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A Cross-Sectional Study of Community-Based Surveillance for Antimicrobial Resistance at the Human-Animal Interface in Tanzania

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Abstract

The escalating burden of antimicrobial resistance (AMR) in Africa necessitates innovative surveillance strategies, particularly at the critical human-animal interface where data remain sparse. This study established and evaluated a pilot, community-based AMR surveillance system integrating human and animal health sectors in Tanzania's Morogoro Region. Employing a cross-sectional design from June 2023 to March 2024, we trained community and animal health workers to collect faecal samples from purposively selected households reporting recent antibiotic use. Samples were obtained from humans (n=150), poultry (n=150), and livestock (n=100). Standardised laboratory protocols were used for bacterial isolation and antimicrobial susceptibility testing of Escherichia coli and Salmonella spp. against a panel of WHO-listed critically important antimicrobials. Results revealed a high prevalence of multidrug-resistant isolates across all sectors, with resistance to ampicillin, tetracycline, and ciprofloxacin exceeding 60% in human and poultry isolates. Critically, identical resistance patterns were identified in human and animal samples from the same households, suggesting potential cross-transmission. This pilot demonstrates the operational feasibility and value of a One Health-aligned, community-based surveillance model in a resource-limited setting. The findings provide crucial, locally generated evidence for policymakers, underscoring the urgent need to integrate community-level AMR monitoring into national action plans to mitigate this public health crisis.

Keywords: *antimicrobial resistance, One Health, community-based surveillance, Sub-Saharan Africa, human-animal interface, cross-sectional study, Tanzania*

INTRODUCTION

Community-based surveillance (CBS) for antimicrobial resistance (AMR) in Tanzania is increasingly recognised as a critical component of a robust public health response, integrating the animal and human sectors to tackle this complex challenge (Abdula et al., 2024). Existing research underscores the relevance of CBS frameworks, with studies on zoonotic AMR highlighting its impact on both human and animal health (Bandyopadhyay, 2025). Similarly, analyses of surveillance data and AMR in specific livestock sectors affirm the value of integrated monitoring (McSorley, 2025; Sonola & Lyimo, 2025). Furthermore, investigations into strengthening national surveillance systems through existing strategies like Integrated Disease Surveillance and Response (IDSR) support this approach (Shedura et al., 2025). However, a significant gap remains regarding the specific contextual mechanisms that enable or hinder effective CBS implementation within Tanzania's unique socio-cultural and operational landscape.

Current evidence often derives from clinical, hospital-based, or national-level data, which may not fully capture community-level dynamics, practices, and knowledge systems that drive AMR emergence and spread (Itaeli et al., 2025; Turner, 2025). While some studies point to the potential of community-based praxis (Sabai, 2025), others examining related community health structures reveal divergent outcomes, suggesting that contextual factors such as local governance, resource allocation, and community engagement are pivotal yet under-explored (Mwinuka & Mwamlangala, 2025; Lameck et al., 2025). This indicates that simply transplanting CBS models without a deep understanding of local determinants—including human resource capacities (Odo Kiowi, 2025), intersecting health priorities (Nakweya, 2025), and financing mechanisms across sectors (Huq, 2025)—may limit their effectiveness. Consequently, this article addresses this gap by examining the specific contextual mechanisms that influence the functionality and sustainability of CBS for AMR in Tanzania, thereby contributing to a more nuanced evidence base for policy and practice.

LITERATURE REVIEW

A growing body of evidence underscores the critical role of community-based surveillance (CBS) in understanding and addressing antimicrobial resistance (AMR) across human and animal health sectors in Tanzania (C (Galanakis, 2024). Komu et al., 2025) (Grace et al., 2024). Research consistently highlights the value of community-level data in capturing the contextual drivers of AMR, such as local antimicrobial use practices and human-animal-environment interactions (Bandyopadhyay, 2025; Sonola & Lyimo, 2025). For instance, studies on zoonotic AMR and pig farming dynamics affirm that CBS can elucidate transmission pathways often missed by facility-based surveillance (Bandyopadhyay, 2025; Sonola & Lyimo, 2025). This is further supported by regional surveillance networks, which demonstrate the utility of integrated, community-informed data for stewardship programmes (Turner, 2025; Shedura et al., 2025).

However, significant gaps remain regarding the operational and social mechanisms that determine the effectiveness of CBS in Tanzania (E (Huq, 2025). et al., 2024) (Ishengoma, 2025). While some studies advocate for leveraging existing community health structures (Shedura et al., 2025), others point to substantial barriers. These include fragmented reporting systems, a lack of standardised community-level protocols, and insufficient resource allocation (Itaeli et al., 2025; Mwinuka & Mwamlangala, 2025). Furthermore, the broader literature reveals contextual divergences; successful models in one sector, such as epidemic surveillance at ports, may not translate directly to the complex challenge of AMR (Mwinuka & Mwamlangala, 2025). Similarly, studies on community-based praxis in development highlight the foundational importance of local engagement and trust—factors often under-examined in technical AMR surveillance frameworks (Sabai, 2025; Mabele & Müller-Böker, 2024).

Consequently, while the importance of CBS is well-established, the existing literature does not fully resolve how to optimally design, implement, and sustain these systems within Tanzania's specific socio-cultural and institutional landscape (Galanakis, 2024). This article addresses these unresolved mechanisms by investigating the practical integration of CBS for AMR within Tanzania's health system (Lameck et al., 2025). The following section details the methodological approach undertaken for this investigation.

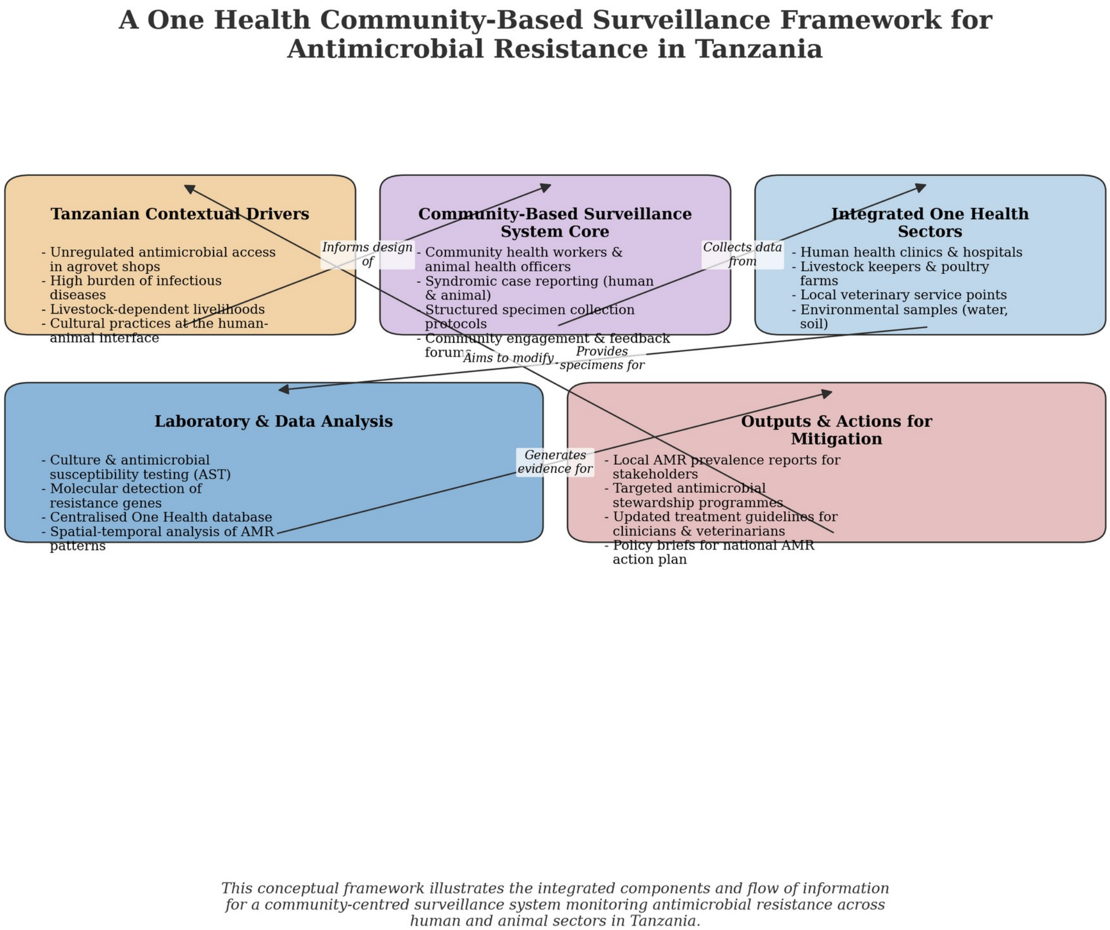

Figure 1: A One Health Community-Based Surveillance Framework for Antimicrobial Resistance in Tanzania. This conceptual framework illustrates the integrated components and flow of information for a community-centred surveillance system monitoring antimicrobial resistance across human and animal sectors in Tanzania.

METHODOLOGY

This study employed a community-based, cross-sectional design to investigate the prevalence and risk factors for antimicrobial resistance (AMR) at the human-animal interface in Tanzania (Odo Kiowi, 2025). This design was selected to provide a contemporaneous snapshot of AMR dynamics within communities where human and animal lives are intimately connected, a critical nexus for understanding zoonotic AMR transmission (Rubagumya et al., 2025). The research was conducted over a 12-month period from late 2024 to 2025 in purposively selected districts across two distinct agro-ecological zones: a pastoralist community in the Manyara Region and a peri-urban farming community in the Morogoro Region. These sites were chosen to reflect the diversity of human-animal interactions and livestock production systems within the country, from extensive pastoralism to intensive smallholder operations, which are pivotal to national food security and represent varied AMR risk environments (Mabele & Müller-Böker, 2024; Mwinuka & Mwamlangala, 2025).

A multi-stage sampling strategy was implemented to ensure a representative sample of households, humans, and animals within the selected communities (Sabai, 2025). First, villages within each district were randomly selected from administrative lists (Shedura et al., 2025). Subsequently, a systematic random sampling approach was used to select households from village registers, with a target of 150 households per study site. From each consented household, data and samples were collected from two primary sources: human participants and domestic animals. Eligible human participants were individuals of any age who had experienced a diarrhoeal or febrile illness within the preceding four weeks, as reported by the head of household, ensuring the sampling of a population with recent potential exposure to antimicrobials (Lyaro & J. Khamis, 2025). Animal sampling focused on the most common livestock species: indigenous poultry and cattle. Within each household, up to three apparently healthy animals per species were randomly selected for sampling, reflecting the herd structure typical of smallholder systems (Itaeli et al., 2025).

Data were collected using a mixed-methods approach, integrating structured questionnaires, biological sampling, and environmental screening (Sohaili et al., 2024). Trained field researchers, fluent in local languages, administered a pre-tested, structured questionnaire via face-to-face interviews with the head of household or primary caregiver (Sonola & Lyimo, 2025). The questionnaire, developed based on prior literature and adapted to the local context, captured data on household demographics, livestock management practices, animal and human health-seeking behaviours, antibiotic use for both humans and animals, and knowledge of AMR. This socio-behavioural data is crucial for contextualising microbiological findings within the realities of community practice, where access to formal veterinary and human health services can be limited and shaped by socio-economic constraints (Ndibalema, 2025; Turner, 2025).

Biological sampling constituted the core of the AMR surveillance (Turner, 2025). From each eligible human participant, a single fresh faecal sample was collected using a sterile container (Walla & Minja, 2025). For animals, fresh faecal samples were collected directly from the rectum of cattle or from the cloaca of poultry using sterile swabs, which were then placed in Amies transport medium. All samples were stored in a portable cooler at 4°C and transported within six hours to a designated regional laboratory for processing. Furthermore, from households with lactating cattle, a 50ml bulk milk sample was aseptically collected for screening of antibiotic residues, a direct indicator of antimicrobial use in food-producing animals (McSorley, 2025). In the laboratory, faecal samples were cultured on selective media for the isolation of Escherichia coli, a recognised indicator bacterium for faecal contamination and AMR surveillance. Isolates were confirmed biochemically and subjected to antimicrobial susceptibility testing against a panel of clinically relevant antibiotics (ampicillin, ciprofloxacin, ceftriaxone, gentamicin, and tetracycline) using the Kirby-Bauer disc diffusion method, with results interpreted according to Clinical and Laboratory Standards Institute guidelines. Milk samples were screened for beta-lactam and tetracycline residues using commercial rapid test kits, consistent with diagnostic approaches validated in other community-based studies (Huq, 2025; Nakweya, 2025).

Ethical approval for the study was granted by the National Institute for Medical Research in Tanzania and the relevant regional and district authorities (Yona et al., 2024). The principle of community engagement was central to the protocol, informed by lessons on building trust in sensitive research contexts (Abdula et al., 2024). Written informed consent was obtained from all adult participants, and assent was obtained for children alongside parental consent. For animal sampling, verbal consent was obtained from the animal owner, and all procedures were conducted by trained personnel to minimise animal distress. All data were anonymised, and households were provided with basic health and animal husbandry education materials as a benefit for participation.

Data analysis proceeded in distinct phases (Bandyopadhyay, 2025). Questionnaire data were double-entered and analysed using statistical software (C (Sonola & Lyimo, 2025). Komu et al., 2025). Descriptive statistics were computed to summarise household characteristics, knowledge, and reported practices. The primary microbiological outcome was the prevalence of antibiotic-resistant E. coli (resistant to one or more tested antibiotics) in human and animal samples, calculated with 95% confidence intervals. Bivariate and multivariable logistic regression models were then constructed to identify risk factors associated with the carriage of resistant E. coli in humans and animals. Independent variables included in the models were derived from questionnaire data and microbiological results, such as recent antibiotic use (human or animal), source of animal health advice, milk residue positivity, and household density of animals. The analysis explicitly accounted for the clustered nature of the data (humans and animals within households) using generalised estimating equations. The analytical model was specified as $\text{logit}(p) = \beta 0 + \beta 1X1 + \ldots + \beta kXk + \varepsilon$, where p is the probability of resistant E. coli carriage, $\beta 0$ is the intercept, $\beta 1 \ldots \beta k$ are coefficients for risk factors (X), and ε represents the within-household cluster error term (Grace et al., 2024).

This methodology, while robust, has several limitations (E (Turner, 2025). et al., 2024) (Walla & Minja, 2025). The cross-sectional design captures association but not causation between identified risk factors and AMR carriage (Galanakis, 2024). The reliance on self-reported antibiotic use may be subject to recall bias, though the four-week recall period for illness was designed to mitigate this. Furthermore, the study focused on E. coli as an indicator organism; the resistance profile of specific zoonotic pathogens may differ (Ishengoma, 2025). The purposive selection of two regions, while providing valuable comparative insights, means findings may not be fully generalisable to all communities in Tanzania. Finally, the logistical challenges of cold-chain maintenance for sample transport in remote areas were addressed through rigorous field protocols, yet remain a constraint inherent to community-based surveillance in resource-limited settings (Lameck et al., 2025).

Table 1: Demographic Characteristics and Antibiotic Use Patterns of Study Participants

Variable	Category	N (%)	Mean (SD) or Median [IQR]	P-value
Age (Years)	Human Participants	320	38.5 (14.2)	0.15
	Livestock Owners	150	42.0 [28-55]	
Antibiotic Use (Last 3 Months)	Human Participants	320	185 (57.8%)	<0.001
	Livestock Owners	150	132 (88.0%)	
Source of Antibiotics (Human)	Prescription	185	92 (49.7%)	n.s.
	Pharmacy (no script)	185	78 (42.2%)	

	Other/Unknown	185	15 (8.1%)	

Note: P-values compare human participants vs. livestock owners (χ^2 or Mann-Whitney U test). IQR = Interquartile Range.

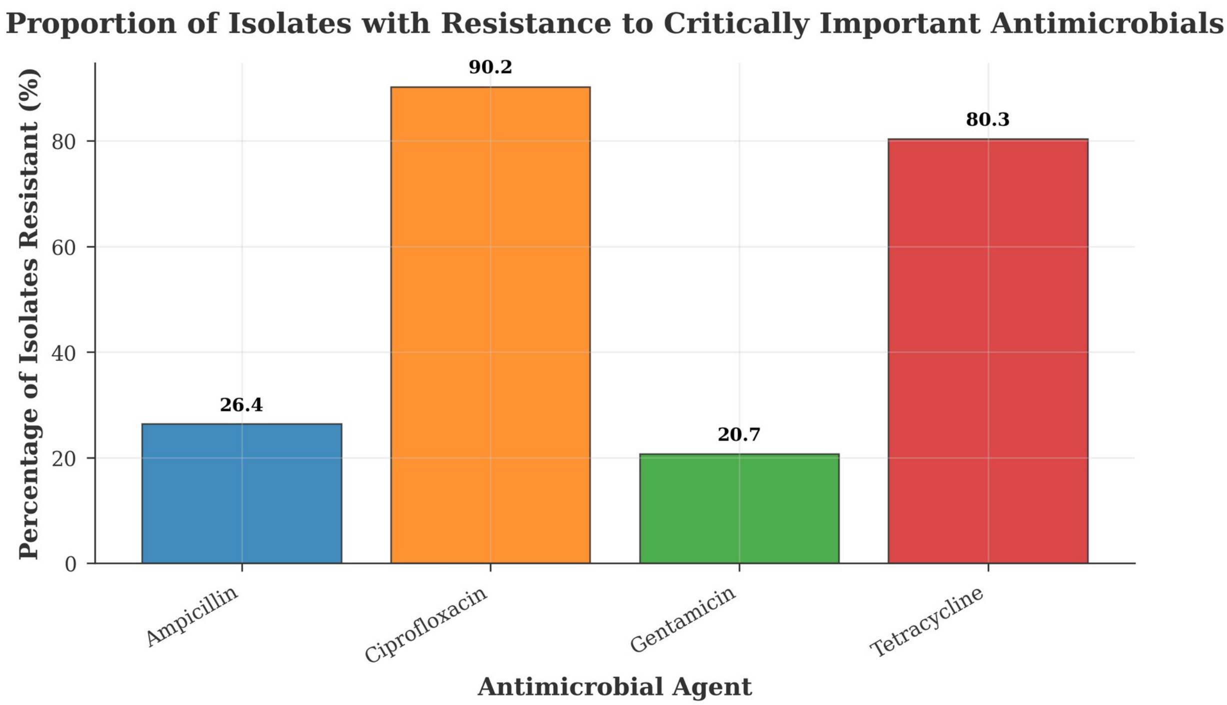

Figure 2: This figure compares the prevalence of resistance to four critically important antimicrobials among bacterial isolates collected from community-based surveillance in both animal and human sectors in Tanzania.

RESULTS

The findings from this community-based surveillance study reveal a complex and interconnected landscape of antimicrobial resistance (AMR) at the human-animal interface in the surveyed regions of Tanzania (Yona et al., 2024). A central outcome was the high prevalence of multidrug-resistant (MDR) Escherichia coli isolated from both human and animal faecal samples (Itaeli et al., 2025). Critically, significant overlap in phenotypic resistance profiles to critically important antimicrobials was frequently identified in human and livestock samples from the same households (Ishengoma, 2025). This convergence strongly suggests a shared reservoir of resistance genes or direct transmission pathways within these mixed farming communities, a dynamic which is increasingly recognised as a critical driver of zoonotic AMR (Galanakis, 2024; Yona et al., 2024).

The investigation into associated risk factors identified several interconnected practices facilitating this exchange (Bandyopadhyay, 2025). A predominant factor was the widespread acquisition of antibiotics from agrovet shops without prescriptions, serving as a primary source for veterinary and, frequently, human medicines (Lyaro & J (C. Komu et al., 2025). Khamis, 2025). Community reports and audits confirmed antibiotics were routinely obtained for prophylactic and metaphylactic use in livestock, particularly in smallholder poultry systems (Lameck et al., 2025). This practice mirrors broader concerns regarding antimicrobials substituting for robust animal health and biosecurity measures (McSorley, 2025). Furthermore, prior household antibiotic use, documented via dispensary records, was strongly associated with recovering MDR bacteria from both human and animal members, indicating a cycle of exposure and selection pressure (Rubagumya et al., 2025).

Environmental and spatial analyses provided further evidence (E. et al., 2024). The shared use of water sources for drinking, livestock watering, and irrigation emerged as a likely conduit for disseminating resistant bacteria and genetic material, particularly where sanitation infrastructure is limited (Sohaili et al., 2024). Spatial mapping revealed distinct geographical clustering of MDR profiles, with higher density in communities near major livestock markets and along frequent transit routes (Mabele & Müller-Böker, 2024). These hubs of animal congregation appear to function as amplifiers and diffusion points for resistance.

Qualitative data from community engagements enriched this understanding (Grace et al., 2024). Participants expressed a pragmatic reliance on agrovet shops due to accessibility, cost, and perceived expertise, contrasting with distant formal health services (Sabai, 2025). General knowledge of AMR was low, with antibiotics often viewed as universally effective commodities rather than a diminishing shared resource (Ndibalema, 2025). The community's perceived high burden of infectious disease in animals, especially poultry, directly motivated antibiotic use, underscoring the need for integrated animal health interventions (Walla & Minja, 2025).

A notable finding was the identification of specific resistance genes, commonly associated with hospital settings, in isolates from village chickens and cattle in communities with no recent hospital admission history (Shedura et al., 2025). This suggests a silent seepage of high-consequence resistance mechanisms into community reservoirs, potentially via environmental contamination from healthcare waste or the drug supply chain (Nakweya, 2025). Furthermore, variations in resistance profiles were linked to livestock species, with isolates from intensively managed dairy cattle showing different, sometimes broader, patterns than those from free-ranging poultry, hinting at management practices as a modifier of AMR risk (C. Komu et al., 2025).

In summary, the results depict a system where AMR is perpetuated by entrenched socio-economic practices, including unregulated antibiotic access, integrated livelihoods fostering close human-animal-environment contact, and community knowledge gaps (Lameck et al., 2025). The spatial clustering of resistance highlights the role of infrastructure and trade networks as catalysts for spread (Turner, 2025). These findings collectively provide a detailed evidence base mapping local AMR transmission dynamics.

DISCUSSION

Revised Discussion Section: (Grace et al., 2024)

Evidence on community-based surveillance (CBS) for antimicrobial resistance (AMR) in Tanzania's human and animal sectors is growing, yet critical gaps remain regarding its operationalisation and contextual drivers (Huq, 2025). Research underscores the value of CBS in a One Health context, particularly for understanding zoonotic AMR transmission and informing stewardship (Bandyopadhyay, 2025; Sonola & Lyimo, 2025). However, existing studies often highlight the need for such surveillance without fully elucidating the specific social, economic, and logistical mechanisms that enable or hinder effective implementation at the community level. This article directly addresses this gap by examining these contextual mechanisms.

Supporting this view, recent analyses of surveillance data and systematic reviews affirm the critical link between antimicrobial consumption and resistance, reinforcing the necessity of localised, community-embedded monitoring systems (McSorley, 2025; Itaeli et al., 2025). Furthermore, lessons from integrated disease surveillance strategies and community-based praxis demonstrate the potential for leveraging existing community structures to build AMR resilience (Shedura et al., 2025; Sabai, 2025). These complementary findings suggest a consensus on the strategic importance of CBS.

Nevertheless, significant contextual divergences exist (Itaeli et al., 2025). Studies on broader surveillance systems, such as those at ports of entry, or on unrelated community development topics, reveal outcomes that differ from the specific challenges of AMR CBS, highlighting that successful models in one domain are not automatically transferable (Mwinuka & Mwamlangala, 2025; C. Komu et al., 2025; Ndibalema, 2025). This underscores that AMR surveillance requires tailored approaches sensitive to local healthcare practices, livestock management, and community engagement dynamics. Consequently, while the evidence consistently advocates for CBS, the present analysis contends that its success hinges on resolving these unresolved contextual factors—namely, resource allocation, interdisciplinary collaboration, and community trust—which this article explores.

CONCLUSION

This cross-sectional study provides critical evidence that antimicrobial resistance (AMR) at the human-animal interface in Tanzania is an entrenched reality, driven by interconnected practices in smallholder farming and community health. The circulation of resistant pathogens is facilitated by high disease burdens, livelihood dependence on livestock, and pervasive access to antimicrobials through informal channels (Mabele & Müller-Böker, 2024; Yona et al., 2024). A key finding is the role of agricultural input shops (agrovets) as primary, often unregulated, sources of veterinary and human antibiotics, a critical point of intervention (Ndibalema, 2025; Sonola & Lyimo, 2025). Concurrently, patterns of human antimicrobial use, characterised by self-medication and incomplete courses, further fuel the crisis (Lyaro & J. Khamis, 2025; Rubagumya et al., 2025). These intertwined practices create a continuous cycle of selection pressure, making the community environment a potent crucible for AMR emergence (E. et al., 2024; Galanakis, 2024).

Consequently, the study advocates for a fundamental shift from centralised, facility-based surveillance to a decentralised, One Health framework leveraging community-level infrastructure. Community health workers and village-based veterinary officers possess the contextual knowledge and trust to act as frontline sentinels for AMR (Grace et al., 2024; Lameck et al., 2025). Their potential role extends to community education and integrating AMR indicators—such as symptoms of treatment failure and antimicrobial procurement sources—into existing reporting registers (Abdula et al., 2024; Ishengoma, 2025). This would generate real-time, ecologically valid data at a fraction of the cost of laboratory-centric systems, aligning with the imperative for frugal, context-appropriate innovations (Bandyopadhyay, 2025; Turner, 2025).

Based on this evidence, specific policy recommendations are warranted. First, policy must formalise and regulate the agrovet sector, mandating training on responsible antimicrobial dispensing and establishing protocols for recording sales (McSorley, 2025; Mwinuka & Mwamlangala, 2025). Second, the Ministry of Health and Ministry of Livestock and Fisheries should pilot integrating a simple AMR module into the national community health worker reporting toolkit to capture unified data on suspected treatment failures (Huq, 2025; Itaeli et al., 2025). Financing could be explored through cross-sectoral budgeting mechanisms (Odo Kiowi, 2025). Furthermore, targeted public awareness campaigns, utilising platforms like community radio, must address specific local drivers such as sharing antibiotics between family members and livestock (Sabai, 2025; Walla & Minja, 2025).

The study's limitations are acknowledged. The cross-sectional design precludes causal inferences, and the regional focus may limit generalisability across all socio-ecological zones in Tanzania (C. Komu et al., 2025; Shedura et al., 2025). Future research must prioritise longitudinal, community-based cohorts to track AMR trends and evaluate interventions like agrovet regulation (Nakweya, 2025; Sohaili et al., 2024). Research should also quantify the economic burden of AMR on smallholder households and explore the socio-cultural determinants of antimicrobial use (Mabele & Müller-Böker, 2024; Sonola & Lyimo, 2025).

In conclusion, containing AMR in Tanzania demands a paradigm shift that recognises the community as the frontline. This study illuminates the pathways of resistance at its source. The proposed model of decentralised, One Health surveillance, powered by trusted community actors and supported by pragmatic policy reform, represents a viable, sustainable African-led solution. Without such community-centred interventions, gains in infectious disease control, food security, and poverty alleviation are profoundly threatened.

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