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Afrique One

One Health Research in Africa: Innovation, Communities and Resilient Health Systems

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Foreword

Emerging and Endemic Zoonoses (EEZs)

TTP Lead

Immune profiling of T cell responses and antibody functions in SARS-CoV-2 infection, exploring differential disease prognosis in African and European populations.

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Introduction: Africa's unexpectedly mild COVID-19 outcomes, despite low vaccination and high HIV prevalence, suggest protective immune factors. A One Health approach is crucial given SARS-CoV-2's zoonotic origin2. While T cells and antibodies confer protection, Sub-Saharan Africa lacks data on SARS-CoV-2-specific T cells and cross-reactive immunity from endemic coronaviruses. Emerging variants challenge vaccine efficacy, necessitating study of viral mutations on immunity.

Objectives: The study aims to reveal immune mechanisms behind Africa's milder COVID19 outcomes by comparing German and Kenyan cohorts through (1) quantifying SARS-CoV-2-specific T cell responses and cross-reactivity with endemic human coronaviruses (HCoVs), (2) generating a library of SARS-CoV-2 variants to assess capacity of neutralizing antibodies against variants of concern (VoCs).

Methodology: This retrospective study compared SARS-CoV-2 immunity across two cohorts using archived samples from acute COVID-19 cases, convalescents, vaccinated individuals, and pre-pandemic controls.

Objective 1: assessed T-cell immunity using SARS-CoV-2 and HCoV peptide stimulation followed by intracellular cytokine staining, and multiparameter flow cytometry to quantify cytokines and T-cell phenotype characterization.

Objective 2: generated VSVΔG-Fluc pseudoviruses bearing Spike variants via site-directed mutagenesis to evaluate serum neutralization by Incucyte and luciferase readouts. Objective 3: profiled anti-cytokine autoantibodies and autoimmune autoantibodies in plasma using multiplex assays to define prevalence and distribution.

Results:
Objective 1: Pre-pandemic (HIV+) cohort showed higher CD4+ counts predominantly naïve and central memory T cells, while convalescents had elevated CD8+ late effector memory phenotypes. TNF-α secretion exceeded IFN-γ in pre-pandemic samples.

Objective 2: SARS-CoV-2 pseudotypes were successfully generated, incorporating Beta and Omicron sub-lineage mutations. Neutralization potency was reduced against the B.1.351 and B.1.1.529 variants compared with the ancestral strain, while the German cohort showed no clear evidence of antibody waning across sampled timepoints.

Objective 3: Autoimmune Autoantibodies (AIMAs) and Anticytokine Autoantibodies (ACAs) indicate heterogeneous immune dysregulation patterns rather than disease-specific signatures, suggesting broad immune perturbations.

Conclusion: Distinct immune patterns emerged within the different populations. Neutralization potency declined against B.1.351 and B.1.1.529 variants, indicating immune escape. Heterogeneous autoantibody dysregulation (AIMAs/ACAs) rather than disease-specific signatures suggests variant evolution and autoimmunity challenge immunity. A One Health approach is needed to explain population-specific outcomes.

Keywords: Immune responses, SARS-CoV-2, Pseudoviruses, COVID-19

Biofilm-Forming and Multidrug-Resistant Enterococcus faecalis in Ready-to-Eat Foods and Water in Accra, Ghana

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Introduction/Background/Objectives: In the food industry *Enterococcus* species play a dual role, functioning as beneficial probiotics in cheese fermentation while also acting as spoilage organisms in meat. Recognized as indicators of fecal contamination, they have been implicated in both foodborne and nosocomial infections. Certain strains produce bacteriocins that inhibit pathogens such as *Listeria monocytogenes*, thereby enhancing food safety; however, their full potential in the food sector remains underexplored. This study investigated bacteriocin production, biofilm formation, and antimicrobial resistance (AMR) profiles of *Enterococcus faecalis* isolates recovered from Ready-to-eat (RTE) foods and water samples in Accra, Ghana, to assess their potential public health implications.

Methodology: *Enterococcus faecalis* isolates recovered from RTE foods around Maamobi General Hospital and Kaneshie Polyclinic in Accra were revived from −80 ˚C glycerol stocks, subcultured on nutrient agar, and confirmed using MALDI-TOF MS. Antimicrobial susceptibility testing was performed using the Epsilometer (E-test) method to determine minimum inhibitory concentrations, with emphasis on detecting vancomycin-resistant *Enterococcus* (VRE), while biofilm formation was assessed using a 96-well microtiter plate crystal violet assay.

Additional phenotypic assays and whole-genome sequencing were conducted to characterize antimicrobial resistance, virulence determinants, and genomic features of the isolates. Fourteen isolates were analyzed using phenotypic assays and whole-genome sequencing to identify resistance determinants, virulence-associated genes, and genetic relatedness.

Results: Genomic analysis revealed that 13 of the 14 isolates harbored biofilm-associated genes *(ebpA, ebpB, ebpC)*, although only eight demonstrated phenotypic biofilm formation, suggesting that environmental or regulatory factors influence gene expression. Antimicrobial susceptibility testing showed that five isolates were multidrug resistant, with notable resistance to erythromycin (5/14) and linezolid (3/14). Additional resistance patterns included chloramphenicol, penicillin, and ciprofloxacin resistance in two isolates, and tetracycline and vancomycin resistance in four isolates. Corresponding resistance genes, including *lsa(A)*, *cat*, *ermB*, *tet(M)*, and *tet(C)*, were detected alongside multiple plasmid replicons *(rep9a, repA (pTW9), rep9b, rep22, rep32*, *rep9*t, *repUS43*, *col3M*), indicating the potential for horizontal gene transfer. Clinically relevant sequence types, including ST16, ST79, ST126, ST81, ST242, and ST376, were identified, highlighting the presence of strains with known clinical significance within the food chain. Phylogenetic analysis demonstrated close genetic relatedness among isolates from diverse food sources and washing water, with clustering patterns suggesting shared contamination pathways.

Conclusions/Outlook: The intermixing of isolates across different sample types indicates possible cross-contamination during food preparation, handling, or through environmental reservoirs such as water used for washing. Overall, the coexistence of antimicrobial resistance, virulence-associated traits, and genetic relatedness among *E. faecalis* isolates from RTE foods underscores their emerging role as food safety hazards. These findings highlight the need for continuous genomic surveillance, improved hygiene practices, and strengthened antimicrobial stewardship within food production and distribution systems.

Keywords: biofilm, ready-to-eat (RTE) food, antimicrobial resistance (AMR), Enterococcus faecalis, Whole genome sequencing (WGS)

Rodent-borne disease risk in West and Central Africa: Mapping pathways and drivers for One Health action

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Introduction/Background/Objectives: Over the past decade, research on wildlife-associated zoonotic diseases has increased substantially. However, previous work has highlighted important limitations, including a strong taxonomic bias toward primates, with comparatively limited attention to rodents, and a lack of interdisciplinary integration, with only a small proportion of studies adopting a One Health approach.

As a result, current evidence remains fragmented and insufficient to capture how zoonotic risks emerge and evolve across the transmission pathway, particularly at the human–animal interface where exposure occurs. In addition, socio-ecological drivers including human behaviors, environmental conditions, and livelihood constraints are often described but rarely integrated into analytical frameworks linking exposure to infection outcomes.

Building on these gaps, this study aims to (i) map rodent-borne disease exposure across the transmission pathway, and (ii) identify key socio-ecological drivers and evidence gaps to inform actionable One Health strategies.

Methodology: A systematic review was conducted following PRISMA guidelines, resulting in the inclusion of 88 studies. Data were extracted

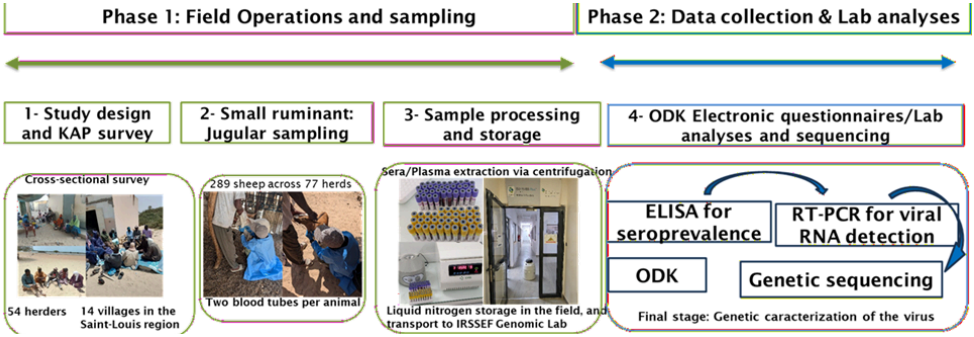
conceptual framework structured around key stages of transmission: reservoir, human exposure, transmission, and human infection. Socio-ecological drivers including knowledge, attitudes and practices (KAP), wild meat-related practices, environmental conditions, livelihoods, and structural factors were systematically identified and mapped across pathway stages. An evidence-to-action gap analysis was then performed to assess the level of evidence available at each stage, identify research gaps, and propose priority actions aligned with a One Health approach.

Results: The review highlights that evidence is unevenly distributed across the transmission pathway and remains largely descriptive. Moderate evidence is available at the exposure stage, where frequent human–rodent interactions are documented through activities such as hunting, handling, and domestic contact. These interactions are shaped by multiple socio-ecological drivers, including environmental conditions, livelihood strategies, and behavioral factors. However, evidence is limited for transmission and human infection stages, with very few studies providing robust data on spillover mechanisms or clear attribution of infection to rodent exposure. Across all stages, links between identified drivers and infection outcomes are rarely quantified, and interdisciplinary integration remains weak. The evidence-to-action matrix further shows that while exposure contexts are relatively well described, critical gaps persist in understanding transmission dynamics and linking exposure to health outcomes.

Conclusions/Outlook: This review maps rodent-borne disease exposure across the transmission pathway, revealing uneven and largely descriptive evidence. While exposure is relatively well documented at human–rodent interfaces, evidence remains limited for transmission and infection, with weak attribution of infection to rodent exposure. Socio-ecological drivers including KAP, practices, environmental, livelihood, and structural factors shape exposure primarily at contact and exposure stages, but their links to infection outcomes remain poorly quantified and weakly integrated. Addressing these gaps requires stage-specific One Health actions, including integrated ecological surveillance, interface-based interventions, improved animal–human linkage studies, and strengthened health systems.

Keywords: Rodent-borne diseases, Exposure pathways, Socio-ecological drivers; One Health; West and Central Africa

Investigation of Rift Valley Fever at the Edges of Protected Areas: The role of small ruminants, rodents and herding practices in Saint-Louis, Sénégal



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Introduction : Anthropogenic pressure and rapid land-use changes around protected areas intensify human-livestock-wildlife interactions fostering zoonotic emergence (Jones et al., 2008; Karesh et al., 2012). The ecological shifts reshape vector habitats and enhance mosquito-borne pathogens transmission (Chevalier et al. 2010; Ba et al., 2017), while concurrently increasing rodent exposure, suspected as cryptic reservoirs of interspecies transmission (Meerburg et al., 2009; Han et al., 2015). In Senegal, repeated outbreaks of Rift Valley Fever (RFV) which is a vector-borne disease, occurs regularly, particularly in the northern region of Saint-Louis where the degree of cohabitation between wildlife and livestock is especially high. The large -scale RVF epidemic which began in the last quarter of 2025 in Saint-Louis and subsequently spread to several other regions of Senegal offers a unique opportunity to investigate the molecular characteristics of circulating stains and to better understand the factors triggering recurrent outbreaks. Within this framework, this study aims to achieve five specific objectives.

Firstly, to estimate RVF seroprevalence in small ruminants. Secondly, to characterize circulating viral genomes. Thereafter, to assess risk factors at the human-animal-environment interface. Furthermore, to evaluate herders' knowledge, attitudes and practices regarding the RVF; and finally, to investigate rodents as potential viral host in the epidemiology of the RVF.

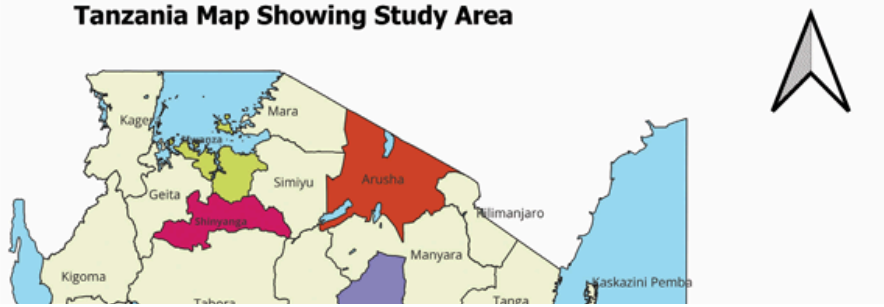
Material and methods : This research was designed as a cross-sectional field study employing stratified cluster sampling (villages as strata, and herds as clusters) to collect data around two wildlife reserves in Saint-Louis, Senegal. From October to December 2025, blood samples were collected from 289 small ruminants across 77 herds in 14 villages. Samples were processed and transferred to the "Institut de Recherche en Santé, de Surveillance Epidémiologique et de Formation" (IRESSEF) genomics laboratory in Dakar. Epidemiological data were gathered via Open Data Kit (ODK) mobile questionnaires.

Results : Initial data from the late 2025 collection phase show a male-to-female ratio of 0.3 in sampled animals. The sampled population comprises 88.6% sheep and 11.4% goats, aligning with the initial targeted species focus. The initial phase of knowledge, attitude and practice (KAP) survey related to the RVF was successfully implemented among 54 herds during the census of sheep flocks that took place as the first field activity of this work in the first quarter of 2025.

Conclusion : Preliminary findings from the KAP survey highlight a critical gap in disease awareness, emphasizing the need for targeted community education. Moving forward, this study will integrate continued small ruminants and rodents sampling with ELISA, RT-PCR analyses and sequencing at the IRESSEF. Through this work, I will develop competence in advanced bioinformatic and phylogenetic analyses. Ultimately, the results will be shared with the herders' communities of the study zone during an engagement session involving all local health and livestock stakeholders.

Keywords: rift valley fever; small ruminants; One Health

Genetic relationship of mycobacteria culture isolates from the human-livestock interface using next generation sequencing in Tanzania



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Introduction/Background/Objectives: Tanzania being among the African leading countries in livestock husbandry, the risk of transmission of mycobacteria between hosts is high. Genetic relationship of mycobacteria isolated from humans and animals and specifically livestock has not been thoroughly investigated in Tanzania. Kazwala et al. 2006 studied *M.bovis* in specific using classical molecular techniques such as RFLT. However, this current study broadly investigates all types of mycobacteria strains circulating between humans and livestock using the next generation sequencing. It determines the similarities and differences between these two hosts. Ongoing DNA extraction and sequencing is going to provide more detailed information on the similarities and differences.

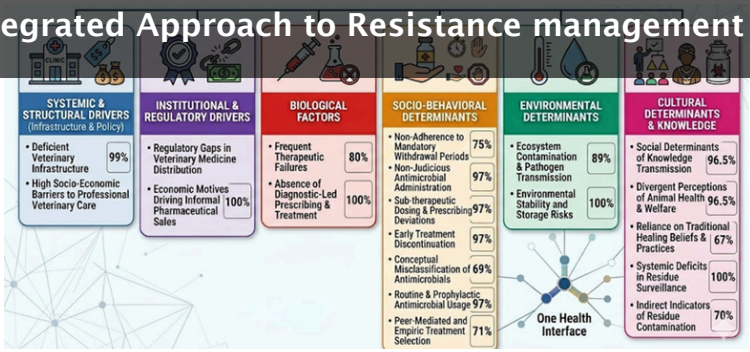
Methodology: This was a cross-sectional study that involved collecting and processing of aseptically collected tissue, 132 (96%) from livestock and sputum, 137 (100%) from humans in CPC. Eight slaughterhouses from five regions with highest meat production were included. These samples were cultured on LJ for isolation of mycobacteria at the Central Reference TB laboratory. Culture positive samples (N=46) are subcultured for DNA extraction using CTAB before the next generation sequencing.

Results: A total of 296 samples were cultured. A total of 132 (96%) tissue samples and 137 (100%101 (74%) humans have been collected and cultured on LJ media. Smear microscopy reported 2.3% positivity on the tissue and 20% on sputum samples. This was slightly higher by LJ culture; 6.8% by 27% respectively. Most of the tissue samples (80%) came from cattle and the remaining were from goats. Organs from which tissue were collected included Liver (40%), Lungs (37%), and Lymphnodes (23%). Dar es Salaam led in the number of tissue samples collected while Dodoma had the list.
More male (60%) patients with classical TB symptoms were recruited and collected a sample than females. Most of the enrolled patients were between the age of 35 to 44 years. While most of enrolled patients were from Dar es Salaam, 29% of enrolled were previously treated TB patients. 27% of the sputum samples turn out positive for culture.

Conclusions/Outlook: Risk of transmission of mycobacterial infections between human and livestock is not negligible in Tanzania. This study has identified significant burdens and similarities of the strain between the two hosts suggesting cross-species transmission. Elimination of mycobacterial infections in humans such as Tuberculosis strongly requires a deep understanding and elimination of the infection in animals and specifically livestock.

Keywords: Mycobacteria, relationship, human, animal, and sequencing

Drivers and Dynamics of AMR in Togo's Dairy Value Chain: An Integrated Approach to Resistance management



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Introduction/Background/Objectives: Livestock systems are key drivers of antimicrobial resistance (AMR) through veterinary antibiotic use and informal products value chain dynamics. Yet the data on Togo's expanding dairy sector and related risks remain scarce. This study aims to maps antibiotic access and use, assess human, social, and environmental drivers of resistance, characterize resistance genes in key dairy pathogens, and co-develop mitigation strategies.

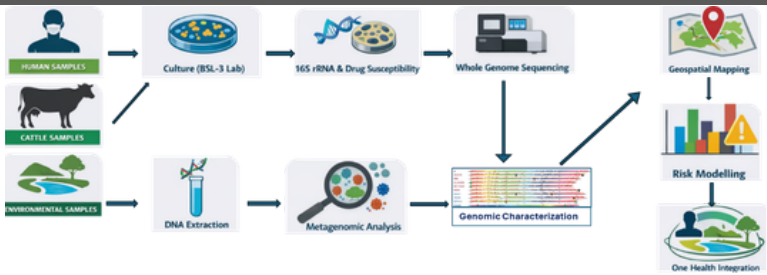
Methodology: A cross-sectional, mixed-methods design combining qualitative and quantitative approaches was employed in the Haho region. Data on antibiotic use patterns (drug selection, dose adherence, peer-influenced decision-making) and socioeconomic determinants were collected via structured questionnaires and in-depth interviews with 150 dairy farmers, 322 households, 50 milk vendors, 3 drug sellers, and 2 formal animal health practitioners. Samples collected included 150 cow dung, 115 milk, 50 soil, 40 cheese, and 21 animal drinking waters. A socio-ecological framework is applied to derive collective action in AMR mitigation through participatory stakeholders group modelling.

Results : The first findings reveal a predominantly traditional mobile system (89%) with low seasonal milk yields that generate low revenues and pressure on therapeutic decisions. The results reveal that 99% of the stakeholders demonstrate an extremely low level of knowledge (KN) on antibiotics ($p<0,0387$). This KN deficit is critically widespread within street drug vendors and milk sellers due to their downstream position outside of the veterinary and health system targets. Only 8% of stakeholders maintain a good overall perception of AMR risk, leaving the vast majority (92%) conceptualizing antibiotics as ordinary, multipurpose products rather than regulated medicines. The consequence of this KN gap is the near-universal adoption of inappropriate practices. While all livestock farmers engage in poor practices due to structural constraints and economic pressure, nearly 100% of animal health professionals admit dispensing antibiotics without a systematic prescription to maintain business viability. These systemic conditions facilitate high-risk behaviors, including the frequent failure to observe mandatory withdrawal periods (75.33%) and the empirical co-administration of traditional medicinal plants. Stakeholders primarily identify training (42%) and awareness-raising (37%) as the most vital mitigation strategies. However, 21% of respondents are unable to suggest any solution, underscoring a significant blind spot of KN in the dairy value chain. To achieve effective mitigation, an integrated strategy derived from a group model building will align financial incentives with regulation, as AMR currently acts as an invisible tax that increases production costs and threatens the long-term livelihoods and food security of rural communities.

Conclusions : The AMR risk is systemic, driven by structural, economic, and institutional failures. Limited veterinary access has normalized informal antibiotic markets, undermining stewardship. Persistent KN gaps drive self-medication in a context of poor residue surveillance. Formal education remains the strongest determinant of rational antibiotic use. Awaiting laboratory results, urgent integrated interventions are required to address AMR risks at the human–animal–environment interface.

Keywords: AMR; antibiotics; Dairy value chain; One Health, Togo

Transmission Dynamics and Genomic Characterization of Mycobacteria Across the One Health Ecosystem in Northern Ghana



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Background : Mycobacterial infections remain a major global health concern, with tuberculosis (TB) caused by the *Mycobacterium tuberculosis* complex (MTBC) continuing to pose significant morbidity and mortality burdens. In addition to MTBC, nontuberculous mycobacteria (NTM) are increasingly recognized as important pathogens in both humans and animals. Environmental changes, including climate variability, and expanding human–animal interactions have contributed to the rising prevalence of NTM infections, and are further complicating drug-resistant TB treatment, due to horizontal gene transfers. In Ghana, a nationwide study in 2017 reported that over 50% of mycobacterial isolates were NTMs, with *Mycobacterium fortuitum* identified as the predominant species. Despite these findings, there is paucity of data on the transmission pathways, evolutionary relationships, and genomic drivers of pathogenicity and spread of Mycobacteria across the human–animal–environment interface in northern Ghana.

Objectives : This study aims to investigate transmission dynamics of Mycobacteria within the One Health ecosystem in northern Ghana and to characterize their evolutionary relationships and functional genomic diversity across human, animal, and environmental reservoirs.

Methodology : A cross-sectional study was conducted across the Northern, North-East, and Upper East Regions of Ghana. A total of 533 samples were collected, comprising 264 human samples (49.5%), 193 cattle tissue samples (36.2%), and 76 environmental samples (14.3%). Human samples included sputum from presumptive TB patients, nasal swabs from abattoir workers and butchers, and treatment-resistant wound swabs. Cattle tissues exhibiting TB-like lesions were obtained during post-slaughter inspections. Environmental samples (water and soil) were collected from dams, abattoir environments, cattle markets, and grazing fields characterized by close human–animal interactions. Environmental samples were processed using membrane filtration (0.44 µm) and DNA extracted using the guanidine hydrochloride method for metagenomic next-generation sequencing (mNGS). Human sputum and cattle tissues are undergoing mycobacterial culture in a BSL-3 laboratory, followed by phenotypic drug susceptibility testing and whole genome sequencing (WGS). Nasal and wound swabs are being analyzed using 16S rRNA metagenomic sequencing. Comparative genomic analysis will assess evolutionary relationships and functional gene diversity, while geospatial mapping and statistical risk modelling will identify transmission hotspots and pathways

Results : Among human participants, 76.9% were male, 51.5% were sputum samples, 46.2% nasal swabs, the rest were wound swabs. Also, from human participants, 52.7% were animal handlers, 20.1% livestock keepers, the rest, farmers. Of the 193 cattle sampled, 58.0% exhibited lung lesions, and 29.0% had lymph node involvement. Environmental sampling covered 39 high-risk sites, predominantly dams (79.5%). Genomic and culture analyses are ongoing to determine species distribution, resistance profiles, and cross-reservoir genomic relatedness.

Conclusions/Outlook : This study integrates genomic epidemiology and geospatial modelling within a One Health framework to clarify transmission pathways of Mycobacteria in northern Ghana. Findings will strengthen surveillance, inform targeted control strategies, and contribute to understanding the role of environmental and zoonotic reservoirs in sustaining mycobacterial transmission.

Keywords: Mycobacteria, Tuberculosis, One Health, Zoonotic tuberculosis, Transmission dynamics

Blockchain-enabled Rabies control in Côte d'Ivoire and Mali: Ethical dimensions of technical and social adoption

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Introduction/Background/Objectives: Rabies is a priority zoonosis targeted for elimination by 2030 in Côte d'Ivoire and Mali. However, fragmented inter-sectoral communication remains a significant barrier to coordinated control. Within a One Health framework, where data integration is paramount, blockchain technology offers novel avenues for strengthening stakeholder coordination through secure and transparent information sharing. To address these systemic gaps, the transdisciplinary BlockRabies App pilot test project based on blockchain was established for both countries. But technological hesitation, knowledge deficits about security, transparency, social, and ethical conditions of its adoption, in the pilot areas create uncertainty about the initial uptake of the application. This study analyses the socio-technical and institutional dynamics that shape the co-design, participatory implementation and initial use of the app, to understand the conditions for its adoption, scale-up and long-term viability.

Methodology: This inductive qualitative study was conducted in Côte d'Ivoire and Mali, the two countries where the BlockRabies App. is being implemented. A total of 35 involved participants of the project were recruited across both countries, including researchers, laboratory technicians, veterinary and public health professionals, software developers, decision-makers, and community representatives in the study sites.

Data were collected through (i) participant observation during introduction workshops and field tests in rabies and veterinary centers; (ii) semi-structured interviews focusing on stakeholders' perceptions and representations; and (iii) a comprehensive desk review of project documents and ethical review process documents. The transcribed recording and paper-based data were both coded subjected to thematic content analysis assisted by Nvivo 14. The data analysis was guided by approaches from transdisciplinarity, new institutional economics, the ethics of health technology, and the sociology of innovation and use.

Results: The results highlight a dynamic of social interaction and inclusive participation among stakeholders around technology, thereby fostering its acceptance. The BlockRabies App was implemented through good collaboration between rabies centres, veterinary services researchers, IT-experts and laboratories. This cross-sector partnership was supported by mutual learning and institutional agreements, helped structure data governance and facilitate the circulation of Rabies cases information.
The results also show local adjustments and adaptations of the technology. Practical training was key to support users to gradually adjust and adapt the interface and functionalities of the application to professional needs and practices. The initial use of technology reflected a gradual integration of it into existing professional practices. The application is not rejected, but its adoption remains limited. Information management continues to be hybrid, combining paper forms, telephone communication and digital tools, due to technical constraints, particularly unstable and irregular Internet access, highlight the need for an offline version.

Conclusions/Outlook: The viability of blockchain depends on an appropriate legal framework, the availability of reliable IT infrastructure, the involvement and commitment of the relevant institutions, training, and users' motivation.

Keywords: Ethical and social adoption, One Health, west Africa, Blockchain technology

Integrated management of the Clinical Decision Support Tool and community engagement in rabies control in Moyen-Chari, Chad

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Introduction/Background/Objectives: The implementation of the Digital Health in Chad (SANU TD) clinical decision support Tool and community engagement against rabies are innovations for improving basic health services and access to Post-Exposure Prophylaxis (PEP) rabies vaccine. In Chad, the inaccessibility of human and animal vaccines is due to geographical, institutional, economic, and cultural difficulties. This study aims to evaluate the implementation of the Clinical Decision Support System (CDSS) and community engagement strategies aimed at improving access to rabies care.

Methodology: The survey was conducted using a mixed-method approach among human and animal health workers and community leaders based on the five dimensions of successful CDSS, namely adaptation, adoption, feasibility, acceptability, and sustainability. Data were collected using FGDs, questionnaires and individual interviews. The data were processed using SPSS and Maxqda.

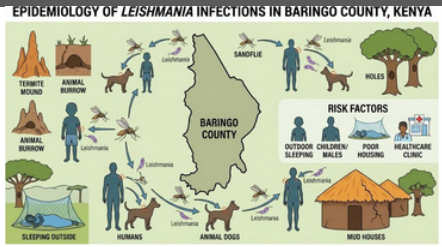
Results: The results are presented according to the five dimensions of successful CDSS. In terms of adaptability, the implementation of the tool was carefully prepared by the team in order to adapt it to the local context.

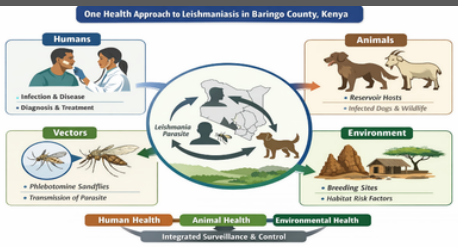
The SANU TD tool is accepted by the majority of users and appreciated by the beneficiary communities. Its adoption is marked by the motivation of agents to use the tool and the community's satisfaction with the treatment received. Feasibility is positively influenced by acceptance, but negatively influenced by insufficient power supply for recharging tablets. Another positive aspect for sustainability is the high level of acceptance among patients and caregivers. The participants in our study strongly desire the extension of the project to other health centers. The CDSS tool has had a positive impact on healthcare activities at the user level and has satisfied communities. In terms of community engagement strategy, one major element stands out: community engagement marked by the involvement of community leaders and health workers in activities to ensure ownership and sustainability. The use of CDSS within the One Health framework is accepted and appreciated by human and animal health actors in the fight against zoonoses. Agents lament the lack of qualified personnel and collaboration between different sectors. This study contributes to the strengthening of the District Health Information System, phase 2 (DHS2) implemented by the Ministry of Public Health and opens up research opportunities for researchers in the field of digital health.

Conclusions/Outlook: This study has revealed the importance of using digital tools. Users are seeking support from partners and authorities for the sustainable use and scaling up of this tool.

Keywords: Rage, digital tools, community engagement, surveillance, Chad

A One Health Perspective on Transmission of leishmaniasis: Human, Canine and environmental interactions in Baringo County, Kenya





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Introduction/Background: Leishmaniases is a group of zoonotic infections caused by leishmania parasites, transmitted by sandflies and affecting a wide range of hosts including humans, domestic and wild animals. The disease is presented as Visceral Leishmaniasis (VL), Cutaneous leishmaniasis (CL), or mucocutaneous (MCL) forms. As one of the 20 WHO-targeted neglected tropical diseases (NTD), it thrives in poor, marginalized communities lacking proper housing and healthcare. Understanding the connections between people, animals, and the environment is key to controlling its spread Kenya is one of the five countries with the heaviest burden with the current transmission foci at Baringo County. Domestic dogs are known to be the reservoir for VL in humans and Canine leishmaniasis. Understanding the connections between people, animals, and the environment is key to controlling the spread of infections.

Objectives: The study assessed the resident's knowledge, attitudes, and practices (KAP) regarding leishmaniasis, determined the prevalence of leishmania infection in dogs and humans; identified risk factors and ecological factors associated with infection. The leishmania genotypes circulating in dogs, humans and vectors will be characterized.

Methodology: A cross-sectional study was carried out in Baringo County to assess leishmaniasis prevalence, risk and ecological factors and KAP among residents. Blood samples from 380 humans and 140 dogs were tested via RDT, the positives will be confirmed by ELISA/PCR. Sandflies were captured in the same locality where dogs and humans tested positive using CDC light traps from (termite mounds, caves, tree holes) and identified morphologically in the lab pending DNA extraction and characterization.

Results: The KAP survey (n=135) revealed high awareness (94.8%) of the infection with 86.7%, 76% and 77.7% of respondents demonstrating overall moderate to good knowledge, attitude and practice respectively. Age and education significantly predicted KAP. Health workers demonstrated technical expertise in detection and management. Preliminary data on prevalence showed 6.9% and 7.8% of humans and dogs were positive for leishmania respectively by RDT/microscopy (pending ELISA/PCR confirmation). Key risk factors included young age, male sex, sleeping outside, muddy cracked houses, thatched roofs, termite mounds, and proximity to dogs. Vectors identified were *Sergentomyia*, *P. martini* and *P. duboscqi* from termite mounds, houses, sheds, and vegetation as identified by their mouth parts and genitalia.

Conclusions/Outlook: The study shows respondents have strong knowledge, attitudes, and practices regarding leishmaniasis, but gaps remain, particularly on dogs as reservoirs. Addressing these through schools, media, and a One Health approach involving veterinarians, medical, and environmental professionals are needed, supported by medical personnel's expertise and ongoing surveillance.

Keywords: Leishmania infection, Human, dogs, prevalence, KAP, risk factor, one Heath

Building an integrated psychosocial intervention model for epidemiological surveillance: Evidence based on Covid-19 and CCHF Case Studies in Senegal

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In West Africa, the resurgence of pathogens such as Crimean Congo Hemorrhagic fever (CCHF) and Covid-19, following the Ebola outbreak, have caused major social and psychological disruptions, generating fear and denial of disease and control measures. Despite progress in One Health (OH) implementation, the approach often insufficiently integrates mental health and remains poorly adapted to local contexts. While biomedical strategies have shown a certain level of effectiveness, the psychosocial dimensions, often overlooked, reveal significant gaps for affected communities.

This study aims to assess the psychosocial effects associated with the emergence of zoonotic diseases to develop an integrated psychosocial intervention model within the epidemiological surveillance system. The research draws on experiences in Senegal from Permanent Secretariat of the National High Council for Global Health Security OH in 2022, epidemiological investigations during first case detection CCHF in 2023 with Institut Pasteur de Dakar in collaboration with Prevention Division (DP) and COUS at Ministry of health, and further field investigation in 2024. A mixed method approach was used to collect data through participatory observations, field reports from 8 OH platform meetings, and 9 interviews from IPD/DP epidemiological investigation.

55 Key informant interviews were conducted both with governmental and local actors involved in epidemic management. 434 livestock keepers were surveyed to assess their knowledge on zoonotic diseases and OH interventions in their localities during public health events. Case stories from 31 victims-caregivers affected by Covid-19 (10), rabies (10), CCHF (9), and unknown diseases (2) and from livestock keepers (4) who lost animals due to these diseases.

The study identified indicators of psychological distress among victims. Case narratives highlighted that psychological distress was linked to multiple factors, including fear of infection and death, experienced stigmatization, the loss of family members and livestock, socio-economic consequences, and limited psychosocial support and mental health services during outbreaks, while presenting healthcare professionals with complex ethical challenges.

Analysis of the OH coordination platform showed that emergency responses are primarily organized around multisectoral collaboration between sectors, with operational activities largely focused on surveillance, case detection, and contact tracing. However, this coordination rarely includes social scientists, psychologists, resulting in limited integration of mental health considerations in zoonotic disease preparedness and response.The study further identified substantial knowledge disparities among central authorities, operational personnel, and communities regarding zoonotic diseases. Among 434 livestock keepers, 81.6% demonstrated limited knowledge due to low-risk perception, which showed a significant association with poor level of formal education ($p <= 0.03$). Most farmers (87.1%) reported being unaware of the OH approach, finding the concept largely unfamiliar.

The study suggests interventions should be designed to bridge central, operational, and community levels by integrating local knowledge, while strengthening cross-sector collaboration, including social workers and mental health actors.

Integrated framework to improve the effectiveness of interventions against Rabies and Dracunculiasis in sedentary and nomadic communities of the province of Moyen-Chari in Chad

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Background: Chad is an endemic country for rabies and guinea worm disease. This study explores the interactions between human and animal health governance to improve the control of these zoonosis in sedentary and nomadic communities in two districts of Moyen-Chari in Chad

Methodology: A cross-sectional mixed-methods study was conducted in December 2025 involving 37 human and 3 animal health facilities. Quantitative data was collected from 106 human and 8 animal health professionals on socio-professional characteristics, job satisfaction, knowledge, attitudes and practices related to rabies and dracunculiasis, as well as resource availability and inter-sectoral collaboration. Clinical data from 80 cases (bite exposures, rabies and dracunculiasis cases) were collected from health facilities. Semi-structured interviews were conducted with 23 community members and 12 health governance stakeholders. Quantitative data were analysed using R, while interview transcripts were analysed through thematic content analysis in NVivo 12.

Results: Human health professionals are younger and more gender-balanced, while their animal health colleagues tend to be older, mostly male, and have about twice as much work experience. The male-female ratio was 49.1% in human health and 87.5% in animal health. These ratios are reflected in the refusal of nomadic women to interact with veterinary men for the observation of a dog or to treat a sick ruminant.

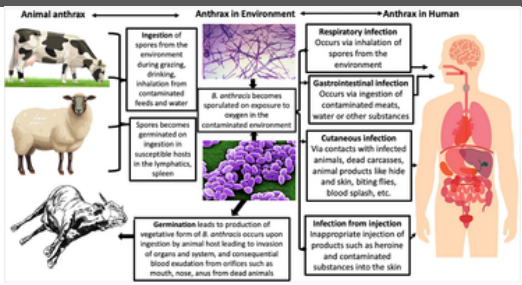
Regarding work satisfaction there is a notable difference between health sectors, 95% of human health workers are associated with positive satisfaction, while 75% of their animal health colleagues remain less satisfied. The capacity assessment revealed that the availability of equipment is very limited in animal health structures compared to human health facilities (exp. cold chain lacking in 5% in human health compared to 75% in animal health facilities), highlighting the under-funding of the animal sector also deplored by heads of veterinary posts. Collaboration analysis showed stronger internal collaboration within the health centre, while intersectoral collaboration between human and animal health sectors was weaker. Health centers act as frontline structures against zoonosis, but veterinarians are the main drivers encouraging intersectoral collaboration.

Health records showed an average of reported 3.2 bite cases per facility per month (95% CI: 2.4–4.2). Compared with incidence estimates from previous studies, this suggests significant underreporting. Veterinary registries recorded only 29 dogs placed under observation despite 49 reported bite cases, illustrating weak follow-up. Two human and 17 animal guinea worm cases have been documented jointly by human health and the Guinea worm program, including the animal sector, which remains under-reported.

Conclusion: This study identifies key resource and governance gaps, including underfunding of the elevator sector, a lack of equipment and collaboration between sectors that hinder the effectiveness of One Health interventions and zoonotic disease control in rural areas of Chad.

Keywords: Zoonosis, One Health, Human-animal interface, Health governance, Chad

Integrated Anthrax risk mapping outbreak zones in the North of Benin



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Introduction: Anthrax is a major zoonotic disease endemic in Benin and is commonly associated with areas characterized by extensive livestock production systems. Pastoral areas, where livestock farming (ruminants) is widespread, are particularly prone to sporadic cases of Anthrax. Livestock farmers and population in close contact with animals and their environment are most at risk of contracting Anthrax. Anthrax therefore represents a high risk for humans and the animal production system due to sporadic outbreaks with infected animals and humans dying every year. Despite annual vaccination programmes against Anthrax, Benin experienced regular outbreaks of anthrax in the Northern municipalities of Boukombé, Cobly, Matéri, Tanguiéta, Toucountouna and Natitingou in 2005, 2007 and 2012, which resulted in 10 deaths among individuals who consumed meat from carcasses of animals that had died of anthrax. Without biosecurity measures, areas where animals have been infected or have died remain at risk for animal and human infections for decades. The study seeks to spatially map affected zones and assess the potential risk of pathogen spread as well as the risk of human and animal infections risks associated with human activities and climatic seasons. The aim is to raise awareness and guide targeted preventive measures.

Methods: This will involve close collaboration between veterinary and medical epidemiologists, municipalities, local communities, and key stakeholders engaged in seasonal activities such as crop farming, livestock production, and charcoal production. The activities will consist of collecting data on the incidence of the disease from national archives and institutions. An epidemiological field survey for risk factors identification. Suspected contaminated sites will be georeferenced. Where feasible, soil samples will be collected and analysed using environmental PCR assays for Bacillus anthracis to characterize the level of environmental contamination and associated risks. The resulting data will be used to generate spatial maps indicating the locations of contaminated land and to estimate the potential risk of pathogen spread based risk factors.

Expected results: The outcome of this study will facilitate the rapid and targeted implementation of preventive measures in affected areas. They will help improve the protection of human and animal health and guide agricultural practices, land-use planning. In emergency situations, knowledge of at-risk areas would also support faster and more coordinated responses by medical teams and emergency services, thereby contributing to a more effective outbreak management and control.

Key words: anthrax; zoonosis; sporadic

Investigating the Role of Small Ruminants in Transmission Dynamics of African Trypanosomiasis in Kibondo and Serengeti districts, Tanzania.

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Introduction/Background/Objectives: African trypanosomiasis remains a major zoonotic and livestock disease in sub-Saharan Africa. In Tanzania, both Animal African Trypanosomiasis (AAT) and Human African Trypanosomiasis (HAT) persist in tsetse-infested ecosystems, especially near wildlife areas such as the Serengeti and Kibondo districts. While wildlife are recognized reservoirs of *Trypanosoma brucei rhodesiense*, the role of small ruminants—goats and sheep—remains poorly understood despite their abundance and close contact with humans. These animals are often overlooked in surveillance programs that mainly target cattle. This study investigates the role of small ruminants in AAT and HAT transmission by determining trypanosome prevalence in goats and sheep, assessing the presence of the human-infective *T. b. rhodesiense*, and identifying animal- and management-level risk factors at the wildlife–livestock–human interface.

Methodology: This cross-sectional study uses multistage cluster sampling in two endemic districts (Serengeti and Kibondo), targeting high-risk villages near wildlife areas, with 576 small ruminants sampled. Fieldwork is ongoing, with blood collected under a cold chain. Molecular analysis includes ITS1-PCR (species identification), TBR-PCR (*T. brucei* confirmation), and SRA PCR (*T. b. rhodesiense* detection). Questionnaires capture herd, management, and exposure data. Analysis combines prevalence estimation, GIS mapping, and mixed-effects logistic regression to identify risk factors while accounting for clustering.

Results: Field data collection is currently ongoing in Serengeti district. Initial findings indicate that all livestock keepers graze their sheep and goats, and a large proportion of them frequently observe wildlife (30/40) and tsetse flies (31/40) during grazing. While most farmers report using insecticides (30/40), very few administer trypanocides to small ruminants (37/40 do not use them). In addition, a substantial proportion of farmers (35/40) are unaware that sheep and goats can be infected with African trypanosomiasis. Knowledge about sleeping sickness is also very limited, with only 10% (4/40) of respondents aware of the disease.

Conclusions/Outlook: Preliminary findings indicate high livestock exposure to tsetse-infested wildlife interfaces alongside low farmer awareness of trypanosomiasis in small ruminants and its public health risks. Ongoing lab analyses will clarify infection prevalence and reservoir potential, supporting targeted control strategies including awareness, surveillance, and One Health interventions.

Keywords: African animal trypanosomiasis; Trypanosoma brucei rhodesiense; Small ruminants; One Health; Tanzania

Whole-Genome Sequencing Based Characterization of the Mycobacterium tuberculosis Complex in Humans and Cattle with Drug Susceptible Tuberculosis

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Introduction/Background/Objectives: Tuberculosis (TB) remains a persistent public health challenge worldwide, particularly in settings characterized by close human and livestock interactions and constrained diagnostic capacity. In Tanzania, progress toward TB control is increasingly threatened by the emergence and circulation of multidrug-resistant tuberculosis (MDR-TB), with limited genomic data available from pastoralist regions. This study investigated the genetic diversity, resistance-associated mutations, and phylogenetic relationships of Mycobacterium tuberculosis complex (MTBC) strains circulating in human and cattle populations in the Manyara Region of northern Tanzania. Specifically, it aimed to characterize multidrug-resistant MTBC strains by identifying prevalent resistance markers and determining their phylogenetic relationships across human and livestock hosts

Methodology: A cross-sectional study was conducted between September 2024 through February 2025 in Manyara region Tanzania, enrolling 178 presumptive human TB cases and collecting 161 cattle-derived samples. Diagnostic workflows combined GeneXpert MTB/RIF, Lowenstein Jensen culture, MPB64 antigen detection, and whole-genome sequencing (WGS) to enable both phenotypic and genomic characterization.

Results: Among human participants, 14 (7.8%) sputum samples were GeneXpert positive and LJ culture confirmed as M. Tuberculosis.

In cattle samples 1 (0.62%) lymph node aspirate in LJ culture yielded *M. Tuberculosis* as well. A Multivariate regression analysis identified a previous history of TB as the only statistically significant independent variable predictor of *M. Tuberculosis* positivity (p = 0.003). For Whole-genome sequencing, only five positive human isolates had good quality and revealed the presence of Lineages 1 (Indo-Oceanic), 3 (East African Indian), and 4 (Euro-American).The isolates harbored multiple resistance conferring mutations to Isoniazid, Rifampicin, Ethambutol, Pyrazinamide, Fluoroquinolone (Moxifloxacin and Levofloxacin), Bedaquiline, Streptomycin, Clofazimine, and Ethionamide resistance linked respectively to mutations detected in katG (Ser315Thr), rpoB (Gln432Glu), embB (Met306Leu), pncA (Glu111, Gln 10, p. Trp119), gyrA (Asp94Gly) , mmpR5 (198dupG) rpsl (Lys88Met), mmpR (198dupG), ald (436_437dupGC), inhA (c. -777C>7). These mutations showed different types of variation in the gene, like missense, upstream_gene_variant, stop gained, and frameshift, which indicate reduced drug susceptibility that can compromise regimen effectiveness, especially in combination therapies. Phylogenetic reconstruction showed clustering with regional sequences obtained from public databases, which reveals ongoing local circulation and potential recent transmission events.

Conclusions/Outlook: These findings suggest that TB transmission in Manyara is primarily due to human-to-human spread, with limited zoonotic contribution. They also highlight a silent yet significant burden of MDR and emerging XDR strains in pastoralist communities. The identification of various Mycobacterium tuberculosis lineages with high-confidence resistance mutations, particularly in katG, rpoB, and gyrA, indicates the likely presence of phenotypic resistance that could compromise both first- and second-line treatments. Moreover, mutations associated with newer drugs like bedaquiline and clofazimine raise concerns about the development of more advanced resistance. Some of these mutations are outside the detection scope of routine diagnostics, exposing critical gaps in current testing and treatment approaches. Overall, these results stress the need to combine genomic surveillance with phenotypic assessment in routine TB programs to enable earlier detection, more accurate treatment, and better control of resistant TB spread in northern Tanzania. Future research with larger samples is essential to validate and expand these findings.

Keywords: Phylogenetic, Lineages, Mycobacteria Tuberculosis Complex (MTBC), Whole-genome sequencing, Manyara

Antimicrobial resistance among Isolates recovered from avian and human origin in N'djamena, Chad

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Introduction: Antimicrobial resistance (AMR) is a growing public health problem. Around the world, as well as in Chad, antibiotic resistance in bacteria is on the rise, both in humans and animals. These bacteria can become resistant to antibiotics through mutation, amplification or the acquisition of resistance genes. Some studies have shown a strong correlation between the use of antibiotics in farm animals such as poultry and the emergence of antibiotic resistance in certain bacteria associated with human food-borne illnesses. Poultry products, such as meat and eggs, and poultry droppings are often considered sources of contamination for humans.

Methodology: We intend to use the "One Health" approach to isolate and assess the antimicrobial resistance of bacteria that will be isolated from eggs, deli meats, meat and feces from poultry and poultry farm workers, as well as from patients admitted to hospitals in Ndjamena and its peri-urban area. Then, using whole-genome sequencing of antimicrobial-resistant strains, we will determine the relationship between AMR genes in recovered isolates and poultry/humans.

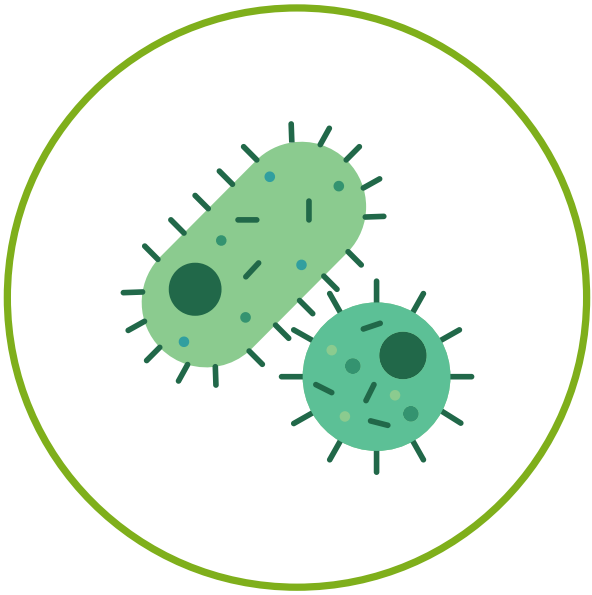
Results/Conclusions: The results of this work will enable us to understand the presence and transfer mechanisms associated with (isolates). The knowledge gained will be used in the surveillance and control of AMR among food-borne pathogens recovered from poultry meat, eggs and droppings.

With the completion of our first-year master's course in microbiology at UCAD, we have started our research with an exchange with one of the poultry farming actors who monitors poultry farms in the peri-urban areas of N'Djamena. He will put us in contact with at least twenty farms, some towards the northern exit of N'Djamena and the rest towards the southern exit.

Almost all farms produce eggs, and there are rarely broiler chicken farms. Moreover, during this heatwave period, many have restarted and are waiting for chicks to restart. We have noticed that the poultry farmers' cooperative is not operational. The questionnaire for poultry farmers will be finalized and the sampling kits acquired by July-August 2026, as well as the culture media and reagents for the lab work. Data collection and laboratory analyses are planned for October-November 2026.

Keywords: AMR, One Health, Central Africa, whole-genome sequencing

Neglected tropical diseases (NTDs)



TTP Lead

Assessing Stakeholder Interactions and Influence in One Health Implementation: A Net Mapping Study in Tanzania

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Background: Net mapping is a valuable tool essential for identifying One Health (OH) relationships, connections, interactions, and influence among OH actors. An example of this exercise was conducted in Tanzania under Capacitation OH in Eastern and Southern Africa project in September 2023 involving 26 relevant OH stakeholders. The aim was to understand how various potential OH stakeholders interact and influence the implementation of the OH strategic plan in Tanzania, which was recently reviewed for the period 2022-2027.

Methodology: The netmapping, which is preceded by purposive sampling of multi-sectoral and multi-disciplinary teams with knowledge, involvement and expertise within the OH sector. The process involves five steps i) identifying a specific goal ii) Identifying relevant OH actors who are relevant in responding to the overarching issue iii) using a stakeholder's grid to place stakeholders according to the perceived levels of influence and interest iv) defining the linkages relevant to implementation of the identified goal i.e. implementation of OH strategic plan v) building influence towers depending on how much the actors can influence the overarching goal, and finally analysing using visualizer software.

Results: Five key linkages were defined for studying the connections influencing the implementation of the OH strategic plan: coordination, funding, collaboration, capacity development and advocacy. Findings will be well displayed in a visualizer/illustrative mode. Here are the summary of key linkages.

- Coordination: The One Health Section (OHS) at the Prime Minister's office showed strong coordination, but some OH actors were less coordinated.
- Funding: Weak linkages of funding were observed, with funds mainly coming from development and implementing partners, favoring academia and national research institutes.
- Collaboration: Fairly good collaboration was observed among OH actors, with strong ties with the OHS office, Ministry of Health, Ministry of Livestock Development and Fisheries (MOLF), and implementing partners.
- Capacity Development: Weak capacity development activities were noted, indicating a need for targeted efforts aligned with the OH strategic plan.
- Advocacy/lobbying: Advocacy was weak among OH actors, with OHS showing more influence than others. Some key OH actors were also unaware of OH initiatives in Tanzania.

Conclusion: Despite some advancements of OH in Tanzania with an operational office, the five assessed linkages need to be strengthened. Tanzania has taken a significant step to operationalize OH, even at subnational levels. However, OHS needs to develop a framework for resource mobilization to sustain the OH activities. Importantly, advocacy on OH needs to be improved to strengthen integration and implementation of OH activities. Grassroot communities need to be engaged through community-based organizations which need to be capacitated to undertake OH activities.

Keywords: One Health, stakeholders, interactions , Net Mapping, Tanzania

Illegal mining 'galamsey' effects from a One Health lenses-shared narratives and contested realities from a rural district in Ghana

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Introduction/Background/Objectives: For many years, water sources, land, wildlife, human health, and safety have all been adversely impacted by the unrestrained growth of illegal artisanal small-scale gold mining (ASM) in Africa. The effect from One health perspectives had not been fully assessed in Ghana. This study assessed the effect of illegal mining from a One-health lense in a rural district in Ghana.

Methodology: A qualitative exploratory design was selected for this study. Data were collected from 20 participants who were purposefully selected and interviewed utilizing an interview guide. The qualitative data were manually evaluated using Bran and Clark's theme content analysis.

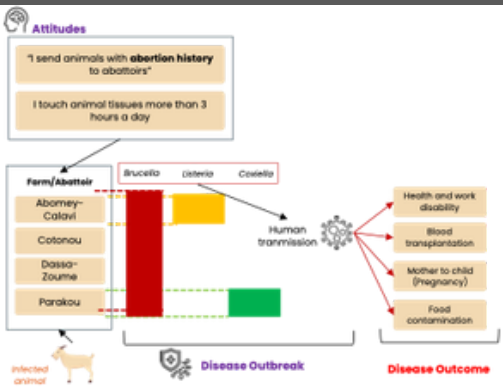
Results: The study found that water pollution, death of livestock, destruction of lands, spread of infectious diseases and environmental degradation where the environmental effects of galamsey activities. Participants consistently linked galamsey to health issues, including outbreak of infectious disease, dermatological problem, body pains increase incidence of human death and lung issues.

Pertaining to the effect of galamsey on water bodies; two themes emerged; reduction in water quality and destruction of water bodies. Participants preferred treatment options include self- medication and usage of herbal medicine. Notably, all participants reported the lack of educational programs as a major setback to the mitigation of galamsey activities in their communities.

Conclusion /Outlook: Implementing an integrated educational program in impacted communities to promote knowledge about the adverse effects of galamsey and supportive sustainable strategies is an effective way to reduce galamsey activities in Ghana.

Keywords: One health, effect, galamsey, illegal mining, Ghana

Assessment of abortive zoonoses in small ruminants integrating stakeholder knowledge, perceptions, and attitudes with animal prevalence from farm to abattoir of Benin



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Background/Objectives: In sub-Saharan Africa, abortive zoonoses such as brucellosis, Q fever, leptospirosis, and listeriosis severely impact livestock productivity and public health. However, baseline epidemiological data for small ruminants in countries like Benin remain significantly underreported. This study aims to understand psychometric parameters, prevalence, and risk factors associated with abortive zoonosis in Benin.

Methodology: A cross-sectional study was conducted between August 2024 and September 2025 across four municipalities of Benin (Parakou, Dassa-Zoumé, Abomey-Calavi, and Cotonou).

A structured questionnaire was administered to 115 respondents in four professional groups (breeders, paraveterinarians, butchers, and meat inspectors) to assess their knowledge, perception, and attitude (KPA) toward these diseases. Up to 308 sheep and goat sera and 127 tissue samples were collected, respectively, from farms and abattoirs in four municipalities. Prevalence and animal transmission risk factors were assessed through the Rose Bengal test on farms and multiplex qPCR assays in abattoirs.

Results: The respondents demonstrated limited knowledge (50.4 ± 25.2%), highly undesirable attitudes (71.0 ± 23.2%), and likely desirable attitudes (65.0 ± 24.4%) toward zoonotic diseases. Most participants perceived abortive diseases as a serious threat, yet this awareness did not translate into safer practices. They mainly think, "They are taking enough protection toward abortive zoonosis," when the most separating knowledge question was, "Cite at least three abortive zoonoses," and the most common habit in managing abortion cases is “to quickly sell the animals that have abortion histories. " Brucellosis seroprevalence at the farm level was 6.17% (95% CI: 3.93-9.53). Male sex (OR = 3.75, 95% CI: 1.18-10.65) and origin from Parakou commune (OR = 7.95, 95% CI: 1.01-1025) were identified as significant risk factors. At the abattoir level, *Brucella spp.* were detected in 6.30% (95% CI: 3.20-12.02) of samples, with male sex again strongly associated with positivity (OR = 17.56, 95% CI: 3.06-188.9). *Coxiella burnetii* and *Listeria spp.* were each detected in one sample (0.79%, 95% CI: 0.14-4.34), constituting the first molecular evidence of these pathogens in Benin's small ruminant production system. No *Leptospira spp.* was detected in tissue samples.

Conclusion: The most common habit of sending animals with abortion history to human consumption suggests a high risk of infection in abattoirs where workers usually work more than 3 hours a day with bare hands. The presence of brucellosis, listeriosis, and Q fever in all communes enhances the risk of work disability for abattoir workers and food safety.

Keywords: Abortion, Zoonoses, Small ruminant, Neglected tropical disease, One Health.

Designing a One Health Early Warning System for Toxoplasmosis in Prenatal Women and Pigs in Nairobi, Kenya: Epidemiologically Driven.

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Background/Objectives: Toxoplasmosis, caused by *Toxoplasma gondii*, is a neglected zoonosis that threatens pregnant women and the foetus, yet routine antenatal screening and integrated surveillance are lacking. Also, despite the growth of peri-urban pig farming and the established zoonotic risk posed by *T. gondii*, data on its infection in pigs, risk factors, and transmission to humans in Kenya remain limited. This study aims to develop an epidemiologically driven, mobile-based One Health early warning system for toxoplasmosis in pregnancy and enhance food safety.

Methodology: A One Health cross-sectional design was used to generate the evidence required to develop the early warning system, combining systematic review, serology, molecular analysis, and KAP assessment. A systematic review identified early warning signs, risk factors, & diagnostic indicators in pregnant women.

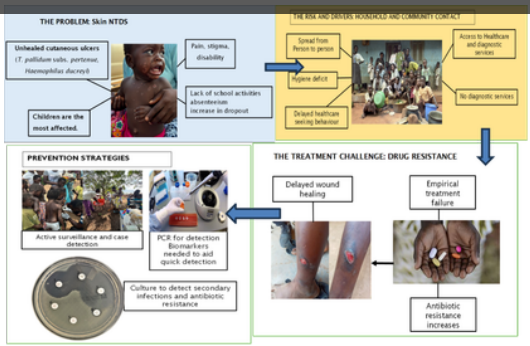
Pregnant women (n=299; Pumwani Maternity Hospital) and pigs (n=240; peri-urban farms) were tested for anti-*T. gondii* IgG by ELISA; two RDTs were evaluated against ELISA. Respondents to the KAP survey were pregnant women, pig farmers, and healthcare practitioners. Polymerase Chain Reaction (PCR) genotyping and sequencing are ongoing to assess zoonotic linkage. The integration of human, animal, laboratory, behavioural, and environmental data under the One Health framework will directly be used to develop a mobile early warning system for toxoplasmosis.

Results: Scoping review (28/407 studies) identified lymphadenopathy and flu-like illness as key maternal signs; congenital anomalies and miscarriage as major foetal outcomes; reported risk factors included contact with cat faeces and contaminated soil, consumption of undercooked or raw pork meat, raw vegetables, and contaminated water; ELISA- major diagnostic approach. Pig seroprevalence was 44.6%, associated with age, poor biosecurity, unsafe water, and low awareness. Maternal seroprevalence was 24.4%; RDT sensitivity was lower than ELISA. KAP showed low awareness among pig farmers, with only 22.5% having heard of toxoplasmosis, and risky practices, including the presence of cats and limited biosecurity measures. Preliminary gel electrophoresis shows positive bands indicating potential target presence; however, PCR optimisation and amplification are still in progress, after which Sanger or next-generation sequencing will be conducted to confirm variants.

Conclusion/Outlook: The exposure to *Toxoplasma gondii* in pigs and pregnant women confirms ongoing zoonotic and environmental transmission. This calls for routine antenatal screening, improved farm biosecurity, targeted education, strengthened surveillance, and integration of a digital One Health early warning system to enhance maternal health and food safety in Kenya. This system will enable timely detection, risk alerts, and targeted intervention in antenatal care and pig production systems.

Keywords: Toxoplasmosis; epidemiology; One Health; Early warning system; pigs; Prenatal health

Molecular Epidemiology, Secondary Infections and Infection Pathways of Wound Causing Skin-NTDs in Rural Northern Ghana.



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Background/Objectives: Skin related Neglected tropical diseases (skin NTDs) such as Buruli ulcer, yaws and other ulcerative skin disease caused by *Haemophilus ducreyi* remain a public health concern in low resource communities in Northern Ghana. These affect many children living in settings with limited access to health care and are linked with chronic wounds, stigma, disability and negative physical and mental health outcomes. The lack of routine screening often leads to empirical treatment which may delay wound healing process, risk secondary microbial infection, promote antimicrobial resistance and eventual treatment failure. The study aims to investigate the epidemiology of wound causing skin-NTDs, assess secondary microbial infections and identify infection pathways and intervention strategies for prevention and control in rural Northern Ghana.

Methodology: A cross-sectional study was conducted in the Northern Region of Ghana. A structured questionnaire was used to collect data. From one participant, three swabs and 2.5 ml of venous blood were aseptically obtained. One swab was processed for DNA extraction and others for culture and antimicrobial sensitivity testing.

Serum form blood samples were stored for cytokine analysis. Polymerase chain reaction (PCR) was used to detect *Treponema pallidum* sub species *pertenue*, *Haemophilus ducreyi*, and *Mycobacterium ulcerans* from ulcers.

Results: A total of 9,725 individuals were screened and 1428 suspected of yaws consented to participate in the study. Among the study participants 971(68%) were males and 457(32%) were females. Only 169 tested positives for RDT.

For those whose samples were tested, 38.5% (65/169) were from children aged 1 to 5 years, 58.6% (99/169) from those aged 6–15 and 2.9% (6/169) were above 15 years. PCR detected *T. pallidum* in 24 of the169 representing 14.2% of tested lesions, and 1.7% (24/1428) of all suspected cases. The genes detected were pol A in 14.2% (24/169), tp0548 in 2.9% (5/169), and tp1031(tprL) in 2.3% (4/169). *H. ducreyi* was detected among 1.8% (3/169) of the participants and coinfection was detected in 1.8% (3/169). No lesion was positive for *mycobacterium ulcerans*.

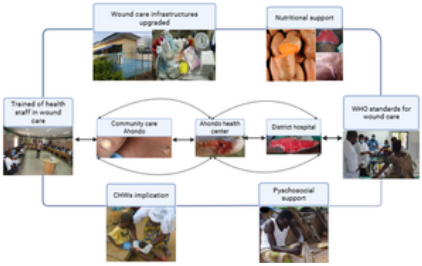
Household (aOR=4.04, 95% CI = 1.2- 5.5, p= 0.0003) and community (aOR = 1.97, 95% CI: 1.40–2.50, p = 0.0043) exposure were significant predictors of infection.

For secondary infected ulcers, A total of 95 bacterial were isolated. The predominant ones included *Staphylococcus aureus* 59(34.9%), *Pseudomonas aeruginosa* 14(8.3%) and *Streptococcus pyogenes* 9(5.3%). High resistance was detected among the broad-spectrum antibiotics such as Ampicillin ranging from 88% to 98%, and erythromycin (55 to 90%). Also 62% of the isolates were multi-drug resistant (MDR).

Conclusion/Outlook: These findings support the need for routine laboratory confirmation and target therapy, early health seeking behavior and strengthened community prevention measures.

Keywords: Infectious cutaneous ulcers, Yaws, *Hemophilus ducreyi*, Neglected Tropical Disease

Access to care and mitigation of wounds burden in Africa through community-based interventions: A One Health wound management model in rural Côte d'Ivoire



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Background/Objectives: Wounds are often the result of multiple interacting factors at the ecological, social, economic and public health interface. In Côte d'Ivoire, wound care has typically been delivered through vertical, clinically driven structures within formal health facilities (health centres, district hospitals, tertiary hospitals), with limited community health workers (CHWs) involvement despite evidence supporting community-based interventions for early active case detection. From 2019 to 2024, a community based wound care model (CBWM) for early detection and treatment of wounds was developed in Taabo HDSS, and endemic place of skin diseases in Côte d'Ivoire. The model develops relied on CHWs identified locally and trained in early detection and treatment of wound at household level including basic wound management, patient follow-up, and referral of complicated cases to formal health facilities. This study aims to assess the performance, effectiveness and associated socio-economic and psychosocial benefits of the community-based wound management model implemented.

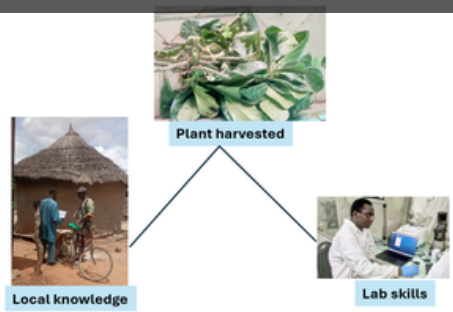
Methodology: We conducted a mixed-method cross-sectional study to assess (i) the performance of the model; community satisfaction, perceived benefits and conditions for adoption (ii) the cost-benefit of care from patients, health-system and societal perspectives and (iii) the psychosocial impact related to anxiety and depression disorders. The model performance data from community perspective were collected from 191 randomly selected household heads and 297 patients with wounds ranging from minor to chronic. Socioeconomic and psychosocial burden parameters were compared across patients who received treatment community level (n=105), health centre (n=99), district hospital (n=93). All patients were included in the socio-economic analysis. The psychosocial assessment (anxiety and depression) was conducted only among patients aged 16 years and older (n=175) using the Hospital Anxiety and Depression Scale (HADS) and established criteria reported in the literature. Additional qualitative data were collected through 16 in-depth interviews with recovered patients, village leaders, traditional healers, health staff and adult and adolescent community members. Quantitative data were analyzed using descriptive and inferential statistics while qualitative data were examined using deductive thematic content analysis.

Results: Ninety-seven (97%) of households that received wound care in the community reported satisfaction with the CBWM model. Significant positive aspects identified were healing effectiveness (44%), the availability and friendliness of CHWs (50%) and the speed of care delivery (6%). The prevalence of anxiety and depression was lower among patients treated early by CHWs (<30%) compared with those treated at hospital (> 50%). Treatment costs were lower in community care (0,41€ per case) than the health centres and district hospital (2,40€-89€).

Conclusion/Outlook: The community-based wound care model implemented is highly perceived as effective due to healing effectiveness, flexibility, availability and friendliness of CHWs. Integrating community-based interventions into wound management can reduce the economic and psychosocial burden of wounds while improving access to and uptake of care in rural settings.

Keywords: Wounds, community-based interventions, CHW, early detection, added value

Identification and Biological Characterization of Traditional Medicinal Plants Used in the Treatment Against Meningitis in Northern Côte d'Ivoire



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Background/Objectives: Meningitis remains a significant public health concern, prompting a WHO initiative for global elimination by 2030. While antibiotics are currently the primary treatment, their excessive use has accelerated the emergence of multidrug-resistant pathogens. Consequently, there is an urgent need to explore alternative therapeutics, such as indigenous medicinal plants, which require rigorous biological validation to ensure efficacy and safety.

Objective: To identify effective local plants traditionally used against meningitis or meningeal symptoms and evaluate their biological activity against pathogens in vitro.

Methodology: Plant species were selected based on literature review combined with ethnobotanical surveys conducted among traditional healers and herbal practitioners in Tengréla and Korhogo. Selected plant materials were harvested, processed, and freeze-dried. The antioxidant activity of the extracts was evaluated using DPPH radical scavenging and FRAP (Ferric Reducing Antioxidant Power) assays.

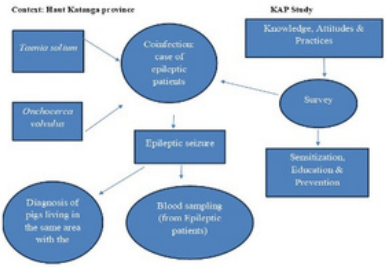
76 plants extracts were prepared and used for antibacterial assay. This activity was assessed using the agar well diffusion method. The extracts were subsequently tested against selected bacterial strains using agar diffusion assays, and the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were determined in liquid medium. To investigate the potential development of resistance, bacterial strains will be continuously exposed to sub-inhibitory concentrations of the plant extracts over an extended period. Resistant phenotypes, if obtained, will undergo whole-genome analysis using next-generation sequencing (NGS) to characterize genomic alterations associated with resistance. Finally, chromatographic techniques will be employed to isolate and identify the bioactive compounds responsible for the observed antibacterial activity.

Preliminary Results: 23 plants have been selected for antioxidant and antibacterial activity. Of the 76 plant extracts tested against meningitis bacteria, 8 showed high antimicrobial activity, 20 showed moderate activity, while 48 extracts were ineffective. The antioxidant activity of the extracts ranged from 6.27 to 20.83 µM vitamin C equivalent.

Conclusion/Outlook: This study bridges local knowledge and experimental research to evaluate the antioxidant and antibacterial potential of selected medicinal plants. By investigating resistance development and characterizing genomic adaptations, the work also addresses key challenges related to antimicrobial resistance. In line with the One Health approach, these findings support the sustainable use of plant-based bioactive compounds as potential alternatives to conventional antibiotics, contributing to global health and environmental sustainability.

Keywords: Bacterial meningitis, medicinal plants, antimicrobial resistance, antioxidant activity, Côte d'Ivoire

Co infection of Taenia Solium and Onchocerca Volvulus: Case of Epileptic Patients in Haut Katanga Province, DR Congo



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Background/Objectives: Neglected Tropical Diseases (NTDs) such as Taeniasis and Onchocerciasis are devastating diseases in sub-Saharan Africa including the Democratic Republic of Congo. In Haut-Katanga (H-K) province both diseases are highly prevalent with estimates of around 45% of people suffering from taeniasis and onchocerciasis. Epilepsy is also a significant public health concern in these endemic areas among patients examined for neurological disorders. A substantial proportion of epilepsy cases have been associated with these infections, with over 65% linked to onchocerciasis and 38.9% to cysticercosis. There is limited information on current seroprevalence of these two diseases in this community of Haut Katanga area. Previous studies carried out in H-K province did not determine the seroprevalence either for neurocysticercosis or for onchocerciasis. This study aims to determine the seroprevalence of neurocysticercosis and onchocerciasis among epileptic patients in H-K province.

Methodology: This is a cross-sectional study in the province of Haut-Katanga. A ousehold survey using a structured questionnaire was administered to 202 people with a final target of 400 participants for taeniasis and onchocerciasis associated risk factors assessment. Blood samples have been taken from 14 patients (out of the targeted 74 patients) diagnosed with epilepsy and admitted in neurological centers of Haut-Katanga province for evaluation of neurocysticercosis due to cystcercosis and onchocerciasis. A pig's tongue palpation was done for cysticercosis test among 131(Out of 384 targeted pigs). These samples have been taken to the lab for analysis.

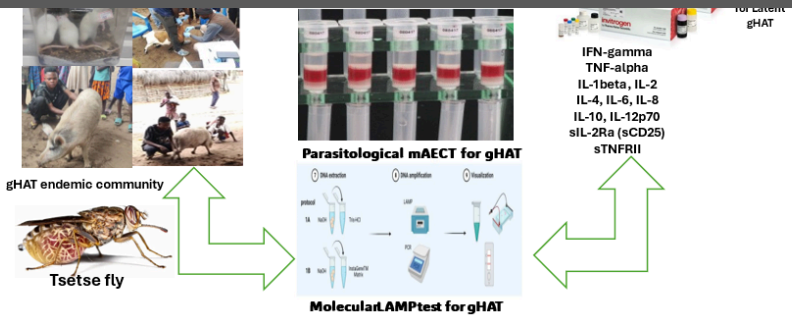
Expected outcomes

- Detection of *Taenia solium* antigen to determine the seroprevalence of taeniasis
- Detection of *Onchocerca volvulus* antigen to determine the seroprevalence of Onchocerciasis in epileptic patients
- These seroprevalence results will help us to find out the real impact of the association of these diseases among epileptic patients in H-K province.
- Understanding the level of taeniasis infection in pigs as primary intermediate hosts

Outlook: This study will demonstrate the existence of a co-infection of Taenia solium and *Onchocerca volvulus* among epileptic patients. These results will suggest a possible role for parasitic infections in the onset or worsening of epilepsy in endemic areas. This study will also help us determine the level of knowledge, practices, and attitudes of the community where these epileptic patients live regarding these parasites. It will also allow us to determine the prevalence of cysticercosis in pigs living around these patients. The study will strengthen screening of the diseases and management of these infections in Haut Katanga province.

Keywords: *Taenia solium*, *Onchocerca volvulus*, pigs, epileptic, Haut Katanga

Exploiting the Human and Animal Host Interaction with Trypanosoma brucei gambiense for Rapid Diagnostic Test Development



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Background/Objectives: Human African trypanosomiasis (HAT), caused by *T. b. gambiense*, remains a public health challenge in West and Central Africa. While traditionally considered an anthroponotic disease, emerging evidence suggests that animal reservoirs may contribute to transmission dynamics, complicating elimination efforts. This study explores advances in serological, parasitological and molecular tools for detecting *T. b. gambiense* in diverse hosts.

Methodology: Forty human (22 *T. b. gambiense* HAT positive cases and 18 negative controls), 6 pig, 7 goat and 4 sheep blood samples were collected from Kwilu Province in the Democratic Republic of Congo. Immunological, Coris HAT Sero-k-SeT RDT, CATT, and Trypanolysis tests, parasitological, mini-Anion Exchange Centrifugation Test (mAECT) and molecular, Loop-mediated Isothermal Amplification (LAMP) test were used to confirm positivity of gHAT in blood.

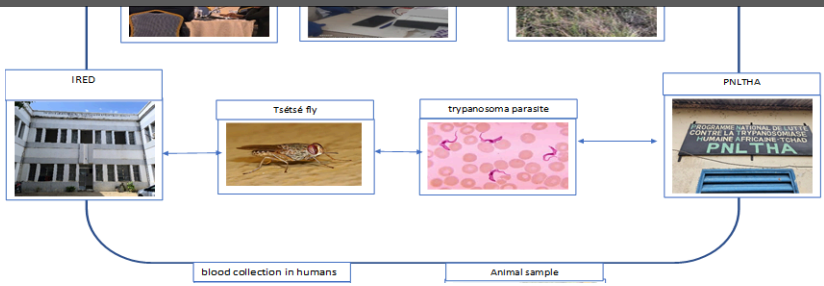
Whole blood stimulation assay was done using LiTat 1.3, LiTat 1.5 and Phytohemagglutinin (PHA) as stimulants for human blood and *T. b. brucei* antigen in addition to human blood stimulants for all animal samples to identify potential animal reservoirs of T. b. gambiense and compare this to *T. b. brucei* exposure. In addition, 11 human, 10 pig and 10 goat blood samples were collected from Greater Accra Region in Ghana. Coris HAT Sero-k-SeT RDT was used for screening Ghana samples. Plasma from humans and animals were stored at -80°C and tested by multiplex assay to measure the concentrations of cytokine biomarkers IL-1beta, IL-2, sIL-2R, IL-4, IL-6, IL-8, IL-10, IFN-gamma, sTNFRII, TNF-alpha, and IL-12p70. Data was entered into MS Excel and analyzed using GraphPad Prism 9.0.

Preliminary Results: Coris HAT Sero-k-SeT RDT detected no case of gHAT in human and animal samples collected in Ghana. However, Coris HAT Sero-k-SeT RDT and CATT tests detected 22/22 (100.0%) gHAT cases from human blood, 2/6 (33.3%) pig, 2/7 (28.6%) goat and none of the 4 sheep blood sampled in DRC. Trypanolysis test detected 17/22 (77.3%) gHAT cases from human blood and no gHAT in pigs, goats and sheep. mAECT and LAMP test detected 16/22 (72.7%) gHAT cases from human blood and no gHAT in pigs, goats and sheep. All 18 human control samples were negative by the immunological, parasitological and molecular tests mentioned above. Human and animal' plasma from whole blood stimulation assays have been analyzed for cytokine production and results are yet to be analyzed statistically for potential and useful biomarkers for latent gHAT.

Conclusion/Outlook: The detection of *Trypanosoma brucei gambiense* across species in human and animals is essential for effective surveillance through rapid early diagnosis and One Health management strategies. Identification of potential host cytokine biomarkers that are predictive for latent gHAT in plasma will be novel for humans and domestic animals.

Keywords: Sleeping sickness, Latent Human African Trypanosomiasis, *Trypanosoma brucei gambiense*, host cytokines/chemokine biomarkers, One Health

Diversity of Trypanosoma spp. in animals and tsetse flies in latent foci of African human trypanosomiasis (HAT) in Chad



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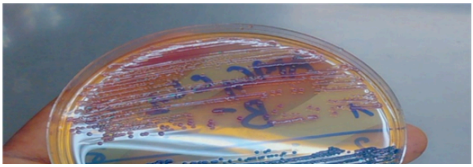
Background/Objectives: African trypanosomiasis (AT) is a major parasitic disease in sub-Saharan Africa, affecting both humans and animals. It is caused by extracellular protozoa of the genus Trypanosoma, transmitted by blood-feeding vectors of the genus Glossina (tsetses). In Chad, significant control efforts have led to a notable reduction in cases in certain historically active foci. However, the concept of a “latent focus” does not rule out the silent persistence of the parasite in human or animal reservoirs. To date, the parasitological status of trypanosomiasis in latent foci remains insufficiently documented, particularly in Tapol and Goré. This study aims to Conduct a literature review and develop the national atlas of tsetse flies and trypanosomes in Chad, evaluate existing data and knowledge on the diversity of trypanosomiasis circulating among animals and tsetse flies in Chad, and to identify the species of trypanosomes circulating among tsetse flies, and livestock in these two latent foci. The overall objective is to determine trypanosomal infections in animals and tsetse flies in the Goré and Tapol latent foci of sleeping sickness in Chad, to define appropriate strategies within a One Health approach.

Methodology: A database has been compiled using all available documents containing data on tsetse flies and African trypanosomiasis (AT) collected from 2010 to 2024 in Chad. These data pertain to research activities or efforts to control tsetse flies and AT. Surveys are being conducted in the latent foci of Tapol and Goré. Captured tsetse flies are morphologically identified and stored in appropriate tubes. At the same time, blood samples are collected from domestic animals (cattle, goats, and sheep). Genomic DNA is extracted from various matrices (tsetse fly tissues and blood). A nested PCR targeting the ITS1 (Internal Transcribed Spacer 1) region is used to detect trypanosomes.

Preliminary Results: Of the 2,225 trapping sites surveyed, three species and subspecies of tsetse flies involved in the transmission of African trypanosomiasis in Chad were detected: G. tachinoides, G. fuscipes fuscipes, and G. morsitans submorsitans. G. morsitans submorsitans was the most common species in the surveys (47.4%, n=927), followed by G. fuscipes (32.2%; n=631) and G. tachinoides (20.04%; n=400). For TAA, 6,277 blood samples were collected from 4,833 cattle, 444 goats, 339 sheep, 228 dogs, 157 donkeys, 119 pigs, 138 horses, and 19 camels. Six hundred fifty-five animals were infected with five species of trypanosomiasis: T. brucei, T. congolense, T. vivax, T. godfreyi, and T. simiae. TAA is present in the south and southeast of the country. A total of 238 tsetse flies, all belonging to the species G. f. fuscipes, were captured in two foci. In addition, 1,004 blood samples were collected in 10 villages, including 395 samples from humans, 529 from cattle, 53 from goats, and 27 from sheep. All of these samples are currently being analyzed at the IRED laboratory.

Conclusion/Outlook: This study provides essential insights into the distribution of tsetse flies and African trypanosomiasis, as well as the current circulation of trypanosomes in the Tapol and Goré foci. Looking ahead, the completion of PCR and geospatial analyses will enable a more refined risk assessment, strengthen targeted surveillance, and guide sustainable prevention strategies tailored to the local epidemiological context.

Integrating Medico social and Dairy Value Chain Drivers of AMR in the Haho Region, Togo.



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Background: The systemic misuse of antibiotics in both human and veterinary medicine drives the accumulation of residues in animal-source foods and environmental contamination, fostering horizontal gene transfer across the human–animal–environment continuum. In Togo, antimicrobial resistance (AMR) surveillance remains predominantly hospital-based, leaving the community, livestock and food-chain dimensions largely uncharacterized. Consequently, milk and its derivatives in rural diets represent a critical yet neglected reservoir and vector for the transmission of resistant pathogens. The aim of this study is to characterize the medical, social, and environmental determinants of AMR while quantifying the prevalence of selected resistant pathogens among dairy consumers in Togo through an integrated socio-epidemiological and microbiological assessment.

Methodology: A cross-sectional study will be implemented using structured interviews targeting key stakeholders in the Haho region. The interviews will collect data on a broad range of medico-social and environmental independent variables, encompassing self-medication practices, clinical prescription patterns, health-seeking behaviors, socioeconomic and educational profiles, sanitation infrastructure, hygiene practices, and environmental contamination pathways. All these variables will be systematically correlated with the dependent variable AMR.

Associations between response variables (knowledge, attitudes, and practices) and socio-demographic or institutional characteristics were first assessed using Chi-square tests. Variables with significant associations were subsequently included in multivariate logistic regression models performed using RStudio.

Results: In the community, although 520(86.67%) of respondents were aware of rabies, only 271(45.16%) had actual knowledge about risks associated with animal bites, preventive measures, notable signs of rabies, progression of declared rabies, and modes of transmission. There was a marked contrast between attitude with 598(99.67%) indicating they would go to a health facility in the event of a bite while in actual practice only 38 (46.25%) of 80 bite victims had sought medical care. The determinants of "sufficient knowledge" include *marital status* (widowers are better informed with OR=3.20 and p-value=0.01), *occupation* (employees and traders are better informed than the unemployed with OR=25.61 and 2.98 respectively and a p-value of less than 0.001 for both) and *socio-economic status* (respondents with low socio-economics status are better informed compared to those with an average socio-economic status with OR=2.43 and p-value=0.001, whilst those with a high socio-economic status are less well informed than the latter with OR=0.26 and p-value=0.02). Belonging to the Bambara ethnic group is associated with poorer attitude than to the Wolof (the majority ethnic group) with OR= 0.04 and p-value=0.01. There was a notable disparity among service providers with 90% of animal health workers having sufficient knowledge, compared to only 15.91% of human health providers. Nurses showed more appropriate attitudes than doctors with OR=97.13 and p-value=0.04, probably due to their proximity to rural realities. Finally, only 26.92% of the 78 dog owners had vaccinated their animals, with lower accessibility in rural areas.

Conclusion/Outlook : Rabies control in Kaffrine is hindered by insufficient knowledge and unfavourable practices that limit effective prevention and elimination of the disease. We recommend strengthening the training of human healthcare providers, enhancing community awareness through inclusive approaches, revising the regulatory framework, and strengthening intersectoral collaboration in line with the One Health approach.

Keywords: AMR, Medico social, Milk, One Health, Togo.

Seroprevalence and Molecular Characterization of Treponemal Species in Non-human primates and Humans in Proximity to Selected Zoos and Wildlife Reserves in Ghana.

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Background/Objectives: Yaws, a neglected tropical disease caused by *Treponema pallidum* subspecies *pertenue*, remains endemic in Ghana despite decades of eradication efforts. Recent evidence suggests non-human primates (NHPs) may harbor *T. pallidum* subsp. *pertenue*, potentially acting as wildlife reservoirs that complicate elimination strategies. However, data on the prevalence and transmission dynamics between humans and NHPs in Ghana remain limited. This study investigated the occurrence of *T. pallidum subsp. pertenue* in humans and NHPs at human-wildlife interfaces in Ghana and assessed knowledge, attitudes, and practices (KAP) related to yaws among at-risk populations.

Methodology: A cross-sectional study was conducted at Accra Zoo, Kumasi Zoo, and Mole National Park in Ghana. Structured KAP questionnaires were administered to 19 participants (zoo staff, park rangers, and community members). NHP species sampled included *Cercocebus atys* (white-naped mangabeys), *Erythrocebus patas* (patas monkeys), *Chlorocebus sabaeus* (green monkeys), Papio anubis (olive baboons), *Cercopithecus petaurista* (lesser spot-nosed monkeys), and *Cercopithecus mona* (mona monkeys). Knowledge was scored as low (0–1 correct responses), moderate (2–3), or high (4–5).

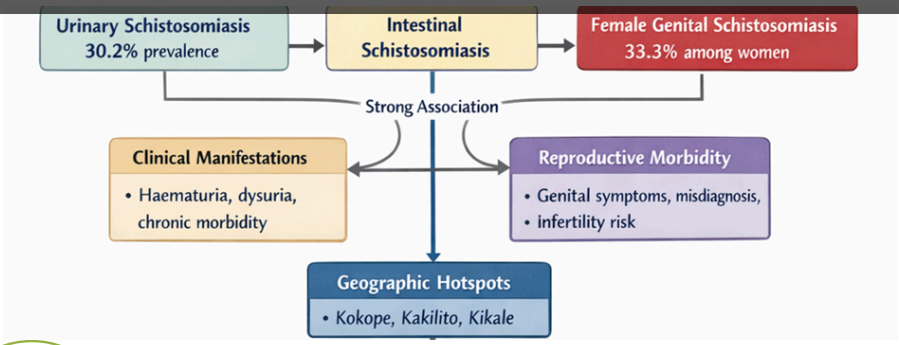
For, HIGHTOP Syphilis Ab rapid diagnostic tests was used for serological screening of *Treponema pallidum* in finger prick blood of humans (n=19) and serum from NHPs (n=21). Molecular analysis involved DNA extraction from human stool samples (n=18) and NHP rectal swabs (n=21), followed by PCR amplification targeting tp0548 and polA genes specific to *T. pallidum subsp. pertenue.* Amplicons were visualized using 2% agarose gel electrophoresis.

Results: KAP assessment revealed critical gaps in occupational health preparedness. Only 10.5% of participants had received formal training on zoonotic diseases. While 89.5% consistently wore boots, PPE use was inconsistent: 21.1% never wore gloves, 73.7% never used masks, and 42.1% never wore coveralls. Only 47.4% had been vaccinated (primarily rabies and COVID-19). All participants expressed interest in receiving yaws education. Serological tests were negative in humans and NHPs. In contrast, molecular analysis detected *T. pallidum subsp. pertenue* DNA in 22.2% (4/18) of human samples and 71.4% (15/21) of NHP samples. Specifically, tp0548 was amplified in 16.7% (3/18) of human samples and 47.6% (10/21) of NHP samples, while *polA* was detected in 5.6% (1/18) of humans and 23.8% (5/21) of NHPs.

Conclusion/Outlook: This study provides molecular evidence that NHPs in Ghana harbor *T. pallidum subsp. pertenue*, with significantly higher detection rates than in humans despite negative serology in both populations. The detection of identical gene targets in both species at human-wildlife interfaces, combined with critical gaps in occupational health knowledge and biosecurity practices, underscores the need for integrated One Health surveillance. Yaws eradication programs focusing exclusively on human populations may be insufficient without wildlife monitoring. We recommend incorporating molecular diagnostics and wildlife surveillance into national control programs and strengthening occupational health training for zoo and wildlife workers.

Keywords: Yaws, *Treponema pallidum subsp. pertenue,* non-human primates.

Epidemiology and Characterisation of Schistosomiasis in the Central Gonja District of Ghana



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Background/Objectives: Schistosomiasis, a neglected tropical disease caused by Schistosoma parasites, remains endemic in sub-Saharan Africa, accounting for over 90% of global cases. In Ghana, communities near freshwater bodies face high transmission and infection risk due to the frequent contact with water contaminated with snail intermediate hosts. Although a common chronic parasitic infection, some types of schistosomiases are often underdiagnosed and poorly understood, compounded by low awareness among healthcare providers and affected populations. This study assessed the epidemiology, clinical manifestations and knowledge gaps surrounding schistosomiasis in the Central Gonja District.

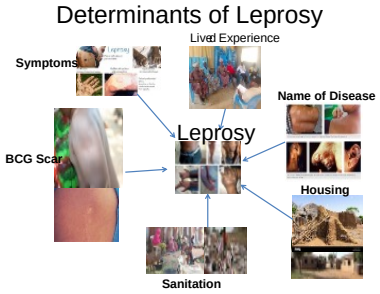
Methodology: A cross-sectional study was conducted using Kobo Toolbox-administered questionnaires to collect data on demographics, knowledge, attitudes, perceptions, water, hygiene, and sanitation practices, as well as the diagnostic and treatment capabilities of health workers and facilities regarding schistosomiasis. Participants included riparian community residents, healthcare workers and women of reproductive age, selected via stratified, purposive and convenience sampling. Urine, stool and high/cervicovaginal swabs were analysed using urine sedimentation to detect urinary schistosomiasis, Kato-Katz technique to determine intestinal schistosomiasis and PCR to detect DNA of schistosomes for female genital schistosomiasis diagnosis, respectively.

Results: Among 524 participants (mean age 14.9 years; 56.9% female), urinary schistosomiasis prevalence was 30.2%, with hotspots in Kokope (63.0%), Kakilito (46.3%) and Kikale (45.9%) communities. Males had higher infection rates (35.8%) compared to females (25.8%). FGS prevalence among 132 women of childbearing age was 33.3% and strongly associated with urinary schistosomiasis ($p = 0.001$). The community had severe Knowledge gaps: 82.4% lacked schistosomiasis awareness; only 1.9% had good knowledge. Healthcare workers (n=237) demonstrated limited FGS knowledge (16.9%), Poor Water, Sanitation and Hygiene practices exacerbated transmission risks.

Conclusion/Outlook: The study highlights the significant burden of schistosomiasis and FGS in the district, exacerbated by geographic disparities, weak mass drug administration impact and systemic knowledge gaps. Appropriate diagnostics, community education, provision of Water Sanitation and Health infrastructure and healthcare worker training are urgently needed.

Keywords: Female Genital Schistosomiasis, Knowledge, Perceptions, Central Gonja District, Ghana.

Characterization of Sociocultural, Environmental and Community Determinants of Leprosy in Bongo District, Ghana.



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Background/Objectives: Leprosy persists as a public health challenge in several endemic districts of Ghana despite national elimination targets. Bongo District in the Upper East Region has recorded a three-fold increase in cases between 2021-2023, emerging as a documented hotspot. While individual risk factors are known, the combined influence of sociocultural, environmental, and community-level determinants within hyper-endemic settings remains poorly characterized. This study investigated these interconnected drivers to generate evidence for context-specific health policy and practice.

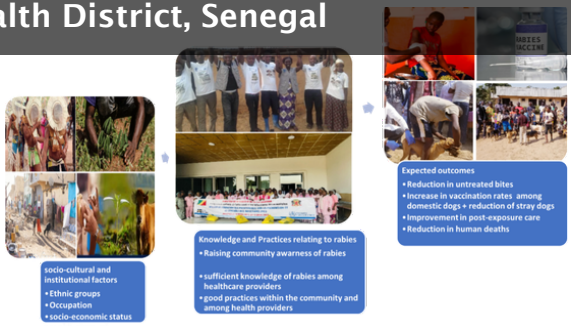
Methodology: An explanatory sequential mixed-methods design, grounded in a One Health framework, was employed. The quantitative component comprised a matched case-control study with 17 confirmed leprosy cases and 34 community controls, matched by sex, age, residence, education, occupation, and marital status. BCG vaccination was verified through scar inspection. The qualitative component involved five focus group discussions (n=25) with affected persons, family members, health workers, and community leaders. Data were analysed using STATA v17 (quantitative) and thematic analysis in NVivo (qualitative), with integration at the interpretation stage to inform policy recommendations.

Results: Among cases, 15(88.2%) were diagnosed with multibacillary leprosy and 2(47.0%) presented with Grade 2 disability indicating advanced disease and delayed detection. BCG vaccination was strongly protective, associated with a 90% reduction in leprosy odds (aOR: 0.10; 95% CI: 0.01-0.98; p=0.048). Environmental risks were evident, with open defecation significantly more common among cases 16(94.1%) vs. 18(60.0%); p=0.017). Health literacy was poor: only 8(17.0%) correctly identified germs as the cause, while beliefs in heredity 17(36.2%), witchcraft 9(19.2%), and divine punishment 5(10.6%) were prevalent. Stigma was profound. 31(90.0%) of controls were unwilling to buy food from affected persons, and 26(76.7%) would not permit marriage into affected families. Qualitative themes revealed delayed help-seeking (often first consulting traditional healers), structural health system barriers (cost, distance, and insurance gaps), pervasive stigma leading to social isolation, and strong sociocultural beliefs attributing leprosy to supernatural causes as key determinants sustaining transmission.

Conclusion/Outlook: Leprosy resurgence is driven by complex interactions across sociocultural, environmental and community-level systems. Policy implications include: (1) integrating leprosy messaging into routine health education to address misconceptions; (2) strengthening BCG immunization coverage with community awareness of its protective benefits; (3) implementing targeted WASH interventions in endemic communities; (4) developing community-led anti-stigma programmes; and (5) enhancing surveillance and contact tracing. These findings support the need for holistic, multisectoral strategies aligned with the WHO NTD Roadmap to achieve zero leprosy.

Keywords: Leprosy; Hansen's disease; neglected tropical diseases; mixed-methods; stigma; health policy

Socio-cultural and Institutional Determinants of Knowledge, Attitudes and Practices Related to Rabies Risk in the Kaffrine Health District, Senegal



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Background/Objectives: Rabies is a neglected disease in developing countries, heavily burdening poor rural communities and disproportionately affecting children. In Senegal, reported data underestimate reality, with one case for every six unreported. The Kaffrine region is particularly alarming, with several fatal cases. While some studies on knowledge, attitudes, and practices (KAP) exist, socio-cultural, economic, and institutional determinants remain underexplored. This study examines factors influencing rabies-related knowledge, attitudes, and practices among community members and health providers in Kaffrine, Senegal.

Methods: The study was conducted in the Kaffrine health district among 600 community members (Two-stage cluster random sampling) and healthcare providers (44 in human health and 10 in animal health). Data were collected using structured questionnaires.

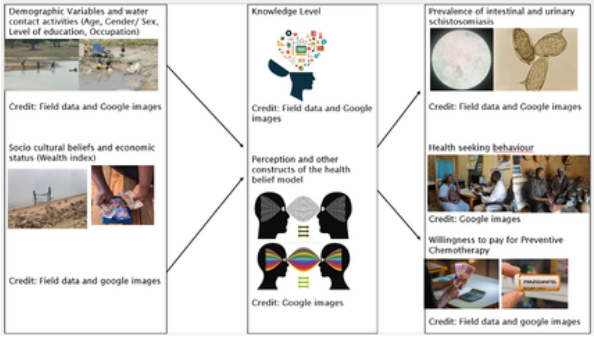
Associations between response variables (knowledge, attitudes, and practices) and socio-demographic or institutional characteristics were first assessed using Chi-square tests. Variables with significant associations were subsequently included in multivariate logistic regression models performed using RStudio.

Results: In the community, although 520(86.67%) of respondents were aware of rabies, only 271(45.16%) had actual knowledge about risks associated with animal bites, preventive measures, notable signs of rabies, progression of declared rabies, and modes of transmission. There was a marked contrast between attitude with 598(99.67%) indicating they would go to a health facility in the event of a bite while in actual practice only 38 (46.25%) of 80 bite victims had sought medical care. The determinants of "sufficient knowledge" include *marital status* (widowers are better informed with OR=3.20 and p-value=0.01), *occupation* (employees and traders are better informed than the unemployed with OR=25.61 and 2.98 respectively and a p-value of less than 0.001 for both) and *socio-economic status* (respondents with low socio-economics status are better informed compared to those with an average socio-economic status with OR=2.43 and p-value=0.001, whilst those with a high socio-economic status are less well informed than the latter with OR=0.26 and p-value=0.02). Belonging to the Bambara ethnic group is associated with poorer attitude than to the Wolof (the majority ethnic group) with OR= 0.04 and p-value=0.01. There was a notable disparity among service providers with 90% of animal health workers having sufficient knowledge, compared to only 15.91% of human health providers. Nurses showed more appropriate attitudes than doctors with OR=97.13 and p-value=0.04, probably due to their proximity to rural realities. Finally, only 26.92% of the 78 dog owners had vaccinated their animals, with lower accessibility in rural areas.

Conclusion/Outlook : Rabies control in Kaffrine is hindered by insufficient knowledge and unfavourable practices that limit effective prevention and elimination of the disease. We recommend strengthening the training of human healthcare providers, enhancing community awareness through inclusive approaches, revising the regulatory framework, and strengthening intersectoral collaboration in line with the One Health approach.

Keywords: KAP, Determinants, socio-economic, Rabies, Sénégal

Prevalence of Schistosomiasis, Household Healthcare Seeking Behaviour and Willingness to Pay for Preventive Chemotherapy for Schistosomiasis Prevention in Upper East Region, Ghana



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Background: Schistosomiasis remains a major public health challenge in Ghana despite sixteen years of Mass Drug Administration (MDA) with praziquantel. Although national prevalence has declined, transmission hotspots persist in several districts, and MDA faces funding constraints. Effective long-term control and elimination strategies require identifying infection prevalence hotspots, assessing household knowledge of schistosomiasis, understanding healthcare-seeking behavior, and evaluating willingness to invest in preventive measures. This study examined the prevalence of Schistosoma haematobium and S. mansoni infections, household awareness and perceptions, healthcare-seeking practices, and willingness to pay for preventive chemotherapy in the Kassena-Nankana East and Bongo Districts of the Upper East Region of Ghana.

Methodology: The study used mixed-methods approach with a cross-sectional design informed by the Health Belief Model (HBM). Quantitative data were obtained from 349 school-aged children (5–17 years) and their household heads through structured questionnaires and parasitological analysis of urine and stool Samples.

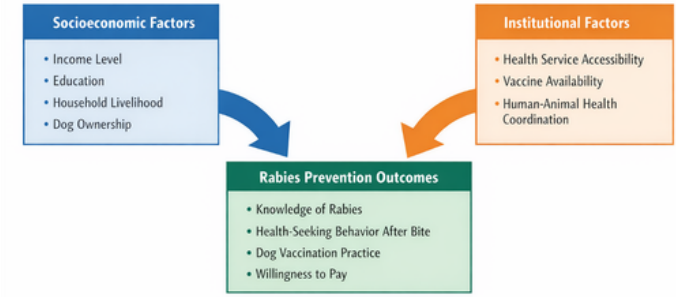
Twenty-one (21) qualitative interviews were conducted with disease control officials, healthcare practitioners, and selected household heads to understand the contextual factors affecting healthcare seeking behaviour. Quantitative data were analyzed using descriptive statistics, logistic regression, and contingent valuation analysis, whilst qualitative data underwent theme analysis.

Results: The general prevalence of schistosomiasis was low, 10/349 (2.87%). Only good (accurate) perception was a significant predictor of infection after adjusting for other variables (OR=10.15, 95% CI: 1.07 – 96.42, p=0.044). Household knowledge of schistosomiasis was moderate with 55.6% scoring > 18 out of the maximum possible score of 30. The average willingness to pay (WTP) for preventive chemotherapy was at GHC 26.7 (SD=9). This was positively linked to good (accurate) perception of schistosomiasis (β=13.7, 95% CI: 1.26 – 26.15, p=0.031) and female headed household (β=14.2, 95% CI: 1.85 – 26.56, p=0.024) but negatively linked to household wealth index (β=-21.18, 95% CI: -36.77 – -5.59, p=0.008). Household healthcare seeking behaviour was affected by perceptions of susceptibility, seriousness, barriers as against benefits and participants motivation to seek health. Most households relied on home and herbal remedies first to treat schistosomiasis and only went to hospital when the herbs failed, or symptoms were severe. There was a favorable community acceptance of MDA. There were however some challenges of MDA including heavy dependance on donor funding, inconsistent drug supply, inadequate community sensitization, and financial challenges.

Conclusion/Outlook: The study showed significant progress had been made in lowering the prevalence of schistosomiasis. Sustainable control will require the incorporation of schistosomiasis control programs into primary healthcare services, enhancement of community engagement, and the creation of innovative financial arrangements in the wake of declining global support These strategies are required to be led by the local people, based on health beliefs and be economically viable.

Keywords: Schistosomiasis, Prevalence, Willingness to pay, healthcare seeking behaviour.

Socio-economic and Institutional Determinants Influencing Health-Seeking Behavior and Willingness to Pay for Rabies Prophylaxis in Abomey-Calavi and Cotonou, Benin



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Background: Rabies remains a neglected tropical disease affecting vulnerable populations in Benin, with nearly 130 human deaths reported between 2017 and 2024. Despite multisectoral control efforts, transmission persists, particularly in Abomey-Calavi and Cotonou. Control is hindered by limited public awareness, reliance on ineffective traditional treatments, poor access to healthcare, and weak coordination between human and animal health sectors. These barriers reflect broader socioeconomic vulnerabilities and institutional constraints. This study therefore examines determinants influencing care-seeking behaviour and community willingness to pay for rabies prophylaxis.

Methodology: A mixed-methods study was conducted in Abomey-Calavi and Cotonou, Benin. The quantitative component included 422 households involving all available health providers, and bite victims identified from health and veterinary records. Households were selected using two-stage cluster sampling. Data were analysed using descriptive statistics, Chi-square tests, and multivariate logistic regression ($p < 0.05$) to identify factors influencing rabies prevention knowledge, care-seeking behaviour, and dog vaccination.

The qualitative component involved four groups: bite victims, dog owners, human health providers and veterinary staff. Two focus groups were conducted per community: one with bite victims and dog owners (20 participants) and one with health providers (15 participants), complemented by individual interviews. Qualitative data were analyzed through thematic content analysis using Nvivo12. Willingness to pay for human post-exposure prophylaxis (PEP) and dog vaccination was assessed using the contingent valuation method.

Results: The study showed satisfactory rabies knowledge among respondents (70%) and service providers, but only 39.6% fully mastered preventive measures, which was significantly associated with education (AOR = 2.3; p = 0.006). Those with good knowledge also demonstrated appropriate attitudes and practices, and most dog owners reported vaccinating their animals.

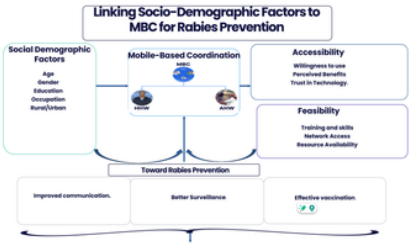
After animal bites, 65% of victims did not consult formal health services, particularly in Abomey-Calavi; 43.5% took no action and 56.5% relied on traditional treatments. Care-seeking behaviour was influenced by income (AOR = 1.8), risk perception (AOR = 2.1), and living environment (AOR = 1.9). Similar associations were observed for dog vaccination, particularly among households owning dogs. Qualitative data highlighted barriers to care, including high costs of vaccines and PEP, geographic constraints, reliance on traditional treatments, limited communication, and weak coordination between human and animal health sectors.

Despite these constraints, 68.2% were willing to pay for human post-exposure prophylaxis and 75.4% for dog vaccination, with willingness to pay higher in Cotonou, especially when availability, and accessibility of services were improved.

Conclusion/Outlook: Rabies prevention depends on awareness, financial and geographic accessibility. Strengthening access to care, vaccine supply, and One Health coordination can reduce exposure, improve care-seeking, and accelerate progress toward elimination nationwide in an equitable and sustainable manner for public health.

Keywords: Rabies; Health-seeking behavior; Willingness to pay; One Health; Benin.

Acceptability and Feasibility of Sustained Mobile-Based Coordination Among Healthcare Professionals (Human & Animal) for Rabies Prevention in Ilala Municipality, Dar es Salaam, Tanzania



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Background/Objectives: Rabies prevention requires timely coordination among health care professionals across human and animal health sectors, and mobile-based coordination (MBC) could streamline multidisciplinary collaboration in Ilala Municipality, Dar es Salaam, Tanzania, while there is limited evidence on the acceptability and feasibility of MBC for cross-sector rabies prevention among healthcare professionals in this setting. Thus, this study aims to assess the acceptability and feasibility of mobile-based coordination among health professionals in the human and animal sectors in Ilala Municipality, a densely populated urban area with over 7,600 dogs, a major risk vector for rabies transmission.

Methodology: A cross-sectional study using a mixed-method approach was conducted from September to November 2024. Quantitative data was collected using the Kobo toolbox, then transferred to Microsoft Excel, cleaned, and analyzed using SPSS version 20. Sequentially, qualitative data from in-depth interviews and focus group discussions were collected to have complementary information on MBC, and then they were thematically analyzed and presented in quotations. The qualitative analysis was conducted to identify recurring themes and insights related to MBC, with quotations used to illustrate key findings.

Results: Among the 72 healthcare professionals who participated, 48(68%) had a positive perception of MBC. While all respondents 72(100%) acknowledged its potential to improve information sharing, only 31(43%) were positive about using mobile technology in their work. Key barriers cited included digital illiteracy 47(65%), poor infrastructure 52(72%), and work overload 65(90%). Qualitative findings highlighted additional challenges such as a lack of financial support for mobile communication, policy constraints, and inadequate training. Participants also expressed concerns about stigma, limited collaboration between human and animal health professionals, and difficulties in accessing reliable network coverage.

Conclusion: MBC could help information sharing across sectors, but many professionals remain cautious about daily use. Challenges such as digital illiteracy, weak infrastructure, high workloads, limited funding, policy hurdles, and inadequate training were reported concerns. To improve rabies prevention collaboration through an interdisciplinary, one-health approach, the focus must be on building digital skills, reliable network access, and supportive policies for mobile communication.

Keywords: Rabies, Mobile coordination, One Health, Acceptability, Feasibility.

Assessing slaughter actor's knowledge, perception and practices of human, animal, and environmental health risk management at Port-Bouët abattoir in Abidjan

Source: *Factors that contribute to insanitation practices in Port-Bouët's abattoir*. Soro, 2025.

Insanitation practices as a One Health problem at the Port-Bouët abattoir. Soro Wonna Lacina, 2025.

Wonna Lacina Soro[1], Kouadio Baya Bouaki[1], Kathrin Heitz-Tokpa[2], Esther Gwae Kimaro[3], Gloria Ivy Mensah[4], Bassirou Bonfoh[2]

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Background/Objectives: Poor handling and sanitation practices in abattoirs pose significant threats to human, animal, and environmental health. The Ivorian government has instituted regulations prohibiting practices that compromise sanitary standards within its abattoirs. In 2019, the Port-Bouët abattoir was renovated to improve it sanitary standards. Despite these renovations, the facility remains characterized by persistent sanitary deficiencies and substandard hygiene protocols including improper waste management, foul odors, stagnant rainwater, and the presence of various arthropod vectors. This study aimed to identify the factors contributing to persistent substandard sanitary practices at the Port-Bouët abattoir."

Methodology: Qualitative methodology built around semi-structured interviews, direct observations, and documentary research was used. The principle of discourse saturation was used as a sampling technique. Interview guides were sent to 25 actors, divided into 7 categories: 2 veterinarians, 3 butchers, 7 animal sellers, 7 slaughtered beef cleaners, 2 restaurateurs, 1 hygiene officer and 3 customers. An inductive methodology with typological analysis was used to analyze the data.

Results: The study indicates that persistent insanitary practices result from an interplay of organizational, cultural, and behavioral factors. At the organizational level, these practices result from structural constraints: insufficient livestock holding capacity, inadequacy of slaughtering infrastructure to meet daily meat demand, a lack of communication between health authorities and workers, as well as insufficient training on identifying and managing health risks.

At the cultural level, they are rooted in risk perceptions. There is a gap between perceived and actual risks, a minimization of the danger to humans, and a belief that preparation and cooking are sufficient to neutralize health hazards. Additionally, financial and social risks are considered more urgent and more pressing than health risks.

At the behavioral level, actors develop adaptation strategies based on negotiation and risk acceptance rather than elimination. Some seek to limit the effects of risks through control practices (regular cleaning of enclosures, feeding and treating sick animals), while others contribute to the creation of new risks through practices such as corruption, bypassing official channels, clandestine slaughter or slaughtering in waste.

Conclusion/Outlook: This study shows that organizational, cultural, and behavioral factors interact to generate unsanitary practices within the Port-Bouët abattoir. They pose a One Health problem, as they simultaneously threaten human, animal, and environmental health. And as they constitute a systemic risk, this study suggests to:

- Train abattoirs' actors on the real health risks associated with the insanitation practices.
- Realize practical studies with animal sellers on recognizing health risks for animals.
- Organize workshops every six months to share information on human and animal diseases identified within the abattoir.
- Produce economic goods from abattoir wastewater.
- Recycle and reuse wastewater in the abattoir production system.

Keywords: Insanitation practices, health risks, One Health, abattoir, Port-Bouët

Assessment of Bacteriological Water Quality and Perception of Health Risks Associated with the Use of Funa River Water in Kinshasa: An Integrated One Health Approach

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Background/Objectives: Quality water scarcity is a global challenge, necessitating water reuse in agriculture and industry, particularly in urban areas. This multifaceted issue requires a multisectoral approach. In many African cities, waterborne diseases remain a major concern where access to safe drinking water and sanitation is limited. In Kinshasa, riverside communities rely on surface water for domestic and economic activities, potentially exposing them to enteric pathogens. The Funa River, flowing through densely populated areas, receives substantial loads of faecal and environmental waste. This study assessed Enterobacteria risk and user perception regarding Funa River water using a Quantitative Microbial Risk Assessment (QMRA) and sociological surveys to inform public health interventions.

Methodology: A descriptive cross-sectional study was conducted in the Funa River valley in Kinshasa, DRC. We analyzed 96 water samples from six strategic sites during dry and rainy seasons. We isolated *E. coli, Salmonella spp., Klebsiella spp., Proteus spp., Providencia spp.,* and *Pseudomonas spp.* using standard culture methods on MacConkey, SS agar, EMB, and TBX media.

The study included a spatial characterization of the human-animal-environment interface using a Geographic Information System (GIS) and visual observation). We surveyed 150 individuals using the river for household needs, gardening, sand gathering, and vehicle washing. Analysis focused on socio-demographic characteristics, exposure contexts, hazard knowledge, and risk behaviors. We estimated the annual infection risk for E. coli and Salmonella sp. using a beta-Poisson dose-response model with Monte Carlo simulations. Scenarios included bathing, irrigation, and washing utensils or vehicles. Statistical analyses were performed using R software.

Results: Findings revealed critical, persistent faecal contamination. E. coli was detected in 100% of samples (Mean: 249.65 CFU/mL) with no significant seasonal variation, indicating chronic pollution. Other bacteria showed lower sporadic prevalence: *Klebsiella sp.* (11.46%), *Providencia sp.* (2.08%), *Proteus sp.* (2.08%), *Salmonellasp.* (1.04%), and *Pseudomonas sp.* (1.04%). Quantitative Microbial Risk Assessment results indicated that exposed populations face an annual E. coli infection probability approaching 100% under certain scenarios, with a 25% probability of illness. The survey showed that while 86% of users recognized health risks, over 50% continued to dispose of waste including human excreta directly into the river. This highlights how socio-economic constraints and lack of infrastructure drive environmental behaviors.

Conclusion: The Funa River is severely contaminated with microorganisms, predominantly *E. coli*, exposing riverside populations to high health risk. Despite recognition of the danger, observed behaviors contribute to the persistence of pollution. These results highlight the need to strengthen microbiological monitoring, improve sanitation and adopt integrated interventions adapted to the local context.

Keywords: Waterborne diseases risk, water reuse risk, Kinshasa

Modeling Healthcare-seeking Behavior and Determinants of Catastrophic Health Expenditures among Buruli Ulcer Patients in the Kimputu Health Zone, Democratic Republic of Congo

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10. Division Provinciale de Santé Province KWILU, République Démocratique du Congo

Background/Objectives: Buruli ulcer represents a major public health issue in the Democratic Republic of Congo due to its significant health, social, and economic consequences on affected households. In the absence of effective financial protection mechanisms, patients and their families are exposed to a high risk of catastrophic health expenditures (CHE), which may further deepen poverty and limit access to healthcare. This study analyzed the determinants of CHE and healthcare-seeking pathways among

Buruli ulcer patients, while assessing associated socioeconomic inequalities through a mixed-methods approach combining quantitative and qualitative analyses.

Results: The findings reveal a high prevalence of CHE (85.9%), indicating substantial financial vulnerability among households. Multivariate analysis identified wealth status (OR = 0.796), delay in seeking care (OR = 0.465), and household size (OR = 1.242) as the main significant determinants of CHE. Furthermore, delayed healthcare-seeking was estimated at 52%, mainly explained by disease knowledge (OR = 0.586), traditional beliefs (OR = 0.538), and biomedical trust (OR = 1.781).
Econometric analysis using Wagstaff decomposition shows that inequalities in CHE are primarily driven by delay in seeking care (48%), followed by wealth status (25%), social support (17%), and disease stage (7%). Other variables, including education level, disease duration, and distance to health facilities, contribute marginally. Similarly, decomposition of healthcare-seeking determinants indicates that knowledge (61%), traditional beliefs (12%), and low biomedical trust (10%) are key drivers. Qualitative findings highlight that delays in healthcare-seeking are influenced by cultural factors (use of traditional healers), economic constraints (cost of care), and geographic barriers (distance), leading to disease progression and increased healthcare costs.

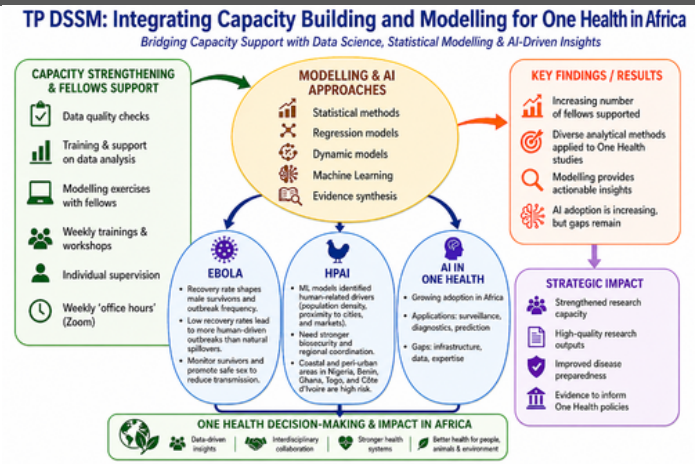
Conclusion/Outlook: Catastrophic health expenditures among Buruli ulcer patients result from a complex interaction between economic vulnerability, healthcare-seeking behavior, and structural barriers to access. These findings underscore the need to strengthen financial protection mechanisms, promote early healthcare utilization, and improve geographic accessibility to reduce health inequalities

Keywords: Buruli ulcer, Catastrophic health spending, Health inequalities, Wagstaff decomposition, Care pathways, Democratic Republic of Congo

Data Science, Statistics and Modeling (DSSM)

TTP Lead

Strengthening One Health Research in Africa through Data Science, Modelling, and Machine Learning: Integrating Capacity Support and Applied Modelling to Complex Health Threats



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3. University of Glasgow, Glasgow, United Kingdom.

Background: The growing burden of health threats in Africa requires robust analytical frameworks that integrate data science, statistical modelling, and machine learning within a One Health perspective. The TP DSSM (Data Science, Statistics, and Modelling) is a core component of the Afrique One-REACH (Research Excellence for African Challenges in Health) consortium. Within this framework, DSSM addresses critical gaps in analytical capacity while advancing modelling applications on health risks at human, animal, and environmental interface for decision-making.

Methodology: TP DSSM adopts a comprehensive, fellows and institutions demand-driven approach combining capacity strengthening and applied modelling. Activities include: (i) data quality assurance through review of study designs, variables, and analytical strategies; (ii) training and technical support in statistical analysis and modelling techniques;

and (iii) collaborative modelling exercises tailored to fellows' research and institutions strategic needs. Capacity development is delivered through weekly workshops and online training sessions, complemented by individual supervision and weekly "office hours" for continuous support. In parallel, DSSM conducted applied research using stochastic epidemic modelling, machine learning-based risk mapping, and systematic evidence synthesis on priority health threats.

Results:

Capacity Strengthening Outcomes

DSSM provides comprehensive analytical support to over 30 fellows, covering study design, data management, statistical testing, regression modelling, and manuscript development. Supported methods include logistic regression, chi-square testing, Poisson regression, and advanced modelling workflows. The number of fellows supported has increased substantially over time, rising from 10 in 2023 to over 30 to date.

Applied modelling and AI insights

Applied modelling activities generated key insights across disease systems. For Ebola disease, stochastic epidemic modelling combined with Bayesian inference demonstrated that male survivor recovery dynamics strongly influence outbreak recurrence, with lower recovery rates associated with increased human-driven transmission.

For Highly Pathogenic Avian Influenza (HPAI) risk in West Africa, machine learning-based spatio-temporal modelling identified anthropogenic drivers, poor compensation particularly population density and proximity to markets, as major determinants of HPAI risk in West Africa. The coastal and peri-urban areas in Nigeria, Benin, Ghana, Togo, and Côte d'Ivoire were consistently identified as the zones of high risk.

A systematic review of AI applications in One Health research across Sub-Saharan Africa revealed increasing adoption of machine learning approaches, alongside persistent gaps in computational infrastructure, data governance, and availability of trained specialists in West Africa.

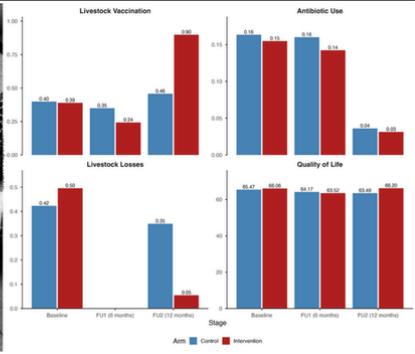
Conclusions/Outlook: Integrating capacity strengthening with advanced modelling approaches enables the generation of actionable insights for disease prevention and control. As part of Afrique One-REACH, DSSM demonstrates how targeted analytical support can enhance research quality and drive scientific innovation. Addressing persistent gaps in infrastructure, data systems, and human capacity will be essential to fully harness the potential of AI and modelling in Africa. Strengthening interdisciplinary collaboration and scaling training initiatives will be critical for advancing evidence-based policymaking and improving health outcomes. Next steps include modelling work on HPAI, Ebola, Rift Valley fever, and other relevant disease. A review of modelling techniques and evaluation metrics used to assess effectiveness of One Health interventions in Africa will be conducted. The cost-effectiveness and added value of interventions implemented by fellows will be assessed. A collaborative proposal with postdocs from other TTPs will be developed. One Health models will be developed to inform evidence-based policy.

Keywords: One Health, Data Science, Statistical Modelling, Machine Learning, Artificial Intelligence, Capacity Building, Health, Africa

Non-Communicable Diseases (NCDs)

TTP Lead

Community-Based Farmer Platforms Improve Livestock Vaccination Uptake, Reduce Losses, and Enhance Wellbeing: a Cluster-Randomized Trial in Ghana



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Introduction: Infectious livestock diseases remain a major constraint to productivity, food security, and farmer wellbeing across sub-Saharan Africa. In Ghana, Contagious Bovine Pleuropneumonia and Peste des Petits Ruminants have been identified as the diseases with the greatest negative impact on ruminant production. Despite the availability of effective vaccines, uptake remains low due to barriers in access, affordability, and service coordination. Formative participatory research suggested that localized farmer platforms, which organize farmers together and coordinate vaccination schedules, share information, and pool resources, could address these constraints. We conducted a cluster randomized controlled trial to evaluate the effectiveness of these platforms on vaccination uptake, antimicrobial use, livestock losses, and farmer wellbeing in three districts in Ghana.

Methodology: Forty-six communities (clusters) were randomized 1:1 to intervention or control arms. About ten households per cluster were enrolled and followed at baseline, 6 months, and 12 months.

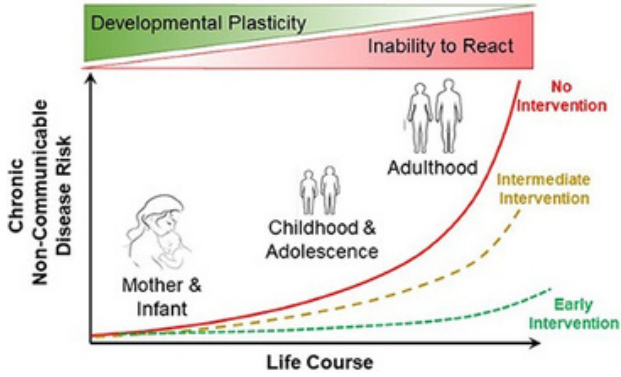
In intervention communities, two trained local leaders established farmer platforms to coordinate vaccine information exchange, schedule vaccination services, and share vaccination costs. Analyses followed an intention-to-treat approach using mixed-effects models with random intercepts for clusters. The primary outcome was livestock vaccination uptake at 12 months. Secondary outcomes included antimicrobial use in the past month, livestock losses over 12 months, and wellbeing measured using the WHOQOL-BREF across physical, psychological, social, and environmental domains.

Results: A total of 1,090 observations were collected across three survey waves, with 211 households contributing endline data. At 12 months, vaccination uptake was substantially higher in intervention communities. The predicted probability of vaccinating was 96% (95% CI: 86–99%) in the intervention arm versus 47% (95% CI: 25–70%) in controls (adjusted OR: 26.8; 95% CI: 5.1–141.0; $p<0.001$). Livestock losses were significantly reduced in intervention communities, predicted probability of 2% compared with 31% in controls (adjusted OR: 0.045; 95% CI: 0.01–0.23; $p<0.001$). Antimicrobial use remained low in both groups, with no significant difference at endline (OR: 0.81; $p=0.823$). Wellbeing scores were modestly higher in the intervention arm (mean difference=2.69; $p=0.053$).

Conclusions/Outlook: This community-led platform intervention led to a significant increase in vaccination uptake and a marked reduction in livestock mortality at 12 months. These findings demonstrate that locally coordinated delivery models can improve utilization of existing vaccines in resource-constrained settings. Although no effect was observed on antimicrobial use, and wellbeing gains were modest, the evidence shows that such local-driven initiatives can overcome persistent demand- and supply-side barriers to livestock vaccination, offer a pragmatic pathway to strengthen preventive health service delivery, and enhance household wellbeing.

Keywords: One Health, Infectious livestock diseases, Vaccination, Antimicrobial use, Wellbeing, Transdisciplinary

Integrated health promotion strategies for children and adolescents for healthy ageing in Taabo health and demographic surveillance system (IHPS)



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Introduction/Background/Objectives: The nutritional and epidemiological transition is accelerating, moving from the stage of declining famine to that of non-communicable diseases (NCDs) linked to nutrition and coupled with infectious diseases. In this multifaceted ecological and socio-economic environment, the health of children and adolescents occupies an important place in the health system. The triple burden of malnutrition, infectious diseases and NCDs refers to the coexistence of undernutrition, micronutrient deficiencies, overnutrition and endemic and emerging infections, including antimicrobial resistance. To overcome these three public health problems, concerted actions targeting children and adolescents in rural areas of Côte d'Ivoire have become a priority. The aim is to promote the lifestyle of children and adolescents to improve their health and healthy aging, through a cohort in the Taabo Demographic and Health Surveillance System (HDSS).

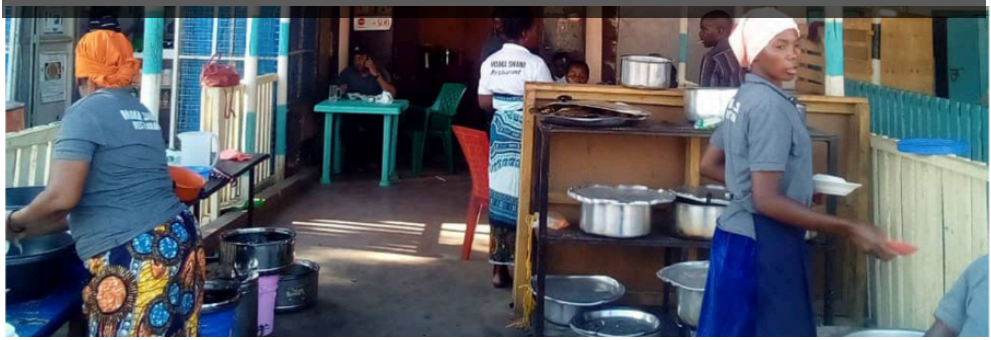
Methodology: Based on workshops and interviews with stakeholders to assess situation analysis, keys area most affected, data collection on prevalence of health condition, health risk mapping to determine influencing factors (geographic, social and economic).

Results: an integrated intervention model developed to be tested incorporating health system strengthening and service integrated, water, hygiene and sanitation couple with environmental health, multi-disease, multisectoral behavioral communication, diseases prevention and control programs, maternal and child health focus, trauma and wound prevention associated to monitoring, evaluation and adaptive learning. The results will improve children and adolescents' health, with better cognitive development and a reduction in overweight, obesity and NCDs (diabetes and hypertension). The result in the long term is the establishment of indicators for healthy aging.

Conclusions/Outlook: In the context of an accelerating nutritional and epidemiological transition in rural Côte d'Ivoire, addressing the triple burden of malnutrition, infectious diseases, and NCDs among children and adolescents requires integrated and multisectoral approaches. The proposed intervention model—combining health system strengthening, environmental health, water, hygiene and sanitation, and behavior change strategies—offers a comprehensive response tailored to local determinants. Its implementation within the Taabo HDSS cohort is expected to generate robust evidence on effective, context-specific interventions, leading to improved health outcomes, enhanced cognitive development, and a reduction in NCD risk factors. Ultimately, this approach provides a sustainable pathway toward healthier life trajectories and the establishment of indicators for healthy aging.

Keywords: NCDs, infectious diseases, malnutrition, health promotion, Côte d'Ivoire

Dietary Salt Intake and Blood Pressure Among Street Food Consumers in Dar es Salaam: A Cross-Sectional Study



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5. Kilimanjaro Christian Research Institute
6. Kampala International University, Tanzania

Introduction: Excessive salt consumption is a major modifiable risk factor for hypertension and cardiovascular diseases. In urban Tanzania, street food consumption is common, yet knowledge and practices related to salt intake among regular street food consumers remain poorly understood. This study assessed knowledge and attitudes regarding salt intake and examined their association with salt-related practices among regular street food consumers in Dar es Salaam.

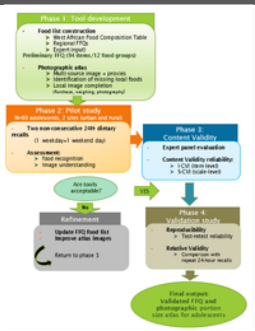
Methodology: A cross-sectional baseline survey was conducted among 313 regular street food consumers aged ≥18 years in nine wards of Dar es Salaam. Aligned with the One Health perspective this study is integrating human health and the role of food system in causing disease. Participants were recruited through multistage sampling from mapped street food vending sites. Salt intake was estimated using the INTERSALT equation from spot urine samples among 244 participants. Data were analyzed using descriptive statistics, logistic regression for determinants of high salt intake, and linear regression to assess the association between salt intake and blood pressure.

Results: The majority had excessive salt intake, with a median intake of 9.7 g/day, nearly double the WHO recommended limit. High salt intake was observed across all participant groups. Female participants had significantly higher odds of high salt intake compared to males (AOR = 4.53, 95% CI: 1.02–20.20, p = 0.047). In multivariable linear regression analysis, salt intake was independently associated with systolic blood pressure (β = 1.15, 95% CI: 0.19–2.11, p = 0.019), but not with diastolic blood pressure after adjustment.

Conclusions: Salt intake among street food consumers in Dar es Salaam is markedly higher than recommended levels and is independently associated with increased systolic blood pressure. These findings highlight a substantial public health concern and underscore the need for targeted interventions to reduce dietary salt intake in this population.

Keywords: Dietary salt intake, Street food, blood pressure

Validation of a food Frequency questionnaire and portion size Atlas for adolescents in Côte d'Ivoire.



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3. Université Félix Houphouët Boigny, Abidjan, Côte d'Ivoire.

Background/Objectives: Adolescence represents a critical "second window of opportunity" for growth, yet it remains one of the most under-researched periods in the nutritional transition of Sub-Saharan Africa. Despite this public health challenge, accurately characterizing dietary intake in this cohort remains problematic due to several factors.

Culturally adapted dietary assessment tools are essential for reliable epidemiological research and clinical practice in nutrition. However, such tools remain scarce for adolescents in resource-limited settings, especially in West Africa. In Côte d'Ivoire, no validated Food Frequency Questionnaire (FFQ) or photographic food atlas currently exists, limiting the assessment of dietary patterns in this population. Three primary imperatives: (i) without precise tools like a FFQ, it is impossible to identify the specific dietary patterns driving the divergent health outcomes; (ii) a Photographic Food Atlas is essential to reduce the recall bias and estimation errors, which are particularly prevalent in adolescent populations who often struggle to quantify portion sizes accurately; (iii) the development and validation of these tools provide the necessary infrastructure for longitudinal monitoring, allowing the design, implementation, and the impact evaluation of targeted nutritional interventions.

This study aims to develop and validate the content of a culturally appropriate FFQ and a companion photographic portion size atlas designed to assess the dietary intake of adolescents in Côte d'Ivoire.

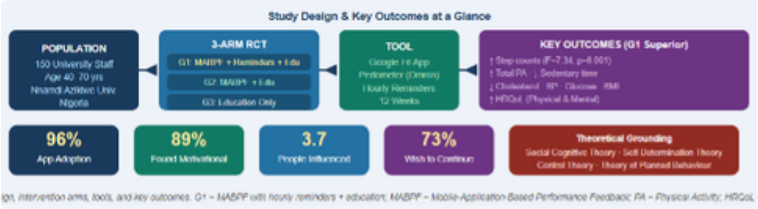
Methodology/Results: In phase 1, a preliminary FFQ was developed using the West African food composition table, existing foods lists from neighboring countries, and expert consultation, resulting in a 94-item food list across 12 food groups. A photographic atlas was constructed using images from existing African atlases (Ghana, Burkina Faso, Togo), supplemented with commercial images. Missing images of local foods are obtained through a small-scale fieldwork involving the purchase, weighing, and standardized photography of food samples.

In phase 2, a pilot study using two repeated 24-hour dietary recalls on non-consecutive days, including one weekday and one weekend will be conducted in two urban sites among 60 randomly selected adolescents. This second phase will be used to refine the FFQ food list while testing the photographic atlas for food recognition, image understanding, and portion size estimation. Content validity of the developed tool will be assessed by a panel of nutrition experts using the Content Validity Index (CVI). The final validation of the FFQ will include assessment of reproducibility and relative validity against repeated 24-hour dietary recalls.

Conclusions: By providing a tool that accounts for community eating and local food preparation, this study shifts the reliance from generic, error-prone global tools to context-specific instruments, significantly improving the quality of nutritional epidemiology in West Africa. This research contributes to filling the global data regarding adolescent nutrition in low- and middle-income countries (LMICs), recognizing this period as a critica.

Keywords: Adolescents, dietary pattern, food frequency questionnaire, food atlas, Côte d'Ivoire.

Mobile-Application-Based Performance Feedback, Physical Activity, Cardiovascular Risk and Quality of Life among University Staff in Nigeria: A Randomised Controlled Trial



IQR, intervention arms, tools, and key outcomes. G1 = MABPF with hourly reminders + education; MABPF = Mobile-Application-Based Performance Feedback; PA = Physical Activity; HRQoL =

Uchechukwu Martha Chukwuemeka[1], Peace Ogechukwu Chukwu[1], Anthony Chinedu Anakor[1,2], Francis Sena Nuvey[3,4], Ifeoma Adaigwe Amaechi[1], Bruno Enagnon Lokonon[5], Janeth Laurean[6], Ignatius Uche Nwankwo[1], Uchenna Prosper Okonkwo[1], Ebele Stella Nwokoye[1], Gilbert Fokou[3], Fatai Adesina Maruf[1], Clemence Esse-Diby[3], Bassirou Bonfoh[3]

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6. Open University of Tanzania, Tanzania

Introduction: Physical inactivity is the fourth leading global mortality risk factor, with a pooled prevalence of approximately 52% among Nigerian adults. University employees are vulnerable due to sedentary work environments that heighten cardiovascular disease (CVD) risk. Despite this, evidence-based, interventions tailored to this workforce remain scarce. Mobile health (mHealth) technologies offer a low-cost avenue for behaviour change, thus, this study evaluated effect of mobile-application-based performance feedback (MABPF) on physical activity, cardiovascular Risk and quality of Life among University Staff in Nigeria: A Randomised Controlled Trial.

Methodology: A 12-week, three-arm parallel randomised controlled trial with qualitative component was conducted among 150 staff aged 40–70 years at Nnamdi Azikiwe University. Overall, 170 participants were randomised 1:1:1 to: (1) MABPF with hourly reminders + CVD education (n = 52); (2) MABPF only + CVD education (n=50) or (3) education-only control (n=48). Google Fit served as the mHealth platform, with Omron HJ-325 pedometers providing objective validation. Outcomes included step counts,

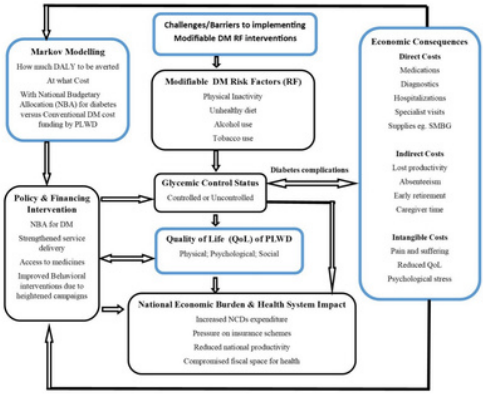
physical activity (PA) levels, sedentary time, CVD risk markers [blood pressure (BP), cholesterol, glucose, body mass index (BMI), waist circumference], stress, stage of change, and health-related quality of life (HRQoL), assessed at baseline, 6 weeks, and 12 weeks. Analyses employed non-parametric Friedman ANOVA, Quade's ANCOVA, Wilcoxon Signed-Rank, and Mann-Whitney U tests ($\alpha = 0.05$). Eleven staff completed qualitative interviews analysed thematically, and 102 staff completed survey on Google Fit app use and diffusion.

Results: App adoption was high (96.1%), with 89.2% reporting MABPF as motivational. Each participant influenced a median of 3.7 additional individuals, demonstrating a snowballing diffusion effect. Between-group analyses revealed that MABPF with hourly reminders produced significantly greater improvements in pedometer step counts ($F = 7.336$, $p = 0.001$), total PA ($F = 3.963$, $p = 0.021$), moderate PA ($F = 6.248$, $p = 0.003$), and sedentary time reduction ($F = 3.405$, $p = 0.038$). Across all groups, significant improvements were observed in diastolic BP, BMI, waist circumference, total cholesterol, HDL cholesterol, blood glucose, and stress (all $p < 0.05$). HRQoL improved in both physical (PCS: $F = 4.874$, $p = 0.009$) and mental (MCS: $F = 3.312$, $p = 0.039$) domains. Qualitative findings showed participants shifted their understanding of PA from routine tasks to intentional exercise, identifying context-specific barriers including infrastructure deficits, time constraints, and low self-motivation, as well as some facilitators such as support from family, community, and religious sources.

Conclusions: This is the first Nigerian evidence that a theory-informed, app-based intervention can simultaneously reduce multiple CVD risk factors, while improve QoL among university employees. The strong behavioural and clinical gains observed support integrating MABPF into institutional wellness policies, and scaling use across universities. Its low cost, feasibility, and adaptability make it a practical tool for strengthening workplace non-communicable disease (NCD) prevention and advancing One Health workforce wellbeing.

Keywords: Physical activity, mHealth, Cardiovascular risk,
Workplace intervention, One Health

Risk Factors, Economic Burden and Quality of Life of people living with Diabetes in Ghana: One Health Approach



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Introduction: Globally, one person dies of diabetes every five seconds. In Ghana, current diabetes prevalence (6.5%) exceeds the sub-Saharan Africa (SSA) average (4.5%). Despite this growing burden, there is no dedicated national budgetary allocation (NBA) to address it. The increasing diabetes prevalence threatens the productivity, livelihood and food security of the population. Meanwhile, adherence to lifestyle interventions such as diet therapy and physical activity remain challenging for many patients. This study evaluates the risk factors, economic burden and Quality of Life (QoL) among persons living with type 2 diabetes (PLWD) in Ghana using an inter-disciplinary One Health approach.

Methodology: The study will apply mixed-methods, including a systematic review, cross-sectional survey and a cost-effectively analysis. In Part I, the study will conduct a systematic review to synthesize evidence on QoL among PLWD and challenges to implementing behavioural risk-factor interventions in SSA, including built-environment and food-system barriers.

Electronic databases (PubMed, EMBASE, LILACS, CINAHL, African Journals Online, African Index Medicus, HINARI, IMSEAR, Google Scholar, and grey literature) will be searched without language restriction. Screening will be conducted using Rayyan, and independent quality appraisal assessed using standard risk of bias tools. Random- or fixed-effects meta-analysis will be applied based on heterogeneity assessed by the I^2 statistic, and evidence quality graded using the GRADE framework. The protocol is registered with PROSPERO.

Part II will entail a multi-center cross-sectional study in six randomly selected regional hospitals in Ghana involving 618 PLWD. A structured questionnaire which incorporates the validated EuroQol-5D-5L instrument will be used to assess direct, indirect and intangible costs of diabetes. A composite variable (including livelihood, productivity, transportation network, proximity to fast-food hubs, walkable green spaces, reliance on local agricultural products vs. ultra-processed imports) will be used to assess the effects of the physical environment and food system on physical activity and diet among PLWD. Descriptive statistics, t-tests, regression analyses, probability modelling, and conditional log-cost models will be applied at a 95% confidence level ($p<0.05$), using STATA 15.1.

In Part III, the study estimates cost-effectiveness of introducing a diabetes care component in Ghana's national budget using a 3-state Markov's model with a one-year cycle length and a 25-year time horizon. The model will compare (a) introducing an NBA for diabetes care with (b) the current standard of practice, where PLWD largely bear out-of-pocket costs.

Expected Outcomes: This study will generate evidence on the economic burden and QoL impacts of diabetes in Ghana and evaluate the cost-effectiveness of dedicated national funding for diabetes care. Findings are expected to inform policymaking diabetes control financing, support integrated One Health strategies for diabetes control, and contribute to improving the wellbeing of PLWD in Ghana and across SSA.

Keywords: Type 2 Diabetes Mellitus, Systematic Review, Markov's Model, Cost-effectiveness analysis; Behavioural life-style modifications

Detection of high-risk human papillomaviruses using the GeneXpert platform in cervical cancer screening in Burkina Faso

Photo: Cartridge launch procedure with the GeneXpert device

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Introduction: Cervical cancer is the fourth most common cancer among women worldwide, with an estimated 660,000 new cases and approximately 350,000 deaths in 2022. In Burkina Faso, cervical cancer is the most commonly diagnosed cancer and the second leading cause of female mortality, with 775 deaths reported in 2022. GeneXpert assays are the primary method for detecting high-risk Human papillomavirus (HPV) in Burkina Faso. However, their limited panel restricts genotypic coverage and typing accuracy. This study aims to thoroughly characterize the genetic diversity and distribution of HPV genotypes identified by the GeneXpert platform in the Burkinabe population.

Methodology: This was a cross-sectional study involving women aged 23 years or older, selected from Bobo-Dioulasso in Burkina Faso. Highly sensitive vaginal swabs were collected, and the samples were genotyped using Cepheid's GeneXpert system.Data were collected from health center across Burkina Faso, particularly focusing of CMA Dô, utilizing GeneXpert technology and the Xpert® HPV kit. The assay reports HPV16, HPV18/45, and pooled channels for 11 HPV types (P3: 31/33/35/52/58; P4: 51/59; P5: 39/56/66/68). Descriptive analysis was conducted.

Results: Of 1,666 valid tests, 309 were positive for high-risk HPV, yielding a prevalence of 18.6%. The most common HPV genomes identified were 11 other genotypes as a pooled result (HPV-31, 33, 35, 39, 51, 52, 56, 58, 59, 66, and 68), constituting 84.8% of HPV-positive women.
Conversely, HPV-18/45, HPV-16, and infections involving two or three genotypes (multiple HPV genome infections) were detected in 4.2; 4.5 and 6.5%, of cases.

Conclusions/Outlook: High-risk HPV infections among women in Burkina Faso were predominantly due to genotypes grouped as "other high-risk HPV types which accounted for 91.3%. These findings highlight the diversity of circulating HPV genotypes and underscore the limitations of the GeneXpert assay in providing detailed genotype-specific information. Future studies should therefore employ advanced genotyping methods to accurately characterize circulating HPV genotypes and better inform vaccine selection in Burkina Faso.

Keywords: GeneXpert, Cervical cancer, Human papillomavirus, Burkina Faso

Recurrent Drought and Mental Health among Pastoralist Communities in Northern Tanzania: A Mixed-Methods Study of Psychosocial Vulnerability and Coping Systems

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Introduction: Recurrent drought in pastoralist regions of Northern Tanzania disrupts livestock-based livelihoods, food systems, mobility patterns, and community support networks. While the environmental and economic impacts of droughts are well documented, limited attention has been given to how repeated climatic shocks reshape psychosocial systems and drive common mental health disorders among livestock-dependent populations. This study conceptualizes drought not merely as an environmental exposure but as a systems-level stressor operating through social, economic, and cultural pathways, a framing that aligns with One Health principles linking environmental, animal, and human health. This study, therefore, aims to determine the 12-month prevalence and correlates of depression and anxiety among Maasai pastoralists in Longido and Monduli districts, and to explore cultural perceptions of drought, its influence on mental health, and the coping mechanisms employed by affected communities.

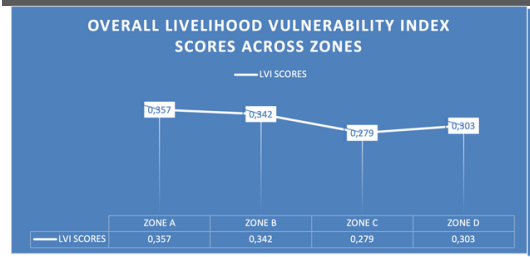
Methodology: A community-based cross-sectional mixed-methods study will be conducted among 554 adult pastoralists in Longido and Monduli districts. Quantitative measures will include household food insecurity (HFIAS), depression (PHQ-9 ≥10), anxiety (GAD-7 ≥10), and alcohol use (AUDIT).

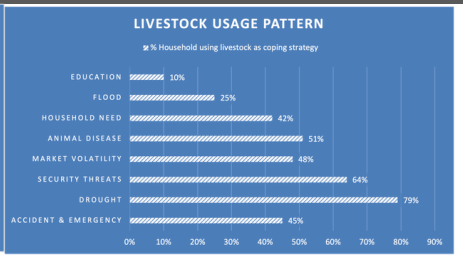
Multivariable logistic regression models, adjusted for village-level clustering, will be used to identify independent predictors of mental health outcomes. Qualitative data will be collected through in-depth interviews and focus group discussions to explore cultural idioms of distress, local understandings of drought-related stress, and perceived pathways linking drought to mental health. Findings will be triangulated across three data sources: the quantitative survey, in-depth interviews, and focus group discussions.

Expected Outcomes: This study will generate the first population-level estimates of 12-month depression and anxiety among Maasai pastoralists in Longido and Monduli, stratified by gender, age, and drought exposure severity. Multivariable logistic regression will produce a predictors profile identifying independent sociodemographic, economic, cultural, and environmental determinants of common mental health disorders. Qualitative components will document cultural pathways through which drought is perceived and experienced as a driver of mental distress, including local idioms of distress, stigma, and traditional meaning systems. The study will also generate evidence on adaptive coping strategies, including kinship networks, spirituality, and livestock diversification, alongside maladaptive responses such as alcohol use and social withdrawal, clarifying their roles as buffers or amplifiers of drought-related psychological distress. Collectively, these findings will advance a psychosocial systems perspective within the One Health evidence base and inform the integration of mental health screening and psychosocial support into drought-response programs, with dissemination through Tanzania's National Mental Health Program and the One Health Platform.

Keywords: Recurrent drought; Maasai Pastoralists; Depression; Anxiety; Coping Systems.

Assessing the contribution of Livestock System in Mitigating Livelihood Vulnerability of Rural Populations in Kwara state





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Introduction/Background/Objectives: Livestock constitutes a significant amount of household wealth, and pastoralists depend on it for their livelihoods and well-being. Livestock has been used to mitigate risk directly through the sale of animal products and indirectly by serving as collateral and insurance for investments. Investment in livestock and social capital are among the most effective coping strategies and form the basis of the majority of the households' shock response plans. For pastoralists in Africa who depend entirely or mostly on livestock for their livelihoods, drought is the leading cause of livestock death. The damaging effects of drought and the resulting high rate of livestock death could be averted through the adoption of Index-Based Livestock Insurance (IBLI). IBLI provides proactive protection by paying herders before animals are lost, enabling them to take preventive actions to save livestock and livelihoods. Given the increasing threats of climate change on pastoralist communities, developing feasible, affordable, and context-specific IBLI products is crucial for sustainable livestock management, poverty reduction, and climate adaptation. This study examines the livelihood vulnerability index (LVI), risks, and coping strategies of pastoral communities to generate evidence on the technical, socioeconomic, and market feasibility of IBLI in Kwara state.

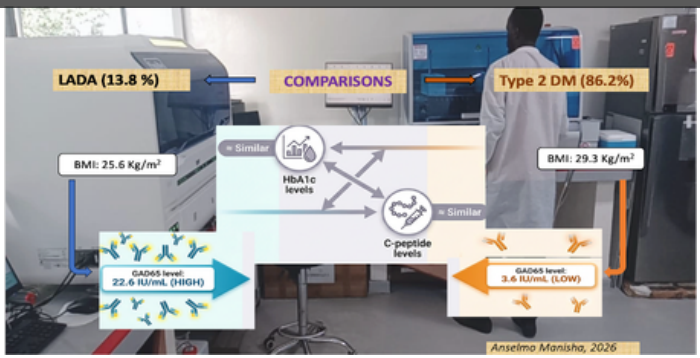
Methodology: A total of 384 households selected using multistage sampling procedure across eight communities from the four ADP zones were surveyed using structured interview. Livelihood vulnerability index (LVI) was calculated using a balanced weighted average method that includes institutional, environmental and socioeconomic factors to assess the degree of vulnerability between zones. Three focus group discussions and key informant interviews (KII) with community members and household heads were conducted across livestock dependent communities from the four ADP zones to identify usage pattern of livestock as domestic insurance. Vulnerability of livestock asset was modelled using Group Model Building (GMB) to better understand the main feedback loops that impact the resilience of livestock as domestic insurance. To assess the feasibility and the degree of favorability of introducing IBLI in Kwara state, biophysical analysis using geospatial data was used to assess the rangeland dominance, seasonality and forage availability. KII with community leaders, extension agents and community members was used to assess the socioeconomic and institutional factors that favors the introduction of IBLI in the study area.

Results: The LVI of livestock-dependent communities across the zones show considerable differences in susceptibility by location. Zone A which has the highest LVI score of 0.357 has the highest vulnerability followed by Zone B, D & C with LVI of 0.342, 0.303 & 0.279 (lowest vulnerability) respectively (Fig 1.0). Household survey revealed a high reliance on livestock liquidation for shocks with >88% using livestock sales as primary coping mechanism. Key factors that count as shocks and the percentage of households using livestock sales to combat them include Drought (79%), Security threat (64%), Animal disease outbreak/mortality (51%) Market volatility (48%), and health emergencies (45%) (Fig 2.0). Drought is the greatest trigger driving livestock sales for adaptation. Five Reinforcing (R) and two Balancing (B) feedback loop that influences system behaviour were identified during the GMB workshop and the major leverage point identified in the system is to reduce the impact of drought through the deployment of Index-based livestock insurance.

Conclusions/Outlook: The thematic analysis underscores that while pastoral livelihoods remain economically and culturally foundational in Kwara State, they face intersectional stresses from climatic shocks, insecurity, disease outbreak, and market inefficiencies. Yet, the resilience demonstrated through adaptive feeding, livelihood diversification, and community mediation reveals significant adaptation. Formal reinforcement - through insurance literacy, implementation of IBLI, infrastructure, and policy trust - is central to strengthening pastoral resilience pathways.

Keywords: Livestock system, Livelihood vulnerability index, Drought, Index-based livestock insurance

The magnitude, β-cell function, and insulin resistance of Latent Autoimmune Diabetes in Adults among patients of phenotypic Type 2 Diabetes in a tertiary hospital in Mwanza, Tanzania



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Introduction/Background/Objectives: Latent Autoimmune Diabetes in Adults (LADA) is a borderline type of diabetes, with genetic and immunological characteristics of Type 1 Diabetes (T1DM) and clinical factors such as overweight/obesity and insulin resistance resembling Type 2 Diabetes Mellitus (T2DM). Despite the recognition of LADA as a distinct type of diabetes mellitus, there is a paucity of data on its prevalence, immunological and metabolic characteristics, and optimal diagnostic approaches within African populations, particularly in resource-limited settings. In Tanzania, LADA remains underdiagnosed due to lack of serum autoantibody testing in routine screening of adult on set diabetes mellitus. Consequently, many patients may receive suboptimal management, leading to poor glycemic control and accelerated beta-cell decline. Therefore, this study aimed to determine the magnitude of LADA among T2DM and to characterize its immunological and clinical features associated with LADA to inform better diagnostic and management practices.

Methodology: This hospital-based cross-sectional study design enrolled 246 participants at Bugando Medical Center (BMC) from August 2024 to August 2025. A standardized questionnaire was used to gather social demographic and patients' history from study participants, which was confirmed by the extracted medical records from the BMC hospital database. We collected blood samples for the HbA1c, GAD65, and C-peptide laboratory analysis. We performed the analyses using R software and STATA v15, and presented the data in mean, median, standard deviation, and proportion. Comparisons between LADA and Type 2 Diabetes groups were performed using the Mann–Whitney U test, and the association was analyzed using Chi-Square and Logistic regression.

Results: LADA accounted for 13.8% of the study participants, whereas 86.2% were classified as T2DM. The main differences between the two groups were observed in GAD65 autoantibody levels and body mass index (BMI). Mean GAD65 levels were significantly higher in the LADA group (22.63 ± 13.3 IU/mL) compared with the T2DM group (3.61 ± 3.53 IU/mL, $p < 0.001$). In contrast, BMI was significantly lower among LADA patients (25.61 ± 3.97 kg/m²) than among those with T2DM (29.31 ± 5.02 kg/m², $p < 0.001$). The distribution of weight categories also differed significantly between the two groups ($p = 0.0002$). A greater proportion of LADA patients had a normal weight (43.75%), whereas obesity was more common among T2DM patients (41.85%). However, C-peptide levels, HbA1c values, and duration of disease management did not show significant differences between the two groups. Logistic regression analysis identified GAD65 levels and BMI as the only variables significantly associated with LADA. Specifically, each 1 kg/m² increase in BMI was associated with a 22.5% decrease in the odds of having LADA (OR = 0.775; $p = 0.03$), while each 1 IU/mL increase in GAD65 level increased the odds of LADA by 53.8% (OR = 1.538; $p < 0.001$).

Conclusions/Outlook: We established that LADA constitutes a substantial subset of apparent T2DM in northwestern Tanzania. LADA has been shown to have distinguished characteristics, which include higher levels of GAD65 autoantibody and a slightly slim body type. The current diagnosis and standard of care practices are inadequate in the proper diagnosis of adult-onset diabetes, which may be improved by the addition of auto-antibody laboratory testing.

Keywords: Latent Autoimmune Diabetes in Adults, Insulin Resistance, β-cell function

Epidemiology of multimorbidity and potential intervention strategies among people living with HIV in Tanzania and Uganda

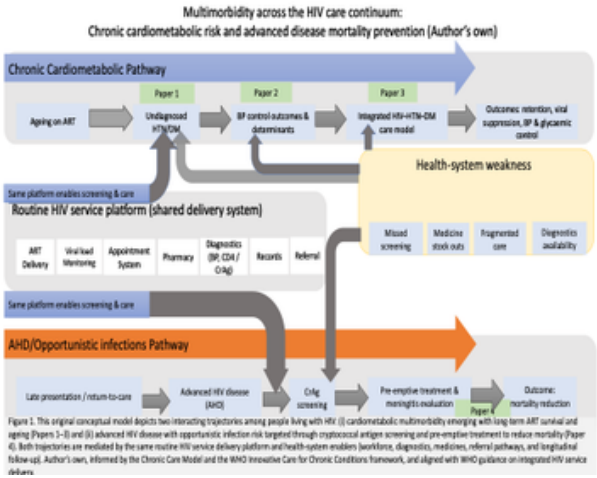

Figure 1. This original conceptual model depicts two interacting trajectories among people living with HIV: (i) cardiometabolic multimorbidity emerging with long-term ART survival and ageing (Papers 1–3) and (ii) advanced HIV disease with opportunistic infection risk targeted through cryptococcal antigen screening and pre-emptive treatment to reduce mortality (Paper 4). Both trajectories are mediated by the same routine HIV service delivery platform and health-system enablers (workforce, diagnostics, medicines, referral pathways, and longitudinal follow-up). Author's own, informed by the Chronic Care Model and the WHO Innovative Care for Chronic Conditions framework, and aligned with WHO guidance on integrated HIV service delivery.

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Background and Objectives: As survival improves with antiretroviral therapy (ART), people living with HIV (PLHIV) in sub-Saharan Africa increasingly experience multimorbidity spanning cardiometabolic conditions and advanced HIV disease (AHD)–related opportunistic infections. Fragmented service delivery can delay detection and compromise chronic disease control, while gaps in AHD packages contribute to preventable mortality. This PhD project aimed to characterize multimorbidity burden and to evaluate pragmatic intervention strategies to improve outcomes among PLHIV in Tanzania and Uganda.

Methodology: TThis thesis comprises four linked studies. (1) A cross-sectional study in large HIV clinics in Dar es Salaam systematically measured blood pressure and glucose among clinically stable PLHIV without known hypertension/diabetes. (2) A secondary analysis of a pragmatic multi-country cluster-randomised trial (Tanzania and Uganda) compared blood pressure (BP) control between PLHIV and participants

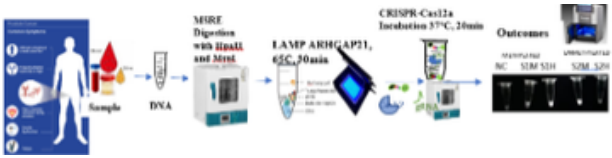
without HIV receiving identical hypertension management. (3) The INTE-AFRICA pragmatic cluster-randomised trial evaluated integrated management of HIV, hypertension, and diabetes versus standard vertical care, with co-primary endpoints of retention among people with hypertension/diabetes and viral load suppression among PLHIV. (4) The TRIP stepped-wedge implementation study evaluated large-scale cryptococcal antigen (CrAg) screening with pre-emptive treatment in routine services, including mortality outcomes. Figure 1 summarizes the thesis logic across the HIV care continuum and maps each study to the relevant pathway and outcomes."

Results: Among 975 PLHIV assessed for glycaemia in Dar es Salaam, 54.6% (95% CI 51.3–57.7) had abnormal glucose levels and 37.7% (95% CI 34.5–40.9) of those without a prior hypertension diagnosis had elevated BP (≥140/90), including 3.4% with severe hypertension (≥180/120). In the multicountry BP analysis (n=3,084 hypertensive participants; 17.4% PLHIV), BP control at 12 months was lower among PLHIV than among those without HIV (32.7% vs 46.9%), with an adjusted risk difference of 11.9% (95% CI 6.0–17.8; p<0.001). In INTE-AFRICA (32 facilities), retention among participants with hypertension/diabetes was high in both arms (89.0% vs 89.8%), and viral suppression remained high, with non-inferiority demonstrated (97.0% vs 97.3%). In TRIP (n=5,358), CrAg positivity was 4.42% in screening facilities; mortality was highest among CrAg-positive symptomatic participants (51.3%) and remained elevated among CrAg-positive asymptomatic participants (22.4%) compared with CrAg-negative participants (9.0%).

Conclusions: Multimorbidity among PLHIV in Tanzania and Uganda is substantial and spans both cardiometabolic disease and AHD-related mortality risk. These findings support strengthening routine HIV platforms to deliver integrated cardiometabolic screening and management while ensuring effective implementation of AHD mortality-prevention pathways such as CrAg screening and timely treatment.

Keywords: HIV; multimorbidity; hypertension; diabetes; advanced HIV disease

A non-invasive CRISPR-Cas12a-Based test for early prostate cancer detection in Nigeria: Integrating genomic innovation with community health systems.



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Background: Prostate cancer (PCa) mortality in Nigeria is high, driven by the low specificity of the standard Prostate-Specific Antigen (PSA) screening test and late clinical presentation. This delay is linked to complex health-seeking behaviours, the high cost of diagnostics, and cultural fears of invasive, painful, and uncomfortable biopsies. Furthermore, the lack of Black population-specific genetic markers associated with early-stage PCa. To bridge this gap, this project translates population-specific epigenetic and mutation signatures of caretaker genes (*BARD1, ARHGAP21*) and androgen pathway genes (*PCA3, KLK3*) into a non-invasive Clustered Regularly Interspaced Short Palindromic Repeat-associated Cas12a coupled to Loop Mediated Isothermal amplification assay. This provides a painless diagnostic alternative designed to empower communities and traditional health practitioners to shift health-seeking behaviours toward early screening.

Methods: Following ethical clearance, 128 participants (44 PCa cases, 42 BPH, and 42 Healthy men) were recruited at the Lagos State University Teaching Hospital (LASUTH), Nigeria. Blood and urine were collected, and

we conducted Sanger sequencing n=74 for mutation identification and MSRE-PCR n=100 for methylation profiling of *KLK3*, *PCA3*, *BARD1*, and *ARHGAP21*. A CRISPR-Cas12a-LAMP assay was developed for methylation-based detection.

Results: Genetic screening revealed no *PCA3* or *ARHGAP21* variants, while *BARD1* and *KLK3* showed multiple variants, with 47% unregistered in dbSNP. *BARD1* rs11896262, one of the recurrent variants (rs11896262, rs1694222860, and rs11897384), trended toward PCa association (OR=2.9, 95% CI [0.59- 15.8], p=0.17), discrimination from Benign Prostatic Hyperplasia (BPH) (OR=3.76, 95%CI: [0.40-53.02], p= 0.192), and improved PSA-based diagnosis (PSA_AUC=0.73, rs11896262_AUC=0.612). KLK3 variants showed risk signals rs8104556 trended towards discriminating PCa from BPH (p=0.068), whereas an unknown variant (C>A) correlated significantly with early-age PCa (<60 years; p=0.02). *ARHGAP21* was hypermethylated (10%) in PCa cases only. A fluorescent CRISPR-Cas12a-LAMP assay was developed for methylation identification and achieved 75% sensitivity and 50% specificity.

Conclusion: This study identified potential population-specific variants and successfully developed a non-invasive fluorescent CRISPR-Cas12a-LAMP diagnostic platform. Integrating these genetic and epigenetic signatures with current PSA screening provides a promising, non-invasive framework for improving early PCa diagnosis in resource-limited settings in Nigeria

Keywords: CRISPR-cas12a-lamp, Prostate cancer, KLK3, PCA3, ARHGAP21, BARD1, Methylation

Hypertension and Mortality in Ageing PLHIV in Kenya, Uganda and Tanzania (AFRICOS, 2013–2023)

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Introduction: Although mortality among people living with HIV (PLHIV) in sub-Saharan Africa has decreased markedly with the scale-up of antiretroviral therapy (ART), the demographic consequences of this success remain underexamined. This study sought to examine how hypertension shapes all-cause mortality trajectories among people living with HIV (PLHIV) aged 40 years and above.

Methods: Using ten years of longitudinal data from the African Cohort Study (AFRICOS; 2013–2023) in Kenya, Tanzania, and Uganda, we estimated the association of hypertension with all-cause mortality among adults aged 40 years and older. We combined descriptive decremental life-table analysis with discrete-time logistic regression, applying both lagged and exponentially weighted moving-average (EWMA) exposure models to capture cumulative risk.

Results: At baseline, 18.6% of participants were hypertensive; 60.1% experienced hypertension during follow-up, and all-cause mortality was 6.4%. Life-table estimates showed cumulative excess mortality (Δq_x) among hypertensive participants increased from 0.6% (95% CI: -0.7-1.9%) in year 1 to 3.4% (95% CI: 1.3-5.6%) by year 9, becoming statistically significant from year 7 onward (2.1%; 95% CI: 0.0-4.0%). Excess mortality was larger among adults aged 50-59 years (4.9%; 95% CI: 1.8-8.0%), men (6.0%; 95% CI: 1.4-10.5% by year 8), underweight participants (27.1%; 95% CI: 5.4-48.8% by year 9), and those with suppressed viral load (5.5%; 95% CI: 3.3-7.8% by year 9). In adjusted discrete-time models controlling for age, sex, body mass index, viral load, and country, hypertension was associated with higher mortality under a standard lag specification (aOR = 2.04; 95% CI 1.10–3.80) and under EWMA exposure definitions (aOR = 3.25; 95% CI 1.26–8.40 at α = 0.3; aOR = 2.51; 95% CI 1.16–5.44 at α = 0.7). Mortality odds were higher among participants aged ≥60 years (aOR = 2.23–2.40; 95% CIs 0.85–6.16) and those with high viral load (aOR = 2.36–2.44; 95% CIs 1.28–4.51), while overweight and obese participants had substantially lower odds of death (aOR = 0.29; 95% CI 0.10–0.85 and aOR = 0.14; 95% CI 0.04–0.56).

Conclusions: These findings highlight a demographic transformation of the HIV epidemic in East Africa, where mortality among PLHIV increasingly reflects a growing influence of chronic diseases in addition to infection control. Hypertension has become a key driver of excess mortality and a demographic indicator of the region's compressed health transition.

Keywords: HIV, hypertension, mortality, life-course, demography, East Africa, AFRICOS

Assessment of the Health Seeking Behaviours and Utilization of NCD-related Services Among the Fulani Community in the Asante Akim North Municipality, Ghana

Image credit: Abubakaringim

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Introduction : Non-communicable diseases (NCDs) are a significant public health challenge in Ghana, reflecting a global epidemiological transition from infectious diseases to chronic conditions. Worldwide, annual NCD-related deaths are projected to rise from 43 million in 2021 to 52 million by 2030. Timely access to appropriate NCD care plays a crucial role in shaping individuals' health-seeking behaviour (HSB). While choice is central to HSB, it is often constrained by structural factors beyond individual control. In LMICs, these constraints are further exacerbated by the double burden facing health systems, where NCDs must compete for limited resources alongside infectious diseases and maternal and child health, reducing the visibility and availability of NCD-specific services. When healthcare systems are inaccessible, unresponsive and unaffordable, individuals may delay seeking care, turn to informal or traditional providers or forgo treatment entirely. Among pastoralist populations such as the Fulbe (Fulani), HSB is shaped by additional barriers — language and communication challenges, limited education and healthcare services, financial constraints, dietary transitions, social stigma, and urbanisation — further shaping healthcare utilisation and perceptions of health systems. This study therefore examines health-seeking behaviours, knowledge, and barriers to NCD healthcare utilisation among the Fulani in the Asante Akim North Municipality of Ghana.

Methodology : This study employs a convergent parallel mixed-method design. A multistage sampling procedure will survey 277 Fulani individuals across five communities (three semi-nomadic and two transhumant). The qualitative component includes 6–8 focus group discussions (elderly men and women, caregivers, semi-nomadic and transhumant individuals) and 5–10 in-depth interviews (NCD patients, traditional healers, and community and religious leaders). Analysis will be guided by a One Health perspective, recognising interconnected relationships between human, animal, and environmental systems and their influence on healthcare utilisation. Quantitative data will be analysed with STATA using descriptive and inferential statistical methods, while qualitative data will be analysed with NVivo through thematic analysis. Findings will be compared and synthesised to produce a fuller and more contextualised interpretation of the research problem.

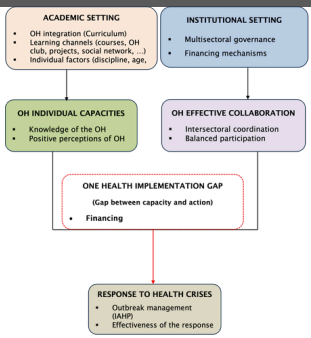
Expected Outcomes : This study will generate insights into lived experiences, cultural beliefs, decision-making processes, gender dynamics, and structural barriers influencing NCD healthcare utilisation among Fulbe populations. It will shed light on the coexistence of biomedical and traditional healthcare systems within these communities. The evidence will inform culturally appropriate and accessible interventions aimed at reducing the NCD burden among livestock-dependent pastoralist populations.

Keywords : Noncommunicable diseases, health-seeking behaviour, healthcare utilisation, Fulani, One Health

Collection Action and Behavioral Change (CABEC)

TTP Lead

Exploring the One Health implementation gap: A cross-analysis of the link between academic curricula and field practice in Senegal



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Introduction/Background/Objectives: One Health (OH) approach represents an essential framework for the prevention and control of complex public health threats, particularly in resource-limited settings. Its effectiveness depends both on the training of pre-services and on the capacity of health systems to ensure effective multisectoral collaboration. However, few studies have jointly examined these two dimensions to assess their coherence in operational implementation. This study aims to identify an underline convergence and gap through integrated analysis of the relationship between academic training and operational implementation of the OH approach in Senegal.

Methodology: A sociological perspective of collaboration was adopted to examine the relational dynamics, power structures, and institutional constraints shaping multisectoral interactions in the implementation of the One Health approach, through integrated analysis of two distinct cross-sectional surveys. The first, conducted among 200 medical and veterinary students at Cheikh Anta Diop University of Dakar, assessed the integration of OH competencies into curricula, as well as students' knowledge and perceptions. The second, carried out among 24 One Health actors involved in the response to the 2023 Highly Pathogenic Avian Influenza (HPAI) outbreak in Senegal, examined multisectoral collaboration dynamics,

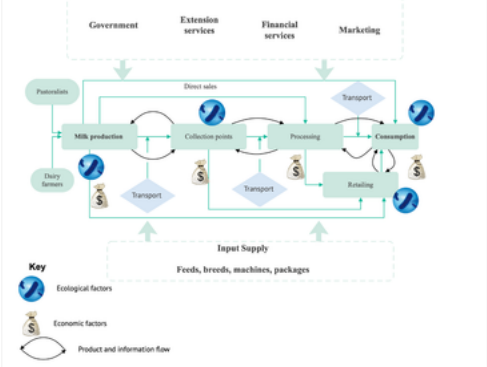
additional training received, and institutional constraints. A cross-analysis and interpretative approach was used to identify convergences and gaps between academic training and operational practices.

Results: The findings show uneven integration of OH core competencies within training programs, with greater advancement in veterinary education than in medical training. Veterinary students demonstrated higher levels of knowledge (78% vs 21%, $p < 0,001$) and generally positive perceptions of the OH approach (56.5%). On the field side, stakeholders reported that, beyond pre-service education, they strengthened their competencies mainly through continuous training (risk communication and community engagement, epidemiology, surveillance, and OH leadership), reflecting adaptation to operational demands. However, multisectoral collaboration during the HPAI response was present but limited and unbalanced, with a dominance of the animal health sector (50%) and major institutional constraints, including insufficient funding for joint actions (62.5%), fragmented budgets and institutional frameworks (37.5%), and weak public health infrastructure (37.5%).
The cross-analysis highlights some convergences, particularly the shared recognition of the OH concept and the central role of the animal health sector in both academic and operational settings. However, it also reveals major gaps, including limited interdisciplinarity with under-representation of the environmental sector, as well as structural and institutional barriers that hinder the operationalization of acquired competencies and the translation of collaborative intentions into effective actions.

Conclusions/Outlook: Despite growing integration of the OH approach into academic training, its translation into effective collaborative practice remains constrained by structural and institutional barriers, suggesting the existence of OH implementation gap between academic knowledge, institutional capacity, and operational practice. Strengthening interdisciplinary pedagogical approaches, integrated governance mechanisms, and sustainable financing systems is essential to reduce these gaps. Future research should focus on evaluating integrated training–action models in different African contexts to identify the most effective strategies for reducing these gaps.

Keywords: One Health, multisectoral collaboration, academic training, knowledge–practice gap, Senegal

Application of systems and value chain approaches in the prevention and control of Brucellosis in Tanzania



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Introduction/Background/Objectives: Brucellosis is a contagious bacterial zoonotic disease which affects livestock, wildlife and humans. It is highly prevalent in cattle population in Tanzania (0.6% to 23%) and abortion rate of up to 80%. Humans are primarily infected through direct contact with infected animals or by consuming contaminated animal products, such as unpasteurized milk. The complex interplay between ecological and socio-economic factors, compounded by limited collaboration and coordination between the human and animal health sectors, has led to the persistence of the disease. Therefore, this study integrates value chain analysis with systems thinking to identify hotspots and action levers, informing the development of a targeted bio-economic intervention model

Methodology: Guided by systems thinking and value chain analysis frameworks, an exploratory study design was employed to identify risk hotspots and action levers across the milk and dairy product production-to-consumption chain in Monduli district, Arusha, Tanzania. Systems thinking guides how incentives and feedback mechanisms shapes actors' responses towards risk while value chain analysis provides how the risk (brucellosis) travels with product and information flow. The interaction between ecological and economic factors determines the risk hotspots.

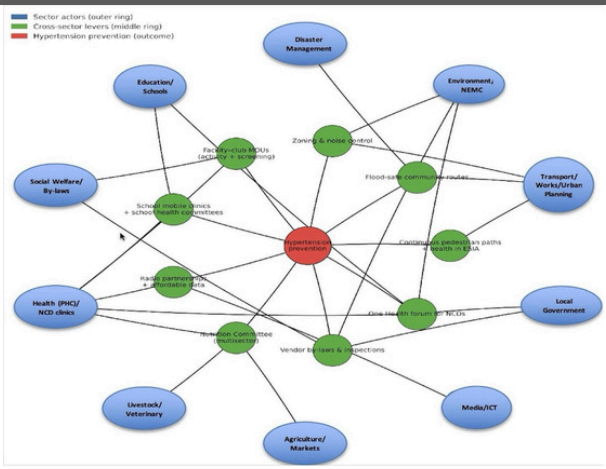
Data were collected through a combination of literature and desk review, mapping of dairy value chain, non-participant field observation (4) and semi-structured and key informant interviews involving value chain actors such as livestock farmers (n=11), milk collectors (n=4), processors (n=2), transporters (n=1), retailers (n=3), consumers (n=2), district medical officers (n=1) and veterinarians (n=2). The value chain analysis was used to identify market structures and risk and intervention nodes.

Results: The dairy value chain in Monduli was highly informal, seasonal, and predominantly female-led, with most actors being semi-mobile. Milk is collected from multiple small-scale livestock keepers at small volumes, often 0.5-10 litres per farmer. During high seasons, between 60 and 200 litres are collected a day at USD 0.4-0.6 per litre. Milk collectors supply hotels and local customers in nearby towns but seldom follow hygiene practices, thereby exposing more women to the risk of contracting the disease. Brucellosis risk hotspots include infected farms, milk collection points, and retail outlets due to higher transaction volumes and poor hygiene. Despite the flow of dairy products along the value chain, there was information asymmetry: most actors were aware of the brucellosis risks associated with the dairy value chain but lacked knowledge of its symptoms.

Conclusions/Outlook: The study identified farms, milk collection points and retail outlets as the key risk hotspots in the dairy value chain due to high human involvement, poor hygiene, and large milk volumes. However, due to limited data availability, it was difficult to map all processes, actors, and actual economic/transactional costs between people and points along the value chain nodes to inform the bio-economic model. Therefore, the next step is to reconstruct the value chain map using the group model-building approach guided by the integrated conceptual framework.

Keywords: Brucellosis, Dairy value chain, zoonotic disease, risk hotspots, Tanzania

Understanding Individual, Social, and System Determinants of Hypertension Prevention in Tanzania: A One Health Perspective



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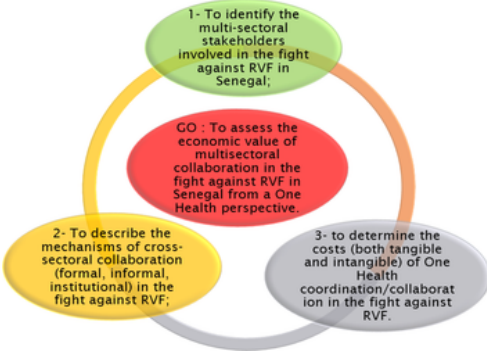
Introduction/Background/Objectives: Hypertension is highly prevalent in Tanzania, with notable rural–urban disparities and low levels of awareness and prevention. While traditional hypertension prevention efforts have primarily focused on individual and biomedical lifestyle risk factors, there is limited evidence regarding how social networks and broader system-level conditions influence the adoption of prevention behaviors. This study examined individual, social, and system-level determinants of hypertension-preventive behaviors among adults in rural and urban Morogoro.

Methodology: A mixed-methods study was conducted in Kilombero District Council (rural) and Morogoro Municipal Council (urban). Quantitative data were collected from 838 adults using a structured survey and analyzed using multivariable logistic regression. Qualitative data were obtained through 16 key informant interviews and 8 focus group discussions and analyzed using thematic analysis. The study was guided by a social-ecological and One Health perspective by examining how individual, social, and system-level factors jointly influence hypertension prevention.

Results: Adoption of healthy lifestyle behaviors (physical activity, smoking, alcohol consumption, and fruit and vegetable intake) was higher in rural than urban areas (55.5% vs 47.0% ; p = 0.017), reflecting differences in prevention across settings. At the individual level, adoption was influenced by income, employment, and age in rural areas, while income was the primary determinant in urban areas. At the social level, the proximity of influential network members was associated with prevention behavior. Individuals reported a higher number of people within their personal network who lived within walking distance and were perceived to influence their lifestyle were more likely to adopt healthy behaviours in both rural (aOR = 1.42, 95% CI: 1.15–1.76) and urban settings (aOR = 1.18, 95% CI: 1.01–1.38), suggesting that closer social ties may facilitate behaviour change through more frequent interaction and support. At the system level, environmental and structural conditions, including the built environment, food systems, communication infrastructure, and governance, shaped opportunities for healthy behaviors by influencing access to safe spaces for physical activity, availability and affordability of healthy foods, access to health information, and regulatory enforcement. Weak coordination across sectors is evident in the limited integration of health initiatives with urban planning, food systems, and community platforms. Although structures such as nutrition committees, school health programs, and community bylaws exist, they operate largely in isolation, with no sustained multisector platform to coordinate action, resulting in fragmented prevention across both rural and urban settings. Together, these findings demonstrate that hypertension prevention is shaped by interacting individual-, social-, and system-level factors, consistent with a social-ecological model and a One Health perspective that links human health to broader environmental and institutional systems.

Conclusions/Outlook: Hypertension prevention is shaped by individual, social, and system-level factors operating across rural and urban contexts. Social proximity and environmental conditions influence behavior adoption, highlighting limitations of individual-focused approaches. Strengthening prevention requires context-specific and multisectoral strategies, with opportunities to extend One Health approaches to non-communicable diseases.

Economic evaluation of multisectoral « One Health » collaboration in the fight against Rift Valley fever in Senegal



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Introduction/Background/Objectives: The resurgence of emerging and endemic zoonoses represents a major public health challenge globally, particularly in West Africa where interactions between humans, animals and ecosystems are intensified. The One Health (OH) approach that recognizes the interdependence of human, animal, and environmental health, promoting collaboration, coordination, communication, and capacity building (4Cs) to prevent and control zoonoses, stands as an open call for intersectoral collaboration. Multisectoral strategies and interventions are being increasingly implemented within the framework of Quadripartite, and One Health platform created in various African countries, including Senegal. However, there is still a paucity of knowledge on the economic value of institutional collaboration and coordination of OH initiatives. Building on the example of the management of recent outbreaks of Rift Valley fever (RVF) in Senegal, this study aims to assess the economic value of multisectoral collaboration, and coordination in disease control.

Methodology: A mixed-method approach was used, involving key institutions engaged in One Health implementation in Senegal.

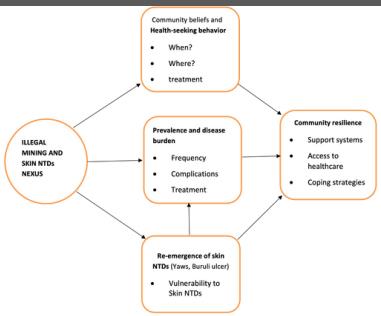
Data collection includes document review (activities reports and terme of references) to idendity OH actors. Primary data were collected through participant observations during activities of the OH platform in Senegal. An economic evaluation of OH collaboration was conducted with data from the incident action plan for November to January 2025. Economic evaluation relies on Activity-Based Costing (ABC), categorizing costs according to the "4Cs" of One Health: collaboration, communication, coordination, and capacity building. After estimation of cost activities have been classified according to the level of intervention.

Results: Preliminary findings highlight a complex and multi-actor system involving public institutions, research bodies, communities and international partners. During the RVF response, the One Health approach fostered strong collaboration among actors, linking technical teams, policymakers, and partners to support coordination, funding, and resource mobilization. Formal structures at centraland regional levels ensured collective action, while informal collaborations on the ground complemented and strengthened overall response effectiveness. Cost distribution analysis shows that coordination represents the largest share of financial resources (47%), followed by collaboration (33%), communication (15%), and capacity building (5%). In contrast, activity frequency is more balanced, with collaboration and communication each accounting for 33% and 22% respectively, suggesting disparities between resource allocation and operational engagement. Furthermore, budget distribution indicates a predominance of regional-level implementation (60%) compared to national-level coordination (40%), reflecting decentralised response dynamics. These findings reveal that while coordination is resource-intensive, frontline collaborative actions occur more frequently with relatively fewer resources.

Conclusion/Outlook: This study provides new evidence on the economic and organizational dimensions of One Health implementation in RVF control in Senegal. The results support more efficient planning, improved intersectoral coordination, and sustainable institutionalization of One Health strategies. Beyond Senegal, these findings offer valuable insights for other West African countries facing recurrent zoonotic threats and seeking cost-effective, integrated response frameworks.

Keywords: One Health, Economic evaluation, Collaboration, Rift Valley Fever, Senegal.

Illegal mining activities and vulnerability of residents to skin neglected tropical diseases in the Amansie West District, Ghana



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Introduction/Background/Objectives: Vector-borne diseases cause 22.8% of all emerging infectious diseases, driven by anthropization and disruption of ecosystems. This makes the environment conducive to the spread of diseases like NTDs. The rising global prices for Gold have led to increased mining activities on several continents. Ghana is one of the leading gold exporters in Africa; however, the proliferation of illegal mining activities poses a significant threat to public health. Illegal mining creates tailings ponds that can harbor mycobacteria, leading to the spread of skin-related NTDs. However, there is limited research on illegal mining activities and the skin NTDs nexus in affected communities in Ghana. Anecdotal reports suggest the prevalence of skin diseases in illegal mining communities, but scientific investigations seldom disaggregate cases to determine whether they are skin NTDs. Understanding the link between illegal mining and skin NTDs will strengthen the one-health approach to reduce disease risk. This study explores the effect of illegal mining activities on the emergence and vulnerability of residents to skin NTDs. Specifically, the study determines the disease burden of skin NTDs; indicators of vulnerability and re-emergence of Skin NTDs in illegal mining communities; and the resilience of communities in the Amansie West District to the health and livelihood impact of Skin NTDs.

Methodology: A concurrent mixed-method design will guide the conduct of the study. Purposive sampling techniques will be adopted to select ten illegal mining and non-endemic communities in the Amansie West district. A total of 944 community members will be sampled using a multistage cluster sampling for the quantitative arm of the study. In contrast, participant selection for the qualitative interviews will be guided by saturation. Secondary data (2010-2015, i.e., 15 years) on selected skin NTDs will be analyzed to compare the prevalence of skin NTDs between mining and non-mining communities. Both descriptive and inferential statistics will be performed for the quantitative data using STATA version 25. A six-step thematic analysis will serve as the foundation for qualitative data analysis using NVIVO software. The study will be guided by the socio-ecological model proposed by Urie Bronfenbrenner, which explains how individual and environmental factors influence health outcomes.

Results: Drawing on existing literature, it is hypothesized that illegal mining activities increase environmental exposures and thereby heighten the transmission vulnerability and re-emergence of skin NTDs in affected communities. It is expected that gaps in community knowledge and health-seeking behavior contribute to sustained transmission and delayed treatment of these conditions. Also, environmental degradation undermines community resilience against skin NTDs.

Conclusions/Outlook: The findings are expected to demonstrate how illegal mining activities shape environmental and social conditions that increase transmission vulnerability and the burden of skin NTDs in affected communities.

Keywords: Illegal mining, Vulnerability, Resilience, Skin, Neglected tropical disease, Ghana


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