

Review Articles



Agriculture-Driven Emergence and Spread of Bacterial Zoonotic Diseases

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ABSTRACT

Zoonotic diseases constitute more than 75% of emerging infectious diseases, with bacterial pathogens representing a substantial and growing proportion of this burden. Agricultural practices—encompassing intensive livestock production, antimicrobial use, land-use change, and expansion into wildlife habitats—have emerged as primary drivers of bacterial zoonosis emergence, amplification, and dissemination. This narrative review synthesizes current evidence on how modern agriculture facilitates the spillover, evolution, and transmission of bacterial zoonotic pathogens, including *Salmonella* spp., *Campylobacter* spp., Shiga toxin-producing *Escherichia coli* (STEC), livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA), *Brucella* spp., *Coxiella burnetii*, *Leptospira* spp., *Mycobacterium bovis*, and emerging multidrug-resistant organisms such as carbapenem-resistant *Klebsiella pneumoniae* and *Acinetobacter baumannii*. We examine the mechanisms by which agricultural intensification, antimicrobial misuse, land-use change, and climate interactions create favorable conditions for pathogen emergence and cross-species transmission. The review further discusses transmission pathways—direct contact, foodborne routes, environmental contamination, and vector-mediated spread—and the critical role of antimicrobial resistance (AMR) in exacerbating the public health impact of agricultural zoonoses. Finally, we evaluate One Health-based mitigation strategies, including antimicrobial stewardship, biosecurity enhancement, surveillance integration, and policy interventions, and identify research gaps and priorities for future action.

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1. Introduction

The global burden of zoonotic diseases ^[1] continues to escalate, with bacterial pathogens representing a particularly concerning category due to their adaptability, environmental persistence, and capacity to acquire antimicrobial resistance. It is estimated that zoonotic diseases account for more than 75% of emerging infectious diseases ^{[2][3]}, and agricultural activities are increasingly recognized as a dominant driver of this trend. The agriculture–environment nexus has undergone profound transformation over the past century, characterized by the intensification of livestock production, expansion of agricultural frontiers into natural ecosystems, massive deployment of antimicrobials, and increasing globalization of food supply chains. These changes have fundamentally altered the interfaces between wildlife, livestock, humans, and the environment, creating novel

opportunities for bacterial pathogen spillover, adaptation, and dissemination.

The emergence and re-emergence of bacterial zoonoses are inextricably linked to the evolution of agricultural systems. Land-use change is cited as the cause of over 30% of emerging infectious diseases and correlates significantly with the emergence of novel zoonoses globally ^[4]. Agricultural intensification, particularly the transition to concentrated animal feeding operations (CAFOs) and industrialized production systems, has created high-density environments that facilitate rapid pathogen transmission and evolution ^[5]. Concurrently, the widespread and often inappropriate use of antibiotics in livestock agriculture has emerged as a critical selective pressure driving the proliferation of multidrug-resistant (MDR) bacterial strains, with profound implications for human health ^{[6][7]}.

This review aims to provide a comprehensive synthesis of current evidence on the role of agriculture in driving the emergence and spread of bacterial zoonotic diseases. We examine the key agricultural drivers, the major

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bacterial pathogens involved, transmission pathways, the intersection with antimicrobial resistance, and potential mitigation strategies within a One Health framework.

This narrative review was conducted by systematically searching PubMed, Web of Science, Scopus, and CABI Abstracts for peer-reviewed articles published between 2000 and 2026. Search terms included combinations of "agriculture," "livestock," "zoonosis," "bacterial infection," "antimicrobial resistance," "land-use change," "climate change," and "One Health." Reference lists of identified systematic reviews and meta-analyses were hand-searched to capture additional relevant studies. Due to the broad interdisciplinary scope of the topic, a narrative synthesis approach was adopted rather than a formal systematic review protocol. Studies were selected based on relevance to the review themes, with priority given to high-impact primary research, systematic reviews, meta-analyses, and reports from international organizations (WHO, FAO, WOA). Data on antimicrobial resistance prevalence, disease burden, and intervention outcomes were extracted and synthesized thematically. The review focuses predominantly on bacterial zoonoses with established or emerging links to agricultural practices; viral, parasitic, and fungal zoonoses are excluded due to scope limitations.

2. Agricultural Drivers of Bacterial Zoonoses

2.1. Intensive Livestock Production and High-Density Farming

The intensification of livestock and poultry production represents one of the most significant transformations in global agriculture over the past several decades. Industrial livestock systems, where large numbers of animals are confined in high-density settings, create ideal conditions for pathogen amplification and transmission [6]. Close contact between large numbers of food-producing animals plays an important role in the spread of antibiotic-resistant bacteria, with population density acting as a catalytic factor [5].

High-density farming environments are characterized by compromised animal immune systems due to stress, overcrowding, and poor biosecurity measures, rendering animals more susceptible to infections. These conditions not only facilitate the rapid spread of pathogens within herds and flocks but also promote the emergence of novel strains through mutation and horizontal gene transfer. The prevalence of Q fever, for example, has been directly linked to stocking density of sheep and goats, illustrating how intensive management practices can amplify zoonotic transmission risk.

Furthermore, the movement and mixing of livestock across farms, markets, and regions amplify the dissemination of resistant strains. A multistate outbreak of multidrug-resistant *Salmonella* Heidelberg in the United States, linked to dairy calves, exemplified how animal transport and shared equipment contribute to pathogen spread across geographic boundaries [8].

2.2. Agricultural Expansion and Land-Use Change

Agricultural expansion into natural habitats represents a major ecological driver of zoonotic disease emergence. Deforestation, habitat fragmentation, and the conversion of wildlands to cropland or pasture disrupt ecosystems, alter wildlife population dynamics, and bring humans and livestock into closer proximity to wildlife reservoirs and vectors [4][9]. These landscape transformations create new interfaces for pathogen spillover and facilitate the establishment of novel transmission cycles.

The expansion of agriculture promotes encroachment into wildlife habitats, leading to ecosystem changes that increase the intensity of interactions

between wildlife, livestock, and humans. Forest edges created by agricultural expansion often function as ecological corridors that facilitate vector dispersal, bridging sylvatic and human transmission cycles [10]. A global-scale analysis demonstrated that outbreaks of vector-borne and zoonotic diseases are significantly associated with changes in forest cover and oil palm expansion, highlighting the role of specific land-use transformations in disease emergence.

Different types of agricultural land-use change exert differentiated effects on zoonotic disease risk. Pasture expansion into forested areas, particularly in the Amazon basin and sub-Saharan Africa, creates extensive wildlife–livestock interfaces where cattle come into contact with reservoir species such as bats and rodents, increasing the risk of pathogen spillover [5][11]. Monoculture crop expansion (e.g., soybean, maize) often involves large-scale habitat simplification, reducing biodiversity and potentially increasing the relative abundance of competent reservoir hosts—a phenomenon known as the "dilution effect" reversal. Oil palm plantations, which have expanded dramatically in Southeast Asia and increasingly in Africa and Latin America, create novel agro-ecosystems with simplified vertebrate communities and high densities of generalist reservoir species [10]. These plantations have been linked to increased risk of malaria, dengue, and other vector-borne diseases, and may similarly facilitate bacterial zoonosis transmission by altering rodent and primate communities.

Agricultural intensification also affects less extensive areas than expansion, but these localized impacts are significant. The contamination of water, soil, and air from animal waste, biomass burning, fertilizers, and pesticides can increase spillover risk by shifting the range of vector species or increasing human vulnerability to infectious diseases. The building of hydraulic infrastructures for irrigation, such as dams and canals, has been associated with the occurrence of epidemic diseases by altering vector habitats and creating new breeding sites [12].

2.3. Antimicrobial Use in Agriculture

The use of antibiotics in intensive animal farming first emerged in the 1940s in the United States, and within a decade, the marketing of antibiotics as feed additives for growth promotion became globalized. This practice has been demonstrated to be associated with an increase in antimicrobial resistance in both pathogens and commensals involved in zoonotic infections [13].

In the United States, approximately 80% of all antibiotic usage is focused on animal agriculture, with 70% of these antibiotics recognized as important to human medicine [6]. Antibiotics are used not only for their antimicrobial properties but are commonly employed as growth promoters, although this practice has been restricted in the European Union since 2006 [14][15].

The excessive use of antibiotics, including prophylactic and metaphylactic administration as well as growth-promotion applications, exacerbates selective pressures, fostering the proliferation of multidrug-resistant bacterial strains. Approximately 70% of antibiotics administered to animals are excreted into the environment, where they are not fully degraded, increasing bacterial exposure and promoting resistance development. Antibiotic residues in manure, often used as fertilizer, contribute to the spread of resistance genes in soil and water systems, creating environmental reservoirs of MDR bacteria [8][16].

2.4. Climate Change Interactions

Climate change interacts with agricultural practices^[17] to further exacerbate zoonotic disease risks. Rising temperatures and changing precipitation patterns influence the distribution of disease vectors, alter host and vector ranges, and affect the survival and replication of bacterial pathogens^{[18][19]}. The spore-forming bacterium *Bacillus anthracis* is causing increased livestock and zoonotic infections worldwide, often as a result of climate change-induced environmental alterations. Climate variability interacts with environmental changes to contribute to disease emergence, affecting ecological systems at landscape and community levels, as well as host and pathogen population dynamics^[5]. The complex interactions between climate change and land use create feedback loops that exacerbate environmental challenges, including increased frequency of floods, droughts, and wildfires that can further degrade ecosystems and amplify disease transmission risks^[4].

Temperature effects on pathogen ecology are particularly significant for bacterial zoonoses. Rising ambient temperatures accelerate bacterial growth rates and can extend seasonal windows of transmission by improving survival in water, soil, and food surfaces^{[19][20]}. Laboratory investigations have shown that higher temperatures correlate with increased proliferation of *E. coli* in seafood species, with proliferation escalating as water surface temperatures rise from 24 to 32°C. Similarly, the frequency of *E. coli* O157:H7 infections in humans and the shedding of Shiga toxin-producing *E. coli* by cattle exhibit seasonality, partly attributed to enhanced survival and proliferation of the pathogen in faeces at higher temperatures. Extreme weather events pose additional risks. Heavy rainfall and flooding can overwhelm wastewater treatment^[21] facilities, contaminating water bodies with pathogenic *E. coli* strains and other zoonotic bacteria^[19]. Flood events mobilize faecal material from animal production sites into surface water and irrigation systems, increasing contamination of fresh produce. Conversely, prolonged drought periods lead to water scarcity and water reuse practices that concentrate bacteria and antimicrobial residues while increasing dependence on suboptimal storage and handling practices. In aquaculture and coastal systems, warmer sea surface temperatures have been associated with increased *Vibrio* suitability and outbreaks^[20].

Indirect effects of climate change on zoonotic disease risk operate through agricultural adaptation. Climate-induced stress in high-density production systems can increase disease incidence in livestock, promoting greater prophylactic or therapeutic antibiotic use, which in turn increases selection pressure for resistant strains. Changes in cropping patterns and irrigation practices driven by altered precipitation regimes may create novel habitats for disease vectors or bring livestock into contact with new wildlife reservoirs^[5].

3. Major Bacterial Zoonotic Pathogens in Agricultural Settings

3.1. Enteric Pathogens: *Salmonella*, *Campylobacter*, and *E. coli*

Enteric bacterial pathogens represent the most common foodborne zoonotic agents associated with agricultural production. The WHO Foodborne Disease Burden Epidemiology Reference Group estimated that 600 million infections and 33 million disability-adjusted life years (DALYs) are caused by foodborne diseases each year, resulting in 420,000 deaths, including 125,000 children under five years of age^[22].

Salmonella spp. remain a leading cause of bacterial gastroenteritis worldwide. In Europe, a significant proportion of *Salmonella* spp. isolates

from human infections in 2023 demonstrated resistance to ampicillin (21.3%), sulphonamides (20.8%), and tetracyclines (21.8%)^[23]. A high prevalence of fluoroquinolone resistance was observed among *Salmonella* spp. isolated from broiler chickens (55.5% ciprofloxacin), with 21.8% of human strains demonstrating resistance to ciprofloxacin in 2023.

Campylobacter jejuni represents another critical foodborne pathogen, with resistance levels in isolates of human and animal origin to fluoroquinolones sufficiently high to exclude this antibiotic class from the recommended therapeutic treatment for humans. In 2022, 78.1% of *C. jejuni* isolates from turkeys and 70.9% from broilers exhibited resistance to ciprofloxacin.

Shiga toxin-producing *Escherichia coli* (STEC), particularly serotype O157:H7, represents a significant zoonotic threat linked to ruminant agriculture. High-intensity farming allows pathogens such as *E. coli* O157:H7 that may occur in small numbers to spread rapidly among concentrated animal populations^[24]. Genomic studies have demonstrated genetic relatedness between STEC strains recovered from dairy calves, animal handlers, and their surrounding environments, underscoring the potential for zoonotic transmission.

3.2. *Staphylococcus aureus*: Livestock-Associated MRSA

Livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA), particularly clone CC398, has emerged as a significant zoonotic pathogen linked to intensive pig and poultry farming. Although LA-MRSA CC398 exhibits low pathogenicity to humans, it has the potential to serve as a reservoir for antimicrobial resistance genes that could be transmissible to virulent human *S. aureus* strains^[25].

The levels of MRSA vary between species and countries, with isolation rates ranging from 0% in pigs in Norway to 80% in pigs in Belgium. MRSA ST398 has been identified on dairy farms, with contamination of raw milk and environmental factors contributing to its spread. In Spain, 72.5% of healthy pigs and 60% of pig farmers carried coagulase-negative staphylococci (CoNS) in their nasal cavities, with 92% of these isolates being MDR^[8].

3.3. *Brucella* spp. and *Coxiella burnetii*: Occupational Zoonoses

Brucellosis and Q fever represent classical occupational zoonoses with strong links to agricultural practices. Brucellosis, caused by Gram-negative *Brucella* spp., is the most common zoonotic disease in humans worldwide, with more than 500,000 new cases reported annually according to WHO estimates^[26]. Transmission to humans occurs mainly via the consumption of unpasteurized dairy products from infected animals, as well as direct or indirect contact with infected animals or exposure to tissues such as the placenta and birth products.

Among high-risk occupational groups, seroprevalence rates are alarmingly high. In western Iran (Lorestan Province), the seroprevalence of brucellosis among butchers and slaughterhouse workers reached 43.7%, with Q fever seroprevalence at 29.8%, significantly higher than the general population. Similarly, in South Africa, abattoir workers face substantial risk of brucellosis infection through direct contact with infected animals' secretions or blood and aerosol dispersion of *Brucella*-containing droplets^[27].

Q fever, caused by *Coxiella burnetii*, is considered a significant public health problem globally. Human infections most commonly occur through contaminated aerosols generated by ruminants, particularly during parturition^[26]. Q fever should be considered an occupational hazard for

farmers, slaughterhouse workers, veterinarians, and butchers who have regular exposure to livestock or their products [26].

3.4. *Leptospira* spp.: An Underappreciated Agricultural Zoonosis

Leptospirosis, caused by pathogenic *Leptospira* spp. [28] represents a significant yet frequently underrecognized bacterial zoonosis with strong agricultural associations. The bacterium is maintained in the renal tubules of reservoir animals—particularly rodents, cattle, pigs, and dogs—and excreted in urine, contaminating water, soil, and vegetation [29][30]. Agricultural workers are disproportionately affected due to occupational exposure to contaminated environments.

A systematic review of environmental and occupational risk factors identified multiple agriculture-related exposures significantly associated with leptospirosis risk: contact with livestock (adjusted odds ratio [AOR] 1.3–10.4), contact with pigs (AOR 1.54–7.9), living on agricultural land (OR 2.09), and contact with mud (AOR 1.57–4.58) [30]. Outdoor workers (AOR 1.95–3.95) and slaughterhouse workers (AOR 5.1–7.5) face elevated infection risk.

Flooding events dramatically amplify leptospirosis transmission risk. Systematic review evidence indicates that flood exposure increases leptospirosis risk (AOR 1.54–6.04), while *Leptospira* can survive in water for up to 12 weeks and in soil for up to 9 weeks [29][30]. The historic 2024 floods in Rio Grande do Sul, Brazil, triggered epidemiological investigations confirming leptospirosis as a major post-flood health concern. In sub-Saharan Africa, pooled seroprevalence of leptospirosis in cattle ranges from 9.7% (PCR) to 30.1% (MAT), indicating substantial animal reservoirs. The intersection of agricultural expansion, irrigation practices, and increasingly frequent extreme precipitation events under climate change is likely to expand the geographic range and seasonal intensity of leptospirosis transmission [20][29].

3.5. *Mycobacterium bovis*: Bovine Tuberculosis as a Persistent Zoonotic Threat

Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, remains a persistent zoonotic threat in agricultural systems worldwide, particularly in low- and middle-income countries where pasteurization is inconsistently applied, and test-and-slaughter control programs are inadequately resourced. Cattle serve as the primary reservoir, though the pathogen can infect a broad range of mammalian species including humans, buffalo, goats, and wildlife [31][32].

Global prevalence estimates vary substantially by region. A 2024 systematic review and meta-analysis reported an overall bTB prevalence of 6.06% in Pakistan, with higher rates in cattle (6.44%) than buffalo (5.54%). In Africa, prevalence estimates are considerably higher: 19% in Ghana, 28% in South Africa, and 22% in Ethiopia. The economic impact is substantial, with estimated global losses of USD 3 billion annually from decreased production, higher mortality, culling, and trade restrictions. Individual farm-level impacts include 10–18% decreases in milk production, 10–25% losses in productive efficiency, 15% reductions in meat production, and increased condemnation of edible organs [32].

Zoonotic transmission occurs primarily through consumption of unpasteurized milk and dairy products, as well as via inhalation of infectious droplets during close contact with infected animals [31][33]. A systematic review and meta-analysis of *M. bovis* in milk on dairy cattle farms found that milk samples showed the highest pathogen prevalence (14.66%) among all sample types, underscoring the critical role of raw milk

consumption in human exposure. High-density breeding environments in commercial dairy farms facilitate animal-to-animal transmission through close contact, defective ventilation, improper waste disposal, and poor floor sanitation. Larger herds (101–500 animals) show higher prevalence (10.59%) compared to smaller operations, and pregnant and lactating animals exhibit increased susceptibility due to physiological stress and immune suppression [32].

3.6. Emerging Multidrug-Resistant Pathogens

Beyond classical zoonotic agents, emerging MDR bacterial pathogens are increasingly detected in livestock and agricultural environments, raising concerns about their zoonotic potential. Carbapenem-resistant *Klebsiella pneumoniae* harboring resistance genes such as blaNDM and blaOXA-48 have been isolated from bovine respiratory infections, with genomic analyses showing phylogenetic relatedness to human clinical isolates [34]. *Acinetobacter baumannii*, traditionally considered a nosocomial pathogen, has been increasingly identified in agricultural settings. It has been recovered from raw milk samples in Kenya and approximately 15% of chicken litter samples in Ethiopian poultry farms, often exhibiting multidrug resistance. Genomic epidemiology studies have demonstrated zoonotic potential, underscoring the need for surveillance within a One Health context [35].

Coagulase-negative staphylococci (CoNS) are also widespread in dairy and swine operations, with a 2023 study in Italy finding CoNS in 72.7% of sampled swine and poultry farms, with over half of the isolates classified as MDR [8]. These findings highlight agricultural settings' significant role in the spread of AMR beyond traditionally recognized pathogens.

4. Transmission Pathways at the Agriculture–Human Interface

4.1. Direct Contact and Occupational Exposure

Direct contact with livestock represents one of the most important transmission routes for bacterial zoonoses. Farmers, veterinarians, slaughterhouse workers, and butchers are at elevated risk of infection through handling of infected animals, contact with bodily fluids, and exposure to birth products [26]. The presence of ESBL-producing Enterobacteriaceae in both livestock and farmers [36] in rural settings highlights the interconnected nature of resistance across humans, animals, and the environment.

Close contact with animals and practices such as raw milk consumption are significant risk factors for zoonotic transmission of MDR *Staphylococcus* spp. [8]. In Kenya, MDR *Staphylococcus* spp. were widespread in livestock environments, with genomic studies demonstrating phylogenetic links between livestock and human isolates.

4.2. Foodborne Transmission

Consumption of contaminated animal products remains a primary route of zoonotic bacterial infection. Undercooked meat, unpasteurized dairy products, and contaminated eggs serve as vehicles for *Salmonella*, *Campylobacter*, STEC, *Brucella*, and *M. bovis* transmission [8][33]. The globalized food supply chain facilitates the rapid dissemination of contaminated products across international borders, amplifying the public health impact of localized agricultural contamination events [24].

The complexity of modern food systems creates multiple critical control points where bacterial contamination can occur. At the pre-harvest stage, pathogens from livestock manure can contaminate soil, water, and crops used for animal feed. During slaughter and processing, cross-contamination between carcasses, equipment, and environmental surfaces is a well-documented risk factor for *Salmonella* and *Campylobacter* dissemination [23]. Post-harvest contamination during transportation, storage, and retail distribution further extends the reach of agricultural pathogens. The increasing demand for minimally processed and "farm-fresh" products, including raw milk and unpasteurized cheeses, has created niche markets where traditional pasteurization barriers are bypassed, elevating zoonotic risk [31][33].

Climate change compounds foodborne transmission risks. Warmer temperatures along supply chains accelerate bacterial proliferation in perishable products, while extreme weather events disrupt cold chain integrity and increase contamination of irrigation water used for produce [19][20]. The detection of *E. coli* O157:H7 in pre-harvested leafy green vegetables, linked to contaminated irrigation water and manure-amended soil [37], exemplifies the convergence of agricultural practices and environmental factors in foodborne disease emergence.

4.3. Environmental Pathways

Environmental contamination via manure, wastewater, and agricultural runoff creates persistent reservoirs of zoonotic pathogens and resistance genes. In rural China, antibiotic-resistant bacteria and resistance genes were detected in agricultural soils treated with manure from antibiotic-fed livestock, with significant enrichment of genes conferring resistance to tetracyclines, sulfonamides, and β -lactams. Mobile genetic elements, such as integrons, facilitate horizontal gene transfer between bacterial populations in the environment, accelerating resistance dissemination. Intensive livestock farming degrades freshwater ecosystems and has the potential to create stores of zoonotic bacteria in rivers. The bovine rumen is a known reservoir for AMR bacteria, and in pastoral farming systems, these bacteria are excreted onto land where they are potentially transported into waterways.

4.4. Vector-Mediated and Wildlife Interface Transmission

Agricultural landscapes facilitate pathogen transmission through multiple vector-mediated mechanisms that extend beyond direct and foodborne routes. Houseflies (*Musca domestica*) and other filth flies serve as particularly important mechanical vectors in intensive livestock operations [38]. Flies acquire bacteria through contact with contaminated manure, feed, and animal surfaces, and can subsequently transfer pathogens to humans, other animals, and food products [39][40].

The vector potential of houseflies is substantial. A single housefly can carry up to 2×10^{12} *E. coli* cells and approximately 0.1 mg of food material between landing sites. Flies have been found to externally carry *Enterococcus faecium* in poultry farms, *Klebsiella pneumoniae* in kitchens and farms, *Salmonella enterica* in swine farms, and *Staphylococcus aureus* in urban areas. Female flies carry more bacteria than males due to their visitation of oviposition sites that are heavily contaminated. In cattle operations, 73% of houseflies carried one or more antimicrobial-resistant bacterial isolates, with individual flies harboring as many as nine different resistant isolates.

Importantly, houseflies are not merely passive mechanical vectors. Studies have demonstrated that bacteria can proliferate within the fly gut and that

horizontal gene transfer of antibiotic resistance genes occurs in the housefly digestive tract. Resistance genes—including those conferring chloramphenicol resistance and Shiga toxin production—have been shown to transfer between *E. coli* strains in the fly midgut and crop within one hour of feeding [39]. Vertical transmission of antimicrobial resistance has also been documented: *E. coli* containing resistance plasmids fed to adult flies were subsequently detected in immature and adult life stages of the next generation. When these immature stages were fed to chickens, resistant *E. coli* persisted in cecal contents for at least 16 days [40].

Dispersal range is a critical factor in vector-mediated transmission. Stable flies from pig farms can reach neighboring farms in 6–53% of cases within 24 hours, and house flies have been observed to travel offsite while carrying multiple bacterial pathogens [41]. Although house fly dispersal is often resource-dependent, their movement between animal production facilities, waste disposal sites, and human habitation creates a continuous bridge for pathogen and resistance gene dissemination.

The wildlife–livestock–human interface at agricultural frontiers creates additional opportunities for pathogen spillover. Livestock often act as a bridge across this interface, amplifying and transmitting pathogens that originate in wildlife populations [42]. Forest edges function as ecological corridors facilitating movement of reservoir species and vectors between natural habitats and agricultural areas. Rodents, which thrive in agricultural landscapes, serve as reservoirs for *Leptospira* spp. and can contaminate feed stores and water sources. Bats, increasingly brought into contact with livestock through habitat fragmentation, have been implicated in the maintenance of multiple zoonotic pathogens. The convergence of wildlife encroachment, intensive livestock production, and inadequate biosecurity creates high-risk interfaces where bacterial zoonoses can emerge and establish sustained transmission cycles.

5. Antimicrobial Resistance in Agricultural Zoonoses

5.1. Mechanisms and Drivers of Resistance

Antimicrobial resistance in agricultural settings is driven by multiple interconnected mechanisms. The primary driver is the selective pressure exerted by antibiotic use in livestock, which promotes the survival and proliferation of resistant strains [43]. Subtherapeutic antibiotic use with limited supervision increases selective pressures, promoting intrinsic resistance and horizontal gene transfer (HGT) of resistance genes.

Resistance mechanisms include enzymatic modification of antibiotic molecules (e.g., β -lactamases such as CTX-M-15), target site modification, efflux pump overexpression, and reduced membrane permeability [44]. The high prevalence of CTX-M-15-type ESBL genes across humans, animals, and the environment underscores the bidirectional flow of resistance in rural ecosystems.

5.2. Global Patterns of Resistance

The prevalence of MDR bacteria in livestock exhibits significant regional variability, often correlated with differences in regulatory frameworks, farming practices, and resource availability. Regions with limited regulatory oversight and intensive farming systems experience higher resistance rates. In Nigeria, 99% of *E. coli* isolates from beef cattle were ESBL producers, exhibiting resistance to multiple antibiotic classes. In rural Nepal, 47.7% of bacterial isolates from livestock were ESBL producers, with 39.4% exhibiting multidrug resistance, even in subsistence farms with limited antibiotic use.

A particularly concerning development is the increased resistance to last-resort antibiotics, including colistin and carbapenems. Colistin-resistant *E. coli* isolates carrying the *mcr-1* gene have been documented in farm animals and farmers, with evidence of direct transfer from calves to farmers [45]. This poses serious challenges to public health and treatment outcomes, as these antibiotics represent the final therapeutic options for MDR infections.

5.3. Public Health Implications

The public health implications of AMR in agricultural zoonoses are profound. Infections caused by MDR *E. coli*, *Salmonella* spp., and LA-MRSA have been associated with prolonged hospital stays, increased morbidity and mortality, and higher healthcare costs [46]. In 2019, an estimated 4.95 million deaths were linked to bacterial AMR, with 1.27 million deaths directly attributable to bacterial AMR. Described as a "silent pandemic," antibiotic resistance is spreading rapidly through trade, human mobility, wildlife migration, and environmental flows [47].

AMR is projected to reduce livestock production by 3% to 8% annually by 2050, disrupting global food systems and placing severe financial burdens on farmers. The growing prevalence of zoonotic outbreaks linked to MDR bacteria further escalates healthcare costs, increases hospitalizations, and reduces the efficacy of last-resort antibiotics.

6. One Health Approaches and Mitigation Strategies

6.1. Antimicrobial Stewardship

Addressing the challenge of agriculture-driven bacterial zoonoses requires a paradigm shift toward responsible antimicrobial use. The implementation of sustainable practices, enhanced antibiotic stewardship, and strengthened interdisciplinary collaboration are critical. Safe and judicious use of antibiotics must be implemented in veterinary and human medical procedures to slow down the emergence of antibiotic resistance. This includes restricting the use of antibiotics as growth promoters, ensuring veterinary oversight of antimicrobial use, and promoting the use of organic and sustainable therapeutic agents [48].

Evidence for antimicrobial stewardship interventions [49] is accumulating. The European Union's ban on antibiotic growth promoters (AGPs), implemented between 1997 (avoparcin) and 2006 (complete ban), provides the most extensively studied natural experiment. Following the ban, Denmark observed a substantial reduction in antimicrobial resistance in commensal *Enterococcus faecium* to avoparcin and virginiamycin in pigs. However, the ban also revealed that these agents had important prophylactic activity; their withdrawal was associated with increased diarrhoea, weight loss, and mortality due to *E. coli* and *Lawsonia intracellularis* in post-weaning pigs, and clostridial necrotic enteritis in broilers. A directly attributable effect was an increase in therapeutic antibiotic usage in food animals, including tetracyclines, aminoglycosides, trimethoprim/sulphonamides, macrolides, and lincosamides—all of direct importance in human medicine.

More recent evaluations show mixed but generally positive trends. A Korean study analyzing *E. coli* isolates from diarrheic weaned piglets before and after the AGP ban (2007–2017) found that resistance to gentamicin decreased from 68.8% to 39.0%, neomycin from 84.9% to 57.8%, ciprofloxacin from 49.5% to 39.6%, and amoxicillin/clavulanic acid from 40.8% to 23.5% [50]. However, resistance to cephalothin increased (51.4% to 69.5%), and colistin resistance rose from 7.3% to 11.0%, with the emergence of cefepime resistance (0.0% to 2.1%). Multidrug resistance

remained high before (95.0%) and after (96.6%) the ban, underscoring that AGP restriction alone is insufficient without comprehensive stewardship.

The Netherlands provides a notable example of successful MRSA control through antibiotic stewardship. Dutch studies indicated that reducing antibiotic use correlated with lower MRSA prevalence in pigs and cattle [51]. The country's rigorous "search and destroy" strategy for healthcare-associated MRSA, combined with livestock antibiotic reduction programs, has maintained one of the lowest MRSA prevalence rates globally [52].

6.2. Biosecurity and Farm Management

Improved biosecurity measures are essential for preventing the introduction and spread of zoonotic pathogens in agricultural settings. Key interventions include:

- Herd/flock health management: Implementing vaccination programs, quarantine protocols for new animals, and all-in/all-out production systems. Vaccination against *Brucella* and *M. bovis* has proven effective in reducing herd prevalence where systematically applied [53].
- Hygiene and sanitation: Ensuring adequate facility management, proper waste disposal, and regular cleaning and disinfection of equipment. Cleaning and disinfection between batches can effectively reduce LA-MRSA levels in subsequent pig batches.
- Vector control: Managing housefly populations and other potential mechanical vectors through integrated pest management, proper manure handling, and physical barriers.
- Personal protective equipment (PPE): Ensuring access to and proper use of PPE among farmers, slaughterhouse workers, and veterinarians.

Implementation challenges are substantial, particularly in resource-limited settings. Biosecurity measures increase production costs, requiring capital investment in infrastructure, training, and ongoing maintenance. In LMICs, smallholder farmers often lack the financial resources and technical knowledge to implement comprehensive biosecurity programs [54]. Cultural practices, such as consumption of raw milk and traditional slaughtering methods, present additional barriers to infection control.

Inadequate knowledge and preventive practices have been identified as barriers to controlling diseases such as brucellosis, highlighting the value of targeted farmer education and disease prevention programs. Community-based education programs that engage local leaders and incorporate traditional knowledge have shown greater success than top-down regulatory approaches in changing high-risk behaviors [54].

6.3. Surveillance and Early Warning Systems

Enhanced surveillance and improved diagnostic awareness are essential for early detection and prevention of potential outbreaks originating from agricultural settings. Regular monitoring of antibiotic-resistant bacteria in humans and animals can help identify growing patterns of resistance and develop effective control measures. Integrated surveillance systems that capture data across human health, animal health, and environmental domains are critical for detecting spillover events and tracking resistance trends.

The integration of whole-genome sequencing (WGS) into routine surveillance has transformed the ability to trace transmission pathways and identify emerging resistance mechanisms. In the Netherlands, continued WGS-based monitoring of MRSA from a One Health perspective has enabled early detection of emerging lineages and guided targeted control measures [52]. Genomic surveillance of *A. baumannii* and *K. pneumoniae* in

agricultural settings has revealed phylogenetic links between livestock and human clinical isolates, providing actionable intelligence for intervention. However, surveillance capacity remains highly uneven globally. LMICs face disproportionate risks but often lack the laboratory infrastructure, trained personnel, and funding required for effective AMR and zoonotic disease surveillance. The absence of climate-informed AMR risk models further limits the ability to predict and prepare for seasonal or weather-driven outbreaks.

6.4. Policy and Regulatory Frameworks

Strengthened regulatory frameworks are urgently needed, particularly in low- and middle-income countries (LMICs) where antibiotics are frequently used without veterinary oversight or diagnostic confirmation of infections. Projections indicate a 50% increase in antimicrobial use in livestock by 2030 [55], underscoring the urgent need for stricter regulations. Policy interventions should include:

- Banning or restricting antimicrobial growth promoters: The EU experience demonstrates that regulatory bans can reduce resistance in specific bacterial populations, though compensatory increases in therapeutic use must be monitored.
- Implementing prescription requirements for veterinary antibiotics: Ensuring that antimicrobial use is guided by diagnostic confirmation rather than empirical administration.
- Establishing maximum residue limits and enforcement mechanisms: Preventing environmental contamination through antibiotic-laden manure and wastewater.
- Promoting alternative farming systems: Supporting organic and agroecological approaches that reduce reliance on antibiotics while maintaining productivity.
- Supporting international cooperation: Harmonizing standards, sharing surveillance data, and coordinating responses to transboundary zoonotic threats through frameworks such as the Codex Alimentarius and the Global Action Plan on AMR.

Political and economic barriers to policy implementation are significant. The livestock industry often resists regulatory restrictions due to concerns about production costs and competitive disadvantage in international markets. In countries where antibiotics remain inexpensive and readily available over the counter, enforcement of prescription requirements faces substantial challenges [54]. The lack of economic incentives for farmers to adopt biosecurity measures, combined with the non-food-borne nature of many zoonotic transmission pathways, complicates cost-benefit analyses for policymakers [51].

6.5. The One Health Framework

The One Health approach—which recognizes the interconnectedness of human, animal, and environmental health—provides the most effective framework for addressing agriculture-driven bacterial zoonoses. The One Health strategy collaborates across human, animal, and environmental sectors, playing a positive role in identifying and managing the development of antibiotic-resistant microbes at the human–animal–environment interface [48].

This integrated approach is essential because the implications of MDR bacteria extend across all three domains. Resistant pathogens originating from cattle not only limit treatment options in human medicine but also threaten economic stability and ecological integrity. Effective One Health

implementation requires sustained political commitment, adequate resource allocation, and genuine collaboration across sectors and disciplines.

Success stories demonstrate the potential of One Health approaches. Norway's zero-tolerance strategy for LA-MRSA, in which infected herds are immediately culled, cleaned, and disinfected—with contact herds also tested and culled if positive—has successfully maintained negligible MRSA prevalence. While this strategy is costly and likely sustainable only in countries with low baseline prevalence, it illustrates the effectiveness of coordinated, multi-sectoral action when political will and resources are available [51].

The Tripartite collaboration (WHO, FAO, WOAH) and the Quadripartite (plus UNEP) have established global frameworks for AMR and zoonotic disease governance, but implementation at national and subnational levels remains inconsistent [53][56]. Capacity building, particularly in LMICs, and the integration of climate adaptation into One Health planning represent critical priorities for future action.

7. Conclusions and Future Perspectives

Agricultural practices have become a dominant force shaping the emergence, amplification, and global dissemination of bacterial zoonotic diseases. The intensification of livestock production, expansion of agricultural frontiers, massive deployment of antimicrobials, and interactions with climate change have created a complex web of drivers that facilitate pathogen spillover, evolution, and transmission across the human–animal–environment interface.

The evidence synthesized in this review demonstrates that modern agriculture is implicated in the emergence and spread of a broad spectrum of bacterial zoonoses, from classical foodborne pathogens such as *Salmonella* and *Campylobacter* to neglected occupational diseases such as leptospirosis and bovine tuberculosis, and emerging MDR organisms such as carbapenem-resistant *K. pneumoniae* and *A. baumannii*. The acquisition and dissemination of antimicrobial resistance in agricultural settings represent a particularly urgent threat, with projections of substantially increased AMR-related mortality and economic losses in the coming decades.

Addressing these challenges requires a fundamental rethinking of agricultural practices within a One Health framework. Key priorities for future action include:

1. Reducing antimicrobial use in agriculture through regulatory restrictions, improved diagnostics, and promotion of alternative disease prevention strategies such as vaccination, probiotics, and improved biosecurity.
2. Enhancing surveillance capacity through integrated human, animal, and environmental monitoring systems capable of detecting spillover events and tracking resistance trends in real time, with particular emphasis on WGS-based genomic surveillance.
3. Improving biosecurity and farm management practices to reduce pathogen transmission within and between farms, with particular attention to high-risk interfaces such as slaughterhouses, live animal markets, and peri-urban dairy operations.
4. Addressing land-use change by implementing sustainable agricultural practices that minimize encroachment into wildlife habitats, preserve ecosystem integrity, and reduce the creation of high-risk spillover interfaces.
5. Strengthening international cooperation to harmonize standards, share surveillance data, and coordinate responses to transboundary zoonotic threats, with enhanced support for LMIC capacity building.

6. Investing in research to better understand the complex ecological, evolutionary, and socioeconomic drivers of bacterial zoonosis emergence in agricultural systems. Priority research gaps include:

- Longitudinal studies quantifying the dose–response relationships between land-use change and zoonotic spillover risk across different agro-ecological systems;
- Genomic epidemiology of MDR pathogens at the agriculture–human interface, particularly in underrepresented regions such as sub-Saharan Africa, South Asia, and Latin America;
- Climate-informed AMR risk models that integrate meteorological data, agricultural practices, and resistance surveillance;
- Economic evaluations of One Health interventions to inform cost-effective policy decisions;
- The role of mechanical vectors (flies, rodents) in environmental dissemination of AMR bacteria, including dispersal distances and gene transfer dynamics;
- The impact of alternative farming systems (organic, agroecological, regenerative) on zoonotic disease risk and AMR prevalence.

The rate of future zoonotic disease emergence or re-emergence will be closely linked to the evolution of the agriculture–environment nexus [5]. However, available research inadequately addresses the complexity and interrelatedness of environmental, biological, economic, and social dimensions of zoonotic pathogen emergence, which significantly limits our ability to predict, prevent, and respond to these threats.

Ultimately, safeguarding global public health from agriculture-driven bacterial zoonoses will require transformative changes in how we produce food, manage antimicrobial use, and steward our shared environment. The One Health approach offers the conceptual and operational framework for these changes, but its successful implementation will depend on sustained political commitment, adequate resource allocation, and genuine collaboration across sectors and disciplines. The window for proactive intervention is narrowing; the time for coordinated global action is now.

CRedit authorship contribution statement

Jarunee Siengsanun-Lamont: Conceptualization, Methodology, Investigation, Data curation, Formal analysis, Visualization, Writing – original draft, Writing – review & editing. **Zubaidah Ya'cob:** Conceptualization, Methodology, Investigation, Resources, Validation, Writing – review & editing. **Sinh Dang-Xuan:** Methodology, Investigation, Formal analysis, Validation, Writing – review & editing. **Budi Utomo:** Conceptualization, Methodology, Resources, Supervision, Project administration, Funding acquisition, Writing – review & editing.

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The free versions of Grammarly were used for spell-checking and grammar corrections. After using these tools, the author(s) reviewed and edited the content as needed and took full responsibility for the content of the publication.

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