver.</p> <p>Conclusion: It was evident, combined first line of treatment is a more effective strategy in managing co-infection of <i>L. major</i> and <i>S. mansoni</i>. The findings denote simultaneous chemotherapy compliments immunomodulation in the helminth-protozoa comorbidity hence, less severe pathological effects following the parasites infection. Recent cases of increased incidences of polyparasitism in vertebrates call for better ways to manage co-infections. The findings presented necessitate intrinsic biological interest on examining optimal combined chemotherapeutic agents strategies in helminth-protozoa concomitance and the related infections abatement trends vis-a-vis host-parasite relationships.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31348915/</p>



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42.	<p>Njuguna P, Maitland K, Nyaguara A, Mwanga D, Mogeni P, Mturi N, Mohammed S, Mwambingu G, Ngetsu C, Awuondo K, Lowe B, Adetifa I, Scott JAG, Williams TN, Atkinson S, Osier F, Snow RW, Marsh K, Tsofa B, Peshu N, Hamaluba M, Berkley JA, Newton CRJ, Fondo J, Omar A, Bejon P. Observational study: 27 years of severe malaria surveillance in Kilifi, Kenya. <i>BMC Med.</i> 2019 Jul 8;17(1):124.</p> <p>Abstract</p> <p>Background: Many parts of Africa have witnessed reductions in <i>Plasmodium falciparum</i> transmission over the last 15 years. Since immunity to malaria is acquired more rapidly at higher transmission, the slower acquisition of immunity at lower transmission may partially offset the benefits of reductions in transmission. We examined the clinical spectrum of disease and predictors of mortality after sustained changes in transmission intensity, using data collected from 1989 to 2016.</p> <p>Methods: We conducted a temporal observational analysis of 18,000 children, aged 14 days to 14 years old, who were admitted to Kilifi County Hospital, Kenya, from 1989 to 2016 with malaria. We describe the trends over time of the clinical and laboratory criteria for severe malaria and associated risk of mortality.</p> <p>Results: During the time periods 1989-2003, 2004-2008, and 2009-2016, Kilifi County Hospital admitted averages of 657, 310, and 174 cases of severe malaria per year including averages of 48, 14, and 12 malaria-associated deaths per year, respectively. The median ages in years of children admitted with cerebral malaria, severe anaemia, and malaria-associated mortality were 3.0 (95% confidence interval (CI) 2.2-3.9), 1.1 (95% CI 0.9-1.4), and 1.1 (95% CI 0.3-2.2) in the year 1989, rising to 4.9 (95% CI 3.9-5.9), 3.8 (95% CI 2.5-7.1), and 5 (95% CI 3.3-6.3) in the year 2016. The ratio of children with cerebral malaria to severe anaemia rose from 1:2 before 2004 to 3:2 after 2009. Hyperparasitaemia was a risk factor for death after 2009 but not in earlier time periods.</p> <p>Conclusion: Despite the evidence of slower acquisition of immunity, continued reductions in the numbers of cases of severe malaria resulted in lower overall mortality. Our temporal data are limited to a single site, albeit potentially applicable to a secular trend present in many parts of Africa.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31280724/</p>
43.	<p>Denckla CA, Ongeru L, Ouma L, Singa B, Maingi C, Bosire R, Otieno P, Omolo D, Henderson DC, Chibnik LB, Koenen KC, Manduku V. Prevalence of parental bereavement among female sex workers (FSW) in Kibra, Kenya. <i>J Loss Trauma.</i> 2019;24(2):129-142.</p> <p>Abstract</p> <p>Female sex workers (FSW) residing in Kibra, Kenya experience elevated exposure to adverse events, yet the prevalence of parental bereavement is not well characterized. This cross-sectional pilot study on 301 FSWs residing in Kibra, Kenya found that 67.7% of these women were parentally bereaved. Significantly fewer parentally bereaved women reported historical use of condoms and emergency contraception compared to non-bereaved women, and older age of paternal bereavement was significantly associated with</p>



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	<p>current contraceptive use. Prevalence rates of bereavement among this cohort are well over the national Kenyan average, and further research on the specific impact of bereavement is warranted.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31598099/</p>
44.	<p>Kamau E, Agoti CN, Ngoi JM, de Laurent ZR, Gitonga J, Cotten M, Phan MVT, Nokes DJ, Delwart E, Sanders E, Warimwe GM. Complete Genome Sequences of Dengue Virus Type 2 Strains from Kilifi, Kenya. <i>Microbiol Resour Announc</i>. 2019 Jan 24;8(4):e01566-18.</p> <p>Abstract</p> <p>Dengue infection remains poorly characterized in Africa and little is known regarding its associated viral genetic diversity. Here, we report dengue virus type 2 (DENV-2) sequence data from 10 clinical samples, including 5 complete genome sequences of the cosmopolitan genotype, obtained from febrile adults seeking outpatient care in coastal Kenya.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30701251/</p>
45.	<p>Tusting LS, Bisanzio D, Alabaster G, Cameron E, Cibulskis R, Davies M, Flaxman S, Gibson HS, Knudsen J, Mbogo C, Okumu FO, von Seidlein L, Weiss DJ, Lindsay SW, Gething PW, Bhatt S. Mapping changes in housing in sub-Saharan Africa from 2000 to 2015. <i>Nature</i>. 2019 Apr;568(7752):391-394.</p> <p>Abstract</p> <p>Access to adequate housing is a fundamental human right, essential to human security, nutrition and health, and a core objective of the United Nations Sustainable Development Goals^{1,2}. Globally, the housing need is most acute in Africa, where the population will more than double by 2050. However, existing data on housing quality across Africa are limited primarily to urban areas and are mostly recorded at the national level. Here we quantify changes in housing in sub-Saharan Africa from 2000 to 2015 by combining national survey data within a geostatistical framework. We show a marked transformation of housing in urban and rural sub-Saharan Africa between 2000 and 2015, with the prevalence of improved housing (with improved water and sanitation, sufficient living area and durable construction) doubling from 11% (95% confidence interval, 10-12%) to 23% (21-25%). However, 53 (50-57) million urban Africans (47% (44-50%) of the urban population analysed) were living in unimproved housing in 2015. We provide high-resolution, standardized estimates of housing conditions across sub-Saharan Africa. Our maps provide a baseline for measuring change and a mechanism to guide interventions during the era of the Sustainable Development Goals.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30918405/</p>
46.	<p>Malinga J, Maia M, Moore S, Ross A. Can trials of spatial repellents be used to estimate mosquito movement? <i>Parasit Vectors</i>. 2019 Sep 3;12(1):421.</p> <p>Abstract</p> <p>Background: Knowledge of mosquito movement would aid the design of effective intervention strategies against malaria. However, data on mosquito movement through</p>



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	<p>mark-recapture or genetics studies are challenging to collect, and so are not available for many sites. An additional source of information may come from secondary analyses of data from trials of repellents where household mosquito densities are collected. Using the study design of published trials, we developed a statistical model which can be used to estimate the movement between houses for mosquitoes displaced by a spatial repellent. The method uses information on the different distributions of mosquitoes between houses when no households are using spatial repellents compared to when there is incomplete coverage. The parameters to be estimated are the proportion of mosquitoes repelled, the proportion of those repelled that go to another house and the mean distance of movement between houses. Estimation is by maximum likelihood.</p> <p>Results: We evaluated the method using simulation and found that data on the seasonal pattern of mosquito densities were required, which could be additionally collected during a trial. The method was able to provide accurate estimates from simulated data, except when the setting has few mosquitoes overall, few repelled, or the coverage with spatial repellent is low. The trial that motivated our analysis was found to have too few mosquitoes caught and repelled for our method to provide accurate results.</p> <p>Conclusions: We propose that the method could be used as a secondary analysis of trial data to gain estimates of mosquito movement in the presence of repellents for trials with sufficient numbers of mosquitoes caught and repelled and with coverage levels which allow sufficient numbers of houses with and without repellent. Estimates from this method may supplement those from mark-release-recapture studies, and be used in designing effective malaria intervention strategies, parameterizing mathematical models and in designing trials of vector control interventions.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31477155/</p>
47.	<p>Muriuki JM, Mentzer AJ, Band G, Gilchrist JJ, Carstensen T, Lule SA, Goheen MM, Joof F, Kimita W, Mogire R, Cutland CL, Diarra A, Rautanen A, Pomilla C, Gurdasani D, Rockett K, Mturi N, Ndungu FM, Scott JAG, Sirima SB, Morovat A, Prentice AM, Madhi SA, Webb EL, Elliott AM, Bejon P, Sandhu MS, Hill AVS, Kwiatkowski DP, Williams TN, Cerami C, Atkinson SH. The ferroportin Q248H mutation protects from anemia, but not malaria or bacteremia. <i>Sci Adv.</i> 2019 Sep 4;5(9):eaaw0109.</p> <p>Abstract</p> <p>Iron acquisition is critical for life. Ferroportin (FPN) exports iron from mature erythrocytes, and deletion of the Fpn gene results in hemolytic anemia and increased fatality in malaria-infected mice. The FPN Q248H mutation (glutamine to histidine at position 248) renders FPN partially resistant to hepcidin-induced degradation and was associated with protection from malaria in human studies of limited size. Using data from cohorts including over 18,000 African children, we show that the Q248H mutation is associated with modest protection against anemia, hemolysis, and iron deficiency, but we found little evidence of protection against severe malaria or bacteremia. We additionally observed no excess Plasmodium growth in Q248H erythrocytes ex vivo, nor evidence of</p>



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	<p>selection driven by malaria exposure, suggesting that the Q248H mutation does not protect from malaria and is unlikely to deprive malaria parasites of iron essential for their growth.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31517041/</p>
48.	<p>Pyra MN, Haberer JE, Hasen N, Reed J, Mugo NR, Baeten JM. Global implementation of PrEP for HIV prevention: setting expectations for impact. <i>J Int AIDS Soc.</i> 2019 Aug;22(8):e25370.</p> <p>Abstract</p> <p>Introduction: Questions remain whether HIV pre-exposure prophylaxis (PrEP) can be translated into a successful public health intervention, leading to a decrease in population-level HIV incidence. We use examples from HIV treatment and contraceptives to discuss expectations for PrEP uptake, adherence, and persistence and their combined impact on the epidemic.</p> <p>Discussion: Targets for PrEP uptake must be based on the local HIV epidemic and will depend on appropriate estimates of the key populations at risk for HIV. However, there is evidence that targets, once established, can successfully be met and that uptake may increase with awareness. Messaging around adherence should include that daily adherence is the goal (except for those MSM for whom event-driven dosing is a good fit), but perfect adherence should not be a barrier. Ideally, clients persist on PrEP for as long as they are at risk for HIV. While PrEP will be most effective when coverage is focused on high-risk populations, normalizing rather than stigmatizing PrEP will be highly beneficial.</p> <p>Conclusions: While many challenges to PrEP implementation exist, we focused on the three key steps of uptake, adherence and persistence as measurable processes that can lead to improved coverage and decreased HIV incidence.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31456348/</p>
49.	<p>Kamau E, Luka MM, de Laurent ZR, Adema I, Agoti CN, Nokes DJ. Genome Sequences of Human Coronavirus OC43 and NL63, Associated with Respiratory Infections in Kilifi, Kenya. <i>Microbiol Resour Announc.</i> 2019 Nov 14;8(46):e00730-19.</p> <p>Abstract</p> <p>Coding-complete genomes of two human coronavirus OC43 strains and one NL63 strain were obtained by metagenomic sequencing of clinical samples collected in 2017 and 2018 in Kilifi, Kenya. Maximum likelihood phylogenies showed that the OC43 strains were genetically dissimilar and that the NL63 strain was closely related to NL63 genotype B viruses.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31727697/</p>
50.	<p>Cook J, Owaga C, Marube E, Baidjoe A, Stresman G, Migiro R, Cox J, Drakeley C, Stevenson JC. Risk factors for <i>Plasmodium falciparum</i> infection in the Kenyan Highlands: a cohort study. <i>Trans R Soc Trop Med Hyg.</i> 2019 Mar 1;113(3):152-159.</p> <p>Abstract</p>



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	<p>Background: Malaria transmission in African highland areas can be prone to epidemics, with minor fluctuations in temperature or altitude resulting in highly heterogeneous transmission. In the Kenyan Highlands, where malaria prevalence has been increasing, characterising malaria incidence and identifying risk factors for infection is complicated by asymptomatic infection.</p> <p>Methods: This all-age cohort study, one element of the Malaria Transmission Consortium, involved monthly follow-up of 3155 residents of the Kisii and Rachuonyo South districts during June 2009-June 2010. Participants were tested for malaria using rapid diagnostic testing at every visit, regardless of symptoms.</p> <p>Results: The incidence of Plasmodium falciparum infection was 0.2 cases per person, although infections were clustered within individuals and over time, with the majority of infections detected in the last month of the cohort study. Overall, incidence was higher in the Rachuonyo district and infections were detected most frequently in 5-10-year-olds. The majority of infections were asymptomatic (58%). Travel away from the study area was a notable risk factor for infection.</p> <p>Conclusions: Identifying risk factors for malaria infection can help to guide targeting of interventions to populations most likely to be exposed to malaria.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30496556/</p>
51.	<p>Karuitha M, Bargul J, Lutomiah J, Muriu S, Nzovu J, Sang R, Mwangangi J, Mbogo C. Larval habitat diversity and mosquito species distribution along the coast of Kenya. Wellcome Open Res. 2019 Nov 13;4:175.</p> <p>Abstract</p> <p>Background: Management of arboviruses relies heavily on vector control. Implementation and sustenance of effective control measures requires regular surveillance of mosquito occurrences, species abundance and distribution. The current study evaluated larval habitat diversity and productivity, mosquito species diversity and distribution in selected sites along the coast of Kenya. Methods: A cross-sectional survey of mosquito breeding habitats, species diversity and distribution was conducted in urban, peri-urban and forested ecological zones in Mombasa and Kilifi counties. Results: A total of 13,009 immature mosquitoes were collected from 17 diverse aquatic habitats along the coast of Kenya. Larval productivity differed significantly ($F(16, 243) = 3.21, P < 0.0001$) among the aquatic habitats, with tyre habitats recording the highest larval population. <i>Culex pipiens</i> (50.17%) and <i>Aedes aegypti</i> (38.73%) were the dominant mosquito species in urban areas, while <i>Ae. vittatus</i> (89%) was the dominant species in forested areas. In total, 4,735 adult mosquitoes belonging to 19 species were collected in Haller Park, Bamburi, Gede and Arabuko Sokoke forest. Urban areas supported higher densities of <i>Ae. aegypti</i> compared to peri-urban and forest areas, which, on the other hand, supported greater mosquito species diversity. Conclusions: High <i>Ae. aegypti</i> production in urban and peri-urban areas present a greater risk of arbovirus outbreaks. Targeting productive habitats of <i>Aedes aegypti</i>, such as discarded tyres, containers and poorly maintained drainage systems in urban areas and preventing human-vector contact in peri-urban and</p>



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	<p>forested areas could have a significant impact on the prevalence of arboviruses along the coast of Kenya, forestalling the periodic outbreaks experienced in the region. Pubmed link- https://pubmed.ncbi.nlm.nih.gov/32509966/</p>
52.	<p>Maitland K, Ohuma EO, Mpoya A, Uyoga S, Hassall O, Williams TN. Informing thresholds for paediatric transfusion in Africa: the need for a trial. Wellcome Open Res. 2019 Aug 12;4:27. Abstract Background: Owing to inadequate supplies of donor blood for transfusion in sub-Saharan Africa (sSA) World Health Organization paediatric guidelines recommend transfusion practices, based on expert opinion. We examined whether survival amongst hospitalised children by admission haemoglobin and whether this was influenced by malaria infection and/or transfusion. Methods: A retrospective analysis of standardised clinical digital records in an unselected population of children admitted to a rural hospital in Kenya over an 8-year period. We describe baseline parameters with respect to categories of anaemia and outcome (in-hospital death) by haemoglobin (Hb), malaria and transfusion status. Results: Among 29,226 children, 1,143 (3.9%) had profound anaemia (Hb <4g/dl) and 3,469 (11.9%) had severe anaemia (Hb 4-6g/d). In-hospital mortality rate was 97/1,143 (8.5%) if Hb<4g/dl or 164/2,326 (7.1%) in those with severe anaemia (Hb ≥4.0-<6g/dl). Admission Hb <3g/dl was associated with higher risk of death versus those with higher Hbs (OR=2.41 (95%CI: 1.8 - 3.24; P<0.001), increasing to OR=6.36, (95%CI: 4.21-9.62; P<0.001) in malaria positive children. Conversely, mortality in non-malaria admissions was unrelated to Hb level. Transfusion was associated with a non-significant improvement in outcome if Hb<3g/dl (malaria-only) OR 0.72 (95%CI 0.29 - 1.78), albeit the number of cases were too few to show a statistical difference. For those with Hb levels above 4g/dl, mortality was significantly higher in those receiving a transfusion compared to the non-transfused group. For non-malarial cases, transfusion did not affect survival-status, irrespective of baseline Hb level compared to children who were not transfused at higher Hb levels. Conclusion: Although severe anaemia is common among children admitted to hospital in sSA (~16%), our data do not indicate that outcome is improved by transfusion irrespective of malaria status. Given the limitations of observational studies, clinical trials investigating the role of transfusion in outcomes in children with severe anaemia are warranted. Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31633055/</p>
53.	<p>Davies A, Mwangome N, Yeri B, Mwangi G, Mumba N, Marsh V, Kamuya D, Molyneux S, Kinyanjui S, Jones C. Evolution of a programme to engage school students with health research and science in Kenya. Wellcome Open Res. 2019 Feb 28;4:39. Abstract Facilitating mutually-beneficial educational activities between researchers and school students is an increasingly popular way for research institutes to engage with communities who host health research, but these activities have rarely been formally</p>



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	<p>examined as a community or public engagement approach in health research. The KEMRI-Wellcome Trust Research Programme (KWTRP) in Kilifi, Kenya, through a Participatory Action Research (PAR) approach involving students, teachers, researchers and education stakeholders, has incorporated 'school engagement' as a key component into their community engagement (CE) strategy. School engagement activities at KWTRP aim at strengthening the ethical practice of the institution in two ways: through promoting an interest in science and research among school students as a form of benefit-sharing; and through creating forums for dialogue aimed at promoting mutual understanding between researchers and school students. In this article, we provide a background of CE in Kilifi and describe the diverse ways in which health researchers have engaged with communities and schools in different parts of the world. We then describe the way in which the KWTRP school engagement programme (SEP) was developed and scaled-up. We conclude with a discussion about the challenges, benefits and lessons learnt from the SEP implementation and scale-up in Kilifi, which can inform the establishment of SEPs in other settings.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30906884/</p>
53.	<p>Smit MR, Ochomo EO, Waterhouse D, Kwambai TK, Abong'o BO, Bousema T, Bayoh NM, Ginnig JE, Samuels AM, Desai MR, Phillips-Howard PA, Kariuki SK, Wang D, Ter Kuile FO, Ward SA, Aljayoussi G. Pharmacokinetics-Pharmacodynamics of High-Dose Ivermectin with Dihydroartemisinin-Piperaquine on Mosquitocidal Activity and QT-Prolongation (IVERMAL). <i>Clin Pharmacol Ther.</i> 2019 Feb;105(2):388-401.</p> <p>Abstract High-dose ivermectin, co-administered for 3 days with dihydroartemisinin-piperaquine (DP), killed mosquitoes feeding on individuals for at least 28 days posttreatment in a recent trial (IVERMAL), whereas 7 days was predicted pretrial. The current study assessed the relationship between ivermectin blood concentrations and the observed mosquitocidal effects against <i>Anopheles gambiae</i> s.s. Three days of ivermectin 0, 300, or 600 mcg/kg/day plus DP was randomly assigned to 141 adults with uncomplicated malaria in Kenya. During 28 days of follow-up, 1,393 venous and 335 paired capillary plasma samples, 850 mosquito-cluster mortality rates, and 524 QTcF-intervals were collected. Using pharmacokinetic/pharmacodynamic (PK/PD) modeling, we show a consistent correlation between predicted ivermectin concentrations and observed mosquitocidal-effects throughout the 28-day study duration, without invoking an unidentified mosquitocidal metabolite or drug-drug interaction. Ivermectin had no effect on piperaquine's PKs or QTcF-prolongation. The PK/PD model can be used to design new treatment regimens with predicted mosquitocidal effect. This methodology could be used to evaluate effectiveness of other endectocides.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30125353/</p>
55.	<p>van den Berg M, Ogotu B, Sewankambo NK, Biller-Andorno N, Tanner M. RTS,S malaria vaccine pilot studies: addressing the human realities in large-scale clinical trials. <i>Trials.</i> 2019 May 31;20(1):316.</p>



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	<p>Abstract</p> <p>A malaria vaccine as part of the integrated malaria control and elimination efforts will have a major impact on public health in sub-Saharan Africa. The first malaria vaccine, RTS,S, now enters pilot implementation in three African countries. These pilot implementation studies are being initiated in Kenya, Malawi, and Ghana to inform the broader roll-out recommendation. Based on the malaria vaccine clinical trial experiences, key ethical practices for effective clinical trial research in low-resource settings are described. For successful vaccine integration into malaria intervention programs, the relational dynamics between researchers and trial communities must be made explicit. Incorporating community values and returning to research practices that serve the intended benefactors are key strategies that address the human realities in large-scale clinical trials and pilot implementation, leading to positive public health outcomes.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31151473/</p>
56.	<p>Oyando R, Njoroge M, Nguhiu P, Kirui F, Mbui J, Sigilai A, Bukania Z, Obala A, Munge K, Etyang A, Barasa E. Patient costs of hypertension care in public health care facilities in Kenya. <i>Int J Health Plann Manage.</i> 2019 Apr;34(2):e1166-e1178.</p> <p>Abstract</p> <p>Objective: To estimate the direct and indirect costs of diabetes mellitus care at five public health facilities in Kenya.</p> <p>Methods: We conducted a cross-sectional study in two counties where diabetes patients aged 18 years and above were interviewed. Data on care-seeking costs were obtained from 163 patients seeking diabetes care at five public facilities using the cost-of-illness approach. Medicines and user charges were classified as direct health care costs while expenses on transport, food, and accommodation were classified as direct non-health care costs. Productivity losses due to diabetes were classified as indirect costs. We computed annual direct and indirect costs borne by these patients.</p> <p>Results: More than half (57.7%) of sampled patients had hypertension comorbidity. Overall, the mean annual direct patient cost was KES 53 907 (95% CI, 43 625.4-64 188.6) (US\$ 528.5 [95% CI, 427.7-629.3]). Medicines accounted for 52.4%, transport 22.6%, user charges 17.5%, and food 7.5% of total direct costs. Overall mean annual indirect cost was KES 23 174 (95% CI, 20 910-25 438.8) (US\$ 227.2 [95% CI, 205-249.4]). Patients reporting hypertension comorbidity incurred higher costs compared with diabetes-only patients. The incidence of catastrophic costs was 63.1% (95% CI, 55.7-70.7) and increased to 75.4% (95% CI, 68.3-82.1) when transport costs were included.</p> <p>Conclusion: There are substantial direct and indirect costs borne by diabetic patients in seeking care from public facilities in Kenya. High incidence of catastrophic costs suggests diabetes services are unaffordable to majority of diabetic patients and illustrate the urgent need to improve financial risk protection to ensure access to care.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31621953/</p>



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57.	<p>Githang'a D, Anzala O, Mutegi C, Agweyu A. The effects of exposures to mycotoxins on immunity in children: A systematic review. <i>Curr Probl Pediatr Adolesc Health Care</i>. 2019 May;49(5):109-116.</p> <p>Abstract</p> <p>The majority of childhood deaths occur in low-income countries, with vaccine-preventable infections contributing greatly. Of the many possible environmental factors that could hamper a child's immune response, mycotoxins rank among the least studied in spite of the high exposure in vulnerable populations. Aflatoxin crosses the placenta, is secreted in breast milk and is consumed widely in weaning diets by children with developing organ systems. This review describes the effects of mycotoxin exposure on immunity in children that may contribute to sub-optimal vaccine effectiveness. We searched electronic databases and references of identified articles for relevant studies on the effects of mycotoxins on the immune system in children. Geographical location, publication year, study design, sample selection, sample size, mean age, route of exposure were extracted on a standard template. Quality was assessed using Joanna Briggs Institute tool for appraisal of systematic reviews for prevalence studies. Our analyses and reporting were conducted in accordance with the preferred reporting items for systematic reviews and meta-analyses (PRISMA) guidelines. Out of 806 articles screened, 5 observational studies met criteria for inclusion for review. The definition of exposures to mycotoxins and outcomes varied across the studies. Exposure to mycotoxins was positively associated with low birth weight and concentration of antibodies to asexual malaria parasites and hepatitis B surface antigen, and negatively associated with death and sIgA, antibodies to pneumococcal antigen 23. Despite the far-reaching clinical and public health effects of mycotoxin exposure among children, studies on the effects of mycotoxin exposure on immunity in children were few, small and mostly of low quality. There is an urgent need for carefully designed prospective studies in this neglected field to inform policy interventions for child health in settings where exposure to mycotoxins is high.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31126742/</p>
58.	<p>Uyoga S, Macharia AW, Ndila CM, Nyutu G, Shebe M, Awuondo KO, Mturi N, Peshu N, Tsofa B, Scott JAG, Maitland K, Williams TN. The indirect health effects of malaria estimated from health advantages of the sickle cell trait. <i>Nat Commun</i>. 2019 Feb 20;10(1):856.</p> <p>Abstract</p> <p>Most estimates of the burden of malaria are based on its direct impacts; however, its true burden is likely to be greater because of its wider effects on overall health. Here we estimate the indirect impact of malaria on children's health in a case-control study, using the sickle cell trait (HbAS), a condition associated with a high degree of specific malaria resistance, as a proxy indicator for an effective intervention. We estimate the odds ratios for HbAS among cases (all children admitted to Kilifi County Hospital during 2000-2004) versus community controls. As expected, HbAS protects strongly against malaria admissions (aOR 0.26; 95%CI 0.22-0.31), but it also protects against other syndromes,</p>



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	<p>including neonatal conditions (aOR 0.79; 0.67-0.93), bacteraemia (aOR 0.69; 0.54-0.88) and severe malnutrition (aOR 0.67; 0.55-0.83). The wider health impacts of malaria should be considered when estimating the potential added benefits of effective malaria interventions.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30787300/</p>
59.	<p>Kivata MW, Mbuchi M, Eyase FL, Bulimo WD, Kyanya CK, Oundo V, Muriithi SW, Andagalu B, Mbinda WM, Soge OO, McClelland RS, Sang W, Mancuso JD. <i>gyrA</i> and <i>parC</i> mutations in fluoroquinolone-resistant <i>Neisseria gonorrhoeae</i> isolates from Kenya. <i>BMC Microbiol.</i> 2019 Apr 8;19(1):76.</p> <p>Abstract</p> <p>Background: Phenotypic fluoroquinolone resistance was first reported in Western Kenya in 2009 and later in Coastal Kenya and Nairobi. Until recently gonococcal fluoroquinolone resistance mechanisms in Kenya had not been elucidated. The aim of this paper is to analyze mutations in both <i>gyrA</i> and <i>parC</i> responsible for elevated fluoroquinolone Minimum Inhibitory Concentrations (MICs) in <i>Neisseria gonorrhoeae</i> (GC) isolated from heterosexual individuals from different locations in Kenya between 2013 and 2017.</p> <p>Methods: Antimicrobial Susceptibility Tests were done on 84 GC in an ongoing Sexually Transmitted Infections (STI) surveillance program. Of the 84 isolates, 22 resistant to two or more classes of antimicrobials were chosen for analysis. Antimicrobial susceptibility tests were done using E-test (BioMerieux) and the results were interpreted with reference to European Committee on Antimicrobial Susceptibility Testing (EUCAST) standards. The isolates were sub-cultured, and whole genomes were sequenced using Illumina platform. Reads were assembled de novo using Velvet, and mutations in the GC Quinolone Resistant Determining Regions identified using Bioedit sequence alignment editor. Single Nucleotide Polymorphism based phylogeny was inferred using RaxML.</p> <p>Results: Double <i>GyrA</i> amino acid substitutions; S91F and D95G/D95A were identified in 20 isolates. Of these 20 isolates, 14 had an additional E91G <i>ParC</i> substitution and significantly higher ciprofloxacin MICs ($p = 0.0044^*$). On the contrary, norfloxacin MICs of isolates expressing both <i>GyrA</i> and <i>ParC</i> QRDR amino acid changes were not significantly high ($p = 0.82$) compared to MICs of isolates expressing <i>GyrA</i> substitutions alone. No single <i>GyrA</i> substitution was found in the analyzed isolates, and no isolate contained a <i>ParC</i> substitution without the simultaneous presence of double <i>GyrA</i> substitutions. Maximum likelihood tree clustered the 22 isolates into 6 distinct clades.</p> <p>Conclusion: Simultaneous presence of amino acid substitutions in <i>ParC</i> and <i>GyrA</i> has been reported to increase gonococcal fluoroquinolone resistance from different regions in the world. Our findings indicate that <i>GyrA</i> S91F, D95G/D95A and <i>ParC</i> E91G amino acid substitutions mediate high fluoroquinolone resistance in the analyzed Kenyan GC.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30961546/</p>



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60.	<p>Hendriksen RS, Lukjancenko O, Munk P, Hjelmshø MH, Verani JR, Ng'eno E, Bigogo G, Kiplangat S, Oumar T, Bergmark L, Röder T, Neatherlin JC, Clayton O, Hald T, Karlsmose S, Pamp SJ, Fields B, Montgomery JM, Aarestrup FM. Pathogen surveillance in the informal settlement, Kibera, Kenya, using a metagenomic approach. <i>PLoS One</i>. 2019 Oct 10;14(10):e0222531.</p> <p>Abstract</p> <p>Background: Worldwide, the number of emerging and re-emerging infectious diseases is increasing, highlighting the importance of global disease pathogen surveillance. Traditional population-based methods may fail to capture important events, particularly in settings with limited access to health care, such as urban informal settlements. In such environments, a mixture of surface water runoff and human feces containing pathogenic microorganisms could be used as a surveillance surrogate.</p> <p>Method: We conducted a temporal metagenomic analysis of urban sewage from Kibera, an urban informal settlement in Nairobi, Kenya, to detect and quantify bacterial and associated antimicrobial resistance (AMR) determinants, viral and parasitic pathogens. Data were examined in conjunction with data from ongoing clinical infectious disease surveillance.</p> <p>Results: A large variation of read abundances related to bacteria, viruses, and parasites of medical importance, as well as bacterial associated antimicrobial resistance genes over time were detected. Significant increased abundances were observed for a number of bacterial pathogens coinciding with higher abundances of AMR genes. <i>Vibrio cholerae</i> as well as rotavirus A, among other virus peaked in several weeks during the study period whereas <i>Cryptosporidium</i> spp. and <i>Giardia</i> spp, varied more over time.</p> <p>Conclusion: The metagenomic surveillance approach for monitoring circulating pathogens in sewage was able to detect putative pathogen and resistance loads in an urban informal settlement. Thus, valuable if generated in real time to serve as a comprehensive infectious disease agent surveillance system with the potential to guide disease prevention and treatment. The approach may lead to a paradigm shift in conducting real-time global genomics-based surveillance in settings with limited access to health care.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31600207/</p>
61.	<p>Ochola-Oyier LI, Wamae K, Omedo I, Ogola C, Matharu A, Musabyimana JP, Njogu FK, Marsh K. Few <i>Plasmodium falciparum</i> merozoite ligand and erythrocyte receptor pairs show evidence of balancing selection. <i>Infect Genet Evol</i>. 2019 Apr;69:235-245.</p> <p>Abstract</p> <p>Erythrocyte surface proteins have been identified as receptors of <i>Plasmodium falciparum</i> merozoite proteins. The ligand-receptor interactions enable the parasite to invade human erythrocytes, initiating the clinical symptoms of malaria. These interactions are likely to have had an evolutionary impact on the genes that encode the ligand and receptor proteins. We used sequence data from Kilifi, Kenya to detect departures from neutrality in a paired analysis of <i>P. falciparum</i> merozoite ligands and their erythrocyte receptor genes from the same population. We genotyped parasite and human DNA obtained from</p>



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	<p>93 individuals with severe malaria. We examined six merozoite ligands EBA175, EBL1, EBA140, MSP1, Rh4 and Rh5, and their corresponding erythrocyte receptors, glycophorin (Gyp) A, GypB, GypC, band 3, complement receptor (CR) 1 and basigin, focusing on the regions involved in the ligand-receptor interactions. Positive Tajima's D values (>1) were observed only in the MSP1 C-terminal region and EBA175 region II, while negative values (<-1) were observed in EBL-1 region II, Rh4, basigin exons 3 and 5, CR1 exon 5, Gyp B exons 2, 3 and 4 and Gyp C exon 2. Additionally, ebl-1 region II and basigin exon 3 showed extreme negative values in all three tests, Tajima's D, Fu & Li D* and F*, ≤ -2. A large majority of the erythrocyte receptor and merozoite genes have a negative Tajima's D even when compared with previously published whole genome data. Thus, highlighting EBA175 region II and MSP1-33, as outlier genes with a positive Tajima's D (>1). Both these genes contain multiple polymorphisms, which in the case of EBA175 may counteract receptor polymorphisms and/or evade host immune responses and in MSP1 the polymorphisms may primarily evade host immune responses.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30735814/</p>
62.	<p>George EC, Kiguli S, Olupot PO, Opoka RO, Engoru C, Akech SO, Nyeko R, Mtove G, Mpoya A, Thomason MJ, Crawley J, Evans JA, Gibb DM, Babiker AG, Maitland K, Walker AS. Mortality risk over time after early fluid resuscitation in African children. <i>Crit Care</i>. 2019 Nov 27;23(1):377.</p> <p>Abstract</p> <p>Background: African children hospitalised with severe febrile illness have a high risk of mortality. The Fluid Expansion As Supportive Therapy (FEAST) trial (ISCRTN 69856593) demonstrated increased mortality risk associated with fluid boluses, but the temporal relationship to bolus therapy and underlying mechanism remains unclear.</p> <p>Methods: In a post hoc retrospective analysis, flexible parametric models were used to compare change in mortality risk post-randomisation in children allocated to bolus therapy with 20-40 ml/kg 5% albumin or 0.9% saline over 1-2 h or no bolus (control, 4 ml/kg/hour maintenance), overall and for different terminal clinical events (cardiogenic, neurological, respiratory, or unknown/other).</p> <p>Results: Two thousand ninety-seven and 1041 children were randomised to bolus vs no bolus, of whom 254 (12%) and 91 (9%) respectively died within 28 days. Median (IQR) bolus fluid in the bolus groups received by 4 h was 20 (20, 40) ml/kg and was the same at 8 h; total fluids received in bolus groups at 4 h and 8 h were 38 (28, 43) ml/kg and 40 (30, 50) ml/kg, respectively. Total fluid volumes received in the control group by 4 h and 8 h were median (IQR) 10 (6, 15) ml/kg and 10 (10, 26) ml/kg, respectively. Mortality risk was greatest 30 min post-randomisation in both groups, declining sharply to 4 h and then more slowly to 28 days. Maximum mortality risk was similar in bolus and no bolus groups; however, the risk declined more slowly in the bolus group, with significantly higher mortality risk compared to the no bolus group from 1.6 to 101 h (4 days) post-randomisation. The delay in decline in mortality risk in the bolus groups was most pronounced for cardiogenic modes of death.</p>



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	<p>Conclusions: The increased risk from bolus therapy was not due to a mechanism occurring immediately after bolus administration. Excess mortality risk in the bolus group resulted from slower decrease in mortality risk over the ensuing 4 days. Thus, administration of modest bolus volumes appeared to prevent mortality risk declining at the same rate that it would have done without a bolus, rather than harm associated with bolus resulting from a concurrent increased risk of death peri-bolus administration.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31775837/</p>
63.	<p>Chadeka EA, Nagi S, Cheruiyot NB, Bahati F, Sunahara T, Njenga SM, Hamano S. A high-intensity cluster of <i>Schistosoma mansoni</i> infection around Mbita cause way, western Kenya: a confirmatory cross-sectional survey. Trop Med Health. 2019 Apr 15;47:26.</p> <p>Abstract</p> <p>In Kenya, communities residing along the shores and islands of Lake Victoria bear a substantial burden of schistosomiasis. Although there is a school-based deworming program in place, the transmission of <i>Schistosoma mansoni</i> varies even at a fine scale. Given the focal nature of schistosomes' transmission, we aim to identify areas with high intensity of <i>S. mansoni</i> infection in Mbita, Homabay County, western Kenya, for prioritized integrated control measures. Our findings confirm a high intensity of <i>S. mansoni</i> infection cluster around Mbita causeway. While the current efforts to curtail morbidity due to schistosomiasis through preventive chemotherapy in schools are crucial, fine-scale mapping of risk areas is necessary for specific integrated control measures.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31015786/</p>
64.	<p>Munge K, Mulupi S, Barasa E, Chuma J. A critical analysis of purchasing arrangements in Kenya: the case of micro health insurance. BMC Health Serv Res. 2019 Jan 18;19(1):45.</p> <p>Abstract</p> <p>Background: Strategic purchasing can ensure that financial resources are used in a way that optimally enhances the attainment of health system goals. A number of low- and middle-income countries, including Kenya, have experimented with micro health insurance (MHIs) as a means to purchase health services for the informal sector. This study aimed to examine the purchasing practices of MHIs in Kenya.</p> <p>Methods: The study was guided by an analytical framework that compared purchasing practices of MHIs with the ideal actions for strategic purchasing along three pairs of principal-agent relationships (government-purchaser, purchaser-provider and citizen-purchaser). The study adopted a qualitative descriptive case study design with 2 MHIs as cases. Data were collected through document reviews (regulation, marketing materials, websites) and semi-structured interviews with key informants (n = 27).</p> <p>Results: The regulatory framework for MHIs did not adequately support strategic purchasing practice and was exacerbated by poor coordination between health and financial sectors. The MHIs strategically contracted health providers over whom they</p>



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	<p>could exercise bargaining power, sometimes at the expense of quality. There were no clear channels for beneficiaries to provide timely feedback to the purchaser. MHIs premium payments were family-based, low-cost and offered limited benefits. Coverage was based on ability to pay, which may have excluded low-income households from membership.</p> <p>Conclusions: Adequate policy, legal and regulatory frameworks that integrate MHIs into the broader health financing system and support strategic purchasing practices are required. The state departments responsible for finance and health should form coordinating structures that ensure that MHI's role in universal health coverage is owned across all relevant sectors, and that actors, such as regulators, perform in a coordinated manner. The frameworks should also seek to align purchasers' relationships with providers so that clear and consistent signals are received by providers from all purchasing mechanisms present within the health system.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30658639/</p>
65.	<p>Campbell ZA, Thumbi SM, Marsh TL, Quinlan MB, Shirima GM, Palmer GH. Why isn't everyone using the thermotolerant vaccine? Preferences for Newcastle disease vaccines by chicken-owning households in Tanzania. PLoS One. 2019 Aug 15;14(8):e0220963.</p> <p>Abstract</p> <p>Understanding preferences for veterinary vaccines in low and middle-income countries is important for increasing vaccination coverage against infectious diseases, especially when the consumer is responsible for choosing between similar vaccines. Over-the-counter sales of vaccines without a prescription gives decision-making power to consumers who may value vaccine traits differently from national or international experts and vaccine producers and distributors. We examine consumer preferences for La Sota and I-2 Newcastle disease vaccines in Tanzania to understand why two vaccines co-exist in the market when I-2 is considered technically superior because of its thermotolerance. Household survey and focus group results indicate consumers perceive both vaccines to be effective, use the two vaccines interchangeably when the preferred vaccine is unavailable, and base preferences more on administration style than thermotolerance. Considering the consumers' perspectives provides a way to increase vaccination coverage by targeting users with a vaccine that fits their preferences.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31415629/</p>
66.	<p>Samia P, Hassell J, Hudson JA, Murithi MK, Kariuki SM, Newton CR, Wilmshurst JM. Epilepsy diagnosis and management of children in Kenya: review of current literature. Res Rep Trop Med. 2019 Jun 28;10:91-102.</p> <p>Abstract</p> <p>Introduction: The growing impact of non-communicable diseases in low- to middle-income countries makes epilepsy a key research priority. We evaluated peer-reviewed published literature on childhood epilepsy specific to Kenya to identify knowledge gaps</p>



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	<p>and inform future priorities. Methodology: A literature search utilizing the terms "epilepsy" OR "seizure" as exploded subject headings AND "Kenya" was conducted. Relevant databases were searched, generating 908 articles. After initial screening to remove duplications, irrelevant articles, and publications older than 15 years, 154 papers remained for full-article review, which identified 35 publications containing relevant information. Data were extracted from these reports on epidemiology, etiology, clinical features, management, and outcomes. Results: The estimated prevalence of lifetime epilepsy in children was 21-41 per 1,000, while the incidence of active convulsive epilepsy was 39-187 cases per 100,000 children per year. The incidence of acute seizures was 312-879 per 100,000 children per year and neonatal seizures 3,950 per 100,000 live births per year. Common risk factors for both epilepsy and acute seizures included adverse perinatal events, meningitis, malaria, febrile seizures, and family history of epilepsy. Electroencephalography abnormalities were documented in 20%-41% and neurocognitive comorbidities in more than half. Mortality in children admitted with acute seizures was 3%-6%, and neurological sequelae were identified in 31% following convulsive status epilepticus. Only 7%-29% children with epilepsy were on antiseizure medication. Conclusion: Active convulsive epilepsy is a common condition among Kenyan children, remains largely untreated, and leads to extremely poor outcomes. The high proportion of epilepsy attributable to preventable causes, in particular neonatal morbidity, contributes significantly to the lifetime burden of the condition. This review reaffirms the ongoing need for better public awareness of epilepsy as a treatable disease and for national-level action that targets both prevention and management.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31388319/</p>
67.	<p>Lee JC, Westgate K, Boit MK, Mwaniki DL, Kiplamai FK, Friis H, Tetens I, Christensen DL, Brage S. Physical activity energy expenditure and cardiometabolic health in three rural Kenyan populations. <i>Am J Hum Biol.</i> 2019 Jan;31(1):e23199.</p> <p>Abstract</p> <p>Objectives: Physical activity is beneficial for metabolic health but the extent to which this may differ by ethnicity is still unclear. Here, the objective was to characterize the association between physical activity energy expenditure (PAEE) and cardiometabolic risk among the Luo, Kamba, and Maasai ethnic groups of rural Kenya.</p> <p>Methods: In a cross-sectional study of 1084 rural Kenyans, free-living PAEE was objectively measured using individually-calibrated heart rate and movement sensing. A clustered metabolic syndrome risk score (zMS) was developed by averaging the sex-specific z-scores of five risk components measuring central adiposity, blood pressure, lipid levels, glucose tolerance, and insulin resistance.</p> <p>Results: zMS was 0.08 (-0.09; -0.06) SD lower for every 10 kJ/kg/day difference in PAEE after adjustment for age and sex; this association was modified by ethnicity (interaction with PAEE $P < 0.05$). When adjusted for adiposity, each 10 kJ/kg/day difference in PAEE was predicted to lower zMS by 0.04 (-0.05, -0.03) SD, without</p>



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	<p>evidence of interaction by ethnicity. The Maasai were predicted to have higher cardiometabolic risk than the Kamba and Luo at every quintile of PAEE, with a strong dose-dependent decreasing trend among all ethnicities.</p> <p>Conclusion: Free-living PAEE is strongly inversely associated with cardiometabolic risk in rural Kenyans. Differences between ethnic groups in this association were observed but were explained by differences in central adiposity. Therefore, targeted interventions to increase PAEE are more likely to be effective in subgroups with high central adiposity, such as Maasai with low levels of PAEE.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30537282/</p>
68.	<p>Deichsel EL, Pavlinac PB, Richardson BA, Mbori-Ngacha D, Walson JL, McGrath CJ, Farquhar C, Bosire R, Maleche-Obimbo E, John-Stewart GC. Birth size and early pneumonia predict linear growth among HIV-exposed uninfected infants. <i>Matern Child Nutr.</i> 2019 Oct;15(4):e12861.</p> <p>Abstract</p> <p>Stunting remains a global health priority, particularly in sub-Saharan Africa. Identifying determinants of linear growth in HIV-exposed uninfected (HEU) infants can inform interventions to prevent stunting in this vulnerable population. HIV-infected mothers and their uninfected infants were followed monthly from pregnancy to 12-month post-partum in Nairobi, Kenya. Mixed-effects models estimated the change in length-for-age z-score (LAZ) from birth to 12 months by environmental, maternal, and infant characteristics. Multivariable models included factors univariately associated with LAZ. Among 372 HEU infants, mean LAZ decreased from -0.54 (95% confidence interval [CI] [-0.67, -0.41]) to -1.09 (95% CI [-1.23, -0.96]) between 0 and 12 months. Declines in LAZ were associated with crowding (≥ 2 persons per room; adjusted difference [AD] in 0-12 month change: -0.46; 95% CI [-0.87, -0.05]), use of a pit latrine versus a flush toilet (AD: -0.29; 95% CI [-0.57, -0.02]), and early infant pneumonia (AD: -1.14; 95% CI [-1.99, -0.29]). Infants with low birthweight (<2,500 g; AD: 1.08; 95% CI [0.40, 1.76]) and birth stunting (AD: 1.11; 95% CI [0.45, 1.78]) experienced improved linear growth. By 12 months of age, 46 infants were stunted, of whom 11 (24%) were stunted at birth. Of the 34 infants stunted at birth with an available 12-month LAZ, 68% were not stunted at 12 months. Some low birthweight and birth-stunted HEU infants had significant linear growth recovery. Early infant pneumonia and household environment predicted poor linear growth and may identify a subgroup of HEU infants for whom to provide growth-promoting interventions.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31222958/</p>
69.	<p>Ngari MM, Iversen PO, Thitiri J, Mwalekwa L, Timbwa M, Fegan GW, Berkley JA. Linear growth following complicated severe malnutrition: 1-year follow-up cohort of Kenyan children. <i>Arch Dis Child.</i> 2019 Mar;104(3):229-235.</p> <p>Abstract</p> <p>Background: Stunting is the most common manifestation of childhood undernutrition worldwide. Children presenting with severe acute malnutrition (SAM) are often also</p>



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	<p>severely stunted. We evaluated linear growth and its determinants after medically complicated SAM.</p> <p>Methods: We performed secondary analysis of clinical trial data (NCT00934492) from HIV-uninfected Kenyan children aged 2-59 months hospitalised with SAM. Outcome was change in height/length-for-age z-score (HAZ) between enrolment and 12 months later. Exposures were demographic, clinical, anthropometric characteristics and illness episodes during follow-up.</p> <p>Results: Among 1169 children with HAZ values at month 12 (66% of those in original trial), median (IQR) age 11 (7-17) months and mean (SD) HAZ -2.87 (1.6) at enrolment, there was no change in mean HAZ between enrolment and month 12: -0.006Z (95% CI -0.07 to 0.05Z). While 262 (23%) children experienced minimal HAZ change (within ± 0.25 HAZ), 472 (40%) lost >0.25 and 435 (37%) gained >0.25 HAZ. After adjusting for regression to the mean, inpatient or outpatient episodes of diarrhoea and inpatient severe pneumonia during follow-up were associated with HAZ loss. Premature birth and not being cared by the biological parent were associated with HAZ gain. Increases in mid-upper arm circumference and weight-for-age were associated with HAZ gain and protected against HAZ loss. Increase in weight-for-height was not associated with HAZ gain but protected against HAZ loss. No threshold of weight gain preceding linear catch-up growth was observed.</p> <p>Conclusions: Interventions to improve dietary quality and prevent illness over a longer period may provide opportunities to improve linear growth.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30266874/</p>
70.	<p>Kagaya W, Gitaka J, Chan CW, Kongere J, Md Idris Z, Deng C, Kaneko A. Malaria resurgence after significant reduction by mass drug administration on Ngodhe Island, Kenya. <i>Sci Rep.</i> 2019 Dec 13;9(1):19060.</p> <p>Abstract</p> <p>Although WHO recommends mass drug administration (MDA) for malaria elimination, further evidence is required for understanding the obstacles for the optimum implementation of MDA. Just before the long rain in 2016, two rounds of MDA with artemisinin/piperaquine (Artequick) and low-dose primaquine were conducted with a 35-day interval for the entire population of Ngodhe Island (~500 inhabitants) in Lake Victoria, Kenya, which is surrounded by areas with moderate and high transmission. With approximately 90% compliance, Plasmodium prevalence decreased from 3% to 0% by microscopy and from 10% to 2% by PCR. However, prevalence rebounded to 9% by PCR two months after conclusion of MDA. Besides the remained local transmission, parasite importation caused by human movement likely contributed to the resurgence. Analyses of 419 arrivals to Ngodhe between July 2016 and September 2017 revealed Plasmodium prevalence of 4.6% and 16.0% by microscopy and PCR, respectively. Risk factors for infection among arrivals included age (0 to 5 and 11 to 15 years), and travelers from Siaya County, located to the north of Ngodhe Island. Parasite importation caused by</p>



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	<p>human movement is one of major obstacles to sustain malaria elimination, suggesting the importance of cross-regional initiatives together with local vector control.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31836757/</p>
71.	<p>Moyes CL, Wiebe A, Gleave K, Trett A, Hancock PA, Padonou GG, Chouaïbou MS, Sovi A, Abuelmaali SA, Ochomo E, Antonio-Nkondjio C, Dengela D, Kawada H, Dabire RK, Donnelly MJ, Mbogo C, Fornadel C, Coleman M. Analysis-ready datasets for insecticide resistance phenotype and genotype frequency in African malaria vectors. <i>Sci Data</i>. 2019 Jul 15;6(1):121.</p> <p>Abstract</p> <p>The impact of insecticide resistance in malaria vectors is poorly understood and quantified. Here a series of geospatial datasets for insecticide resistance in malaria vectors are provided, so that trends in resistance in time and space can be quantified, and the impact of resistance found in wild populations on malaria transmission in Africa can be assessed. Specifically, data have been collated and geopositioned for the prevalence of insecticide resistance, as measured by standard bioassays, in representative samples of individual species or species complexes. Data are provided for the <i>Anopheles gambiae</i> species complex, the <i>Anopheles funestus</i> subgroup, and for nine individual vector species. Data are also given for common genetic markers of resistance to support analyses of whether these markers can improve the ability to monitor resistance in low resource settings. Allele frequencies for known resistance-associated markers in the Voltage-gated sodium channel (Vgsc) are provided. In total, eight analysis-ready, standardised, geopositioned datasets encompassing over 20,000 African mosquito collections between 1957 and 2017 are released.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31308378/</p>
72.	<p>Ojal J, Griffiths U, Hammitt LL, Adetifa I, Akech D, Tabu C, Scott JAG, Flasche S. Sustaining pneumococcal vaccination after transitioning from Gavi support: a modelling and cost-effectiveness study in Kenya. <i>Lancet Glob Health</i>. 2019 May;7(5):e644-e654.</p> <p>Abstract</p> <p>Background: In 2009, Gavi, the World Bank, and donors launched the pneumococcal Advance Market Commitment, which helped countries access more affordable pneumococcal vaccines. As many low-income countries begin to reach the threshold at which countries transition from Gavi support to self-financing (3-year average gross national income per capita of US\$1580), they will need to consider whether to continue pneumococcal conjugate vaccine (PCV) use at full cost or to discontinue PCV in their childhood immunisation programmes. Using Kenya as a case study, we assessed the incremental cost-effectiveness of continuing PCV use.</p> <p>Methods: In this modelling and cost-effectiveness study, we fitted a dynamic compartmental model of pneumococcal carriage to annual carriage prevalence surveys and invasive pneumococcal disease (IPD) incidence in Kilifi, Kenya. We predicted disease incidence and related mortality for either continuing PCV use beyond 2022, the start of Kenya's transition from Gavi support, or its discontinuation. We calculated the</p>



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	<p>costs per disability-adjusted life-year (DALY) averted and associated 95% prediction intervals (PI).</p> <p>Findings: We predicted that if PCV use is discontinued in Kenya in 2022, overall IPD incidence will increase from 8.5 per 100 000 in 2022, to 16.2 per 100 000 per year in 2032. Continuing vaccination would prevent 14 329 (95% PI 6130-25 256) deaths and 101 513 (4386-196 674) disease cases during that time. Continuing PCV after 2022 will require an estimated additional US\$15.8 million annually compared with discontinuing vaccination. We predicted that the incremental cost per DALY averted of continuing PCV would be \$153 (95% PI 70-411) in 2032.</p> <p>Interpretation: Continuing PCV use is essential to sustain its health gains. Based on the Kenyan GDP per capita of \$1445, and in comparison to other vaccines, continued PCV use at full costs is cost-effective (on the basis of the assumption that any reduction in disease will translate to a reduction in mortality). Although affordability is likely to be a concern, our findings support an expansion of the vaccine budget in Kenya.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31000132/</p>
73.	<p>Macharia PM, Giorgi E, Thurania PN, Joseph NK, Sartorius B, Snow RW, Okiro EA. Sub national variation and inequalities in under-five mortality in Kenya since 1965. BMC Public Health. 2019 Feb 4;19(1):146.</p> <p>Abstract</p> <p>Background: Despite significant declines in under five mortality (U5M) over the last 3 decades, Kenya did not achieve Millennium Development Goal 4 (MDG 4) by 2015. To better understand trends and inequalities in child mortality, analysis of U5M variation at subnational decision making units is required. Here the comprehensive compilation and analysis of birth history data was used to understand spatio-temporal variation, inequalities and progress towards achieving the reductions targets of U5M between 1965 and 2013 and projected to 2015 at decentralized health planning units (counties) in Kenya.</p> <p>Methods: Ten household surveys and three censuses with data on birth histories undertaken between 1989 and 2014 were assembled. The birth histories were allocated to the respective counties and demographic methods applied to estimate U5M per county by survey. To generate a single U5M estimate for year and county, a Bayesian spatio-temporal Gaussian process regression was fitted accounting for variation in sample size, surveys and demographic methods. Inequalities and the progress in meeting the goals set to reduce U5M were evaluated subnationally.</p> <p>Results: Nationally, U5M reduced by 61.6%, from 141.7 (121.6-164.0) in 1965 to 54.5 (44.6-65.5) in 2013. The declining U5M was uneven ranging between 19 and 80% across the counties with some years when rates increased. By 2000, 25 counties had achieved the World Summit for Children goals. However, as of 2015, no county had achieved MDG 4. There was a striking decline in the levels of inequality between counties over time, however, disparities persist. By 2013 there persists a 3.8 times difference between</p>



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	<p>predicted U5M rates when comparing counties with the highest U5M rates against those with the lowest U5M rates.</p> <p>Conclusion: Kenya has made huge progress in child survival since independence. However, U5M remains high and heterogeneous with substantial differences between counties. Better use of the current resources through focused allocation is required to achieve further reductions, reduce inequalities and increase the likelihood of achieving Sustainable Development Goal 3.2 on U5M by 2030.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30717714/</p>
74.	<p>Kubicek-Sutherland JZ, Vu DM, Noormohamed A, Mendez HM, Stromberg LR, Pedersen CA, Hengartner AC, Klosterman KE, Bridgewater HA, Otieno V, Cheng Q, Anyona SB, Ouma C, Raballah E, Perkins DJ, McMahon BH, Mukundan H. Direct detection of bacteremia by exploiting host-pathogen interactions of lipoteichoic acid and lipopolysaccharide. <i>Sci Rep.</i> 2019 Apr 17;9(1):6203.</p> <p>Abstract</p> <p>Bacteremia is a leading cause of death in sub-Saharan Africa where childhood mortality rates are the highest in the world. The early diagnosis of bacteremia and initiation of treatment saves lives, especially in high-disease burden areas. However, diagnosing bacteremia is challenging for clinicians, especially in children presenting with co-infections such as malaria and HIV. There is an urgent need for a rapid method for detecting bacteremia in pediatric patients with co-morbidities to inform treatment. In this manuscript, we have developed and clinically validated a novel method for the direct detection of amphiphilic pathogen biomarkers indicative of bacteremia, directly in aqueous blood, by mimicking innate immune recognition. Specifically, we have exploited the interaction of amphiphilic pathogen biomarkers such as lipopolysaccharides (LPS) from Gram-negative bacteria and lipoteichoic acids (LTA) from Gram-positive bacteria with host lipoprotein carriers in blood, in order to develop two tailored assays - lipoprotein capture and membrane insertion - for their direct detection. Our assays demonstrate a sensitivity of detection of 4 ng/mL for LPS and 2 ng/mL for LTA using a waveguide-based optical biosensor platform that was developed at LANL. In this manuscript, we also demonstrate the application of these methods for the detection of LPS in serum from pediatric patients with invasive <i>Salmonella Typhimurium</i> bacteremia (n = 7) and those with <i>Staphylococcal</i> bacteremia (n = 7) with 100% correlation with confirmatory culture. Taken together, these results demonstrate the significance of biochemistry in both our understanding of host-pathogen biology, and development of assay methodology, as well as demonstrate a potential new approach for the rapid, sensitive and accurate diagnosis of bacteremia at the point of need.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30996333/</p>
75.	<p>Tanaka J, Yoshizawa K, Hirayama K, Karama M, Wanjihia V, Changoma MS, Kaneko S. Relationship between dietary patterns and stunting in preschool children: a cohort analysis from Kwale, Kenya. <i>Public Health.</i> 2019 Aug; 173:58-68.</p> <p>Abstract</p>



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	<p>Objectives: Stunting is a significant cause of poor cognitive performance and lower school achievement. Stunting is observed among pre-school children in several areas in Africa; however, not all children are affected, and children with and without stunting are seen in the same communities. Therefore, this study aimed to identify nutritional and other factors that prevent stunting that may exist in local communities. Study design: This is a prospective cohort study.</p> <p>Methods: Data were extracted from the Health and Demographic Surveillance System conducted in Kwale County, Kenya. The cohort consisted of all households with children less than five years old, within a radius of 2.2 km from a local health centre. A dietary pattern (DP) survey with a semi-quantitative food frequency questionnaire was conducted on caretakers of children who were voluntary participated from the cohort between June 2012 and August 2012. Using cluster analysis, the children were assigned to a DP group. Logistic regression analysis was applied to calculate the adjusted odds ratios (aORs) of DPs for stunting controlling for other factors.</p> <p>Results: In total, 402 children were included in the analysis. By cluster analysis, three DPs were identified: protein-rich DP; traditional DP; and traditional DP complemented by breastfeeding. The aOR of a child becoming stunted from a normal height during the study period among children who received a traditional DP compared with those who had a protein-rich DP was 2.78 (95% confidence interval [CI]: 1.02-7.55). However, the aOR for children who were already stunted at the start of the study and had a traditional DP was 1.49 (95% CI: 0.82-2.72). Increased aORs of stunting were observed among children aged over 12 months compared with children aged 6-11 months, and the effects of DPs were modified by age in months from 12 to 35 months; however, the effects were near the null value for children over 36 months of age, although these were not statistically significant.</p> <p>Conclusions: We found that the traditional DP showed a higher risk for stunting compared with the protein-rich DP, and the most vulnerable age range for stunting was between 12 and 35 months. Interventions to prevent stunting should focus on providing 12- to 35-month-old children with locally available, protein-rich foods.</p>
76.	<p>Fiorella KJ, Gavenus ER, Milner EM, Moore M, Wilson-Anumudu F, Adhiambo F, Mattah B, Bukusi E, Fernald LCH. Evaluation of a social network intervention on child feeding practices and caregiver knowledge. <i>Matern Child Nutr.</i> 2019 Jul;15(3):e12782.</p> <p>Abstract</p> <p>Food insecurity and poor infant and young child feeding (IYCF) practices contribute to undernutrition. The Kanyakla Nutrition Program was developed in rural Kenya to provide knowledge alongside social support for recommended IYCF practices. Utilizing a social network approach, the Kanyakla Nutrition Program trained community health workers (CHWs) to engage mothers, fathers, and grandparents in nutrition education and discussions about strategies to provide instrumental, emotional, and information support</p>



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	<p>within their community. The 12-week programme included six sessions and was implemented on Mfangano Island, Kenya, in 2014-2015. We analysed intervention effects on (a) nutrition knowledge among community members or CHWs and (2) IYCF practices among children 1-3 years. Nutrition knowledge was assessed using a postintervention comparison among intervention (community, n = 43; CHW, n = 22) and comparison groups (community, n = 149; CHW, n = 64). We used a quasi-experimental design and difference-in-difference to assess IYCF indicators using dietary recall data from an ongoing cohort study among intervention participants (n = 48) with individuals living on Mfangano Island where the intervention was not implemented (n = 178) before the intervention, within 1 month postintervention, and 6 months postintervention. Findings showed no effect of the intervention on IYCF indicators (e.g., dietary diversity and meal frequency), and less than 15% of children met minimum acceptable diet criteria at any time point. However, knowledge and confidence among community members and CHWs were significantly higher 2 years postintervention. Thus, a social network approach had an enduring effect on nutrition knowledge, but no effects on improved IYCF practices.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30676696/</p>
77.	<p>Tuju J, Mackinnon MJ, Abdi AI, Karanja H, Musyoki JN, Warimwe GM, Gitau EN, Marsh K, Bull PC, Urban BC. Antigenic cartography of immune responses to Plasmodium falciparum erythrocyte membrane protein 1 (PfEMP1). PLoS Pathog. 2019 Jul 1;15(7):e1007870.</p> <p>Abstract</p> <p>Naturally acquired clinical immunity to Plasmodium falciparum is partly mediated by antibodies directed at parasite-derived antigens expressed on the surface of red blood cells which mediate disease and are extremely diverse. Unlike children, adults recognize a broad range of variant surface antigens (VSAs) and are protected from severe disease. Though crucial to the design and feasibility of an effective malaria vaccine, it is not yet known whether immunity arises through cumulative exposure to each of many antigenic types, cross-reactivity between antigenic types, or some other mechanism. In this study, we measured plasma antibody responses of 36 children with symptomatic malaria to a diverse panel of 36 recombinant proteins comprising part of the DBLα domain (the 'DBLα-tag') of PfEMP1, a major class of VSAs. We found that although plasma antibody responses were highly specific to individual antigens, serological profiles of responses across antigens fell into one of just two distinct types. One type was found almost exclusively in children that succumbed to severe disease (19 out of 20) while the other occurred in all children with mild disease (16 out of 16). Moreover, children with severe malaria had serological profiles that were narrower in antigen specificity and shorter-lived than those in children with mild malaria. Borrowing a novel technique used in influenza-antigenic cartography-we mapped these dichotomous serological profiles to amino acid sequence variation within a small sub-region of the PfEMP1 DBLα domain. By applying our methodology on a larger scale, it should be possible to identify epitopes</p>



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	<p>responsible for eliciting the protective version of serological profiles to PfEMP1 thereby accelerating development of a broadly effective anti-disease malaria vaccine. Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31260501/</p>
78.	<p>Bediako Y, Adams R, Reid AJ, Valletta JJ, Ndungu FM, Sodenkamp J, Mwacharo J, Ngoi JM, Kimani D, Kai O, Wambua J, Nyangweso G, de Villiers EP, Sanders M, Lotkowska ME, Lin JW, Manni S, Addy JWG, Recker M, Newbold C, Berriman M, Bejon P, Marsh K, Langhorne J. Repeated clinical malaria episodes are associated with modification of the immune system in children. <i>BMC Med.</i> 2019 Mar 13;17(1):60. Abstract Background: There are over 200 million reported cases of malaria each year, and most children living in endemic areas will experience multiple episodes of clinical disease before puberty. We set out to understand how frequent clinical malaria, which elicits a strong inflammatory response, affects the immune system and whether these modifications are observable in the absence of detectable parasitaemia. Methods: We used a multi-dimensional approach comprising whole blood transcriptomic, cellular and plasma cytokine analyses on a cohort of children living with endemic malaria, but uninfected at sampling, who had been under active surveillance for malaria for 8 years. Children were categorised into two groups depending on the cumulative number of episodes experienced: high (≥ 8) or low (< 5). Results: We observe that multiple episodes of malaria are associated with modification of the immune system. Children who had experienced a large number of episodes demonstrated upregulation of interferon-inducible genes, a clear increase in circulating levels of the immunoregulatory cytokine IL-10 and enhanced activation of neutrophils, B cells and CD8+ T cells. Conclusion: Transcriptomic analysis together with cytokine and immune cell profiling of peripheral blood can robustly detect immune differences between children with different numbers of prior malaria episodes. Multiple episodes of malaria are associated with modification of the immune system in children. Such immune modifications may have implications for the initiation of subsequent immune responses and the induction of vaccine-mediated protection. Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30862316/</p>
79.	<p>Kamaara E, Oketch D, Chesire I, Coats CS, Thomas G, Ransome Y, Willie TC, Nunn A. Faith and healthcare providers' perspectives about enhancing HIV biomedical interventions in Western Kenya. <i>Glob Public Health.</i> 2019 Dec;14(12):1744-1756. Abstract Adult HIV prevalence in Kenya was 5.9% in 2017. However, in the counties of Kisumu, Siaya, and Homa Bay, HIV prevalence was over 15%. Biomedical interventions, including home-based testing and counselling (HBTC), HIV treatment and pre-exposure prophylaxis (PrEP) provide opportunities to reduce HIV transmission, particularly in rural communities with limited access to health services. Faith-based institutions play an important role in the Kenyan social fabric, providing over 40% of all health care services</p>



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	<p>in Kenya, but have played limited roles in promoting HIV prevention interventions. We conducted qualitative interviews with 45 medical professionals and focus groups with 93 faith leaders in Kisumu and Busia Counties, Kenya. We explored their knowledge, opinions, and experiences in promoting biomedical HIV prevention modalities, including HBTC and PrEP. Knowledge about and engagement in efforts to promote HIV prevention modalities varied; few health providers had partnered with faith leaders on HIV prevention programmes. Faith leaders and health providers agreed about the importance of increasing faith leaders' participation in HIV prevention and were positive about increasing their HIV prevention partnerships. Most faith leaders requested capacity building to better understand biomedical HIV prevention modalities and expressed interest in collaborating with clinical partners to spread awareness about HIV prevention modalities.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31390958/</p>
80.	<p>Slater HC, Ross A, Felger I, Hofmann NE, Robinson L, Cook J, Gonçalves BP, Björkman A, Ouedraogo AL, Morris U, Msellem M, Koepfli C, Mueller I, Tadesse F, Gadisa E, Das S, Domingo G, Kapulu M, Midega J, Owusu-Agyei S, Nabet C, Piarroux R, Doumbo O, Doumbo SN, Koram K, Lucchi N, Udhayakumar V, Mosha J, Tiono A, Chandramohan D, Gosling R, Mwingira F, Sauerwein R, Paul R, Riley EM, White NJ, Nosten F, Imwong M, Bousema T, Drakeley C, Okell LC. The temporal dynamics and infectiousness of subpatent Plasmodium falciparum infections in relation to parasite density. <i>Nat Commun.</i> 2019 Mar 29;10(1):1433.</p> <p>Abstract</p> <p>Malaria infections occurring below the limit of detection of standard diagnostics are common in all endemic settings. However, key questions remain surrounding their contribution to sustaining transmission and whether they need to be detected and targeted to achieve malaria elimination. In this study we analyse a range of malaria datasets to quantify the density, detectability, course of infection and infectiousness of subpatent infections. Asymptomatically infected individuals have lower parasite densities on average in low transmission settings compared to individuals in higher transmission settings. In cohort studies, subpatent infections are found to be predictive of future periods of patent infection and in membrane feeding studies, individuals infected with subpatent asexual parasite densities are found to be approximately a third as infectious to mosquitoes as individuals with patent (asexual parasite) infection. These results indicate that subpatent infections contribute to the infectious reservoir, may be long lasting, and require more sensitive diagnostics to detect them in lower transmission settings.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30926893/</p>
81.	<p>Kimani M, van der Elst EM, Chiro O, Oduor C, Wahome E, Kazungu W, Shally M, Rinke de Wit TF, Graham SM, Operario D, Sanders EJ. PrEP interest and HIV-1 incidence among MSM and transgender women in coastal Kenya. <i>J Int AIDS Soc.</i> 2019 Jun;22(6):e25323.</p> <p>Abstract</p>



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	<p>Introduction: There is emerging data on HIV-1 incidence among MSM in sub-Saharan Africa (SSA), but no known estimate of HIV-1 incidence among transgender women (TGW) in the region has yet been reported. We assessed HIV-1 incidence and pre-exposure prophylaxis (PrEP) interest in men who have sex with men exclusively (MSME), men who have sex with men and women (MSMW) and TGW in coastal Kenya. Methods: HIV-1-seronegative individuals who had participated in an HIV testing study in 2016 were traced and retested in 2017 according to Kenyan guidelines. All participants were assigned male sex at birth and had male sex partners; additional data on gender identity and sexual orientation were obtained. We assessed the factors associated with HIV-1 acquisition using Poisson regression and calculated HIV-1 incidence in MSME, MSMW and TGW. PrEP interest was assessed through focus group discussions to characterize subcategories' perceived PrEP needs.</p> <p>Results: Of the 168 cohort participants, 42 were classified as MSME, 112 as MSMW and 14 as TGW. Overall, HIV-1 incidence was 5.1 (95% confidence interval (CI): 2.6 to 9.8) per 100 person-years (PY): 4.5 (95% CI: 1.1 to 17.8] per 100 PY among MSME, 3.4 (95% CI: 1.3 to 9.1) per 100 PY among MSMW and 20.6 (95% CI: 6.6 to 63.8] per 100 PY among TGW. HIV-1 acquisition was associated with exclusive receptive anal intercourse (aIRR 13.0, 95% CI 1.9 to 88.6), history of an STI in preceding six months (aIRR 10.3, 95% CI 2.2 to 49.4) and separated/divorced marital status (aIRR 8.2 (95%: 1.1 to 62.2). Almost all (98.8%) participants were interested in initiating PrEP. MSME and TGW felt that PrEP would lead to increases in condomless anal or group sex.</p> <p>Conclusions: TGW had a very high HIV-1 incidence compared with MSME and MSMW. Subcategories of MSM anticipated different PrEP needs and post-PrEP risk behaviour. Further studies should assess if TGW may have been wrongly categorized as MSM in other HIV-1 incidence studies in the region.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31194291/</p>
82.	<p>Ghansah A, Kamau E, Amambua-Ngwa A, Ishengoma DS, Maiga-Ascofare O, Amenga-Etego L, Deme A, Yavo W, Randrianarivelosia M; Plasmodium Diversity Network Africa, Ochola-Oyier LI, Helegbe GK, Bailey J, Alifrangis M, Djimde A. Targeted Next Generation Sequencing for malaria research in Africa: current status and outlook. <i>Malar J.</i> 2019 Sep 23;18(1):324.</p> <p>Abstract</p> <p>Targeted Next Generation Sequencing (TNGS) is an efficient and economical Next Generation Sequencing (NGS) platform and the preferred choice when specific genomic regions are of interest. So far, only institutions located in middle and high-income countries have developed and implemented the technology, however, the efficiency and cost savings, as opposed to more traditional sequencing methodologies (e.g. Sanger sequencing) make the approach potentially well suited for resource-constrained regions as well. In April 2018, scientists from the Plasmodium Diversity Network Africa (PDNA) and collaborators met during the 7th Pan African Multilateral Initiative of Malaria (MIM) conference held in Dakar, Senegal to explore the feasibility of applying TNGS to genetic</p>



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	<p>studies and malaria surveillance in Africa. The group of scientists reviewed the current experience with TNGS platforms in sub-Saharan Africa (SSA) and identified potential roles the technology might play to accelerate malaria research, scientific discoveries and improved public health in SSA. Research funding, infrastructure and human resources were highlighted as challenges that will have to be mitigated to enable African scientists to drive the implementation of TNGS in SSA. Current roles of important stakeholders and strategies to strengthen existing networks to effectively harness this powerful technology for malaria research of public health importance were discussed.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31547818/</p>
83.	<p>Lockhart A, Senkomago V, Ting J, Chitwa M, Kimani J, Gakure H, Kwatampora J, Patel S, Mugo N, Smith JS. Prevalence and Risk Factors of Trichomonas vaginalis Among Female Sexual Workers in Nairobi, Kenya. <i>Sex Transm Dis.</i> 2019 Jul;46(7):458-464.</p> <p>Abstract</p> <p>Background: Trichomonas vaginalis (TV) is the most common curable sexually transmitted infection (STI) worldwide. Trichomonas vaginalis infection is associated with an increased risk of pelvic inflammatory disease, human immunodeficiency virus transmission, and preterm birth in women. Data on the prevalence and risk factors for TV infection in sub-Saharan African countries remain scarce.</p> <p>Methods: A total of 350 Kenyan female sex workers, aged 18 to 50 years, participated in a 2-year longitudinal study of the acquisition of STIs, including TV infection. Every 3 months, cervical and vaginal brush samples were collected for STI testing. At baseline, a sociodemographic and behavior questionnaire was administered. Testing for TV, Chlamydia trachomatis (CT), Neisseria gonorrhoeae, Mycoplasma genitalium, and high-risk human papillomavirus was performed using APTIMA assays.</p> <p>Results: The TV baseline prevalence was 9.2% (95% confidence interval [95% CI], 6.3-12.7%) and 2-year cumulative TV incidence was 8.1 per 1000 person months (6.9-9.3). Risk factors for higher TV prevalence at baseline were CT infection (adjusted prevalence ratio [PR], 8.53; 95% CI, 3.35-21.71), human immunodeficiency virus seropositivity (PR, 3.01; 95% CI, 1.45, 6.24) and greater than 4 years of sex work (PR, 2.66; 95% CI, 1.07-6.60). Risk factors for elevated 2-year TV incidence were CT (hazard ratio [HR], 4.28; 95% CI, 1.36-13.50), high-risk human papillomavirus infection (HR, 1.91; 95% CI, 1.06-3.45) and history of smoking (HR, 2.66; 95% CI, 1.24-5.73).</p> <p>Discussion: CT infection was positively associated with both prevalent and 2-year incident TV infections.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31194717/</p>
84.	<p>McCollum R, Taegtmeier M, Otiso L, Tolhurst R, Mireku M, Martineau T, Karuga R, Theobald S. Applying an intersectionality lens to examine health for vulnerable individuals following devolution in Kenya. <i>Int J Equity Health.</i> 2019 Jan 30;18(1):24.</p> <p>Abstract</p>



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	<p>Background: Power imbalances are a key driver of avoidable, unfair and unjust differences in health. Devolution shifts the balance of power in health systems. Intersectionality approaches can provide a 'lens' for analysing how power relations contribute to complex and multiple forms of health advantage and disadvantage. These approaches have not to date been widely used to analyse health systems reforms. While the stated objectives of devolution often include improved equity, efficiency and community participation, past evidence demonstrates that there is a need to create space and capacity for people to transform existing power relations these within specific contexts.</p> <p>Methods: We carried out a qualitative study between March 2015 and April 2016, involving 269 key informant and in-depth interviews from across the health system in ten counties, 14 focus group discussions with community members in two of these counties and photovoice participatory research with nine young people. We adopted an intersectionality lens to reveal how power relations intersect to produce vulnerabilities for specific groups in specific contexts, and to identify examples of the tacit knowledge about these vulnerabilities held by priority-setting stakeholders, in the wake of the introduction of devolution reforms in Kenya.</p> <p>Results: Our study identified a range of ways in which longstanding social forces and discriminations limit the power and agency individuals can exercise, but are mediated by their unique circumstances at a given point in their life. These are the social determinants of health, influencing an individual's exposure to risk of ill health from their living environment, their work, or their social context, including social norms relating to their gender, age, geographical residence or socio-economic status. While a range of policy measures have been introduced to encourage participation by typically 'unheard voices', devolution processes have yet to adequately challenge the social norms, and intersecting power relations which contribute to discrimination and marginalisation.</p> <p>Conclusions: If key actors in devolved decision-making structures are to ensure progress towards universal health coverage, there is need for intersectoral policy action to address social determinants, promote equity and identify ways to challenge and shift power imbalances in priority-setting processes.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30700299/</p>
85.	<p>Kitsao-Wekulo P, Holding PA, Kvalsvig JD, Alcock KJ, Taylor HG. Measurement of expressive vocabulary in school-age children: Development and application of the Kilifi Naming Test (KNT). <i>Appl Neuropsychol Child</i>. 2019 Jan-Mar;8(1):24-39.</p> <p>Abstract</p> <p>The dearth of locally developed measures of language makes it difficult to detect language and communication problems among school-age children in sub-Saharan African settings. We sought to describe variability in vocabulary acquisition as an important element of global cognitive functioning. Our primary aims were to establish the psychometric properties of an expressive vocabulary measure, examine sources of variability, and investigate the measure's associations with non-verbal reasoning and</p>



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	<p>educational achievement. The study included 308 boys and girls living in a predominantly rural district in Kenya. The developed measure, the Kilifi Naming Test (KNT), had excellent reliability and acceptable convergent validity. However, concurrent validity was not adequately demonstrated. In the final regression model, significant effects of schooling and area of residence were recorded. Contextual factors should be taken into account in the interpretation of test scores. There is need for future studies to explore the concurrent validity of the KNT further.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/29023138/</p>
86.	<p>Mauti J, Gautier L, De Neve JW, Beiersmann C, Tosun J, Jahn A. Kenya's Health in All Policies strategy: a policy analysis using Kingdon's multiple streams. <i>Health Res Policy Syst.</i> 2019 Feb 6;17(1):15.</p> <p>Abstract</p> <p>Background: Health in All Policies (HiAP) is an intersectoral approach that facilitates decision-making among policy-makers to maximise positive health impacts of other public policies. Kenya, as a member of WHO, has committed to adopting HiAP, which has been included in the Kenya Health Policy for the period 2014-2030. This study aims to assess the extent to which this commitment is being translated into the process of governmental policy-making and supported by international development partners as well as non-state actors.</p> <p>Methods: To examine HiAP in Kenya, a qualitative case study was performed, including a review of relevant policy documents. Furthermore, 40 key informants with diverse backgrounds (government, UN agencies, development agencies, civil society) were interviewed. Analysis was carried out using the main dimensions of Kingdon's Multiple Streams Approach (problems, policy, politics).</p> <p>Results: Kenya is facing major health challenges that are influenced by various social determinants, but the implementation of intersectoral action focusing on health promotion is still arbitrary. On the policy level, little is known about HiAP in other government ministries. Many health-related collaborations exist under the concept of intersectoral collaboration, which is prominent in the country's development framework - Vision 2030 - but with no specific reference to HiAP. Under the political stream, the study highlights that political commitment from the highest office would facilitate mainstreaming the HiAP strategy, e.g. by setting up a department under the President's Office. The budgeting process and planning for the Sustainable Development Goals were found to be potential windows of opportunity.</p> <p>Conclusion: While HiAP is being adopted as policy in Kenya, it is still perceived by many stakeholders as the business of the health sector, rather than a policy for the whole government and beyond. Kenya's Vision 2030 should use HiAP to foster progress in all sectors with health promotion as an explicit goal.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30728042/</p>



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87. Tickell KD, Mangale DI, Tornberg-Belanger SN, Bourdon C, Thitiri J, Timbwa M, Njirammadzi J, Voskuijl W, Chisti MJ, Ahmed T, Shahid ASMSB, Diallo AH, Ouédraogo I, Khan AF, Saleem AF, Arif F, Kazi Z, Mupere E, Mukisa J, Sukhtankar P, Berkley JA, Walson JL, Denno DM; Childhood Acute Illness and Nutrition Network. A mixed method multi-country assessment of barriers to implementing pediatric inpatient care guidelines. *PLoS One*. 2019 Mar 25;14(3):e0212395.

Abstract

Introduction: Accelerating progress in reducing child deaths is needed in order to achieve the Sustainable Development Goal child mortality target. This will require a focus on vulnerable children-including young children, those who are undernourished or with acute illnesses requiring hospitalization. Improving adherence to inpatient guidelines may be an important strategy to reduce child mortality, including among the most vulnerable. The aim of our assessment of nine sub-Saharan African and South Asian hospitals was to determine adherence to pediatric inpatient care recommendations, in addition to capacity for and barriers to implementation of guideline-adherent care prior to commencing the Childhood Acute Illness and Nutrition (CHAIN) Cohort study. The CHAIN Cohort study aims to identify modifiable risk factors for poor inpatient and post discharge outcomes above and beyond implementation of guidelines.

Methods: Hospital infrastructure, staffing, durable equipment, and consumable supplies such as medicines and laboratory reagents, were evaluated through observation and key informant interviews. Inpatient medical records of 2-23 month old children were assessed for adherence to national and international guidelines. The records of children with severe acute malnutrition (SAM) were oversampled to reflect the CHAIN study population. Seven core adherence indicators were examined: oximetry and oxygen therapy, fluids, anemia diagnosis and transfusion, antibiotics, malaria testing and antimalarials, nutritional assessment and management, and HIV testing.

Results: All sites had facilities and equipment necessary to implement care consistent with World Health Organization and national guidelines. However, stockouts of essential medicines and laboratory reagents were reported to be common at some sites, even though they were mostly present during the assessment visits. Doctor and nurse to patient ratios varied widely. We reviewed the notes of 261 children with admission diagnoses of sepsis (17), malaria (47), pneumonia (70), diarrhea (106), and SAM (119); 115 had multiple diagnoses. Adherence to oxygen therapy, antimalarial, and malnutrition refeeding guidelines was >75%. Appropriate antimicrobials were prescribed for 75% of antibiotic-indicative conditions. However, 20/23 (87%) diarrhea and 20/27 (74%) malaria cases without a documented indication were prescribed antibiotics. Only 23/122 (19%) with hemoglobin levels meeting anemia criteria had recorded anemia diagnoses. HIV test results were infrequently documented even at hospitals with universal screening policies (66/173, 38%). Informants at all sites attributed inconsistent guideline implementation to inadequate staffing.



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	<p>Conclusion: Assessed hospitals had the infrastructure and equipment to implement guideline-consistent care. While fluids, appropriate antimalarials and antibiotics, and malnutrition refeeding adherence was comparable to published estimates from low- and high-resource settings, there were inconsistencies in implementation of some other recommendations. Stockouts of essential therapeutics and laboratory reagents were a noted barrier, but facility staff perceived inadequate human resources as the primary constraint to consistent guideline implementation.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30908499/</p>
88.	<p>Tagoe N, Molyneux S, Pulford J, Murunga VI, Kinyanjui S. Managing health research capacity strengthening consortia: a systematised review of the published literature. <i>BMJ Glob Health</i>. 2019 Apr 14;4(2):e001318.</p> <p>Abstract</p> <p>Background: Locally relevant research is considered critical for advancing health and development in low- and middle-income countries (LMICs). Accordingly, health research capacity strengthening (HRCS) efforts have intensified, increasingly through consortia. Yet, the knowledge base for managing such consortia is not well defined. This review aimed to ascertain the scope and quality of published literature on HRCS consortium management processes, management-related factors influencing consortium operations and outcomes, and the knowledge gaps.</p> <p>Methods: Given the paucity of published HRCS literature, a 'systematised review' as outlined by Grant and Booth was conducted, modelling the systematic review process without restriction to research-based publications. A systematic search in PubMed and Scopus was carried out coupled with a manual search for papers using reference checking and citation searching. A quality appraisal of eligible articles using the Mixed Method Appraisal Tool was undertaken. Thematic synthesis was used to analyse the extracted data.</p> <p>Results: The search identified 55 papers, made up of 18 empirical papers and 37 commentaries focusing on consortium-based HRCS initiatives involving LMICs and reporting management-related data. The review indicates increasing efforts being made in the HRCS field in reporting consortia outcomes. However, it highlights the dearth of high-quality empirical research on HRCS consortium management and the nascent nature of the field with most papers published after 2010. The available literature highlights the importance of relational management factors such as equity and power relations in influencing consortium success, though these factors were not explored in depth. Operational management processes and their role in the capacity strengthening pathway were rarely examined.</p> <p>Conclusion: Findings indicate a weak evidence base for HRCS consortium management both in terms of quantity and conceptual depth, demonstrating the need for an expanded research effort to inform HRCS practice.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31139450/</p>



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89.	<p>Ssewanyana D, van Baar A, Mwangala PN, Newton CR, Abubakar A. Inter-relatedness of underlying factors for injury and violence among adolescents in rural coastal Kenya: A qualitative study. <i>Health Psychol Open</i>. 2019 May 13;6(1):2055102919849399.</p> <p>Abstract</p> <p>We utilized a socio-ecological model to explore views from 85 young people and 10 local stakeholders on forms and underlying factors for unintentional injury, violence, self-harm, and suicidal behavior of adolescents in Kilifi County, Kenya. Young people took part in 11 focus group discussions, whereas 10 in-depth interviews were conducted with the local stakeholders. Road traffic accidents, falls, fights, sexual and gender-based violence, theft, and vandalism were viewed as common. There was an overlap of risk factors, especially at intra- and interpersonal levels (gender, poverty, substance use, parenting behavior, school drop-out). Some broader-level risk factors were insecure neighborhoods and risky sources of livelihood. Research is needed to quantify burden and to pilot feasible injury prevention interventions in this setting.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31205735/</p>
90.	<p>Nyongesa MK, Mwangi P, Wanjala SW, Mutua AM, Newton CRJC, Abubakar A. Prevalence and correlates of depressive symptoms among adults living with HIV in rural Kilifi, Kenya. <i>BMC Psychiatry</i>. 2019 Nov 1;19(1):333.</p> <p>Abstract</p> <p>Background: Published research on depression among people living with HIV/AIDS (PLWHA) from Africa is increasing, but data from Kenya remains scarce. This cross-sectional study measured the prevalence and correlates of depressive symptoms among PLWHA in rural Kilifi, on the Kenyan coast.</p> <p>Methods: Between February and April 2018, we consecutively recruited and interviewed 450 adults living with HIV and on combination antiretroviral therapy (cART). Depressive symptoms were assessed with the 9-item Patient Health Questionnaire (PHQ-9), with a positive depression screen defined as PHQ-9 score ≥ 10. Measures of psychosocial, health, and treatment characteristics were also administered.</p> <p>Results: The overall prevalence of depressive symptoms was 13.8% (95% Confidence Interval (95%CI): 10.9, 17.3). Multivariable logistic regression analysis identified current comorbid chronic illness (adjusted Odds Ratio (aOR) 5.72, 95% CI: 2.28, 14.34; $p < 0.001$), cART regimen (aOR 6.93, 95%CI: 2.34, 20.49; $p < 0.001$), perceived HIV-related stigma (aOR 1.10, 95%CI: 1.05, 1.14, $p < 0.001$) and difficulties accessing HIV care and treatment services (aOR 2.37, 95%CI: 1.14, 4.91; $p = 0.02$) as correlates of depressive symptoms.</p> <p>Conclusion: The prevalence of depressive symptoms among adults living with HIV on the Kenyan coast is high. Those at high risk for elevated depressive symptoms (e.g., with comorbid chronic illnesses, on second-line cART, experiencing perceived HIV-stigma or with problems accessing HIV care) may benefit from early identification, treatment or referral, which requires integration of mental health programmes into HIV primary care.</p>



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	Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31675938/
91.	<p>Githang'a D, Wangia RN, Mureithi MW, Wandiga SO, Mutegi C, Ogutu B, Agweyu A, Wang JS, Anzala O. The effects of aflatoxin exposure on Hepatitis B-vaccine induced immunity in Kenyan children. <i>Curr Probl Pediatr Adolesc Health Care</i>. 2019 May;49(5):117-130.</p> <p>Abstract</p> <p>Background: Globally, approximately three million children die each year from vaccine preventable infectious diseases mainly in developing countries. Despite the success of the expanded immunization program, not all infants and children around the world develop the same protective immune response to the same vaccine. A vaccine must induce a response over the basal immune response that may be driven by population-specific, environmental or socio-economic factors. Mycotoxins like aflatoxins are immune suppressants that are confirmed to interfere with both cell-mediated and acquired immunity. The mechanism of aflatoxin toxicity is through the binding of the bio-activated AFB1-8, 9-epoxide to cellular macromolecules.</p> <p>Methods: We studied Hepatitis B surface antibodies [anti-HBs] levels to explore the immune modulation effects of dietary exposure to aflatoxins in children aged between one and fourteen years in Kenya. Hepatitis B vaccine was introduced for routine administration for Kenyan infants in November 2001. To assess the effects of aflatoxin on immunogenicity of childhood vaccines Aflatoxin B1-lysine in blood serum samples were determined using High Performance Liquid Chromatography with Fluorescence detection while anti-HBs were measured using Bio-ELISA anti-HBs kit.</p> <p>Results: The mean \pm SD of AFB1-lysine adducts in our study population was 45.38 ± 87.03 pg/mg of albumin while the geometric mean was 20.40 pg/mg. The distribution of AFB1-lysine adducts was skewed to the right. Only 98/205 (47.8%) of the study population tested positive for Hepatitis B surface antibodies. From regression analysis, we noted that for</p>



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	<p>every unit rise in serum aflatoxin level, anti-HBs dropped by 0.91 mIU/ml (-0.9110038; 95% C.I -1.604948, -0.21706).</p> <p>Conclusion: Despite high coverage of routine immunization, less than half of the study population had developed immunity to HepB. Exposure to aflatoxin was high and weakly associated with low anti-HBs antibodies. These findings highlight a potentially significant role for environmental factors that may contribute to vaccine effectiveness warranting further research.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31103452/</p>
92	<p>Radovich E, Dennis ML, Barasa E, Cavallaro FL, Wong KL, Borghi J, Lynch CA, Lyons-Amos M, Abuya T, Benova L. Who pays and how much? A cross-sectional study of out-of-pocket payment for modern contraception in Kenya. <i>BMJ Open</i>. 2019 Feb 20;9(2):e022414.</p> <p>Abstract</p> <p>Objectives: Out-of-pocket (OOP) payment for modern contraception is an understudied component of healthcare financing in countries like Kenya, where wealth gradients in met need have prompted efforts to expand access to free contraception. This study aims to examine whether, among public sector providers, the poor are more likely to receive free contraception and to compare how OOP payment for injectables and implants-two popular methods-differs by public/private provider type and user's sociodemographic characteristics.</p> <p>Design, setting and participants: Secondary analyses of nationally representative, cross-sectional household data from the 2014 Kenya Demographic and Health Survey. Respondents were women of reproductive age (15-49 years). The sample comprised 5717 current modern contraception users, including 2691 injectable and 1073 implant users with non-missing expenditure values.</p>



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	<p>Main outcome: Respondent's self-reported source and payment to obtain their current modern contraceptive method.</p> <p>Methods: We used multivariable logistic regression to examine predictors of free public sector contraception and compared average expenditure for injectable and implant. Quintile ratios examined progressivity of non-zero expenditure by wealth.</p> <p>Results: Half of public sector users reported free contraception; this varied considerably by method and region. Users of implants, condoms, pills and intrauterine devices were all more likely to report receiving their method for free ($p < 0.001$) compared with injectable users. The poorest were as likely to pay for contraception as the wealthiest users at public providers (OR: 1.10, 95% CI: 0.64 to 1.91). Across all providers, among users with non-zero expenditure, injectable and implant users reported a mean OOP payment of Kenyan shillings (KES) 80 (US\$0.91), 95% CI: KES 78 to 82 and KES 378 (US\$4.31), 95% CI: KES 327 to 429, respectively. In the public sector, expenditure was pro-poor for injectable users yet weakly pro-rich for implant users.</p> <p>Conclusions: More attention is needed to targeting subsidies to the poorest and ensuring government facilities are equipped to cope with lost user fee revenue.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30787074/</p>
93	<p>Morobe JM, Nyiro JU, Brand S, Kamau E, Gicheru E, Eyase F, Otieno GP, Munywoki PK, Agoti CN, Nokes DJ. Human rhinovirus spatial-temporal epidemiology in rural coastal Kenya, 2015-2016, observed through outpatient surveillance. <i>Wellcome Open Res.</i> 2019 Mar 27;3:128.</p> <p>Abstract</p> <p>Background: Human rhinovirus (HRV) is the predominant cause of upper respiratory tract infections, resulting in a significant public health burden. The virus circulates as many different types (168), each generating strong homologous, but weak heterotypic, immunity. The influence of these features on transmission patterns of HRV in the community is understudied. Methods: Nasopharyngeal swabs were collected from patients with</p>



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	<p>symptoms of acute respiratory infection (ARI) at nine out-patient facilities across a Health and Demographic Surveillance System between December 2015 and November 2016. HRV was diagnosed by real-time RT-PCR, and the VP4/VP2 genomic region of the positive samples sequenced. Phylogenetic analysis was used to determine the HRV types. Classification models and G-test statistic were used to investigate HRV type spatial distribution. Demographic characteristics and clinical features of ARI were also compared. Results: Of 5,744 NPS samples collected, HRV was detected in 1057 (18.4%), of which 817 (77.3%) were successfully sequenced. HRV species A, B and C were identified in 360 (44.1%), 67 (8.2%) and 390 (47.7%) samples, respectively. In total, 87 types were determined: 39, 10 and 38 occurred within species A, B and C, respectively. HRV types presented heterogeneous temporal patterns of persistence. Spatially, identical types occurred over a wide distance at similar times, but there was statistically significant evidence for clustering of types between health facilities in close proximity or linked by major road networks. Conclusion: This study records a high prevalence of HRV in out-patient presentations exhibiting high type diversity. Patterns of occurrence suggest frequent and independent community invasion of different types. Temporal differences of persistence between types may reflect variation in type-specific population immunity. Spatial patterns suggest either rapid spread or multiple invasions of the same type, but evidence of similar types amongst close health facilities, or along road systems, indicate type partitioning structured by local spread.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30483602/</p>
94	<p>Abdullahi OA, Ngari MM, Sanga D, Katana G, Willetts A. Mortality during treatment for tuberculosis; a review of surveillance data in a rural county in Kenya. PLoS One. 2019 Jul 11;14(7):e0219191.</p> <p>Abstract</p>



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	<p>Background: Globally in 2016, 1.7 million people died of Tuberculosis (TB). This study aimed to estimate all-cause mortality rate, identify features associated with mortality and describe trend in mortality rate from treatment initiation.</p> <p>Method: A 5-year (2012-2016) retrospective analysis of electronic TB surveillance data from Kilifi County, Kenya. The outcome was all-cause mortality within 180 days after starting TB treatment. The risk factors examined were demographic and clinical features at the time of starting anti-TB treatment. We performed survival analysis with time at risk defined from day of starting TB treatment to time of death, lost-to-follow-up or completing treatment. To account for 'lost-to-follow-up' we used competing risk analysis method to examine risk factors for all-cause mortality.</p> <p>Results: 10,717 patients receiving TB treatment, median (IQR) age 33 (24-45) years were analyzed; 3,163 (30%) were HIV infected. Overall, 585 (5.5%) patients died; mortality rate of 12.2 (95% CI 11.3-13.3) deaths per 100 person-years (PY). Mortality rate increased from 7.8 (95% CI 6.4-9.5) in 2012 to 17.7 (95% CI 14.9-21.1) in 2016 per 100PY (Ptrend<0.0001). 449/585 (77%) of the deaths occurred within the first three months after starting TB treatment. The median time to death (IQR) declined from 87 (40-100) days in 2012 to 46 (18-83) days in 2016 (Ptrend = 0.04). Mortality rate per 100PY was 7.3 (95% CI 6.5-7.8) and 23.1 (95% CI 20.8-25.7) among HIV-uninfected and HIV-infected patients respectively. Age, being a female, extrapulmonary TB, being undernourished, HIV infected and year of diagnosis were significantly associated with mortality.</p> <p>Conclusions: We found most deaths occurred within three months and an increasing mortality rate during the time under review among patients on TB treatment. Our results therefore warrant further investigation to explore host, disease or health system factors that may explain this trend.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31295277/</p>
95	Etyang AO, Sigilai A, Odipo E, Oyando R, Ong'ayo G, Muthami L, Munge K,



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Kirui F, Mbui J, Bukania Z, Mwai J, Obala A, Barasa E. Diagnostic Accuracy of Unattended Automated Office Blood Pressure Measurement in Screening for Hypertension in Kenya. *Hypertension*. 2019 Dec;74(6):1490-1498.

Abstract

Despite increasing adoption of unattended automated office blood pressure (uAOBP) measurement for determining clinic blood pressure (BP), its diagnostic performance in screening for hypertension in low-income settings has not been determined. We determined the validity of uAOBP in screening for hypertension, using 24-hour ambulatory BP monitoring as the reference standard. We studied a random population sample of 982 Kenyan adults; mean age, 42 years; 60% women; 2% with diabetes mellitus; none taking antihypertensive medications. We calculated sensitivity using 3 different screen positivity cutoffs ($\geq 130/80$, $\geq 135/85$, and $\geq 140/90$ mm Hg) and other measures of validity/agreement. Mean 24-hour ambulatory BP monitoring systolic BP was similar to mean uAOBP systolic BP (mean difference, 0.6 mm Hg; 95% CI, -0.6 to 1.9), but the 95% limits of agreement were wide (-39 to 40 mm Hg). Overall discriminatory accuracy of uAOBP was the same (area under receiver operating characteristic curves, 0.66-0.68; 95% CI range, 0.64-0.71) irrespective of uAOBP cutoffs used. Sensitivity of uAOBP displayed an inverse association ($P < 0.001$) with the cutoff selected, progressively decreasing from 67% (95% CI, 62-72) when using a cutoff of $\geq 130/80$ mm Hg to 55% (95% CI, 49-60) at $\geq 135/85$ mm Hg to 44% (95% CI, 39-49) at $\geq 140/90$ mm Hg. Diagnostic performance was significantly better ($P < 0.001$) in overweight and obese individuals (body mass index, > 25 kg/m²). No differences in results were present in other subanalyses. uAOBP misclassifies significant proportions of individuals undergoing screening for hypertension in Kenya. Additional studies on how to improve screening strategies in this setting are needed.

Pubmed link-<https://pubmed.ncbi.nlm.nih.gov/31587589/>

96 Kabia E, Mbau R, Oyando R, Oduor C, Bigogo G, Khagayi S, Barasa E. "We are



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called the et cetera": experiences of the poor with health financing reforms that target them in Kenya. *Int J Equity Health*. 2019 Jun 24;18(1):98.

Abstract

Background: Through a number of healthcare reforms, Kenya has demonstrated its intention to extend financial risk protection and service coverage for poor and vulnerable groups. These reforms include the provision of free maternity services, user-fee removal in public primary health facilities and a health insurance subsidy programme (HISP) for the poor. However, the available evidence points to inequity and the likelihood that the poor will still be left behind with regards to financial risk protection and service coverage. This study examined the experiences of the poor with health financing reforms that target them.

Methods: We conducted a qualitative cross-sectional study in two purposively selected counties in Kenya. We collected data through focus group discussions (n = 8) and in-depth interviews (n = 30) with people in the lowest wealth quintile residing in the health and demographic surveillance systems, and HISP beneficiaries. We analyzed the data using a framework approach focusing on four healthcare access dimensions; geographical accessibility, affordability, availability, and acceptability.

Results: Health financing reforms reduced financial barriers and improved access to health services for the poor in the study counties. However, various access barriers limited the extent to which they benefited from these reforms. Long distances, lack of public transport, poor condition of the roads and high transport costs especially in rural areas limited access to health facilities. Continued charging of user fees despite their abolition, delayed insurance reimbursements to health facilities that HISP beneficiaries were seeking care from, and informal fees exposed the poor to out of pocket payments. Stock-outs of medicine and other medical supplies, dysfunctional medical equipment, shortage of healthcare workers, and frequent strikes adversely affected the availability of health services. Acceptability of care was further limited by discrimination by healthcare workers and



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	<p>ineffective grievance redress mechanisms which led to a feeling of disempowerment among the poor.</p> <p>Conclusions: Pro-poor health financing reforms improved access to care for the poor to some extent. However, to enhance the effectiveness of pro-poor reforms and to ensure that the poor in Kenya benefit fully from them, there is a need to address barriers to healthcare seeking across all access dimensions.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31234940/</p>
97	<p>Roxby AC, Yuhas K, Farquhar C, Bosire R, Mbori-Ngacha D, Richardson BA, Totten PA, John-Stewart G. Mycoplasma genitalium infection among HIV-infected pregnant African women and implications for mother-to-child transmission of HIV. AIDS. 2019 Nov 15;33(14):2211-2217.</p> <p>Abstract</p> <p>Objective: Many sexually transmitted infections increase risk of mother-to-child transmission (MTCT) of HIV, but the effect of Mycoplasma genitalium is not known. We hypothesized that M. genitalium infection would be common among HIV-infected pregnant women and could be associated with in-utero and intrapartum MTCT.</p> <p>Design: Observational case-cohort study.</p> <p>Methods: The current study used specimens from a Kenyan perinatal MTCT cohort (1999-2005) involving HIV-infected women and their infants, who received short-course zidovudine for prevention of MTCT. Vaginal swabs collected at 32 weeks gestation were tested for M. genitalium using a transcription-mediated amplification assay. Infant perinatal HIV infection was determined at birth and 4 weeks of age by DNA PCR. Using a case-cohort design, a random sample was generated with 3 : 1 control : case ratio; prevalence and correlates of M. genitalium were assessed with chi-squared and t tests; predictors of infant outcomes were analyzed using logistic regression.</p>



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	<p>Results: Among 220 HIV-infected pregnant women evaluated, 47 women (21.4%) had <i>M. genitalium</i>. Antenatal <i>M. genitalium</i> infection was associated with higher HIV RNA in plasma (5.0 vs. 4.6 log₁₀ copies/ml in <i>M. genitalium</i>-positive vs. <i>M. genitalium</i>-negative women, $P = 0.02$) at 32 weeks. Women with <i>M. genitalium</i> were less likely to report prior sexually transmitted infections and genital ulcers (both $P = 0.05$). There was no association found between exposure to <i>M. genitalium</i> and perinatal MTCT (odds ratio = 0.72, 95% confidence interval 0.35, 1.51, $P = 0.39$).</p> <p>Conclusion: Vaginal <i>M. genitalium</i> infection was frequently detected among Kenyan HIV-infected pregnant women and was associated with higher plasma HIV levels, but was not associated with perinatal transmission of HIV.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31385863/</p>
98	<p>Mwandawiro C, Okoyo C, Kihara J, Simiyu E, Kepha S, Campbell SJ, Freeman MC, Brooker SJ, Njenga SM. Results of a national school-based deworming programme on soil-transmitted helminths infections and schistosomiasis in Kenya: 2012-2017. <i>Parasit Vectors</i>. 2019 Feb 7;12(1):76.</p> <p>Abstract</p> <p>Background: Soil-transmitted helminth (STH) and schistosome infections are among the most prevalent neglected tropical diseases (NTDs) in the world. School-aged children are particularly vulnerable to these chronic infections that can impair growth, nutritional status and cognitive ability. Mass drug administration (MDA) delivered either once or twice annually is a safe and effective approach recommended by the World Health Organization (WHO) to reduce worm burden. In 2012, Kenya began a national school-based deworming programme (NSBDP) aimed at reducing infection and associated morbidity. The change in prevalence and intensity of these infections was monitored over five years (2012-2017). Here, we present the changes in STH and schistosome infections between baseline and endline assessments, as well as explore the yearly patterns of infection reductions.</p>



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	<p>Methods: We used series of pre- and post-MDA intervention, repeat cross-sectional surveys in a representative, stratified, two-stage sample of schools in 16 counties of Kenya. The programme consisted of two tiers of monitoring; a national baseline, midterm and endline surveys consisting of 200 schools, and pre- and post-MDA surveys conducted yearly consisting of 60 schools. Stool and urine samples were collected from randomly selected school children and examined for STH and schistosome infections using Kato-Katz and urine filtration techniques respectively.</p> <p>Results: Overall, 32.3%, 16.4% and 13.5% of the children were infected with any STH species during baseline, midterm and endline assessment, respectively, with a relative reduction of 58.2% over the five-year period. The overall prevalence of <i>S. mansoni</i> was 2.1%, 1.5% and 1.7% and of <i>S. haematobium</i> was 14.8%, 6.8% and 2.4%, respectively, for baseline, midterm and endline surveys. We observed inter-region and inter-county heterogeneity variation in the infection levels.</p> <p>Conclusions: The analysis provided robust assessment of the programme and outlined the current prevalence, mean intensity and re-infection pattern of these infections. Our findings will allow the Government of Kenya to make informed decisions on the strategy to control and eliminate these NTDs. Our results suggest that complimentary interventions may have to be introduced to sustain the chemotherapeutic gains of MDA and accelerate attainment of elimination of these NTDs as a public health problem in Kenya.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30732642/</p>
99	<p>Toy T, Pak GD, Duc TP, Campbell JI, El Tayeb MA, Von Kalckreuth V, Im J, Panzner U, Cruz Espinoza LM, Eibach D, Dekker DM, Park SE, Jeon HJ, Konings F, Mogeni OD, Cosmas L, Bjerregaard-Andersen M, Gasmelseed N, Hertz JT, Jaeger A, Krumkamp R, Ley B, Thriemer K, Kabore LP, Niang A, Raminosa TM, Sampo E, Sarpong N, Soura A, Owusu-Dabo E, Teferi M, Yeshitela B, Poppert S, May J, Kim JH, Chon Y, Park JK, Aseffa A, Breiman RF, Schütt-Gerowitt H, Aaby P, Adu-</p>



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Sarkodie Y, Crump JA, Rakotozandrainy R, Meyer CG, Sow AG, Clemens JD, Wierzba TF, Baker S, Marks F. Multicountry Distribution and Characterization of Extended-spectrum β -Lactamase-associated Gram-negative Bacteria From Bloodstream Infections in Sub-Saharan Africa. *Clin Infect Dis*. 2019 Oct 30;69(Suppl 6):S449-S458.

Abstract

Background: Antimicrobial resistance (AMR) is a major global health concern, yet, there are noticeable gaps in AMR surveillance data in regions such as sub-Saharan Africa. We aimed to measure the prevalence of extended-spectrum β -lactamase (ESBL) producing Gram-negative bacteria in bloodstream infections from 12 sentinel sites in sub-Saharan Africa.

Methods: Data were generated during the Typhoid Fever Surveillance in Africa Program (TSAP), in which standardized blood cultures were performed on febrile patients attending 12 health facilities in 9 sub-Saharan African countries between 2010 and 2014. Pathogenic bloodstream isolates were identified at the sites and then subsequently confirmed at a central reference laboratory. Antimicrobial susceptibility testing, detection of ESBL production, and conventional multiplex polymerase chain reaction (PCR) testing for genes encoding for β -lactamase were performed on all pathogens.

Results: Five hundred and five pathogenic Gram-negative bloodstream isolates were isolated during the study period and available for further characterization. This included 423 Enterobacteriaceae. Phenotypically, 61 (12.1%) isolates exhibited ESBL activity, and genotypically, 47 (9.3%) yielded a PCR amplicon for at least one of the screened ESBL genes. Among specific Gram-negative isolates, 40 (45.5%) of 88 *Klebsiella* spp., 7 (5.7%) of 122 *Escherichia coli*, 6 (16.2%) of 37 *Acinetobacter* spp., and 2 (1.3%) of 159 nontyphoidal *Salmonella* (NTS) showed phenotypic ESBL activity.

Conclusions: Our findings confirm the presence of ESBL production among pathogens causing bloodstream infections in sub-Saharan Africa. With few alternatives for managing



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	<p>ESBL-producing pathogens in the African setting, measures to control the development and proliferation of AMR organisms are urgently needed.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31665776/</p>
100	<p>Camlin CS, Akullian A, Neilands TB, Getahun M, Bershteyn A, Ssali S, Geng E, Gandhi M, Cohen CR, Maeri I, Eyul P, Petersen ML, Havlir DV, Kanya MR, Bukusi EA, Charlebois ED. Gendered dimensions of population mobility associated with HIV across three epidemics in rural Eastern Africa. <i>Health Place</i>. 2019 May;57:339-351.</p> <p>Abstract</p> <p>Mobility in sub-Saharan Africa links geographically-separate HIV epidemics, intensifies transmission by enabling higher-risk sexual behavior, and disrupts care. This population-based observational cohort study measured complex dimensions of mobility in rural Uganda and Kenya. Survey data were collected every 6 months beginning in 2016 from a random sample of 2308 adults in 12 communities across three regions, stratified by intervention arm, baseline residential stability and HIV status. Analyses were survey-weighted and stratified by sex, region, and HIV status. In this study, there were large differences in the forms and magnitude of mobility across regions, between men and women, and by HIV status. We found that adult migration varied widely by region, higher proportions of men than women migrated within the past one and five years, and men predominated across all but the most localized scales of migration: a higher proportion of women than men migrated within county of origin. Labor-related mobility was more common among men than women, while women were more likely to travel for non-labor reasons. Labor-related mobility was associated with HIV positive status for both men and women, adjusting for age and region, but the association was especially pronounced in women. The forms, drivers, and correlates of mobility in eastern Africa are complex and</p>



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	<p>highly gendered. An in-depth understanding of mobility may help improve implementation and address gaps in the HIV prevention and care continua.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31152972/</p>
101	<p>Laidemitt MR, Brant SV, Mutuku MW, Mkoji GM, Loker ES. The diverse echinostomes from East Africa: With a focus on species that use Biomphalaria and Bulinus as intermediate hosts. <i>Acta Trop.</i> 2019 May;193:38-49.</p> <p>Abstract</p> <p>Echinostomes are a diverse group of digenetic trematodes that are globally distributed. The diversity of echinostomes in Africa remains largely unknown, particularly in analyses using molecular markers. Therefore, we were interested in the composition and host usage patterns of African echinostomes, especially those that also use schistosome transmitting snails as intermediate hosts. We collected adults and larval stages of echinostomes from 19 different localities in East Africa (1 locality in Uganda and 18 in Kenya). In this study we provide locality information, host use, museum vouchers, and genetic data for two loci (28S and nad1) from 98 samples of echinostomes from East Africa. Combining morphological features, host use information, and phylogenetic analyses we found 17 clades of echinostomes in East Africa. Four clades were found to use more than one genus of freshwater snails as their first intermediate hosts. We also determined at least partial life cycles (2 of the 3) of four clades using molecular markers. Of the 17 clades, 13 use Biomphalaria or Bulinus as a first intermediate host. The overlap in host usage creates opportunities for competition, including against human schistosomes. Thus, our study can be used as a foundation for future studies to ascertain the interactions between schistosomes and echinostomes in their respective intermediate hosts.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30710531/</p>



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102 Huerga H, Ferlazzo G, Wanjala S, Bastard M, Bevilacqua P, Ardizzoni E, Sitienei J, Bonnet M. Mortality in the first six months among HIV-positive and HIV-negative patients empirically treated for tuberculosis. *BMC Infect Dis.* 2019 Feb 11;19(1):132.

Abstract

Background: Empirical treatment of tuberculosis (TB) may be necessary in patients with negative or no Xpert MTB/RIF results. In a context with access to Xpert, we assessed mortality in the 6 months after the initial TB consultation among HIV-positive and HIV-negative patients who received empirical TB treatment or TB treatment based on bacteriological confirmation and we compared it with the mortality among those who did not receive TB treatment.

Methods: This prospective cohort study included consecutively adult patients with signs and symptoms of TB attending an outpatient TB clinic in Western Kenya. At the first consultation, patients received a clinical exam and chest X-ray. Sputum was collected for microscopy, Xpert and Mycobacterium tuberculosis complex (MTB) culture. Patients not started on TB treatment were reassessed after 5 days. All patients bacteriologically confirmed (positive Xpert or culture) received TB treatment. Empirical treatment was defined as a decision to start TB treatment without bacteriological confirmation. Patients were reassessed after 6 months.

Results: Of 606 patients included, 344/606 (56.8%) were women. Median age was 35 years [Interquartile Range (IQR):27-47] and 398/594 (67.0%) were HIV-positive. In total, 196/606 (32.3%) patients were Xpert- or culture-positive and 331/606 (54.6%) started TB treatment. Overall, 100/398 (25.1%) HIV-positive and 31/196 (15.8%) HIV-negative patients received empirical treatment. Mortality in the 6 months following the first consultation was 1.6 and 0.8/100 patient-months among HIV-positive and HIV-negative patients respectively. In the multivariate analyses, TB treatment - whether empirical or based on bacteriological confirmation- was not associated with increased mortality among HIV-positive patients (aHR:2.51, 95%CI:0.79-7.90 and aHR:1.25, 95%CI:0.37-4.21



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	<p>respectively). However, HIV-negative patients who received empirical treatment had a higher risk of mortality (aHR:4.85, 95%CI:1.08-21.67) compared to those not started on treatment. HIV-negative patients treated for TB based on bacteriological confirmation did not have a different risk of mortality (aHR:0.77, 95%CI:0.08-7.41).</p> <p>Conclusions: Our findings suggest that in a context with access to Xpert, clinicians should continue using empirical TB treatment in HIV-positive patients with signs and symptoms of TB and negative Xpert results. However, differential diagnoses other than TB should be actively sought before initiating empirical TB treatment, particularly in HIV-negative patients.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30744603/</p>
103	<p>Maina J, Ouma PO, Macharia PM, Alegana VA, Mitto B, Fall IS, Noor AM, Snow RW, Okiro EA. A spatial database of health facilities managed by the public health sector in sub Saharan Africa. <i>Sci Data</i>. 2019 Jul 25;6(1):134.</p> <p>Abstract</p> <p>Health facilities form a central component of health systems, providing curative and preventative services and structured to allow referral through a pyramid of increasingly complex service provision. Access to health care is a complex and multidimensional concept, however, in its most narrow sense, it refers to geographic availability. Linking health facilities to populations has been a traditional per capita index of health care coverage, however, with locations of health facilities and higher resolution population data, Geographic Information Systems allow for a more refined metric of health access, define geographic inequalities in service provision and inform planning. Maximizing the value of spatial health access requires a complete census of providers and their locations. To-date there has not been a single, geo-referenced and comprehensive public health facility database for sub-Saharan Africa. We have assembled national master health facility lists from a variety of government and non-government sources from 50 countries and islands</p>



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	<p>in sub Saharan Africa and used multiple geocoding methods to provide a comprehensive spatial inventory of 98,745 public health facilities.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31346183/</p>
104	<p>Musimbi ZD, Rono MK, Otieno JR, Kibinge N, Ochola-Oyier LI, de Villiers EP, Nduati EW. Peripheral blood mononuclear cell transcriptomes reveal an over-representation of down-regulated genes associated with immunity in HIV-exposed uninfected infants. <i>Sci Rep.</i> 2019 Dec 2;9(1):18124.</p> <p>Abstract</p> <p>HIV-exposed uninfected (HEU) infants are disproportionately at a higher risk of morbidity and mortality, as compared to HIV-unexposed uninfected (HUU) infants. Here, we used transcriptional profiling of peripheral blood mononuclear cells to determine immunological signatures of in utero HIV exposure. We identified 262 differentially expressed genes (DEGs) in HEU compared to HUU infants. Weighted gene co-expression network analysis (WGCNA) identified six modules that had significant associations with clinical traits. Functional enrichment analysis on both DEGs and the six significantly associated modules revealed an enrichment of G-protein coupled receptors and the immune system, specifically affecting neutrophil function and antibacterial responses. Additionally, malaria pathogenicity genes (thrombospondin 1-(THBS 1), interleukin 6 (IL6), and arginine decarboxylase 2 (ADC2)) were down-regulated. Of interest, the down-regulated immunity genes were positively correlated to the expression of epigenetic factors of the histone family and high-mobility group protein B2 (HMGB2), suggesting their role in the dysregulation of the HEU transcriptional landscape. Overall, we show that genes primarily associated with neutrophil mediated immunity were repressed in the HEU infants. Our results suggest that this could be a contributing factor to the increased susceptibility to bacterial infections associated with higher morbidity and mortality commonly reported in HEU infants.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31792230/</p>



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Musimbi ZD, Rono MK, Otieno JR, Kibinge N, Ochola-Oyier LI, de Villiers EP, Nduati EW. Peripheral blood mononuclear cell transcriptomes reveal an over-representation of down-regulated genes associated with immunity in HIV-exposed uninfected infants. *Sci Rep.* 2019 Dec 2;9(1):18124.

Abstract

HIV-exposed uninfected (HEU) infants are disproportionately at a higher risk of morbidity and mortality, as compared to HIV-unexposed uninfected (HUU) infants. Here, we used transcriptional profiling of peripheral blood mononuclear cells to determine immunological signatures of in utero HIV exposure. We identified 262 differentially expressed genes (DEGs) in HEU compared to HUU infants. Weighted gene co-expression network analysis (WGCNA) identified six modules that had significant associations with clinical traits. Functional enrichment analysis on both DEGs and the six significantly associated modules revealed an enrichment of G-protein coupled receptors and the immune system, specifically affecting neutrophil function and antibacterial responses. Additionally, malaria pathogenicity genes (thrombospondin 1-(THBS 1), interleukin 6 (IL6), and arginine decarboxylase 2 (ADC2)) were down-regulated. Of interest, the down-regulated immunity genes were positively correlated to the expression of epigenetic factors of the histone family and high-mobility group protein B2 (HMGB2), suggesting their role in the dysregulation of the HEU transcriptional landscape. Overall, we show that genes primarily associated with neutrophil mediated immunity were repressed in the HEU infants. Our results suggest that this could be a contributing factor to the increased susceptibility to bacterial infections associated with higher morbidity and mortality commonly reported in HEU infants.

Pubmed link- <https://pubmed.ncbi.nlm.nih.gov/31792230/>



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105 Masha SC, Owuor C, Ngoi JM, Cools P, Sanders EJ, Vaneechoutte M, Crucitti T, de Villiers EP. Comparative analysis of the vaginal microbiome of pregnant women with either *Trichomonas vaginalis* or *Chlamydia trachomatis*. PLoS One. 2019 Dec 12;14(12):e0225545.

Abstract

Background: Although the significance of the human vaginal microbiome for health and disease is increasingly acknowledged, there is paucity of data on the differences in the composition of the vaginal microbiome upon infection with different sexually transmitted pathogens.

Method: The composition of the vaginal bacterial community of women with *Trichomonas vaginalis* (TV, N = 18) was compared to that of women with *Chlamydia trachomatis* (CT, N = 14), and to that of controls (N = 21) (women negative for TV, CT and bacterial vaginosis). The vaginal bacterial composition was determined using high throughput sequencing with the Ion 16S metagenomics kit of the variable regions 2, 4 and 8 of the bacterial 16S ribosomal RNA gene from the vaginal swab DNA extract of the women. QIIME and R package "Phyloseq" were used to assess the α - and β -diversity and absolute abundance of the 16S rRNA gene per sample in the three groups. Differences in taxa at various levels were determined using the independent T-test.

Results: A total of 545 operational taxonomic units (OTUs) were identified in all the three groups of which 488 occurred in all three groups (core OTUs). Bacterial α -diversity, by both Simpson's and Shannon's indices, was significantly higher, ($p = 0.056$) and ($p = 0.001$) respectively, among women with either TV or CT than among controls (mean α -diversity TV-infected > CT-infected > Controls). At the genus level, women infected with TV had a significantly ($p < 0.01$) higher abundance of *Parvimonas* and *Prevotella* species compared to both controls and CT-infected women, whereas women infected with CT had a significantly ($p < 0.05$) higher abundance of *Anaerococcus*, *Collinsella*, *Corynebacterium* and *Dialister*.



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	<p>Conclusion: The vaginal microbiomes of TV and CT-infected women were markedly different from each other and from women without TV and CT. Future studies should determine whether the altered microbiomes are merely markers of disease, or whether they actively contribute to the pathology of the two genital infections.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31830061/</p>
106	<p>Agoti CN, Phan MVT, Munywoki PK, Githinji G, Medley GF, Cane PA, Kellam P, Cotten M, Nokes DJ. Genomic analysis of respiratory syncytial virus infections in households and utility in inferring who infects the infant. <i>Sci Rep.</i> 2019 Jul 11;9(1):10076.</p> <p>Abstract</p> <p>Infants (under 1-year-old) are at most risk of life threatening respiratory syncytial virus (RSV) disease. RSV epidemiological data alone has been insufficient in defining who acquires infection from whom (WAIFW) within households. We investigated RSV genomic variation within and between infected individuals and assessed its potential utility in tracking transmission in households. Over an entire single RSV season in coastal Kenya, nasal swabs were collected from members of 20 households every 3-4 days regardless of symptom status and screened for RSV nucleic acid. Next generation sequencing was used to generate >90% RSV full-length genomes for 51.1% of positive samples (191/374). Single nucleotide polymorphisms (SNPs) observed during household infection outbreaks ranged from 0-21 (median: 3) while SNPs observed during single-host infection episodes ranged from 0-17 (median: 1). Using the viral genomic data alone there was insufficient resolution to fully reconstruct within-household transmission chains. For households with clear index cases, the most likely source of infant infection was via a toddler (aged 1 to <3 years-old) or school-aged (aged 6 to <12 years-old) co-occupant. However, for best resolution of WAIFW within households, we suggest an integrated analysis of RSV genomic and epidemiological data.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31296922/</p>
107	<p>Murphy JL, Ayers T, Foote A, Woods E, Wamola N, Fagerli K, Waiboci L, Mugoh</p>



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	<p>R, Mintz ED, Zhao K, Marano N, O'Reilly CE, Hill VR. Efficacy of a solar concentrator to Inactivate <i>E. coli</i> and <i>C. perfringens</i> spores in latrine waste in Kenya. <i>Sci Total Environ.</i> 2019 Nov 15;691:401-406.</p> <p>Abstract</p> <p>Alternative sanitation options are needed for effective waste management in low-income countries where centralized, large-scale waste treatment is not easily achievable. A newly designed solar concentrator technology utilizes solar thermal energy to treat feces contained in drums. This pilot study assessed the efficacy of the new design to inactivate microbes in 13 treatment drums under field conditions in Kenya. Three-quarters of the drums contained <1000 <i>E. coli</i>/g of total solids following 6 h of solar thermal treatment and inactivation of thermotolerant <i>C. perfringens</i> spores ranged from <1.8 to >5.0 log₁₀. Nearly all (94%) samples collected from treatment drums achieved thermophilic temperatures (>50 °C) during the treatment period, however this alone did not ensure samples met the WHO <i>E. coli</i> guideline; higher, sustained thermophilic temperatures tended to be more effective in reaching this guideline. The newly designed solar concentrator was capable of inactivating thermotolerant, environmentally-stable microorganisms as, or possibly more, efficiently than a previous design. Additional data are needed to better characterize how temperature, time, and other parameters affect the ability of the solar concentrator to inactivate microbes in feces.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31323585/</p>
108	<p>Sande CJ, Njunge JM, Ngoi JM, Mutunga MN, Chege T, Gicheru ET, Gardiner EM, Gwela A, Green CA, Drysdale SB, Berkley JA, Nokes DJ, Pollard AJ. Author Correction: Airway response to respiratory syncytial virus has incidental antibacterial effects. <i>Nat Commun.</i> 2019 Jul 18;10(1):3291.</p> <p>Abstract</p>



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	<p>RSV infection is typically associated with secondary bacterial infection. We hypothesise that the local airway immune response to RSV has incidental antibacterial effects. Using coordinated proteomics and metagenomics analysis we simultaneously analysed the microbiota and proteomes of the upper airway and determined direct antibacterial activity in airway secretions of RSV-infected children. Here, we report that the airway abundance of Streptococcus was higher in samples collected at the time of RSV infection compared with samples collected one month later. RSV infection is associated with neutrophil influx into the airway and degranulation and is marked by overexpression of proteins with known antibacterial activity including BPI, EPX, MPO and AZU1. Airway secretions of children infected with RSV, have significantly greater antibacterial activity compared to RSV-negative controls. This RSV-associated, neutrophil-mediated antibacterial response in the airway appears to act as a regulatory mechanism that modulates bacterial growth in the airways of RSV-infected children.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31101811/</p>
109	<p>: Maia MF, Kapulu M, Muthui M, Wagah MG, Ferguson HM, Dowell FE, Baldini F, Ranford-Cartwright L. Correction to: Detection of Plasmodium falciparum infected Anopheles gambiae using near-infrared spectroscopy. Malar J. 2019 Apr 17;18(1):137.</p> <p>Abstract</p> <p>Background: Large-scale surveillance of mosquito populations is crucial to assess the intensity of vector-borne disease transmission and the impact of control interventions. However, there is a lack of accurate, cost-effective and high-throughput tools for mass-screening of vectors.</p> <p>Methods: A total of 750 Anopheles gambiae (Keele strain) mosquitoes were fed Plasmodium falciparum NF54 gametocytes through standard membrane feeding assay (SMFA) and afterwards maintained in insectary conditions to allow for oocyst (8 days) and sporozoite development (14 days). Thereupon, each mosquito was scanned using near</p>



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	<p>infra-red spectroscopy (NIRS) and processed by quantitative polymerase chain reaction (qPCR) to determine the presence of infection and infection load. The spectra collected were randomly assigned to either a training dataset, used to develop calibrations for predicting oocyst- or sporozoite-infection through partial least square regressions (PLS); or to a test dataset, used for validating the calibration's prediction accuracy.</p> <p>Results: NIRS detected oocyst- and sporozoite-stage <i>P. falciparum</i> infections with 88% and 95% accuracy, respectively. This study demonstrates proof-of-concept that NIRS is capable of rapidly identifying laboratory strains of human malaria infection in African mosquito vectors.</p> <p>Conclusions: Accurate, low-cost, reagent-free screening of mosquito populations enabled by NIRS could revolutionize surveillance and elimination strategies for the most important human malaria parasite in its primary African vector species. Further research is needed to evaluate how the method performs in the field following adjustments in the training datasets to include data from wild-caught infected and uninfected mosquitoes.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30890179/</p>
110	<p>Kibe LW, Kamau AW, Gachigi JK, Habluetzel A, Mbogo CM. A formative study of disposal and re-use of old mosquito nets by communities in Malindi, Kenya. <i>Malariaworld J.</i> 2019 Jul 3;6:9. Epub 2015 Jun 29. PMID: 31293898; PMCID: PMC6616035.</p> <p>Abstract</p> <p>Background: About 30 million insecticide treated mosquito nets have been distributed in Kenya since 2001 and ownership is approaching full coverage. As a consequence of this achievement, Kenya is faced with the challenge of disposing old mosquito nets that are no longer in use. The study aimed at investigating ways of disposal and re-use of old and torn nets by end users.</p>



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	<p>Materials and methods: A formative study was conducted in the former Malindi District, which is comprised of Malindi and Magarini sub-counties of Kilifi County in Coastal Kenya. A total of 6 Focus Group Discussions, 10 Key Informant Interviews and 9 transect walks/drives were undertaken. Data from the different sources were analysed separately and triangulated for similarities and differences.</p> <p>Results: There were variations in disposal and re-use of old nets between urban and rural or peri-urban residents. In all settings, people adopted innovative and beneficial ways of re-using old, expired nets, and those that were damaged beyond repair. Common causes of damage were fire, children, domestic animals sharing the sleeping room and friction from the bed poles while hanging or tacking it in under a sleeping mat. Re-use was most prominent in farming activities (78%) and less to for use in mosquito control, like window screening (15%). The remaining 8% was related to making ropes, swings, footballs, goal posts and fishing nets. Advantageous texture and nature of the netting material, perceived economic benefit and lack of guidelines for disposal were the main reasons cited by residents for re-using old nets.</p> <p>Conclusions: It is important that re-use and disposal of old mosquito nets is distinguished from misuse of newly distributed mosquito nets. Alternative uses of old nets as opposed to misuse of new nets was found to be common in our study.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31293898/</p>
111	<p>Truscott JE, Ower AK, Werkman M, Halliday K, Oswald WE, Gichuki PM, Mcharo C, Brooker S, Njenga SM, Mwandariwo C, Walson JL, Pullan R, Anderson R. Heterogeneity in transmission parameters of hookworm infection within the baseline data from the TUMIKIA study in Kenya. <i>Parasit Vectors</i>. 2019 Sep 16;12(1):442.</p> <p>Abstract</p>



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Background: As many countries with endemic soil-transmitted helminth (STH) burdens achieve high coverage levels of mass drug administration (MDA) to treat school-aged and pre-school-aged children, understanding the detailed effects of MDA on the epidemiology of STH infections is desirable in formulating future policies for morbidity and/or transmission control. Prevalence and mean intensity of infection are characterized by heterogeneity across a region, leading to uncertainty in the impact of MDA strategies. In this paper, we analyze this heterogeneity in terms of factors that govern the transmission dynamics of the parasite in the host population.

Results: Using data from the TUMIKIA study in Kenya (cluster STH prevalence range at baseline: 0-63%), we estimated these parameters and their variability across 120 population clusters in the study region, using a simple parasite transmission model and Gibbs-sampling Monte Carlo Markov chain techniques. We observed great heterogeneity in R_0 values, with estimates ranging from 1.23 to 3.27, while k -values (which vary inversely with the degree of parasite aggregation within the human host population) range from 0.007 to 0.29 in a positive association with increasing prevalence. The main finding of this study is the increasing trend for greater parasite aggregation as prevalence declines to low levels, reflected in the low values of the negative binomial parameter k in clusters with low hookworm prevalence. Localized climatic and socioeconomic factors are investigated as potential drivers of these observed epidemiological patterns.

Conclusions: Our results show that lower prevalence is associated with higher degrees of aggregation and hence prevalence alone is not a good indicator of transmission intensity. As a consequence, approaches to MDA and monitoring and evaluation of community infection status may need to be adapted as transmission elimination is aimed for by targeted treatment approaches.

Pubmed link- <https://pubmed.ncbi.nlm.nih.gov/31522687/>

112 Ong'ayo G, Ooko M, Wang'ondur R, Bottomley C, Nyaguara A, Tsofa BK, Williams



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	<p>TN, Bejon P, Scott JAG, Etyang AO. Effect of strikes by health workers on mortality between 2010 and 2016 in Kilifi, Kenya: a population-based cohort analysis. <i>Lancet Glob Health</i>. 2019 Jul;7(7):e961-e967.</p> <p>Abstract</p> <p>Background: Health workers' strikes are a global occurrence. Kenya has had several strikes by health workers in recent years but their effect on mortality is unknown. We assessed the effect on mortality of six strikes by health workers that occurred from 2010 to 2016 in Kilifi, Kenya.</p> <p>Methods: Using daily mortality data obtained from the Kilifi Health and Demographic Surveillance System, we fitted a negative binomial regression model to estimate the change in mortality during strike periods and in the 2 weeks immediately after strikes. We did subgroup analyses by age, cause of death, and strike week.</p> <p>Findings: Between Jan 1, 2010, and Nov 30, 2016, we recorded 1 829 929 person-years of observation, 6396 deaths, and 128 strike days (median duration of strikes, 18.5 days [range 9-42]). In the primary analysis, no change in all-cause mortality was noted during strike periods (adjusted rate ratio [RR] 0.93, 95% CI 0.81-1.08; p=0.34). Weak evidence was recorded of variation in mortality rates by age group, with an apparent decrease among infants aged 1-11 months (adjusted RR 0.58, 95% CI 0.33-1.03; p=0.064) and an increase among children aged 12-59 months (1.75, 1.11-2.76; p=0.016). No change was noted in mortality rates in post-strike periods and for any category of cause of death.</p> <p>Interpretation: The brief strikes by health workers during the period 2010-16 were not associated with obvious changes in overall mortality in Kilifi. The combined effects of private (and some public) health care during strike periods, a high proportion of out-of-hospital deaths, and a low number of events might have led us to underestimate the effect.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31129126/</p>
113	Marsh V, Mwangome N, Jao I, Wright K, Molyneux S, Davies A. Who should



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decide about children's and adolescents' participation in health research? The views of children and adults in rural Kenya. *BMC Med Ethics*. 2019 Jun 14;20(1):41.

Abstract

Background: International research guidance has shifted towards an increasingly proactive inclusion of children and adolescents in health research in recognition of the need for more evidence-based treatment. Strong calls have been made for the active involvement of children and adolescents in developing research proposals and policies, including in decision-making about research participation. Much evidence and debate on this topic has focused on high-income settings, while the greatest health burdens and research gaps occur in low-middle income countries, highlighting the need to take account of voices from more diverse contexts.

Methods: Between January and March 2014, 56 community representatives and secondary school students were involved in eight group discussions to explore views on the acceptability of involving children and adolescents in research, and how these groups should be involved in decision-making about their own participation. Discussions were voice-recorded and transcriptions analyzed using Framework Analysis, combining deductive and inductive approaches.

Results: Across these discussions, the idea of involving children and adolescents in decision-making about research participation was strongly supported given similar levels of responsibility carried in everyday life; existing capacity that should be recognized; the opportunity for learning involved; varying levels of parental control; and generational shifts towards greater understanding of science for adolescents than their parents. Joint decision-making processes were supported for older children and adolescents, with parental control influenced by perceptions of the risks involved in participation.

Conclusions: Moves towards more active involvement of children and adolescents in planning studies and in making decisions about their participation are supported by these



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	<p>findings from Kenya. Important emerging considerations include the need to take account of the nature proposed studies and prevailing attitudes and understanding of research in identifying children's and adolescents' roles. More research is needed to expand diversity and develop approaches to joint assent and consent processes that would fairly represent children's and adolescents' wishes and interests, towards their long term benefit.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31200697/</p>
114	<p>Ndegwa L, Hatfield KM, Sinkowitz-Cochran R, D'Iorio E, Gupta N, Kimotho J, Woodard T, Chaves SS, Ellingson K. Evaluation of a program to improve hand hygiene in Kenyan hospitals through production and promotion of alcohol-based Handrub - 2012-2014. <i>Antimicrob Resist Infect Control</i>. 2019 Jan 3;8:2.</p> <p>Abstract</p> <p>Although critical to prevent healthcare-associated infections, hand hygiene (HH) compliance is poor in resource-limited settings. In 2012, three Kenyan hospitals began onsite production of alcohol-based handrub (ABHR) and HH promotion. Our aim is to determine the impact of local production of ABHR on HH compliance and perceptions of ABHR. We observed 25,738 HH compliance opportunities and conducted 15 baseline and post-intervention focus group discussions. Hand Hygiene compliance increased from 28% (baseline) to 38% (post-intervention, $p = 0.0003$). Healthcare workers liked the increased accessibility of ABHR, but disliked its smell, feel, and sporadic availability. Onsite production and promotion of ABHR resulted in modest HH improvement. Enhancing the quality of ABHR and addressing logistical barriers could improve program impact.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30622703/</p>
115	<p>Fogel JM, Sandfort T, Zhang Y, Guo X, Clarke W, Breaud A, Cummings V, Hamilton EL, Ogendo A, Kayange N, Panchia R, Dominguez K, Chen YQ, Eshleman SH. Accuracy of Self-Reported HIV Status Among African Men and Transgender Women Who Have Sex with Men Who were Screened for Participation in a Research Study: HPTN 075. <i>AIDS Behav</i>. 2019 Jan;23(1):289-294.</p>



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	<p>Abstract</p> <p>Some HIV-infected individuals in research studies may choose not to disclose knowledge of their HIV status to study staff. We evaluated the accuracy of self-reported HIV status among African men and transgender women who have sex with men and who were screened for a research study. Sixty-seven of 183 HIV-infected participants reported a prior HIV diagnosis. Samples from the remaining 116 participants were tested for antiretroviral (ARV) drugs. Thirty-six of the 116 participants had ARV drugs detected, indicating that they were on antiretroviral treatment; these participants were classified as previously diagnosed based on ARV drug testing. Among participants classified as previously diagnosed, disclosure of a prior HIV diagnosis varied among study sites ($p = 0.006$) and was more common among those who reported having sex with men only ($p = 0.002$). ARV drug testing in addition to self-report improves the accuracy for identifying individuals with a prior HIV diagnosis.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30051192/</p>
116	<p>Etyang AO, Kapesa S, Odipo E, Bauni E, Kyobutungi C, Abdalla M, Muntner P, Musani SK, Macharia A, Williams TN, Cruickshank JK, Smeeth L, Scott JAG. Effect of Previous Exposure to Malaria on Blood Pressure in Kilifi, Kenya: A Mendelian Randomization Study. <i>J Am Heart Assoc.</i> 2019 Mar 19;8(6):e011771.</p> <p>Abstract</p> <p>Background Malaria exposure in childhood may contribute to high blood pressure (BP) in adults. We used sickle cell trait (SCT) and α-thalassemia, genetic variants conferring partial protection against malaria, as tools to test this hypothesis. Methods and Results Study sites were Kilifi, Kenya, which has malaria transmission, and Nairobi, Kenya, and Jackson, Mississippi, where there is no malaria transmission. The primary outcome was 24-hour systolic BP. Prevalent hypertension, diagnosed using European Society of Hypertension thresholds was a secondary outcome. We performed regression analyses adjusting for age, sex, and estimated glomerular filtration rate. We studied 1127</p>



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	<p>participants in Kilifi, 516 in Nairobi, and 651 in Jackson. SCT frequency was 21% in Kilifi, 16% in Nairobi, and 9% in Jackson. SCT was associated with -2.4 (95% CI , -4.7 to -0.2) mm Hg lower 24-hour systolic BP in Kilifi but had no effect in Nairobi/Jackson. The effect of SCT in Kilifi was limited to 30- to 59-year-old participants, among whom it was associated with -6.1 mm Hg (CI , -10.5 to -1.8) lower 24-hour systolic BP. In pooled analysis allowing interaction by site, the effect of SCT on 24-hour systolic BP in Kilifi was -3.5 mm Hg (CI , -6.9 to -0.1), increasing to -5.2 mm Hg (CI , -9.5 to -0.9) when replacing estimated glomerular filtration rate with urine albumin to creatinine ratio as a covariate. In Kilifi, the prevalence ratio for hypertension was 0.86 (CI , 0.76-0.98) for SCT and 0.89 (CI , 0.80-0.99) for α+thalassemia. Conclusions Lifelong malaria protection is associated with lower BP in Kilifi. Confirmation of this finding at other sites and elucidating the mechanisms involved may yield new preventive and therapeutic targets.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30879408/</p>
117	<p>Mandal RK, Crane RJ, Berkley JA, Gumbi W, Wambua J, Ngoi JM, Ndungu FM, Schmidt NW. Longitudinal Analysis of Infant Stool Bacteria Communities Before and After Acute Febrile Malaria and Artemether-Lumefantrine Treatment. <i>J Infect Dis.</i> 2019 Jul 19;220(4):687-698.</p> <p>Abstract</p> <p>Background: Gut microbiota were recently shown to impact malaria disease progression and outcome, and prior studies have shown that Plasmodium infections increase the likelihood of enteric bacteria causing systemic infections. Currently, it is not known whether Plasmodium infection impacts human gut microbiota as a prelude to bacteremia or whether antimalarials affect gut microbiota. Our goal was to determine to what degree Plasmodium infections and antimalarial treatment affect human gut microbiota.</p> <p>Methods: One hundred Kenyan infants underwent active surveillance for malaria from birth to 10 months of age. Each malaria episode was treated with artemether-lumefantrine (AL).</p>



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	<p>Any other treatments, including antibiotics, were recorded. Stool samples were collected on an approximately biweekly basis. Ten children were selected on the basis of stool samples having been collected before (n = 27) or after (n = 17) a malaria episode and without antibiotics having been administered between collections. These samples were subjected to 16S ribosomal ribonucleic acid gene (V3-V4 region) sequencing.</p> <p>Results: Bacterial community network analysis revealed no obvious differences in the before and after malaria/AL samples, which was consistent with no difference in alpha and beta diversity and taxonomic analysis at the family and genus level with one exception. At the sequence variant (SV) level, akin to bacterial species, only 1 of the top 100 SVs was significantly different. In addition, predicted metagenome analysis revealed no significant difference in metagenomic capacity between before and after malaria/AL samples. The number of malaria episodes, 1 versus 2, explained significant variation in gut microbiota composition of the infants.</p> <p>Conclusions: In-depth bioinformatics analysis of stool bacteria has revealed for the first time that human malaria episode/AL treatment have minimal effects on gut microbiota in Kenyan infants.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30590681/</p>
118	<p>Bunei M, Muturi P, Otiato F, Njuguna HN, Emukule GO, Otieno NA, Dawa J, Chaves SS. Factors Influencing Acceptance of Post-Mortem Examination of Children at a Tertiary Care Hospital in Nairobi, Kenya. <i>Ann Glob Health</i>. 2019 Jul 3;85(1):95.</p> <p>Abstract</p> <p>Background: Clinical autopsies are not often part of routine care, despite their role in clarifying cause of death. In fact, autopsy rates across the world have declined and are especially low in sub-Saharan Africa.</p>



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	<p>Objectives: We set out to identify factors associated with acceptance of pediatric autopsies among parents of deceased children less than five years old, and examined local preferences for minimally invasive tissue sampling (MITS) procedures during post-mortem (PM) examinations.</p> <p>Methods: From December 2016 to September 2017, we contacted 113 parents/next of kin who had been previously approached to consent to a PM examination of their deceased child as part of a Kenyan study on cause of death. Interviews occurred up to three years after the death of their child.</p> <p>Findings: Seventy-three percent (83/113) of eligible study participants were enrolled, of whom 62/83 (75%) had previously consented to PM examination of their child. Those who previously consented to PM had higher levels of education, were more likely employed, and had more knowledge about certain aspects of autopsies than non-consenters. The majority (97%) of PM consenters did so because they wanted to know the cause of death of their child, and up to a third believed autopsy studies helped advance medical knowledge. Reasons for non-consent to PM examination included: parents felt there was no need for further examination (29%) or they were satisfied with the clinical diagnosis (24%). Overall, only 40% of study participants would have preferred MITS procedures to conventional autopsy. However, 81% of autopsy non-consenters would have accepted PM examination if it only involved MITS techniques.</p> <p>Conclusion: There is potential to increase autopsy rates by strengthening reasons for acceptance and addressing modifiable reasons for refusals. Although MITS procedures have the potential to improve autopsy acceptance rates, they were not significantly preferred over conventional autopsies in our study population.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31276331/</p>
119	Wandera EA, Komoto S, Mohammad S, Ide T, Bundi M, Nyangao J, Kathiiko C, Odoyo E, Galata A, Miring'u G, Fukuda S, Hatazawa R, Murata T, Taniguchi K,



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	<p>Ichinose Y. Genomic characterization of uncommon human G3P[6] rotavirus strains that have emerged in Kenya after rotavirus vaccine introduction, and pre-vaccine human G8P[4] rotavirus strains. <i>Infect Genet Evol.</i> 2019 Mar;68:231-248.</p> <p>Abstract</p> <p>A monovalent rotavirus vaccine (RV1) was introduced to the national immunization program in Kenya in July 2014. There was increased detection of uncommon G3P[6] strains that coincided temporally with the timing of this vaccine introduction. Here, we sequenced and characterized the full genomes of two post-vaccine G3P[6] strains, RVA/Human-wt/KEN/KDH1951/2014/G3P[6] and RVA/Human-wt/KEN/KDH1968/2014/G3P[6], as representatives of these uncommon strains. On full-genomic analysis, both strains exhibited a DS-1-like genotype constellation: G3-P[6]-I2-R2-C2-M2-A2-N2-T2-E2-H2. Phylogenetic analysis revealed that all 11 genes of strains KDH1951 and KDH1968 were very closely related to those of human G3P[6] strains isolated in Uganda in 2012-2013, indicating the derivation of these G3P[6] strains from a common ancestor. Because the uncommon G3P[6] strains that emerged in Kenya are fully heterotypic as to the introduced vaccine strain regarding the genotype constellation, vaccine effectiveness against these G3P[6] strains needs to be closely monitored.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30543939/</p>
120	<p>Magai DN, Mwaniki M, Abubakar A, Mohammed S, Gordon AL, Kalu R, Mwangi P, Koot HM, Newton CR. A randomized control trial of phototherapy and 20% albumin versus phototherapy and saline in Kilifi, Kenya. <i>BMC Res Notes.</i> 2019 Sep 23;12(1):617.</p> <p>Abstract</p> <p>Objective: The study evaluated the efficacy of phototherapy and 20% albumin infusion to reduce total serum bilirubin (TSB) in neonates with severe hyperbilirubinemia. The primary outcome was a reduction of TSB at the end of treatment. The secondary outcomes</p>



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	<p>were the need for exchange transfusion, inpatient mortality, neurological outcomes at discharge, and development outcomes at 12-months follow-up.</p> <p>Results: One hundred and eighteen neonates were randomly assigned to phototherapy and 20% albumin (n = 59) and phototherapy and saline (n = 69). The median age at admission was 5 (interquartile range (IQR) 3-6) days, and the median gestation was 36 (IQR 36-38) weeks. No significant differences were found in the change in TSB (Mann-Whitney U = 609, p = 0.98) and rate of change in TSB per hour after treatment (Mann-Whitney U = 540, p = 0.39) between the two groups. There were no significant differences between the two groups in the proportion of participants who required exchange transfusion (χ^2 (2) = 0.36, p = 0.546); repeat phototherapy (χ^2 (2) = 2.37, p = 0.123); and those who died (χ^2 (2) = 0.92, p = 0.337). Trial registration The trial was registered in the International Standardized Randomized Controlled Trial Number (ISRCTN); trial registration number ISRCTN89732754.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31547861/</p>
121	<p>Kibe LW, Habluetzel A, Gachigi JK, Kamau AW, Mbogo CM. Exploring communities' and health workers' perceptions of indicators and drivers of malaria decline in Malindi, Kenya. <i>Malariaworld J.</i> 2019 Jul 3;8:21. Epub 2017 Dec 8. PMID: 31338302; PMCID: PMC6650290.</p> <p>Abstract</p> <p>Background: Since 2000, a decrease in malaria burden has been observed in most endemic countries. Declining infection rates and disease burden and reduction in asymptomatic carriers are the outcome of improved quality of care and related health system factors. These include improved case management through better diagnosis, implementation of highly effective antimalarial drugs and increased use of bednets. We studied communities' and health workers' perceptions of indicators and drivers in the context of decreasing malaria transmission in Malindi, Kenya.</p>



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	<p>Materials and methods: A variety of qualitative methods that included participatory rural appraisal (PRA) tools such as community river of life and trend lines, focus group discussions (FGDs) and key informant interviews were used. Studies took place between November 2013 and April 2014.</p> <p>Results: Providing residents with bednets contributed to malaria reduction, and increasing community awareness on the causes and symptoms of malaria and improved malaria treatment were also perceived to contribute to the decline of malaria. The study identified three perceived drivers to the reported decline in malaria: a) community health workers' enhanced awareness creation towards household owners regarding malaria-related activities through visitations and awareness sessions, b) Women involvement in Savings Internal Lending Community was perceived to have increased their financial base, thereby improving their decision-making power towards the care of their sick child(ren), c) Non-Governmental Organizations (NGOs) and partners played a promoter part in health and general economic development initiatives.</p> <p>Conclusions: To achieve the goal of malaria elimination, collaboration between governmental and NGOs will be crucial when improving the financial base of women and enhancing participation of community health workers.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31338302/</p>
122	<p>Mang'era CM, Hassanali A, Khamis FM, Rono MK, Lwande W, Mbogo C, Mireji PO. Growth-disrupting <i>Murraya koenigii</i> leaf extracts on <i>Anopheles gambiae</i> larvae and identification of associated candidate bioactive constituents. <i>Acta Trop.</i> 2019 Feb;190:304-311.</p> <p>Abstract</p> <p>Plant-based constituents have been proposed as eco-friendly alternatives to synthetic insecticides for control of mosquito vectors of malaria. In this study, we first screened the effects of methanolic leaf extracts of curry tree (<i>Murraya koenigii</i>) growing in tropical (Mombasa, Malindi) and semi-arid (Kibwezi, and Makindu) ecological zones of Kenya on</p>



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third instar *An. gambiae* s.s. larvae. Extracts of the plant from the semi-arid region, and particularly from Kibwezi, led to high mortality of the larvae. Bioassay-guided fractionation of the methanolic extract of the leaves of the plants from Kibwezi was then undertaken and the most active fraction (20 fold more potent than the crude extract) was then analyzed by Liquid chromatography quadruple time of flight coupled with mass spectrometry (LC-QtoF-MS) and a number of constituents were identified, including a major alkaloid constituent, Neplanocin A (5). Exposure of the third instar larvae to a sub-lethal dose (4.43 ppm) of this fraction over 7-day periods induced gross morphogenetic abnormalities in the larvae, with reduced locomotion, and delayed pupation. Moreover, the few adults that emerged from some pupae failed to fly from the water surface, unlike in the untreated control group. These results demonstrate subtle growth-disrupting effects of the phytochemical blend from *M. koenigii* leaves on aquatic stages *An. gambiae* mosquito. The study lays down some useful groundwork for the downstream development of phytochemical blends that can be evaluated for integration into eco-friendly control of *An. gambiae* vector population targeting the often overlooked but important immature stages of the malaria vector.

Pubmed link- <https://pubmed.ncbi.nlm.nih.gov/30529445/>



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123 Hounsoume N, Kassahun MM, Ngari M, Berkley JA, Kivaya E, Njuguna P, Fegan G, Tamiru A, Kelemework A, Amberbir T, Clarke A, Lang T, Newport MJ, McKay A, Enquoselassie F, Davey G. Cost-effectiveness and social outcomes of a community-based treatment for podoconiosis lymphoedema in the East Gojjam zone, Ethiopia. *PLoS Negl Trop Dis*. 2019 Oct 23;13(10):e0007780.

Abstract

Background: Podoconiosis is a disease of the lymphatic vessels of the lower extremities that is caused by chronic exposure to irritant soils. It results in leg swelling, commonly complicated by acute dermatolymphangioadenitis (ADLA), characterised by severe pain, fever and disability.

Methods: We conducted cost-effectiveness and social outcome analyses of a pragmatic, randomised controlled trial of a hygiene and foot-care intervention for people with podoconiosis in the East Gojjam zone of northern Ethiopia. Participants were allocated to the immediate intervention group or the delayed intervention group (control). The 12-month intervention included training in foot hygiene, skin care, bandaging, exercises, and use of socks and shoes, and was supported by lay community assistants. The cost-effectiveness analysis was conducted using the cost of productivity loss due to acute dermatolymphangioadenitis. Household costs were not included. Health outcomes in the cost-effectiveness analysis were: the incidence of ADLA episodes, health-related quality of life captured using the Dermatology Life Quality Index (DLQI), and disability scores measured using the WHO Disability Assessment Schedule 2.0 (WHODAS 2.0).

Results: The cost of the foot hygiene and lymphoedema management supplies was 529 ETB (69 I\$, international dollars) per person per year. The cost of delivery of the intervention as part of the trial, including transportation, storage, training of lay community assistants and administering the intervention was 1,890 ETB (246 I\$) per person. The intervention was effective in reducing the incidence of acute dermatolymphangioadenitis episodes and improving DLQI scores, while there were no significant improvements in the



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	<p>disability scores measured using WHODAS 2.0. In 75% of estimations, the intervention was less costly than the control. This was due to improved work productivity. Subgroup analyses based on income group showed that the intervention was cost-effective (both less costly and more effective) in reducing the number of acute dermatolymphangioadenitis episodes and improving health-related quality of life in families with monthly income <1,000 ETB (130 I\$). For the subgroup with family income \geq1,000 ETB, the intervention was more effective but more costly than the control.</p> <p>Conclusions: Whilst there is evident benefit of the intervention for all, the economic impact would be greatest for the poorest.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31644556/</p>
124	Hanson K, Barasa E, Honda A, Panichkriangkrai W, Patcharanarumol W. Strategic Purchasing: The Neglected Health Financing Function for Pursuing



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	<p>Universal Health Coverage in Low-and Middle-Income Countries Comment on "What's Needed to Develop Strategic Purchasing in Healthcare? Policy Lessons from a Realist Review". <i>Int J Health Policy Manag.</i> 2019 Aug 1;8(8):501-504.</p> <p>Abstract</p> <p>Sanderson et al's realist review of strategic purchasing identifies insights from two strands of theory: the economics of organisation and inter-organisational relationships. Our findings from a programme of research conducted by the RESYST (Resilient and Responsive Health Systems) consortium in seven countries echo these results, and add to them the crucial area of organisational capacity to implement complex reforms. We identify key areas for policy development. These are the need for: (1) a policy design with clearly delineated responsibilities; (2) a task network of organisations to engage in the broad set of functions needed; (3) more effective means of engaging with populations; (4) a range of technical and management capacities; and (5) an awareness of the multiple agency relationships that are created by the broader financing environment and the provider incentives generated by multiple financing flows.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31441291/</p>
125	<p>Lucas ER, Rockett KA, Lynd A, Essandoh J, Grisales N, Kemei B, Njoroge H, Hubbart C, Rippon EJ, Morgan J, Van't Hof AE, Ochomo EO, Kwiatkowski DP, Weetman D, Donnelly MJ. A high throughput multi-locus insecticide resistance marker panel for tracking resistance emergence and spread in <i>Anopheles gambiae</i>. <i>Sci Rep.</i> 2019 Sep 16;9(1):13335.</p> <p>Abstract</p> <p>The spread of resistance to insecticides in disease-carrying mosquitoes poses a threat to the effectiveness of control programmes, which rely largely on insecticide-based interventions. Monitoring mosquito populations is essential, but obtaining phenotypic measurements of resistance is laborious and error-prone. High-throughput genotyping offers the prospect of quick and repeatable estimates of resistance, while also allowing resistance markers to be</p>



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	<p>tracked and studied. To demonstrate the potential of highly-multiplexed genotypic screening for measuring resistance-association of mutations and tracking their spread, we developed a panel of 28 known or putative resistance markers in the major malaria vector <i>Anopheles gambiae</i>, which we used to screen mosquitoes from a wide swathe of Sub-Saharan Africa (Burkina Faso, Ghana, Democratic Republic of Congo (DRC) and Kenya). We found resistance association in four markers, including a novel mutation in the detoxification gene <i>Gste2</i> (<i>Gste2</i>-119V). We also identified a duplication in <i>Gste2</i> combining a resistance-associated mutation with its wild-type counterpart, potentially alleviating the costs of resistance. Finally, we describe the distribution of the multiple origins of <i>kdr</i> resistance, finding unprecedented diversity in the DRC. This panel represents the first step towards a quantitative genotypic model of insecticide resistance that can be used to predict resistance status in <i>An. gambiae</i>.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31527637/</p>
126	<p>Muthui MK, Mogeni P, Mwai K, Nyundo C, Macharia A, Williams TN, Nyangweso G, Wambua J, Mwangi D, Marsh K, Bejon P, Kapulu MC. Gametocyte carriage in an era of changing malaria epidemiology: A 19-year analysis of a malaria longitudinal cohort. <i>Wellcome Open Res.</i> 2019 May 28;4:66.</p> <p>Abstract</p> <p>Background: Interventions to block malaria transmission from humans to mosquitoes are currently in development. To be successfully implemented, key populations need to be identified where the use of these transmission-blocking and/or reducing strategies will have greatest impact. Methods: We used data from a longitudinally monitored cohort of children from Kilifi county located along the Kenyan coast collected between 1998-2016 to describe the distribution and prevalence of gametocytaemia in relation to transmission intensity, time and age. Data from 2,223 children accounting for 9,134 person-years of follow-up assessed during cross-sectional surveys for asexual parasites and gametocytes were used in logistic regression models to identify factors predictive of gametocyte carriage in this</p>



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	<p>cohort. Results: Our analysis showed that children 1-5 years of age were more likely to carry microscopically detectable gametocytes than their older counterparts. Carrying asexual parasites and recent episodes of clinical malaria were also strong predictors of gametocyte carriage. The prevalence of asexual parasites and of gametocyte carriage declined over time, and after 2006, when artemisinin combination therapy (ACT) was introduced, recent episodes of clinical malaria ceased to be a predictor of gametocyte carriage. Conclusions: Gametocyte carriage in children in Kilifi has fallen over time. Previous episodes of clinical malaria may contribute to the development of carriage, but this appears to be mitigated by the use of ACTs highlighting the impact that gametocidal antimalarials can have in reducing the overall prevalence of gametocytaemia when targeted on acute febrile illness.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31223663/</p>
127	<p>Mwanga EP, Minja EG, Mrimi E, Jiménez MG, Swai JK, Abbasi S, Ngowo HS, Siria DJ, Mapua S, Stica C, Maia MF, Olotu A, Sikulu-Lord MT, Baldini F, Ferguson HM, Wynne K, Selvaraj P, Babayan SA, Okumu FO. Detection of malaria parasites in dried human blood spots using mid-infrared spectroscopy and logistic regression analysis. <i>Malar J.</i> 2019 Oct 7;18(1):341.</p> <p>Abstract</p> <p>Background: Epidemiological surveys of malaria currently rely on microscopy, polymerase chain reaction assays (PCR) or rapid diagnostic test kits for Plasmodium infections (RDTs). This study investigated whether mid-infrared (MIR) spectroscopy coupled with supervised machine learning could constitute an alternative method for rapid malaria screening, directly from dried human blood spots.</p> <p>Methods: Filter papers containing dried blood spots (DBS) were obtained from a cross-sectional malaria survey in 12 wards in southeastern Tanzania in 2018/19. The DBS were scanned using attenuated total reflection-Fourier Transform Infrared (ATR-FTIR)</p>



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	<p>spectrometer to obtain high-resolution MIR spectra in the range 4000 cm⁻¹ to 500 cm⁻¹. The spectra were cleaned to compensate for atmospheric water vapour and CO₂ interference bands and used to train different classification algorithms to distinguish between malaria-positive and malaria-negative DBS papers based on PCR test results as reference. The analysis considered 296 individuals, including 123 PCR-confirmed malaria positives and 173 negatives. Model training was done using 80% of the dataset, after which the best-fitting model was optimized by bootstrapping of 80/20 train/test-stratified splits. The trained models were evaluated by predicting Plasmodium falciparum positivity in the 20% validation set of DBS.</p> <p>Results: Logistic regression was the best-performing model. Considering PCR as reference, the models attained overall accuracies of 92% for predicting P. falciparum infections (specificity = 91.7%; sensitivity = 92.8%) and 85% for predicting mixed infections of P. falciparum and Plasmodium ovale (specificity = 85%, sensitivity = 85%) in the field-collected specimen.</p> <p>Conclusion: These results demonstrate that mid-infrared spectroscopy coupled with supervised machine learning (MIR-ML) could be used to screen for malaria parasites in human DBS. The approach could have potential for rapid and high-throughput screening of Plasmodium in both non-clinical settings (e.g., field surveys) and clinical settings (diagnosis to aid case management). However, before the approach can be used, we need additional field validation in other study sites with different parasite populations, and in-depth evaluation of the biological basis of the MIR signals. Improving the classification algorithms, and model training on larger datasets could also improve specificity and sensitivity. The MIR-ML spectroscopy system is physically robust, low-cost, and requires minimum maintenance.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31590669/</p>
128	Akama E, Nimz A, Blat C, Moghadassi M, Oyaro P, Maloba M, Cohen CR, Bukusi



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	<p>EA, Abuogi LL. Retention and viral suppression of newly diagnosed and known HIV positive pregnant women on Option B+ in Western Kenya. <i>AIDS Care</i>. 2019 Mar;31(3):333-339.</p> <p>Abstract</p> <p>Kenya introduced universal antiretroviral treatment (ART) for pregnant and breastfeeding women living with HIV (Option B+) in 2014. A retrospective study was conducted to review consecutive records for HIV positive pregnant women presenting for antenatal care (ANC) at five clinics in western Kenya. Known positive women (KP :HIV diagnosis prior to current pregnancy) were compared to newly positive (NP) women regarding virologic suppression and retention in care. Among 165 women included, 71 (43%) NP and 94 (57%) KP, NP were younger (24.5 years (SD 4.6) vs. 28.1 years (SD 5.6) compared to KP ($p < .001$). Almost all NP (97%) were initiated on Option B+ while over half of KP (59%) started ART for clinical/immunological criteria ($p < .0001$). KPs were more likely than NPs to have a VL performed following Kenyan guidelines (64% vs. 31%; $p < .001$). Among those tested, virologic suppression was high in both groups (92% KP vs. 100% NP; $p = .31$). More KPs (82%) vs. NPs (66%) remained active in care at 15-18 months of follow-up ($p = .02$). Women newly diagnosed with HIV during pregnancy show poorer uptake of VL testing and worse retention in care than those diagnosed prior to pregnancy.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30261742/</p>
129	<p>Gilbertson A, Ongili B, Odongo FS, Hallfors DD, Rennie S, Kwaro D, Luseno WK. Voluntary medical male circumcision for HIV prevention among adolescents in Kenya: Unintended consequences of pursuing service-delivery targets. <i>PLoS One</i>. 2019 Nov 4;14(11):e0224548.</p> <p>Abstract</p> <p>Introduction: Voluntary medical male circumcision (VMMC) provides significant reductions in the risk of female-to-male HIV transmission. Since 2007, VMMC has been a</p>



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	<p>key component of the United States President's Emergency Plan for AIDS Relief's (PEPFAR) strategy to mitigate the HIV epidemic in countries with high HIV prevalence and low circumcision rates. To ensure intended effects, PEPFAR sets ambitious annual circumcision targets and provides funding to implementation partners to deliver local VMMC services. In Kenya to date, 1.9 million males have been circumcised; in 2017, 60% of circumcisions were among 10-14-year-olds. We conducted a qualitative field study to learn more about VMMC program implementation in Kenya.</p> <p>Methods and results: The study setting was a region in Kenya with high HIV prevalence and low male circumcision rates. From March 2017 through April 2018, we carried out in-depth interviews with 29 VMMC stakeholders, including "mobilizers", HIV counselors, clinical providers, schoolteachers, and policy professionals. Additionally, we undertook observation sessions at 14 VMMC clinics while services were provided and observed mobilization activities at 13 community venues including, two schools, four public marketplaces, two fishing villages, and five inland villages. Analysis of interview transcripts and observation field notes revealed multiple unintended consequences linked to the pursuit of targets. Ebbs and flows in the availability of school-age youths together with the drive to meet targets may result in increased burdens on clinics, long waits for care, potentially misleading mobilization practices, and deviations from the standard of care.</p> <p>Conclusion: Our findings indicate shortcomings in the quality of procedures in VMMC programs in a low-resource setting, and more importantly, that the pursuit of ambitious public health targets may lead to compromised service delivery and protocol adherence. There is a need to develop improved or alternative systems to balance the goal of increasing service uptake with the responsible conduct of VMMC.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31682626/</p>
130	Elson L, Wiese S, Feldmeier H, Fillinger U. Prevalence, intensity and risk factors of tungiasis in Kilifi County, Kenya II: Results from a school-based



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observational study. PLoS Negl Trop Dis. 2019 May 16;13(5):e0007326.

Abstract

Introduction: Awareness of the public health importance of tungiasis has been growing in East Africa in recent years, but data on epidemiological characteristics necessary for the planning and implementation of control measures do not exist. The work presented here was part of a larger cross-sectional study on the epidemiology of tungiasis in coastal Kenya and aims at identifying risk factors of tungiasis and severe disease in school children.

Methods: A total of 1,829 students of all age groups from five schools and 56 classes were clinically examined for tungiasis on their feet based on standardized procedures and observations made about the school infrastructure. To investigate the impact of school holidays, observations were repeated after school holidays in a subset of children in one school. In an embedded case-control study, structured interviews were conducted with 707 students in the five schools to investigate associations between tungiasis and household infrastructure, behaviour and socio-economic status.

Results: The overall prevalence of tungiasis was 48%; children below the age of 15 years were the most affected, and boys were twice as likely as girls to be infected. The highest risk of disease was associated with the socio-economic circumstances of the individual student at home. The study indicated that mild to moderate tungiasis could be reduced by a third, and severe tungiasis by over half, if sleeping places of children had hardened floors, whilst approximately a seventh of the cases could be prevented by sealing classroom floors in schools, and another fifth by using soap for daily feet washing.

Conclusion: There is a clear role for public health workers to expand the WASH policy to include washing of feet with soap in school-aged children to fight tungiasis and to raise awareness of the importance of sealed floors.

Pubmed link- <https://pubmed.ncbi.nlm.nih.gov/31095558/>



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associated neurocognitive disorders among adults living with HIV in sub-Saharan Africa: A scoping review. *AAS Open Res.* 2019 Oct 30;1:28.

Abstract

Background: People living with HIV are at risk of developing HIV-associated neurocognitive disorders (HAND) which adversely affects their quality of life. Routine screening of HAND in HIV care is recommended to identify clinically important changes in cognitive functioning and allow for early interventions. However, HAND detection in routine clinical practice has never been reported in sub-Saharan Africa (SSA), partly due to a lack of adequately standardized screening tools. This review was conducted to identify the commonly used screening tools for HAND in SSA and document their psychometric properties and diagnostic accuracy. **Methods:** We searched Ovid Medline, PsycINFO and Web of Sciences databases for empirical studies published from 1/1/1980 to 31/8/2018 on HAND among adults living with HIV in SSA. **Results:** We identified 14 eligible studies, of which 9 were from South Africa. The International HIV Dementia Scale (IHDS) was the most frequently reported tool, being used in more than half of the studies. However most studies only reported the diagnostic accuracy of this and other tools, with specificity ranging from 37% to 81% and sensitivity ranging from 45% to 100%. Appropriate data on construct validity and reliability of tools was rarely documented. Although most tools performed well in screening for severe forms of HAND, they lacked sensitivity and specificity for mild forms of HAND. NeuroScreen, one of the newer tools, yielded good diagnostic accuracy in its initial evaluation in South Africa (81% to 93% sensitivity and 71% to 81% specificity). **Conclusions:** This review identified a lack of adequately standardized and contextually relevant HAND screening tools in SSA. Most screening tools for HAND used in SSA possess inadequate psychometric properties and diagnostic accuracy. There is a need for further validation of existing tools and development of new HAND screening tools in SSA.

Pubmed link- <https://pubmed.ncbi.nlm.nih.gov/31844836/>



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132	<p>Luseno WK, Field SH, Iritani BJ, Rennie S, Gilbertson A, Odongo FS, Kwaro D, Ongili B, Hallfors DD. Consent Challenges and Psychosocial Distress in the Scale-up of Voluntary Medical Male Circumcision Among Adolescents in Western Kenya. <i>AIDS Behav.</i> 2019 Dec;23(12):3460-3470.</p> <p>Abstract</p> <p>In priority sub-Saharan African countries, on the ground observations suggest that the success of voluntary medical male circumcision (VMMC) programs should not be based solely on numbers of males circumcised. We identify gaps in the consent process and poor psychosocial outcomes among a key target group: male adolescents. We assessed compliance with consent and assent requirements for VMMC in western Kenya among males aged 15-19 (N = 1939). We also examined differences in quality of life, depression, and anticipated HIV stigma between uncircumcised and circumcised adolescents. A substantial proportion reported receiving VMMC services as minors without parent/guardian consent. In addition, uncircumcised males were significantly more likely than their circumcised peers to have poor quality of life and symptoms of depression. Careful monitoring of male adolescents' well-being is needed in large-scale VMMC programs. There is also urgent need for research to identify effective strategies to address gaps in the delivery of VMMC services.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31375957/</p>
133	<p>Mbuthia D, Molyneux S, Njue M, Mwalukore S, Marsh V. Kenyan health stakeholder views on individual consent, general notification and governance processes for the re-use of hospital inpatient data to support learning on healthcare systems. <i>BMC Med Ethics.</i> 2019 Jan 8;20(1):3.</p> <p>Abstract</p> <p>Background: Increasing adoption of electronic health records in hospitals provides new opportunities for patient data to support public health advances. Such learning healthcare models have generated ethical debate in high-income countries, including on the role of</p>



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patient and public consent and engagement. Increasing use of electronic health records in low-middle income countries offers important potential to fast-track healthcare improvements in these settings, where a disproportionate burden of global morbidity occurs. Core ethical issues have been raised around the role and form of information sharing processes for learning healthcare systems, including individual consent and individual and public general notification processes, but little research has focused on this perspective in low-middle income countries.

Methods: We conducted a qualitative study on the role of information sharing and governance processes for inpatient data re-use, using in-depth interviews with 34 health stakeholders at two public hospitals on the Kenyan coast, including health managers, providers and researchers. Data were collected between March and July 2016 and analysed using a framework approach, with Nvivo 10 software to support data management.

Results: Most forms of clinical data re-use were seen as an important public health good. Individual consent and general notification processes were often argued as important, but contingent on interrelated influences of the type of data, use and secondary user. Underlying concerns were linked to issues of patient privacy and autonomy; perceived risks to trust in health systems; and fairness in how data would be used, particularly for non-public sector re-users. Support for engagement often turned on the anticipated outcomes of information-sharing processes, as building or undermining trust in healthcare systems.

Conclusions: As reported in high income countries, learning healthcare systems in low-middle counties may generate a core ethical tension between supporting a public good and respecting patient autonomy and privacy, with the maintenance of public trust acting as a core requirement. While more evidence is needed on patient and public perspectives on learning healthcare activities, greater collaboration between public health and research governance systems is likely to support the development of efficient and locally responsive learning healthcare activities in LMICs.

Pubmed link- <https://pubmed.ncbi.nlm.nih.gov/30621693/>



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134 Owor BE, Mwanga MJ, Njeru R, Mugo R, Ngama M, Otieno GP, Nokes DJ, Agoti CN. Molecular characterization of rotavirus group A strains circulating prior to vaccine introduction in rural coastal Kenya, 2002-2013. Wellcome Open Res. 2019 May 15;3:150.

Abstract

Background: Kenya introduced the monovalent Rotarix® rotavirus group A (RVA) vaccine nationally in mid-2014. Long-term surveillance data is important prior to wide-scale vaccine use to assess the impact on disease and to investigate the occurrence of heterotypic strains arising through immune selection. This report presents baseline data on RVA genotype circulation patterns and intra-genotype genetic diversity over a 7-year period in the pre-vaccine era in Kilifi, Kenya, from 2002 to 2004 and from 2010 to 2013. **Methods:** A total of 745 RVA strains identified in children admitted with acute gastroenteritis to a referral hospital in Coastal Kenya, were sequenced using the di-deoxy sequencing method in the VP4 and VP7 genomic segments (encoding P and G proteins, respectively). Sequencing successfully generated 569 (76%) and 572 (77%) consensus sequences for the VP4 and VP7 genes respectively. G and P genotypes were determined by use of BLAST and the online RotaC v2 RVA classification tool. **Results:** The most common GP combination was G1P[8] (51%), similar to the Rotarix® strain, followed by G9P[8] (15%), G8P[4] (14%) and G2P[4] (5%). Unusual GP combinations-G1P[4], G2P[8], G3P[4,6], G8P[8,14], and G12P[4,6,8]-were observed at frequencies of <5%. Phylogenetic analysis showed that the infections were caused by both locally persistent strains as evidenced by divergence of local strains occurring over multiple seasons from the global ones, and newly introduced strains, which were closely related to global strains. The circulating RVA diversity showed temporal fluctuations both season by season and over the longer-term. None of the unusual strains increased in frequency over the observation period. **Conclusions:** The circulating RVA diversity showed temporal fluctuations with several



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	<p>unusual strains recorded, which rarely caused major outbreaks. These data will be useful in interpreting genotype patterns observed in the region during the vaccine era.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31020048/</p>
135	<p>Dauncey JW, Olupot-Olupot P, Maitland K. Healthcare-provider perceptions of barriers to oxygen therapy for paediatric patients in three government-funded eastern Ugandan hospitals; a qualitative study. <i>BMC Health Serv Res.</i> 2019 May 24;19(1):335.</p> <p>Abstract</p> <p>Background: This study aimed to assess on-the-ground barriers to the provision of oxygen therapy for paediatric patients in three government-funded Eastern Ugandan district general hospitals (DGHs).</p> <p>Methods: Site visits to DGHs during March 2017 involved semi-structured interviews with medical officers, clinical officers, paediatric nurses and non-clinical staff (n = 29). MAXQDA qualitative data software was used to assist with response analysis.</p> <p>Results: The healthcare professionals reported that erratic electricity supplies, few and/or malfunctioning oxygen cylinders and concentrators, limited or no access to pulse oximetry, inadequate staffing and lack of continued professional training were key barriers to the delivery of oxygen therapy. Local populations were reportedly fearful of oxygen therapy and reluctant to consent for oxygen therapy to be administered to their children.</p>



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	<p>Conclusion: According to healthcare providers in three Eastern Ugandan DGHs, numerous barriers exist to oxygen therapy for paediatric patients. Healthcare professionals reported lack of facilities and training to effectively deliver oxygen therapy. Quality improvement work prioritising oxygen therapy in government-funded district general hospitals should focus on oxygen supply and delivery issues on a site-specific level and sensitizing communities to the potential benefits of oxygen.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31126269/</p>
136	<p>Luseno WK, Iritani BJ, Maman S, Mbai I, Ongili B, Otieno FA, Hallfors DD.</p> <p>"If the mother does not know, there is no way she can tell the adolescent to go for drugs": Challenges in promoting health and preventing transmission among pregnant and parenting Kenyan adolescents living with HIV. <i>Child Youth Serv Rev</i>. 2019 Aug;103:100-106.</p> <p>Abstract</p> <p>Adolescents living with HIV (ALHIV) who are pregnant, or parenting, are an important but understudied group. This study explores the challenges in promoting the health of these adolescents and preventing onward transmission. We used existing semi-structured interview data from a 2014 study conducted among Kenyan ALHIV (ages 15-19), their family members, and local health staff to examine adolescent HIV-testing, disclosure, and treatment engagement, focusing on participants who were pregnant, had given birth, or had fathered a child. A total of 28 participant interviews were analyzed, including those conducted with nine ALHIV, four family members, and 15 HIV providers. Four adolescent participants were not in care at the time of their interview. Our analysis also included a transcript from a stakeholder meeting involving HIV providers and associated administrators, held to disseminate and garner feedback on, preliminary findings from the original study. Based on our analysis, adolescents frequently reported being alone during</p>



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	<p>testing, experiencing fear and denial on receiving their results, and delaying disclosure to family and linkage to treatment. They also mentioned a lack of contraceptive counseling, with some reporting multiple pregnancies. Providers voiced misgivings and uncertainty about disclosing HIV diagnoses to minor adolescents without a family member present and reported severe shortages of personnel and resources to adequately serve ALHIV in rural clinics. These findings highlight gaps in services that limit adolescent engagement in HIV treatment prior to sexual debut and conceiving a child, and in PMTCT during and after pregnancy. Greater research attention is needed to address ALHIV reproductive health needs, improve linkage to HIV treatment, and prevent onward sexual transmission. Empirical ethics studies of current adolescent disclosure policies are also warranted to examine cultural and developmental appropriateness, and effectiveness in fostering support and engagement in HIV services.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31308586/</p>
137	<p>Muthui MK, Kamau A, Bousema T, Blagborough AM, Bejon P, Kapulu MC. Immune Responses to Gametocyte Antigens in a Malaria Endemic Population-The African <i>falciparum</i> Context: A Systematic Review and Meta-Analysis. <i>Front Immunol.</i> 2019 Oct 22;10:2480.</p> <p>Abstract</p> <p>Background: Malaria elimination remains a priority research agenda with the need for interventions that reduce and/or block malaria transmission from humans to mosquitoes. Transmission-blocking vaccines (TBVs) are in development, most of which target the transmission stage (i.e., gametocyte) antigens Pfs230 and Pfs48/45. For these interventions to be implemented, there is a need to understand the naturally acquired immunity to gametocytes. Several studies have measured the prevalence of immune responses to Pfs230 and Pfs48/45 in populations in malaria-endemic areas. Methods: We conducted a systematic review of studies carried out in African populations that measured the prevalence of immune responses to the gametocyte antigens Pfs230 and Pfs48/45. We</p>



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	<p>assessed seroprevalence of antibody responses to the two antigens and investigated the effects of covariates such as age, transmission intensity/endemicity, season, and parasite prevalence on the prevalence of these antibody responses by meta-regression. Results: We identified 12 studies covering 23 sites for inclusion in the analysis. We found that the range of reported seroprevalence to Pfs230 and Pfs48/45 varied widely across studies, from 0 to 64% for Pfs48/45 and from 6 to 72% for Pfs230. We also found a modest association between increased age and increased seroprevalence to Pfs230: adults were associated with higher seroprevalence estimates in comparison to children (β coefficient 0.21, 95% CI: 0.05-0.38, $p = 0.042$). Methodological factors were the most significant contributors to heterogeneity between studies which prevented calculation of pooled prevalence estimates. Conclusions: Naturally acquired sexual stage immunity, as detected by antibodies to Pfs230 and Pfs48/45, was present in most studies analyzed. Significant between-study heterogeneity was seen, and methodological factors were a major contributor to this, and prevented further analysis of epidemiological and biological factors. This demonstrates a need for standardized protocols for conducting and reporting seroepidemiological analyses.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31695697/</p>
138	<p>Omoro R, Khagayi S, Ogwel B, Onkoba R, Ochieng JB, Juma J, Munga S, Tabu C, Kibet S, Nuorti JP, Odhiambo F, Mwenda JM, Breiman RF, Parashar UD, Tate JE. Rates of hospitalization and death for all-cause and rotavirus acute gastroenteritis before rotavirus vaccine introduction in Kenya, 2010-2013. <i>BMC Infect Dis.</i> 2019 Jan 11;19(1):47.</p> <p>Abstract</p> <p>Background: Rotavirus vaccine was introduced in Kenya immunization program in July 2014. Pre-vaccine disease burden estimates are important for assessing vaccine impact.</p> <p>Methods: Children with acute gastroenteritis (AGE) (≥ 3 loose stools and/or ≥ 1 episode of unexplained vomiting followed by loose stool within a 24-h period), hospitalized in Siaya County Referral Hospital (SCRH) from January 2010 through December 2013 were</p>



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	<p>enrolled. Stool specimens were tested for rotavirus (RV) using an enzyme immunoassay (EIA). Hospitalization rates were calculated using person-years of observation (PYO) from the Health Demographic Surveillance System (HDSS) as a denominator, while adjusting for healthcare utilization at household level and proportion of stool specimen collected from patients who met the case definition at the surveillance hospital. Mortality rates were calculated using PYO as the denominator and number of deaths estimated using total deaths in the HDSS, proportion of deaths attributed to diarrhoea by verbal autopsy (VA) and percent positive for rotavirus AGE (RVAGE) hospitalizations.</p> <p>Results: Of 7760 all-cause hospitalizations among children < 5 years of age, 3793 (49%) were included in the analysis. Of these, 21% (805) had AGE; RV was detected in 143 (26%) of 541 stools tested. Among children < 5 years, the estimated hospitalization rates per 100,000 PYO for AGE and RVAGE were 2413 and 429, respectively. Mortality rate associated with AGE and RVAGE were 176 and 45 per 100,000 PYO, respectively.</p> <p>Conclusion: AGE and RVAGE caused substantial health care burden (hospitalizations and deaths) before rotavirus vaccine introduction in Kenya.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30634922/</p>
139	<p>Schoenbuchner SM, Dolan C, Mwangome M, Hall A, Richard SA, Wells JC, Khara T, Sonko B, Prentice AM, Moore SE. The relationship between wasting and stunting: a retrospective cohort analysis of longitudinal data in Gambian children from 1976 to 2016. <i>Am J Clin Nutr.</i> 2019 Aug 1;110(2):498-507.</p> <p>Abstract</p> <p>Background: The etiologic relationship between wasting and stunting is poorly understood, largely because of a lack of high-quality longitudinal data from children at risk of undernutrition.</p> <p>Objectives: The aim of this study was to describe the interrelationships between wasting and stunting in children aged <2 y.</p>



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	<p>Methods: This study involved a retrospective cohort analysis, based on growth-monitoring records spanning 4 decades from clinics in rural Gambia. Anthropometric data collected at scheduled infant welfare clinics were converted to z scores, comprising 64,342 observations on 5160 subjects (median: 12 observations per individual). Children were defined as "wasted" if they had a weight-for-length z score <-2 against the WHO reference and "stunted" if they had a length-for-age z score <-2.</p> <p>Results: Levels of wasting and stunting were high in this population, peaking at approximately (girls-boys) 12-18% at 10-12 months (wasted) and 37-39% at 24 mo of age (stunted). Infants born at the start of the annual wet season (July-October) showed early growth faltering in weight-for-length z score, putting them at increased risk of subsequent stunting. Using time-lagged observations, being wasted was predictive of stunting (OR: 3.2; 95% CI: 2.7, 3.9), even after accounting for current stunting. Boys were more likely to be wasted, stunted, and concurrently wasted and stunted than girls, as well as being more susceptible to seasonally driven growth deficits.</p> <p>Conclusions: We provide evidence that stunting is in part a biological response to previous episodes of being wasted. This finding suggests that stunting may represent a deleterious form of adaptation to more overt undernutrition (wasting). This is important from a policy perspective as it suggests we are failing to recognize the importance of wasting simply because it tends to be more acute and treatable. These data suggest that stunted children are not just short children but are children who earlier were more seriously malnourished and who are survivors of a composite process.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30753251/</p>
140	Roberts DJ, Njuguna HN, Fields B, Fligner CL, Zaki SR, Keating MK, Rogena E, Walong E, Gachii AK, Maleche-Obimbo E, Irimu G, Mathaiya J, Orata N, Lopokoiyit R, Michuki J, Emukule GO, Onyango CO, Gikunju S, Owuor C, Muturi PK, Bunei M, Widdowson MA, Mott JA, Chaves SS. Comparison of Minimally Invasive



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	<p>Tissue Sampling With Conventional Autopsy to Detect Pulmonary Pathology Among Respiratory Deaths in a Resource-Limited Setting. <i>Am J Clin Pathol.</i> 2019 Jun 5;152(1):36-49.</p> <p>Abstract</p> <p>Objectives: We compared minimally invasive tissue sampling (MITS) with conventional autopsy (CA) in detection of respiratory pathology/pathogens among Kenyan children younger than 5 years who were hospitalized with respiratory disease and died during hospitalization.</p> <p>Methods: Pulmonary MITS guided by anatomic landmarks was followed by CA. Lung tissues were triaged for histology and molecular testing using TaqMan Array Cards (TACs). MITS and CA results were compared for adequacy and concordance.</p> <p>Results: Adequate pulmonary tissue was obtained by MITS from 54 (84%) of 64 respiratory deaths. Comparing MITS to CA, full histologic diagnostic concordance was present in 23 (36%) cases and partial concordance in 19 (30%), an overall 66% concordance rate. Pathogen detection using TACs had full concordance in 27 (42%) and partial concordance in 24 (38%) cases investigated, an overall 80% concordance rate.</p> <p>Conclusions: MITS is a viable alternative to CA in respiratory deaths in resource-limited settings, especially if combined with ancillary tests to optimize diagnostic accuracy.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31006817/</p>
141	<p>Gichuki PM, Mbugua G, Kiplelgo EK, Irungu TW, Mwandawiro C. Long Term School Based Deworming against Soil-Transmitted Helminths Also Benefits the Untreated Adult Population: Results from a Community-Wide Cross Sectional Survey. <i>J Trop Med.</i> 2019 May 2;2019:4151536.</p> <p>Abstract</p> <p>Background: Soil-transmitted helminths (STH) are a public health problem in Kenya. The primary control strategy for these infections is preventive chemotherapy (PC) delivered</p>



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	<p>through school based deworming (SBD) programs. The World Health Organization (WHO) recommends the inclusion of other at-risk groups in the PC. The untreated groups in endemic areas have been shown to act as reservoirs for STH transmission. Few field based studies have focused on the possible benefits of SBD to the untreated groups in the community. This study sought to determine the levels of STH among all age groups in a community where SBD has been going on for more than 10 years.</p> <p>Methods: This was a cross sectional study where 3,292 individuals, ranging from 2 to 98 years, were enrolled. Stool samples were analyzed using duplicate Kato Katz thick smear technique for presence of STH eggs. Statistical analysis was conducted using STATA software 14.0 (Stata corporation).</p> <p>Results: Out of the total 3,292 stool samples analyzed, only 13 were positive for any STH. Of these, 12 were infected with <i>Trichuris trichiura</i> and one case was of hookworm. There was no <i>Ascaris lumbricoides</i> infection detected. Of the 13 STH infections, seven of the infections were of school going age (6-18 years), 5 were of preschool age (<6 years), and one was of adult age group (18>). More male (61.5%) than female were infected with STH.</p> <p>Conclusion: This study shows very low prevalence of STH among all age groups in Mwea, suggesting that long term SBD may also be benefitting the untreated groups in the community and thus the potential to achieve STH elimination in such endemic areas.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31186652/</p>
142	<p>Mburu M, Guzé MA, Ong'wen P, Okoko N, Moghadassi M, Cohen CR, Bukusi EA, Wolf HT. Evaluating the effectiveness of the HIV adolescent package of care (APOC) training on viral load suppression in Kenya. <i>Public Health</i>. 2019 Aug;173:146-149.</p> <p>Abstract</p> <p>Objectives: To evaluate the effectiveness of the implementation of the adolescent package of care (APOC) training on adolescent viral suppression at Family AIDS Care & Education Services (FACES)-supported sites.</p>



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	<p>Study design: The effect of APOC training was evaluated based on viral load suppression (<1000 copies/mL) of 10-19-year-olds in 13 FACES-supported sites in six months before (January 2015-August 2016) and after (November 2015-March 2017) the APOC training for each site.</p> <p>Methods: Patient-level data were abstracted from the FACES electronic medical records (OpenMRS) and the National AIDS and STI Control Programme viral load website. Information on adolescent clinic day implementation and utilization of an APOC checklist as a proxy for services provided at each site was collected. Generalized estimating equations with repeated measures clustered by patients were used for bivariate and multivariate modeling to assess factors associated with viral suppression.</p> <p>Results: In the pretraining period, 60% of adolescents received services at clinics offering adolescent clinic days compared to 95% in the post-training period. Among those tested, 65% were virally suppressed during the pretraining period compared to 72% during the post-training period (odds ratio [OR] = 1.31, 95% confidence interval [CI] 1.12, 1.53, $P < 0.01$). In multivariable analysis, there was no statistically significant change in viral load suppression due to APOC training (adjusted OR [aOR] = 0.97, 95% CI: 0.72, 1.30, $P = 0.84$). However, at clinics offering adolescent-friendly clinic days, adolescents were nearly 2 times more likely to be virally suppressed than at facilities not offering these specialized clinic days (aOR = 1.86, 95% CI: 1.04, 3.32, $P = 0.04$).</p> <p>Conclusions: This study suggests that adolescent clinic days greatly improve adolescent viral load suppression and should be considered for implementation across HIV programs.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31310874/</p>
143	<p>Wekesa Sifuna M, Wambui M, Kang'ethe Nganga J, Wainaina Kariuki D, Kimani FT, Muregi FW. Antiplasmodial Activity Assay of 3-Chloro-4-(4-chlorophenoxy) Aniline Combinations with Artesunate or Chloroquine <i>In Vitro</i> and in a Mouse Model. <i>Biomed Res Int.</i> 2019 Oct 17;2019:5153482.</p> <p>Abstract</p>



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	<p>Malaria is the eighth highest contributor to global disease burden with 212 million cases and 429,000 deaths reported in 2015. There is an urgent need to develop multiple target drug to curb growing resistance by Plasmodia due to use of single target drugs and lack of vaccines. Based on a previous study, 3-chloro-4-(4-chlorophenoxy) aniline (ANI) inhibits Plasmodia enoyl acyl carrier protein reductase. This study aimed at evaluating the antiplasmodial activity of ANI combinations with artesunate (AS) or chloroquine (CQ) against <i>P. falciparum</i> in vitro based on the semiautomated microdilution assay and <i>P. berghei</i> in vivo based on Peters' 4-day test. Data were analysed by linear regression using version 5.5 of Statistica, 2000. From the results, on the one hand, a combination of 1.1 ng/ml AS and 3.3 µg/ml of ANI inhibited 50% growth of W2, while a combination of 0.8 ng/ml of AS and 2.6 µg/ml of ANI inhibited 50% growth of 3D7. On the other hand, a combination of 22 ng/ml CQ and 3.7 µg/ml of ANI inhibited 50% growth of W2, while a combination of 4.6 ng/ml CQ and 3.1 µg/ml of ANI inhibited 50% growth of 3D7. In in vivo assays, a combination of ED50 concentrations of AS and ANI cleared all parasites, while 1/2 and 1/4 ED50 combinations inhibited 67.0% and 35.4% parasite growth, respectively. ED50 combinations of CQ and ANI inhibited 81.0% growth of parasites, while 1/2 and 1/4 ED50 combinations inhibited 27.3% and 10.2% parasite growth. Assuming a linear relationship between percentage chemosuppression and combination ratios, only 0.88 mg/kg of AS combined with 1.68 mg/kg of ANI or 1.78 mg/kg of CQ with 3.15 mg/kg of ANI inhibited 50% parasite growth in vivo. ANI combinations with AS or CQ are thus potential antimalarial drug combinations if their clinical efficacy and safety are ascertained.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31781619/</p>
144	<p>Aluvaala J, Collins GS, Maina B, Mutinda C, Wayiego M, Berkley JA, English M. Competing risk survival analysis of time to in-hospital death or discharge in a large urban neonatal unit in Kenya. Wellcome Open Res. 2019 Jun 17;4:96. doi: 10.12688/wellcomeopenres.15302.1. PMID: 31289756; PMCID: PMC6611136.</p>
145	<p>Oiye S, Safari N, Anyango J, Arimi C, Nyawa B, Kimeu M, Odinge J, Kambona</p>



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O, Kahindi R, Mutisya R. Programmatic implications of some vitamin A supplementation and deworming determinants among children aged 6-59 months in resource-poor rural Kenya. *Pan Afr Med J.* 2019 Feb 28;32:96.

Abstract

Introduction: Controlling vitamin A deficiency and soil-transmitted helminth infections are public health imperatives. We aimed at revealing some caregiver and child-related determinants of uptake of vitamin A supplementation and deworming, and examine their programmatic implications in Kenyan context.

Methods: A cross-sectional study of randomly selected 1,177 households with infants and young children aged 6-59 months in three of the 47 counties of Kenya. The number of times a child was

given vitamin A supplements and dewormed 6 months and one year preceding the study was extracted from mother-child health books.

Results: Coverage for age-specific deworming was considerably depressed compared to corresponding vitamin A supplementation and for both services, twice-yearly provisions were disproportionately lower than half-yearly. Univariate and multivariate analyses showed relatively younger children, of Islam-affiliated caregivers (vis a vis Christians) and those who took less time to nearest health facilities as more likely to be supplemented with vitamin A. Similar observations were made for deworming where additionally, maternal and child ages were also determinants in favour of older groups. Other studied factors were not significant determinants. Programmatic allusions of the determining factors were discussed.

Conclusion: Key to improving uptake of vitamin A supplementation and deworming among Kenyan 6-59 months olds are: increasing access to functional health facilities, expanding outreaches and campaigns, dispelling faith-related misconceptions and probably modulating caregiver and child age effects by complementing nutrition literacy with robust



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	<p>and innovative caregiver reminders. Given analogous service points and scheduling, relative lower uptake of deworming warrants further investigations.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31231453/</p>
146	<p>Marzouk M, Kelley M, Fadhil I, Slama S, Longuere KS, Ariana P, Carson G, Marsh V. "If I have a cancer, it is not my fault I am a refugee": A qualitative study with expert stakeholders on cancer care management for Syrian refugees in Jordan. PLoS One. 2019 Sep 27;14(9):e0222496.</p> <p>Abstract</p> <p>Background: Noncommunicable diseases including cancer are widespread amongst the 5.6 million Syrian refugees currently hosted in the Middle East. Given its prevalence as the third leading cause of death in Syria, cancer is likely to be an important health burden among Syrian refugees. Against this background, our aim was to describe the clinical, ethical and policy decision-making experiences of health actors working within the current refugee cancer care system; the impact of refugee cancer care health policies on health care providers and policy makers in this context; and provide suggestions for the way delivery of care should be optimised in a sustained emergency situation.</p> <p>Methods: From April-July 2016, we conducted in-depth interviews with 12 purposively sampled health officials and health care workers from the Jordanian Ministry of Health, multilateral donors and international non-governmental organisations. Data were analysed using a framework analysis approach to identify systemic, practical and ethical challenges to optimising care for refugees, through author agreement on issues emerging from the data and those linked more directly to areas of questioning.</p> <p>Results: As has been previously reported, central challenges for policy makers and health providers were the lack of quality cancer prevalence data to inform programming and care delivery for this refugee population, and insufficient health resource allocation to support services. In addition, limited access to international funding for the host country, the absence of long-term funding schemes, and barriers to coordination between institutions</p>



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	<p>and frontline clinicians were seen as key barriers. In this context where economic priorities inevitably drive decision-making on public health policy and individual care provision, frontline healthcare workers and policy makers experienced significant moral distress where duties of care and humanitarian values were often impossible to uphold.</p> <p>Conclusions: Our findings confirm and expand understanding of the challenges involved in resource allocation decisions for cancer care in refugee populations, and highlight these for the particular situation of long term Syrian refugees in Jordan. The insights offered by frontline clinicians and policy makers in this context reveal the unintended personal and moral impact of resource allocation decisions. With many countries facing similar challenges in the provision of cancer care for refugees, the lessons learned from Jordan suggest key areas for policy revision and international investment in developing cancer care policies for refugees internationally.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31560701/</p>
147	<p>Muraya KW, Govender V, Mbachu C, Uguru NP, Molyneux S. 'Gender is not even a side issue...it's a non-issue': career trajectories and experiences from the perspective of male and female healthcare managers in Kenya. <i>Health Policy Plan.</i> 2019 May 1;34(4):249-256.</p> <p>Abstract</p> <p>Women comprise a significant proportion of the health workforce globally but remain under-represented in the higher professional categories. Concern about the under-representation of women in health leadership positions has resulted in increased research on the topic, although this research has focused primarily on high-income countries. An improved understanding of the career trajectories and experiences of healthcare leaders in low- and middle-income countries (LMICs), and the role of gender, is therefore needed. This qualitative case study was undertaken in two counties in coastal Kenya. Drawing on the life-history approach, 12 male and 13 female healthcare leaders were interviewed between August 2015 and July 2016 on their career progression and related experiences.</p>



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	<p>Although gender was not spontaneously identified as a significant influence, closer exploration of responses revealed that gendered factors played an important role. Most fundamentally, women’s role as child bearers and gendered societal expectations including child nurturing and other domestic responsibilities can influence their ability to take up leadership opportunities, and their selection and appointment as leaders. Women’s selection and appointment as leaders may also be influenced by positive discrimination policies (in favour of women), and by perceptions of women and men as having different leadership styles (against women, who some described as more emotive and reactive). These gendered influences intersect in relatively invisible ways with other factors more readily identified by respondents to influence their progression and experience. These factors included: professional cadre, with doctors more likely to be selected into leadership roles; and personal and professional support systems ranging from family support and role models, through to professional mentorship and continuing education. We discuss the implications of these findings for policy, practice and research, including highlighting the need for more in-depth intersectionality analyses of leadership experience in LMICs.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/</p>
148	<p>Macpherson L, Ogero M, Akech S, Aluvaala J, Gathara D, Irimu G, English M, Agweyu A. Risk factors for death among children aged 5-14 years hospitalised with pneumonia: a retrospective cohort study in Kenya. <i>BMJ Glob Health</i>. 2019 Sep 3;4(5):e001715.</p> <p>Abstract</p> <p>Introduction: There were almost 1 million deaths in children aged between 5 and 14 years in 2017, and pneumonia accounted for 11%. However, there are no validated guidelines for pneumonia management in older children and data to support their development are limited. We sought to understand risk factors for mortality among children aged 5-14 years hospitalised with pneumonia in district-level health facilities in Kenya.</p>



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	<p>Methods: We did a retrospective cohort study using data collected from an established clinical information network of 13 hospitals. We reviewed records for children aged 5-14 years admitted with pneumonia between 1 March 2014 and 28 February 2018. Individual clinical signs were examined for association with inpatient mortality using logistic regression. We used existing WHO criteria (intended for under 5s) to define levels of severity and examined their performance in identifying those at increased risk of death.</p> <p>Results: 1832 children were diagnosed with pneumonia and 145 (7.9%) died. Severe pallor was strongly associated with mortality (adjusted OR (aOR) 8.06, 95% CI 4.72 to 13.75) as were reduced consciousness, mild/moderate pallor, central cyanosis and older age (>9 years) (aOR >2). Comorbidities HIV and severe acute malnutrition were also associated with death (aOR 2.31, 95% CI 1.39 to 3.84 and aOR 1.89, 95% CI 1.12 to 3.21, respectively). The presence of clinical characteristics used by WHO to define severe pneumonia was associated with death in univariate analysis (OR 2.69). However, this combination of clinical characteristics was poor in discriminating those at risk of death (sensitivity: 0.56, specificity: 0.68, and area under the curve: 0.62).</p> <p>Conclusion: Children >5 years have high inpatient pneumonia mortality. These findings also suggest that the WHO criteria for classification of severity for children under 5 years do not appear to be a valid tool for risk assessment in this older age group, indicating the urgent need for evidence-based clinical guidelines for this neglected population.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31544003/</p>
149	<p>Gichuki PM, Kepha S, Mulewa D, Masaku J, Kwoba C, Mbugua G, Mazigo HD, Mwandawiro C. Association between <i>Schistosoma mansoni</i> infection and access to improved water and sanitation facilities in Mwea, Kirinyaga County, Kenya. <i>BMC Infect Dis.</i> 2019 Jun 7;19(1):503.</p> <p>Abstract</p> <p>Background: Schistosomiasis remains a public health problem in Central Kenya despite concerted control efforts. Access to improved water and sanitation has been emphasized as</p>



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important control measures. Few studies have assessed the association between access to improved water sources and sanitation facilities with *Schistosoma mansoni* infection in different environmental settings. This study assessed the association between *S. mansoni* infection and household access to improved water sources and sanitation facilities in Mwea, Kirinyaga County, Kenya.

Methods: A cross sectional study was conducted between the months of August and October 2017. A total of 905 household heads from seven villages were interviewed and their stool samples screened for *S. mansoni* using the Kato Katz technique. Comparisons of demographic factors by *S. mansoni* infection were tested for significance using the chi-square test (χ^2) or the Fisher exact test for categorical variables. Variables associated with *S. mansoni* infection were analyzed using univariable analysis and the strength of the association measured as odds ratio (OR) using mixed effects logistic regression at 95% CI, with values considered significant at $p < 0.05$.

Results: The overall prevalence of *S. mansoni* was, 23.1% (95% CI: 20.5-26.0%), with majority of the infections being of light intensity. Rurumi village had the highest prevalence at 33.3%, with Kirogo village having the least prevalence at 7.0%. Majority (84.1%) of the households lacked access to improved water sources but had access to improved sanitation facilities (75%). Households with access to piped water had the lowest *S. mansoni* infections. However, there was no significant association between *S. mansoni* infections with either the main source of water in the household (Odds Ratio (OR) =0.782 (95% CI: 0.497-1.229) $p = 0.285$ or sanitation facilities (OR = 1.018 (95% CI: 0.705-1.469) $p = 0.926$).

Conclusion: Our study suggests that *S. mansoni* is still a public health problem among all age groups in Mwea irrigation scheme, Kirinyaga County, Central Kenya. Majority of the households lacks access to improved water sources but have access to improved sanitation facilities. This study recommends initiatives to ensure adequate provision of improved



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	<p>water sources, and the inclusion of the adult community in preventive chemotherapy programs.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31174478/</p>
150	<p>Juma DW, Muiruri P, Yuhas K, John-Stewart G, Ottichilo R, Waitumbi J, Singa B, Polyak C, Kamau E. The prevalence and antifolate drug resistance profiles of <i>Plasmodium falciparum</i> in study participants randomized to discontinue or continue cotrimoxazole prophylaxis. <i>PLoS Negl Trop Dis</i>. 2019 Mar 21;13(3):e0007223.</p> <p>Abstract</p> <p>Objective: Cotrimoxazole prevents opportunistic infections including <i>falciparum</i> malaria in HIV-infected individuals but there are concerns of cross-resistance to other antifolate drugs such as sulphadoxine-pyrimethamine (SP). In this study, we investigated the prevalence of antifolate-resistance mutations in <i>Plasmodium falciparum</i> that are associated with SP resistance in HIV-infected individuals on antiretroviral treatment randomized to discontinue (STOP-CTX), or continue (CTX) cotrimoxazole in Western Kenya.</p> <p>Design: Samples were obtained from an unblinded, non-inferiority randomized controlled trial where participants were recruited on a rolling basis for the first six months of the study, then followed-up for 12 months with samples collected at enrollment, quarterly, and during sick visits.</p> <p>Method: <i>Plasmodium</i> DNA was extracted from blood specimens. Initial screening to determine the presence of <i>Plasmodium</i> spp. was performed by quantitative reverse transcriptase real-time PCR, followed by genotyping for the presence of SP-resistance associated mutations by Sanger sequencing.</p> <p>Results: The prevalence of mutant haplotypes associated with SP-resistant parasites in <i>pfdhfr</i> (51I/59R/108N) and <i>pfdhps</i> (437G/540E) genes were significantly higher ($P = 0.0006$ and $P = 0.027$, respectively) in STOP-CTX compared to CTX arm. The prevalence of quintuple haplotype (51I/59R/108N/437G/540E) was 51.8% in STOP-CTX vs. 6.3% (P</p>



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	<p>= 0.0007) in CTX arm. There was a steady increase in mutant haplotypes in both genes in STOP-CTX arm overtime through the study period, reaching statistical significance ($P < 0.0001$).</p> <p>Conclusion: The frequencies of mutations in <i>pfdhfr</i> and <i>pfdhps</i> genes were higher in STOP-CTX arm compared to CTX arm, suggesting cotrimoxazole effectively controls and selects against SP-resistant parasites.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30897090/</p>
151	<p>Tamari N, Minakawa N, Sonye GO, Awuor B, Kongere JO, Munga S, Larson PS. Antimalarial bednet protection of children disappears when shared by three or more people in a high transmission setting of western Kenya. <i>Parasitology</i>. 2019 Mar;146(3):363-371.</p> <p>Abstract</p> <p>A sizeable proportion of households is forced to share single long-lasting insecticide treated net (LLIN). However, the relationship between increasing numbers of people sharing a net and the risk for Plasmodium infection is unclear. This study revealed whether risk for Plasmodium falciparum infection is associated with the number of people sharing a LLIN in a holoendemic area of Kenya. Children ≤ 5 years of age were tested for P. falciparum infection using polymerase chain reaction. Of 558 children surveyed, 293 (52.5%) tested positive for parasitaemia. Four hundred and fifty-eight (82.1%) reported sleeping under a LLIN. Of those, the number of people sharing a net with the sampled child ranged from 1 to 5 (median = 2). Children using a net alone or with one other person were at lower risk than non-users (OR = 0.29, 95% CI 0.10-0.82 and OR = 0.47, 95% CI 0.22-0.97, respectively). On the other hand, there was no significant difference between non-users and children sharing a net with two (OR = 0.88, 95% CI 0.44-1.77) or more other persons (OR = 0.75, 95% CI 0.32-1.72). LLINs are effective in protecting against Plasmodium infection in children when used alone or with one other person compared with not using them. Public health professionals should inform caretakers of the risks of too many people sharing a net.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30198452/</p>



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152 Obbo CJD, Kariuki ST, Gathirwa JW, Olaho-Mukani W, Cheplogoi PK, Mwangi EM. In vitro antiplasmodial, antitrypanosomal and antileishmanial activities of selected medicinal plants from Ugandan flora: Refocusing into multi-component potentials. *J Ethnopharmacol.* 2019 Jan 30;229:127-136.

Abstract

Ethnopharmacological relevance: Seven medicinal plants from Ugandan flora, namely *Entada abyssinica*, *Khaya anotheca*, *Vernonia amygdalina*, *Baccharoides adoensis*, *Schkuhria pinnata*, *Entandropagma utile* and *Momordica foetida*, were selected in this study. They are used to treat conditions and infections ranging from inflammations, pains and fevers to viruses, bacteria, protozoans and parasites. Two of the plants, *V. amygdalina* and *M. foetida*, are also used as human food or relish, while others are important in ethnoveterinary practices and in zoopharmacognosy in the wild. The aim of this study was to evaluate the in vitro antiplasmodial, antitrypanosomal and antileishmanial activities, along with cytotoxicity of the multi-component extracts of these plants.

Materials and methods: Different parts of the plants were prepared and serially extracted with hexane, petroleum ether, dichloromethane, ethyl acetate, methanol and double distilled water. Solvent free extracts were assayed for in vitro inhibition against four reference parasite strains, *Plasmodium falciparum* (K1), *Trypanosoma brucei rhodesiense* (STIB 900), *Trypanosoma cruzi* (Talahuen C2C4) and *Leishmania donovani* (MHOM-ET-67/L82) using standard methods. Toxicity was assessed against L6 skeletal fibroblast and mouse peritoneal macrophage (J774) cells and selectivity indices (SIs) calculated for the most active extracts.

Results: The strongest activities, demonstrating median inhibitory concentration (IC₅₀) values $\leq 2 \mu\text{g/ml}$, were observed for the dichloromethane and petroleum ether extracts of *K. anotheca*, *B. adoensis* and *S. pinnata*. Overall, IC₅₀ values ranged from $< 1 \mu\text{g/ml}$ to $> 90 \mu\text{g/ml}$. Out of 22 extracts demonstrating IC₅₀s $< 20 \mu\text{g/ml}$, seven were against *T. b. rhodesiense* (IC₅₀: 1.6-16.2 $\mu\text{g/ml}$), six against *T. cruzi* (IC₅₀: 2.1-18.57 $\mu\text{g/ml}$), none



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	<p>against <i>L. donovani</i> (IC₅₀: falling > 3.3 and >10 µg/ml), and nine against <i>P. falciparum</i> (IC₅₀: 0.96 µg/ml to 4.69 µg/ml). Selectivity indices (SI) calculated for the most active extracts ranged from <1.00 to 94.24. However, the <i>B. adoensis</i> leaf dichloromethane extract (a) was equipotent (IC₅₀ = 3.3 µg/ml) against <i>L. donovani</i> and L6 cells respectively, indicating non-specific selection. Trypanosome and Plasmodium parasites were comparatively more sensitive to the test extracts.</p> <p>Conclusions: The benefits achieved from the seven tested plant species as traditional ethnomedicinal and ethnoveterinary therapies or in zoopharmacognosy against infections and conditions of animals in the wild are strongly supported by results of this study. The synergy of plant extracts, so achieved by concerted actions of the ligands, produces adequate perturbation of targets in the four parasite genera, resulting in the strong potencies exhibited by low IC₅₀ values. The total inhibitory effect, achieved as a sum of perturbations contributed by each participating compound in the extract, minimises toxic effects of the compounds as seen in the high SI's obtained with some extracts. Those extracts demonstrating SI ≥ 4 form promising candidates for further cell-based and system pharmacology studies.6.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30273736/</p>
153	<p>Sandbulte MR, Gautney BJ, Maloba M, Wexler C, Brown M, Mabachi N, Goggin K, Lwembe R, Nazir N, Odeny TA, Finocchiaro-Kessler S. Infant HIV testing at birth using point-of-care and conventional HIV DNA PCR: an implementation feasibility pilot study in Kenya. <i>Pilot Feasibility Stud.</i> 2019 Jan 25;5:18.</p> <p>Abstract</p> <p>Background: Infant HIV diagnosis by HIV DNA polymerase chain reaction (PCR) testing at the standard 6 weeks of age is often late to mitigate the mortality peak that occurs in HIV positive infants' first 2-3 months of life. Kenya recently revised their early infant diagnosis (EID) guidelines to include HIV DNA PCR testing at birth (pilot only), 6 weeks, 6 months, and 12 months postnatal and a final 18-month antibody test. The World Health</p>



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	<p>Organization (WHO) approved point-of-care (POC) diagnostic platforms for infant HIV testing in resource-limited countries that could simplify logistics and expedite infant diagnosis. Sustainable scale-up and optimal utility in Kenya and other high-prevalence countries depend on robust implementation studies in diverse clinical settings.</p> <p>Methods: We will pilot the implementation of birth testing by HIV DNA PCR, as well as two POC testing systems (Xpert HIV-1 Qual [Xpert] and Alere q HIV-1/2 Detect [Alere q]), on specimens collected from Kenyan infants at birth (0 to 2 weeks) and 6 weeks (4 to < 24 weeks) postnatal. The formative phase will inform optimal implementation of birth testing and two POC testing technologies. Qualitative interviews with stakeholders (providers, parents of HIV-exposed infants, and community members) will assess attitudes, barriers, and recommendations to optimize implementation at their respective sites. A non-blinded pilot study at four Kenyan hospitals (n = 2 Xpert, n = 2 Alere q platforms) will evaluate infant HIV POC testing compared with standard of care HIV DNA PCR testing in both the birth and 6-week windows. Objectives of the pilot are to assess uptake, efficiency, quality, implementation variables, user experiences of birth testing with both POC testing systems or with HIV DNA PCR, and costs.</p> <p>Discussion: This study will generate data on the clinical impact and feasibility of adding HIV testing at birth utilizing POC and traditional PCR HIV testing strategies in resource-limited settings. Data from this pilot will inform the optimal implementation of Kenya's birth testing guidelines and of POC testing systems for the improvement of EID outcomes.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30701079/</p>
154	<p>Ogari CO, Nyamache AK, Nonoh J, Amukoye E. Prevalence and detection of drug resistant mutations in Mycobacterium tuberculosis among drug naïve patients in Nairobi, Kenya. BMC Infect Dis. 2019 Mar 25;19(1):279.</p> <p>Abstract</p>



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Background: Tuberculosis (TB), an ancient scourge of humanity known for several thousands of years, is still a significant public health challenge in many countries today even though some progress has been made in recent years in controlling the disease. The study's aim was to determine the prevalence of mutations responsible for drug resistance in *Mycobacterium tuberculosis* among patients visiting selected health centers in Nairobi, Kenya.

Methods: The cross-sectional study involved 132 TB positive patients visiting Mbagathi and Chandaria hospitals between September 2015 and August 2016. Sputum samples were collected from the participants and handled in a biosafety level 3 laboratory at the Kenya Medical Research Institute (KEMRI). Samples were decontaminated using N-Acetyl-L-Cysteine (NALC) - Sodium Hydroxide (NALC-NaOH), stained using Zeihl-Neelsen (ZN), and cultured in *Mycobacterium* Growth Indicator Tube (MGIT). DNA extracted from cultured isolates using Genolyse™ technique was subjected to Multiplex PCR amplification and reverse hybridization for detection of drug resistance mutations on *rpoB*, *katG*, *inhA*, *gyrA*, *gyrB*, *rrs* and *eis* genes using Hain Genotype MTBDRplus and MTBDRsl.

Results: All 132 (100%) patients included in the study were culture positive for *M. tuberculosis*. Among them, 72 (54%) were male while the remaining 60 (46%) were female. The mean age of the patients was 26.4 ± 19.4 (SD) with a range of 18 to 60 years. Overall, the prevalence of the resistance to first and second-line TB drugs was 1.5% (2/132). Resistance to isoniazid (INH) was observed in 1 of 132 patients (0.8%), as was multi-drug resistant tuberculosis (MDR-TB), also at 0.8%. No resistance to fluoroquinolones (FQ) or kanamycin (KAN) was observed. The INH resistant strain had the *katG* mutations S315 T, while mutations detected for the MDR-TB were *katG* S513 T for INH, *rpoB* S531 L for rifampicin (RIF) and *rrs* G1484 T for cross-resistance to aminoglycosides/capreomycin (AG/CP).



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	<p>Conclusions: Molecular analysis confirms transmission of the drug-resistant M. tuberculosis strains. The data suggested that there is homogeneity when it comes to the type of drug resistance and mutation that occurs in the region. This calls for intensified drug resistance surveillance and drug adherence among patients infected with TB.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30909867/</p>
155	<p>Mmeje O, Njoroge B, Wekesa P, Murage A, Ondondo RO, van der Poel S, Guzé MA, Shade SB, Bukusi EA, Cohan D, Cohen CR. Empowering HIV-infected women in low-resource settings: A pilot study evaluating a patient-centered HIV prevention strategy for reproduction in Kisumu, Kenya. PLoS One. 2019 Mar 6;14(3):e0212656.</p> <p>Abstract</p> <p>Background: Female positive/male negative HIV-serodiscordant couples express a desire for children and may engage in condomless sex to become pregnant. Current guidelines recommend antiretroviral treatment in HIV-serodiscordant couples, yet HIV RNA viral suppression may not be routinely assessed or guaranteed and pre-exposure prophylaxis may not be readily available. Therefore, options for becoming pregnant while limiting HIV transmission should be offered and accessible to HIV-affected couples desiring children.</p> <p>Methods: A prospective pilot study of female positive/male negative HIV-serodiscordant couples desiring children was conducted to evaluate the acceptability, feasibility, and effectiveness of timed vaginal insemination. Eligible women were 18-34 years with regular menses. Prior to timed vaginal insemination, couples were observed for two months, and tested and treated for sexually transmitted infections. Timed vaginal insemination was performed for up to six menstrual cycles. A fertility evaluation and HIV RNA viral load assessment was offered to couples who did not become pregnant.</p> <p>Findings: Forty female positive/male negative HIV-serodiscordant couples were enrolled; 17 (42.5%) exited prior to timed vaginal insemination. Twenty-three couples (57.5%) were introduced to timed vaginal insemination; eight (34.8%) achieved pregnancy, and six live</p>



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	<p>births resulted without a case of HIV transmission. Seven couples completed a fertility evaluation. Four women had no demonstrable tubal patency bilaterally; one male partner had decreased sperm motility. Five women had unilateral/bilateral tubal patency; and seven women had an HIV RNA viral load (≥ 400 copies/mL).</p> <p>Conclusion: Timed vaginal insemination is an acceptable, feasible, and effective method for attempting pregnancy. Given the desire for children and inadequate viral suppression, interventions to support safely becoming pregnant should be integrated into HIV prevention programs.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30840672/</p>
156	<p>Abeijon C, Alves F, Monnerat S, Wasunna M, Mbui J, Viana AG, Bueno LL, Siqueira WF, Carvalho SG, Agrawal N, Fujiwara R, Sundar S, Campos-Neto A. Development of a Multiplexed Assay for Detection of <i>Leishmania donovani</i> and <i>Leishmania infantum</i> Protein Biomarkers in Urine Samples of Patients with Visceral Leishmaniasis. J Clin Microbiol. 2019 Apr 26;57(5):e02076-18.</p> <p>Abstract</p> <p>Visceral leishmaniasis (VL) is a serious and fatal disease caused by the parasites <i>Leishmania infantum</i> and <i>Leishmania donovani</i>. The gold standard diagnostic test for VL is the demonstration of parasites or their DNA in spleen, lymph node, or bone marrow aspirates. Serological tests exist but cannot distinguish active VL from either prior exposure to the parasites or previously treated VL disease. Using mass spectroscopy, we have previously identified three <i>L. infantum</i> protein biomarkers (Li-isd1, Li-txn1, and Li-ntf2) in the urine of VL patients and developed a sensitive and specific urine-based antigen detection assay for the diagnosis of VL that occurs in Brazil (where VL is caused by <i>L. infantum</i>). However, unpublished observations from our laboratory at DetectoGen showed that these biomarkers were detected in only 55% to 60% of VL patients from India and Kenya, where the disease is caused by <i>L. donovani</i>. Here, we report the discovery and</p>



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	<p>characterization of two new biomarkers of <i>L. donovani</i> (Ld-mao1 and Ld-ppi1) present in the urine of VL patients from these two countries. Capture enzyme-linked immunosorbent assays using specific rabbit IgG and chicken IgY were developed, and the assays had sensitivities of 44.4% and 28.8% for the detection of Ld-mao1 and Ld-ppi1, respectively. In contrast, a multiplexed assay designed to simultaneously detect all five leishmanial biomarkers markedly increased the assay sensitivity to 82.2%. These results validate the utility of leishmanial protein biomarkers found in the urine of VL patients as powerful tools for the development of an accurate diagnostic test for this disease.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30787142/</p>
157	<p>Silverman RA, John-Stewart GC, Beck IA, Milne R, Kiptinness C, McGrath CJ, Richardson BA, Chohan B, Sakr SR, Frenkel LM, Chung MH. Predictors of mortality within the first year of initiating antiretroviral therapy in urban and rural Kenya: A prospective cohort study. <i>PLoS One</i>. 2019 Oct 4;14(10):e0223411.</p> <p>Abstract</p> <p>Introduction: Despite increased treatment availability, HIV-infected individuals continue to start antiretroviral therapy (ART) late in disease progression, increasing early mortality risk.</p> <p>Materials and methods: Nested prospective cohort study within a randomized clinical trial of adult patients initiating ART at clinics in urban Nairobi and rural Maseno, Kenya, between 2013-2014. We estimated mortality incidence rates following ART initiation and used Cox proportional hazards regression to identify predictors of mortality within 12 months of ART initiation. Analyses were stratified by clinic site to examine differences in mortality correlates and risk by location.</p> <p>Results: Among 811 participants initiated on ART, the mortality incidence rate within a year of initiating ART was 7.44 per 100 person-years (95% CI 5.71, 9.69). Among 207 Maseno and 612 Nairobi participants initiated on ART, the mortality incidence rates (per 100 person-years) were 12.78 (95% CI 8.49, 19.23) and 5.72 (95% CI 4.05, 8.09). Maseno</p>



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	<p>had a 2.20-fold greater risk of mortality than Nairobi (95% CI 1.29, 3.76; P = 0.004). This association remained [adjusted hazard ratio (HR) = 2.09 (95% CI 1.17, 3.74); P = 0.013] when adjusting for age, gender, education, pre-treatment drug resistance (PDR), and CD4 count, but not when adjusting for BMI. In unadjusted analyses, other predictors (P<0.05) of mortality included male gender (HR = 1.74), age (HR = 1.04 for 1-year increase), fewer years of education (HR = 0.92 for 1-year increase), unemployment (HR = 1.89), low body mass index (BMI<18.5 m/kg²; HR = 4.99), CD4 count <100 (HR = 11.67) and 100-199 (HR = 3.40) vs. 200-350 cells/μL, and pre-treatment drug resistance (PDR; HR = 2.49). The increased mortality risk associated with older age, males, and greater education remained when adjusted for location, age, education and PDR, but not when adjusted for BMI and CD4 count. PDR remained associated with increased mortality risk when adjusted for location, age, gender, education, and BMI, but not when adjusted for CD4 count. CD4 and BMI associations with increased mortality risk persisted in multivariable analyses. Despite similar baseline CD4 counts across locations, mortality risk associated with low CD4 count, low BMI, and PDR was greater in Maseno than Nairobi in stratified analyses. Conclusions: High short-term post-ART mortality was observed, partially due to low CD4 count and BMI at presentation, especially in the rural setting. Male gender, older age, and markers of lower socioeconomic status were also associated with greater mortality risk. Engaging patients earlier in HIV infection remains critical. PDR may influence short-term mortality and further studies to optimize management will be important in settings with increasing PDR.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31584992/</p>
158	<p>Nduba V, Van't Hoog AH, de Bruijn A, Mitchell EMH, Laserson K, Borgdorff M. Estimating the annual risk of infection with Mycobacterium tuberculosis among adolescents in Western Kenya in preparation for TB vaccine trials. BMC Infect Dis. 2019 Aug 2;19(1):682.</p> <p>Abstract</p>



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	<p>Background: Adolescents are a prime target group for tuberculosis (TB) vaccine trials that include prevention of infection (POI). The BCG vaccine is given at birth and does not prevent TB infection. TB infection, a critical endpoint for POI vaccine trials would need to be documented to estimate sample sizes in target populations.</p> <p>Methods: Adolescents aged 12-18 years of age were enrolled in an area under continuous demographic surveillance. A tuberculin skin test (TST) survey was conducted as part of a study on TB prevalence and incidence. All adolescents got TSTs at enrolment and returned after 72 h for reading. A TST of ≥ 10 mm if HIV negative or ≥ 5 mm if HIV positive, was considered positive.</p> <p>Results: Of 4808 adolescents returning for TST readings (96% of those enrolled), mean age was 14.4 (SD 1.9), 4518(94%) were enrolled in school and 21(0.4%) gave a previous history of tuberculosis. Among adolescents with TST reactivity, the mean TST induration was 13.2 mm (SD 5.4). The overall prevalence of latent TB infection was 1544/4808 (32.1, 95% CI 29.2-35.1) with a corresponding annual risk of TB infection (ARTI) of 2.6% (95% CI 2.2-3.1). Risk factors for a positive TST included being male (OR 1.3, 95% CI 1.2,1.5), history of having a household TB contact (OR 1.5, 95% CI 1.2,1.8), having a BCG scar (OR 1.5,95% CI 1.2,1.8), living in a rural area (OR 1.4, 95% CI 1.1,1.9), and being out of school (OR 1.8, 95% CI 1.4,2.3).</p> <p>Conclusion: We conclude that the high TB transmission rates we found in this study, suggest that adolescents in this region may be an appropriate target group for TB vaccine trials including TB vaccine trials aiming to prevent infection.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31375068/</p>
159	<p>Hassan AS, Bibby DF, Mwaringa SM, Agutu CA, Ndirangu KK, Sanders EJ, Cane PA, Mbisa JL, Berkley JA. Presence, persistence and effects of pre-treatment HIV-1 drug resistance variants detected using next generation sequencing: A Retrospective longitudinal study from rural coastal Kenya. PLoS One. 2019 Feb 13;14(2):e0210559.</p>



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	<p>Abstract</p> <p>Background: The epidemiology of HIV-1 drug resistance (HIVDR) determined by Sanger capillary sequencing, has been widely studied. However, much less is known about HIVDR detected using next generation sequencing (NGS) methods. We aimed to determine the presence, persistence and effect of pre-treatment HIVDR variants detected using NGS in HIV-1 infected antiretroviral treatment (ART) naïve participants from rural Coastal Kenya.</p> <p>Methods: In a retrospective longitudinal study, samples from HIV-1 infected participants collected prior [n = 2 time-points] and after [n = 1 time-point] ART initiation were considered. An ultra-deep amplicon-based NGS assay, calling for nucleotide variants at >2.0% frequency of viral population, was used. Suspected virologic failure (sVF) was defined as a one-off HIV-1 viral load of >1000 copies/ml whilst on ART.</p> <p>Results: Of the 50 eligible participants, 12 (24.0% [95% CI: 13.1-38.2]) had at least one detectable pre-treatment HIVDR variant against Protease Inhibitors (PIs, n = 6 [12%]), Nucleoside Reverse Transcriptase Inhibitors (NRTIs, n = 4 [8.0%]) and Non-NRTIs (n = 3 [6.0%]). Overall, 15 pre-treatment resistance variants were detected (frequency, range: 2.3-92.0%). A positive correlation was observed between mutation frequency and absolute load for NRTI and/or NNRTI variants ($r = 0.761$ [$p = 0.028$]), but not for PI variants ($r = -0.117$ [$p = 0.803$]). Participants with pre-treatment NRTI and/or NNRTI resistance had increased odds of sVF (OR = 6.0; 95% CI = 1.0-36.9; $p = 0.054$).</p> <p>Conclusions: Using NGS, pre-treatment resistance variants were common, though observed PI variants were unlikely transmitted, but rather probably generated de novo. Even when detected from a low frequency, pre-treatment NRTI and/or NNRTI resistance variants may adversely affect treatment outcomes.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/30759103/</p>
160	Lee JS, Mogasale V, Lim JK, Ly S, Lee KS, Sorn S, Andia E, Carabali M,



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Namkung S, Lim SK, Ridde V, Njenga SM, Yaro S, Yoon IK. A multi-country study of the economic burden of dengue fever based on patient-specific field surveys in Burkina Faso, Kenya, and Cambodia. *PLoS Negl Trop Dis*. 2019 Feb 28;13(2):e0007164.

Abstract

Background: Dengue fever is a rapidly growing public health problem in many parts of the tropics and sub-tropics in the world. While there are existing studies on the economic burden of dengue fever in some of dengue-endemic countries, cost components are often not standardized, making cross-country comparisons challenging. Furthermore, no such studies have been available in Africa.

Methods/principal findings: A patient-specific survey questionnaire was developed and applied in Burkina Faso, Kenya, and Cambodia in a standardized format. Multiple interviews were carried out in order to capture the entire cost incurred during the period of dengue illness. Both private (patient's out-of-pocket) and public (non-private) expenditure were accessed to understand how the economic burden of dengue is distributed between private and non-private payers. A substantial number of dengue-confirmed patients were identified in all three countries: 414 in Burkina Faso, 149 in Kenya, and 254 in Cambodia. The average cost of illness for dengue fever was \$26 (95% CI \$23-\$29) and \$134 (95% CI \$119-\$152) per inpatient in Burkina Faso and Cambodia, respectively. In the case of outpatients, the average economic burden per episode was \$13 (95% CI \$23-\$29) in Burkina Faso and \$23 (95% CI \$19-\$28) in Kenya. Compared to Cambodia, public contributions were trivial in Burkina Faso and Kenya, reflecting that a majority of medical costs had to be directly borne by patients in the two countries.

Conclusions/significance: The cost of illness for dengue fever is significant in the three countries. In particular, the current study sheds light on the potential economic burden of the disease in Burkina Faso and Kenya where existing evidence is sparse in the context of dengue fever, and underscores the need to achieve Universal Health Coverage. Given the



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	<p>availability of the current (CYD-TDV) and second-generation dengue vaccines in the near future, our study outcomes can be used to guide decision makers in setting health policy priorities.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/30817776/</p>
161	<p>Sandfort TGM, Dominguez K, Kayange N, Ogendo A, Panchia R, Chen YQ, Chege W, Cummings V, Guo X, Hamilton EL, Stirratt M, Eshleman SH. HIV testing and the HIV care continuum among sub-Saharan African men who have sex with men and transgender women screened for participation in HPTN 075. <i>PLoS One</i>. 2019 May 31;14(5):e0217501.</p> <p>Abstract</p> <p>Throughout the world, men who have sex with men (MSM) are at increased risk for HIV infection compared to heterosexual men. Little is known about awareness of HIV infection and other gaps in the HIV care continuum for MSM, especially in sub-Saharan Africa (SSA). This information is urgently needed to address the HIV epidemic in this population. This study assessed gaps in the HIV care continuum among persons screened for participation in a multi-country prospective study that evaluated the feasibility of recruiting and retaining MSM for HIV prevention studies in SSA (HIV Prevention Trials Network (HPTN) 075, conducted in four cities in Kenya, Malawi, and South Africa). Participants were recruited using site-specific strategies, that included outreach and informal networks. Transgender women (TW) were eligible to participate. During screening, 601 MSM and TW were tested for HIV infection and asked about prior HIV testing, HIV status, engagement in care, and HIV treatment. Viral load testing and retrospective antiretroviral (ARV) drug testing were performed for HIV-infected participants. Most participants (92.2%) had a prior HIV test; 42.1% were last tested >6 months earlier. HIV prevalence was 30.4%. HIV infection was associated with older age and identifying as female or transgender; 43.7% of the HIV-infected participants were newly diagnosed, especially younger persons and persons with a less recent HIV test. Almost a third of previously-</p>



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	<p>diagnosed participants were not linked to care. Most participants (88.7%) in care were on ARV treatment (ART). Only about one-quarter of all HIV-infected participants were virally suppressed. These findings demonstrate substantial prevalence of undiagnosed HIV infection and sub-optimal HIV care engagement among MSM and TW in SSA. Increased HIV testing frequency and better linkage to care represent critical steps in preventing further HIV transmission in this population. Once in care, gaps in the HIV care continuum appear less critical.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31150447/</p>
162	<p>Oliwa JN, Gathara D, Ogero M, van Hensbroek MB, English M, Van't Hoog A; Clinical Information Network. Diagnostic practices and estimated burden of tuberculosis among children admitted to 13 government hospitals in Kenya: An analysis of two years' routine clinical data. PLoS One. 2019 Sep 4;14(9):e0221145.</p> <p>Abstract</p> <p>Background: True burden of tuberculosis (TB) in children is unknown. Hospitalised children are low-hanging fruit for TB case detection as they are within the system. We aimed to explore the process of recognition and investigation for childhood TB using a guideline-linked cascade of care.</p> <p>Methods: This was an observational study of 42,107 children admitted to 13 county hospitals in Kenya from 01Nov 15-31Oct 16, and 01Nov 17-31Oct 18. We estimated those that met each step of the cascade, those with an apparent (or "Working") TB diagnosis and modelled associations with TB tests amongst guideline-eligible children.</p> <p>Results: 23,741/42,107 (56.4%) met step 1 of the cascade (≥ 2 signs and symptoms suggestive of TB). Step 2(further screening of history of TB contact/full respiratory exam) was documented in 14,873/23,741 (62.6%) who met Step 1. Step 3(chest x-ray or Mantoux test) was requested in 2,451/14,873 (16.5%) who met Step 2. Step 4(≥ 1 bacteriological test) was requested in 392/2,451 (15.9%) who met Step 3. Step 5("Working TB" diagnosis) was</p>



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	<p>documented in 175/392 (44.6%) who met Step 4. Factors associated with request of TB tests in patients who met Step 1 included: i) older children [AOR 1.19(CI 1.09-1.31)]; ii) co-morbidities of HIV, malnutrition or pneumonia [AOR 3.81(CI 3.05-4.75), 2.98(CI 2.69-3.31) and 2.98(CI 2.60-3.40) respectively]; iii) sicker children, readmitted/referred [AOR 1.24(CI 1.08-1.42) and 1.15(CI 1.04-1.28) respectively]. "Working TB" diagnosis was made in 2.9%(1,202/42,107) of all admissions and 0.2%(89/42,107) were bacteriologically-confirmed.</p> <p>Conclusions: More than half of all paediatric admissions had symptoms associated with TB and nearly two-thirds had more specific history documented. Only a few amongst them got TB tests requested. TB was diagnosed in 2.9% of all admissions but most were inadequately investigated. Major challenges remain in identifying and investigating TB in children in hospitals with access to Xpert MTB/RIF and a review is needed of existing guidelines.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31483793/</p>
163	<p>Odero NA, Samuels AM, Odongo W, Abong'o B, Gimnig J, Otieno K, Odero C, Obor D, Ombok M, Were V, Sang T, Hamel MJ, Kachur SP, Slutsker L, Lindblade KA, Kariuki S, Desai M. Community-based intermittent mass testing and treatment for malaria in an area of high transmission intensity, western Kenya: development of study site infrastructure and lessons learned. <i>Malar J.</i> 2019 Jul 29;18(1):255.</p> <p>Abstract</p> <p>Background: Malaria transmission is high in western Kenya and the asymptomatic infected population plays a significant role in driving the transmission. Mathematical modelling and simulation programs suggest that interventions targeting asymptomatic infections through mass testing and treatment (MTaT) or mass drug administration (MDA) have the potential to reduce malaria transmission when combined with existing interventions.</p> <p>Objective: This paper describes the study site, capacity development efforts required, and lessons learned for implementing a multi-year community-based cluster-randomized</p>



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	<p>controlled trial to evaluate the impact of MTaT for malaria transmission reduction in an area of high transmission in western Kenya.</p> <p>Methods: The study partnered with Kenya's Ministry of Health (MOH) and other organizations on community sensitization and engagement to mobilize, train and deploy community health volunteers (CHVs) to deliver MTaT in the community. Within the health facilities, the study availed staff, medical and laboratory supplies and strengthened health information management system to monitor progress and evaluate impact of intervention.</p> <p>Results: More than 80 Kenya MOH CHVs, 13 clinical officers, field workers, data and logistical staff were trained to carry out MTaT three times a year for 2 years in a population of approximately 90,000 individuals. A supply chain management was adapted to meet daily demands for large volumes of commodities despite the limitation of few MOH facilities having ideal storage conditions. Modern technology was adapted more to meet the needs of the high daily volume of collected data.</p> <p>Conclusions: In resource-constrained settings, large interventions require capacity building and logistical planning. This study found that investing in relationships with the communities, local governments, and other partners, and identifying and equipping the appropriate staff with the skills and technology to perform tasks are important factors for success in delivering an intervention like MTaT.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31357997/</p>
164	<p>Kiti MC, Melegaro A, Cattuto C, Nokes DJ. Study design and protocol for investigating social network patterns in rural and urban schools and households in a coastal setting in Kenya using wearable proximity sensors. Wellcome Open Res. 2019 Aug 22;4:84.</p> <p>Abstract</p> <p>Background: Social contact patterns shape the transmission of respiratory infections spread via close interactions. There is a paucity of observational data from schools and households, particularly in developing countries. Portable wireless sensors can record unbiased</p>



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	<p>proximity events between individuals facing each other, shedding light on pathways of infection transmission. Design and methods: The aim is to characterize face-to-face contact patterns that may shape the transmission of respiratory infections in schools and households in Kilifi, Kenya. Two schools, one each from a rural and urban area, will be purposively selected. From each school, 350 students will be randomly selected proportional to class size and gender to participate. Nine index students from each school will be randomly selected and followed-up to their households. All index household residents will be recruited into the study. A further 3-5 neighbouring households will also be recruited to give a maximum of 350 participants per household setting. The sample size per site is limited by the number of sensors available for data collection. Each participant will wear a wireless proximity sensor lying on their chest area for 7 consecutive days. Data on proximal dyadic interactions will be collected automatically by the sensors only for participants who are face-to-face. Key characteristics of interest include the distribution of degree and the frequency and duration of contacts and their variation in rural and urban areas. These will be stratified by age, gender, role, and day of the week. Expected results: Resultant data will inform on social contact patterns in rural and urban areas of a previously unstudied population. Ensuing data will be used to parameterize mathematical simulation models of transmission of a range of respiratory viruses, including respiratory syncytial virus, and used to explore the impact of intervention measures such as vaccination and social distancing.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31489381/</p>
165	<p>Ermel A, Tonui P, Titus M, Tong Y, Wong N, Ong'echa J, Muthoka K, Kiptoo S, Moormann A, Hogan J, Mwangi A, Cu-Uvin S, Loehrer PJ, Orang'o O, Brown D. A cross-sectional analysis of factors associated with detection of oncogenic human papillomavirus in human immunodeficiency virus-infected and uninfected Kenyan women. BMC Infect Dis. 2019 Apr 27;19(1):352.</p> <p>Abstract</p>



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Background: Cervical cancer is caused by oncogenic human papillomaviruses (HPV) and is one of the most common malignancies in women living in sub-Saharan Africa. Women infected with the human immunodeficiency virus (HIV) have a higher incidence of cervical cancer, but the full impact on HPV detection is not well understood, and associations of biological and behavioral factors with oncogenic HPV detection have not been fully examined. Therefore, a study was initiated to investigate factors that are associated with oncogenic HPV detection in Kenyan women.

Methods: Women without cervical dysplasia were enrolled in a longitudinal study. Data from enrollment are presented as a cross-sectional analysis. Demographic and behavioral data was collected, and HPV typing was performed on cervical swabs. HIV-uninfected women (n = 105) and HIV-infected women (n = 115) were compared for demographic and behavioral characteristics using t-tests, Chi-square tests, Wilcoxon sum rank tests or Fisher's exact tests, and for HPV detection using logistic regression or negative binomial models adjusted for demographic and behavioral characteristics using SAS 9.4 software.

Results: Compared to HIV-uninfected women, HIV-infected women were older, had more lifetime sexual partners, were less likely to be married, were more likely to regularly use condoms, and were more likely to have detection of HPV 16, other oncogenic HPV types, and multiple oncogenic types. In addition to HIV, more lifetime sexual partners was associated with a higher number of oncogenic HPV types (aIRR 1.007, 95% CI 1.007-1.012). Greater travel distance to the clinic was associated with increased HPV detection (aOR for detection of ≥ 2 HPV types: 3.212, 95% CI 1.206-8.552). Older age (aOR for HPV 16 detection: 0.871, 95% CI 0.764-0.993) and more lifetime pregnancies (aOR for detection of oncogenic HPV types: 0.706, 95% CI, 0.565-0.883) were associated with reduced detection.

Conclusion: HIV infection, more lifetime sexual partners, and greater distance to health-care were associated with a higher risk of oncogenic HPV detection, in spite of ART use in those who were HIV-infected. Counseling of women about sexual practices, improved



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	<p>access to health-care facilities, and vaccination against HPV are all potentially important in reducing oncogenic HPV infections.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31029097/</p>
166	<p>Levy R, Mathai M, Chatterjee P, Ongeru L, Njuguna S, Onyango D, Akena D, Rota G, Otieno A, Neylan TC, Lukwata H, Kahn JG, Cohen CR, Bukusi D, Aarons GA, Burger R, Blum K, Nahum-Shani I, McCulloch CE, Meffert SM. Implementation research for public sector mental health care scale-up (SMART-DAPPER): a sequential multiple, assignment randomized trial (SMART) of non-specialist-delivered psychotherapy and/or medication for major depressive disorder and posttraumatic stress disorder (DAPPER) integrated with outpatient care clinics at a county hospital in Kenya. <i>BMC Psychiatry</i>. 2019 Dec 28;19(1):424.</p> <p>Abstract</p> <p>Background: Mental disorders are a leading cause of global disability, driven primarily by depression and anxiety. Most of the disease burden is in Low and Middle Income Countries (LMICs), where 75% of adults with mental disorders have no service access. Our research team has worked in western Kenya for nearly ten years. Primary care populations in Kenya have high prevalence of Major Depressive Disorder (MDD) and Posttraumatic Stress Disorder (PTSD). To address these treatment needs with a sustainable, scalable mental health care strategy, we are partnering with local and national mental health stakeholders in Kenya and Uganda to identify 1) evidence-based strategies for first-line and second-line treatment delivered by non-specialists integrated with primary care, 2) investigate presumed mediators of treatment outcome and 3) determine patient-level moderators of treatment effect to inform personalized, resource-efficient, non-specialist treatments and sequencing, with costing analyses. Our implementation approach is guided by the Exploration, Preparation, Implementation, Sustainment (EPIS) framework.</p> <p>Methods/design: We will use a Sequential, Multiple Assignment Randomized Trial (SMART) to randomize 2710 patients from the outpatient clinics at Kisumu County</p>



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	<p>Hospital (KCH) who have MDD, PTSD or both to either 12 weekly sessions of non-specialist-delivered Interpersonal Psychotherapy (IPT) or to 6 months of fluoxetine prescribed by a nurse or clinical officer. Participants who are not in remission at the conclusion of treatment will be re-randomized to receive the other treatment (IPT receives fluoxetine and vice versa) or to combination treatment (IPT and fluoxetine). The SMART-DAPPER Implementation Resource Team, (IRT) will drive the application of the EPIS model and adaptations during the course of the study to optimize the relevance of the data for generalizability and scale -up.</p> <p>Discussion: The results of this research will be significant in three ways: 1) they will determine the effectiveness of non-specialist delivered first- and second-line treatment for MDD and/or PTSD, 2) they will investigate key mechanisms of action for each treatment and 3) they will produce tailored adaptive treatment strategies essential for optimal sequencing of treatment for MDD and/or PTSD in low resource settings with associated cost information - a critical gap for addressing a leading global cause of disability.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31883526/</p>
167	<p>Wamae K, Okanda D, Ndwiga L, Osoth V, Kimenyi KM, Abdi AI, Bejon P, Sutherland C, Ochola-Oyier LI. No evidence of <i>P. falciparum</i> K13 artemisinin conferring mutations over a 24-year analysis in Coastal Kenya, but a near complete reversion to chloroquine wild type parasites. <i>Antimicrob Agents Chemother.</i> 2019 Oct 7;63(12):e01067-19.</p> <p>Abstract</p> <p>Antimalarial drug resistance is a substantial impediment to malaria control. The spread of resistance has been described using genetic markers which are important epidemiological tools. We carried out a temporal analysis of changes in allele frequencies of 12 drug resistance markers over two decades of changing antimalarial drug policy in Kenya. We did not detect any of the validated kelch 13 (k13) artemisinin resistance markers, nonetheless, a single k13 allele, K189T, was maintained at a stable high frequency (>10%)</p>



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	<p>over time. There was a distinct shift from chloroquine resistant transporter (crt)-76, multi-drug resistant gene 1 (mdr1)-86 and mdr1-1246 chloroquine (CQ) resistance alleles to a 99% prevalence of CQ sensitive alleles in the population, following the withdrawal of CQ from routine use. In contrast, the dihydropteroate synthetase (dhps) double mutant (437G and 540E) associated with sulfadoxine-pyrimethamine (SP) resistance was maintained at a high frequency (>75%), after a change from SP to artemisinin combination therapies (ACTs). The novel cysteine desulfurase (nfs) K65 allele, implicated in resistance to lumefantrine in a West African study, showed a gradual significant decline in allele frequency pre- and post-ACT introduction (from 38% to 20%), suggesting evidence of directional selection in Kenya, potentially not due to lumefantrine. The high frequency of CQ-sensitive parasites circulating in the population suggests that the re-introduction of CQ in combination therapy for the treatment of malaria can be considered in the future. However, the risk of a re-emergence of CQ resistant parasites circulating below detectable levels or being reintroduced from other regions remains.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31591113/</p>
168	<p>Kapulu MC, Njuguna P, Hamaluba MM; CHMI-SIKA Study Team. Controlled Human Malaria Infection in Semi-Immune Kenyan Adults (CHMI-SIKA): a study protocol to investigate <i>in vivo</i> Plasmodium falciparum malaria parasite growth in the context of pre-existing immunity. Wellcome Open Res. 2019 Nov 14;3:155.</p> <p>Abstract</p> <p>Malaria remains a major public health burden despite approval for implementation of a partially effective pre-erythrocytic malaria vaccine. There is an urgent need to accelerate development of a more effective multi-stage vaccine. Adults in malaria endemic areas may have substantial immunity provided by responses to the blood stages of malaria parasites, but field trials conducted on several blood-stage vaccines have not shown high levels of efficacy. We will use the controlled human malaria infection (CHMI) models with malaria-exposed volunteers to identify correlations between immune responses and parasite growth</p>



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	<p>rates in vivo. Immune responses more strongly associated with control of parasite growth should be prioritized to accelerate malaria vaccine development. We aim to recruit up to 200 healthy adult volunteers from areas of differing malaria transmission in Kenya, and after confirming their health status through clinical examination and routine haematology and biochemistry, we will comprehensively characterize immunity to malaria using >100 blood-stage antigens. We will administer 3,200 aseptic, purified, cryopreserved <i>Plasmodium falciparum</i> sporozoites (PfSPZ Challenge) by direct venous inoculation. Serial quantitative polymerase chain reaction to measure parasite growth rate in vivo will be undertaken. Clinical and laboratory monitoring will be undertaken to ensure volunteer safety. In addition, we will also explore the perceptions and experiences of volunteers and other stakeholders in participating in a malaria volunteer infection study. Serum, plasma, peripheral blood mononuclear cells and whole blood will be stored to allow a comprehensive assessment of adaptive and innate host immunity. We will use CHMI in semi-immune adult volunteers to relate parasite growth outcomes with antibody responses and other markers of host immunity.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31803847/</p>
169	<p>Cordero JP, Steyn PS, Gichangi P, Kriel Y, Milford C, Munakampe M, Njau I, Nkole T, Silumbwe A, Smit J, Kiarie J. Community and Provider Perspectives on Addressing Unmet Need for Contraception: Key Findings from a Formative Phase Research in Kenya, South Africa and Zambia (2015-2016). <i>Afr J Reprod Health</i>. 2019 Sep;23(3):106-119.</p> <p>Abstract</p> <p>Unmet need for contraception remains a challenge especially in low and middle-income countries. Community participation or the -active involvement of affected populations in all stages of decision-making and implementation of policies, programs, and services is a precondition for attaining the highest standard of health. Participation as a key component of rights and quality of care frameworks could increase met needs. However, it has been</p>



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	<p>inadequately addressed in contraceptive programs. A qualitative, exploratory methodology that included focus group discussions and in-depth interviews with community members, healthcare providers, and other stakeholders were conducted to identify domains or key thematic areas of action through which stakeholders could be engaged. The study conducted in Kenya, South Africa, and Zambia explored knowledge and use of contraceptives, barriers and enablers to access, quality of care, and participatory practices. Thematic analysis was used, facilitated by NVivo (version 10 QSR International) with a single master codebook. Comparing the thematic areas that emerged from the county data, four domains were selected: quality of care, informed decision-making, acceptability, and accountability. These domains informed the theory of change of a participatory programme aiming to meet unmet needs. Identifying possible generalizable domains establishes measurable and comparable intermediate outcomes for participatory programs despite diverse African contexts.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31782636/</p>
170	<p>Kombe FK, Marsh V, Molyneux S, Kamuya DM, Ikamba D, Kinyanjui SM. Enhancing fieldworkers' performance management support in health research: an exploratory study on the views of field managers and fieldworkers from major research centres in Africa. <i>BMJ Open</i>. 2019 Dec 18;9(12):e028453.</p> <p>Abstract</p> <p>Introduction: Fieldworkers are part of the system that promotes scientific and ethical standards in research, through data collection, consenting and supporting research, due to their insider cultural knowledge and fluency in local languages. The credibility and integrity of health research, therefore, rely on how fieldworkers adhere to institutional and research procedures and guidelines.</p> <p>Objectives: This study mapped out existing practices in training, support and performance management of fieldworkers in Africa, described fieldworkers' and their managers' experiences, and lessons learnt. A consultative process, involving field managers from 15</p>



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	<p>international health research institutions, was used to identify appropriate ways of addressing the challenges fieldworkers face.</p> <p>Methods: In phase 1, we conducted 32 telephone interviews with 20 field managers and 12 senior fieldworkers from 18 major research centres in Africa, Medical Research Council-UK and the INDEPTH Network Secretariat. In phase 2, we held a 2.5-day workshop involving 25 delegates, including 18 field managers from the institutions that were involved in phase 1 and 7 additional stakeholders from the KEMRI Wellcome Trust Research Programme (KWTRP). An earlier report from phase 1 was published in BMC Medical Ethics in 2015. Data transcribed from the interviews and workshop proceedings were analysed thematically using NVivo V.10 software.</p> <p>Results: Most institutions employed fieldworkers, usually with 12 years of formal education and residing within the geographical areas of research, to support studies. Although their roles were common, there were marked differences in the type of training, professional development schemes and fieldworkers support. Fieldworkers faced various challenges, with the potential to affect their ethical and scientific practices.</p> <p>Discussion: Fieldworkers undertake vital tasks that promote data quality and ethical practice in research. There is a need for research institutions to develop a structured support system, provide fieldworkers with interpersonal skills training, and provide space for discussion, reflection and experience sharing to help fieldworkers tackle the practical and ethical challenges they face.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31857297/</p>
171	<p>Elson L, Randu K, Feldmeier H, Fillinger U. Efficacy of a mixture of neem seed oil (<i>Azadirachta indica</i>) and coconut oil (<i>Cocos nucifera</i>) for topical treatment of tungiasis. A randomized controlled, proof-of-principle study. <i>PLoS Negl Trop Dis</i>. 2019 Nov 22;13(11):e0007822.</p> <p>Abstract</p>



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	<p>Background: Tungiasis is a neglected tropical skin disease caused by the female sand flea (<i>Tunga penetrans</i>), which burrows into the skin causing intense pain, itching and debilitation. People in endemic countries do not have access to an effective and safe home treatment. The aim of this study was to determine the efficacy of a traditionally used and readily available mixture of neem and coconut oil for treatment of tungiasis in coastal Kenya.</p> <p>Methodology: Ninety-six children aged 6-14 years with at least one embedded viable flea were randomized to be treated with either a mixture of 20% neem (<i>Azadirachta indica</i>) seed oil in coconut oil (NC), or with a 0.05% potassium permanganate (KMnO₄) foot bath. Up to two viable fleas were selected for each participant and monitored for 6 days after first treatment using a digital microscope for signs of viability and abnormal development. Acute pathology was assessed on all areas of the feet using a previously established score. Children reported pain levels and itching on a visual scale.</p> <p>Results: The NC was not more effective in killing embedded sand fleas within 7 days than the current standard with KMnO₄, killing on average 40% of the embedded sand fleas six days after the initial treatment. However, the NC was superior with respect to the secondary outcomes of abnormal development and reduced pathology. There was a higher odds that fleas rapidly aged in response to NC compared to KMnO₄ (OR 3.4, 95% CI: 1.22-9.49, $p = 0.019$). NC also reduced acute pathology ($p < 0.005$), and there was a higher odds of children being pain free (OR 3.5, $p = 0.001$) when treated with NC.</p> <p>Conclusions: Whilst NC did not kill more fleas than KMnO₄ within 7 days, secondary outcomes were better and suggest that a higher impact might have been observed at a longer observation period. Further trials are warranted to assess optimal mixtures and dosages.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31756189/</p>
172	Mweu MM, Wambua J, Njuga F, Bejon P, Mwangi D. Bayesian evaluation of the



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performance of three diagnostic tests for *Plasmodium falciparum* infection in a low-transmission setting in Kilifi County, Kenya. Wellcome Open Res. 2019 Oct 1;4:67.

Abstract

Background: Central to the successful elimination of *Plasmodium falciparum* malaria, are tests with superior capability of diagnosing low-density parasitaemias. Empirical evidence on the performance of the commonly available diagnostics (light microscopy (LM), rapid diagnostic tests (RDT) and polymerase chain reaction (PCR)) is needed to better inform case management and surveillance activities within primary health care settings where elimination of *falciparum* malaria is targeted. The objective of this study was to estimate the sensitivity (Se) and specificity (Sp) and predictive values of LM, RDT and PCR tests for *P. falciparum* infection in children, while evaluating the effect of specific covariates on the accuracy of the tests. **Methods:** The study enrolled 1,563 children presenting with fever (axillary temperature ≥ 37.5 °C) to the Ngerenya dispensary, Kilifi County between March and December 2014. A Bayesian latent class model (BLCM) was fitted to the participants' diagnostic data obtained from blood samples that were screened for the presence of *P. falciparum* using the three tests. **Results:** The PCR assay registered a higher Se (97.6% [92.0; 99.7]) than LM (84.0% [74.8; 91.0]) but similar to RDT (92.2% [84.4; 97.0]). However, the assay showed a similar Sp (98.9% [98.2; 99.4]) to both RDT (99.4% [98.9; 99.7]) and LM (99.5% [99.0; 99.8]). Regarding predictive values, the tests yielded statistically similar estimates of positive and negative predictive values (PPV and NPV). A serial interpretation of the results of RDT and LM raised the PPVs and NPVs to >98%. **Conclusions:** LM and RDT afford high Se and Sp in symptomatic care-seeking children in this low *P. falciparum* prevalence setting. A serial combination of the tests assures high PPV and NPV estimates. These elements, coupled with the wide deployment and affordability of the tests, lend the tests useful for guiding clinical care and surveillance activities for *P. falciparum* within elimination settings.

Pubmed link- <https://pubmed.ncbi.nlm.nih.gov/31595228/>



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173 Bitilinyu-Bangoh J, Voskuil W, Thitiri J, Menting S, Verhaar N, Mwalekwa L, de Jong DB, van Loenen M, Mens PF, Berkley JA, Bandsma RHJ, Schallig HDFH. Performance of three rapid diagnostic tests for the detection of *Cryptosporidium* spp. and *Giardia duodenalis* in children with severe acute malnutrition and diarrhoea. *Infect Dis Poverty*. 2019 Nov 28;8(1):96.

Abstract

Background: There is significant need for accurate diagnostic tools for *Cryptosporidium* spp. and *Giardia duodenalis* infections in resource limited countries where diarrhoeal disease caused by these parasites is often prevalent. The present study assessed the diagnostic performance of three commercially available rapid diagnostic tests (RDTs) based on faecal-antigen detection for *Cryptosporidium* spp. and/or *G. duodenalis* infections in stool samples of children admitted with severe acute malnutrition (SAM) and diarrhoea. An established multiplex PCR was used as reference test.

Methods: Stool samples from children with SAM and diarrhoea enrolled in a randomized controlled trial (registered at clinicaltrials.gov/ct2/show/NCT02246296) in Malawi (n = 175) and Kenya (n = 120) between December 2014 and December 2015 were analysed by a multiplex PCR for the presence of *Cryptosporidium* spp., *G. duodenalis* or *Entamoeba histolytica* parasite DNA. *Cryptosporidium*-positive samples were species typed using restriction fragment length polymorphism analysis. A sub-sample of the stool specimens (n = 236) was used for testing with three different RDTs. Diagnostic accuracy of the tests under evaluation was assessed using the results of PCR as reference standard using MedCalc software. Pearson Chi-square test and Fisher's exact test were used to determine (significant) difference between the number of cryptosporidiosis or giardiasis cases found by PCR in Malawi and Kenya. The overall diagnostic accuracy of each RDT was calculated by plotting a receiver operating characteristic (ROC) curve for each test and to determine the area under the curve (AUC) using SPSS8 software.



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	<p>Results: Prevalence of <i>Cryptosporidium</i> spp. by PCR was 20.0 and 21.7% in Malawi and Kenya respectively, mostly <i>C. hominis</i>. <i>G. duodenalis</i> prevalence was 23.4 and 5.8% in Malawi and Kenya respectively. <i>E. histolytica</i> was not detected by PCR. RDT testing followed the same pattern of prevalence. RDT sensitivities ranged for cryptosporidiosis from 42.9 to 76.9% and for <i>G. duodenalis</i> from 48.2 to 85.7%. RDT specificities ranged from 88.4 to 100% for <i>Cryptosporidium</i> spp. and from 91.2 to 99.2% for <i>G. duodenalis</i> infections. Based on the estimated area under the curve (AUC) values, all tests under evaluation had an acceptable overall diagnostic accuracy (> 0.7), with the exception of one RDT for <i>Cryptosporidium</i> spp. in Malawi.</p> <p>Conclusions: All three RDTs for <i>Cryptosporidium</i> spp. and <i>Giardia duodenalis</i> evaluated in this study have a moderate sensitivity, but sufficient specificity. The main value of the RDTs is within their rapidness and their usefulness as screening assays in surveys for diarrhoea.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31775877</p>
174	<p>Zulaika G, Kwaro D, Nyothach E, Wang D, Zielinski-Gutierrez E, Mason L, Eleveld A, Chen T, Kerubo E, van Eijk A, Pace C, Obor D, Juma J, Oyaró B, Niessen L, Bigogo G, Ngere I, Henry C, Majiwa M, Onyango CO, Ter Kuile FO, Phillips-Howard PA. Menstrual cups and cash transfer to reduce sexual and reproductive harm and school dropout in adolescent schoolgirls: study protocol of a cluster-randomised controlled trial in western Kenya. <i>BMC Public Health</i>. 2019 Oct 21;19(1):1317.</p> <p>Abstract</p> <p>Background: Adolescent girls in sub-Saharan Africa are disproportionately vulnerable to sexual and reproductive health (SRH) harms. In western Kenya, where unprotected transactional sex is common, young females face higher rates of school dropout, often due to pregnancy, and sexually transmitted infections (STIs), including HIV. Staying in school has shown to protect girls against early marriage, teen pregnancy, and HIV infection. This</p>



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	<p>study evaluates the impact of menstrual cups and cash transfer interventions on a composite of deleterious outcomes (HIV, HSV-2, and school dropout) when given to secondary schoolgirls in western Kenya, with the aim to inform evidence-based policy to improve girls' health, school equity, and life-chances.</p> <p>Methods: Single site, 4-arm, cluster randomised controlled superiority trial. Secondary schools are the unit of randomisation, with schoolgirls as the unit of measurement. Schools will be randomised into one of four intervention arms using a 1:1:1:1 ratio and block randomisation: (1) menstrual cup arm; (2) cash transfer arm, (3) cups and cash combined intervention arm, or (4) control arm. National and county agreement, and school level consent will be obtained prior to recruitment of schools, with parent consent and girls' assent obtained for participant enrolment. Participants will be trained on safe use of interventions, with all arms receiving puberty and hygiene education. Annually, the state of latrines, water availability, water treatment, handwashing units and soap in schools will be measured. The primary endpoint is a composite of incident HIV, HSV-2, and all-cause school dropout, after 3 years follow-up. School dropout will be monitored each term via school registers and confirmed through home visits. HIV and HSV-2 incident infections and risk factors will be measured at baseline, mid-line and end-line. Intention to treat analysis will be conducted among all enrolled participants. Focus group discussions will provide contextual information on uptake of interventions. Monitoring for safety will occur throughout.</p> <p>Discussion: If proved safe and effective, the interventions offer a potential contribution toward girls' schooling, health, and equity in low- and middle-income countries.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31638946/</p>
175	<p>Okello G, Molyneux S, Zakayo S, Gerrets R, Jones C. Producing routine malaria data: an exploration of the micro-practices and processes shaping routine malaria data quality in frontline health facilities in Kenya. <i>Malar J</i>. 2019 Dec 16;18(1):420.</p>



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Abstract

Background: Routine health information systems can provide near real-time data for malaria programme management, monitoring and evaluation, and surveillance. There are widespread concerns about the quality of the malaria data generated through routine information systems in many low-income countries. However, there has been little careful examination of micro-level practices of data collection which are central to the production of routine malaria data.

Methods: Drawing on fieldwork conducted in two malaria endemic sub-counties in Kenya, this study examined the processes and practices that shape routine malaria data generation at frontline health facilities. The study employed ethnographic methods-including observations, records review, and interviews-over 18-months in four frontline health facilities and two sub-county health records offices. Data were analysed using a thematic analysis approach.

Results: Malaria data generation was influenced by a range of factors including human resource shortages, tool design, and stock-out of data collection tools. Most of the challenges encountered by health workers in routine malaria data generation had their roots in wider system issues and at the national level where the framing of indicators and development of data collection tools takes place. In response to these challenges, health workers adopted various coping mechanisms such as informal task shifting and use of improvised tools. While these initiatives sustained the data collection process, they also had considerable implications for the data recorded and led to discrepancies in data that were recorded in primary registers. These discrepancies were concealed in aggregated monthly reports that were subsequently entered into the District Health Information Software 2.

Conclusion: Challenges to routine malaria data generation at frontline health facilities are not malaria or health information systems specific; they reflect wider health system weaknesses. Any interventions seeking to improve routine malaria data generation must



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	<p>look beyond just malaria or health information system initiatives and include consideration of the broader contextual factors that shape malaria data generation.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31842872/</p>
176	<p>Kennedy SH, Victora CG, Craik R, Ash S, Barros FC, Barsosio HC, Berkley JA, Carvalho M, Fernandes M, Cheikh Ismail L, Lambert A, Lindgren CM, McGready R, Munim S, Nellåker C, Noble JA, Norris SA, Nosten F, Ohuma EO, Papageorghiou AT, Stein A, Stones W, Tshivuila-Matala COO, Staines Urias E, Vatish M, Wulff K, Zainab G, Zondervan KT, Uauy R, Bhutta ZA, Villar J. Deep clinical and biological phenotyping of the preterm birth and small for gestational age syndromes: The INTERBIO-21 st Newborn Case-Control Study protocol. Gates Open Res. 2019 Feb 5;2:49.</p> <p>Abstract</p> <p>Background: INTERBIO-21 st is Phase II of the INTERGROWTH-21 st Project, the population-based, research initiative involving nearly 70,000 mothers and babies worldwide coordinated by Oxford University and performed by a multidisciplinary network of more than 400 healthcare professionals and scientists from 35 institutions in 21 countries worldwide. Phase I, conducted 2008-2015, consisted of nine complementary studies designed to describe optimal human growth and neurodevelopment, based conceptually on the WHO prescriptive approach. The studies generated a set of international standards for monitoring growth and neurodevelopment, which complement the existing WHO Child Growth Standards. Phase II aims to improve the functional classification of the highly heterogenous preterm birth and fetal growth restriction syndromes through a better understanding of how environmental exposures, clinical conditions and nutrition influence patterns of human growth from conception to childhood, as well as specific neurodevelopmental domains and associated behaviors at 2 years of age.</p> <p>Methods: In the INTERBIO-21 st Newborn Case-Control Study, a major component of Phase II, our objective is to investigate the mechanisms potentially responsible for preterm</p>



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	<p>birth and small for gestational age and their interactions, using deep phenotyping of clinical, growth and epidemiological data and associated nutritional, biochemical, omic and histological profiles. Here we describe the study sites, population characteristics, study design, methodology and standardization procedures for the collection of longitudinal clinical data and biological samples (maternal blood, umbilical cord blood, placental tissue, maternal feces and infant buccal swabs) for the study that was conducted between 2012 and 2018 in Brazil, Kenya, Pakistan, South Africa, Thailand and the UK. Discussion: Our study provides a unique resource for the planned analyses given the range of potentially disadvantageous exposures (including poor nutrition, pregnancy complications and infections) in geographically diverse populations worldwide. The study should enhance current medical knowledge and provide new insights into environmental influences on human growth and neurodevelopment.</p> <p>Pubmed link-https://pubmed.ncbi.nlm.nih.gov/31172050/</p>
177	<p>Talisuna AO, Zurovac D, Githinji S, Oburu A, Malinga J, Nyandigisi A, Jones CO, Snow RW. Efficacy of Mobile Phone Short Message Service (SMS) Reminders on Malaria Treatment Adherence and Day 3 Post-Treatment Reviews (SMS-RES-MAL) in Kenya: A Study Protocol. <i>J Clin Trials</i>. 2019 Jun 25;5(2):217.</p> <p>Abstract</p> <p>Background: Mobile phone short messaging services (SMS) have been investigated in health information reporting, provider performance, drug and diagnostic stock management and patient adherence to treatment for chronic diseases. However, their potential role in improving patients' adherence to malaria treatment and day 3 post treatment reviews remains unclear.</p> <p>Methods/design: A "proof of concept" open label randomised controlled trial will be conducted at four sites in Western Kenya. Principal research questions are: 1) Can mobile phone SMS reminders improve patient adherence to malaria treatment? 2) Can mobile phone SMS reminders improve day 3 post treatment reviews? Eligible caregivers (n=1000</p>



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	<p>per arm) of children under five years old with uncomplicated malaria will be randomly assigned (one to one) to: a) the current standard of care (provider counselling and health education); and b) the current standard of care plus SMS reminders. Within each arm, caregivers will be further randomized to three different categories. In categories 1 and 2, 300 caregivers per arm per category will be visited at home on day 1 and 2 of follow up respectively, to measure appropriate timing and adherence of the second Artemether-Lumefantrine (AL) dose and doses 3 and 4. Further, caregivers in categories 1 and 2 will be required to come to the health facility for the day 3 post treatment reviews. Finally, in category 3, 400 caregivers per arm will be visited at home on day 3 to measure adherence for the full AL course. Each category will be visited at home only once to avoid biases in the measures of adherence as a result of home consultations. Primary outcomes will be adherence to the full AL course (category 3), as well as, the proportion of patients reporting back for day 3 post treatment reviews (categories 1 and 2). The primary analysis will be intention-to-treat. Costs of the intervention will be measured over the period of the intervention, and a cost-effectiveness ratio will be estimated.</p> <p>Discussion: If successful, evidence from this trial could improve malaria treatment adherence and offer pragmatic approaches for antimalarial drug resistance surveillance and risk mitigation in Africa.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31285980/</p>
178	<p>Houston KA, Gibb J, Olupot-Olupot P, Obonyo N, Mpoya A, Nakuya M, Muhindo R, Uyoga S, Evans JA, Connon R, Gibb DM, George EC, Maitland K. Gastroenteritis aggressive versus slow treatment for rehydration (GASTRO): a phase II rehydration trial for severe dehydration: WHO plan C versus slow rehydration. <i>BMC Med.</i> 2019 Jul 1;17(1):122.</p> <p>Abstract</p> <p>Background: World Health Organization rehydration management guidelines (plan C) for severe dehydration are widely practiced in resource-poor settings, but never formally</p>



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evaluated in a trial. The Fluid Expansion as a Supportive Therapy trial raised concerns regarding the safety of bolus therapy for septic shock, warranting a formal evaluation of rehydration therapy for gastroenteritis.

Methods: A multi-centre open-label phase II randomised controlled trial evaluated two rehydration strategies in 122 Ugandan/Kenyan children aged 60 days to 12 years with severe dehydration secondary to gastroenteritis. We compared the safety and efficacy of standard rapid rehydration using Ringer's lactate (100 ml/kg over 3 h (6 h if < 1 year), incorporating 0.9% saline boluses for children with shock (plan C) versus slower rehydration: 100 ml/kg Ringer's lactate over 8 h (all ages) without boluses (slow: experimental). The primary outcome was the frequency of serious adverse events (SAE) within 48 h including cardiovascular, respiratory and neurological complications. Secondary outcomes included clinical, biochemical and physiological measures of response to treatment by intravenous rehydration.

Results: One hundred twenty-two eligible children (median (IQR) age 8 (6-12) months) were randomised to plan C (n = 61) or slow (n = 61), with two (2%) lost to follow-up at day 7). Following randomisation mean (SD) time to start intravenous rehydration started was 15 min (18) in both arms. Mean (SD) fluid received by 1 hour was greater in plan C (mean 20.2 ml/kg (12.2) and 33.1 ml/kg (17) for children < 1 year and >- 1 year respectively) versus 10.4 ml/kg (6.6) in slow arm. By 8 hours volume received were similar mean (SD) plan C: 96.3 ml/kg (15.6) and 97.8 ml/kg (10.0) for children < 1 and \geq 1 year respectively vs 93.2 ml/kg (12.2) in slow arm. By 48-h, three (5%) plan C vs two (3%) slow had an SAE (risk ratio 0.67, 95% CI 0.12-3.85, p = 0.65). There was no difference in time to the correction of dehydration (p = 0.9) or time to discharge (p = 0.8) between groups. Atrial natriuretic peptide levels rose substantially by 8 hours in both arms, which persisted to day 7. Day 7 weights suggested only 33 (29%) could be retrospectively classified as severely dehydration (\geq 10% weight loss).



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	<p>Conclusion: Slower rehydration over 8 hours appears to be safe, easier to implement than plan C. Future large trials with mortality as the primary endpoint are warranted.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31256761/</p>
179	<p>Kimathi D, Juan A, Bejon P, Grais RF, Warimwe GM; YEFE and NIFTY vaccine trials teams. Randomized, double-blinded, controlled non-inferiority trials evaluating the immunogenicity and safety of fractional doses of Yellow Fever vaccines in Kenya and Uganda. Wellcome Open Res. 2019 Nov 20;4:182.</p> <p>Abstract</p> <p>Introduction: Yellow fever is endemic in specific regions of sub-Saharan Africa and the Americas, with recent epidemics occurring on both continents. The yellow fever vaccine is effective, affordable and safe, providing life-long immunity following a single dose vaccination. However, the vaccine production process is slow and cannot be readily scaled up during epidemics. This has led the World Health Organization (WHO) to recommend the use of fractional doses as a dose-sparing strategy during epidemics, but there are no randomized controlled trials of fractional yellow fever vaccine doses in Africa. Methods and analysis: We will recruit healthy adult volunteers, adults living with HIV, and children to a series of randomized controlled trials aiming to determine the immunogenicity and safety of fractional vaccine doses in comparison to the standard vaccine dose. The trials will be conducted across two sites; Kilifi, Kenya and Mbarara, Uganda. Recruited participants will be randomized to receive fractional or standard doses of yellow fever vaccine. Scheduled visits will include blood collection for serum and peripheral blood mononuclear cells (PBMCs) before vaccination and on various days - up to 2 years - post-vaccination. The primary outcome is the rate of seroconversion as measured by the plaque reduction neutralization test (PRNT 50) at 28 days post-vaccination. Secondary outcomes include antibody titre changes, longevity of the immune response, safety assessment using clinical data, the nature and magnitude of the cellular immune response and post-vaccination control of viremia by vaccine dose. Ethics and dissemination: The clinical trial</p>



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	<p>protocols have received approval from the relevant institutional ethics and regulatory review committees in Kenya and Uganda, and the WHO Ethics Review Committee. The research findings will be disseminated through open-access publications and presented at relevant conferences and workshops. Registration: ClinicalTrials.gov NCT02991495 (registered on 13 December 2016) and NCT04059471 (registered on 15 August 2019).</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31984244/</p>
180	<p>Enoch AJ, English M; Clinical Information Network, McGivern G, Shepperd S.</p> <p>Variability in the use of pulse oximeters with children in Kenyan hospitals: A mixed-methods analysis. <i>PLoS Med.</i> 2019 Dec 31;16(12):e1002987.</p> <p>Abstract</p> <p>Background: Pulse oximetry, a relatively inexpensive technology, has the potential to improve health outcomes by reducing incorrect diagnoses and supporting appropriate treatment decisions. There is evidence that in low- and middle-income countries, even when available, widespread uptake of pulse oximeters has not occurred, and little research has examined why. We sought to determine when and with which children pulse oximeters are used in Kenyan hospitals, how pulse oximeter use impacts treatment provision, and the barriers to pulse oximeter use.</p> <p>Methods and findings: We analyzed admissions data recorded through Kenya's Clinical Information Network (CIN) between September 2013 and February 2016. We carried out multiple imputation and generated multivariable regression models in R. We also conducted interviews with 30 healthcare workers and staff from 14 Kenyan hospitals to examine pulse oximetry adoption. We adapted the Integrative Model of Behavioural Prediction to link the results from the multivariable regression analyses to the qualitative findings. We included 27,906 child admissions from 7 hospitals in the quantitative analyses. The median age of the children was 1 year, and 55% were male. Three-quarters had a fever, over half had a cough; other symptoms/signs were difficulty breathing (34%), difficulty feeding (34%), and indrawing (32%). The most common diagnoses were</p>



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pneumonia, diarrhea, and malaria: 45%, 35%, and 28% of children, respectively, had these diagnoses. Half of the children obtained a pulse oximeter reading, and of these, 10% had an oxygen saturation level below 90%. Children were more likely to receive a pulse oximeter reading if they were not alert (odds ratio [OR]: 1.30, 95% confidence interval (CI): 1.09, 1.55, $p = 0.003$), had chest indrawing (OR: 1.28, 95% CI: 1.17, 1.40, $p < 0.001$), or a very high respiratory rate (OR: 1.27, 95% CI: 1.13, 1.43, $p < 0.001$), as were children admitted to certain hospitals, at later time periods, and when a Paediatric Admission Record (PAR) was used (OR PAR used compared with PAR not present: 2.41, 95% CI: 1.98, 2.94, $p < 0.001$). Children were more likely to be prescribed oxygen if a pulse oximeter reading was obtained (OR: 1.42, 95% CI: 1.25, 1.62, $p < 0.001$) and if this reading was below 90% (OR: 3.29, 95% CI: 2.82, 3.84, $p < 0.001$). The interviews indicated that the main barriers to pulse oximeter use are inadequate supply, broken pulse oximeters, and insufficient training on how, when, and why to use pulse oximeters and interpret their results. According to the interviews, variation in pulse oximeter use between hospitals is because of differences in pulse oximeter availability and the leadership of senior doctors in advocating for pulse oximeter use, whereas variation within hospitals over time is due to repair delays. Pulse oximeter use increased over time, likely because of the CIN's feedback to hospitals. When pulse oximeters are used, they are sometimes used incorrectly and some healthcare workers lack confidence in readings that contradict clinical signs. The main limitations of the study are that children with high levels of missing data were not excluded, interview participants might not have been representative, and the interviews did not enable a detailed exploration of differences between counties or across senior management groups. Conclusions: There remain major challenges to implementing pulse oximetry—a cheap, decades old technology—into routine care in Kenya. Implementation requires efficient and transparent procurement and repair systems to ensure adequate availability. Periodic training, structured clinical records that include prompts, the promotion of pulse oximetry by senior doctors, and monitoring and feedback might also support pulse oximeter use. Our



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	<p>findings can inform strategies to support the use of pulse oximeters to guide prompt and effective treatment, in line with the Sustainable Development Goals. Without effective implementation, the potential benefits of pulse oximeters and possible hospital cost-savings by targeting oxygen therapy might not be realized.</p> <p>Pubmed link- https://pubmed.ncbi.nlm.nih.gov/31891572/</p>
181	<p>Tuti T, Winters N, Muinga N, Wanyama C, English M, Paton C. Evaluation of Adaptive Feedback in a Smartphone-Based Serious Game on Health Care Providers' Knowledge Gain in Neonatal Emergency Care: Protocol for a Randomized Controlled Trial. <i>JMIR Res Protoc</i>. 2019 Jul 26;8(7):e13034.</p> <p>Abstract</p> <p>Background: Although smartphone-based clinical training to support emergency care training is more affordable than traditional avenues of training, it is still in its infancy and remains poorly implemented. In addition, its current implementations tend to be invariant to the evolving learning needs of the intended users. In resource-limited settings, the use of such platforms coupled with serious-gaming approaches remain largely unexplored and underdeveloped, even though they offer promise in terms of addressing the health workforce skill imbalance and lack of training opportunities associated with the high neonatal mortality rates in these settings.</p> <p>Objective: This randomized controlled study aims to assess the effectiveness of offering adaptive versus standard feedback through a smartphone-based serious game on health care providers' knowledge gain on the management of a neonatal medical emergency.</p> <p>Methods: The study is aimed at health care workers (physicians, nurses, and clinical officers) who provide bedside neonatal care in low-income settings. We will use data captured through an Android smartphone-based serious-game app that will be downloaded to personal phones belonging to the study participants. The intervention will be adaptive feedback provided within the app. The data captured will include the level of feedback provided to participants as they learn to use the mobile app, and performance data from</p>



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attempts made during the assessment questions on interactive tasks participants perform as they progress through the app on emergency neonatal care delivery. The primary endpoint will be the first two complete rounds of learning within the app, from which the individuals' "learning gains" and Morris G intervention effect size will be computed. To minimize bias, participants will be assigned to an experimental or a control group by a within-app random generator, and this process will be concealed to both the study participants and the investigators until the primary endpoint is reached.

Results: This project was funded in November 2016. It has been approved by the Central University Research Ethics Committee of the University of Oxford and the Scientific and Ethics Review Unit of the Kenya Medical Research Institute. Recruitment and data collection began from February 2019 and will continue up to July 31, 2019. As of July 18, 2019, we enrolled 541 participants, of whom 238 reached the primary endpoint, with a further 19 qualitative interviews conducted to support evaluation. Full analysis will be conducted once we reach the end of the study recruitment period.

Conclusions: This study will be used to explore the effectiveness of adaptive feedback in a smartphone-based serious game on health care providers in a low-income setting. This aspect of medical education is a largely unexplored topic in this context. In this randomized experiment, the risk of performance bias across arms is moderate, given that the active ingredient of the intervention (ie, knowledge) is a latent trait that is difficult to comprehensively control for in a real-world setting. However, the influence of any resulting bias that has the ability to alter the results will be assessed using alternative methods such as qualitative interviews.

Pubmed link- <https://pubmed.ncbi.nlm.nih.gov/31350837/>