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Editorial

Antimicrobial resistance in zoonotic bacteria in Bangladesh: a converging crisis at the human–animal–environment interface

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Antimicrobial resistance (AMR) is widely recognized as one of the most formidable global public health threats of the 21st century (Salam *et al.*, 2023; Haq *et al.*, 2025). Its impact is particularly profound in low- and middle-income countries, where rapid population growth, intensified animal production, unregulated antimicrobial use, and weak surveillance systems converge (Gandra *et al.*, 2020; Baweja *et al.*, 2025). Bangladesh exemplifies this challenge and over more than a decade, a substantial body of nationally generated scientific evidence has documented the emergence, persistence, and spread of antimicrobial-resistant zoonotic bacteria across humans, food animals, foods of animal and plant origin, and environmental compartments. Collectively, these findings indicate that AMR in Bangladesh is no longer a localized or sector-specific problem but a systemic One Health crisis requiring urgent, coordinated action (Hoque *et al.*, 2020; Chowdhury *et al.*, 2021; Rafiq *et al.*, 2022).

Food animals, particularly poultry, have consistently been identified as major reservoirs of antimicrobial-resistant bacteria in Bangladesh. Early studies reported resistant *Salmonella*, *Escherichia coli*, *Aeromonas hydrophila* and *Campylobacter* species in broiler meat and poultry processing environments, highlighting the risk of foodborne exposure to consumers and workers (Ferdous *et al*., 2013; Kabir *et al*., 2014; Sarker *et al*., 2020; Hossain *et al*., 2025). Subsequent investigations confirmed that these pathogens were not only prevalent but frequently multidrug resistant (MDR), especially within commercial poultry production systems (Neogi *et al*., 2020; Uddin *et al*., 2021). The isolation of *Salmonella* Gallinarum with diverse resistance patterns from small-scale layer farms further underscored the circulation of resistant bacteria within poultry value chains that often operate with limited biosecurity and minimal veterinary oversight (Haque *et al*., 2021).

Crucially, similar resistance profiles have been documented in human clinical cases. Studies from Mymensingh reported a high prevalence of antimicrobial-resistant *Campylobacter* spp. in diarrheal patients, mirroring resistance patterns observed in poultry and farm environments (Karmaker *et al*., 2018; Rahman *et al*., 2021). This overlap provides compelling evidence of zoonotic transmission and illustrates how resistant bacteria originating in animal production systems can directly compromise human health. The findings reinforce concerns that current patterns of antimicrobial use in food animals are undermining the effectiveness of critically important antimicrobials for human medicine (Elbehiry and Marzouk, 2025).

Beyond poultry, resistant zoonotic bacteria have been detected across a wide range of livestock species. Antibiotic-resistant *E. coli* have been isolated from apparently healthy and diarrheic goats, indicating that small ruminants can act as silent carriers of resistant bacteria (Begum *et al*., 2016). Dairy production systems have also been implicated, with resistant *E. coli*, *Salmonella* spp., and *Campylobacter* spp. detected in cattle, milk-associated environments, and farm surroundings (Kabir *et al*., 2018; Sobur *et al*., 2019). More recently,

Campylobacter spp. with notable resistance profiles were reported from farmed sheep in the Mymensingh division, extending the spectrum of animal reservoirs contributing to the national AMR burden (Nobi *et al*., 2024).

Environmental dissemination represents another critical dimension of AMR in Bangladesh. Resistant bacteria originating from farms and households are frequently released into the environment through inadequately treated waste. Tetracycline-resistant *E. coli* and *Salmonella* spp. have been detected in sewage, rivers, ponds, and even swimming pools, highlighting widespread contamination of shared water resources (Nahar *et al*., 2019). Similarly, *Vibrio cholerae* isolated from dairy excreta exhibited resistance to commonly used antimicrobials, raising concerns about environmental persistence and reintroduction into human populations in cholera-endemic settings (Eashmen *et al*., 2021). These environmental reservoirs not only sustain resistant organisms but also facilitate horizontal gene transfer, accelerating the spread of resistance determinants across bacterial species.

In recent years, research in Bangladesh has expanded beyond conventional food animal and environmental matrices to include everyday exposure pathways that were previously underappreciated. Fresh vegetables and betel leaves—often consumed raw—have been shown to harbor virulent and antimicrobial-resistant *C. jejuni* and *E. coli*, indicating contamination during cultivation, irrigation, handling, or marketing (Al-Mamun *et al*., 2023; Islam *et al*., 2024). These findings blur the traditional boundaries between "animal-origin" and "plant-origin" foods, emphasizing that AMR risks extend throughout the entire food system.

Perhaps most alarming is the recent detection of diarrheagenic and extended-spectrum β-lactamase (ESBL)–producing *E. coli* on publicly shared common touch surfaces, such as door handles and handrails (Arif *et al*., 2025). This evidence suggests that antimicrobial-resistant bacteria have moved beyond farms, markets, and hospitals into routine public spaces, increasing the likelihood of community-level transmission. Such findings underscore the pervasive nature of AMR and challenge conventional assumptions that resistant zoonotic bacteria are confined to specific high-risk settings (Cave *et al.*, 2021; Aslam and Aljasir, 2025).

The problem of antimicrobial residues in foods of animal origin further compounds the AMR crisis. A recent comprehensive review highlighted widespread detection of antimicrobial residues in meat, milk, and eggs in developing countries, including Bangladesh, largely due to non-compliance with withdrawal periods and weak regulatory enforcement (Arif *et al*., 2022; Hosain *et al*., 2025). Residual antimicrobials exert continuous selective pressure on bacterial populations within the human gut and the environment, even in the absence of active infections. This "low-dose exposure" pathway is increasingly recognized as a critical driver of resistance evolution and persistence, yet remains inadequately addressed in national food safety frameworks (Nicz *et al.*, 2025; Tan and Xi, 2025).

Taken together, the accumulated evidence clearly demonstrates that AMR in zoonotic bacteria in Bangladesh is multifactorial, entrenched, and sustained by interconnected human, animal, and environmental systems. Addressing this challenge therefore requires more than isolated technical solutions or sector-specific policies. A genuinely integrated One Health approach is essential. Within this framework, public health veterinarians have a pivotal role to play by bridging animal health, food safety, environmental monitoring, and human health priorities (Kabir, 2025). Their involvement is critical in antimicrobial stewardship, farm-level biosecurity, surveillance of zoonotic pathogens, and risk communication to farmers, food handlers, and the public.

Strengthening national AMR surveillance across human, animal, food, and environmental sectors must be a priority. Surveillance systems should move beyond pathogen detection to include systematic monitoring of resistance patterns and antimicrobial residues. Rational use of antimicrobials in veterinary and human medicine, enforcement of prescription-only policies, and regulation of antimicrobial sales are equally important. At the farm level, improved hygiene, vaccination, and biosecurity can reduce reliance on antimicrobials, while in the food sector, adherence to good agricultural and manufacturing practices can limit contamination (Zhao *et al.*, 2024; Lautan *et al.*, 2025).

The antimicrobial resistance in zoonotic bacteria represents a clear and escalating threat to public health, food safety, and environmental sustainability in Bangladesh. The extensive body of local scientific evidence leaves little doubt about the scale and complexity of the problem. What is now urgently needed is the translation of this evidence into coherent policy, sustained intersectoral collaboration, and practical interventions grounded in the One Health paradigm. Without decisive action, AMR risks undermining decades of progress in infectious disease control and compromising the health and livelihoods of future generations in Bangladesh.

Ethical approval and informed consent

Not applicable.

Data availability
Not applicable.

Conflict of interest
None to declare.

Author's contribution
Conceptualization, formal analysis, writing-original draft preparation, review and editing: S. M. Lutful Kabir. The author has read and approved the final version of the published editorial.

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