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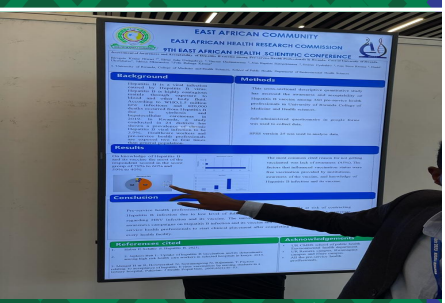
The best oral presenter Ms. Olga Mashedi receiving a trophy during the 9th EAHSC



A participant presenting an e-poster of the 9th EAHSC

The exhibition booth of the National Institute of Medical Research, Tanzania

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CONFERENCE ABSTRACTS

THE 9TH EAST AFRICAN HEALTH AND SCIENTIFIC CONFERENCE:

Challenges and Strategies to Preparedness and Response to Communicable and Non-Communicable Diseases: LessonsLearnt from the COVID-19 Pandemic

27th- 29th September 2023

Kigali, Republic of Rwanda

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CONFERENCES ABSTRACTS

Sub-theme 1: Innovative approaches and interventions to strengthen health systems, leadership and governance for management of communicable and non-communicable diseases

1. Antimicrobial and Antibiofilm Activities of Selected Essential Oils and Phytochemicals Against *Campylobacter jejuni* strains

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Introduction: *Campylobacter jejuni*, one of the major etiologies of human gastroenteritis, forms persistent biofilms which are considered a public health concern. This complicated the management of antimicrobial-resistant infections. Existing antibiofilm interventions have shown various shortcomings while natural products (NPs) are viewed as potential and effective alternative sources of biofilm modulators. The aim of this study was to assess the antimicrobial and antibiofilm activities of selected essential oils and phytochemicals against *C. jejuni* strains.
Methods: Three C. jejuni strains (ATCC® 33560TM, MT947450, and 200605), two EOs [clove oil (CLO) and cinnamon oil (CIO], and their major phytochemicals [eugenol (EUG) and trans-cinnamaldehyde (TRC)] were used in this study. The used strains included preserved samples and purchased reference strain. The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were assessed by broth microdilution. The antibiofilm activity on the polystyrene surface was assessed by crystal violet assay. Data were analyzed using GraphPad Prism software.
Results: The MIC and MBC varied between 25-50 µg/mL and 50-100 µg/mL, respectively. The inhibition of biofilm formation ranged between 21.9-34.5% while the degradation of pre-formed biofilm ranged between 7.2-28.4%. CIO and TRC were more effective in inhibiting biofilm while CLO exhibited more degradation of mature biofilm.
Conclusion: Further studies are required to test the efficacy of the used NPs using in vivo models or in mixed cultures.
Keywords: Biofilm, natural products, antimicrobial activity, *C. jejuni*

2. Synergism in Antiplasmodial activities of Artemether and Lumefantrine in Combinations with Extracts of Securidaca longipedunculata Fresen (Polygalaceae)

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Background: Malaria caused about 1,700 deaths per day in 2020, globally. The sustained malaria burden and prevalence is majorly due to the development of resistance of malaria parasites to available antimalarial drugs. One strategy to combat drug resistance is the use of combinations of two drugs with different modes of action. Limited access to hospitals in East Africa, especially during the COVID-19 lockdowns, led people to use antimalarial plants for treatment of malaria in traditional medicine. When malaria condition persists, they seek orthodox treatment in hospitals. This leads to herb-drug interactions. The antiplasmodial activity of such herb-drug interactions for *Securidaca longipedunculata*, that is widely used in traditional medicine for treatment of malaria in Africa remains unknown. Therefore, the current study aimed to determine the antiplasmodial activity of extracts of *S. longipedunculata*, in fixed combinations with standard antimalarial drugs (Artemether and Lumefantrine).
Methodology: Artemether and lumefantrine were each combined with methanol roots, stems and leaves extracts of *S. longipedunculata* at fixed extract to drug ratios of: 4:1, 3:1, 1:1, 1:2, 1:3 and 1:4. These combinations were tested for ex vivo antiplasmodial activity using fresh clinical isolates which were also characterized for molecular ex vivo drug resistance profiles. In vitro antiplasmodial activity was tested against three cultured *Plasmodium falciparum* strains (W2, D6 and DD2) using SYBR Green I assay. The concentration that inhibits 50% of P. falciparum parasites (IC50) was determined for each drug and extract when used singly and in combination. The IC50s were then used to determine the mean sum of fifty-percent fractional inhibition concentration (FIC50) that are

grouped into synergism (FIC50<1), additivity (FIC50 =1) and antagonism (FIC50>1). All sum FIC50 means were subjected to analysis of variance (ANOVA).
Results: Synergism was observed across all the fixed doses when the root extracts were combined with artemether against D6 clone (FIC50 0.403±0.068). The stem extracts in combination with lumefantrine showed synergism across all the fixed doses against DD2 clone (FIC50 0.376±0.096) as well as field isolates (FIC50 0.656±0.067). Similarly, synergism was observed along all ratios when leaf extracts were combined with lumefantrine against W2 clone (FIC50 0.456±0.165). All tests caused significant (P<0.05) parasite reduction.
Conclusion: The observed synergism is suggestive of the use of *S. longipedunculata* in combination with Artemether and Lumefantrine in combating antimalarial drug resistance.

3. Plasmid Characterization in Bacterial Isolates of Public Health Relevance in a Tertiary Healthcare Facility in Kilimanjaro Region, Tanzania
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Co-authors: Marco van Zwetselaar, Happiness Kumburu, Frank M. Aarestrup, Katharina Kreppel, Elingarami Sauli, Tolbert Sonda
Affiliation: Kilimanjaro Clinical Research Institute, Tanzania
Background: Antibiotic resistance of human pathogens is becoming a serious public threat globally and is causing morbidity and mortality. Transmission of acquired resistance to human pathogens can occur horizontally through plasmids.
Objective: Limited knowledge regarding the spread of antibiotic resistance genes and virulence genes among clinical isolates in Tanzania, influenced plasmids characterization in bacterial isolates from inpatients at Kilimanjaro Christian Medical Centre to establish their resistance and virulence in humans.
Materials and Methods: All bacterial sequences were de-novo assembled using Unicycler before extraction of plasmids. Assembly graphs were submitted to Gplas+plasflow for plasmid contiguous prediction. The predicted plasmid contigs were validated using PlasmidFinder. The assembled putative plasmid sequences for each isolate were submitted to Resfinder and VirulenceFinder to identify antibiotic resistance and virulence genes carried in plasmid replicons. Pearson correlation approach was used to determine the relationship between number of antibiotic resistance and virulence genes in plasmid replicons.
Results: A total of 159 (56.2%) out of 283 bacterial isolates were found to carry plasmid replicons, with Escherichia coli, Klebsiella pneumoniae, and Staphylococcus aureus being the most prevalent plasmid carriers. A total of 26 (86.7%) multiple-replicon types were found to carry both resistance and virulence genes compared to 4 (13.3%) single plasmid replicons. No statistically significant correlation was found between the number of antibiotic resistance and virulence genes in multiple-replicon types ($r = -0.14$, $P > 0.05$).
Conclusion and Recommendation: Our findings show a relatively high proportion of plasmid replicon-carrying isolates suggesting selection pressure due to antibiotic use in the hospital. Co-occurrence of antibiotic resistance and virulence genes in clinical isolates is a public health problem warranting attention.

4. Whole Genome Sequenced-based Characterization and Determination of Quinolone Resistance Among Methicillin-resistant and Methicillin-susceptible *S. aureus* Isolates from Patients Attending Regional Referral Hospitals in Tanzania
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Co-authors: Happiness Kumburu, Boaz Wadugu, Marian Shayo, Tolbert Sonda
Affiliation: Kilimanjaro Christian Medical University College
Background: *S. aureus* has become an important infectious agent in both hospital and community settings. The emergency of multidrug-resistant MRSA driven by acquisition of resistance genes the mecA gene imposes a substantial challenge in the treatment and control of their related infections. Quinolone, the affordable broad class of antibiotics have historically been effective against both MRSA and MSSA strains. However, the escalating rise of quinolones resistance particularly in MRSA has severely hampered their potency and further diminish the therapeutic options.
Material and Methods: A descriptive cross-sectional laboratory-based study involving a total of 140 archieved clinical S. aureus isolates collected from six Tanzanian regional referral hospitals including Dodoma, Songea, Kigoma, Kitete, and Morogoro Regional Referral Hospitals, as well as Mnazi Mmoja Referral Hospital of Zanzibar. Bacterial identification was accomplished through both classical microbiology and whole genome sequencing utilizing the Illumina Nextseq 550 sequencer. Bioinformatics analysis was done for species identification, Multilocus Sequence typing, SCCmec type, identification of resistance determinants and a phylogenetic relationship.

Results: From the 140 isolates, 69 (49.3%) were identified as MRSA, among which 57 (82.6%) exhibited quinolone resistance. Conversely, 71 isolates identified as MSSA with none of them exhibiting resistance to quinolone. Spa-typing revealed 6 spa types with the predominant ones being t355, t1476, and t498 respectively. Moreover, all MRSA were found to harbor SCCmec type IV. There was a significant genetic diversity among the isolates with detection of 14 sequence types (ST) and 6 genetic clusters comprised of isolates with ST8-spa-t1476-SCCmecIV and ST8-spa-t498-SCCmecIV genotypes. Notably, ST152 was prevalent sequence type among MSSA while ST8 was predominant among MRSA. The antimicrobial resistance profile revealed that, the isolates carried at least three horizontally acquired resistance genes, with blaZ, dfrG, tet(K), and aac (6')-aph (2'') genes being highly prevalent.
Conclusion: There is a high genetic diversity among the S. aureus isolates existing in Tanzania regional hospitals, with a concerning burden of quinolone resistance in MRSA isolates. The significant presence of diverse resistance genes among MRSA lineages emphasizes the necessity of developing sustainable antimicrobial stewardship and evidence-based guidelines for the treatment and control of MRSA-related infections in both community and hospital settings.
Recommendations: From a given result, there is a dire necessity on emphasizing heightened screening for MRSA, proper sanitation, and advanced decontamination practice in our referral hospitals to control the nosocomial spreading of MRSA, as well as in the communities through initiating education campaigns and control practices such as hand washing.

5. Nano-Diagnostics: Illuminating the Path to Swift and Reliable Tuberculosis Diagnosis. A Perspective
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Background: *Mycobacterium tuberculosis* (MTB) is the most prevalent infectious disease and leading cause of mortality worldwide. Diagnostic testing for TB is crucial for prevention worldwide, using techniques such as bacterial culture, microscopy, radiography, and clinical and immunological methods.
Main Text: Common tests include chest radiography (CXR), tuberculin skin test (TST), interferon gamma release assays (IGRAs), drug susceptibility tests (DSTs), DNA microarray chips and loop-mediated isothermal amplification (LAMP). However, conventional diagnostic approaches have drawbacks such as low sensitivity, time-consuming procedures, false-negative results, and lack of strain separation and bacterial viability detection. Advanced diagnostic approaches, such as Droplet polymerase chain reaction(D-PCR), Next-Generation sequencing (NGS), microRNAs, and Whole Genome sequencing (WGS), are needed to combat the TB epidemic. Nano-diagnostics, using specialized nanoparticles like quantum dots, magnetic Nano-diagnostics, optical biosensors, Nucleic Acid hybridization, and electro-immuno-sensors, offer high specificity and sensitivity.
Conclusion: To eradicate TB completely, light should be shed further to explore cutting-edge techniques and Nano-diagnostics for TB diagnosis.

6. Use of Infection Control Assessment Tool to Monitor the Progress of the IPC Program Pre and Post COVID at Kitale County Referral Hospital
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Introduction: Infection Prevention and Control (IPC) is a key aspect of patient care and a cornerstone of global health security in terms of prevention and response to infectious disease outbreak threats including antimicrobial resistance and healthcare associated infections (HAIs). ICAT is used to systematically assess a healthcare facility's IPC practices and guide quality improvement activities. The aim of this study was to monitor progress of the IPC program at Kitale County Referral Hospital (KCRH).
Methods: A cross sectional survey was conducted using the Infection Control Assessment Tool (ICAT) in December 2022. The tool was administered to the KCRH departmental in-charges through interviews, document reviews and practice observations. The 2022 findings were compared to the previous results in 2016 (baseline), 2017 and 2019. All IPC key areas; hand hygiene, healthcare waste management, standard precautions and occupational health were assessed. The data was summarized in proportions with the numerator being the actual score and the denominator the highest possible score of each key indicator monitored.
Results: The average score of the IPC program in 2022 was 60%; 49% in 2019; 33% in 2017 and 11% in 2016 (baseline). The isolation and standard precautions score was 25% in 2022, 49% in 2019, 55% in 2017 and 5% in 2016. The occupational health score was 41% in 2022, 49% in 2019, 55% in 2017 and 37% in 2016.The pharmacy scored 45% in 2022, 30% in 2019 and 53% in 2017. Healthcare waste management score was 69% in 2022, 30% in 2019, 53% in 2017 and 25% at baseline.

Conclusion: The ICAT tool provides a simple, practical standardized way of monitoring progress in the IPC program as it identifies the gaps and recommendations for improvement. Generally, there was improvement in IPC programs post covid 19 infection.

7. Taking Stock of Various Research Studies on Potential Leishmaniasis Vaccine Development in KEMRI, Kenya
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Co-authors: Ruttoh Reuben, Ingonga Johstone, Chebet Alphine, Mwangi Milka
Affiliation: Centre for Biotechnology Research for Development, KEMRI1
Background: Leishmaniasis is a neglected tropical disease caused by Leishmania protozoa that is transmitted by infected female sand flies. Currently there are no effective vaccines against leishmaniasis, hence need for continued research on new effective vaccines. The aim of the study was to take stock of research studies on potential leishmaniasis vaccines to ascertain if there are of future prospects.
Methods: The salivary glands from Phlebotomus duboscqi were vortexed to obtain salivary gland lysates (SGLs). Soluble Leishmania major exoantigens (LmSEAgs) were obtained from short culture systems of dividing promastigotes and soluble Leishmania antigens (SLA) were obtained by sonication (3-5cycles) of promastigotes and protein concentration determined by the Bio-Rad protein assay. BALB/c mice were immunized with SGLs, LmSEAgs and SLA and seven days after the second immunization, all the mice were challenged with metacyclic promastigotes. Lesion sizes were measured and parasite burden were determined using limited dilution assay whereas IFN-γ, IL-4 and IL-5 were measured using ELISA.
Results: The data reported here is from three experimental animal model studies carried out in Leishmaniasis Laboratory at KEMRI. We report that immunizations with LPG alone gave effective protection against L. major infection ($P < 0.05$) compared to controls, whereas SGLs, and the LPG + SGLs cocktail failed to protect. In another study, using soluble Leishmania antigens to vaccinate BALB/c mice, it showed promising results when combined with BCG. Briefly, there was increased IFN-γ and decreased IL-4 and IL-5 as detected using ELISA. In our lab we have also shown vaccinating mice with soluble exoantigens of L. major i.e recombinant nucleoside hydrolase have led to significant decrease in lesion sizes and parasite burden with concomitant increase in IFN-γ and decrease in IL-10. Mice immunized with L. major SEAgs had significantly smaller lesions with fewer parasites. When lymphoid cells from L. major SEAg-immunized mice were stimulated with leishmanial antigen in vitro, they proliferated and secreted a mixed profile of type 1 and type 2 cytokines. The study was limited to CL caused by L. major parasite, hence no cross protection has been studied in other CL causing Leishmania spp.
Conclusions: We conclude that mice immunized with LmSEAgs alone and SLA in combination with BCG were protected from L. major infections. Hence, they could be potential vaccine candidates for further clinical studies.

8. Urogenital Schistosomiasis and Molecular Characterization of *Schistosoma bovis* and *Schistosoma haematobium* Hybrids in Shinyanga and Misungwi Districts, Northwestern Tanzania.
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Background: Schistosomiasis is a water-borne parasitic disease with the second highest global socioeconomic impact after Malaria. Preventive chemotherapy using praziquantel is the main intervention in endemic countries including Tanzania. Recent studies have reported the occurrence of Schistosoma hybrid species among humans of up to 36% in West Africa. This is one of the factors which are suspected to affect the efficacy of the treatment.
Objective: To determine the burden of urogenital schistosomiasis and the occurrence of Schistosoma haematobium and Schistosoma bovis hybrids and their effect on treatment outcomes in Northwestern Tanzania.
Methodology: A population-based cross-sectional study involving 1,910 study participants was conducted. A standard parasitological survey through urine filtration technique was used to determine the prevalence of schistosomiasis in study participants. A Rapid Diagnostic Multiplex PCR was carried out to identify individuals infected with Schistosoma bovis or Schistosoma haematobium or hybrids of the two species in the studied population. The cure rate and egg reduction rate were assessed at day 21.
Results: The overall prevalence of S. haematobium before treatment was 6.4% (range 1.3% - 9.3%) with significant differences among villages (χ 2 = 24.4, $P < 0.001$). The infection intensity of S. haematobium was 4.5 (1.6 – 6.8 eggs/10ml urine). The prevalence of S. haematobium decreased to 0.3% (range 0 - 9.5%) after treatment, therefore praziquantel yielded a satisfactory cure rate above 90% in people with Schistosoma haematobium infection and those carrying hybrids. The occurrence of Schistosoma haematobium and Schistosoma bovis hybrid infections was (3.5%), detected only in one village.

Conclusion: These findings suggest that schistosomiasis is still a public health problem in the study area and that Schistosoma haematobium and Schistosoma bovis hybrids exist. Our results highlight the importance of adopting the one health approach in schistosomiasis control and elimination.

9. Multidrug-resistant *Escherichia coli* and *Klebsiella pneumoniae* isolated from Hospital Sewage Flowing Through the Community Sewage System and Discharging into the Indian Ocean

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Affiliation: Kilimanjaro Christian Medical Centre, Tanzania

Background: Hospital sewage is a significant reservoir of antimicrobial-resistant pathogens and genes that pose a huge public health threat. In this study, we determined the occurrence of multidrug-resistant *Escherichia coli* and *Klebsiella pneumoniae* in sewage flowing from a referral hospital through the urban sewage system to the point of discharge in the Indian Ocean.
Results: A total of 400 sewage samples were collected, yielding 517 isolates. Of these, 32.3% (167/517) were from hospital sewage, while 67.7% (350/517) were from the community. *E. coli* was the most common isolate (44.5% (230/517), followed by *K. pneumoniae* at 27.3% (141/517), and other gram-negative bacteria constituted 28.2% (146/517) of the isolates. Multidrug resistance (MDR) was seen in 80.9% (186/230) E. coli and 71.6% (101/141) K. pneumoniae. Of the MDR isolates, 27.2% (78/287) were resistant to four different classes of antibiotics, while 6.9% (20/287) exhibited resistance to eight classes. The most frequent MDR pattern was PEN/CEP/TET/QNL/SUL, seen in 14.2% (38/287) of the isolates. The isolation frequency of MDR *E. coli* and *K. pneumoniae* at different sampling sites was high, being 47.6% in hospital chambers, 62.0% in hospital ponds, 58.1% in the treated hospital wastewater, and 55.6% in the community stream draining into the Indian Ocean. Extended-spectrum beta-lactamase production was observed in 40% (92/230) of E. coli and 36.2% (51/141) of K. pneumoniae isolates. Resistance to quinolones among *E. coli* was 54.8% (126/230) and 39.7% in K. pneumoniae (56/141). Carbapenem resistance in E. coli was 39.6% (91/230), while among K. pneumoniae isolates was 32.6% (46/141).
Conclusions: We found high proportions of multidrug-resistant E. coli and K. pneumoniae in the wastewater flowing from the hospital through the community sewage system to the point where it enters the Indian Ocean. Biological treatment did not significantly reduce the proportion of resistant bacteria, posing a very serious public health threat. The release of these highly resistant pathogens into the Indian Ocean is of international concern.

10. Nanotechnology-based Formulation and Preclinical Assessment of Antimalarial Efficacy of Dihydroartemisinin-lumefantrine in a Mouse Model

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Background: The challenges posed by expanding health issues necessitate advanced healthcare solutions. Nanotechnology, focusing on atomic and molecular levels, offers promising tools for diagnostics, vaccines, and treatments. For instance, during the COVID-19 pandemic, nanotechnology played a pivotal role in delivery of the Moderna's mRNA and Pfizer vaccines in which the mRNA was designed and delivered enclosed in lipid nanoparticles (NPs). Malaria remains a significant health concern, and artemisinin-based combinations are recommended by the World Health Organization for treatment. However, artemisinin and its derivatives is dodged by challenges such as low aqueous solubility, low bioavailability, and short half-life thus requiring increased dose frequency to maintain adequate therapeutic drug-plasma concentration.
Objectives: This study aimed to formulate a combination of dihydroartemisinin and lumefantrine as a duo-drug using solid lipid nanoparticles (SLNs) and evaluate its antimalarial efficacy in a mouse model.
Methods: SLNs were prepared via a modified solvent extraction method using a water-in-oil-in-water double emulsion. The nanoparticles underwent physicochemical characterization, safety evaluation, and preclinical assessment for antimalarial efficacy.
Results: The SLNs exhibited a mean particle size of 308.4 nm, a polydispersity index of 0.29, and a zeta potential of -16.0 mV. DHA and LUM encapsulation efficiencies were 93.9% and 33.7%, with drug loading capacities of 11.9% and 24.10%, respectively. The drugs demonstrated sustained release according to the Kors-Peppas model, with continuous release for over 72 hours. The nanoparticles, presenting a spherical shape, effectively encapsulated the drugs as confirmed by Fourier transform infrared overlay spectra. Nano-formulated DHA-LUM-SLNs exhibited a 31% higher efficacy in clearing Plasmodium berghei from infected Swiss albino mice compared to conventional oral doses.

Conclusion: This study underscores the potential of nanotechnology to address complex health challenges, exemplified by the enhanced antimalarial efficacy achieved through the formulation of dihydroartemisinin-lumefantrine duo-drug using solid lipid nanoparticles. By harnessing the capabilities of nanotechnology, innovative therapeutic strategies can be developed to combat diseases that continue to affect global health.

11. Application of Nanopore Sequencing Technology for Clinical Diagnosis of Infectious Diseases: a Case Report of *Campylobacter jejuni*

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Affiliation: Kilimanjaro Christian Medical Centre, Tanzania

Background: In resource-limited settings, patients are often first presented to clinical settings when seriously ill, and access to proper clinical microbial diagnostics is often very limited or non-existing. On February 16th, 2022, we were on a field trip to test a completely field-deployable metagenomics sequencing set-up that includes DNA purification, sequencing, and bioinformatics analyses using bioinformatics tools installed on a laptop for water samples, just outside Moshi, Tanzania. On our way to the test site, we were contacted by the nearby Machame hospital regarding a 3 years toddler who was seriously ill with diarrhea and not responding to treatment.
Methods: On the same day, we conducted an onsite metagenomics examination of a fecal sample from the child. The portable laboratory equipment bento-lab (Portable DNA Laboratory) and Oxford Nanopore Technology were employed to study the case in this instance
Results: Routine hospital diagnoses, including PITS, MRDT, HB, RBG, and stool analysis, found no causative agent. *Campylobacter jejuni* was identified as the causative agent as a result of sequencing. The treatment was subsequently changed, with almost immediate improvement, and the child was discharged on February 21st just after 4 days.
Conclusion: This case report demonstrated the feasibility of using a streamlined approach combining rapid sample preparation, ONT sequencing, and user-friendly bioinformatics software to quickly identify the causative agent in patients, resulting in improved treatment outcomes, which is especially important in low and middle-income countries with limited diagnostic capabilities. The ONT devices do not require a large capital investment: initial costs, including start up reagents, are around GBP 1,000. These advantages together make the device a suitable tool for infectious disease surveillance in resource-limited countries.

12. Rapid Assessment of the Expansion of Artemisinin-Resistant *Plasmodium falciparum kelch13* R561H and First Report of G449A in Rwanda using Pooled Nanopore Amplicon Sequencing

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Affiliation: Brown University, Providence, RI, USA

Background: The emergence and spread of drug-resistant parasites such as the *Plasmodium falciparum kelch13* (*PfK13)* gene mutations have been associated with *in vitro* resistance to artemisinin and delayed clearance after treatment with ACTs. There has been a recent increase of mutations such as R561H, C469Y/F, and A675V in East Africa, primarily in Rwanda, Uganda, and Tanzania.
Methods: We genotyped 280 samples collected as whole blood samples from Tanda Health Center in Rwanda between May-July 2022 from malaria positive patients. Eight samples of similar parasitemia identified by microscopy were pooled in equal volume, generating 35 pools, and nucleic acids were extracted using magnetic beads. We used qPCR to amplify a short fragment spanning amino acid sites *Pfk13* 434-562. Products were balanced by qPCR output, rapid barcoded and sequenced on MinION. Allele frequency within pools was calculated as the number of reads mapped to each mutant strain. Overall prevalence was calculated as the average of pool prevalence. Pooled sequencing is a high throughput approach applicable in low resource settings, previously shown to accurately estimate population allele frequency and prevalence of antimalarial resistance.
Results: R561H was detected in 9 out of 35 pools, with a population allele frequency of 16.7%. G449A, a WHO candidate resistance mutation not previously seen in Africa, was detected in 5 pools with a frequency of 8.7%. R561H is expanding in Rwanda, in this instance having spread to Tanda, a high transmission region. However, the R561H mutation has not swept the parasite population.
Conclusion: The novel appearance of G449A at a relatively high prevalence in Africa is concerning. G449A was previously reported in China at low frequency and is associated with a two-fold PC1/2 increase. Monitoring mutations associated with *in vitro* resistance is vital to the control of drug-resistant parasites, allowing therapeutic efficacy studies to be focused in sites with mutants and inform treatment protocols.

13. The Role of *Plasmodium falciparum* HSP90 in Antimalarial Drug Treatment Outcome in a Malaria Endemic Region, Kisumu County

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Background: The protozoan parasite *P. falciparum* is responsible for the most severe form of malaria in Kenya and is developing mechanisms to circumvent challenges encountered in the human host and stress brought about by drugs. *P. falciparum* nuclear genome consists of 14 chromosomes which encode 5,300 genes with many genes being devoted to immune evasion and host–parasite interactions. In the host and especially during fever periods observed in clinical malaria, *P. falciparum* adapts to the environment by translocating heat shock proteins 90 (Hsps90) for its survival. There is scarcity in data to determine the role of PfHsp90 based on clinical malaria isolates from high prevalence *P. falciparum* zones of Kenya.
Objective: To determine the role of HSP90 in *P. falciparum* clinical isolates from malaria infected individuals following treatment with Artemether-lumefantrine and its correlation with the treatment outcome.
Methods: A cross sectional study on 45 *P. falciparum* positive blood samples collected from Nyando, Kisumu County. DNA extracted for day 0 and day 2, amplified HSP90 gene using real time PCR in triplicates. Average Ct and fold change between HSP90 expression at day 0 and day 2 computed using the 2^{a}-($\Delta\Delta$Ct) method.
Results: HSP90 gene expression was compared between day 0 and day 2 samples from the same patients. A fold difference of >1.6 was used as an indication of a twofold increase in the gene expression levels. 15 out of 45 (33%) samples showed an increase in HSP90 expression levels. 8/15 (53.3%) had a twofold increase. 3/15 (20%) had a threefold increase, 15 (6.7%) showed a 4X, 5X, 7X, and 9X fold increase.
Conclusion: Varied expression pattern of HSP90 after antimalarial treatment. Downregulation at Day 2 suggesting that expression might be associated with malaria symptoms. Upregulation in treated samples which suggest that drug pressure may have an impact on the expression of HSP90 protein. In Africa, ACT resistance has not been widely reported yet and this is due to minimal studies that have been conducted. Heat shock proteins are essential for the survival of the most virulent malaria parasite, P. falciparum and play a major role when the parasite encounters stress as it changes host, from the vector to the human, and mediate in malaria pathogenesis (Archya *et al.*, 2007). PfHsp90 constitute the hub that drives drug resistance in malaria parasites.

14. Genomics Insights into Antibiotic Resistance and Virulence: Landscape of Quinolone Resistant and ESBL Producing *Klebsiella pneumoniae* in Tanzanian Referral Hospitals

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Background: Multidrug-resistant Gram-negative bacteria, particularly Extended Spectrum Beta-Lactamase (ESBL)-producing Klebsiella pneumoniae, poses a significant global public health challenge due to the production of beta-lactamases and the presence of mobile genetic elements. The coexistence of quinolone and beta-lactam resistance exacerbates the problem by limiting treatment options and making treatment challenging. This study aimed elucidating the genomic landscape of these resistant strains and explore their virulence factors.
Methods: The study involved 38 K. pneumoniae isolates collected from referral hospitals across Tanzania between September 2020 and December 2022. Classical microbiological procedures were used for the isolation of this bacteria. Genomic DNA was extracted, library prepared, and whole genome paired end sequenced using Illumina NextSeq 550 platform.
Results: A high diversity of K. pneumoniae was observed, with the most prevalent being ST307 (7.9%), ST35 (7.9%), and ST45 (7.9%). 27(71%) isolates were collected from outpatients, while 11(29%) from inpatients. Among these isolates, 35 (92%) were collected from adults, with 13(34%) collected from pus or wound swabs. Phenotypically, all isolates (100%) were resistant to ampicillin. 25(65.8%) were Extended-Spectrum Beta-lactamases (ESBL), and 24(63.2%) showed resistance to (Fluoro)quinolones. Genotypically, all isolates were identified as multidrug-resistant (MDR), with 37 (97.4%) carrying at least one beta-lactam resistance gene determinant. The most frequently detected resistant genes were blaCTX-M-15 19(50%) and blaTEM-1D 21(55%). Yersinibactin was the most predominant virulence factor, with hypervirulence strain determinants present in 18.4% of the isolates. Comparing the two resistance detection methods, an average agreement of 70.1% was observed between the isolates, with Ampicillin exhibiting perfect agreement between the two methods.
Conclusion: There is a high diversity of *K. pneumoniae* strains in referral hospitals. The ESBL-producing and quinolones resistance are alarmingly high. There is a need for robust surveillance and intervention strategies to address antibiotic resistance as a significant public health concern.

15. Presence of an Invasive Exotic Freshwater Snail, *Pomacea Canaliculata* (Gastropoda: Ampullaridae) in Mwea Irrigation Scheme, Kenya: Potential implications on Control of Schistosomiasis and Public Health

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Background: The apple snail, *Pomacea canaliculata* (Gastropoda: Ampullaridae), a native of South America, was recently reported to be present in Kenya. This invasive freshwater snail is considered a devastating agricultural and ecological pest, and a potential public health threat. *P. canaliculata* serves as intermediate host of the rat lungworm, *Angiostrongylus cantonensis*, which causes human eosinophilic meningitis, an emerging disease. Long term impact of this snail in Kenya, remains unknown. A survey was recently done in Mwea irrigation scheme to assess the spread of this snail in the area and impact it has on population of native *Biomphalaria pfeifferi* snails; intermediate host for *Schistosoma mansoni*.
Methods: Sampling was done using a standard snail scoop in 30 freshwater habitats within the Mwea rice irrigation scheme. The snails and snail egg masses collected were identified using snail taxonomic keys based on morphological features, with the aid of a dissecting microscope.
Results: The presence of a thriving population of *P. canaliculata* in the Mwea rice irrigation scheme canals, ponds and rice paddies were confirmed, and numerous *Pomacea* egg masses observed. Out of all 30 sites sampled, no *B. pfeifferi* snails were recovered.
Conclusions: Absence of vector snails in Mwea provides an excellent opportunity for interruption of *S. mansoni* lifecycle at the intermediate host level, which can be complimented by mass drug administration (MDA) using Praziquantel to eliminate intestinal schistosomiasis in the area. There should be continuous snail surveillance in regions surrounding Mwea to monitor for spread of *Pomacea* snails into new localities. Need for further studies to determine presence of *A. Cantonensis* in *pomacea* snails or rodents, which act as the intermediate hosts and the potential public health threat of eosinophilic meningitis in humans who act as accidental hosts.

16. Exosome-based Malaria vaccine, a Miracle of Nanomedicine

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Abstract: Malaria is a parasitic infection that led to a large population of death worldwide. Exosome is a nano-size subpopulation of extracellular vesicles (EVs). Exosomes and malaria interrelation is the most complicated event. Infected cells derived exosomes devolve host-pathogen cellular communication and support in infection advanced stage enrichment. Exosome molecular cargos (miRNA, protein, etc.) efficiently participate in infection progression. In malaria, exosomes based theranostic approach is very exciting. Exosome develops a platform where the nanomedicine overcomes several traditional limitations (toxicity, biocompatibility, stability, target specificity). Exosome-based several drugs and micromolecular transportation showing promising results in malaria. This exosome and malaria research domain has the most challenging event called exosome heterogeneity (it is based on source, size, and internal molecular diversity). This limitation is possible to overcome with a single exosome profiling approach. Exosome is a new effective solution for a malaria-associated global health crisis.

17. Genomic Insights into Multidrug Resistance *Enterobacter cloacae* and *Escherichia coli* through Nanopore Sequencing of Clinical Isolates from Benjamin Mkapa Hospital, Tanzania: A case report

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Background: Antimicrobial resistance (AMR) remains a critical global health challenge, urging the need for innovative diagnostic approaches to combat infectious diseases effectively. Both *Enterobacter cloacae (E. cloacea)* and *Escherichia coli (E. coli)* belong to the Enterobacteriaceae family of bacteria, which also includes many other common bacteria found in the human digestive tract and other surroundings. In this study, we investigated isolates from a pleural fluid sample obtained from a patient suspected of having pneumonia at Benjamin Mkapa Hospital. The initial cultures revealed potential mixed cultures of Gram-negative rods exhibiting resistance to all tested antimicrobial agents. To gain deeper insights into the AMR profile and species identity, we performed whole genome sequencing using nanopore technology.
Methods: DNA was extracted from both agar-plate cultures and sub-cultures of putative pure isolates. Oxford Nanopore Technology was employed to study the case in this instance. Through genomic analysis, we elucidated the genetic basis of antimicrobial resistance and identified the implicated species.
Results: The examined clinical isolates, encompassing *E. cloacae* and *E. coli*, showcase an alarming degree of resistance to a wide range of antimicrobial drugs. Despite this resistance, few antimicrobial drugs remain effective: Colistin, florfenicol, and

carbapenem classes for *E. cloacae*, and colistin, florfenicol, fosfomycin, and chloramphenicol for *E. coli*.
Conclusion: The application of whole genome sequencing in this report provided valuable insights into the antimicrobial resistance landscape, underscoring the need for comprehensive genomic analysis to guide targeted therapeutic interventions. The findings emphasize the importance of understanding the genomic determinants of resistance to design effective treatment strategies.

18. In Vitro Study on The Immunomodulatory Effects of Free & Chitosan Antitubercular Flavonoid Nanocapsules on thp-1-Derived Macrophages
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Background: Macrophages are an integral part of the innate immune system. In response to bacterial infections, these cells release cytokines that promote inflammation. On the other hand, persistent inflammation may play a role in the etiology of a number of illnesses, including diabetes, TB, rheumatoid arthritis, multiple sclerosis, and psoriasis. Reducing the secretion of pro-inflammatory cytokines is a successful therapy method for these conditions. Synthesized free and chitosan encapsulated selected antitubercular flavonoids have been shown to have immunomodulatory effects.
Purpose: This study is designed to investigate the immunological response after treating human leukemia monocyte cells (THP-1) with free & chitosan nano-encapsulated selected antitubercular flavonoids.
Methodology: Free & chitosan nano-encapsulated selected antitubercular flavonoids were synthesized, and the treatment groups were as follows: naringenin encapsulated chitosan nanoparticles (ChN-nps), quercetin encapsulated chitosan nanoparticles (ChQ-nps), and non-encapsulated chitosan nanoparticles (Ch-nps). THP-1 cells were differentiated into macrophages and characterized by measuring the expression of macrophage surface markers by Enzyme-linked immunosorbent assay (ELISA). Then, differentiated cells were activated by lipopolysaccharide (LPS). Afterwards, the activated macrophages were treated with Ch-nps, ChN-nps and ChQ-nps for 24 hrs. After treatment, the production levels of the inflammatory cytokines were measured by using ELISA.
Results: Our results show that THP-1 cells were successfully differentiated into macrophages. For inflammatory cytokine expression response, ChN-nps, ChQ-nps and Ch-nps showed the same expression level of cytokines, as the expression of IL-1β, TNF-α and IL-8 were expressively downregulated ($p < 0:0001$, $p < 0:0001$, $p < 0:0001$), respectively, while IL-6 was downregulated in a statistically significant manner for both Ch-nps and ChN-nps ($p < 0:0002$, $p < 0:0002$) compared to the control untreated group.
Conclusion: We can conclude that the quercetin loaded chitosan nanoparticles are potent effectors that prevent tuberculosis progression by activating two main immunological strategies: switching the surface expression profile of the activated macrophages into a proinflammatory M1-like phenotype and downregulating the expression of proinflammatory cytokines.

19. Mycological and Mycotoxin Quality of Commonly Consumed Beverages from Selected Counties in Kenya
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Introduction: Mycotoxin contamination of foods is estimated at 25% globally with a half a billion people exposed to mycotoxin. According to IARC, aflatoxin is classified as group 1 carcinogens resulting in adverse health effects, including but not limited to immunosuppression and cancer. In 2004, outbreak of acute aflatoxicosis in Kenya was one of the unprecedented human aflatoxin poisonings. *Camellia sinensis* tea is the world's second most popular beverage after water with several health-promoting properties. Like other food commodities, it is susceptible to fungal and mycotoxin contamination (Pouretedal et al., 2013). There are limited studies on fungal and mycotoxin contamination in *C. sinensis* black tea in Kenya.
Objective: To establish the fungal infestation and aflatoxins contamination in *Camellia sinensis* black tea retailed in selected Counties in Kenya.
Methodology: Forty *C. sinensis* tea were sampled from retailed shops. Fungal infestation was done by fungal culture and identified based on phenotypic features Aflatoxin quantifications was done using ELISA (Envirologix quicktox kit) according to manufacturer's instructions.
Results: The study established that *C. sinensis* harbor toxigenic fungi; *Aspergillus flavus*, *Aspergillus fumigatus*, *Aspergillus niger*, *Rrhizopus, Penicillium spp.* and *other toxigenic Aspergillus spp*. with 14.29% of the samples with aflatoxins above 30ppband 85.71% above 20 ppb. This is relatively high levels above the set standard of 10 ppb for aflatoxins residues in black tea.
Conclusion: The link between mycotoxin exposures and cancer risk has been established and IARC confirms aflatoxins as a carcinogen. This necessitates more research on mycotoxin contamination on non-cereal food for human and animal safety.

20. Technologies for Climate Data Analysis: Evaluating Long-term Climate Patterns and Implications for Disease Transmission

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Background: Climate is an important determinant of transmission of vector borne diseases as it affects the biology and ecology of disease vectors. Increased temperatures increase vector reproduction rates and shorten pathogen incubation periods within vectors thus directly affecting disease transmission. Climate change may also shift the geographic ranges of vectors. Additionally, some adaptive strategies to climate change, such as irrigated agriculture, may result in increased risk of diseases due to the proliferation of vector breeding sites. The phenomenon of global warming that has been observed is forecasted to continue in the foreseeable future.
Methods: Climate data for the 60-year period from 1961 – 2020 was obtained from *Climate Engine* (Climate.org) for three sites in Kenya where there are anecdotal reports of occurrence of vector-borne diseases but where definitive studies have not been conducted, namely Busia, Tharaka Nithi and Kikuyu. The data were analysed to evaluate long-term climate patterns and postulate how these might affect transmission of vector-borne diseases.
Results: When data were averaged over ten-year periods, differences in precipitation between these periods were not statistically significant for all the three site (One-way ANOVA: $p < 0.05$ in all cases). However, there were significant differences in both the mean minimum and maximum temperatures in all three sites (One-way ANOVA: $p = 0.00$ in all cases). Increases in the annual mean minimum and maximum temperatures ranged from 1.3°C - 2.6°C and 1.3°C - 2.9°C, respectively in concordance with the prediction that average global temperatures are expected to rise by 1.0 – 3.5^0C by 2100.
Discussion: Studies have demonstrated climate-related expansion of the geographical range of vector-borne disease as well as the occurrence of disease outbreaks. Access to climate data and integration of these data into research to aid disease risk mapping and development of early warning systems followed by appropriate and timely actions can significantly contribute to the goal of disease elimination.

21. Nano Biosensor for the Rapid Detection of the blaNDM-1 Resistant Gene

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Abstract: Antimicrobial resistant (AMR) pathogens have manifested a damaging effect across the world. They are estimated to contribute to nearly 700,000 deaths each year and projected to cause 10 million deaths in 2050 if adequate mitigation plans are not put in place. Carbapenemases in gram-negative resistant strains, among them *Escherichia coli, Klebsiella pneumoniae,* are significant mechanisms of carbapenem resistance. The New Delhi metallo-*b*-lactamase-1 (NDM-1), coded by the $bla_{\text{NDM-1}}$ gene expressed by *Escherichia coli* isolates, has drawn attention as they compromise almost all b-lactam antibiotics. This leads to long hospitalization times and high mortality rates, consequently impacting on the financial status of the economies. The current rapid diagnostic tools require costly equipment and pure culture; separation and enrichment of samples are time-consuming. Therefore, there is unmet need for an inexpensive, rapid, sensitive, specific field friendly diagnostic tool for detecting the carriers of this gene to contain these outbreaks that threaten the efficacy of medicine. This study highlights the use of glycan coated magnetic nanoparticle (MNP) to isolate and concentrate the pure culture of NDM-1producing *Escherichia coli* (ATCC 2471) in phosphate buffered saline (PBS). A colorimetric dextrin coated gold nanoparticle (GNP) biosensing platform for its detection was developed. From the study, bacterial capture of carbapenem-susceptible and carbapenem-resistant strains from pure cultures in PBS were analyzed by the plating method and microscopic imaging and high concentration factors for the bacterial strains have been realized. The biosensor was also optimized and tested for the presence of the target DNA that was observed by the GNPs retaining the red color and the absence of non-target DNA that turned blue/violet. The estimated sensitivity of the biosensor is 2.5 ng/μL which is equivalent to 10^3 CFU/ml. The biosensor is expected to advance an inexpensive and rapid method for detecting resistant superbugs. Comprehensive results will be presented.

22. Tuberculosis diagnosis using African Giant Pouched Rats among Culture Positives: Does Bacillary Load Matter?

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Background: Over the years, African giant pouched rats (Cricetomys ansorgei), trained by Anti-Persoonsmijnen Ontmijnende Product Ontwikkeling (APOPO) to identify tuberculosis (TB) by smell, have demonstrated their ability to detect TB from sputum. Rat's indication as TB has not been described before by mycobacterium bacillary load.
Methods: From Jun-August 2022, in an ongoing collaboration between APOPO and the University of Manchester in Dar es Salaam outpatient health facilities, sputum samples were collected from purposefully selected sputum-smear positive (smear) and asymptomatic control participants, and tested using a set of five trained rats, Xpert MTB/RIF and culture. We analyzed: 1) Rat's indication as TB by mycobacterium bacillary load, and 2) Compared sensitivity of rat's and Xpert MTB/RIF using Mc Nemar's test. Specificity was not determined since the controls were asymptomatic participants.
Results: From a total of 57 participants enrolled, 17 were all smear and culture positive. Sensitivity was 71% (95% confidence interval, CI: 49%-92%) and 65% (95% CI: 42%-87%) for rat's indication and Xpert MTB/RIF, *p=0.134,* respectively. From a set of five rats, an average of 4.3 (range 2-5 rat indication) rats indicated TB among those with Acid Fast Bacilli +2 or +3 on smear compared to an average of 2 (range 1-3 rat indication) with +1 or scanty. And, an average individual rat sensitivity was 68% compared to 28% among the two groups, respectively.
Conclusion: The higher the bacillary load the smaller number of rats needed to identify TB. In identifying TB, rats performed as good as Xpert MTB/RIF. Further evaluation of the usefulness of rats for active TB case finding is needed, especially in low- and middle-income countries, where resources are limited.

23. The Impact of Titanium Mining and Other Major Economic Anthropogenic Activities on Malaria Transmission and Burden in Kwale County, Kenya

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Introduction: In 2021, Africa was home to 95% of malaria cases and deaths. The negative impacts of malaria can be aggravated by social-economic-environmental factors especially agro-economic practices such as irrigation, mining and dam construction.
Objective: The aim of this study was to investigate the impact of three major economic and anthropogenic activities on *P. falciparum* transmission in Kwale.
Methods: A cross-sectional concurrent mixed methods (quantitative and qualitative) study was used to collect data. Kwale County was purposively selected due to the nuanced high malaria endemicity possibly attributable to the suitable vector habitat from the major anthropogenic activities. The study had five different arms of investigation; the first arm was the Control (C), second Dam site (D), third Sugarcane site (S), fourth Mining site (M) and fifth Dam-Sugarcane-Mining site (DSM). Each of the 1,025 consenting participants from 208 households provided a single blood sample for determining malaria prevalence and parasitaemia using rapid diagnostic kit and microscopy.
Results: Overall, the malaria positivity rate was 22.9% by RDT and 20.1% by microscopy. *Plasmodium falciparum* observation by RDT was highest in the DSM site with 33.7% followed by S site with 26.8%, D site with 23.3%, M site with 17.6%, and least the C site with 11.0%. The overall parasitaemia density (parasite counts per 200 white blood cells) was 8.4 with site-specific density of 18.7, 8.6, 7.1, 3.7 and 3.1 for DMS, S, D, M and C sites respectively. Univariable analysis of factors associated with malaria infection showed that participants in the DSM site were four times more likely to be infected with malaria, OR = 4.1 $p<0.001$ compared to those in the Control (C) site.
Discussion: Malaria vector and human host interactions are often enhanced by suitable environmental conditions especially ambient temperature which accelerate parasite growth in the mosquito and humidity. Anthropogenic activities may open up new breeding sites for the vector or increase human – anopheles contact hours hence different intensities in *P. falciparum* transmission and positivity rates.
Conclusion: The study results showed that prevalence of malaria and parasitaemia were high in areas where all the three anthropogenic activities were taking place. In the single activities site, sugarcane farming predisposed participants to high malaria burden. Characterized relational interplay between these anthropogenic activities and *P. falciparum* parasitemia will be useful in developing tailored strategies towards optimized malaria control interventions in areas with anthropogenic activities.

24. Optimizing the Pharmacy Retail Channel for Provision of a Self-injectable Contraceptive in Kenya Using Human-Centered Design

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Background: Self-injectable subcutaneous depot medroxyprogesterone acetate (DMPA-SC SI) offers women greater autonomy, privacy and convenience in pregnancy prevention and can help circumvent some health system barriers imposed by pandemic-related restrictions. We sought to tap into the pharmacy retail channel's potential to expand access to self-injectable contraceptives and other self-care products in a way that meets women's needs while ensuring viable pharmacy business models.
Methods: In 2021-2022, we used human-centered design (HCD) to explore the challenges facing self-injectable contraceptive provision through the pharmacy retail channel in Kenya and to design interventions to address these challenges. We conducted participant observations and interviews with pharmacy staff, clients and stakeholders drawn from 11 Kenyan towns, and analyzed the data to identify key insights which were further synthesized into design opportunities. For each opportunity identified, we generated ideas, developed prototypes, and refined solutions through interviews with contraceptive users, pharmacy providers and key stakeholders to come up with a final set of interventions.
Results: Observations with 30 pharmacy providers and clients, and interviews with 43 pharmacy providers, clients and stakeholders revealed 16 insights addressing pharmacy provider, client and DMPA-SC SI provision gaps. Three design opportunities that focused on demand generation, product availability and capacity building of pharmacy providers produced 35 ideas which translated to 12 prototypes. Through two rounds of prototype testing, rating, and ranking, with 34 pharmacy clients, 30 pharmacy providers and 16 stakeholders, we refined the prototypes into a multicomponent intervention: (1) "Ni-Consult" capacity building for pharmacies and providers, (2) "Jipende-Jipange" brand network of pharmacies and (3) pharmacy trainee mentor ship.
Conclusion: We recommend expanding DMPA-SC SI provision in the pharmacy retail channel through capacity building and re-positioning of pharmacies as a comprehensive, respectful and high-quality source of self-care products and contraceptives to women. Our intervention is being pilot-tested for feasibility and business viability in pharmacies across Kenya.

Sub-theme 2: Is the world prepared for future pandemics? Success, opportunities, and challenges in management of COVID19 and Ebola

25. Clinical Trial Experience on Cold Chain Management in the COVID-19 vaccine study
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Introduction: Cold chain management is a crucial aspect of clinical trials involving temperature-sensitive investigational medicinal products (IMPs). Maintaining the required temperature range throughout the supply chain is essential to preserve the integrity and efficacy of these products. This abstract presents the experience and insights gained from implementing a comprehensive cold chain management system during a clinical trial to safeguard product integrity and ensure participant safety.
Methods: The clinical trial involved a double-blind, randomized, multicenter study evaluating the efficacy, safety and immunogenicity of two SARS-CoV-2 Adjuvanted Recombinant protein Vaccines (Monovalent and Bivalent) for prevention against COVID-19 in adults 18 years of age and older. The investigational product required strict temperature control to maintain its potency and efficacy. An online Temperature Monitoring system was attached in two of the fridges that contained the Investigational products. In case of power outage, the monitoring system sends an email alert to the pharmacist who can do the necessary action in case the backup generator is not functioning well. Robust logistics planning is necessary to ensure that IMPs are transported and stored within the specified temperature range. Cold storage facilities, temperature monitoring devices and contingency plans are critical components of an effective cold chain system. For example in our set Up the courier team will also transport the Investigational products for example Covid 19 vaccine in a cold chain box/container with an electronic data logger device attached to it. Upon arrival to the site, the pharmacy team will stop the data logger and confirm if the Investigational drug was transported according to the required temperature range mostly between 2 to 8°C.
Results: Throughout the trial, the cold chain management system demonstrated exceptional performance. One temperature excursions was reported during transportation from the depo to the site, upon informing the sponsor and the Monitor the Investigational products was fit for use. All recording were acceptable.
Conclusions: The implementation of a meticulous cold chain management strategy was fundamental to maintaining the potency and efficacy of the investigational products throughout the trial. The utilization of online temperature monitoring systems, particularly within refrigeration units housing the investigational products, showcased its effectiveness in safeguarding the products from temperature excursions.

26. Evaluation of the Hygiene Hypothesis by Gross Domestic product and Death Rates of COVID-19

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Introduction: Industrialization is associated with a decrease of the infectious burden and a rise of allergic and autoimmune diseases, according to the 'hygiene hypothesis'. The hypothesis states that exposure to parasitic infections strengthens ones immune system. We analysed this hypothesis based on the COVID-19 mortality rates.

Methods: The 2018 Gross domestic product (GDP) for selected countries was used as a marker of hygiene and evaluated using linear regression against the impact of COVID -19 as indicated by the number of deaths per million population as the mortality rates.

Results: Positive linear regression showed a significant positive correlation between GDP and mortality. Four groups were observed. The first group comprised of high-income countries that experienced high mortality rates including USA, UK, Spain, Italy, France, Canada, Germany and Saudi Arabia. In these countries, parasitic infections were completely eradicated before the 2nd world war. The second group comprised high income countries that experiences relatively low mortality rates like including countries like Australia, Japan South Korea, Taiwan, Malaysia, China and Thailand which are the latest countries to industrialized. In these countries parasites have been widespread in until the recent past. The third group comprised middle-income countries with high mortality rates like Peru, Brazil, Mexico, Columbia, Argentina, South Africa, turkey and Poland where economic inequality is evident. The high mortality rate in the countries could be explained by the fact that the very rich in the country were susceptible to infection as suggested by the hygiene hypothesis. A fourth group comprised middle to low-income countries including Kenya, Uganda and other developing countries where low mortality rates were experienced; indeed the populations seemed resistant to COVID 19 infection. Parasites are still endemic in the countries.

Conclusion: In summary eradication of parasitic diseases has been a struggle by Scientists, ironically this is leading to their own extinction!! However, with the successful eradication, can it be said 'and the people lived happy ever after!

27. Post vaccination SARS-CoV-2 Antibody Responses among Healthcare Workers at a Tertiary Health Facility in Kenya

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Background: Vaccination against SARS-CoV-2 has greatly reduced the spread and severity of COVID-19 infections since widespread rollout begun around March 2021. In Kenya, a total of 23,750,431 vaccine doses had been administered by July 2023 with only 21.4% population having completed the primary vaccination series. Healthcare workers were categorised as high-risk individuals at the onset and during the epidemic and were thus prioritized to get vaccinated alongside other vulnerable groups.

We assessed how demographics and the different vaccines administered impacted antibody responses and COVID-19 infections among clinical and non-clinical healthcare workers at Aga Khan University Hospital, Nairobi (AKUHN).

Methods: This was a continuation of a previous prevaccine SARS-CoV-2 seroprevalence study among healthcare workers at AKUHN which had enrolled over 1600 participants.

For this continuation phase conducted between November2021 and February 2023, both SARS-CoV-2 spike and nucleocapsid antibodies were measured at two time intervals after vaccination. Spike antibodies were determined using the Wantai total spike antibody kit (Beijing Wantai Biological Pharmacy Enterprise, China) on an ELISA platform and nucleocapsid antibodies using the Elecsys Anti-SARS-CoV-2 kit (Roche Diagnostics, Germany) on an automated chemiluminescent platform.

Results: Out of the initial 1631 participants in the parent study, 981 and 764 healthcare workers participated in the 1st and 2nd phases of the post vaccine study, respectively.

The median age was 35 years [Interquartile range (IQR): 30-42] and females comprised 56% (554) of the participants. Clinical staff were 542 (56%) and 119 (12%) worked in a COVID-19 designated area. AstraZeneca was the most administered vaccine (80%) for the two doses followed by Moderna (12%).

Spike antibodies were detected in 100% and in 93% (708) of participants at the first and second post-vaccine tests, respectively.

Nucleocapsid antibodies were present in 59% (575) and in 26% (201) of participants at the first and second post-vaccine tests, respectively. A positive nucleocapsid result at the second test was associated with a positive anti-spike result at the second test ($X2 = 95.9$, $p<0.001$) but not at the 1st pair of tests ($X2 = 2.9$, $p = 0.09$)

Seventy-six participants tested positive by PCR for COVID-19 after full vaccination.

Conclusion: Almost all participants developed spike antibodies after vaccination but the levels decreased significantly by the time of second test, hence vigilance should continue. Age, sex and type of vaccine administered did not significantly impact antibody response.

Sub-theme 3: Addressing social, economic and political impacts caused by COVID-19 pandemic

28. Association between COVID 19 and Fungi Isolated from Indoor Urban Environments in Nairobi Kenya
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Introduction: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) causes direct damage to the respiratory epithelium and immune dysregulation leading patients to an increase in their susceptibility to fungal superinfections.
Coronavirus disease 2019 (COVID-19)-associated invasive pulmonary aspergillosis presents a diagnostic challenge due to its non-specific clinical/imaging features, as well as the fact that the proposed clinically diagnostic algorithms do not necessarily apply to COVID-19 patients. In addition, Fusarium spp. is a rare cause of opportunistic life-threatening fungal infections. Disseminated Fusarium infection in an immunocompromised host is intractable, with a high likelihood of resulting mortality. Anthropogenic indoor air pollution continues to be seen as an environmental and public health problem. Its seriousness lies in exposure to fungi that can trigger allergic reactions, hypersensitivity pneumonitis, allergic rhinitis, and some types of asthma. Fungi are ubiquitous in nature and contribute to 10% of bioaerosols' biodiversity. Identification of these fungi is based on phenotypic methods whereas genotypic identification is seldom applied. This study sought to identify and characterize indoor fungi by molecular methods.
Material and methods: 150 fungi strains isolated from indoor environments in urban settings in Kenya were used. Molecular characterization was performed with Polymerase chain reaction and Sequencing of the β-tubulin, Fum6, and Calmodulin genes. Immunochromatography, High-performance liquid chromatography (HPLC) was employed for the detection of mycotoxins
Results: The most frequently isolated was Penicillium spp 63% (81/127), followed by Fusarium spp 19% (25/127) and Aspergillus spp11%(15/127). 5% (7/127) of the strains were contaminated. The fum6 and fum8 genes in the fumonisin-producing gene cluster, and the idh gene in the patulin-producing were detected. Citrinin was not detected.

Sub-theme 4: Harnessing digital technologies for preparedness and responses to communicable and non-communicable diseases

29. Predicting Adverse Pregnancy Outcome in Rwanda Using Machine Learning Techniques
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Background: Adverse pregnancy outcomes have significant short-term and long-term effects on both the mother and the infant, these outcomes can lead to neonatal and maternal morbidity and mortality, with long-term consequences such as developmental delays, chronic health conditions, and increased healthcare costs. The main objective of this study was to predict the adverse pregnancy outcomes in Rwanda using supervised machine learning algorithms Analyzing data from Rwanda demographic and health survey 2019-2020.
Methods: This study was cross-sectional and utilized the data from Rwanda demographic and health survey carried on 14634 women (RDHS, 2019-2020). K-Fold cross validation (k=10) was used to split the dataset, SMOTE solved class imbalance. Descriptive analysis determined the observed adverse pregnancy outcomes, Multivariate analysis employed to identify the factors associated with adverse pregnancy outcomes. Seven ML algorithms were employed and model performance metrics (accuracy, precision, recall, F1 Score and AUC) were evaluated to identify the best performance algorithms.
Results: The findings revealed that 93.4% of pregnancies resulted in live births, 4.5% ended in miscarriage or stillbirths (2.1%). The multiple logistic regression analysis indicated that Advanced maternal age (AOR: 3.452, 95% CI: 1.946-6.680), a higher age at first sexual intercourse (AOR: 1.421, 95% CI: 1.300 – 1.611), and many unions (AOR: 1.320, 95% CI: 1.104 – 1.573) were risk factors for adverse pregnancy outcomes. However, the risk was lower among married women (AOR: 0.894, 95% CI: 0.787 – 0.966) and women who attended antenatal care (ANC) visits (AOR: 0.801, 95% CI: 0.664 – 0.9615). The K-nearest neighbors (KNN) model was the most effective model for predicting adverse pregnancy outcomes with 86% accuracy, precision (89%), recall score (97%), F1 score (93%) and AUC (0.842).
Conclusions: Promote essential antenatal care (ANC) visits, particularly for high-risk groups such as those with advanced maternal age is essential for minimizing risks of adverse pregnancy outcome. ML algorithms can be used for accurately identifying potential risks at an early stage of pregnancy to enable healthcare professionals to intervene promptly and implement appropriate interventions and treatments.

30. E-commerce; Bridging the Gap to Contraceptive Accessibility in Kenya

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Background: COVID-19 pandemic affected access to contraceptive services for women in Kenya and globally. There is need to develop alternative channels for women to access contraceptives in case of future pandemics. E-commerce offers a discreet and streamlined option for accessing sexual and reproductive health products. We set out to assess women's perceptions on the effects of COVID-19 on access to contraceptive products and to explore the potential of e-commerce to improve access to contraception in Kenya.
Methods: This was a mixed method study involving qualitative data collection among women 15-45 years in Nairobi and Kisumu Counties in Kenya and a descriptive web-analysis of an e-commerce platform following an intervention to increase awareness and visibility of the platform. From February to May 2021, 61 IDIs assessing perceptions on contraceptive access during COVID-19 were conducted. The web-analysis followed the e-commerce intervention in 2022-2023. Qualitative data was analyzed thematically using comparative analysis while descriptive analysis was applied to analyze the web data by comparing pre and post intervention sales.
Results: Women faced uncertainty as to when and how to access contraceptive products during COVID-19 lockdown. Due to limited work hours they had challenges accessing health facilities. They also had to grappled with an increased cost of the contraceptive products. Web-analytic results showed that before our intervention only 78 (∼3%) customers out of (N = 2874) visited the site to purchase a contraceptive product while 2661 (∼93%) accessed it post-intervention. Most customers who accessed the site post intervention were young 20-24 years (37%) compared to only 17% of those aged 31-39 years.
Conclusion: COVID 19 highlighted the need for alternative channels for accessing contraceptives. E-commerce is an avenue that can be explored. With awareness creation, particularly younger women, may be willing to adopt this as a service provision model.

31. Development and Implementation of a Digital Application for Infectious Disease Surveillance in Tanzanian Referral Hospitals

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Introduction: Electronic health records systems (EHRS) have improved overall health information management activities. In many African hospitals, the primary focus has been on reducing paperwork and increasing efficiency to the benefit of patient care. EHRS including DHIS2 are sources of information to improve the quality of healthcare, clinical research, epidemiological surveillance and clinical decision-making support systems. In the pursuit of effective infectious disease surveillance, various digital tools and technologies have been harnessed to track and manage diseases. Currently, DHIS2 does not provide an option for integrating epidemiological information and pathogen genomics data. Developing a novel application that combines DHIS2-aggregated data with pathogen genomics data can enhance information management and utilization, and proactively respond to public health emergencies including outbreaks.
Methods: This study presents the development and implementation of a novel digital application for disease surveillance in six regional referral hospitals in Tanzania. Conducted over a period of 4 months, starting from April 2023.The study focused on patients presenting with fever and diarrhea because of their significance as common symptoms of various infectious diseases. Stool and blood samples were collected from these patients for sequence-based infectious pathogens investigation. The application was built on the DHIS-2 open-source platform and designed to capture essential demographic, socio-economic, infectious diagnostics, environmental, and epidemiological information.
Results: As of the present study is still ongoing, and a total of 530 samples have been successfully gathered within a four-month timeframe. Among these, 403 blood samples and 127 stool samples were collected. The collected samples are slated for sequencing, which will generate crucial bio-informatics data. This data holds the potential for precise diagnostic insights, further enhancing disease detection and management capabilities.
Conclusion: The digital application developed will play a vital role in bolstering preparedness against various infectious diseases. The data integration will enable valuable insights for early preparedness, response, and management of infectious diseases. However, during its development, certain challenges were encountered, such as data completeness issues where some variables had inadequate crucial information and complexities in extracting and integrating genomic data, requiring specialized expertise.

32. Innovations in Cancer Registration for Automated Data Collection with Electronic Medical Health Information: Integration of Rwanda Cancer Registry into DHIS2

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Background: Population-based cancer registries play an essential role in providing reliable data on cancer incidence and mortality. Most registries in low- and middle-income countries use cancer registrars travelling to various sources of information for data collection using paper forms and data entry in a centralized office, posing sustainability challenges with limited funding for staff and travel costs. Rwanda's Ministry of Health has integrated the cancer registry into the existing health surveillance system, DHIS2, to ensure sustainability.
Methods: Historically since 2010, in Rwanda, cancer registration was paper based and data entry into a centralized canreg5 software. DHIS2 was first introduced in Rwanda in 2011 for reporting routine health aggregate data and later upgraded to host individual records with TB, HIV, Immunization et c. Since 2019, the cancer registry was also integrated into DHIS2 according to international standards of cancer registration as defined by IARC to ensure sustainability. The interoperability between DHIS2 and Canreg5 was done to ensure data exchange and advanced analysis with Canreg 5.
Results: The oncology module of the DHIS2 cancer registry has nationwide coverage. 90 focal persons from 73 information sources, including hospitals, clinics, laboratories and mortality databases, have been trained in cancer registration within their respective institutions, under the coordination of the Rwanda Biomedical Centre (RBC) cancer registration office. A total of 35,132 cases from 2007 to 2021 are recorded in the DHIS2 database. We analyzed data for the last 5 years (2016 to 2020) (n = 17, 290). Prostate cancer was the main cancer in men (36.6%), followed by stomach cancer (8.6%). In women, the main cancers were cervical cancer (22.2%) and breast cancer (22.4%).
Conclusion: Integrating the cancer registry into existing health surveillance system including electronic health information system such as DHIS2 for automated data management, is the cornerstone of the cancer registry's sustainability.

33. Utilization of Digital Health Systems to Describe Trends and Spatial Distribution of Organophosphate Poisoning in Uganda, 2017–2022: A Case Study of the District Health Information System-2 Digital Health Platform

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Introduction: Digital health systems track progress and provide timely information on routinely collected disease surveillance information. Organophosphate (OP) poisoning is mainly attributed to pesticide use and is the leading cause of poisoning worldwide, with >3,000,000 poisonings and >300,000 deaths globally per year. As a country with an agriculture-based economy, Uganda has widespread use of pesticides, creating an elevated risk for OP poisoning, yet this information is not routinely analyzed in digital health platforms. We assessed the temporal trends and spatial distribution of OP poisoning admissions in Uganda during 2017—2022 to guide control and prevention.
Methods: We analyzed secondary data from the national digital health platform; the District Health Information System version-2 (DHIS-2) about OP poisoning admissions and deaths. We calculated the annual incidence of OP poisoning admissions per population and case-fatality rates. We used line graphs to describe national OP admission trends. The Mann-Kendall (MK) test was used to determine the direction and strength of the trend and $p \leq 0.05$ was considered significant.
Results: Over the study period, a total of 37,883 (average: 6,314 per year) OP admissions and 1,599 (average: 267 per year) deaths were reported (case-fatality rate [CFR] = 4.2%). The average OP admission incidence was 15/100,000. Males (incidence = 18/100,000), children <5 years (incidence = 20/100,000), and residents of Ankole Region (incidence = 26/100,000) were the most affected. The incidence of OP admissions declined by 3-fold over the study period (MK = -13, p = 0.02). Reporting rates of OP poisoning increased from 79% to 94%.
Conclusion: From 2017-2022, there was increased uptake of digital health system reporting and a reduction in the incidence of OP poisonings. Males, children <5 years, and residents in Ankole Region were the most affected. Routine analysis of OP poisoning data, continued use of digital health systems, and sensitization amongst high-risk populations could further reduce the OP burden and mortality in Uganda.

34. Use of Digital Technologies to Promote Real-time Disease Outbreak Surveillance and Responses: A Desktop Review

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Introduction: The rapid spread of infectious diseases poses significant challenges to global public health systems. In recent years, digital technologies have emerged as powerful tools to enhance disease surveillance and response efforts. This desktop review aims to explore the utilization of digital technologies in promoting real-time disease outbreak surveillance and responses.
Methods: This review draws on a comprehensive search of peer-reviewed literature, reports, and case studies from reputable databases. Such as PubMed, EBSCOhost and Web of Science, with search dates ranging from 2013–2023. The keywords used in the search included digital technologies, disease outbreak, surveillance, real-time, and response. Relevant studies were selected based on their contribution to the understanding of the topic and the diversity of approaches explored. Data was extracted into a summative table and data synthesized through grouping digital technology domains, using data charting forms.
Results: From the three databases a total of 145 publications were found. A further 26 publications were obtained from the Google scholar search engine. Inclusion and exclusion criteria were met by 35 papers: they described digital forms of technologies designed for disease surveillance, between 2013 and 2023, The publications discussed 13 technologies, of which 8 were for community-based surveillance, 2 were for facility-based surveillance, and 3 combined both forms of surveillance.
Conclusion: In conclusion, digital technologies, including medical devices, wearables, online surveillance-mapping tools, mHealth technologies, and digital syndromic surveillance systems, have shown promise in promoting real-time disease outbreak surveillance and responses. These technologies have the potential to enhance disease detection, monitoring, and response, ultimately improving public health outcomes. Further research and implementation are needed to fully leverage the potential of digital technologies in disease surveillance and response efforts, especially in the East African region,
Keywords: Digital technologies, disease outbreak, surveillance, real-time

35. Leveraging Digital Technology to Combat Covid-19: A Case Study from Nyeri County, Kenya

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Background: The COVID-19 pandemic has led to significant global public health challenges, and Nyeri County, Kenya, was no exception. To curb the spread of the virus, Kenya launched a national vaccination program in 2020 to vaccinate 90% of individuals aged 12 years and above. The government implemented the Chanjo system, a digital platform with six modules for efficient monitoring and data capture to facilitate this.
Methods: A cross-sectional study was conducted to assess the impact of digital technology on COVID-19 vaccination in Nyeri County.
Results: By June 2023, 71% of the population had received at least one vaccine dose, and 57% were fully vaccinated. The real-time documentation of vaccination data by the county, with support from the Ministry of Health contributed to Nyeri County's success, making it a leader in COVID-19 vaccination nationwide. However, some modules, particularly inventory commodity management and AEFI reporting, scored below 50% and require improvement.
Conclusion: The study emphasizes the importance of digital technology in public health responses, particularly in managing pandemics through vaccination. The efficient implementation of the Chanjo system enabled real-time tracking, effective planning, and informed decision-making. To maximize the benefits of digital platforms, it is essential to address accessibility and equity concerns to ensure all segments of the population can benefit from these technologies.
Recommendations: Based on the findings, it is recommended to prioritize enhancing the inventory commodity management and AEFI modules to improve vaccination rates and data management. Continued investment in digital infrastructure and efforts to bridge the digital divide will help ensure equitable access to vaccination and public health services, enhancing the fight against infectious diseases like COVID-19. By harnessing the potential of digital technology while upholding principles of accessibility and inclusivity, Nyeri County and other regions can strengthen global pandemic response efforts and protect public health.

Sub-theme 6: Traditional and herbal medicines use, practices and believes during COVID-19 Pandemic

36. Accelerating South Africa's Indigenous Knowledge Systems for Antiviral Drug Discovery Using Computational Modelling

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Background: Natural products or related drugs such as botanicals or herbal medicines make up approximately 35% of the annual global market, followed by 25% from plants, 13% from microorganisms and 3% from animal sources. The use of indigenous medicinal plant species used on traditional medicines has been used for centuries to treat viral infections. The constant growth of the human population and human interaction with the environment have led to several emerging and re-emerging RNA viruses responsible for diseases and pandemics. Considering the continuous spread of major viral pathogens as well as unpredictable viral outbreaks of emerging or reemerging viral strains, it is essential to ensure preparedness interventions to treat and manage yet another global health crisis.
Aim: The review article explores the potential application of computational modelling in identifying antiviral drugs informed by indigenous knowledge systems for future pandemic preparedness by the pharmaceutical industry.
Methods: The South Africa' National Recordal System, which has been developed under the IKS Policy (2007), was used to identify the indigenous medicinal plant species used to treat respiratory diseases. The plants species, *Bulbine frutescens, Cyclopia genistoides, Harpagophytum procumbens, Kigelia Africana, Siphonochilus aethopicus, Sutherlandia frutescens, Trichilia emetic, Warburgia salutaris, Xysmalobium undulatum and Lippia javanica* were identified. A systemic review of these plant species was conducted using past literature papers.
Results: From the literature, most of these plants have been shown to exhibit a wide range of chemical compounds with potential health benefits as shown in in vitro and in vivo studies for inhibition of the Human Immunodeficiency virus (HIV). The use of the computational modelling in small molecule drug discovery will proficiently accelerate the drug development process thereby impacting on the pharmaceutical industry while ensuring benefit sharing arrangements are released with the communities in terms of the Nagoya Protocol on Access and benefit sharing.

37. In-vitro Cytotoxic Effects of *Plantago major L, Ranunculus acris* and *Cannabis sativa L* Plant Species-crude Extracts against Cervical Cancer Cells

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Background: African traditional medicine incorporates herbal remedies to address diverse health conditions. Moreover, research on medicinal plants, aimed at discovering therapeutic compounds, offers societal benefits, including improving patient's quality of life and providing economic advantages for patients and herbalists. This study utilises plants with traditional medicinal benefits, such as wound healing and inflammation. Previous studies suggest potential anti-cancer characteristics in the leaves from Plantago major L., Ranunculus acris L., and Cannabis sativa L. plants, since their extracts are rich in bioactive compounds known for anti-cancer properties. However, thorough, and comprehensive research is crucial to establish their efficacy and safety. The aim of this study was to assess the impact of plant crude extracts on cervical cancer cell lines in an in-vitro setting and to isolate bioactive compounds against cervical cancer HeLa cell lines.
Methods: Leaves from Plantago major L., Ranunculus acris L., and Cannabis sativa L. plants were collected in November 2022, in the morning from Weavind Park, in the East of Pretoria, Gauteng Province, South Africa. These plants were transported back to the Council for Scientific and Industrial Research (CSIR), Agro-processing laboratory for post-sample processing and analysis, such as drying, fraction isolation, and to performing in-vitro cancer screening assays. The Presto-Blue cell viability assay was used to assess and measure the cytotoxic effects of different concentrations of the crude plant extract when administered to HeLa cells after 72 hours. The isolation of crude extracts was performed using the filtration method, wherein all ground plant samples were soaked in 100% Dichloromethane: Methanol (1:1) solvent overnight and then extracted at a flow rate of 20 mL per 8 hours for 8 hours. The solvent was vacuum-dried, and subsequently, four dilutions were prepared from each crude extract in 0.1% DMSO for cancer screening assays.
Results: Preliminary results suggest effective in-vitro inhibition of cancer cell growth by the three crude extracts. Extracts isolated from Plantago major L., Ranunculus acris, and Cannabis sativa L. plant species significantly reduced cell viability of HeLa cells when compared to the control ($p < 0.05$) in a dose-dependent manner. IC50 values in HeLa cells were: Plantago major L., (36.89 µg/mL), Ranunculus acris L., (35.14 µg/mL), and Cannabis sativa L., (34.38 µg/mL). Therefore, ongoing investigations aim to unravel their mechanisms of action and validate their ability to selectively inhibit cancer proliferation in-vitro.
Conclusion: the study underscores the anti-cancer potential of plant extracts, providing groundwork for future therapeutic application of traditional medicine.

38. Antidiabetic Pharmaceutical Drugs as Adulterants in Herbal Medicines Sold in Selected Counties in Kenya

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Background: Herbal medicines are usually marketed as natural products with multiple beneficial health claims. However, several studies have established that some of these products are adulterated with pharmaceuticals to increase their treatment effectiveness. Adulterating herbal products with pharmaceuticals can result in adverse herb–drug interactions, undermining their safety. Therefore, it is important to routinely analyze herbal products to determine if they have been adulterated with pharmaceuticals.
Methods: A liquid chromatography coupled with tandem mass spectroscopy (LC–MS/MS) method was developed and validated for simultaneous identification and quantification of four commonly used antidiabetics—metformin (MET), gliclazide (GLZ), glibenclamide (GLC), and glimepiride (GLP)—in herbal medicines. Chromatographic separation of these analytes was done using a C-18 column and a gradient elution program of 0.1% formic acid in acetonitrile.
Results: The developed method showed detection limits and quantification limits ranging from 2.86 to 7.67 ng/mL and 8.64 to 23.24 ng/mL, respectively. The accuracy was above 80% for all analytes except MET (52%). This method was then applied to analyze 24 powdered herbal drugs sourced from the Kenyan market to check for adulteration. MET was detected in 17% of the samples, with concentrations ranging from 900 to 1969 ng/g. GLC, GLZ, and GLP were not detected in any sample.
Conclusion: This method can therefore be used to analyze herbal medicines indicated for diabetes for adulteration using the four pharmaceuticals. It is envisaged that data from this study will contribute towards guiding policy on regulation of the traditional medicine practice in Kenya.

39. Gossypol and Its L-Ascorbyl Palmitate Coagel Susceptibility of Methicillin-resistant *Staphylococcus aureus* and *Staphylococcus epidermidis* in Vitro

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Introduction: Antibacterial resistance threatens the effective prevention and treatment of an ever-increasing range of infections caused by bacteria, it is an increasingly serious threat to global public health that requires action across all government sectors and society. Therefore, the new antibacterial agents in innovative therapeutic strategies are need in order to counteract the issue. In this study, gossypol, a polyphenolic compound from cotton seeds with several biological activities such as antiretroviral, antimicrobial, antischistosomal, antimalarial and anticancer properties, coupled with its L-Ascorbyl Palmitate coagels were investigated separately for their inhibiting activities against methicillin resistant Staphylococcus aureus (MRSA), Vancomycin Resistant Staphylococcus aureus (VRSA) and methicillin resistant Staphylococcus epidermidis (MRSE) strains.
Methods: The synergy between gossypol and vancomycin was investigated against Vancomycin Resistant Staphylococcal strains (VRSA) by the checkerboard method.
The antibacterial studies of pure gossypol and gossypol coagel were investigated separately for their inhibiting activities against MRSA and MRSE strains using Disc and well diffusion technique, Agar dilution technique, and Broth macrodilution technique.
Results: The complete growth inhibition of tested bacteria, MRSA ATCC 43300, SA ATCC 6538, MRSA CMCC (B) 26001, MRSE ATCC 35964, SE CMCC (B) 26069, VRSA ATCC 700699 and VRSA ATCC 700698 respectively occurred at 16µg/ml, 4µg/ml, 8µg/ml, 8 µg/ml, 8µg/ml, 2µg/ml and 2µg/ml. Gossypol coagel 7% (w/w) and 30mg were respectively considered as an optimal concentration and amount to exhibit a maximum antimicrobial activity for this system. The synergy between gossypol and vancomycin was investigated using broth checkerboard method, it resulted to the synergy and additive combinations; for strains resistant to vancomycin, VRSA ATCC 700699 and VRSA ATCC 700698 the synergy occurs at ΣFIC = 0.5 each. Generally, ΣFIC indices of gossypol and vancomycin among other strains were arranged between 0.375 and 0.75. The mechanism of identification of gossypol against staphylococcal strains revealed that it interacts with peptidoglycan of cell wall which probably led to the bacteria lysis.
Conclusion: These findings can serve as pillar from which gossypol will be used alone or in combination as antibiotic against staphylococcal infections. But further in vivo and clinical studies are needed before conferring gossypol in clinical use.

40. Assessing the Antibacterial Activity of *Aloe vera* against *Staphylococcus aureus* and *Escherichia coli* Isolates

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Introduction: Staphylococcus aureus and Escherichia coli are two bacteria that have become resistant to frequently used antibiotics. Aloe vera plant is known to have antibacterial properties and can serve as alternative source of effective antimicrobials.
Methods: This study aimed at assessing antibacterial activity of Aloe vera leaves. Aloe vera leaves were collected from Karongi district and transported to the microbiology laboratory of the University of Rwanda, College of Science and Technology. The antibacterial

activity of A. vera leaves against E. coli and S. aureus isolates was evaluated using its gel and crude extracts by the disk diffusion and broth microdilution methods. Amoxicillin and penicillin V were used as positive controls. Escherichia coli was isolated from wastewater and cultured on MacConkey Agar (MCA) while S. aureus was isolated from sweat and cultured on Mannitol Salt Agar (MSA). Aloe vera leaves were stripped of their gel while A. vera powder was dissolved in dimethyl sulfoxide [DMSO]. The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were recorded.
Results: The results obtained for disk diffusion showed that the inhibition zones for amoxicillin on E. coli and S. aureus were 30 mm and 20 mm, respectively. Inhibition zones of crude extract of A. vera on E. coli and S. aureus were 18mm and 17mm, respectively while the ones for the gel on E. coli and S. aureus were 16mm and 14mm, respectively. MIC of A. vera crude for both E. coli and S. aureus was 0.125 g/ml. MICs of A. vera gel for *E. coli* and *S. aureus* were 0.0625 ml/ml and 0.03125 ml/ml, respectively. For penicillin V, MICs on *E. coli* and *S. aureus* were 0.03125 g/ml and 0.015625 g/ml, respectively. The MBCs ranged between 0.06-0.5 g/ml.
Conclusion: The findings showed that A. vera has antibacterial activity closer to that of conventional antibiotics. Further studies are needed for characterization of phytochemicals of Aloe vera and screen their antimicrobial activities.

41. Challenges Mapping of Medicinal Resources with Potential to Mitigate COVID-19 and Other SARS-like Ailments in the K1-7 Flora Regions of Kenya: Field Experience

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Introduction: The COVID-19 pandemic prompted a global search for effective treatments and preventive measures. In the absence of a known cure for COVID-19, many turned to the use of alternative medicine which have been used for centuries in various cultures to treat illnesses and boost immunity, Kenya was no exception. This paper presents field experiences while collecting traditional medicine and medicinal products with the potential to mitigate COVID-19.
Methods: Participatory ethno-botanical and ethno-medical surveys were done in the K1-K7 plant distribution regions of Kenya and mapping of medicinal plants, herbal products and food resources used to mitigate COVID-19 and other SARS-like ailments. Local healers, herbalists, and Traditional Health Practitioners (THPs) were engaged in interviews and discussions. Forest transects walks guided by lead practitioners were conducted to identify, quantify, document, and collect medicinal resources known for their medicinal properties believed to possess antiviral or immune-boosting properties.
Results: Samples from 434 medicinal plants mentioned by the THPs to be in use in the management of COVID-19 and related respiratory illnesses were collected. The field experiences were as follows: The THPs and communities were very protective of their resources and only allowed collection of very small quantities of some of the medicinal plants. In some instances, there was theft of the medicinal plant samples collected from the forests presumably by the THPs, who are otherwise denied access to the forests. Following a new directive by Chief Conservator of Forests the research team was denied permission to access government forests in Trans Nzoia County hence they resorted to collecting samples in farmers' fields, open grounds and along roadsides. The plant collection took place during the dry season, resulting in difficulties obtaining certain plant parts, such as leaves or, at times, the entire plant. The THPs expressed research fatigue and skepticism, likely stemming from past experiences of exploitation by researchers or quacks. Some of the survey areas like Pokot and Baringo were insecure due to banditry hence could not be accessed.
Conclusion: This paper explored the challenges faced during COVID-19 plant collection, including limited access to medicinal plant resources, regulatory barriers, and cultural factors. The findings underscore the importance of integrating traditional knowledge with scientific approaches to develop effective and culturally appropriate interventions against COVID-19.

42. Toxicity and In vivo Anti-diabetic Evaluation of a Poly Herbal Formulation Containing *Azadirachta indica*, *Kigelia africana* and Vernonia amygdalina

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Background: Diabetes mellitus presented significant health challenges during COVID-19. This study examined the phytochemical and pharmacological antidiabetic potential of a polyherbal extract containing *Azadirachta indica*, *Kigelia africana* and *Vernonia amygdalina*.
Methods: The acidified ethanolic extract was analyzed for bioactive compounds using GC-MS. The acute toxicity of the extract as LD_{50} was determined with Wistar albino rats at increasing doses that ranged from 2500- 12,500mg/kg Body weight (BW). Sub-acute toxicity and antiabetic activity were also determined by administering extract to four groups of twelve Wistar

albino rats. Three of the groups were Alloxan- induced diabetic and one group was a control. Group I received 200 mg/Kg BW (metformin) and group II and III received poly herbal extract 200 and 400 mg/Kg BW, once daily for 28 days and Group IV received water. Blood biochemical parameters (glucose, total cholesterol, HDL Cholesterol, LDL-Cholesterol triglycerides and liver enzymes) were analyzed.

Results: The results showed polyherbal extracts to contain 40 bioactive compounds with Hexadecanoic acid, ethyl ester; Triethyl citrate; Tricyclo [4.3.1.0(2,5)] decane; DL-Proline, 5-oxo-, ethyl ester and Linoleic acid ethyl ester being major The LD_{50} of the extract was more than 12,500mg/kgBW. At 200 and 400mg/kg, the extract significantly ($p \leq 0.05$) reduced glucose (76% and 75%), cholesterol (6% and 25%), triglycerides (83% and 74%), urea (81% and 84%) and creatinine (73% and 76%) respectively. Moreover, the extract at 400mg/kg BW was comparable to the normal control group. There was no significant difference ($P \leq 0.05$) in blood glucose, urea and creatinine level between 200mg/kg and 400mg/kg extract but not for blood cholesterol and triglycerides.

Conclusion: Therefore, poly herbal extract of *A. indica*, *K. africana* and *V. amygdalina* was found to be safe and exhibits strong anti-diabetic activity with improved the biochemical parameters of diabetic rats. There is need to formulate polyherbal antidiabetic herbal for clinical trial.

43. In vitro Antimycobacterial Activity of Medicinal Plants *Lantana camara, Cryptolepis sanguinolenta,* and *Zanthoxylum Leprieurii*

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Background: Imperative need exists to search for new anti-TB drugs that are safer, and more effective against drug-resistant strains. Medicinal plants have been the source of active ingredients for drug development. However, the slow growth and biosafety level requirements of *M. tuberculosis* culture are considerable challenges. *M. smegmatis* can be used as a surrogate for *M. tuberculosis*.

Objective: To conduct preliminary phytochemical screening and evaluate anti-mycobacterial activity of crude methanolic extracts of medicinal plants against M. smegmatis (mc2155) and two M. tuberculosis strains, pan-sensitive (H37Rv), and rifampicin-resistant (TMC-331).

Materials and Methods: Crude methanolic extracts, obtained from the leaves of *L. camara*, roots of *C. sanguinolenta*, and stem barks of *Z. leprieurii*, were tested for antimycobacterial activity against *M. smegmatis* (mc2155), pan-sensitive (H37Rv), and rifampicin-resistant (TMC-331) M. tuberculosis, using visual Resazurin Microtiter Assay (REMA) on 96 well plates. Preliminary qualitative phytochemical screening tests were performed using standard chemical methods.

Results: The three methanolic extracts inhibited mycobacterial growth in vitro. They were more active against rifampicin-resistant strain with MICs of 176, 97, and 45 µg/mL for L. camara, *C. sanguinolenta*, and *Z. leprieurii* extracts, respectively. The lowest activity was observed against mc2155 with MICs of 574, 325, and 520 µg/mL, respectively. Against H37Rv, activity was intermediate to those of TMC-331 and mc2155. However, *L. camara* extract showed the same activity against H37Rv and mc2155. Preliminary phytochemical analysis revealed alkaloids, flavonoids, phenolic compounds, saponins, tannins, and terpenoids.

Conclusion: Leaves of *L. camara*, roots of *C. sanguinolenta*, and stem barks of *Z. leprieurii* exhibit antimycobacterial activity against M. smegmatis, pan-sensitive, and rifampicin-resistant M. tuberculosis. This offers the possibilities for novel therapeutic opportunities against TB including multidrug-resistant TB. Further investigations on safety and mechanisms of action are required. These studies could be done using *M. smegmatis* as a surrogate for the highly pathogenic *M. tuberculosis*.

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