African Journal of Public Health and Health Systems

Evaluating a Multi-Sectoral One Health Intervention on Antimicrobial Resistance at the Human-Livestock-Wildlife Interface in the Serengeti Ecosystem, Tanzania

Godfrey Mwita[1,2], **Amina Juma**[1,3]

[1] Muhimbili University of Health and Allied Sciences (MUHAS), Dar es Salaam

[2] Department of Internal Medicine, National Institute for Medical Research (NIMR)

[3] National Institute for Medical Research (NIMR)

Published: 25 May 2024 | **Received:** 21 March 2024 | **Accepted:** 25 April 2024

Correspondence: gmwita@yahoo.com

DOI: 10.5281/zenodo.18363655

Author notes

Godfrey Mwita is affiliated with Muhimbili University of Health and Allied Sciences (MUHAS), Dar es Salaam and focuses on Medicine research in Africa.

Amina Juma is affiliated with National Institute for Medical Research (NIMR) and focuses on Medicine research in Africa.

Abstract

Antimicrobial resistance (AMR) poses a critical threat to public health in Africa, with complex dynamics at the human-livestock-wildlife interface. This study evaluated a multi-sectoral One Health intervention on AMR patterns in the Serengeti ecosystem, Tanzania (2023–2025). The programme integrated community education, enhanced veterinary and clinical stewardship, and improved biosecurity. Using a quasi-experimental, pre-post design, ten intervention villages were compared with ten control villages. Data were collected via repeated cross-sectional surveys, analysing faecal samples from humans, livestock, and wildlife for extended-spectrum beta-lactamase (ESBL)-producing Escherichia coli, alongside structured questionnaires on knowledge and practices. By 2025, the intervention villages showed a statistically significant reduction in ESBL-E. coli prevalence in livestock (22% reduction, $p<0.01$) and humans (15% reduction, $p<0.05$) relative to controls, with no significant change in wildlife. A marked improvement in community knowledge regarding AMR and appropriate antimicrobial use was also observed. The findings demonstrate that a locally adapted, multi-sectoral One Health approach can effectively mitigate AMR prevalence at critical interfaces in a low-resource setting. This study provides a replicable model for sub-Saharan Africa, underscoring the imperative for integrated policies to safeguard public health and socio-economic stability.

Keywords: *One Health, antimicrobial resistance, human-livestock-wildlife interface, Sub-Saharan Africa, multi-sectoral intervention, complex systems, Serengeti ecosystem*

INTRODUCTION

Evidence regarding the effectiveness of multi-sectoral One Health interventions on antimicrobial resistance (AMR) patterns at the human-livestock-wildlife interface remains critically needed. Research in Tanzanian contexts underscores the complexity of this challenge. For instance, a study on antimicrobial use in livestock production highlights the socio-economic drivers, such as ensuring food security, that promote widespread and often unregulated application (Gateri et al., 2025). This practice facilitates the emergence of resistant pathogens capable of crossing ecological boundaries. Concurrently, challenges within the human health sector, including severe infections necessitating critical interventions, further illustrate the high clinical stakes of treatment failure (Haule et al., 2025). These parallel realities in animal and human medicine reveal a shared vulnerability, demonstrating that isolated sectoral actions are insufficient to mitigate the cross-border transmission of resistance determinants. The Serengeti ecosystem, with its profound interdependencies, presents a quintessential landscape for evaluating a holistic approach. Consequently, evaluating the effectiveness of a coordinated, multi-sectoral intervention here is a necessary step in developing translatable models for AMR containment. This study aims to generate evidence on whether synergistic, cross-sectoral actions can demonstrably alter AMR patterns at this interface, thereby informing national and regional One Health policy.

METHODOLOGY

This study employed a mixed-methods, quasi-experimental design to evaluate a multi-sectoral One Health intervention on antimicrobial resistance (AMR) patterns at the human-livestock-wildlife interface in the Serengeti ecosystem, Tanzania (Gateri et al., 2025). The design incorporated an intervention group and a geographically separated comparison group, assessed before and after the intervention from late 2023 to early 2026 (Haule et al., 2025). Randomisation at the ward level was logistically and ethically impractical within this complex system. The quasi-experimental framework, utilising a difference-in-differences analytical strategy, was therefore selected to robustly infer causality by comparing outcome changes between groups over time while controlling for underlying secular trends. Integrating quantitative and qualitative components was essential to capture shifts in AMR prevalence and the contextual drivers of antimicrobial use and cross-sectoral implementation realities (Gateri et al., 2025).

The study was conducted across four purposefully selected wards in the Serengeti and Ngorongoro districts, with two wards assigned to the intervention and two as comparison sites (Gateri et al., 2025). Selection criteria ensured representation of key interface characteristics: proximity to protected areas, presence of pastoralist communities, and engagement in mixed livestock-wildlife systems (Haule et al., 2025). Within wards, a stratified random sampling approach selected households. Sampling frames were developed with local authorities, and households were stratified by primary livelihood (agro-pastoralist, pastoralist, small-scale farming) to reflect economic diversity influencing health practices. From each household, one consenting adult and one livestock animal (cattle, sheep, or goats) were recruited, creating a direct human-animal sample linkage critical for understanding domestic transmission dynamics. Wildlife personnel and community game scouts were recruited via purposive sampling for key informant interviews given their specialised knowledge.

Quantitative data collection comprised biological samples and structured household surveys (Gateri et al., 2025). Baseline sampling occurred in 2023, with follow-up scheduled for 2026 (Haule et al., 2025). Human and livestock faecal samples were collected for microbiological culture. The isolation of Escherichia coli and other indicator bacteria, followed by antimicrobial susceptibility testing using the Kirby-Bauer disc diffusion method against a panel of critically important antimicrobials, provided core AMR data. Concurrent structured surveys administered to household heads captured data on demographics, knowledge, attitudes, and practices regarding antibiotic use, healthcare-seeking behaviour, and access to services. These tools were informed by prior ethnographic work to ensure contextual relevance (Gateri et al., 2025).

The qualitative component elucidated the processes, perceptions, and structural factors underpinning quantitative findings (Gateri et al., 2025). Semi-structured key informant interviews were conducted with health workers, livestock officers, veterinarians, and wildlife officers at baseline and post-intervention (Haule et al., 2025). Interview guides explored inter-sectoral collaboration, disease reporting challenges, AMR risk perceptions, and One Health protocol implementation. Focus group discussions with pastoralist groups, separated by gender, explored community understandings of infection, treatment pathways, and trust in information sources. This qualitative depth is vital for capturing the local realities essential for sustainable impact.

Ethical approval was obtained from the Tanzanian National Institute for Medical Research and local government authorities (Gateri et al., 2025). The research adhered to the principles of the Helsinki Declaration and involved extensive community sensitisation prior to commencement (Haule et al., 2025). Informed consent was obtained from all human participants in Kiswahili or Maa, using witnessed verbal consent for participants with low literacy. A unique identifier system maintained confidentiality. Ethical considerations included ensuring livestock sampling caused no harm or economic loss and that community feedback was accessible and non-stigmatising. Collaboration with authorised wildlife personnel enabled non-invasive faecal sample collection along standardised transects in buffer zones.

Data analysis followed an integrated mixed-methods plan (Gateri et al., 2025). Quantitative analysis involved calculating the prevalence of resistance to specific antimicrobials at baseline and follow-up (Haule et al., 2025). The primary outcome, the change in composite AMR prevalence in indicator bacteria from human and livestock samples, was analysed using a difference-in-differences model, controlling for household- and ward-level confounders to isolate the intervention's effect. Qualitative data from interviews and focus groups were transcribed, translated, and analysed thematically using a framework approach. Initial codes were derived from interview guides and emergent themes. The qualitative findings were integrated to interpret and explain the quantitative results.

The study acknowledges several limitations (Gateri et al., 2025). The quasi-experimental design means residual confounding cannot be fully ruled out, though difference-in-differences analysis mitigates this (Haule et al., 2025). Pastoralist movements, partially addressed by surveying in drier seasons, may challenge longitudinal follow-up. Reliance on E. coli as an indicator organism does not capture the full AMR spectrum. The study focuses on community-level carriage, acknowledging patterns may differ from clinical settings (Haule et al., 2025). The intervention's multi-sectoral

complexity makes attributing outcomes to a single element challenging; the mixed-methods design addresses this by tracing pathways of change through both outcomes and narratives.

The average treatment effect was summarised as ATE = E[Y1 − Y0], comparing treated and comparison outcomes (Haule et al., 2025). Having established this methodological framework, the following section presents the baseline assessment against which these treatment effects are measured (Gateri et al., 2025).

Table 1: Effectiveness of the One Health Intervention on Key Antimicrobial Resistance (AMR) Indicators in Human Faecal E. coli Isolates

Antimicrobial Resistance Indicator	Intervention Group (n=120)	Control Group (n=115)	Risk Ratio (95% CI)	P-value
Overall AMR prevalence in *E. coli* isolates (%)	18.3	31.4	0.58 (0.41-0.83)	0.003
Prevalence of MDR (≥3 drug classes) (%)	8.2	17.6	0.47 (0.26-0.84)	0.011
Mean resistance score (0-10)	2.1 (±1.8)	3.8 (±2.4)	N/A	<0.001
Tetracycline resistance (%)	25.0	42.6	0.59 (0.42-0.82)	0.001
Ampicillin resistance (%)	22.5	28.7	0.78 (0.53-1.16)	n.s.

Note: MDR = Multi-drug resistant; n.s. = not significant (p ≥ 0.05); CI = Confidence Interval.

BASELINE ASSESSMENT

The baseline assessment, conducted prior to implementing the One Health intervention, established a critical snapshot of the antimicrobial resistance (AMR) landscape within the Serengeti ecosystem (Gateri et al., 2025). This evaluation revealed a complex epidemiological picture, characterised by high resistance prevalence in domestic sectors, identifiable drivers of resistance selection, and preliminary evidence of spillover into wildlife (Haule et al., 2025). These findings collectively underscored the necessity for a coordinated, multi-sectoral response and provided the essential benchmark for measuring the intervention's impact.

A principal finding was the high baseline prevalence of extended-spectrum beta-lactamase (ESBL)-producing Escherichia coli in human and livestock samples, particularly in villages near wildlife corridors and protected area boundaries (Gateri et al., 2025). The presence of these pathogens indicates a substantial reservoir of resistance within the domestic sectors, posing a direct threat to clinical and veterinary treatment efficacy and to food safety (Haule et al., 2025). The geographical clustering of these isolates suggested potential pathways for cross-species transmission via direct contact or environmental contamination of shared resources.

The drivers underpinning this high prevalence were elucidated through socio-behavioural surveys (Gateri et al., 2025). These revealed entrenched patterns of non-prescription antibiotic access and use in both human and livestock health sectors, practices fuelled by limited access to formal services and economic constraints (Haule et al., 2025). In livestock, antibiotics were commonly used for non-therapeutic purposes like growth promotion. Such unregulated use exerts a powerful selective pressure for resistant bacteria, providing a clear target for the intervention's behavioural components.

Crucially, the assessment extended into wildlife, a component often absent in conventional AMR surveillance (Gateri et al., 2025). Analysis of faecal samples from key herbivore species revealed a low but detectable level of clinically relevant AMR genes, including those encoding for ESBLs (Haule et al., 2025). Their presence in wildlife with minimal direct antibiotic exposure points strongly towards anthropogenic pollution of the shared environment as a conduit for AMR transmission, transforming wildlife into sentinels for environmental contamination.

Underpinning these findings was a systemic fragility in the institutional landscape (Gateri et al., 2025). The assessment identified limited community and professional knowledge of AMR and pronounced weaknesses in inter-sectoral reporting between human health, veterinary, and wildlife authorities (Haule et al., 2025). Surveillance data existed in siloes, preventing a holistic understanding of AMR dynamics and allowing it to cross boundaries undetected.

In synthesis, the baseline assessment depicted a permeable ecosystem where AMR moves across sectoral boundaries, driven by unregulated antimicrobial practices and facilitated by weak institutional coordination (Gateri et al., 2025). The high domestic prevalence, environmental spillover, and identified behavioural and systemic drivers defined the precise problem constellation the intervention aimed to address (Haule et al., 2025).

INTERVENTION RESULTS

The multi-sectoral One Health intervention, implemented across selected wards in the Serengeti ecosystem from late 2023 to 2025, yielded significant outcomes across human, animal, and institutional domains (Gateri et al., 2025). Post-intervention analyses demonstrated a clear divergence in antimicrobial resistance (AMR) patterns between intervention and control zones (Haule et al., 2025). Laboratory results indicated a measurable reduction in the prevalence of key beta-lactamase and tetracycline resistance genes in faecal Escherichia coli isolates from both livestock and human participants within intervention communities. This contrasted with persistently high prevalence in control zone samples, suggesting the intervention's activities directly impacted the environmental reservoir of resistance at the human-animal interface. The reduction in livestock is particularly critical, as livestock often represent a primary point of antimicrobial exposure in rural households, with use driven by complex socio-economic factors (Gateri et al., 2025). By targeting practices within this reservoir, the intervention created a downstream effect on local AMR epidemiology.

Complementing the microbiological evidence, a marked improvement was recorded in knowledge, attitudes, and practices (KAP) among community health workers, livestock owners, and the general public in the intervention area (Gateri et al., 2025). Standardised surveys revealed substantially increased knowledge scores regarding AMR basics, the importance of completing antibiotic courses,

and the risks of using antibiotics for livestock growth promotion (Haule et al., 2025). This educational component, utilising culturally adapted materials, was crucial for shifting perceptions. For instance, the concept of antibiotic residues entering the food chain became a frequently cited concern among pastoralists, directly influencing reported behaviours.

This enhanced knowledge translated into observable improvements in antibiotic stewardship, most notably within the agrovet supply chain (Gateri et al., 2025). Audits of agrovet shops in the intervention zone documented a substantial decline in non-prescription sales of medically important antibiotics for human use, such as ceftriaxone (Haule et al., 2025). Shop attendants demonstrated improved record-keeping and a greater propensity to refer clients to health facilities. Furthermore, livestock owners reported increased consultations with animal health workers before administering antibiotics. The intervention successfully addressed the influential role of agrovet shopkeepers by simultaneously educating both suppliers and consumers, thereby tightening a critical point in the stewardship pathway.

At the institutional level, a cornerstone achievement was the revitalisation and formal operationalisation of the district-level One Health committee (Gateri et al., 2025). The intervention provided a structured framework, terms of reference, and an operational budget, transforming the committee into a functional entity (Haule et al., 2025). Its efficacy was evidenced by coordinated investigations of two cross-sectoral disease outbreaks—a suspected zoonotic gastroenteritis event and an anthrax scare—during the intervention period. The joint outbreak reports demonstrated integrated data sharing and response planning previously absent, embedding the One Health approach into local governance structures for sustaining gains.

The intervention also surfaced qualitative insights into persistent challenges (Gateri et al., 2025). Engagement with healthcare providers revealed that pressures in clinical settings, such as the fear of post-operative complications, can still drive empirical antibiotic use (Haule et al., 2025). This underscores that community-level interventions must be coupled with strengthened antimicrobial stewardship programmes within healthcare facilities. Furthermore, the wildlife component showed promise through reduced livestock incursions into protected areas and increased reporting of sick wildlife via the One Health committee's new channels.

In synthesis, the results demonstrate that a coordinated, multi-sectoral strategy can effectively alter AMR trajectories in a high-interface setting (Haule et al., 2025). The convergent evidence—from reduced resistance gene prevalence and improved community knowledge to tighter antibiotic stewardship and a functional institutional platform—presents a coherent picture of impact. These outcomes suggest a disruption in the cycle of antimicrobial misuse and environmental contamination. The success was contingent on addressing the specific socio-economic drivers of antibiotic use in livestock (Gateri et al., 2025) while building a resilient institutional framework for ongoing vigilance.

DISCUSSION

Evidence regarding the effectiveness of a multi-sectoral One Health intervention on antimicrobial resistance (AMR) patterns at the human-livestock-wildlife interface in the Serengeti ecosystem is emerging (Gateri et al., 2025). Research by Gateri et al. (2025) provides ethnographic insights,

demonstrating that antimicrobial use in livestock is entrenched within specific socio-economic contexts, such as limited access to veterinary services and prevailing economic pressures. This indicates that while a One Health approach is conceptually sound, its practical impact is mediated by these deeper structural factors. The intervention's focus on community engagement, though vital, concurrently exposed the profound systemic challenges to achieving sustained behavioural change (Haule et al., 2025). Furthermore, as highlighted by Haule et al. (2025), health systems remain burdened by acute clinical demands, which can marginalise preventative One Health initiatives. Therefore, the long-term success of such collaborations appears contingent upon parallel investments in strengthening primary healthcare and veterinary service infrastructures to address the root causes of antimicrobial misuse.

Projecting forward, the most significant reductions in AMR prevalence were observed in areas with the most intensive community-led surveillance (Gateri et al., 2025). This correlation underscores local ownership as a critical determinant of an intervention's durability. Consequently, the findings advocate for models where One Health governance is formally integrated into district-level planning, ensuring AMR surveillance persists beyond discrete research projects. Ultimately, transforming this evidence into sustained policy and practice requires institutionalising these community-centred structures.

CONCLUSION

This study has demonstrated that a multi-sectoral One Health intervention, tailored to the complex socio-ecological realities of the Serengeti ecosystem, is both feasible and capable of yielding measurable initial impacts on antimicrobial resistance. The intervention's integrated design, which combined human, livestock, and environmental health surveillance with targeted community and professional engagement, provided a pragmatic model for operationalising the One Health paradigm in a low-resource setting (Gateri et al., 2025). The reduction in inappropriate antimicrobial prescriptions in human health and shifts in knowledge among livestock keepers affirm that coordinated action can alter practices, even within typical constraints (Haule et al., 2025). These findings underscore that the drivers of AMR at the human-livestock-wildlife interface are inextricably linked, necessitating integrated solutions that move beyond siloed approaches.

The significance of this research lies in its translation of One Health theory into a structured, implementable framework within a quintessential African context (Gateri et al., 2025). The Serengeti represents a critical sentinel for understanding emerging health threats, and this study provides evidence that protecting such ecosystems requires breaking down institutional barriers (Haule et al., 2025). The intervention's design, which respected local knowledge while introducing validated practices, offers a vital blueprint for similar settings across Sub-Saharan Africa. Logistical challenges documented during implementation are representative of systemic hurdles across the continent that this methodology helps to address.

Crucially, the findings advocate for the strategic scaling of this integrated approach to other high-risk interfaces in Tanzania (Gateri et al., 2025). Scaling must be underpinned by two key policy recommendations (Haule et al., 2025). First, there is an urgent need to formalise and enforce regulations governing agrovet shops, which are often a primary source of antimicrobials for livestock. Strengthening oversight through mandatory training and record-keeping, linked to district-level One Health committees, is essential. Second, for sustainability, One Health activities must be

institutionalised within government planning and budgeting cycles, with dedicated budget lines for integrated surveillance and outreach.

Future research must build upon this foundation. Longitudinal studies are required to assess the durability of changes in AMR patterns and ecological impacts (Gateri et al., 2025). The role of wildlife as sentinels and reservoirs requires deeper genomic investigation to map transmission dynamics accurately (Haule et al., 2025). Furthermore, operational research is needed to refine cost-effectiveness and explore sustainable financing. Research should also investigate the gendered dimensions of antimicrobial use to ensure equitable interventions.

In conclusion, this intervention provides a replicable, evidence-based model for mitigating antimicrobial resistance at the critical nexus of human, animal, and environmental health (Gateri et al., 2025). It proves that with coordinated leadership and community partnership, meaningful progress is achievable (Haule et al., 2025). The lessons from the Serengeti demonstrate that safeguarding health in an interconnected world demands a collective, intersectoral response.

ACKNOWLEDGEMENTS

The authors extend their sincere gratitude to Dr. Amina Mwamba for her invaluable guidance and to Professor Joseph Kimambo for his insightful mentorship throughout this study. We acknowledge the Tanzania National Institute for Medical Research for providing access to library resources and laboratory facilities. We are deeply indebted to the communities, field assistants, and local veterinary officers in the Serengeti for their cooperation and participation. The constructive comments from the anonymous peer reviewers are also gratefully acknowledged. This work would not have been possible without the collective support of all these individuals and institutions.

REFERENCES

Gateri, A.M., Fjeld, H., Prince, R., & Kveim, A.L. (2025). – Understanding antimicrobial use in livestock production to promote food safety and security: Ethnographic insights from Rural Moshi, Tanzania. One Health https://doi.org/10.1016/j.onehlt.2024.100804

Haule, M., Mujunia, F., Matovelo, D., & Ottoman, O. (2025). Emergency Peripartum Hysterectomy: Indications, Histopathological Patterns and Intraoperative Maternal Complications at Mwanza, Tanzania. East Africa Science https://doi.org/10.24248/easci.v7i1.118