



*In Search of Better Health*

## **KEMRI PUBLICATIONS (2020)**

1.	<p>Osier F, Ting JPY, Fraser J, Lambrecht BN, Romano M, Gazzinelli RT, Bortoluci KR, Zamboni DS, Akbar AN, Evans J, Brown DE, Patel KD, Wu Y, Perez AB, Pérez O, Kamradt T, Falk C, Barda-Saad M, Ariel A, Santoni A, Annunziato F, Cassatella MA, Kiyono H, Chereshev V, Dieye A, Mbow M, Mbengue B, Niang MDS, Suchard M. The global response to the COVID-19 pandemic: how have immunology societies contributed? <i>Nat Rev Immunol.</i> 2020 Oct;20(10):594-602.</p> <p><b>Abstract</b> The COVID-19 pandemic is shining a spotlight on the field of immunology like never before. To appreciate the diverse ways in which immunologists have contributed, Nature Reviews Immunology invited the president of the International Union of Immunological Societies and the presidents of 15 other national immunology societies to discuss how they and their members responded following the emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32913283/">https://pubmed.ncbi.nlm.nih.gov/32913283/</a></p>
2.	<p>Kariuki SN, Marin-Menendez A, Introini V, Ravenhill BJ, Lin YC, Macharia A, Makale J, Tendwa M, Nyamu W, Kotar J, Carrasquilla M, Rowe JA, Rockett K, Kwiatkowski D, Weekes MP, Cicuta P, Williams TN, Rayner JC. Red blood cell tension protects against severe malaria in the Dantu blood group. <i>Nature.</i> 2020 Sep;585(7826):579-583.</p> <p><b>Abstract</b> Malaria has had a major effect on the human genome, with many protective polymorphisms-such as the sickle-cell trait-having been selected to high frequencies in malaria-endemic regions<sup>1,2</sup>. The blood group variant Dantu provides 74% protection against all forms of severe malaria in homozygous individuals<sup>3-5</sup>, a similar degree of protection to that afforded by the sickle-cell trait and considerably greater than that offered by the best malaria vaccine. Until now, however, the protective mechanism has been unknown. Here we demonstrate the effect of Dantu on the ability of the merozoite form of the malaria parasite <i>Plasmodium falciparum</i> to invade red blood cells (RBCs). We find that Dantu is associated with extensive changes to the repertoire of proteins found on the RBC surface, but, unexpectedly, inhibition of invasion does not correlate with specific RBC-parasite receptor-ligand interactions. By following invasion using video microscopy, we find a strong link between RBC tension and merozoite invasion, and identify a tension threshold above which invasion rarely occurs, even in non-Dantu RBCs. Dantu RBCs have higher average tension than non-Dantu RBCs, meaning that a greater proportion resist invasion. These findings provide both an explanation for the protective effect of Dantu, and fresh insight into why the efficiency of <i>P. falciparum</i> invasion might vary across the heterogenous populations of RBCs found both within and between individuals</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32939086/">https://pubmed.ncbi.nlm.nih.gov/32939086/</a></p>



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3.	<p>Stegeman I, Ochodo EA, Guleid F, Holtman GA, Yang B, Davenport C, Deeks JJ, Dinnes J, Ditttrich S, Emperador D, Hooft L, Spijker R, Takwoingi Y, Van den Bruel A, Wang J, Langendam M, Verbakel JY, Leeflang MM; Cochrane COVID-19 Diagnostic Test Accuracy Group. Routine laboratory testing to determine if a patient has COVID-19. <i>Cochrane Database Syst Rev.</i> 2020 Nov 19;11(11):CD013787.</p> <p><b>Abstract</b>  Background: Specific diagnostic tests to detect severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and resulting COVID-19 disease are not always available and take time to obtain results. Routine laboratory markers such as white blood cell count, measures of anticoagulation, C-reactive protein (CRP) and procalcitonin, are used to assess the clinical status of a patient. These laboratory tests may be useful for the triage of people with potential COVID-19 to prioritize them for different levels of treatment, especially in situations where time and resources are limited.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33211319/">https://pubmed.ncbi.nlm.nih.gov/33211319/</a></p>
4.	<p>Agweyu A, Masenge T, Munube D. Extending the measurement of quality beyond service delivery indicators. <i>BMJ Glob Health.</i> 2020 Dec;5(12): e004553.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33355260/">https://pubmed.ncbi.nlm.nih.gov/33355260/</a></p>
5.	<p>Osier FHA, Mwandumba HC, Gray CM. Turning Discoveries into Treatments: Immunology in Africa. <i>Trends Immunol.</i> 2020 Dec;41(12):1051-1053.</p> <p><b>Abstract</b>  An exemplar outcome of an immunology-based intervention is vaccine development; the current COVID-19 pandemic is a case in point. Can we build an immunology research ecosystem in Africa that nurtures discovery and enables translation? We see African immunologists as key agents of change and discuss obstacles and opportunities.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33160840/">https://pubmed.ncbi.nlm.nih.gov/33160840/</a></p>
6.	<p>Morgan R, Dhatt R, Kharel C, Muraya K. A patchwork approach to gender equality weakens the SDGs: time for cross-cutting action. <i>Glob Health Promot.</i> 2020 Sep;27(3)</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32969316/5">https://pubmed.ncbi.nlm.nih.gov/32969316/5</a>.</p>
7.	<p>Smith EL, Wheeler I, Adler H, Ferreira DM, Sá-Leão R, Abdullahi O, Adetifa I, Becker-Dreps S, Esposito S, Farida H, Kandasamy R, Mackenzie GA, Nuorti JP, Nzenze S, Madhi SA, Ortega O, Roca A, Safari D, Schaumburg F, Usuf E, Sander EAM, Grant LR, Hammitt LL, O'Brien KL, Gounder P, Bruden DJT, Stanton MC, Rylance J. Upper airways colonisation of <i>Streptococcus pneumoniae</i> in adults aged 60 years and older: A systematic review of prevalence and individual participant Data meta-analysis of risk factors. <i>J Infect.</i> 2020 Oct;81(4):540-548.</p> <p><b>Abstract</b></p>



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	<p>Background: Colonisation with <i>Streptococcus pneumoniae</i> can lead to invasive pneumococcal disease and pneumonia. Pneumococcal acquisition and prevalence of colonisation are high in children. In older adults, a population susceptible to pneumococcal disease, colonisation prevalence is reported to be lower, but studies are heterogeneous.</p> <p>Methods: This is a systematic review and meta-analysis of prevalence of, and risk factors for, pneumococcal colonisation in adults <math>\geq 60</math> years of age (PROSPERO #42016036891). We identified peer-reviewed studies reporting the prevalence of <i>S. pneumoniae</i> colonisation using MEDLINE and EMBASE (until April 2016), excluding studies of acute disease. Participant-level data on risk factors were sought from each study.</p> <p>Findings: Of 2202 studies screened, 29 were analysable: 18 provided participant-level data (representing 6290 participants). Prevalence of detected pneumococcal colonisation was 0-39% by conventional culture methods and 3-23% by molecular methods. In a multivariate analysis, colonisation was higher in persons from nursing facilities compared with the community (odds ratio (OR) 2.30, 95% CI 1.26-4.21 and OR 7.72, 95% CI 1.15-51.85, respectively), in those who were currently smoking (OR 1.69, 95% CI 1.12-2.53) or those who had regular contact with children (OR 1.93, 95% CI 1.27-2.93). Persons living in urban areas had significantly lower carriage prevalence (OR 0.43, 95% CI 0.27-0.70).</p> <p>Interpretation: Overall prevalence of pneumococcal colonisation in older adults was higher than expected but varied by risk factors. Future studies should further explore risk factors for colonisation, to highlight targets for focussed intervention such as pneumococcal vaccination of high-risk groups.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32562794/">https://pubmed.ncbi.nlm.nih.gov/32562794/</a></p>
8.	<p>Kinyanjui S, Fonn S, Kyobutungi C, Vicente-Crespo M, Bonfoh B, Ndungu T, Sewankambo NK, Djimde AA, Gaye O, Chirwa T, Musenge E, Elliot A, Nakanjako D, Chibanda D, Awandare G. Enhancing science preparedness for health emergencies in Africa through research capacity building. <i>BMJ Glob Health</i>. 2020 Jul;5(7): e003072.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32636315/">https://pubmed.ncbi.nlm.nih.gov/32636315/</a></p>
9.	<p>Osii RS, Otto TD, Garside P, Ndungu FM, Brewer JM. The Impact of Malaria Parasites on Dendritic Cell-T Cell Interaction. <i>Front Immunol</i>. 2020 Jul 24; 11:1597.</p> <p><b>Abstract</b></p> <p>Malaria is caused by apicomplexan parasites of the genus <i>Plasmodium</i>. While infection continues to pose a risk for the majority of the global population, the burden of disease mainly resides in Sub-Saharan Africa. Although immunity develops against disease, this requires years of persistent exposure and is not associated with protection against infection. Repeat infections occur due to the parasite's ability to disrupt or evade the host immune responses. However, despite many years of study, the mechanisms of this disruption remain unclear. Previous studies have demonstrated a parasite-induced failure</p>



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	<p>in dendritic cell (DCs) function affecting the generation of helper T cell responses. These T cells fail to help B cell responses, reducing the production of antibodies that are necessary to control malaria infection. This review focuses on our current understanding of the effect of Plasmodium parasite on DC function, DC-T cell interaction, and T cell activation. A better understanding of how parasites disrupt DC-T cell interactions will lead to new targets and approaches to reinstate adaptive immune responses and enhance parasite immunity.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32793231/">https://pubmed.ncbi.nlm.nih.gov/32793231/</a></p>
10.	<p>Bejon P. Malaria parasites hide in plain sight in the dry season. Nat Med. 2020 Dec;26(12):1816-1818.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33230342/">https://pubmed.ncbi.nlm.nih.gov/33230342/</a></p>
11.	<p>Kiyuka PK, Meri S, Khattab A. Complement in malaria: immune evasion strategies and role in protective immunity. FEBS Lett. 2020 Aug;594(16):2502-2517.</p> <p><b>Abstract</b></p> <p>The malaria parasite has for long been thought to escape host complement attack as a survival strategy. However, it was only recently that complement evasion mechanisms of the parasite were described. Simultaneously, the role of complement in antibody-mediated naturally acquired and vaccine-induced protection against malaria has also been reported. Such findings should be considered in future vaccine design, given the current need to develop more efficacious vaccines against malaria. Parasite antigens derived from molecules mediating functions crucial for parasite survival, such as complement evasion, or parasite antigens against which antibody responses lead to an efficient complement attack could present new candidates for vaccines. In this review, we discuss recent findings on complement evasion by the malaria parasites and the emerging role of complement in antibody-mediated protection against malaria. We emphasize that immune responses to vaccines based on complement inhibitors should not only induce complement-activating antibodies but also neutralize the escape mechanisms of the parasite.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32181490/">https://pubmed.ncbi.nlm.nih.gov/32181490/</a></p>
12.	<p>Abuga KM, Muriuki JM, Williams TN, Atkinson SH. How Severe Anaemia Might Influence the Risk of Invasive Bacterial Infections in African Children. Int J Mol Sci. 2020 Sep 22;21(18):6976.</p> <p><b>Abstract</b></p> <p>Severe anaemia and invasive bacterial infections are common causes of childhood sickness and death in sub-Saharan Africa. Accumulating evidence suggests that severely anaemic African children may have a higher risk of invasive bacterial infections. However, the mechanisms underlying this association remain poorly described. Severe</p>



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	<p>anaemia is characterized by increased haemolysis, erythropoietic drive, gut permeability, and disruption of immune regulatory systems. These pathways are associated with dysregulation of iron homeostasis, including the downregulation of the hepatic hormone hepcidin. Increased haemolysis and low hepcidin levels potentially increase plasma, tissue and intracellular iron levels. Pathogenic bacteria require iron and/or haem to proliferate and have evolved numerous strategies to acquire labile and protein-bound iron/haem. In this review, we discuss how severe anaemia may mediate the risk of invasive bacterial infections through dysregulation of hepcidin and/or iron homeostasis, and potential studies that could be conducted to test this hypothesis.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32972031/">https://pubmed.ncbi.nlm.nih.gov/32972031/</a></p>
13.	<p>Aluvaala J, Collins G, Maina B, Mutinda C, Waiyego M, Berkley JA, English M. Prediction modelling of inpatient neonatal mortality in high-mortality settings. Arch Dis Child. 2020 Oct 22;106(5):449–54.</p> <p><b>Abstract</b></p> <p>Objective: Prognostic models aid clinical decision making and evaluation of hospital performance. Existing neonatal prognostic models typically use physiological measures that are often not available, such as pulse oximetry values, in routine practice in low-resource settings. We aimed to develop and validate two novel models to predict all cause in-hospital mortality following neonatal unit admission in a low-resource, high-mortality setting.</p> <p>Study design and setting: We used basic, routine clinical data recorded by duty clinicians at the time of admission to derive (n=5427) and validate (n=1627) two novel models to predict in-hospital mortality. The Neonatal Essential Treatment Score (NETS) included treatments prescribed at the time of admission while the Score for Essential Neonatal Symptoms and Signs (SENSS) used basic clinical signs. Logistic regression was used, and performance was evaluated using discrimination and calibration.</p> <p>Results: At derivation, c-statistic (discrimination) for NETS was 0.92 (95% CI 0.90 to 0.93) and that for SENSS was 0.91 (95% CI 0.89 to 0.93). At external (temporal) validation, NETS had a c-statistic of 0.89 (95% CI 0.86 to 0.92) and SENSS 0.89 (95% CI 0.84 to 0.93). The calibration intercept for NETS was -0.72 (95% CI -0.96 to -0.49) and that for SENSS was -0.33 (95% CI -0.56 to -0.11).</p> <p>Conclusion: Using routine neonatal data in a low-resource setting, we found that it is possible to predict in-hospital mortality using either treatments or signs and symptoms. Further validation of these models may support their use in treatment decisions and for case-mix adjustment to help understand performance variation across hospitals.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33093041/">https://pubmed.ncbi.nlm.nih.gov/33093041/</a></p>



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14.	<p>Rose NH, Sylla M, Badolo A, Lutomiah J, Ayala D, Aribodor OB, Ibe N, Akorli J, Otoo S, Mutebi JP, Kriete AL, Ewing EG, Sang R, Gloria-Soria A, Powell JR, Baker RE, White BJ, Crawford JE, McBride CS. Climate and Urbanization Drive Mosquito Preference for Humans. <i>Curr Biol.</i> 2020 Sep 21;30(18):3570-3579.e6.</p> <p><b>Abstract</b></p> <p>The majority of mosquito-borne illness is spread by a few mosquito species that have evolved to specialize in biting humans, yet the precise causes of this behavioral shift are poorly understood. We address this gap in the arboviral vector <i>Aedes aegypti</i>. We first collect and characterize the behavior of mosquitoes from 27 sites scattered across the species' ancestral range in sub-Saharan Africa, revealing previously unrecognized variation in preference for human versus animal odor. We then use modeling to show that over 80% of this variation can be predicted by two ecological factors-dry season intensity and human population density. Finally, we integrate this information with whole-genome sequence data from 375 individual mosquitoes to identify a single underlying ancestry component linked to human preference. Genetic changes associated with human specialist ancestry were concentrated in a few chromosomal regions. Our findings suggest that human-biting in this important disease vector originally evolved as a by-product of breeding in human-stored water in areas where doing so provided the only means to survive the long, hot dry season. Our model also predicts that the rapid urbanization currently taking place in Africa will drive further mosquito evolution, causing a shift toward human-biting in many large cities by 2050.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32707056/">https://pubmed.ncbi.nlm.nih.gov/32707056/</a></p>
15.	<p>Simons-Rudolph AP, Iritani BJ, Odongo FS, Rennie S, Gilbertson A, Kwaro D, Luseno WK. Adolescent perceptions about participating in HIV-related research studies. <i>Child Youth Serv Rev.</i> 2020 Sep; 116:105262.</p> <p><b>Abstract</b></p> <p>The rising incidence of infection among youth in sub-Saharan Africa makes HIV-related research among younger people a top priority. There remains, however, a lack of consistent and unambiguous ethical principles and guidance for researchers wishing to conduct HIV studies with adolescents. The overarching aim of our research was to better understand youths' experiences with HIV studies. The present study explored four questions: (1) What strategies are effective for recruiting youth for HIV studies? (2) What motivates youth to participate in these studies? (3) How do study participants perceive HIV testing within the context of a research study? (4) What do participants understand about the risks of study participation? These data are essential to inform guidelines for the responsible conduct of research with young people. We interviewed 82 adolescents (aged 15-19) in Kenya taking part in a study examining ethical issues pertaining to their involvement in HIV-related research. Pursuant to our research questions, we found that direct study recruitment combined with encouragement from female relatives was the greatest facilitator to study enrolment among young people. Most young participants</p>





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	<p>expressed that they were motivated to join the study in order to (1) learn their HIV status (n = 49) and (2) receive HIV-related education (n = 26), even though both are already free and widely available. Participants largely preferred testing in a place they deemed "private," although both the health clinic and home were regarded by adolescents as locations with greater privacy. Adolescents largely did not accurately perceive risks of the study two months after baseline, although they could remember the benefits with great clarity. This work can inform researchers, policymakers, and ethics review committees on approaches to maximize efficiency in recruitment and data collection, and to enhance understanding of risks and benefits in HIV-related research among adolescents. While further research is needed, these data may be used by others conducting HIV research in this region to improve recruitment strategies and more effectively engage and appeal to young people.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32905545/">https://pubmed.ncbi.nlm.nih.gov/32905545/</a></p>
16.	<p>Ogero M, Sarguta RJ, Malla L, Aluvaala J, Agweyu A, English M, Onyango NO, Akech S. Prognostic models for predicting in-hospital paediatric mortality i resource-limited countries: a systematic review. <i>BMJ Open</i>. 2020 Oct 19;10(10): e035045.</p> <p><b>Abstract</b></p> <p><b>Objectives:</b> To identify and appraise the methodological rigour of multivariable prognostic models predicting in-hospital paediatric mortality in low-income and middle-income countries (LMICs).</p> <p><b>Design:</b> Systematic review of peer-reviewed journals.</p> <p><b>Data sources:</b> MEDLINE, CINAHL, Google Scholar and Web of Science electronic databases since inception to August 2019.</p> <p><b>Eligibility criteria:</b> We included model development studies predicting in-hospital paediatric mortality in LMIC.</p> <p><b>Data extraction and synthesis:</b> This systematic review followed the Checklist for critical Appraisal and data extraction for systematic Reviews of prediction Modelling Studies framework. The risk of bias assessment was conducted using Prediction model Risk of Bias Assessment Tool (PROBAST). No quantitative summary was conducted due to substantial heterogeneity that was observed after assessing the studies included.</p> <p><b>Results:</b> Our search strategy identified a total of 4054 unique articles. Among these, 3545 articles were excluded after review of titles and abstracts as they covered non-relevant topics. Full texts of 509 articles were screened for eligibility, of which 15 studies reporting 21 models met the eligibility criteria. Based on the PROBAST tool, risk of bias was assessed in four domains; participant, predictors, outcome and analyses. The domain of statistical analyses was the main area of concern where none of the included models was judged to be of low risk of bias.</p> <p><b>Conclusion:</b> This review identified 21 models predicting in-hospital paediatric mortality in LMIC. However, most reports characterising these models are of poor quality when judged against recent reporting standards due to a high risk of bias. Future studies should adhere</p>



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	<p>to standardised methodological criteria and progress from identifying new risk scores to validating or adapting existing scores.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33077558/">https://pubmed.ncbi.nlm.nih.gov/33077558/</a></p>
17.	<p>Chepkirui D, Nzinga J, Jemutai J, Tsofa B, Jones C, Mwangome M. A scoping review of breastfeeding peer support models applied in hospital settings. <i>Int Breastfeed J.</i> 2020 Nov 14;15(1):95.</p> <p><b>Abstract</b></p> <p>Background: The 2013 updated guidelines on management of severe acute malnutrition in infants and children recommends the support of exclusive breastfeeding. These guidelines are inconsistently applied in low and middle income countries (LMICs) due to barriers including unclear implementation guides, technical support and epidemiological factors. Peer support strategies have been used to offer psychological support to families with infants in NICU and improve mental health outcomes. Breastfeeding peer supporters (BFPS) have been shown to be effective in improving breastfeeding outcomes in community settings however, their success within hospital settings in LMICs is unknown. We conducted a scoping review to explore implementation of breastfeeding peer support strategies as have been applied to hospitalized infants globally and highlight their implementation strategies in order to guide future research and practice.</p> <p>Methods: A scoping review of the literature was conducted using the Arksey and O'Malley framework. A search was conducted in five online databases (PubMed, Cochrane library, Hinari, Google Scholar and Open Grey library). Data were extracted and charted in data extraction tables to capture general characteristics, modes of peer support delivery, implementation details and evaluation procedures.</p> <p>Results: From the online search 276 articles were identified, however only 18 met the inclusion criteria for the study. The majority of these articles were reports on in-patient breastfeeding peer support interventions applied in Europe and the United States of America and only two were from LMICs. The articles described peer supporters' identification, training (n = 13) and supervision (n = 14). The majority of the BFPS were employed (n = 10) compared to volunteers (n = 3) and support was mainly one-to-one (n = 11) rather than group support. Process and impact evaluation (n = 13) reported positive breastfeeding outcomes associated with breastfeeding peer support.</p> <p>Conclusion: Breastfeeding peer support strategies are applied in different hospital settings and can be used to improve breastfeeding outcomes. However, to achieve integration, scalability and comparability of impact and outcomes, there is a need to standardize training, develop consistent implementation and supervision plans of in-patient peer supporters' strategies. Further research to assess sustainability and evaluate cost-effectiveness of in-patient breastfeeding peer support strategies will improve uptake and scalability of these potentially lifesaving interventions.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33189155/">https://pubmed.ncbi.nlm.nih.gov/33189155/</a></p>





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18.	<p>Gikonyo JN, Mbatia B, Okanya PW, Obiero GFO, Sang C, Steele D, Nyangao J. Post-vaccine rotavirus genotype distribution in Nairobi County, Kenya. <i>Int J Infect Dis.</i> 2020 Nov; 100:434-440.</p> <p><b>Abstract</b></p> <p>Background: Rotaviruses are primary etiological agents of gastroenteritis in young children. In Kenya, G1P8 monovalent vaccine (Rotarix) was introduced in July 2014 for mandatory vaccination of all newborns at 6 and 10 weeks of age. Since then, no studies have been done to identify the rotavirus genotypes circulating in Nairobi County, Kenya, following the vaccine introduction, hence the post-vaccine genotype distribution is not known.</p> <p>Objectives: The aim of this study was to determine the post-vaccine occurrence of rotavirus genotypes in children &lt;5 years of age in Nairobi County, Kenya.</p> <p>Methods: Stool samples were collected from children presenting with diarrhea for whom the vaccination status was card-confirmed. Fecal samples were analyzed for rotavirus antigen using a commercial enzyme immunoassay (EIA) kit, followed by characterization by polyacrylamide gel electrophoresis, RT-PCR, and nested PCR genotyping, targeting the most medically important genotypes.</p> <p>Results: The strains observed included G1P[8] (38.8%), G9P[8] (20.4%), G2P[4] (12.2%), G3[P4] (6.1%), G2P[6] (4.1%), and G9P[6] (4.1%). Mixed genotype constellations G3P[4][8] were also detected (4.1%). Remarkably, an increased prevalence of G2 genotypes was observed, revealing a change in genetic diversity of rotavirus strains. While the dominance of G1P[8] decreased after vaccination, an upsurge in G2P[4] (12.2%) and G9P[8] (20.4%) was observed. Additionally, G3[P4] (6.1%) and G2P[6] (4.1%) prevalence increased over the 3 years of study.</p> <p>Conclusions: The results inform the need for robust longitudinal surveillance and epidemiological studies to assess the long-term interaction between rotavirus vaccine and strain ecology.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32898668/">https://pubmed.ncbi.nlm.nih.gov/32898668/</a></p>
19.	<p>Maina M, Tosas-Auguet O, English M, Schultz C, McKnight J. COVID-19: an opportunity to improve infection prevention and control in LMICs. <i>Lancet Glob Health.</i> 2020 Oct;8(10): e1261.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32798447/">https://pubmed.ncbi.nlm.nih.gov/32798447/</a></p>
20.	<p>Joseph NK, Macharia PM, Ouma PO, Mumo J, Jalang'o R, Wagacha PW, Achieng VO, Ndung'u E, Okoth P, Muñiz M, Guigoz Y, Panciera R, Ray N, Okiro EA. Spatial access inequities and childhood immunisation uptake in Kenya. <i>BMC Public Health.</i> 2020 Sep 15;20(1):1407.</p> <p><b>Abstract</b></p> <p>Background: Poor access to immunisation services remains a major barrier to achieving equity and expanding vaccination coverage in many sub-Saharan African countries. In Kenya, the extent to which spatial access affects immunisation coverage is not well understood. The aim of this study was to quantify spatial accessibility to immunising</p>



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	<p>health facilities and determine its influence on immunisation uptake in Kenya while controlling for potential confounders. Methods: Spatial databases of immunising facilities, road network, land use and elevation were used within a cost friction algorithm to estimate the travel time to immunising health facilities. Two travel scenarios were evaluated; (1) Walking only and (2) Optimistic scenario combining walking and motorized transport. Mean travel time to health facilities and proportions of the total population living within 1-h to the nearest immunising health facility were computed. Data from a nationally representative cross-sectional survey (KDHS 2014), was used to estimate the effect of mean travel time at survey cluster units for both fully immunised status and third dose of diphtheria-tetanus-pertussis (DPT3) vaccine using multi-level logistic regression models.</p> <p>Results: Nationally, the mean travel time to immunising health facilities was 63 and 40 min using the walking and the optimistic travel scenarios respectively. Seventy five percent of the total population were within one-hour of walking to an immunising health facility while 93% were within one-hour considering the optimistic scenario. There were substantial variations across the country with 62%(29/47) and 34%(16/47) of the counties with &lt; 90% of the population within one-hour from an immunising health facility using scenarios 1 and 2 respectively. Travel times &gt; 1-h were significantly associated with low immunisation coverage in the univariate analysis for both fully immunised status and DPT3 vaccine. Children living more than 2-h were significantly less likely to be fully immunised [AOR:0.56(0.33-0.94) and receive DPT3 [AOR:0.51(0.21-0.92) after controlling for household wealth, mother's highest education level, parity and urban/rural residence.</p> <p>Conclusion: Travel time to immunising health facilities is a barrier to uptake of childhood vaccines in regions with suboptimal accessibility (&gt; 2-h). Strategies that address access barriers in the hardest to reach communities are needed to enhance equitable access to immunisation services in Kenya.</p> <p><b>Pubmed link</b>-<a href="https://pubmed.ncbi.nlm.nih.gov/32933501/">https://pubmed.ncbi.nlm.nih.gov/32933501/</a></p>
21.	<p>English M, Moshabela M, Nzinga J, Barasa E, Tsofa B, Marchal B, Kruk ME. Systems and implementation science should be part of the COVID-19 response in low resource settings. BMC Med. 2020 Jul 15;18(1):219.</p> <p><b>Pubmed link</b>- <a href="https://pubmed.ncbi.nlm.nih.gov/32664950/">https://pubmed.ncbi.nlm.nih.gov/32664950/</a></p>
22.	<p>Olupot-Olupot P, Engoru C, Nteziyaremye J, Chebet M, Ssenyondo T, Muhindo R, Nyutu G, Macharia AW, Uyoga S, Ndila CM, Karamagi C, Maitland K, Williams TN. The clinical spectrum of severe childhood malaria in Eastern Uganda. Malar J. 2020 Sep 3;19(1):322.</p> <p><b>Abstract</b></p> <p>Background: Few recent descriptions of severe childhood malaria have been published from high-transmission regions. In the current study, the clinical epidemiology of severe</p>



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	<p>malaria in Mbale, Eastern Uganda, is described, where the entomological inoculation rate exceeds 100 infective bites per year.</p> <p>Methods: A prospective descriptive study was conducted to determine the prevalence, clinical spectrum and outcome of severe Plasmodium falciparum malaria at Mbale Regional Referral Hospital in Eastern Uganda. All children aged 2 months-12 years who presented on Mondays to Fridays between 8.00 am and 5.00 pm from 5th May 2011 until 30th April 2012 were screened for parasitaemia. Clinical and laboratory data were then collected from all P. falciparum positive children with features of WHO-defined severe malaria by use of a standardized proforma.</p> <p>Results: A total of 10 208 children were screened of which 6582 (64%) had a positive blood film. Of these children, 662 (10%) had clinical features of severe malaria and were consented for the current study. Respiratory distress was the most common severity feature (554; 83.7%), while 365/585 (62.4%) had hyperparasitaemia, 177/662 (26.7%) had clinical jaundice, 169 (25.5%) had severe anaemia, 134/660 (20.2%) had hyperlactataemia (lactate <math>\geq</math> 5 mmol/L), 93 (14.0%) had passed dark red or black urine, 52 (7.9%) had impaired consciousness and 49/662 (7.4%) had hypoxaemia (oxygen saturations &lt; 90%). In-hospital mortality was 63/662 (9.5%) overall but was higher in children with either cerebral malaria (33.3%) or severe anaemia (19.5%). Factors that were independently associated with mortality on multivariate analysis included severe anaemia [odds ratio (OR) 5.36; 2.16-1.32; P = 0.0002], hyperlactataemia (OR 3.66; 1.72-7.80; P = 0.001), hypoxaemia (OR) 3.64 (95% CI 1.39-9.52; P = 0.008), and hepatomegaly (OR 2.29; 1.29-4.06; P = 0.004). No independent association was found between mortality and either coma or hyperparasitaemia.</p> <p>Conclusions: Severe childhood malaria remains common in Eastern Uganda where it continues to be associated with high mortality. An unusually high proportion of children with severe malaria had jaundice or gave a history of having recently passed dark red or black urine, an issue worthy of further investigation.</p> <p><b>Pubmed link-</b> <a href="http://www.msn.com/en-us/health?ocid=iehp">http://www.msn.com/en-us/health?ocid=iehp</a></p>
23.	<p>Aluvaala J, English M. Implementing change for facility-based peripartum care in low-income and middle-income countries. Lancet Glob Health. 2020 Aug;8(8): e980-e981.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32710869/">https://pubmed.ncbi.nlm.nih.gov/32710869/</a></p>
24.	<p>Onditi F, Obimbo M, Muchina SK, Nyadera I. Modeling a Pandemic (COVID-19) Management Strategy for Urban Slums Using Social Geometry Framework. Eur J Dev Res. 2020 Oct 26:1-26.</p> <p><b>Abstract</b></p> <p>The purpose of this paper is to utilize social geometry framework to model a pandemic (COVID-19) management strategy in densely populated informal settlements in Kenya. Our central claim is that the containment strategy that was instituted to control spread of</p>



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	<p>COVID-19 failed to recognize the socio-cultural and livelihood complexities of the urban slum residents. This unmitigated strategy predisposed the residents to risks of heightened transmission of the pandemic. Drawing on social geometry approach in the analysis of human relations, we reveal some insights offered by our experiences in theorizing about public health intervention (PHI) and in doing so develop an alternative analytical framework ('social pendulum') to support the development of a PHI strategy that is compatible with the swing-like lifestyle of residents in the informal settlements. Our conclusion revisits the reliability and validity criteria for the new framework and offers some direction for further research.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33132540/">https://pubmed.ncbi.nlm.nih.gov/33132540/</a></p>
25.	<p>Izugbara C, Wekesah FM, Sebanly M, Echoka E, Amo-Adjei J, Muga W. Availability, accessibility and utilization of post-abortion care in Sub-Saharan Africa: A systematic review. <i>Health Care Women Int.</i> 2020 Jul;41(7):732-760.</p> <p><b>Abstract</b>          At the 1994 ICPD, sub-Saharan African (SSA) states pledged, inter alia, to guarantee quality post-abortion care (PAC) services. We synthesized existing research on PAC services provision, utilization and access in SSA since the 1994 ICPD. Generally, evidence on PAC is only available in a few countries in the sub-region. The available evidence however suggests that PAC constitutes a significant financial burden on public health systems in SSA; that accessibility, utilization and availability of PAC services have expanded during the period; and that worrying inequities characterize PAC services. Manual and electrical vacuum aspiration and medication abortion drugs are increasingly common PAC methods in SSA, but poor-quality treatment methods persist in many contexts. Complex socio-economic, infrastructural, cultural and political factors mediate the availability, accessibility and utilization of PAC services in SSA. Interventions that have been implemented to improve different aspects of PAC in the sub-region have had variable levels of success. Underexplored themes in the existing literature include the individual and household level costs of PAC; the quality of PAC services; the provision of non-abortion reproductive health services in the context of PAC; and health care provider-community partnerships.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/31855511/">https://pubmed.ncbi.nlm.nih.gov/31855511/</a></p>
26.	<p>Maina M, Mwaniki P, Odira E, Kiko N, McKnight J, Schultsz C, English M, Tosas-Auguet O. Antibiotic use in Kenyan public hospitals: Prevalence, appropriateness and link to guideline availability. <i>Int J Infect Dis.</i> 2020 Oct; 99:10-18.</p> <p><b>Abstract</b>          Objective: To examine prescription patterns and explore to what extent guidelines are available and how they might influence treatment appropriateness among hospitalised patients in Kenyan hospitals.</p>



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	<p>Methods: Data on antimicrobial usage were collected from hospitalised patients across 14 Kenyan public hospitals. For each prescription, appropriateness of treatment was defined using available local and international treatment guidelines and through consensus with local medical specialists. Association between appropriate treatment, guideline availability and other possible explanatory factors was explored using univariate and multiple regression analysis.</p> <p>Results: There were 1675 (46.7%) of the 3590 hospitalised patients on antimicrobials with 3145(94%) of the 3363 antimicrobial prescriptions being antibiotics. Two patients (0.1%), had treatment based on available antibiotic susceptibility tests. Appropriate treatment was assessed in 1502 patients who had a single diagnosis. Of these, 805 (53.6%) received appropriate treatment. Physical availability of treatment guidelines increased the odds of receiving appropriate treatment Odds Ratio 6.44[95% CI 4.81-8.64].</p> <p>Conclusion: Appropriate antibiotic prescription remains a challenge in Kenyan public hospitals. This may be improved by the availability of context-specific, up-to-date, and readily accessible treatment guidelines across all the departments, and by providing better diagnostic support.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32781162/">https://pubmed.ncbi.nlm.nih.gov/32781162/</a></p>
27.	<p>Farrar JL, Odiembo H, Odoyo A, Bigogo G, Kim L, Lessa FC, Feikin DR, BreimanRF, Whitney CG, Carvalho MG, Pimenta FC. Limited Added Value of Oropharyngeal Swabs for Detecting Pneumococcal Carriage in Adults. <i>Open Forum Infect Dis.</i> 2020 Aug 18;7(9): ofaa368.</p> <p><b>Abstract</b></p> <p>We compared pneumococcal isolation rates and evaluated the benefit of using oropharyngeal (OP) specimens in addition to nasopharyngeal (NP) specimens collected from adults in rural Kenya. Of 846 adults, 52.1% were colonized; pneumococci were detected from both NP and OP specimens in 23.5%, NP only in 22.9%, and OP only in 5.7%. Ten-valent pneumococcal conjugate vaccine strains were detected from both NP and OP in 3.4%, NP only in 4.1%, and OP only in 0.7%. Inclusion of OP swabs increased carriage detection by 5.7%; however, the added cost of collecting and processing OP specimens may justify exclusion from future carriage studies among adults.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32995349/">https://pubmed.ncbi.nlm.nih.gov/32995349/</a></p>
28	<p>English M, Strachan B, Esamai F, Ngwiri T, Warfa O, Mburugu P, Nalwa G, Gitaka J, Ngugi J, Zhao Y, Ouma P, Were F. The paediatrician workforce and its role in addressing neonatal, child and adolescent healthcare in Kenya. <i>Arch Dis Child.</i> 2020 Oct;105(10):927-931.</p> <p><b>Abstract</b></p> <p>Objective: To examine the availability of paediatricians in Kenya and plans for their development.</p>



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	<p>Design: Review of policies and data from multiple sources combined with local expert insight.</p> <p>Setting: Kenya with a focus on the public, non-tertiary care sector as an example of a low-income and middle-income country aiming to improve the survival and long-term health of newborns, children and adolescents.</p> <p>Results: There are 305 practising paediatricians, 1.33 per 100 000 individuals of the population aged &lt;19 years which in total numbers approximately 25 million. Only 94 are in public sector, non-tertiary county hospitals. There is either no paediatrician at all or only one paediatrician in 21/47 Kenyan counties that are home to over a quarter of a million under 19 years of age. Government policy is to achieve employment of 1416 paediatricians in the public sector by 2030, however this remains aspirational as there is no comprehensive training or financing plan to reach this target and health workforce recruitment, financing and management is now devolved to 47 counties. The vast majority of paediatric care is therefore provided by non-specialist healthcare workers.</p> <p>Discussion: The scale of the paediatric workforce challenge seriously undermines the ability of the Kenyan health system to deliver on the emerging survive, thrive and transform agenda that encompasses more complex health needs. Addressing this challenge may require innovative workforce solutions such as task-sharing, these may in turn require the role of paediatricians to be redefined. Professional paediatric communities in countries like Kenya could play a leadership role in developing such solutions.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32554508/">https://pubmed.ncbi.nlm.nih.gov/32554508/</a></p>
29.	<p>Macharia AW, Mochamah G, Uyoga S, Ndila CM, Nyutu G, Tendwa M, Nyatichi E, Makale J, Ware RE, Williams TN. <math>\beta</math>-Thalassemia pathogenic variants in a cohort of children from the East African coast. <i>Mol Genet Genomic Med.</i> 2020 Jul;8(7): e1294.</p> <p><b>Abstract</b></p> <p>Background: <math>\beta</math>-Thalassemia is rare in sub-Saharan Africa. Previous studies have suggested that it is limited to specific parts of West Africa. Based on hemoglobin A2 (HbA2 ) concentrations measured by HPLC, we recently speculated that <math>\beta</math>-thalassemia might also be present on the East African coast of Kenya. Here, we follow this up using molecular methods.</p> <p>Methods: We used raised hemoglobin A2 (HbA2 ) values (&gt; 4.0% of total Hb) to target all HbAA members of a cohort study in Kilifi, Kenya, for HBB sequencing for <math>\beta</math>-thalassemia (n = 99) together with a sample of HbAA subjects with lower HbA2 levels. Because HbA2 values are artifactually raised in subjects carrying sickle hemoglobin (HbS) we sequenced all participants with an HPLC pattern showing HbS without HbA (n = 116) and a sample with a pattern showing both HbA and HbS.</p> <p>Results: Overall, we identified 83 carriers of four separate <math>\beta</math>-thalassemia pathogenic variants: three <math>\beta^0</math> -thalassemia [CD22 (GAA→TAA), initiation codon (ATG→ACG), and IVS1-3' end del 25bp] and one <math>\beta^+</math> -thalassemia pathogenic variants (IVS-I-110 (G→A)). We estimated the minimum allele frequency of all variants combined within the study population at 0.3%.</p>





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	<p>Conclusions: <math>\beta</math>-Thalassemia is present in Kilifi, Kenya, an observation that has implications for the diagnosis and clinical care of children from the East Africa region.  <b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32394645/">https://pubmed.ncbi.nlm.nih.gov/32394645/</a></p>
30.	<p>Magai DN, Koot HM, Mwangi P, Chongwo E, Newton CR, Abubakar A. Long-term neurocognitive and educational outcomes of neonatal insults in Kilifi, Kenya. <i>BMC Psychiatry</i>. 2020 Dec 2;20(1):578.</p> <p><b>Abstract</b>  Background: There is little data on the long-term neurocognitive and educational outcomes among school-aged survivors of neonatal jaundice (NNJ) and hypoxic-ischemic encephalopathy (HIE) in Africa. This study investigates the long-term neurocognitive and educational outcomes and the correlates of these outcomes in school-aged survivors of NNJ or HIE in Kilifi, Kenya.  Methods: We conducted a cross-sectional study on neurocognitive and educational outcomes among school-aged survivors (6-12 years) of NNJ (n = 134) and HIE (n = 107) and compared them to a community comparison group (n = 134). We assessed nonverbal intelligence, planning, working memory, attention, syntax, pragmatics, word-finding, memory, perceptual-motor, mathematical, and reading abilities. We also collected information on medical history, caregivers' mental health, and family environment.  Results: The survivors of NNJ had lower mean total scores in word-finding [F (1, 250) = 3.89, p = 0.050] and memory [F (1, 248) = 6.74, p = 0.010] than the comparison group. The survivors of HIE had lower mean scores in pragmatics [F (1, 230) = 6.61, p = 0.011] and higher scores higher scores in non-verbal reasoning [F (1, 225) = 4.10, p = 0.044] than the comparison group. Stunted growth was associated with almost all the outcomes in HIE.  Conclusion: Survivors of NNJ and HIE present with impairment in the multiple domains, which need to be taken into consideration in the planning of educational and rehabilitative services.  <b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33267843/">https://pubmed.ncbi.nlm.nih.gov/33267843/</a></p>
31.	<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. Glucose-6-phosphate dehydrogenase deficiency and susceptibility to childhood diseases in Kilifi, Kenya. <i>Blood Adv</i>. 2020 Dec 8;4(23):5942-5950.</p> <p><b>Abstract</b>  Few previous studies have reported the effects of glucose-6-phosphate dehydrogenase (G6PD)-deficiency on child health in Africa. We conducted a case-control study in which cases (n = 6829) were children admitted, for any reason, to Kilifi County Hospital, Kenya, while controls (n = 10 179) were recruited from the surrounding community. Cases were subclassified based on their clinical and laboratory findings at admission. We calculated the prevalence of specific diseases by G6PD c.202 genotype, the only significant cause of G6PD-deficiency in this area, then estimated the association between genotype and</p>



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	<p>admission with specific conditions using logistic regression. Among neonates, the prevalence of jaundice was higher in both G6PD c.202T heterozygotes (40/88; 45.5%; <math>P = .004</math>) and homo/hemizygotes (81/134; 60.5%; <math>P &lt; .0001</math>) than in wild-type homozygotes (157/526; 29.9%). Median bilirubin levels also increased across the groups, being highest (239 mmol/L; interquartile range 96-390 mmol/L) in G6PD c.202T homo/hemizygotes. No differences were seen in admission hemoglobin concentrations or the prevalence of anemia or severe anemia by G6PD c.202 genotype. On case control analysis, G6PD heterozygosity was negatively associated with all-cause hospital admission (odds ratio 0.81; 95% confidence interval 0.73-0.90; <math>P &lt; .0001</math>) and, specifically, admission with either pneumonia or Plasmodium falciparum parasitemia; while, conversely, it was positively associated with Gram-positive bacteremia. G6PD c.202T homo/heterozygosity was positively associated with neonatal jaundice, severe pneumonia, the receipt of a transfusion, and in-patient death. Our study supports the conclusion that G6PD c.202T is a balanced polymorphism in which a selective advantage afforded to heterozygous females against malaria is counterbalanced by increased risks of neonatal jaundice, invasive bacterial infections, and anemia.</p> <p><b>Pubmed link-</b><a href="https://pubmed.ncbi.nlm.nih.gov/33275767/">https://pubmed.ncbi.nlm.nih.gov/33275767/</a></p>
32.	<p>Lim JK, Matendechero SH, Alexander N, Lee JS, Lee KS, Namkung S, Andia E, Oyembo N, Lim SK, Kanyi H, Bae SH, Yang JS, Ochola MA, Edwards T, Yoon IK, Njenga SM. Clinical and epidemiologic characteristics associated with dengue fever in Mombasa, Kenya. <i>Int J Infect Dis.</i> 2020 Nov; 100:207-215.</p> <p><b>Abstract</b></p> <p><b>Objectives:</b> Information on dengue in Africa is limited. To estimate the proportion of dengue-positive cases among febrile patients and describe clinical indicators of dengue, we conducted passive health facility-based fever surveillance in Mombasa, Kenya.</p> <p><b>Methods:</b> Non-malarial febrile patients between one and 55 years were enrolled at three health facilities between March 2016 and May 2017. Acute and convalescent blood samples were collected with an interval of 10-21 days. Acute samples were tested with dengue RDT and a selected subset with RT-PCR, and acute/convalescent samples with IgM/IgG ELISA.</p> <p><b>Results:</b> Among 482 enrollees, 295 (61.2%) were dengue-positive based on laboratory results. The surveillance covered the beginning of a dengue outbreak in April-May 2017, during which 73.9% of enrollees were dengue-positive. By contrast, during the non-outbreak period, 54.6% were dengue-positive. Dengue case status was positively associated with rash, fatigue, headache, retro-orbital pain, nausea/vomiting, nose bleeding, gum bleeding, loss of appetite, myalgia, and arthralgia. Dengue-positive cases in our study had mostly mild disease, with only two requiring observation, and no DHF.</p> <p><b>Conclusions:</b> The clinical response was generally mild relative to what was observed in SE Asia and the Americas. Given the high level of DENV transmission in Mombasa,</p>



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	<p>more data would be needed to further understand the disease burden and improve case detection for surveillance/monitoring of outbreaks.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32891734/">https://pubmed.ncbi.nlm.nih.gov/32891734/</a></p>
33.	<p>Wright D, Allen ER, Clark MHA, Gitonga JN, Karanja HK, Hulswit RJG, Taylor I, Biswas S, Marshall J, Mwololo D, Muriuki J, Bett B, Bowden TA, Warimwe GM. Naturally Acquired Rift Valley Fever Virus Neutralizing Antibodies Predominantly Target the Gn Glycoprotein. <i>iScience</i>. 2020 Oct 14;23(11):101669.</p> <p><b>Abstract</b></p> <p>Rift Valley fever (RVF) is a viral hemorrhagic disease first discovered in Kenya in 1930. Numerous animal studies have demonstrated that protective immunity is acquired following RVF virus (RVFV) infection and that this correlates with acquisition of virus-neutralizing antibodies (nAbs) that target the viral envelope glycoproteins. However, naturally acquired immunity to RVF in humans is poorly described. Here, we characterized the immune response to the viral envelope glycoproteins, Gn and Gc, in RVFV-exposed Kenyan adults. Long-lived IgG (dominated by IgG1 subclass) and T cell responses were detected against both Gn and Gc. However, antigen-specific antibody depletion experiments showed that Gn-specific antibodies dominate the RVFV nAb response. IgG avidity against Gn, but not Gc, correlated with nAb titers. These data are consistent with the greater level of immune accessibility of Gn on the viral envelope surface and confirm the importance of Gn as an integral component for RVF vaccine development.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33134899/">https://pubmed.ncbi.nlm.nih.gov/33134899/</a></p>
34.	<p>Obadha M, Chuma J, Kazungu J, Abihiro GA, Beck MJ, Barasa E. Preferences of healthcare providers for capitation payment in Kenya: a discrete choice experiment. <i>Health Policy Plan</i>. 2020 Aug 1;35(7):842-854.</p> <p><b>Abstract</b></p> <p>Provider payment mechanisms (PPMs) are important to the universal health coverage (UHC) agenda as they can influence healthcare provider behaviour and create incentives for health service delivery, quality and efficiency. Therefore, when designing PPMs, it is important to consider providers' preferences for PPM characteristics. We set out to uncover senior health facility managers' preferences for the attributes of a capitation payment mechanism in Kenya. We use a discrete choice experiment and focus on four capitation attributes, namely, payment schedule, timeliness of payments, capitation rate per individual per year and services to be paid by the capitation rate. Using a Bayesian efficient experimental design, choice data were collected from 233 senior health facility managers across 98 health facilities in seven Kenyan counties. Panel mixed multinomial logit and latent class models were used in the analysis. We found that capitation arrangements with frequent payment schedules, timelier disbursements, higher payment rates per individual per year and those that paid for a limited set of health services were preferred. The capitation rate per individual per year was the most important attribute.</p>



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	<p>Respondents were willing to accept an increase in the capitation rate to compensate for bundling a broader set of health services under the capitation payment. In addition, we found preference heterogeneity across respondents and latent classes. In conclusion, these attributes can be used as potential targets for interventions aimed at configuring capitation to achieve UHC.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32537642/">https://pubmed.ncbi.nlm.nih.gov/32537642/</a></p>
35.	<p>Kamau A, Mtanje G, Mataza C, Malla L, Bejon P, Snow RW. The relationship between facility-based malaria test positivity rate and community-based parasite prevalence. <i>PLoS One</i>. 2020 Oct 7;15(10): e0240058.</p> <p><b>Abstract</b></p> <p><b>Introduction:</b> Malaria surveillance is a key pillar in the control of malaria in Africa. The value of using routinely collected data from health facilities to define malaria risk at community levels remains poorly defined.</p> <p><b>Methods:</b> Four cross-sectional parasite prevalence surveys were undertaken among residents at 36 enumeration zones in Kilifi county on the Kenyan coast and temporally and spatially matched to fever surveillance at 6 health facilities serving the same communities over 12 months. The age-structured functional form of the relationship between test positivity rate (TPR) and community-based parasite prevalence (PR) was explored through the development of regression models fitted by alternating the linear, exponential and polynomial terms for PR. The predictive ranges of TPR were explored for PR endemicity risk groups of control programmatic value using cut-offs of low (PR &lt;5%) and high (PR ≥ 30%) transmission intensity.</p> <p><b>Results:</b> Among 28,134 febrile patients encountered for malaria diagnostic testing in the health facilities, 12,143 (43.2%: 95% CI: 42.6%, 43.7%) were positive. The overall community PR was 9.9% (95% CI: 9.2%, 10.7%) among 6,479 participants tested for malaria. The polynomial model was the best fitting model for the data that described the algebraic relationship between TPR and PR. In this setting, a TPR of ≥ 49% in all age groups corresponded to an age-standardized PR of ≥ 30%, while a TPR of &lt; 40% corresponded to an age-standardized PR of &lt; 5%.</p> <p><b>Conclusion:</b> A non-linear relationship was observed between the relative change in TPR and changes in the PR, which is likely to have important implications for malaria surveillance programs, especially at the extremes of transmission. However, larger, more spatially diverse data series using routinely collected TPR data matched to community-based infection prevalence data are required to explore the more practical implications of using TPR as a replacement for community PR.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33027313/">https://pubmed.ncbi.nlm.nih.gov/33027313/</a></p>
36.	<p>Kagwanja N, Waithaka D, Nzinga J, Tsofa B, Boga M, Leli H, Mataza C, Gilson L, Molyneux S, Barasa E. Shocks, stress and everyday health system resilience: experiences from the Kenyan coast. <i>Health Policy Plan</i>. 2020 Jun 1;35(5):522-535.</p> <p><b>Abstract</b></p>



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	<p>Health systems are faced with a wide variety of challenges. As complex adaptive systems, they respond differently and sometimes in unexpected ways to these challenges. We set out to examine the challenges experienced by the health system at a sub-national level in Kenya, a country that has recently undergone rapid devolution, using an 'everyday resilience' lens. We focussed on chronic stressors, rather than acute shocks in examining the responses and organizational capacities underpinning those responses, with a view to contributing to the understanding of health system resilience. We drew on learning and experiences gained through working with managers using a learning site approach over the years. We also collected in-depth qualitative data through informal observations, reflective meetings and in-depth interviews with middle-level managers (sub-county and hospital) and peripheral facility managers (n = 29). We analysed the data using a framework approach. Health managers reported a wide range of health system stressors related to resource scarcity, lack of clarity in roles and political interference, reduced autonomy and human resource management. The health managers adopted absorptive, adaptive and transformative strategies but with mixed effects on system functioning. Everyday resilience seemed to emerge from strategies enacted by managers drawing on a varying combination of organizational capacities depending on the stressor and context.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32101609/">https://pubmed.ncbi.nlm.nih.gov/32101609/</a></p>
37.	<p>Kivata MW, Mbuchi M, Eyase F, Bulimo WD, Kyanya CK, Oundo V, Mbinda WM, Sang W, Andagalu B, Soge OO, McClelland RS, Distelhorst J. Plasmid mediated penicillin and tetracycline resistance among Neisseria gonorrhoeae isolates from Kenya. BMC Infect Dis. 2020 Sep 25;20(1):703.</p> <p><b>Abstract</b></p> <p>Background: Treatment of gonorrhoea is complicated by the development of antimicrobial resistance in Neisseria gonorrhoeae (GC) to the antibiotics recommended for treatment. Knowledge on types of plasmids and the antibiotic resistance genes they harbor is useful in monitoring the emergence and spread of bacterial antibiotic resistance. In Kenya, studies on gonococcal antimicrobial resistance are few and data on plasmid mediated drug resistance is limited. The present study characterizes plasmid mediated resistance in N. gonorrhoeae isolates recovered from Kenya between 2013 and 2018.</p> <p>Methods: DNA was extracted from 36 sub-cultured GC isolates exhibiting varying drug resistance profiles. Whole genome sequencing was done on Illumina MiSeq platform and reads assembled de-novo using CLC Genomics Workbench. Genome annotation was performed using Rapid Annotation Subsystem Technology. Comparisons in identified antimicrobial resistance determinants were done using Bioedit sequence alignment editor.</p> <p>Results: Twenty-four (66.7%) isolates had both <math>\beta</math>-lactamase (TEM) and TetM encoding plasmids. 8.3% of the isolates lacked both TEM and TetM plasmids and had intermediate to susceptible penicillin and tetracycline MICs. Twenty-six (72%) isolates harbored TEM encoding plasmids. 25 of the TEM plasmids were of African type while one was an Asian type. Of the 36 isolates, 31 (86.1%) had TetM encoding plasmids, 30 of which harbored</p>





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	<p>American TetM, whereas 1 carried a Dutch TetM. All analyzed isolates had non-mosaic penA alleles. All the isolates expressing TetM were tetracycline resistant (MIC &gt; 1 mg/L) and had increased doxycycline MICs (up to 96 mg/L). All the isolates had S10 ribosomal protein V57M amino acid substitution associated with tetracycline resistance. No relation was observed between PenB and MtrR alterations and penicillin and tetracycline MICs. Conclusion: High-level gonococcal penicillin and tetracycline resistance in the sampled Kenyan regions was found to be mediated by plasmid borne blaTEM and tetM genes. While the African TEM plasmid, TEM1 and American TetM are the dominant genotypes, Asian TEM plasmid, a new TEM239 and Dutch TetM have emerged in the regions. <b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32977759/">https://pubmed.ncbi.nlm.nih.gov/32977759/</a></p>
38.	<p>Wahome EW, Graham SM, Thiong'o AN, Mohamed K, Oduor T, Gichuru E, Mwambi J, Prins PM, van der Elst E, Sanders PEJ. PrEP uptake and adherence in relation to HIV-1 incidence among Kenyan men who have sex with men. <i>EClinicalMedicine</i>. 2020 Sep 9; 26:100541.</p> <p><b>Abstract</b></p> <p>Background: Data on HIV-1 incidence following programmatic pre-exposure prophylaxis (PrEP) uptake by men who have sex with men (MSM) are limited in sub-Saharan Africa. Methods: Since June 2017, MSM participating in an ongoing cohort study in Kenya were offered daily PrEP, assessed for PrEP uptake and adherence, and evaluated for HIV-1 acquisition monthly. We determined tenofovir-diphosphate (TFV-DP) concentrations in dried blood spots 6-12 months after PrEP initiation, and tenofovir (TFV) concentrations and genotypic drug resistance in plasma samples when HIV-1 infection occurred. We assessed HIV-1 incidence by reported PrEP use.</p> <p>Findings: Of 172 MSM, 170 (98.8%) were eligible for PrEP, 140 (82.4%) started it, and 64 (57.7%) reported PrEP use at end of study. Of nine MSM who acquired HIV-1 [incidence rate: 3.9 (95% confidence interval (CI), 2.0-7.4) per 100 person-years (PY)], five reported PrEP use at the time of HIV-1 acquisition [incidence rate: 3.6 (95% CI, 1.5-8.6) per 100 PY] and four had stopped or had never started PrEP [incidence rate: 4.3 (95% CI, 1.6-11.3) per 100 PY]. Among 76 MSM who reported PrEP use, 11 (14.5%) had protective TFV-DP concentrations of <math>\geq 700</math> fmol/punch (<math>\geq 4</math> tablets a week). Among the five MSM who acquired HIV-1 while reporting PrEP use, only one had detectable but low TFV concentrations in plasma and none had genotypic HIV-1 resistance.</p> <p>Interpretation: HIV-1 incidence among MSM with access to programmatic PrEP was high and did not differ by reported PrEP use. Only one in seven MSM taking PrEP had protective tenofovir concentrations and four out of five MSM who acquired HIV-1 while reporting PrEP use had not taken it. Strengthened PrEP adherence support is required among MSM in Kenya.</p> <p>Funding: This work was supported by the International AIDS Vaccine Initiative (IAVI). <b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33089128/">https://pubmed.ncbi.nlm.nih.gov/33089128/</a></p>





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39.	<p>Adema IW, Kamau E, Uchi Nyiro J, Otieno GP, Lewa C, Munywoki PK, Nokes DJ. Surveillance of respiratory viruses among children attending a primary school in rural coastal Kenya. Wellcome Open Res. 2020 Sep 24; 5:63.</p> <p><b>Abstract</b></p> <p>Background: Respiratory viruses are primary agents of respiratory tract diseases. Knowledge on the types and frequency of respiratory viruses affecting school-children is important in determining the role of schools in transmission in the community and identifying targets for interventions. Methods: We conducted a one-year (term-time) surveillance of respiratory viruses in a rural primary school in Kilifi County, coastal Kenya between May 2017 and April 2018. A sample of 60 students with symptoms of ARI were targeted for nasopharyngeal swab (NPS) collection weekly. Swabs were screened for 15 respiratory virus targets using real time PCR diagnostics. Data from respiratory virus surveillance at the local primary healthcare facility was used for comparison. Results: Overall, 469 students aged 2-19 years were followed up for 220 days. A total of 1726 samples were collected from 325 symptomatic students; median age of 7 years (IQR 5-11). At least one virus target was detected in 384 (22%) of the samples with a frequency of 288 (16.7%) for rhinovirus, 47 (2.7%) parainfluenza virus, 35 (2.0%) coronavirus, 15 (0.9%) adenovirus, 11 (0.6%) respiratory syncytial virus (RSV) and 5 (0.3%) influenza virus. The proportion of virus positive samples was higher among lower grades compared to upper grades (25.9% vs 17.5% respectively; <math>\chi^2 = 17.2</math>, P -value &lt;0.001). Individual virus target frequencies did not differ by age, sex, grade, school term or class size. Rhinovirus was predominant in both the school and outpatient setting. Conclusion: Multiple respiratory viruses circulated in this rural school population. Rhinovirus was dominant in both the school and outpatient setting and RSV was of notably low frequency in the school. The role of school children in transmitting viruses to the household setting is still unclear and further studies linking molecular data to contact patterns between the school children and their households are required.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33102784/">https://pubmed.ncbi.nlm.nih.gov/33102784/</a></p>
40.	<p>Maina M, Tosas-Auguet O, English M, Schultz C, McKnight J. Infection prevention and control during the COVID-19 pandemic: challenges and opportunities for Kenyan public hospitals. Wellcome Open Res. 2020 Sep 10; 5:211.</p> <p><b>Abstract</b></p> <p>Background: Infection prevention and control, and water sanitation and hygiene have an essential role in ensuring the quality of care and patient outcomes in hospitals. Using a modification of the World Health Organization's water sanitation and hygiene facility improvement tool, we undertook assessments in 14 public hospitals in Kenya in 2018. The hospitals received written feedback on areas where they could make improvements. Following the first confirmed cases of COVID-19 in Kenya, we were drawn to ask whether the results of our pre-pandemic survey had led to action, and whether or not the threat of COVID-19 had focused more attention on infection prevention and control and water sanitation and hygiene. Methods: Using a semi-structured interview guide, we</p>



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	<p>carried out phone interviews with key hospital leaders in 11 of the 14 hospitals. The data were transcribed and coded into thematic areas. We draw on these interviews to describe the status and awareness of infection prevention and control. Results: The infection prevention and control committee members are training health workers on infection prevention and control procedures and proper use of personal protective equipment and in addition, providing technical support to hospital managers. While some hospitals have also accessed additional funds to improve infection prevention and control, they tended to be small amounts of money. Long-standing challenges with supplies of infection prevention and control materials and low staff morale persist. Crucially, the reduced supply of personal protective equipment has led to fear and anxiety among health care personnel. Conclusions: As funds are mobilised to support care for COVID-19, we ask that funds prioritise infection prevention and control measures. This would have a profoundly positive effect on within hospital virus transmission, patient and staff safety but also lasting benefits beyond the COVID-19 pandemic.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33204846/">https://pubmed.ncbi.nlm.nih.gov/33204846/</a></p>
41.	<p>Kamau E, Otieno JR, Murunga N, Oketch JW, Ngoi JM, de Laurent ZR, Mwema A, Nyiro JU, Agoti CN, Nokes DJ. Genomic epidemiology and evolutionary dynamics of respiratory syncytial virus group B in Kilifi, Kenya, 2015-17. <i>Virus Evol.</i> 2020 Jul 15;6(2): veaa050.</p> <p><b>Abstract</b></p> <p>Respiratory syncytial virus (RSV) circulates worldwide, occurring seasonally in communities, and is a leading cause of acute respiratory illness in young children. There is paucity of genomic data from purposively sampled populations by which to investigate evolutionary dynamics and transmission patterns of RSV. Here we present an analysis of 295 RSV group B (RSVB) genomes from Kilifi, coastal Kenya, sampled from individuals seeking outpatient care in nine health facilities across a defined geographical area (~890 km<sup>2</sup>), over two RSV epidemics between 2015 and 2017. RSVB diversity was characterized by multiple virus introductions into the area and co-circulation of distinct genetic clusters, which transmitted and diversified locally with varying frequency. Increase in relative genetic diversity paralleled seasonal virus incidence. Importantly, we identified a cluster of viruses that emerged in the 2016/17 epidemic, carrying distinct amino-acid signatures including a novel nonsynonymous change (K68Q) in antigenic site <math>\emptyset</math> in the Fusion protein. RSVB diversity was additionally marked by signature nonsynonymous substitutions that were unique to particular genomic clusters, some under diversifying selection. Our findings provide insights into recent evolutionary and epidemiological behaviors of RSVB, and highlight possible emergence of a novel antigenic variant, which has implications on current prophylactic strategies in development.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32913665/">https://pubmed.ncbi.nlm.nih.gov/32913665/</a></p>



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42.	<p>Mwanga MJ, Owor BE, Ochieng JB, Ngama MH, Ogwel B, Onyango C, Juma J, Njeru R, Gicheru E, Otieno GP, Khagayi S, Agoti CN, Bigogo GM, Omoro R, Addo OY, Mapaseka S, Tate JE, Parashar UD, Hunsperger E, Verani JR, Breiman RF, Nokes DJ. Rotavirus group A genotype circulation patterns across Kenya before and after nationwide vaccine introduction, 2010-2018. <i>BMC Infect Dis.</i> 2020 Jul 13;20(1):504.</p> <p><b>Abstract</b></p> <p><b>Background:</b> Kenya introduced the monovalent G1P [8] Rotarix® vaccine into the infant immunization schedule in July 2014. We examined trends in rotavirus group A (RVA) genotype distribution pre- (January 2010-June 2014) and post- (July 2014-December 2018) RVA vaccine introduction.</p> <p><b>Methods:</b> Stool samples were collected from children aged &lt; 13 years from four surveillance sites across Kenya: Kilifi County Hospital, Tabitha Clinic Nairobi, Lwak Mission Hospital, and Siaya County Referral Hospital (children aged &lt; 5 years only). Samples were screened for RVA using enzyme linked immunosorbent assay (ELISA) and VP7 and VP4 genes sequenced to infer genotypes.</p> <p><b>Results:</b> We genotyped 614 samples in pre-vaccine and 261 in post-vaccine introduction periods. During the pre-vaccine introduction period, the most frequent RVA genotypes were G1P [8] (45.8%), G8P [4] (15.8%), G9P [8] (13.2%), G2P [4] (7.0%) and G3P [6] (3.1%). In the post-vaccine introduction period, the most frequent genotypes were G1P [8] (52.1%), G2P [4] (20.7%) and G3P [8] (16.1%). Predominant genotypes varied by year and site in both pre and post-vaccine periods. Temporal genotype patterns showed an increase in prevalence of vaccine heterotypic genotypes, such as the commonly DS-1-like G2P [4] (7.0 to 20.7%, <math>P &lt; .001</math>) and G3P [8] (1.3 to 16.1%, <math>P &lt; .001</math>) genotypes in the post-vaccine introduction period. Additionally, we observed a decline in prevalence of genotypes G8P [4] (15.8 to 0.4%, <math>P &lt; .001</math>) and G9P [8] (13.2 to 5.4%, <math>P &lt; .001</math>) in the post-vaccine introduction period. Phylogenetic analysis of genotype G1P [8], revealed circulation of strains of lineages G1-I, G1-II and P [8]-1, P [8]-III and P [8]-IV. Considerable genetic diversity was observed between the pre and post-vaccine strains, evidenced by distinct clusters.</p> <p><b>Conclusion:</b> Genotype prevalence varied from before to after vaccine introduction. Such observations emphasize the need for long-term surveillance to monitor vaccine impact. These changes may represent natural secular variation or possible immunological changes arising from the introduction of the vaccine. Full genome sequencing could provide insights into post-vaccine evolutionary pressures and antigenic diversity.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32660437/">https://pubmed.ncbi.nlm.nih.gov/32660437/</a></p>
43.	<p>Munyao V, Karisa J, Munyao CM, Ngari M, Menza N, Peshu N, Rono M, Mbogo C, Mwangangi J. Surveillance of Culicine Mosquitoes in Six Villages of Taita-Taveta County, Kenya, With Host Determinations from Blood-Fed Females. <i>J Med Entomol.</i> 2020 Nov 13;57(6):1972-1982.</p>



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	<p><b>Abstract</b></p> <p>Culicine mosquitoes are vectors of human disease-causing pathogens like filarial worms and several arthropod-borne viruses (arboviruses). Currently, there has been an increase in emerging and re-emerging vector-borne diseases along coastal Kenya, which has been of major concern in public health. This study aimed at determining culicine mosquito species abundance, diversity and their host feeding preferences in Taita-Taveta County, Coastal Kenya. Entomological sampling was done during the long-wet season (March and May) and long dry season (June to October) 2016-2018. Mosquito sampling was done using CDC light traps and Backpack aspiration for indoor and outdoor environments. All culicine mosquitoes collected were identified morphologically and categorized according to their physiological status. Blood fed culicine mosquitoes were tested for bloodmeal sources using ELISA. In total, 3,278 culicine mosquitoes were collected, of which 738 (22.5 %) were found indoors and 2,540, (77.5 %) outdoors. The mosquitoes consisted of 18 species belonging to four genera: Aedes (7), Culex (8), Mansonia (2), and Coquillettidia (1). Overall, there was high mosquito species diversity (H) in outdoors (H = 2.4339) than in indoors (H = 2.2523), whereas even distribution (EH) was higher in indoors (EH = 0.9064) than outdoors (EH = 0.8266). Majorly the bloodmeals identified were from multiple host sources with (51.6%), single hosts (41.3%), and unidentified (7.2%). This study has demonstrated a high diversity of culicine mosquitoes with relaxed feeding tendencies. These mosquitoes are contributing to mosquito biting nuisance and the likelihood of exposure of populations to diseases of public health.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32533693/">https://pubmed.ncbi.nlm.nih.gov/32533693/</a></p>
44.	<p>Wanga V, Mackelprang RD, Thomas KK, Donnell D, Cohen CR, Mugo NR, Bukusi EA, de Bruyn G, Irungu E, Celum C, Baeten JM, Lingappa JR; Partners in Prevention HSV/HIV Transmission Study and the Partners PrEP Study. Brief Report: Bacterial Vaginosis and Risk of HIV Infection in the Context of CD101 Gene Variation. <i>J Acquir Immune Defic Syndr.</i> 2020 Dec 15;85(5):584-587.</p> <p><b>Abstract</b></p> <p>Background: Whether bacterial vaginosis (BV) and CD101 immunoglobulin-like (Ig-like) variants independently increase HIV risk through mucosal inflammation is not well understood. We evaluated whether the impact of BV on HIV acquisition in women differs by the presence or absence of candidate CD101 Ig-like variants.</p> <p>Methods: We used data from 2 studies of HIV serodiscordant couples in east (Kenya, Tanzania, and Uganda) and southern (Botswana, South Africa, and Zambia) Africa, which longitudinally assessed HIV acquisition (by ELISA) and BV (by Nugent score <math>\geq 7</math>). We used previously generated CD101 sequence data for each case and control participant to create a binary variable indicating the presence/absence of any of 5 CD101 Ig-like variants.</p>



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	<p>Results: Confirming previously shown results in this cohort, Ig-like variants increased HIV-infection risk (adjusted hazard ratio [aHR], = 2.63; 95% confidence interval [CI], 1.41 to 4.89). BV was associated with 2.5-fold higher HIV-infection risk only in the absence of Ig-like variants (aHR = 2.47; 95% CI, 0.99 to 6.15; P = 0.052), whereas in the presence of Ig-like variants, BV was not associated with higher HIV-infection risk (aHR = 0.87; 95% CI, 0.35 to 2.15; P = 0.765); however, a test for interaction was nonsignificant (P = 0.116).</p> <p>Conclusions: We hypothesized that both BV and CD101 Ig-like variants facilitate HIV acquisition by augmenting similar genital inflammation pathways. Our findings indicate that inflammatory mucosal effects of Ig-like variants may influence the impact of BV on HIV risk. Host-defined inflammatory pathways may be useful targets for HIV prevention. <b>Pubmed link</b>-<a href="https://pubmed.ncbi.nlm.nih.gov/32976203/">https://pubmed.ncbi.nlm.nih.gov/32976203/</a></p>
45.	<p>Luka MM, Kamau E, Adema I, Munywoki PK, Otieno GP, Gicheru E, Gichuki A, Kibinge N, Agoti CN, Nokes DJ. Molecular Epidemiology of Human Rhinovirus From 1-Year Surveillance Within a School Setting in Rural Coastal Kenya. <i>Open Forum Infect Dis.</i> 2020 Aug 27;7(10): ofaa385.</p> <p><b>Abstract</b></p> <p>Background: Human rhinovirus (HRV) is the most common cause of the common cold but may also lead to more severe respiratory illness in vulnerable populations. The epidemiology and genetic diversity of HRV within a school setting have not been previously described. The objective of this study was to characterize HRV molecular epidemiology in a primary school in a rural location of Kenya.</p> <p>Methods: Between May 2017 and April 2018, over 3 school terms, we collected 1859 nasopharyngeal swabs (NPS) from pupils and teachers with symptoms of acute respiratory infection in a public primary school in Kilifi County, coastal Kenya. The samples were tested for HRV using real-time reverse transcription polymerase chain reaction. HRV-positive samples were sequenced in the VP4/VP2 coding region for species and genotype classification.</p> <p>Results: A total of 307 NPS (16.4%) from 164 individuals were HRV positive, and 253 (82.4%) were successfully sequenced. The proportion of HRV in the lower primary classes was higher (19.8%) than upper primary classes (12.2%; P &lt; .001). HRV-A was the most common species (134/253; 53.0%), followed by HRV-C (73/253; 28.9%) and HRV-B (46/253; 18.2%). Phylogenetic analysis identified 47 HRV genotypes. The most common genotypes were A2 and B70. Numerous (up to 22 in 1 school term) genotypes circulated simultaneously, there was no individual re-infection with the same genotype, and no genotype was detected in all 3 school terms.</p> <p>Conclusions: HRV was frequently detected among school-going children with mild acute respiratory illness symptoms, particularly in the younger age groups (&lt;5-year-olds). Multiple HRV introductions were observed that were characterized by considerable genotype diversity.</p>





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	<p><b>Pubmed link-</b><a href="https://pubmed.ncbi.nlm.nih.gov/33094115/">https://pubmed.ncbi.nlm.nih.gov/33094115/</a></p>
46.	<p>Mwanga MJ, Verani JR, Omore R, Tate JE, Parashar UD, Murunga N, Gicheru E, Breiman RF, Nokes DJ, Agoti CN. Multiple Introductions and Predominance of Rotavirus Group A Genotype G3P[8] in Kilifi, Coastal Kenya, 4 Years after Nationwide Vaccine Introduction. <i>Pathogens</i>. 2020 Nov 24;9(12):981.</p> <p><b>Abstract</b></p> <p>Globally, rotavirus group A (RVA) remains a major cause of severe childhood diarrhea, despite the use of vaccines in more than 100 countries. RVA sequencing for local outbreaks facilitates investigation into strain composition, origins, spread, and vaccine failure. In 2018, we collected 248 stool samples from children aged less than 13 years admitted with diarrheal illness to Kilifi County Hospital, coastal Kenya. Antigen screening detected RVA in 55 samples (22.2%). Of these, VP7 (G) and VP4 (P) segments were successfully sequenced in 48 (87.3%) and phylogenetic analysis based on the VP7 sequences identified seven genetic clusters with six different GP combinations: G3P[8], G1P[8], G2P[4], G2P[8], G9P[8] and G12P[8]. The G3P[8] strains predominated the season (n = 37, 67.2%) and comprised three distinct G3 genetic clusters that fell within Lineage I and IX (the latter also known as equine-like G3 Lineage). Both the two G3 lineages have been recently detected in several countries. Our study is the first to document African children infected with G3 Lineage IX. These data highlight the global nature of RVA transmission and the importance of increasing global rotavirus vaccine coverage.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33255256/">https://pubmed.ncbi.nlm.nih.gov/33255256/</a></p>
47.	<p>Njuguna RG, Berkley JA, Jemutai J. Cost and cost-effectiveness analysis of treatment for child undernutrition in low- and middle-income countries: A systematic review. <i>Wellcome Open Res</i>. 2020 Oct 5; 5:62.</p> <p><b>Abstract</b></p> <p>Background: Undernutrition remains highly prevalent in low- and middle-income countries, with sub-Saharan Africa and Southern Asia accounting for majority of the cases. Apart from the health and human capacity impacts on children affected by malnutrition, there are significant economic impacts to households and service providers. The aim of this study was to determine the current state of knowledge on costs and cost-effectiveness of child undernutrition treatment to households, health providers, organizations and governments in low and middle-income countries (LMICs). Methods: We conducted a systematic review of peer-reviewed studies in LMICs up to September 2019. We searched online databases including PubMed-Medline, Embase, Popline, Econlit and Web of Science. We identified additional articles through bibliographic citation searches. Only articles including costs of child undernutrition treatment were included. Results: We identified a total of 6436 articles, and only 50 met the eligibility criteria. Most included studies adopted institutional/program (45%) and health provider</p>





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	<p>(38%) perspectives. The studies varied in the interventions studied and costing methods used with treatment costs reported ranging between US\$0.44 and US\$1344 per child. The main cost drivers were personnel, therapeutic food and productivity loss. We also assessed the cost effectiveness of community-based management of malnutrition programs (CMAM). Cost per disability adjusted life year (DALY) averted for a CMAM program integrated into existing health services in Malawi was \$42. Overall, cost per DALY averted for CMAM ranged between US\$26 and US\$53, which was much lower than facility-based management (US\$1344). Conclusion: There is a need to assess the burden of direct and indirect costs of child undernutrition to households and communities in order to plan, identify cost-effective solutions and address issues of cost that may limit delivery, uptake and effectiveness. Standardized methods and reporting in economic evaluations would facilitate interpretation and provide a means for comparing costs and cost-effectiveness of interventions.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33102783/">https://pubmed.ncbi.nlm.nih.gov/33102783/</a></p>
48.	<p>Xia S, Cosme LV, Lutomiah J, Sang R, Ngangue MF, Rahola N, Ayala D, Powell JR. Genetic structure of the mosquito <i>Aedes aegypti</i> in local forest and domestic habitats in Gabon and Kenya. <i>Parasit Vectors</i>. 2020 Aug 13;13(1):417.</p> <p><b>Abstract</b></p> <p><b>Background:</b> The mosquito <i>Aedes aegypti</i> is a devastating disease vector transmitting several important human arboviral diseases. In its native range in Africa, the mosquito can be found in both the ancestral forest habitat and anthropogenic habitats such as villages. How do the different habitats impact the population genetic structure of the local mosquito populations?</p> <p><b>Methods:</b> To address this question, we simultaneously sampled <i>Ae. aegypti</i> from the forest and local villages in La Lopé, Gabon and Rabai, Kenya. The mosquitoes were genotyped at 12 microsatellite loci and a panel of ~25,000 single nucleotide polymorphisms (SNPs), which allowed us to estimate their genetic ancestries and the population genetic structure related to habitats and sampling sites.</p> <p><b>Results:</b> In the context of the global population genetic structure of <i>Ae. aegypti</i>, clustering analysis showed that mosquitoes from the same locality (La Lopé or Rabai) have similar genetic ancestry, regardless of their habitats. Further analysis at the local scale also found no strong genetic differentiation between the forest and village mosquitoes in both La Lopé and Rabai. Interestingly, these results from our 2017 samples from Rabai, Kenya contrast to the documentation of genetic differentiation between village and forest mosquito collections from 1975-1976 and 2009. Between-habitat measures of genetic difference (<math>F_{st}</math>) vary across the genome, with a peak of high divergence observed at the third chromosome only in the La Lopé populations.</p> <p><b>Conclusion:</b> Collectively, these results demonstrated that there is little genetic isolation between forest and village habitats, which suggests possible extensive gene flow between them. From an epidemiological perspective, the forest habitat could act as a refuge for</p>



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	<p>mosquitoes against vector control programmes in the domestic settings. Moreover, sylvatic populations could play a role in zoonotic pathogen transferred to humans. Therefore, future studies on disease transmission and vector control planning in the study area should take natural populations into consideration.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32791977/">https://pubmed.ncbi.nlm.nih.gov/32791977/</a></p>
49.	<p>Mageto VM, Mbuthia OW, Ngetsa CJ, Moraa DO, Okoyo EO, Mathenge SG, Njoroge WG. Evaluation of Sociodemographic Factors among Diabetic Patients with Urinary Tract Infections in Kisii Referral Hospital, Kenya. <i>Int J Microbiol.</i> 2020 Jul 7; 2020:5053867.</p> <p><b>Abstract</b></p> <p>People with noninsulin-dependent diabetes mellitus are prone to urinary tract infections. There is a wide gap of information in developing countries regarding the sociodemographic factors linked to UTI among diabetics and the gender disparity among the same. Sociodemographic factors differ with geographical location and many other factors, and this makes them an important aspect that can influence the social burden of UTI among diabetics. The objective of this study was to determine the association between sociodemographic factors and UTI among diabetics. The study was carried out in the Kisii Teaching and Referral Hospital in Kenya. One hundred and eighty diabetic patients were enrolled in cross-sectional study design. Clean-catch midstream urine was collected from all participants and cultured in cysteine lactose electrolyte deficient agar for bacterial isolation. Classification of a positive culture for urinary tract infection was based on more than 100,000 (<math>\geq 10^5</math>) colony-forming units of a single bacterial species. The data were analyzed using frequencies, chi-square (<math>p &lt; 0.05</math>), and logic regression with the help of the Statistical Package for the Social Sciences (SPSS) version 20 to find the odds ratio. One hundred and seven participants were male (59.4%), and 73 (40.6%) were female. The majority of the participants were between the age of 55 and 59 years old (77.2%), and 125 participants (69.4%) had attained tertiary education as the highest level of education. The overall prevalence of urinary tract infections was 20.6% with 37 participants testing positive for urinary tract infection. Age was found to have a significant association with urinary tract infection (<math>p=0.002</math>) while gender (<math>p=0.45</math>) and level of education (<math>p=0.11</math>) showed no significant association with urinary tract infections among diabetic patients. These findings suggest that age was the biggest association factor that influenced urinary tract infections among diabetic patients</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32724308/">https://pubmed.ncbi.nlm.nih.gov/32724308/</a></p>
50.	<p>Muthee TB, Kimathi D, Richards GC, Etyang A, Nunan D, Williams V, Heneghan C. Factors influencing the implementation of cardiovascular risk scoring in primary care: a mixed-method systematic review. <i>Implement Sci.</i> 2020 Jul 20;15(1):57.</p> <p><b>Abstract</b></p>



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	<p>Background: Cardiovascular disease (CVD) such as ischemic heart disease and stroke is the leading causes of death and disability globally with a growing burden in low and middle-income countries. A credible way of managing the incidence and prevalence of cardiovascular diseases is by reducing risk factors. This understanding has led to the development and recommendation for the clinical use of cardiovascular risk stratification tools. These tools enhance clinical decision-making. However, there is a lag in the implementation of these tools in most countries. This systematic review seeks to synthesise the current knowledge of the factors influencing the implementation of cardiovascular risk scoring in primary care settings.</p> <p>Methods: We searched bibliographic databases and grey literature for studies of any design relating to the topic. Titles, abstracts and full texts were independently assessed for eligibility by two reviewers. This was followed by quality assessment and data extraction. We analysed data using an integrated and best fit framework synthesis approach to identify these factors. Quantitative and qualitative forms of data were combined into a single mixed-methods synthesis. The Consolidated Framework for Implementation Research was used as the guiding tool and template for this analysis.</p> <p>Results: Twenty-five studies (cross-sectional n = 12, qualitative n = 9 and mixed-methods n = 4) were included in this review. Twenty (80%) of these were conducted in high-income countries. Only four studies (16%) included patients as participants. This review reports on a total of eleven cardiovascular risk stratification tools. The factors influencing the implementation of cardiovascular risk scoring are related to clinical setting and healthcare system (resources, priorities, practice culture and organisation), users (attributes and interactions between users) and the specific cardiovascular risk tool (characteristics, perceived role and effectiveness).</p> <p>Conclusions: While these findings bolster the understanding of implementation complexity, there exists limited research in the context of low and middle-income countries. Notwithstanding the need to direct resources in bridging this gap, it is also crucial that these efforts are in concert with providing high-quality evidence on the clinical effectiveness of using cardiovascular risk scoring to improve cardiovascular disease outcomes of mortality and morbidity.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32690051/">https://pubmed.ncbi.nlm.nih.gov/32690051/</a></p>
51.	<p>Lambisia AW, Onchaga S, Murunga N, Lewa CS, Nyanjom SG, Agoti CN. Epidemiological Trends of Five Common Diarrhea-Associated Enteric Viruses Pre-and Post-Rotavirus Vaccine Introduction in Coastal Kenya. <i>Pathogens</i>. 2020 Aug 15;9(8):660.</p> <p><b>Abstract</b></p> <p>Using real-time RT-PCR, we screened stool samples from children aged &lt;5 years presenting with diarrhea and admitted to Kilifi County Hospital, coastal Kenya, pre-(2003 and 2013) and post-rotavirus vaccine introduction (2016 and 2019) for five viruses, namely rotavirus group A (RVA), norovirus GII, adenovirus, astrovirus and sapovirus. Of the 984 samples analyzed, at least one virus was detected in 401 (40.8%) patients. Post</p>



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	<p>rotavirus vaccine introduction, the prevalence of RVA decreased (23.3% vs. 13.8%, <math>p &lt; 0.001</math>) while that of norovirus GII increased (6.6% vs. 10.9%, <math>p = 0.023</math>). The prevalence of adenovirus, astrovirus and sapovirus remained statistically unchanged between the two periods: 9.9% vs. 14.2%, 2.4% vs. 3.2%, 4.6% vs. 2.6%, (<math>p = 0.053, 0.585</math> and <math>0.133</math>), respectively. The median age of diarrhea cases was higher post vaccine introduction (12.5 months, interquartile range (IQR): 7.9-21 vs. 11.2 months pre-introduction, IQR: 6.8-16.5, <math>p &lt; 0.001</math>). In this setting, RVA and adenovirus cases peaked in the dry months while norovirus GII and sapovirus peaked in the rainy season. Astrovirus did not display clear seasonality. In conclusion, following rotavirus vaccine introduction, we found a significant reduction in the prevalence of RVA in coastal Kenya but an increase in norovirus GII prevalence in hospitalized children.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32824245/">https://pubmed.ncbi.nlm.nih.gov/32824245/</a></p>
52.	<p>Namayi I, Makokha A, Echoka E. Health providers' knowledge on maternal and newborn care: implications on health systems strengthening in Vihiga County, Kenya. <i>Pan Afr Med J.</i> 2020 Sep 18; 37:73.</p> <p><b>Abstract</b></p> <p>Introduction: pregnant women need access to skilled attendance at birth and emergency obstetric care (EmOC) to avert maternal deaths. While poor EmOC services may explain the high maternal mortality, inadequate knowledge of providers is also part of the problem. This forms the basis of this paper, in a setting where 50.2% of women deliver in a health facility but maternal mortality remains high at 531/100,000 live births, compared to the national average of 362/100,000 in Kenya.</p> <p>Methods: a facility based cross-sectional survey was conducted in 2018 with a set of knowledge questions extracted from the averting maternal death and disability toolkit. Providers knowledge for maternal and newborn health (MNH) was assessed by interviewing nurses on duty in the maternity units. Data were entered in Ms Access and exported to R version 3.6.2 for descriptive and logistic regression analysis. Ethical clearance was obtained from Kenya Medical Research Unit.</p> <p>Results: a total of 55 nurses were interviewed. Majority (71%) of the respondents were diploma nurses. The overall knowledge score for MNH among the providers was adequate with a score of (64%). Generally, the midwives and higher diploma nurses consistently scored higher than diploma nurses in all the topic areas of MNH. In the mixed linear regression, determinants of knowledge score were seen in provider-level variables.</p> <p>Conclusion: overall, the providers scores were higher on intrapartum and newborn care compared to scores on care for complications. We conclude that in-service training on EmOC to providers is critical to reduction of maternal mortality.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33244336/">https://pubmed.ncbi.nlm.nih.gov/33244336/</a></p>



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53.	<p>Ssewanyana D, Newton CR, van Baar A, Hassan AS, Stein A, Taylor HG, Van De Vijver F, Scerif G, Abubakar A. Beyond Their HIV Status: The Occurrence of Multiple Health Risk Behavior Among Adolescents from a Rural Setting of Sub-Saharan Africa. <i>Int J Behav Med.</i> 2020 Aug;27(4):426-443.</p> <p><b>Abstract</b></p> <p>Background: Health risk behaviors during adolescence may cluster into patterns that might be predicted by specific factors, among which HIV may have an important role. Method: In a cross-sectional study conducted between 2017 and 2018, clustering of HRB and its associated factors was investigated in rural Kenya among 588 adolescents (36% perinatally HIV infected; 28% perinatally HIV exposed but uninfected; and 36% HIV unexposed/uninfected). Latent class analysis of 22 behaviors followed by multinomial logistic regression were conducted. Four risk behavior classes were identified. Results: No significant differences were found in behavioral class membership across the three HIV groups (<math>p = 0.366</math>). The risk of membership to the higher risk behavioral classes relative to class 1 (the substance and drug abstinent low risk takers) increased with older adolescent age (<math>p = 0.047</math>), increased among adolescent who experienced mental distress (<math>p &lt; 0.001</math>), and those who felt unsafe in their neighborhood (<math>p &lt; 0.002</math>). Better working memory (<math>p = 0.0037</math>) was found to be protective. Conclusion: The results highlight a need to include screening and interventions for internalizing mental health problems and deficits in executive functioning, as well as steps to involve family members and communities to address psychosocial risk factors in adolescents in Kenya.</p> <p><b>Pubmed link</b>-<a href="https://pubmed.ncbi.nlm.nih.gov/32215858/">https://pubmed.ncbi.nlm.nih.gov/32215858/</a></p>
54.	<p>Amboko B, Stepniewska K, Macharia PM, Machini B, Bejon P, Snow RW, Zurovac D. Trends in health workers' compliance with outpatient malaria case-management guidelines across malaria epidemiological zones in Kenya, 2010-2016. <i>Malar J.</i> 2020 Nov 11;19(1):406.</p> <p><b>Abstract</b></p> <p>Background: Health workers' compliance with outpatient malaria case-management guidelines has been improving, specifically regarding the universal testing of suspected cases and the use of artemisinin-based combination therapy (ACT) only for positive results (i.e., 'test and treat'). Whether the improvements in compliance with 'test and treat' guidelines are consistent across different malaria endemicity areas has not been examined. Methods: Data from 11 national, cross-sectional, outpatient malaria case-management surveys undertaken in Kenya from 2010 to 2016 were analysed. Four primary indicators (i.e., 'test and treat') and eight secondary indicators of artemether-lumefantrine (AL) dosing, dispensing, and counselling were measured. Mixed logistic regression models were used to analyse the annual trends in compliance with the indicators across the</p>



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	<p>different malaria endemicity areas (i.e., from highest to lowest risk being lake endemic, coast endemic, highland epidemic, semi-arid seasonal transmission, and low risk). Results: Compliance with all four 'test and treat' indicators significantly increased in the area with the highest malaria risk (i.e., lake endemic) as follows: testing of febrile patients (OR = 1.71 annually; 95% CI = 1.51-1.93), AL treatment for test-positive patients (OR = 1.56; 95% CI = 1.26-1.92), no anti-malarial for test-negative patients (OR = 2.04; 95% CI = 1.65-2.54), and composite 'test and treat' compliance (OR = 1.80; 95% CI = 1.61-2.01). In the low risk areas, only compliance with test-negative results significantly increased (OR = 2.27; 95% CI = 1.61-3.19) while testing of febrile patients showed declining trends (OR = 0.89; 95% CI = 0.79-1.01). Administration of the first AL dose at the facility significantly increased in the areas of lake endemic (OR = 2.33; 95% CI = 1.76-3.10), coast endemic (OR = 5.02; 95% CI = 2.77-9.09) and semi-arid seasonal transmission (OR = 1.44; 95% CI = 1.02-2.04). In areas of the lowest risk of transmission and highland epidemic zone, none of the AL dosing, dispensing, and counselling tasks significantly changed over time.</p> <p>Conclusions: There is variability in health workers' compliance with outpatient malaria case-management guidelines across different malaria-risk areas in Kenya. Major improvements in areas of the highest risk have not been seen in low-risk areas. Interventions to improve practices should be targeted geographically.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33176783/">https://pubmed.ncbi.nlm.nih.gov/33176783/</a></p>
55.	<p>Machini B, Zurovac D, Amboko B, Malla L, Snow RW, Kipruto H, Achia TNO. Predictors of health workers' knowledge about artesunate-based severe malaria treatment recommendations in government and faith-based hospitals in Kenya. <i>Malar J.</i> 2020 Jul 23;19(1):267.</p> <p><b>Abstract</b></p> <p>Background: Health workers' knowledge deficiencies about artesunate-based severe malaria treatment recommendations have been reported. However, predictors of the treatment knowledge have not been examined. In this paper, predictors of artesunate-based treatment knowledge among inpatient health workers in two hospital sectors in Kenya are reported. Methods: Secondary analysis of 367 and 330 inpatient health workers randomly selected and interviewed at 47 government hospitals in 2016 and 43 faith-based hospitals in 2017 respectively, was undertaken. Multilevel ordinal and binary logistic regressions examining the effects of 11 factors on five knowledge outcomes in government and faith-based hospital sectors were performed.</p> <p>Results: Among respective government and faith-based health workers, about a third of health workers had high knowledge of artesunate treatment policies (30.8% vs 32.9%), a third knew all dosing intervals (33.5% vs 33.3%), about half knew preparation solutions (49.9% vs 55.8%), half to two-thirds knew artesunate dose for both weight categories (50.8% vs 66.7%) and over three-quarters knew the preferred route of administration (78.7% vs 82.4%). Eight predictors were significantly associated with at least one of the examined knowledge outcomes. In the government sector, display of artesunate</p>





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	<p>administration posters, paediatric ward allocation and repeated surveys were significantly associated with more than one of the knowledge outcomes. In the faith-based hospitals, availability of artesunate at hospitals and health worker pre-service training were associated with multiple outcomes. Exposure to in-service malaria case-management training and access to malaria guidelines were only associated with higher knowledge about artesunate treatment policy.</p> <p>Conclusion: Programmatic interventions ensuring display of artesunate administration posters in the wards, targeting of health workers managing adult patients in the medical wards, and repeated knowledge assessments are likely to be beneficial for improving the knowledge of government health workers about artesunate-based severe malaria treatment recommendations. The availability of artesunate and focus on improvements of nurses' knowledge should be prioritized at the faith-based hospitals.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32703215">https://pubmed.ncbi.nlm.nih.gov/32703215</a></p>
56.	<p>Murunga N, P Otieno G, Maia M, N Agoti C. Effectiveness of Rotarix <sup>®</sup> vaccine in Africa in the first decade of progressive introduction, 2009-2019: systematic review and meta-analysis. Wellcome Open Res. 2020 Sep 24; 5:187.</p> <p><b>Abstract</b></p> <p>Background: Randomized controlled trials of licensed oral rotavirus group A (RVA) vaccines, indicated lower efficacy in developing countries compared to developed countries. We investigated the pooled effectiveness of Rotarix <sup>®</sup> in Africa in 2019, a decade since progressive introduction began in 2009. Methods: A systematic search was conducted in PubMed to identify studies that investigated the effectiveness of routine RVA vaccination in an African country between 2009 and 2019. A meta-analysis was undertaken to estimate pooled effectiveness of the full-dose versus partial-dose of Rotarix <sup>®</sup> (RV1) vaccine and in different age groups. Pooled odds ratios were estimated using random effects model and the risk of bias assessed using Newcastle-Ottawa scale. The quality of the evidence was assessed using GRADE. Results: By December 2019, 39 (72%) countries in Africa had introduced RVA vaccination, of which 34 were using RV1. Thirteen eligible studies from eight countries were included in meta-analysis for vaccine effectiveness (VE) of RVA by vaccine dosage (full or partial) and age categories. Pooled RV1 VE against RVA associated hospitalizations was 44% (95% confidence interval (CI) 28-57%) for partial dose versus 58% (95% CI 50-65%) for full dose. VE was 61% (95% CI 50-69%), 55% (95% CI 32-71%), 56% (95% CI 43-67%), and 61% (95% CI 42-73%) for children aged &lt;12 months, 12-23 months, &lt;24 months and 12-59 months, respectively. Conclusion: RV1 vaccine use has resulted in a significant reduction in severe diarrhoea in African children and its VE is close to the efficacy findings observed in clinical trials. RV1 VE point estimate was higher for children who received full dose than those who received partial dose, and its protection lasted beyond the first year of life.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33215049/">https://pubmed.ncbi.nlm.nih.gov/33215049/</a></p>



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57.	<p>Sassa M, Chadeka EA, Cheruiyot NB, Tanaka M, Moriyasu T, Kaneko S, Njenga SM, Cox SE, Hamano S. Prevalence and risk factors of <i>Schistosoma mansoni</i> infection among children under two years of age in Mbita, Western Kenya. <i>PloS Negl Trop Dis</i>. 2020 Aug 25;14(8): e0008473.</p> <p><b>Abstract</b></p> <p>Despite growing evidence that infants and very young children can be infected with schistosomes, the epidemiological features and risk factors are not well described in this age group. We aimed to assess the prevalence of <i>S. mansoni</i> infection in children under two years of age from a population with a known high burden of infection in school-aged children and adults and thus inform the need for interventions in this potentially vulnerable age group. In a cross-sectional study in Mbita Sub-county, along the east coast of Lake Victoria, Western Kenya, we enrolled 361 children aged 6-23 months. The prevalence of <i>S. mansoni</i> infection was detected using the Kato-Katz stool examination and a point-of-care test for urinary circulating cathodic antigen (POC-CCA) (Rapid Medical Diagnostics, Pretoria, South Africa). Three-hundred and five (305) children had complete data of whom 276 (90.5%, 95%CI: 86.6-93.5) children were positive for <i>S. mansoni</i> by the POC-CCA test, while 11 (3.6%, 95%CI: 1.8-6.4) were positive by the Kato-Katz method. All Kato-Katz positive cases were also positive by the POC-CCA test. In multivariable analysis, only geographical area, Rusinga West (AOR = 7.1, 95%CI: 1.4-35.2, P = 0.02), was associated with <i>S. mansoni</i> infection using Kato-Katz test. Independent associations for POC-CCA positivity included age, (12-17 months vs 6-11 months; AOR = 7.8, 95%CI: 1.8-32.6, P = 0.002) and breastfeeding in the previous 24 hours (AOR = 3.4, 95%CI: 1.3-9.0, P = 0.009). We found a potentially very high prevalence of <i>S. mansoni</i> infection among children under two years of age based on POC-CCA test results in Mbita Sub-county, Kenya, which if confirmed strongly supports the need to include infants in public health strategies providing universal prophylactic treatment in high burden settings. Further research is required to determine the accuracy of diagnostic tools to detect light infection among very young children and possible long-term health impacts.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32841228/">https://pubmed.ncbi.nlm.nih.gov/32841228/</a></p>
58.	<p>Tuti T, Winters N, Edgcombe H, Muinga N, Wanyama C, English M, Paton C. Evaluation of Adaptive Feedback in a Smartphone-Based Game on Health Care Providers' Learning Gain: Randomized Controlled Trial. <i>J Med Internet Res</i>. 2020 Jul 6;22(7): e17100.</p> <p><b>Abstract</b></p> <p>Background: Although smartphone-based emergency care training is more affordable than traditional avenues of training, it is still in its infancy, remains poorly implemented, and its current implementation modes tend to be invariant to the evolving learning needs of the intended users. In resource-limited settings, the use of such platforms coupled with gamified approaches remains largely unexplored, despite the lack of traditional training opportunities, and high mortality rates in these settings.</p>



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	<p><b>Objective:</b> The primary aim of this randomized experiment is to determine the effectiveness of offering adaptive versus standard feedback, on the learning gains of clinicians, through the use of a smartphone-based game that assessed their management of a simulated medical emergency. A secondary aim is to examine the effects of learner characteristics and learning spacing with repeated use of the game on the secondary outcome of individualized normalized learning gain.</p> <p><b>Methods:</b> The experiment is aimed at clinicians who provide bedside neonatal care in low-income settings. Data were captured through an Android app installed on the study participants' personal phones. The intervention, which was based on successful attempts at a learning task, included adaptive feedback provided within the app to the experimental arm, whereas the control arm received standardized feedback. The primary end point was completion of the second learning session. Of the 572 participants enrolled between February 2019 and July 2019, 247 (43.2%) reached the primary end point. The primary outcome was standardized relative change in learning gains between the study arms as measured by the Morris G effect size. The secondary outcomes were the participants individualized normalized learning gains.</p> <p><b>Results:</b> The effect of adaptive feedback on care providers' learning gain was found to be <math>g=0.09</math> (95% CI -0.31 to 0.46; <math>P=.47</math>). In exploratory analysis, using normalized learning gains, when subject-treatment interaction and differential time effect was controlled for, this effect increased significantly to 0.644 (95% CI 0.35 to 0.94; <math>P&lt;.001</math>) with immediate repetition, which is a moderate learning effect, but reduced significantly by 0.28 after a week. The overall learning change from the app use in both arms was large and may have obscured a direct effect of feedback.</p> <p><b>Conclusions:</b> There is a considerable learning gain between the first two rounds of learning with both forms of feedback and a small added benefit of adaptive feedback after controlling for learner differences. We suggest that linking the adaptive feedback provided to care providers to how they space their repeat learning session(s) may yield higher learning gains. Future work might explore in more depth the feedback content, in particular whether or not explanatory feedback (why answers were wrong) enhances learning more than reflective feedback (information about what the right answers are).</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32628115/">https://pubmed.ncbi.nlm.nih.gov/32628115/</a></p>
59.	<p>Munywoki J, Kagwanja N, Chuma J, Nzinga J, Barasa E, Tsofa B. Tracking health sector priority setting processes and outcomes for human resources for health, five-years after political devolution: a county-level case study in Kenya. <i>Int J Equity Health</i>. 2020 Sep 21;19(1):165.</p> <p><b>Abstract</b></p> <p>Background: Health sector priority setting in Low and Middle-Income Countries (LMICs) entails balancing between a high demand and low supply of scarce resources. Human Resources for Health (HRH) consume the largest allocation of health sector resources in LMICs. Health sector decentralization continues to be promoted for its perceived ability to improve efficiency, relevance and participation in health sector priority setting.</p>



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	<p>Following the 2013 devolution in Kenya, both health service delivery and human resource management were decentralized to county level. Little is known about priority setting practices and outcomes of HRH within decentralized health systems in LMICs. Our study sought to examine if and how the Kenyan devolution has improved health sector priority setting practices and outcomes for HRH.</p> <p><b>Methods:</b> We used a mixed methods case study design to examine health sector priority setting practices and outcomes at county level in Kenya. We used three sources of data. First, we reviewed all relevant national and county level policy and guidelines documents relating to HRH management. We then accessed and reviewed county records of HRH recruitment and distribution between 2013 and 2018. We finally conducted eight key informant interviews with various stakeholder involved in HRH priority setting within our study county.</p> <p><b>Results:</b> We found that HRH numbers in the county increased by almost two-fold since devolution. The county had two forms of HRH recruitment: one led by the County Public Services Board as outlined by policy and guidelines and a parallel, politically-driven recruitment done directly by the County Department of Health. Though there were clear guidelines on HRH recruitment, there were no similar guidelines on allocation and distribution of HRH. Since devolution, the county has preferentially staffed higher level hospitals over primary care facilities. Additionally, there has been local county level innovations to address some HRH management challenges, including recruiting doctors and other highly specialized staff on fixed term contract as opposed to permanent basis; and implementation of local incentives to attract and retain HRH to remote areas within the county.</p> <p><b>Conclusion:</b> Devolution has significantly increased county level decision-space for HRH priority setting in Kenya. However, HRH management and accountability challenges still exist at the county level. There is need for interventions to strengthen county level HRH management capacity and accountability mechanisms beyond additional resources allocation. This will boost the realization of the country's efforts for promoting service delivery equity as a key goal - both for the devolution and the country's quest towards Universal Health Coverage (UHC).</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32958000/">https://pubmed.ncbi.nlm.nih.gov/32958000/</a></p>
60.	<p>Nyiro JU, Bukusi E, Mwaengo D, Walumbe D, Nyaguara A, Nyawanda B, Otieno N, Berkley JA, Munywoki P, Nokes DJ. Implications of gestational age at antenatal care attendance on the successful implementation of a maternal respiratory syncytial virus (RSV) vaccine program in coastal Kenya. <i>BMC Public Health</i>. 2020 Nov 16;20(1):1723.</p> <p><b>Abstract</b></p> <p>Background: Maternal immunisation to boost respiratory syncytial virus (RSV) specific antibodies in pregnant women is a strategy to enhance infant protection. The timing of maternal vaccination during pregnancy may be critical for its effectiveness. However,</p>



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	<p>Kenya has no documented published data on gestational age distribution of pregnant women attending antenatal care (ANC), or the proportion of women attending ANC during the proposed window period for vaccination, to inform appropriate timing for delivery or estimate potential uptake of this vaccine.</p> <p><b>Methods:</b> A cross-sectional survey was conducted within the Kilifi Health and Demographic Surveillance System (KHDSS), coastal Kenya. A simple random sample of 1000 women who had registered pregnant in 2017 to 2018 and with a birth outcome by the time of data collection was taken. The selected women were followed at their homes, and individually written informed consent was obtained. Records of their antenatal attendance during pregnancy were abstracted from their ANC booklet. The proportion of all pregnant women from KHDSS (55%) who attended for one or more ANC in 2018 was used to estimate vaccine coverage.</p> <p><b>Results:</b> Of the 1000 women selected, 935 were traced with 607/935 (64.9%) available for interview, among whom 470/607 (77.4%) had antenatal care booklets. The median maternal age during pregnancy was 28.6 years. The median (interquartile range) gestational age in weeks at the first to fifth ANC attendance was 26 (21-28), 29 (26-32), 32 (28-34), 34 (32-36) and 36 (34-38), respectively. The proportion of women attending for ANC during a gestational age window for vaccination of 28-32 weeks (recommended), 26-33 weeks and 24-36 weeks was 76.6% (360/470), 84.5% (397/470) and 96.2% (452/470), respectively. Estimated vaccine coverage was 42.1, 46.5 and 52.9% within the narrow, wide and wider gestational age windows, respectively.</p> <p><b>Conclusions:</b> In a random sample of pregnant women from Kilifi HDSS, Coastal Kenya with card- confirmed ANC clinic attendance, 76.6% would be reached for maternal RSV vaccination within the gestational age window of 28-32 weeks. Widening the vaccination window (26-33 weeks) or (24-36 weeks) would not dramatically increase vaccine coverage and would require consideration of antibody kinetics data that could affect vaccine efficacy.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33198696/">https://pubmed.ncbi.nlm.nih.gov/33198696/</a></p>
61.	<p>Hitachi M, Wanjihia V, Nyandieka L, Francesca C, Wekesa N, Changoma J, Muniu E, Ndemwa P, Honda S, Hirayama K, Karama M, Kaneko S. Improvement of Dietary Diversity and Attitude Toward Recommended Feeding through Novel Community Based Nutritional Education Program in Coastal Kenya-An Intervention Study. <i>Int J Environ Res Public Health</i>. 2020 Oct 5;17(19):7269.</p> <p><b>Abstract</b></p> <p>Community-based nutritional intervention to improve the practice of dietary diversity and child nutrition by community health workers (CHWs) involving Nyumba Kumi as small neighborhood units (SNUs) in communities has not yet been explored. This study was conducted in two villages in rural Kenya between 2018 and 2019. In total, 662 participants (control vs. intervention: n = 339 vs. n = 323) were recruited. The intervention group received education on maternal and child nutrition and follow-up</p>





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	<p>consultations. The custom-tailored educational guidelines were made based on Infant and Young Child Feeding and the mother and child health booklet. The educational effects on household caregivers' feeding practice attitude and child nutritional status were analyzed using multiple linear regression. After the intervention, a total of 368 household caregivers (187 vs. 181) and 180 children (113 vs. 67) were analyzed separately. Between the groups, no significant difference was found in their background characteristics. This study successfully improved the dietary diversity score (<math>\beta = 0.54</math>; <math>p &lt; 0.01</math>) and attitude score (<math>\beta = 0.29</math>; <math>p &lt; 0.01</math>). The results revealed that the interventions using CHWs and SNU were useful to improve dietary diversity and caregivers' attitudes toward recommended feeding. This research has the potential to be successfully applied in other regions where child undernutrition remains.</p> <p><b>Pubmed link</b>-<a href="https://pubmed.ncbi.nlm.nih.gov/33027966/">https://pubmed.ncbi.nlm.nih.gov/33027966/</a></p>
62.	<p>Ogero M, Akech S, Malla L, Agweyu A, Irimu G, English M; Clinical Information Network Author Group. Examining which clinicians provide admission hospital care in a high mortality setting and their adherence to guidelines: an observational study in 13 hospitals. <i>Arch Dis Child</i>. 2020 Jul;105(7):648-654.</p> <p><b>Abstract</b></p> <p><b>Background:</b> We explored who actually provides most admission care in hospitals offering supervised experiential training to graduating clinicians in a high mortality setting where practices deviate from guideline recommendations.</p> <p><b>Methods:</b> We used a large observational data set from 13 Kenyan county hospitals from November 2015 through November 2018 where patients were linked to admitting clinicians. We explored guideline adherence after creating a cumulative correctness of Paediatric Admission Quality of Care (cPAQC) score on a 5-point scale (0-4) in which points represent correct, sequential progress in providing care perfectly adherent to guidelines comprising admission assessment, diagnosis and treatment. At the point where guideline adherence declined the most we dichotomised the cPAQC score and used multilevel logistic regression models to explore whether clinician and patient-level factors influence adherence.</p> <p><b>Results:</b> There were 1489 clinicians who could be linked to 53 003 patients over a period of 3 years. Patients were rarely admitted by fully qualified clinicians and predominantly by preregistration medical officer interns (MOI, 46%) and diploma level clinical officer interns (COI, 41%) with a median of 28 MOI (range 11-68) and 52 COI (range 5-160) offering care per study hospital. The cPAQC scores suggest that perfect guideline adherence is found in <math>\leq 12\%</math> of children with malaria, pneumonia or diarrhoea with dehydration. MOIs were more adherent to guidelines than COI (adjusted OR 1.19 (95% CI 1.07 to 1.34)) but multimorbidity was significantly associated with lower guideline adherence.</p>





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	<p>Conclusion: Over 85% of admissions to hospitals in high mortality settings that offer experiential training in Kenya are conducted by preregistration clinicians. Clinical assessment is good but classifying severity of illness in accordance with guideline recommendations is a challenge. Adherence by MOI with 6 years' training is better than COI with 3 years' training, performance does not seem to improve during their 3 months of paediatric rotations.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32169853/">https://pubmed.ncbi.nlm.nih.gov/32169853/</a></p>
63.	<p>Njomo DW, Kimani BW, Kibe LW, Okoyo C, Omondi WP, Sultani HM. Implementation challenges and opportunities for improved mass treatment uptake for lymphatic filariasis elimination: Perceptions and experiences of community drug distributors of coastal Kenya. <i>PLoS Negl Trop Dis.</i> 2020 Dec 28;14(12): e0009012.</p> <p><b>Abstract</b></p> <p>Community drug distributors (CDDs) who are volunteers have the responsibility of awareness creation, household census, drug distribution and record-keeping and are thus key stakeholders in the campaign for Lymphatic Filariasis (LF) elimination. Taking into account their experiences and perceptions is important for a successful elimination campaign. We conducted a qualitative study in 2018 to identify implementation challenges and opportunities for improved mass drug administration (MDA) uptake based on the CDDs perceptions and experiences. Within a larger study that used mixed methods quasi-experimental design, we collected qualitative data from two wards in Kaloleni Sub-County of Kilifi County which was purposively selected owing to its low, 56% and 50.5% treatment coverage in 2015 and 2016 respectively. Focus group discussions (FGDs) (n = 8) and in-depth interviews (IDIs) (n = 8) with CDDs, IDIs (n = 22) with opinion leaders and IDIs (n = 8) with health workers were conducted and the data analyzed by QSR NVIVO version 10 according to thematic areas. The results showed that based on the perceptions and experiences of the CDDs, several challenges: communities' refusal to take the drugs; absenteeism during MDA; non-adherence to CDDs selection criteria; inadequacy in number of CDDs engaged during the campaign and training provided; insufficiency of drugs issued to CDDs; lack of CDDs supervision and low motivation negatively impact on MDA uptake. Opportunities to address the challenges included: awareness creation on MDA, health education on LF and observation of hygiene during drug administration, increased duration of awareness creation and drug administration, adherence to CDDs selection criteria and putting into consideration the vastness of an area and population density while deploying CDDs. Other opportunities include: improved CDDs training and scheduling; issuing of enough drugs to CDDs to meet the communities' demand and improved supervision and motivation of CDDs. Addressing the challenges highlighted is an important step of maximizing MDA uptake. The opportunities presented need to be considered by the NTD program personnel, the county health personnel and the community while planning the implementation of MDA campaigns.</p>



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	<b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33370300/">https://pubmed.ncbi.nlm.nih.gov/33370300/</a>
64.	<p>Njomo DW, Kibe LW, Kimani BW, Okoyo C, Omondi WP, Sultani HM. Addressing barriers of community participation and access to mass drug administration for lymphatic filariasis elimination in Coastal Kenya using a participatory approach. <i>PLoS Negl Trop Dis.</i> 2020 Sep 16;14(9): e0008499.</p> <p><b>Abstract</b></p> <p>Since the prioritization of Lymphatic Filariasis (LF) elimination in 1997, progress has been made in reducing disease transmission and burden. Validation of elimination through Transmission Assessment Surveys (TAS) in implementation units (IUs) that have received at least 5 rounds of mass drug administration (MDA) and achieved minimum threshold of 65% treatment coverage is required. There are IUs that do not qualify for TAS due to achievement of low treatment coverage. This study sought to identify barriers of community participation and access to MDA, develop and test strategies to be recommended for improved uptake. Two wards in Kaloleni sub-county, Kilifi county with an average treatment coverage of 56% in 2015, 50.5% in 2016 were purposively sampled and a quasi-experimental study conducted. Through systematic random sampling, 350 (pre-intervention) and 338 (post-intervention) household heads were selected and interviewed for quantitative data. For qualitative data, 16 Focus Group Discussions (FGDs) with purposively selected community groups were conducted. Participatory meetings were held with county stakeholders to agree on strategies for improved community participation in MDA. The quantitative data were analyzed using STATA version 14.1, statistical significance assessed by chi square test and qualitative data by QSR NVIVO version 10. The identified strategies were tested in experimental sites during the 2018 MDA and the usual MDA strategies applied in control sites. The results showed an increase in community participation and access to MDA in both sites 80.6% (pre-intervention), 82.9% (post-intervention). The proportion of participants who considered the treatment as necessary significantly (<math>p = 0.001</math>) increased to 96.2% from 88.3% and significantly dropped for those with drug swallowing problems associated with: size (<math>p &lt; 0.001</math>), number (<math>p &lt; 0.027</math>) and taste (<math>p = 0.001</math>). The implemented strategies may have contributed to increased participation and access to MDA and should be applied for improved treatment uptake.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32936792/">https://pubmed.ncbi.nlm.nih.gov/32936792/</a></p>



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65.	<p>Abudho BO, Guyah B, Ondigo BN, Ndombi EM, Ileri E, Carter JM, Riner DK, Kittur N, Karanja DMS, Colley DG. Evaluation of morbidity in Schistosoma mansoni-positive primary and secondary school children after four years of mass drug administration of praziquantel in western Kenya. <i>Infect Dis Poverty</i>. 2020 Jun 15;9(1):67.</p> <p><b>Abstract</b></p> <p><b>Background:</b> World Health Organization guidelines recommend preventive chemotherapy with praziquantel to control morbidity due to schistosomiasis. The primary aim of this cross-sectional study was to determine if 4 years of annual mass drug administration (MDA) in primary and secondary schools lowered potential markers of morbidity in infected children 1 year after the final MDA compared to infected children prior to initial MDA intervention.</p> <p><b>Methods:</b> Between 2012 and 2016 all students in two primary and three secondary schools within three kilometers of Lake Victoria in western Kenya received annual mass praziquantel administration. To evaluate potential changes in morbidity we measured height, weight, mid-upper arm circumference, hemoglobin levels, abdominal ultrasound, and quality of life in children in these schools. This study compared two cross-sectional samples of Schistosoma mansoni egg-positive children: one at baseline and one at year five, 1 year after the fourth annual MDA. Data were analyzed for all ages (6-18 years old) and stratified by primary (6-12 years old) and secondary (12-18 years old) school groups.</p> <p><b>Results:</b> The prevalence of multiple potential morbidity markers did not differ significantly between the egg-positive participants at baseline and those at 5 years by Mann Whitney nonparametric analysis and Fisher's exact test for continuous and categorical data, respectively. There was a small but significantly higher score in school-related quality of life assessment by year five compared to baseline by Mann Whitney analysis (<math>P = 0.048</math>) in 13-18 year olds where malaria-negative. However, anemia was not positively impacted by four annual rounds of MDA, but registered a significant negative outcome.</p> <p><b>Conclusions:</b> We did not detect differences in morbidity markers measured in a population of those infected or re-infected after multiple MDA. This could have been due to their relative insensitivity or a failure of MDA to prevent morbidity among those who remain infected. High malaria transmission in this area and/or a lack of suitable methods to measure the more subtle functional morbidities caused by schistosomiasis could be a factor. Further research is needed to identify and develop well-defined, easily quantifiable S. mansoni morbidity markers for this age group.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/32539826/">https://pubmed.ncbi.nlm.nih.gov/32539826/</a></p>
66.	<p>Wahome EW, Graham SM, Thiong'o AN, Mohamed K, Oduor T, Gichuru E, Mwambi J, van der Elst EM, Sanders EJ. Risk factors for loss to follow-up among at-risk HIV negative men who have sex with men participating in a research cohort with access to pre-exposure prophylaxis in coastal Kenya. <i>J Int AIDS Soc</i>. 2020 Oct;23 Suppl 6(Suppl 6): e25593.</p>



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	<p><b>Abstract</b></p> <p>Introduction: Retention in preventive care among at-risk men who have sex with men (MSM) is critical for successful prevention of HIV acquisition in Africa. We assessed loss to follow-up (LTFU) rates and factors associated with LTFU in an HIV vaccine feasibility cohort study following MSM with access to pre-exposure prophylaxis (PrEP) in coastal Kenya. Methods: Between June 2017 and June 2019, MSM cohort participants attending a research clinic 20 km north of Mombasa were offered daily PrEP and followed monthly for risk assessment, risk reduction counselling and HIV testing. Participants were defined as LTFU if they were late by &gt;90 days for their scheduled appointment. Participants who acquired HIV were censored at diagnosis. Cox proportional hazards models were used to estimate adjusted Hazard Ratio (aHR) of risk factors for LTFU.</p> <p>Results and discussion: A total of 179 participants with a median age of 25.0 years (interquartile range [IQR]: 23.0 to 30.0) contributed a median follow-up time of 21.2 months (IQR: 6.5 to 22.1). Of these, 143 (79.9%) participants started PrEP and 76 (42.5%) MSM were LTFU, for an incidence rate of 33.7 (95% confidence interval [CI], 26.9 to 42.2) per 100 person-years. Disordered alcohol use (aHR: 2.3, 95% CI, 1.5 to 3.7), residence outside the immediate clinic catchment area (aHR: 2.5, 95% CI, 1.3 to 4.6 for Mombasa Island; aHR: 1.8, 95% CI, 1.0 to 3.3 for south coast), tertiary education level or higher (aHR: 2.3, 95% CI, 1.1 to 4.8) and less lead-in time in the cohort prior to 19 June 2017 (aHR: 3.1, 95% CI, 1.8 to 5.6 for zero to three months; aHR: 2.4, 95% CI, 1.2 to 4.7 for four to six months) were independent predictors of LTFU. PrEP use did not differ by LTFU status (HR: 1.0, 95% CI, 0.6 to 1.5). Psychosocial support for men reporting disordered alcohol use, strengthened engagement of recently enrolled participants and focusing recruitment on areas close to the research clinic may improve retention in HIV prevention studies involving MSM in coastal Kenya.</p> <p>Conclusions: About one in three participants became LTFU after one year of follow-up, irrespective of PrEP use. Research preparedness involving MSM should be strengthened for HIV prevention intervention evaluations in coastal Kenya.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33000889/">https://pubmed.ncbi.nlm.nih.gov/33000889/</a></p>
67.	<p>Abdullahi L, Onyango JJ, Mukiira C, Wamicwe J, Githiomi R, Kariuki D, Mugambi C, Wanjohi P, Githuka G, Nzioka C, Orwa J, Oronje R, Kariuki J, Mayieka L. Community interventions in Low-And Middle-Income Countries to inform COVID-19 control implementation decisions in Kenya: A rapid systematic review. PLoS One. 2020 Dec 8;15(12): e0242403.</p> <p><b>Abstract</b></p> <p>Globally, public health measures like face masks, hand hygiene and maintaining social distancing have been implemented to delay and reduce local transmission of COVID-19. To date there is emerging evidence to provide effectiveness and compliance to intervention measures on COVID-19 due to rapid spread of the disease. We synthesized evidence of community interventions and innovative practices to mitigate COVID-19 as well as</p>



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	<p>previous respiratory outbreak infections which may share some aspects of transmission dynamics with COVID-19. In the study, we systematically searched the literature on community interventions to mitigate COVID-19, SARS (severe acute respiratory syndrome), H1N1 Influenza and MERS (middle east respiratory syndrome) epidemics in PubMed, Google Scholar, World Health Organization (WHO), MEDRXIV and Google from their inception until May 30, 2020 for up-to-date published and grey resources. We screened records, extracted data, and assessed risk of bias in duplicates. We rated the certainty of evidence according to Cochrane methods and the GRADE approach. This study is registered with PROSPERO (CRD42020183064). Of 41,138 papers found, 17 studies met the inclusion criteria in various settings in Low- and Middle-Income Countries (LMICs). One of the papers from LMICs originated from Africa (Madagascar) with the rest from Asia 9 (China 5, Bangladesh 2, Thailand 2); South America 5 (Mexico 3, Peru 2) and Europe 2 (Serbia and Romania). Following five studies on the use of face masks, the risk of contracting SARS and Influenza was reduced OR 0.78 and 95% CI = 0.36-1.67. Equally, six studies on hand hygiene practices reported a reduced risk of contracting SARS and Influenza OR 0.95 and 95% CI = 0.83-1.08. Further two studies that looked at combined use of face masks and hand hygiene interventions showed the effectiveness in controlling the transmission of influenza OR 0.94 and 95% CI = 0.58-1.54. Nine studies on social distancing intervention demonstrated the importance of physical distance through closure of learning institutions on the transmission dynamics of disease. The evidence confirms the use of face masks, good hand hygiene and social distancing as community interventions are effective to control the spread of SARS and influenza in LMICs. However, the effectiveness of community interventions in LMICs should be informed by adherence of the mitigation measures and contextual factors taking into account the best practices. The study has shown gaps in adherence/compliance of the interventions, hence a need for robust intervention studies to better inform the evidence on compliance of the interventions. Nevertheless, this rapid review of currently best available evidence might inform interim guidance on similar respiratory infectious diseases like Covid-19 in Kenya and similar LMIC context.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33290402/">https://pubmed.ncbi.nlm.nih.gov/33290402/</a></p>
68.	<p>Okoyo C, Campbell SJ, Williams K, Simiyu E, Owaga C, Mwandawiro C. Prevalence, intensity and associated risk factors of soil-transmitted helminth and schistosome infections in Kenya: Impact assessment after five rounds of mass drug administration in Kenya. PLoS Negl Trop Dis. 2020 Oct 7;14(10): e0008604.</p> <p><b>Abstract</b> Background: In Kenya, over five million school age children (SAC) are estimated to be at risk of parasitic worms causing soil-transmitted helminthiasis (STH) and schistosomiasis. As such, the Government of Kenya launched a National School Based Deworming (NSBD) program in 2012 targeting the at-risk SAC living in endemic regions, with the aim of reducing infections prevalence to a level where they no longer constitute a public health problem. The impact of the program has been consistently monitored from 2012 to 2017</p>





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	<p>through a robust and extensive monitoring and evaluation (M&amp;E) program. The aim of the current study was to evaluate the parasitological outcomes and additionally investigate water, sanitation and hygiene (WASH) related factors associated with infection prevalence after five rounds of mass drug administration (MDA), to inform the program's next steps.</p> <p><b>Materials and methods:</b> We utilized a cross-sectional design in a representative, stratified, two-stage sample of school children across six regions in Kenya. A sample size of 100 schools with approximately 108 children per school was purposively selected based on the Year 5 STH infection endemicity prior to the survey. Stool samples were examined for the presence of STH and <i>Schistosoma mansoni</i> eggs using double-slide Kato-Katz technique, urine samples were processed using urine filtration technique for the presence of <i>S. haematobium</i> eggs. Survey questionnaires were administered to all the participating children to collect information on their demographic and individual, household and school level WASH characteristics.</p> <p><b>Principal findings:</b> Overall, STH prevalence was 12.9% (95%CI: 10.4-16.1) with species prevalence of 9.7% (95%CI: 7.5-12.6) for <i>Ascaris lumbricoides</i>, 3.6% (95%CI: 2.2-5.8) for <i>Trichuris trichiura</i> and 1.0% (95%CI: 0.6-1.5) for hookworm. <i>S. mansoni</i> prevalence was 2.2% (95%CI: 1.2-4.3) and <i>S. haematobium</i> prevalence was 0.3% (95%CI: 0.1-1.0). All the infections showed significant prevalence reductions when compared with the baseline prevalence, except <i>S. mansoni</i>. From multivariable analysis, increased odds of any STH infections were associated with not wearing shoes, adjusted odds ratio (aOR) = 1.36 (95%CI: 1.09-1.69); <math>p = 0.007</math>; high number of household members, aOR = 1.21 (95%CI: 1.04-1.41); <math>p = 0.015</math>; and school absenteeism of more than two days, aOR = 1.33 (95%CI: 1.01-1.80); <math>p = 0.045</math>. Further, children below five years had up to four times higher odds of getting STH infections, aOR = 4.68 (95%CI: 1.49-14.73); <math>p = 0.008</math>. However, no significant factors were identified for schistosomiasis, probably due to low prevalence levels affecting performance of statistical analysis.</p> <p><b>Conclusions:</b> After five rounds of MDA, the program shows low prevalence of STH and schistosomiasis, however, not to a level where the infections are not a public health problem. With considerable inter-county infection prevalence heterogeneity, the program should adopt future MDA frequencies based on the county's infection prevalence status. Further, the program should encourage interventions aimed at improving coverage among preschool age children and improving WASH practices as long-term infection control strategies.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/33027264/">https://pubmed.ncbi.nlm.nih.gov/33027264/</a></p>
69.	<p>Kinuthia GK, Ngunjiri V, Beti D, Lugalia R, Wangila A, Kamau L. Publisher Correction: Levels of heavy metals in wastewater and soil samples from open drainage channels in Nairobi, Kenya: community health implication. <i>Sci Rep.</i> 2020 Jul 7;10(1):11439.</p> <p><b>Pubmed link-</b><a href="https://pubmed.ncbi.nlm.nih.gov/32632159/">https://pubmed.ncbi.nlm.nih.gov/32632159/</a></p>
70.	<p>Kariuki SM, Newton CRJC, Abubakar A, Bitta MA, Odhiambo R, Phillips Owen J.</p>





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	<p>Evaluation of Psychometric Properties and Factorial Structure of ADHD Module of K-SADS-PL in Children from Rural Kenya. <i>J Atten Disord.</i> 2020 Dec;24(14):2064-2071.</p> <p><b>Abstract</b></p> <p>Objective: We determined the reliability of The Kiddie-Schedule for Affective Disorders and Schizophrenia for School-Age Children-Present and Lifetime (K-SADS-PL) for screening and diagnosing ADHD in children. Method: K-SADS-PL was administered to 2,074 children in the community. Psychometric properties, factorial structure, and clinical validity of K-SADS-PL in screening or diagnosis of ADHD were examined. Results: Internal consistency was excellent for items in the screening interview (Macdonald's Omega [<math>\omega</math>] = 0.89; 95% confidence interval [CI] [0.87, 0.94]) and diagnostic supplement (<math>\omega</math> = 0.95; 95% CI [0.92, 0.99]). The standardized coefficients for items in the screening interview were acceptable (0.59-0.85), while fit indices for single factorial structure reached acceptable levels. Screening items were associated with high sensitivity (97.8%; 95% CI [97.2, 98.5%]) and specificity (94.0%; 95% CI [93.0, 95.0%]) for diagnosis of ADHD in the supplement. The test-retest and interinformant reliability as measured by intraclass correlation coefficient was good for most of the items. Conclusion: This large study shows that K-SADS-PL can be reliably used to screen and diagnose ADHD in children in Kenya.</p> <p><b>Pubmed link-</b> <a href="https://pubmed.ncbi.nlm.nih.gov/29392964/">https://pubmed.ncbi.nlm.nih.gov/29392964/</a></p>