INTERNATIONAL JOURNAL OF RESEARCH AND INNOVATION IN APPLIED SCIENCE (IJRIAS)
ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume XI Issue VI June 2026

The Role of Agricultural Systems in Antimicrobial Proliferation: Insights from a One Health Framework

Oluwatomiwa Jubilee Sunbare-Funto[1], Timothy Sibanda[2] , and Martins Ajibade Adefisoye[1]

[1]Department of Microbiology, School of Science and Technology, Babcock University, Ilishan-Remo, Ogun State, Nigeria.

[2]School of Molecular and Cell Biology, Faculty of Science, University of the Witwatersrand, P Bag 3, Wits 2050, Johannesburg, South Africa.

DOI: https://doi.org/10.51584/IJRIAS.2026.11060078

Received: 06 June 2026; Accepted: 12 June 2026; Published: 24 June 2026

ABSTRACT

Antimicrobial resistance (AMR) is a major health issue, exacerbated by globalization, population growth, and extensive agricultural practices. The application and overuse of antibiotics in agriculture have played a vital role in AMR development and spread in the environment. Horizontal gene transfer (HGT) contributes significantly to the exchange of antimicrobial resistance genes (ARGs) among pathogens, further complicating the problem of AMR proliferation. The intensive use of antibiotics in livestock farming and animal manure as soil fertilizer, are some of the important agricultural practices which introduce resistant bacteria and ARGs to the soil ecosystems. The application of poorly treated wastewater for irrigation is another significant source of AMR in soils. The use of inorganic pesticides, heavy metals and other chemicals contribute to the selective pressure that favors the emergence of resistant strains. The unabated spread of resistant microorganisms and their ARGs poses a serious threat to the public and environmental health due to their possible transfer into the human food chain via contaminated food crops and animal products. Attempts at mitigating the challenges of AMR in agricultural soil involve a One Health approach, considering the interconnection of human, animal and environmental health. It is vital to curtail the anthropogenic spread of AMR through agroecological measures, adequate wastewater treatment, and a more sustainable use of antibiotics in livestock production. In-depth knowledge of the intricacies of the factors contributing to AMR spread and persistence in soil is necessary to explicate appropriate intervention strategies. Thus, this review critically discusses the concept of sustainable farming practices, improved systems of regulation and international alignment towards combating AMR.

Keywords: Agricultural practices, AMR, HGT, One-Health, Public health, Soil contamination

INTRODUCTION

Interrelated factors contributing to antimicrobial resistance (AMR) spread include globalization, rapid population growth, intensive farming, pollution and climate change (Gauba and Rahman, 2023). These factors have caused increased morbidity and mortality, with an approximate annual death toll predicted to be between 700,000 and 10 million by 2050 (Oliveira et al., 2024). Reflecting on this human health burden, the World Health Organization (WHO) has identified AMR as one of the top ten major global health threats (Aijaz et al., 2023). Poor hygiene and food handling, inappropriate use of antimicrobials in humans, veterinary and agricultural settings, and inadequate measures to combat infections contribute to the occurrence and dissemination of resistance (WHO, 2023). Among this broader phenomenon, the overall subset of AMR is antibiotic resistance, which represents the ability of bacteria to withstand the action of antibiotics (Wasan et al., 2023). Antibiotic-resistant strains adopt various forms of resistance mechanisms, including horizontal gene transfer (Wachino, 2025), enzymatic inactivation of drugs (Tayeb et al., 2025), reduced uptake through altered membrane permeability (Zhou et al., 2023), modifications of the drug target and active efflux (Duffey et al., 2024), all of which reduce the effects of antibiotics.

Horizontal gene transfer facilitates the transfer of resistance genes between groups of bacteria through plasmids, bacteriophages and integrons, thereby accelerating the spread of AMR between and within populations. This process supports the emergence of multidrug-resistant Gram-negative bacteria, including *Acinetobacter*, *Pseudomonas* and members of the Enterobacteriaceae family, which have become important pathogens of public health concern (Macesic et al., 2025). Rising resistance threatens the effectiveness of routine therapy as well as chemotherapy, organ transplantation and major surgery, and is projected to impose substantial economic losses if timely action is not taken (De Oliveira et al., 2020). These challenges demand the adoption of crucial mitigation strategies such as the One Health paradigm which seeks to optimize human, animal and environmental health interfaces in recognition of the interrelatedness of their microbiomes (Despotovic et al., 2023). Within this framework, AMR is understood as a systems problem in which resistant bacteria and resistance genes circulate through food products, direct contact and environmental reservoirs rather than remaining confined to clinical settings. These microbiomes are closely related, as depicted in **Figure 1**, which contributes to the dissemination of AMR through various pathways.

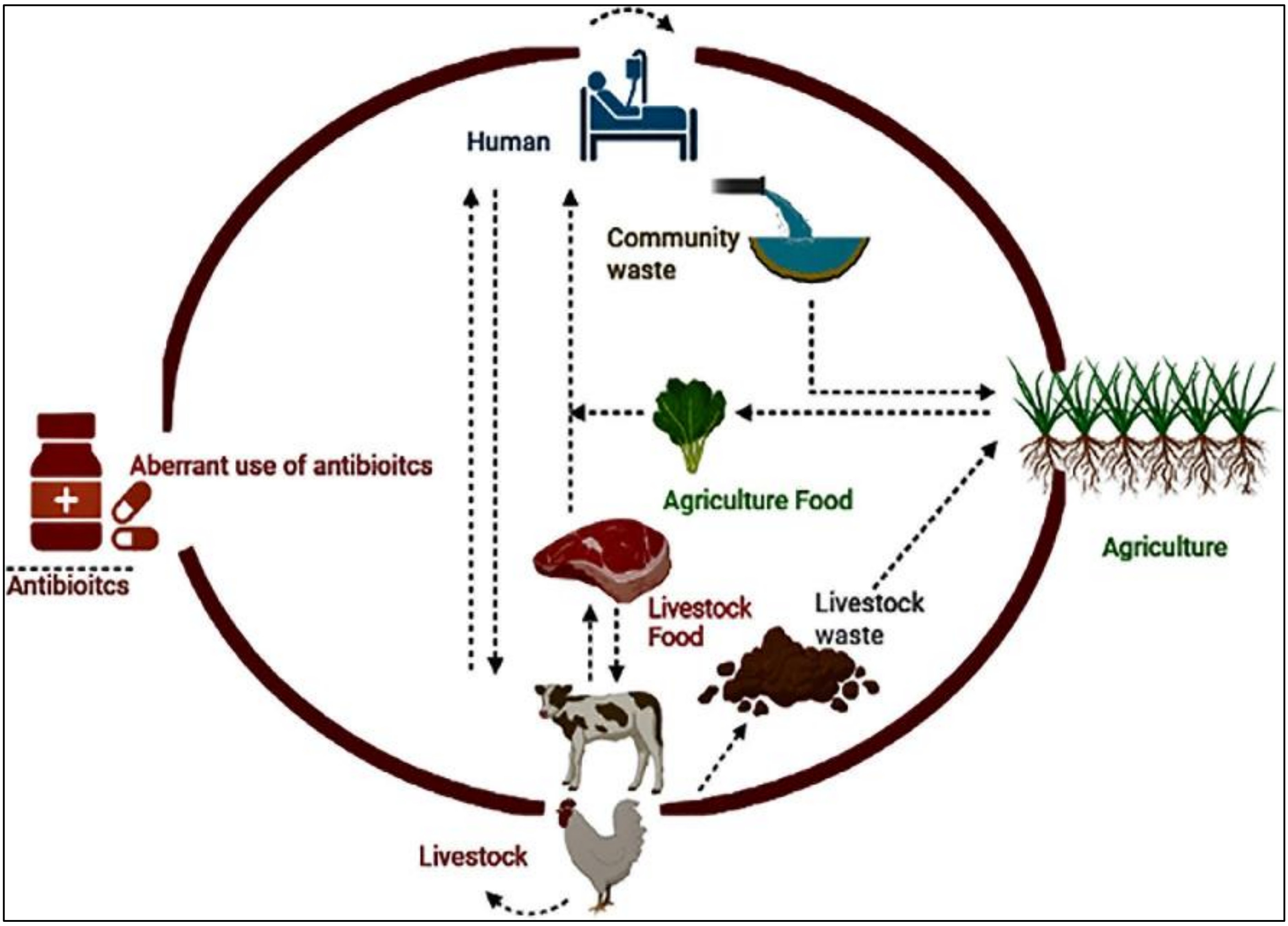

Figure 1: Schematic description of the antibiotic resistance cycle, demonstrating the role of the use of antibiotics in humans, livestock, and agriculture in spreading resistant bacteria in the ecosystems (Aslam et al., 2021).

Agricultural activities are key drivers in this cycle. Inadequate waste management and intensive farming introduce residual antibiotics, resistant bacterial and resistance genes into soil, water and other compartments of the environment (Sassi et al., 2025). Growth promotion and disease prevention antibiotics used in livestock systems are also being selective of gut bacteria resistant to antibiotics, which, together with antibiotic residues, enter soils when manure and other animal wastes are applied as organic fertilizers (Ahmed et al., 2024). Reports of multidrug-resistant *Salmonella* spp. in poultry, cephalosporin-resistant *Escherichia coli* in veal cattle and carbapenem-resistant *E. coli* in swine demonstrate the connections between food and environmental chain AMR transmissions and agricultural practices. Additional inputs also occur through the irrigation of the soils with abattoir effluents and livestock farm wastewater that brings in additional resistant bacteria and resistance-gene to the agricultural soils (Gufe et al., 2025).

Antibiotic use in aquaculture can contaminate adjacent land, while antimicrobial compounds present in some pesticides and fertilizers may indirectly select for resistant soil bacteria; animal faeces with antibiotic residues and those bacteria can create soil conditions that contribute to the survival and transmission of resistance genes (Liu et al., 2025).

Soils are currently being acknowledged as significant sources of antibiotic resistance genes (ARGs) in the environment and as critical interfaces within the One Health system. The accumulation and persistence of ARGs in soils are a public health concern because resistance determinants carried by environmental bacteria can spread to the pathogenic species in human and agricultural environments (Zhao et al., 2025b). The production and distribution of ARGs in soil are influenced by intensive agriculture, climate related changes and pollution with heavy metals. The co-selection of AMR due to metal contamination is possible since resistance determinants to both metals and antibiotics have been found to be genetically linked on mobile genetic elements and, as such, exposure to heavy metals can enrich antibiotic-resistant bacteria even when low antibiotic pressure occurs directly (Gillieatt & Coleman, 2024). Wastewater irrigation, repetitive use of animal-derived manure and fertilizers can hence maintain and increase AMR in the soil ecosystems and soil monitoring is therefore vital in curbing the transmission of resistant bacteria within the agroecosystem to human populations.

Taken together, these observations indicate that agricultural soils are not passive sinks for antimicrobial residues and resistant bacteria but dynamic environments in which resistance is selected, maintained and redistributed along the One Health continuum. The present review analyzes the role of the special agricultural activities in contributing to AMR in the soils like manure and biosolid application, the use of wastewater in irrigation, aquaculture related inputs and the application of pesticides and fertilizers. It also examines how One Health-based soil focused interventions may be useful in reducing the proliferation of resistance in agroecosystem.

METHODOLOGY

Research Design

This article was designed as a literature-based review on the role of agricultural systems in the spread of antimicrobial resistance within a One Health framework. The review focused on how agricultural practices contribute to the introduction, persistence and spread of antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs) in soil, water, food systems and the wider environment.

Literature Search Strategy

Relevant literature was searched using PubMed, Scopus, Web of Science and Google Scholar. The search mainly covered articles published between 2015 and 2025. However, a few older publications were included where they provided important background information, outbreak records or foundational evidence related to antimicrobial resistance transmission. The major search terms used included antimicrobial resistance, antibiotic resistance genes, agricultural soils, livestock antibiotics, animal manure, biosolids, wastewater irrigation, pesticides, heavy metals, horizontal gene transfer, mobile genetic elements, environmental persistence and One Health.

Inclusion and Exclusion Criteria

The literature included in this review consisted of peer-reviewed research articles, review papers, government reports and publications from recognized international organizations such as WHO, FAO and CDC. Studies were included when they discussed the sources, pathways, mechanisms, environmental reservoirs, public health implications or mitigation of antimicrobial resistance in agricultural and One Health-related settings.

Articles that focused only on clinical antimicrobial resistance without any clear link to agriculture, soil, wastewater, food systems or environmental transmission were excluded.

Data Synthesis

The selected literature was organized and discussed thematically. The major themes included livestock antibiotic use, manure and biosolid application, pesticide use, wastewater irrigation, agricultural runoff, soil properties, horizontal gene transfer, mobile genetic elements, co-selection, environmental persistence and One Health-based mitigation strategies. This approach helped to bring together evidence from different agricultural and environmental settings and explain how they contribute to the spread of antimicrobial resistance.

Agricultural Practices and Amr Spread in Soil

The proliferation of AMR in pathogenic bacteria remains a significant safety and health problem (Ho et al., 2025). Current studies confirm that agriculture is just one of several possible sources of bacteria and resistance genes in the environment, much of which focuses on its clinical features (Punch et al., 2025). Agricultural practices contributing significantly to AMR spread include:

Intensive Use of Antibiotics in Livestock Farming

The use of antibiotics in cattle production and animal husbandry is not a new phenomenon, as it has been used over decades as a form of therapy, as well as growth promotion and prophylaxis (Yordanova et al., 2024). At present, thousands of tons of antibiotics are administered annually to cattle, pigs and poultry worldwide (Karwowska, 2024). These drugs span several major classes, and their use differs by species and production phase. . A summary of the examples of commonly used antibiotics in swine, poultry and cattle production systems are summarized in **Table 1** (Zalewska et al., 2021).

Table 1. Examples of Antibiotics Used in Livestock Farming

Livestock Type	**Antibiotics**	**References**
Swine	Pleuromutilins, Tetracyclines, Macrolides, Penicillin, Cephalosporins, Lincosamides, fluoroquinolones, Amoxicillin, Tulathromycin, Tylosin, Colistin	Karwowska, 2024; Enshaie et al., 2025; Kim & Ahn, 2022
Poultry	Bacitracin, Virginiamycin, Salinomycin, Tilmicosin, Penicillin	Zalewska *et al.*, 2021; Trinchera et al., 2025
Cattle	β-lactams, Aminoglycosides, Quinolones, fluoroquinolones, Macrolides, Tetracyclines, Sulfonamides, Streptogramins, Lincosamides, Penicillins	Zalewska *et al.*, 2021; Enshaie et al., 2025
Swine (pig slurry)	Lincosamides, macrolides, phenicols, pleuromutilins, quinolones, sulfonamides, tetracyclines	Massaccesi et al., 2024
Cattle and Poultry	Tetracyclines, sulfonamides	Joseph et al., 2024
Mixed livestock	β-lactams, macrolides, tetracyclines, phenicols, fluoroquinolones, aminoglycosides, polymyxins	Alabi et al., 2025

Source: Karwowska, (2024)

Across regions, frequently used compounds include penicillin, tetracyclines, macrolides, fluoroquinolones, sulfonamides, β-lactams and other classes, many of which are also important in human medicine (Abate & Birhanu, 2025). The amount and type of antibiotics used depend on the age and production stage of the animals, with intensive use during suckling and post weaning periods and in herd-level metaphylactic and prophylactic treatments (Karwowska, 2024). Although growth promotion uses have been banned in many countries and preventive applications are increasingly regulated (Pinho et al., 2025), overall antibiotic consumption in animal production often still exceeds that in human medicine (Abate & Birhanu, 2025). Intensive animal rearing and high antimicrobial inputs mean that livestock and animal husbandry facilities can act as major sources and hotspots of antibiotic-resistant bacteria (ARB) and resistance genes, including multidrug-resistant *Escherichia coli* and extended-spectrum β-lactamase producers, which are then released into the surrounding environment (Pandey et al., 2024; Bava et al., 2024).

In addition to terrestrial livestock, antibiotics are widely used in aquaculture to prevent and treat bacterial infections and, in some settings, to promote growth (Yordanova et al., 2024; Mohammed et al., 2025). They are typically applied in feed or directly into rearing water, and a considerable fraction reaches the wider environment through unconsumed feeds, faeces and farm effluents (Mohammed et al., 2025). This practice selects for ARB and antimicrobial resistance genes in water, sediments and biofilms and can facilitate their transfer to terrestrial systems and the food chain via contaminated aquatic products and irrigation of crops.

Application of Animal Manure and Biosolids

Certain antibiotics administered to farm animals are excreted unaltered or as active metabolites because antibiotic metabolisation can range from 10 to 90% (Patyra et al., 2024). As a result, animal waste contains antibiotics, and their associated metabolites, compounds such as ciprofloxacin and doxycycline have been detected in animal excreta (Wang et al., 2025b). These suboptimal concentrations may be high enough to place microorganisms under selective pressure for antibiotic resistance (Li et al., 2025). Livestock manure often harbours bacteria resistant to multiple antibiotics because of antimicrobial use in feed, and resistance determinants are present in farm waste (Karwowska, 2024). Manure is therefore considered a hotspot for antibiotic resistance expansion since it combines high levels of nutrients, residual antimicrobials and dense microbial communities (Liu et al., 2025). Large numbers of antibiotic resistance genes have been detected in manure, and resistant pathogenic bacteria have been recovered from these matrices. The use of manure from animals treated with antibiotics as soil fertiliser promotes the emergence of drug resistance in soil, and different resistance genes have been reported in manure-fertilised soils compared with unfertilised soils (Nickodem et al., 2025). Drug-resistant microorganisms can persist and be transferred within the environment even after manure application.

Manure-borne antibiotics can directly select for resistant soil bacteria, and antibiotic resistance has been observed to spread into regions not immediately adjacent to farms, suggesting wider environmental dissemination pathways (Karwowska, 2024). Although the increase in resistance genes following manure fertilisation may decline over time, manure-amended soils still tend to contain more resistance genes than unfertilised soils (Nickodem et al., 2025). Biosolids, the primary solid end product of urban wastewater treatment, are likewise applied to soil as organic fertiliser and have been shown to increase the abundance and diversity of ARGs after long term land application, thereby representing an additional source of resistance determinants to agricultural soils (Ste Marie et al., 2025).

Pesticide Application

High levels of agricultural intensification have led to widespread cultivation of densely sown crop monocultures, which has contributed to the prevalence of pests, fungi, bacteria, viruses, insects and weeds (Mihrete and Mihretu, 2025). Biocidal or biostatic compounds are routinely used as pesticides to reduce crop losses, yet many of them also disrupt soil microbial communities (Ni et al., 2025). Pesticide may eliminate microbial diversity, change the composition of the community and promote the formation of antimicrobial resistance in soil bacteria (Shen et al., 2025). For example, fungicides like azoxystrobin and elutriator have been linked with a decrease in the abundance of nitrifying microorganisms, which can reduce soil fertility (Bacmaga et al., 2024), while herbicides such as bromoxynil can suppress soil bacterial populations, decreasing biodegradation potential and prolonging the persistence of chemicals (Kelbrick et al., 2023).

The most common bacterial adaptation to pesticides is down regulation of membrane porins or up regulation of efflux pumps to decrease intracellular levels of harmful substances (Shafiq et al., 2025). Dicamba herbicide, for instance, increases soxRS expression in *Escherichia coli*, which enhances the expression of AcrAB efflux pumps which play a role in pesticide and antibiotic resistance. Copper-based fungicides can induce mutations on the AcrAB TolC multidrug export pump, leading to an inter-antibiotic resistance to tetracycline and chloramphenicol (Murray et al., 2024). Microbial degradation of pesticides may also contribute to AMR, since organophosphate insecticides are broken down by organophosphorus hydrolases produced by soil bacteria, including *Flavobacterium*, *Pseudomonas* and *Bacillus*, and these enzymes can also degrade antibiotics such as streptomycin, ampicillin and chloramphenicol (Paidi et al., 2021). The results from numerous studies have demonstrated that certain pesticides encourage the transfer of AMR genes on mobile genetic elements within natural microbial populations, which is known as co-resistance (Shen et al., 2025). For example, Liao et al. (2021) show that soils treated with glyphosate herbicides contained higher levels of resistance genes and mobile genetic elements than control soils that were not treated with the herbicides. These includes aminoglycoside, vancomycin, chloramphenicol and tetracycline resistance genes. Fungicides aswell as insecticides can further enhance the proliferation of resistance genes by increasing conjugation frequencies in *E. coli* (Zhang et al., 2023), and pesticides may indirectly influence AMR by altering microbial community structure in ways that favour antibiotic-resistant organisms, thereby worsening the AMR burden in agricultural soils (Kelbrick et al., 2023).

Irrigation with Contaminated Water

The water used by agriculture across the world is the greatest consumer of fresh water globally (more than 75% of resources available). As global population is likely to reach a level of over ten billion in the next three decades, farmers are estimated to produce roughly 70% more food, which will place additional pressure on freshwater supplies (Galanakis, 2024; FAO, 2025a). Population growth and water scarcity have driven the adoption of alternative irrigation sources, including wastewater. Nearly half of the world's population depend on water contaminated sources to irrigate their lands, and about 20 million hectares of land are irrigated using sewage water (Bougnom et al., 2020). Wastewater has long been used in agriculture in arid regions and is becoming an important alternative water source where shortages occur (Obijianya et al., 2025; Trotta et al., 2024). Untreated wastewater reuse is economically viable in most low-income nations whereas residential sewage is increasingly reused due to water shortage in high-income nations. Wastewater irrigation can help restore nutrients in soils and reduce the need for mineral fertilisers. However, wastewater may contain heavy metals, microorganisms, pharmaceuticals, plastic additives and other pollutants (La Rosa et al., 2025). Enteric diseass that have been associated with the agricultural use of wastewater include salmonellosis, shigellosis, cholera, giardiasis, amoebiasis, hepatitis A and viral enteritis among farmers, their families and consumers.

The effects of some of these health risks can be mitigated with proper treatment of wastewater before it is used in the agricultural fields, yet most of the contaminants, such as antibiotics, antimicrobial resistant bacteria and antimicrobial resistance genes remain unmitigated by conventional treatment methods (Adefisoye & Olaniran, 2022). Antibiotics may still remain in the treated effluents and resistant bacteria and resistance genes can survive and even thrive when they are in the treatment plants (Brouwir et al., 2025; Kalli et al., 2025). Irrigation with such effluents repeatedly exposes fields to antibiotics and resistant microorganisms, which encourages the selection and propagation of resistant bacteria in the soil. The wastewater derived bacteria can also share resistance genes with the native soil microbiota when resistant bacteria are deposited on fields. Crops grown on wastewater irrigated soils can absorb antimicrobial resistant bacteria and resistance genes and introduce consumers to the risk of AMR in the food chain (Patra and Dubey, 2024). Resistance genes and bacteria in from irrigated fields are also able to contaminate nearby surface and groundwater bodies**. Figure 2** shows the environmental effects of wastewater irrigation such as the distribution of ARB and ARGs.

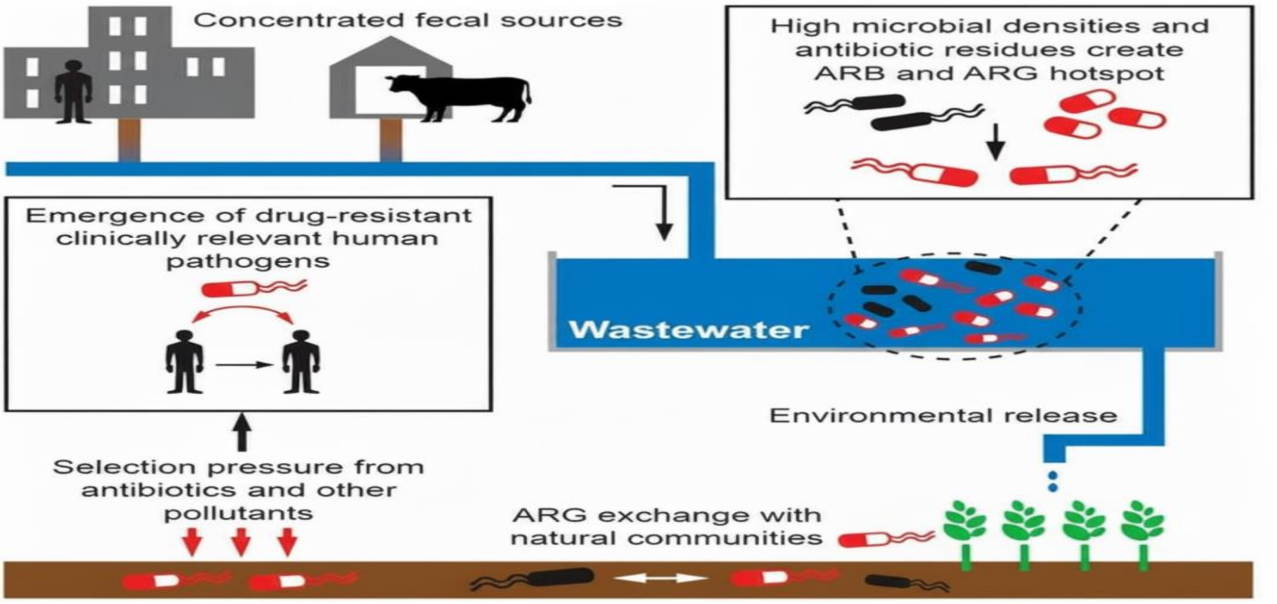

Figure 2: Contribution of wastewater irrigation to the evolution and spread of antimicrobial-resistant bacteria (ARB) and antimicrobial resistance genes (ARGs) in the environment. Slobodiuk *et al*. (2021).

Sources And Transmission Pathways of Amr in Soil

Antimicrobial resistance can be transmitted through human–human interaction, inside and outside the healthcare facility and ARGs may be present in animal-borne pathogens, aquatic environments and the agricultural soil, where they can move within and between these compartments (Godijk et al., 2022). The transmission pathways between bacterial species and the factors driving resistance vary widely. Major environmental hotspots for ARGs include wastewater, sludge of urban wastewater treatment plants, and natural fertilizers, i.e., pig slurry and cow and poultry manure, which are highly active sources of antimicrobial-resistant bacteria (Krzeminski et al., 2020). Direct methods of resistance acquisition include the use of antibiotic-treated feed by the animal, and through indirect means of exposure to humans: by eating animals that have been treated with antibiotic feed or consuming contaminated water and food, and through direct contact between humans and animals.

Agricultural Runoff

Agricultural sector contributes significantly to the spread of AMR in soil by use of manure, agricultural runoff and pesticides and antibiotics. Antibiotics are also commonly applied in animal production to enhance growth, prevent disease and enhance feed efficiency (Olanrewaju & Bezuidenhout, 2025). A large percentage is released in an active form, thus manure used as a fertilizer adds ARB and ARGs into soil, which helps in the survival and reproduction of resistant organisms (Liu et al., 2025).

Agricultural effluents such as irrigation return flows, rainfall runoff from fields and other farm runoffs transport antibiotic residues, ARB and ARGs from farms into surrounding soils and water bodies, thereby contaminating downstream environments (Meradji et al., 2025). Bacteria in these runoffs, whether pathogenic or commensal, can exchange resistance genes via HGT, increasing the overall environmental resistance burden. The level of contamination is pegged on the intensity of rainfall, the soil type, land management and the population of the livestock.

Heavy metals and chemical pesticides also exert co-selection pressure, such that bacteria resistant to both antibiotics and these compounds have a higher chance of survival and proliferation (Sassi et al., 2025; Wang et al., 2025b). This is partly because the antibiotic and the resistance genes of heavy metals are often found on the same mobile genetic element and thus multipe resistances may arise in a single strain. Introduction of ARB, ARGs in the soil environment disrupt normal microbial communities and is a threat to the health of human beings. Human beings may be exposed directly to contaminated soil or ingest polluted foodstuff and the soils may act as the chronic reservoirs of AMR which propagate resistance into the food chains and the entire environment.

Sewage Sludge and Wastewater

Sewage treatment plants (STPs) release a lot of contaminants into the wastewater, such as antibiotics, ARGs and ARB, and even with the conventional methods of wastewater treatment, they are not fully eliminated (Patra et al., 2024).

The primay product of the STPs is the sludge which is closely associated with the distribution of ARGs and ARB into the environment. ARGS, ARB, and heavy metal resistance genes also exist as hotspots of ARGs in the effluents generated by the wastewater and these micropollutants are concentrated in the sewage sludge (Zhao et al., 2025a). Both dry and processed city or industrial sludge contain a high amount of toxic substances. The idea of agricultural land utilization in the use of the raw sewage sludge is also a matter of concern as the sludge has the traces of antibiotic residues, ARB, ARGs and mobile genetic elements (MGEs) (Sorinolu et al., 2021; Zhang et al., 2022). ARB and ARGs are placed in the soil using this sludge as a fertilizer and can be dangerous to the quality of soil, crop safety and human health (da Silva Souza et al., 2020). It is known that soils fed with sewage sludge and biosolids enhance the abundance and spectrum of ARGs in soils and crops that are cultivated in the same seasons.

Soil Properties and AMR Persistence

The survival and stability of antibiotics in soil are controlled by the abiotic and biotic processes, especially sorbing to organic particles and changing (Sharifmand et al., 2024). Sorption is related to the properties of soil and the physicochemical characteristics of the antibiotic; the pH of soil and the amount of the organic matter are of particular importance. Sorption lowers the water solubility and mobility of antibiotics, minimizing ground and surface water leaching but reducing biodegradation of the antibiotic to microbes, making sorption one of the most critical factors in the retention of antibiotics in the soil (Wang et al., 2025a). Degradation and transformation may proceed through abiotic or biotic pathways depending on the compound's structure and properties. The heterogeneity of the half-life of antibiotics in the soil is explained by the fact that the composition of soil, microbial communities, antibiotic concentration, and environmental factors, including moisture, temperature, and pH, can differ across locations and studies (Gurmessa et al., 2020; Zhang et al., 2021). The processes influence not only antibiotics but also the maintenance and propagation of ARGs and resistant microbes (Wu et al., 2025). Sorption can concentrate antibiotics, resistant bacteria and genetic material in the micro-environment of the soil, forming potential hotspots where AMR continues to be present even when the bulk antibiotic concentration is reduced.

Even when antibiotic concentrations decline, selective pressure may persist, since sub-inhibitory levels can still favour resistant strains in soil microbial communities (Sassi et al., 2025). Physical properties of soils like porosity and texture influence bacterial mobility and contact, thereby affecting HGT by various mechanisms like conjugation. Mineral surfaces, in particular the clay, can serve as places of attachment where genes can be exchanged (Hendiani et al., 2025). The availability of soil moisture and organic matter also influences the activity of the microbes and gene transfer rates (Zeng et al., 2025).

Crop Cultivation Practices

One of the major practices is the use of animal manure as fertilizer (Liu et al., 2025). The animal manure from animals treated with antibiotics contains residues of antibiotics and antibiotic resistant bacteria, and when it is shed to the fields, it can cause contamination to soil and water, leading to the spread of resistance to the environmental bacteria, and even to human pathogens. Direct use of antibiotics as crop protection agents, although less frequent than in livestock but is an issue of emerging concern. Examples of such compounds are streptomycin and tetracycline that find their place in controlling bacterial disease in crops such as apples and pears that can also lead to the selection of resistant bacteria in orchards and concentration of resistant genes in soils that can be subsequently transferred into other populations of microbes (Batuman et al., 2024).

Irrigation practices also play a role. AMR can be introduced into fields via water sources contaminated with antibiotic residues and ARB, including treated wastewater and livestock farm runoff. This is particularly an issue in regions where treated wastewater is a common practice in irrigation. The resistant bacteria or ARGs may be absorbed in edible tissues of the crops irrigated with contaminated water, thus increasing human exposure to AMR (Wu et al., 2025).

Biopesticides are often viewed as more sustainable alternatives to chemical pesticides, but they can also influence AMR. Since they are found on living bacteria, they may carry resistance genes that can be transmitted to between bacterial populations can be spread through the horizontal gene transfer in agricultural environments, such as the biopesticides, manure, and the contaminated irrigation water (Barrero-Canosa et al., 2025; Van Laere et al., 2025).

Mechanisms Of Amr Dissemination in Soil Ecosystems

Horizontal Gene Transfer (HGT)

The most significant pathway of ARG transfer among microbial communities in soil is horizontal gene transfer, which occurs through transformation, transduction and conjugation as illustrated in **Figure 3.**

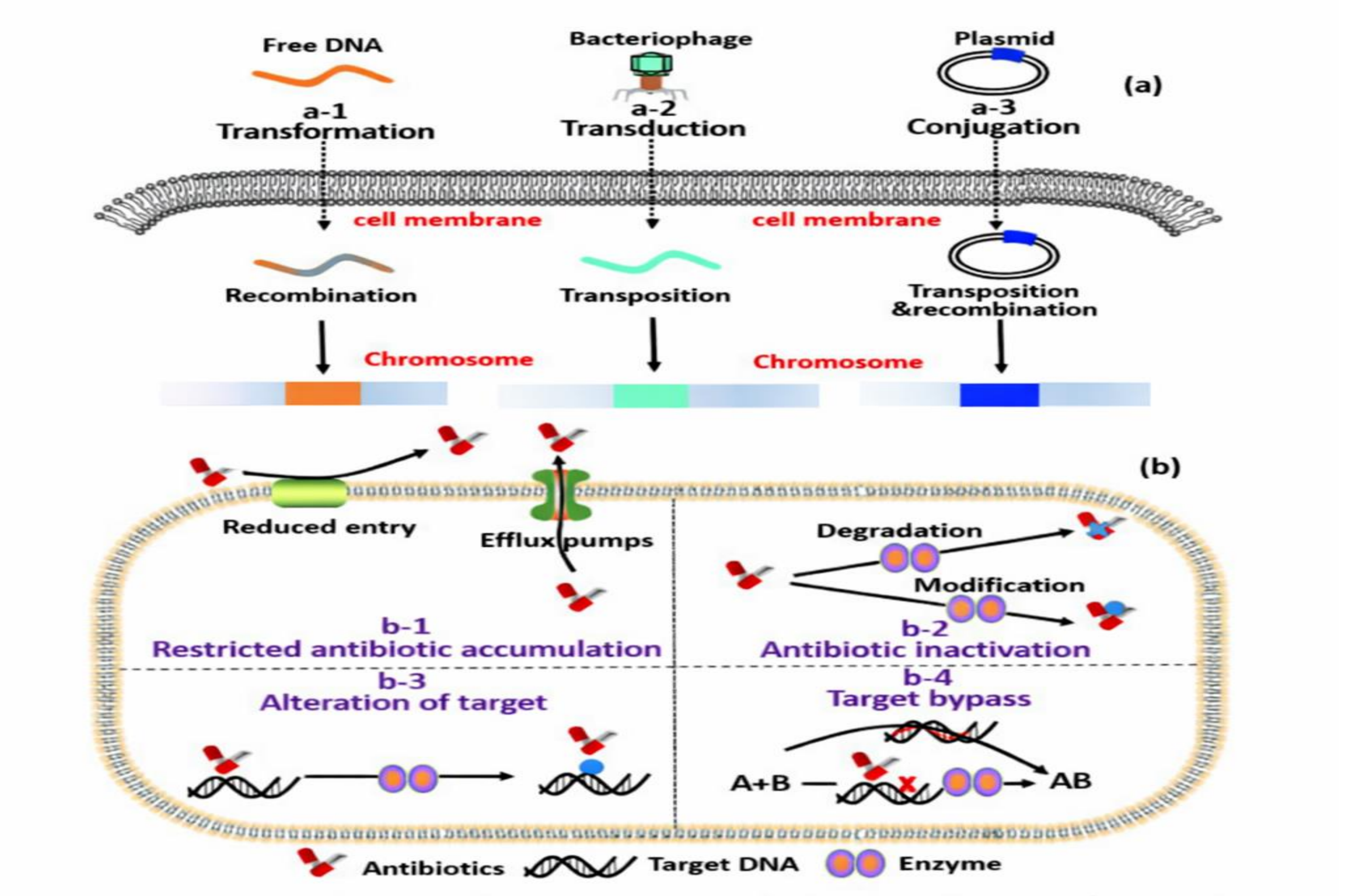

Figure 3: Horizontal Gene Transfer: Dissemination of Antimicrobial Resistance in Microbial Ecosystems. Adopted from Wang et al. (2022).

HGT is important in agricultural soils because it can support the movement of resistance genes between introduced resistant bacteria and native soil bacteria, especially where manure, sewage sludge, wastewater, antibiotics, pesticides and heavy metals occur together in the same environment (Jian et al., 2021; Sassi et al., 2025). These agricultural inputs can increase the presence of antibiotic-resistant bacteria, ARGs and mobile genetic elements in soil, thereby creating conditions that favour the persistence and exchange of resistance determinants (Jian et al., 2021). Soil texture, mineral surfaces, moisture and organic matter may also influence bacterial contact, microbial activity and gene transfer in soil ecosystems (Hendiani et al., 2025). Therefore, HGT remains an important mechanism through which agricultural practices contribute to the persistence and spread of AMR in soil ecosystems.

Mobile Genetic Elements

MGEs such as insertion sequences, transposons, integrons, gene cassettes, plasmids and integrative conjugative elements are important agents of HGT and AMR spread in soil ecosystems (Jian et al., 2021). These elements help resistance genes to move within and between bacterial cells, thereby increasing the spread of ARGs in agricultural soils. Integrons can capture and express resistance gene cassettes, while plasmids and transposons can carry resistance genes across different bacterial groups (Bhat et al., 2023; Jian et al., 2021). In soils affected by manure, wastewater, antibiotics, pesticides and heavy metals, these mobile elements may support the persistence and transfer of resistance genes among soil bacteria. This is important because resistance genes from environmental bacteria may be transferred to bacteria associated with humans, animals, crops and water systems (Liu et al., 2025).

Selective Pressure of Agricultural Input

Antibiotics, heavy metals and pesticides introduced into soils create conditions that suppress susceptible microbes and favour resistant ones. Antibiotic use in animal production is expected to increase markedly, and soil is recognised as one of the largest reservoirs of ARGs, containing an estimated 30% of all known resistance genes (FAO, 2025a; Roy et al., 2025). Soil bacteria are the original source of many clinically used antibiotics, and ARGs have been detected even in 30,000-year-old permafrost sediments, indicating that resistance is an ancient trait. Exogenous ARGs enter soil mainly through manure, sewage and wastewater irrigation. Continuous antibiotic exposure kills susceptible bacteria and allows resistant strains to proliferate; for example, tetracycline residues in manure-amended soils stimulate the growth of tetracycline-resistant bacteria and preserve related ARGs in soil microbiomes (Liu et al., 2025). ARG abundance often correlates positively with soil heavy metal levels, because metal resistance genes frequently co-exist with ARGs on MGEs, resulting in co-selection. Metallotolerant bacteria found in animal feed can also be resistant to macrolides, further contributing to AMR.

The death of susceptible microbes releases cellular contents and opens ecological niches that resistant populations can occupy, increasing overall soil resistance. The relationship between ARG profiles and heavy metal concentrations is dose-dependent; low levels may have limited effects, whereas high levels can strongly select for resistance and alter ARG composition (Murray et al., 2024). Pesticides can drive cross-resistance, since bacteria in contaminated soils may carry plasmids bearing both pesticide degradation and antibiotic resistance genes (Shen et al., 2025). There has been evidence that exposure to organophosphates or glyphosate compounds results in heightened resistance to aminoglycosides and tetracycline, which assist in sustaining AMR when contaminants are mixed.

Environmental Factors

The natural environment harbour different bacterial communities and has conditions favoring the development of resistance and gene transfer (Mustapha et al., 2021). Anthropogenic activities strongly shape these processes by introducing antibiotic residues, antibiotic-resistant bacteria and resistance genes into soil and water environments. In agricultural systems, livestock waste, sewage sludge, wastewater discharge, pesticide use and agricultural runoff can support the persistence of ARB and ARGs in the environment (Zhao et al., 2025b). These environmental conditions can create reservoirs where resistant bacteria survive and resistance genes continue to circulate among microbial communities. Within a One Health perspective, soil, wastewater, sewage and aquatic environments are important storage and transmission routes for resistant bacteria and resistance genes (Sassi et al., 2025). Therefore, environmental factors interact with agricultural practices to support the persistence and spread of AMR in soil ecosystems.

Public Health and Environmental Implications of Amr Spread in Agricultural Soil

The ecological and human health impacts of AMR in agricultural soils are substantial. Soil is an important reservoir of ARGs which can be passed over to other plants, animals and human pathogens, and therefore awareness of soil AMR will be central to both agricultural productivity and the safety of the population (Ifedinezi et al., 2024). ARGs in the soil can reshape crop-associated microbiomes, influence plant disease dynamics and decrease the effectiveness of biocontrol agents, while sewage sludge deposited on soil can further shift resistance patterns in crop microbiomes and introduce ARGs to the food chain.

The existence of resistant bacteria and residual antibiotics may remain in the soil over a long period of time, providing a chance for HGT and increasing the ARG reservoir of agricultural soils. These ARG-contaminated soils, particularly those supplemented with sewage sludge, can alter resistance patterns in crop microbiomes and allow resistance to enter the human food chain. Interactions between bacteriophages and bacteria further promote AMR proliferation and genetic diversification, enhancing resistance gene transfer in soil microbial communities (Gomes et al., 2023). Exposure of human beings occurs by eating infected crops and being in direct contact with resistant microbes in soil. The application of sewage sludge contributes additional resistant bacteria and antibiotic residues from human waste, intensifying selection for resistance in soil microbiota (Markowicz et al., 2021). AMR in soil also threatens wider ecosystems, because ARGs can be mobilised into adjacent water bodies via runoff, spreading resistance through aquatic environments and potentially affecting drinking water supplies (Memesh et al., 2024). The Mitigation would requires sustainable agricultural practices, more cautious use of organic wastes as fertilisers and improved wastewater treatment to reduce AMR transmission risks and protect environmental health.

AMR is now considered a significant epidemic, as microorganisms resistant to antibiotics and their genes are spread to soil, water, animals, and humans. Antimicrobial use in livestock selects and maintains ARB and ARGs, which can enter the environment via animal wastes, contaminated runoff and irrigation water (Enshaie et al., 2025). ARB has the capacity to survive in soil microbiomes and pass resistance genes on to other environmental bacteria, increasing contamination risks for crops, grazing animals and people who contact contaminated soil or consume food grown under these conditions (Wu et al., 2025). Animals may become the reservoirs and carriers of AMR genes, and the resistance can be shared between wild and domestic animals (Mbuthia et al., 2025). The combination of farming practices, food production systems and wastewater management contribute to AMR spread across environmental, animal and human compartments (Woolhouse, 2024). Fields that have not recently been fertilized can still carry significant loads of ARGs that remained as a result of past agricultural practices, and the fact that these genes are not readily destroyed over time highlights the difficulty of controlling their spread (Lin et al., 2024). Addressing this requires integrated management of animal-based fertilizers, better irrigation procedures and strict wastewater treatment policies.

AMR and antibiotic inputs also alter the diversity and functionality of microbial communities of the soil. Antibiotics can reduce the overall microbial abundance and shift the bacteria-fungi ratio, usually by decreasing vulnerable taxa while favouring more resistant ones (Shawver et al., 2021). The magnitude and direction of these effects depend on the type of antibiotic, concentration and duration of exposure, with documented changes in soil microbiome structure and microbial interactions (Lin et al., 2024). Since major processes in the soil are based on microbial communities, the alterations in their composition can interfere with ecosystem functions. The microbes present in the soil are significant in the decomposition of organic matter, nutrient recycling, decomposition and carbon capture and, thus, AMR-induced alterations can result into a reduced soil fertility and the ecosystem stability. A research study by Shawver et al. (2024) discovered that microorganisms activity varied as a result of utilizing antibiotics in cattle manure. In the study, they noted that cephapirin treatment enhanced respiration while pirlimycin slowed it down. Also, antibiotic-treated manure increased the level of NH_4^+ and reduced that of NO_3^- in certain scenarios. These alterations show that AMR associated with antibiotics in agricultural soils can be transferred to wider effects on soil and agroecosystem sustainability.

Case Study: Soil-Associated Amr and Human Infection

Produce-borne outbreaks caused by enteric pathogens are repeatedly traced to upstream agricultural environmental routes, particularly manure-related contamination and irrigation with contaminated surface waters or wastewater (Elbehiry et al., 2025).

These same environmental compartments, especially soil and water, can act as reservoirs and exchange interfaces for antimicrobial-resistant bacteria and resistance genes within a One Health framework (Zhao et al., 2025b). **Table 2.** Summarises representative outbreaks where investigations identified soil-, manure-, or irrigation-linked pathways, and it reports AMR relevance only where it was explicitly described in outbreak investigations or follow-up analyses (CDC, 2006, 2018, 2024).

Table 2. Produce-Associated Outbreaks Linked to Soil, Manure, or Irrigation Pathways, and AMR Relevance

Year, location	**Vehicle**	**Pathogen**	**Soil, manure, or irrigation pathway**	**AMR relevance (as reported)**	**Public health impact (reported)**	**References**
2011, Germany	Sprouts (fenugreek-related supply chain)	*Escherichia coli* O104:H4 (EAEC/STEC hybrid)	Sprout production and supply chain, plausible contamination via agricultural environment and water inputs	Widely discussed as high-virulence and treatment-challenging, resistance features reported in scientific analyses	Large outbreak with extensive HUS and deaths	Beutin and Martin (2012)
2006, USA and Canada	Bagged spinach	*Escherichia coli* O157:H7	Farm-environment contamination suspected, including manure or water influences near production	AMR not emphasised in CDC outbreak summary	High hospitalisation and HUS reported, deaths reported	CDC (2006)
2018, USA (Yuma region)	Romaine lettuce	*Escherichia coli* O157:H7	Outbreak strain identified in irrigation canal water used near production region	AMR not emphasised in CDC outbreak summary	Multistate outbreak, strong environmental water signal reported	CDC (2018)
2024, USA	Cucumbers	*Salmonella* Africana and *Salmonella* Braenderup	Untreated canal water used by a grower linked to outbreak strain detection	CDC WGS reporting included predicted resistance information for some isolates	551 illnesses reported across many states	CDC (2024)

Strategies For Mitigating Amr Spread in Agricultural Soils

Prolonged, non-therapeutic antibiotic use at subtherapeutic concentrations in agriculture has been recognised as a major driver of ARB and resistance gene transfer to humans. Antimicrobial stewardship in food animals aims to ensure judicious antibiotic use, preserve antimicrobial efficacy and minimise residues in animal-derived food products (WHO, 2024). Within agriculture, this involves coordinated action across clinical microbiology, biosecurity and infection control, regulation, prudent antibiotic use and resistance monitoring, as well as improved animal management and the adoption of antibiotic alternatives (Pinho et al., 2025). Effective stewardship requires collaboration between veterinarians, livestock producers, pharmacists, pharmaceutical companies and regulatory agencies to limit unnecessary antibiotic use. Several regions have restricted antimicrobial growth promoters in livestock, and international bodies have updated maximum residue limits for veterinary drugs in foods of animal origin to support resistance control. National measures, such as regulatory amendments specifying withdrawal periods and labelling requirements for veterinary drugs, complement the broader Global Action Plan on Antimicrobial Resistance and the Global Principles for the containment of resistance in food-producing animals, which call on countries to align policies for responsible antibiotic use in livestock (FAO, 2024).

Manure processing can substantially influence the fate of antibiotic residues, ARB and ARGs before land application. Comparative studies suggest that, relative to simple storage in lagoons, composting can more rapidly reduce many antibiotic residues, enteric bacteria, ARB and common ARGs (Marutescu et al., 2022). However, the performance of manure treatments in lowering AMR is still poorly characterised under commercial farm conditions, and systematic studies using harmonised methodologies across regions are needed to evaluate impacts on soil microbiomes and AMR levels before and after application (Wang et al., 2024). Current manure processing technologies are rarely designed or assessed with ARG and ARB removal as a key performance criterion, and many systems do not fully eliminate these targets, allowing further dissemination of resistance in the environment. Thermophilic anaerobic digestion and aerobic thermophilic composting, especially when followed by post digestion composting, can reduce ARG abundances by more than 80%, whereas mesophilic digestion is generally less effective (Liu et al., 2024). Solid manure fractions may be composted, dried, pelletised or burned, while liquid fractions are often applied directly as fertilizer or only lightly treated, which can spread antibiotic residues, ARGs and zoonotic bacteria if management is inadequate.

Safe irrigation practices and water control are equally central to AMR mitigation. Many countries reuse treated wastewater for irrigation, with quality control measures intended to limit AMR risks (Ortega-Pozo et al., 2022). Irrigation with treated effluents can introduce ARB into soils, where these bacteria may survive and multiply in organic-rich microsites (Marano et al., 2021). Evidence on whether treated wastewater irrigation increases ARG levels compared with freshwater irrigation is mixed, and some studies report no major differences, although wastewater clearly functions as a reservoir and conduit for ARB and ARGs (Zhao et al., 2022). Wastewater environments support dense and diverse bacterial communities, facilitate ARG exchange among human, animal and environmental bacteria and can foster the emergence of new resistance variants (La Rosa et al., 2025). To reduce these risks, the European Union has proposed minimum quality standards for wastewater reuse, and harmonisation across member states is expected to improve the safety of irrigated products and reduce trade barriers. The World Health Organization promotes the use of a risk management-based approach that emphasises early detection and mitigation of AMR risks, and a strong implementation mechanism (Drechsel et al., 2024). Runoff and pollution may be reduced through good water management, which involves efficient irrigation technology systems like drip systems, controlled storage and distribution, and water use monitoring. To limit the spread of AMR by irrigation, the availability of recycled water of sufficient treatment, and discouragement of uncontrolled small-scale use of untreated wastewater in the immediate vicinity of streams are important.

Regulatory frameworks and policy interventions form an essential foundation for AMR mitigation. Environmental monitoring and regulations in relation to public health can help to decrease the improper use of antibiotics in human and veterinary practice, control pharmaceutical/industrial discharges and strengthen infection avoidance and control in medical facilities. It can also aid in facilitating the establishment of national and global AMR action plans that expressly embrace the One Health approach, which entails a combination of human, animal and environmental health (WHO, 2024; Woolhouse et al., 2024). The regulatory frameworks can restrict over the counter sales of antibiotics, demand prescription, regulate their use in the agricultural sector and promote alternatives which do not interfere with the health and productivity of livestock without encouraging resistance.

The risk of AMR spread in agricultural systems differs across regions because antibiotic regulation, wastewater treatment, farm management and surveillance capacity are not the same in all countries. In regions with stronger regulatory systems, antimicrobial use in livestock is more controlled, and wastewater reuse is usually guided by treatment and monitoring standards (Truchado et al., 2021). However, resistant bacteria and resistance genes may still persist in manure, wastewater, runoff and food systems, showing that regulation can reduce the risk but may not remove it completely (Marutescu et al., 2022). In many low- and middle-income settings, weak enforcement of veterinary drug regulation, poor wastewater treatment, informal antibiotic access and limited surveillance capacity may increase the movement of ARB and ARGs through agricultural soils and water systems. These differences show that AMR control in agriculture should consider the economic, regulatory and environmental conditions of each region, rather than depending only on general global recommendations (Ouoba et al., 2025; Gozzer et al., 2025). **Table 3** compares selected regions based on livestock antibiotic regulation, wastewater and irrigation control, surveillance capacity and AMR risk implication.

Table 3. Regional Comparison of Agricultural AMR Risk, Regulation and Surveillance Capacity

Region	Antibiotic use regulation in livestock	Wastewater and irrigation control	AMR surveillance capacity	AMR risk implication	References
European Union	More controlled veterinary antimicrobial use, with efforts to reduce unnecessary and routine preventive use.	Reclaimed water use is guided by minimum water quality and monitoring requirements.	AMR monitoring in humans, animals and food is more coordinated through European reporting systems.	Risk is reduced by stronger regulation, but manure, wastewater and food systems can still carry ARB and ARGs.	Truchado et al., 2021; EFSA and ECDC, 2025
United States	Medically important antimicrobials in food animals are under stronger veterinary oversight, but policy gaps remain.	Manure application, livestock waste and agricultural runoff remain important environmental pathways.	NARMS monitors resistance in enteric bacteria from humans, retail meat and food animals.	Risk is moderated by veterinary oversight and surveillance, but intensive livestock production and runoff remain important.	Wallinga et al., 2022; Gens et al., 2022.
Southeast Asia	Regulation and enforcement differ between countries, with livestock and aquaculture antimicrobial use still a concern.	Wastewater treatment and safe irrigation practices vary widely across farming systems.	Surveillance and laboratory capacity are improving, but integrated One Health monitoring still has gaps.	Risk may increase where antimicrobial use, intensive animal production, aquaculture and limited wastewater control occur together.	Chung, 2025; Xie et al., 2025
Sub-Saharan Africa	Veterinary oversight and enforcement are limited in many settings, and antimicrobial use in food animals is often poorly monitored.	Poor sanitation, untreated wastewater, weak waste management and limited treatment infrastructure can increase contamination.	Surveillance is improving, but laboratory, funding, reporting and coordination gaps remain.	Risk is higher where weak regulation, informal drug access, untreated wastewater and poor waste management occur together.	Ouoba et al., 2025; Totaro et al., 2025
Latin America and the Caribbean	Regulation differs across countries, with stronger control in some	Wastewater, surface water and agricultural environments	Surveillance and intervention efforts exist,	Risk varies by country and may increase where livestock production, wastewater contamination	Da Silva et al., 2023; Gozzer et al., 2025

	settings and weak enforcement in others.	can act as AMR reservoirs, but data are uneven.	but monitoring is not equally distributed across countries.	and limited surveillance occur together.	

Integrated One Health approaches therefore remain imperative. In 2015, the WHO Global Action Plan on Antimicrobial Resistance, created in collaboration with FAO and OIE, was endorsed at the World Health Assembly, to offer a coordinated approach to addressing AMR across sectors. The objectives of the Action Plan were the enhancement of awareness and understanding of AMR, reducing the occurrence of infection through hygiene and infection prevention, maximisation of utilisation of antimicrobials in human and animal health, as well as sustainable investment and innovation in diagnostics, vaccines and therapeutic (Adefisoye & Olaniran, 2023). The Global Action Plan has stimulated the development of national action plans in many countries, which adapt its objectives to local contexts while maintaining a One Health orientation (FAO, 2024). Since all the compartments of the human body, animals and the environment can harbour resistant microorganisms, some form of integrated approaches are needed to take care of the transmission pathways between them. This involves regulating environmental dispersion, the control of antimicrobial use and putting into consideration antibiotic alternatives in a rather interconnected relationship of human, animal and ecosystem health (Craddock et al., 2025). Effective AMR mitigation measures must therefore be designed and implemented collaboratively by professionals and researchers across human and veterinary medicine, agriculture and environmental sciences (Woolhouse et al., 2024).

Limitations Of the Review

This review has some limitations. First, the review was based on published literature, and this may be affected by publication bias. Studies that reported strong links between agricultural practices and AMR may be more available than studies that reported weak or no association. This may affect the general interpretation of the evidence presented in the review.

Second, the studies included in this review used different sampling methods, laboratory detection methods, resistance gene targets and data interpretation approaches. Some studies focused on soil, while others focused on wastewater, manure, crops, livestock, food products or aquatic environments. These differences made it difficult to compare all findings directly or carry out a quantitative meta-analysis.

Another limitation is that the available studies are not evenly distributed across all regions. More studies are available from areas with better research facilities, wastewater treatment systems and AMR surveillance structures. This may not fully represent the situation in low- and middle-income settings where untreated wastewater use, poor waste management, informal antibiotic access and limited surveillance may be more common.

In addition, it is difficult to establish a direct causal relationship between one agricultural practice and clinical AMR outcomes. This is because resistant bacteria and resistance genes can move through several connected pathways involving humans, animals, soil, water, food and the wider environment. Despite these limitations, this review provides useful information on how agricultural systems contribute to the persistence and spread of AMR within a One Health framework.

CONCLUSION

The magnitude and scale of AMR are important health concerns that need urgent interventions as a critical global health challenge. Antibiotic misuse and over use in human health, agriculture and livestock production has increased the spread of AMR with animal production playing a significant role by introducing antibiotic residues, ARB and ARGs to the environment through manure, sewage sludge and wastewater irrigation. Soil and water system serve as the main environmental reservoirs and routes of transmission, in which resistance genes can persist, undergo HGTs and selections due to the continued anthropogenic pressures. Addressing

AMR in agricultural soil is pertinent, and requires a complex but appropriately coordinated response that combines responsible antibiotics utilization, enhanced waste and water management and sustainable agricultural practices in a unified One Health framework. The remedies to curbing AMR and ensuring the health of both the people and the environment have been based on the international partnership and strong national action plans and increased antimicrobial stewardship programmes.

RECOMMENDATION AND FUTURE DIRECTION

To curb the problem of antibiotic resistance, rational use of antibiotics in both human and veterinary medicine should be given priority, preference of narrow spectrum agents where feasible and avoidance of unnecessary exposure should be considered. There is a need to have strong antimicrobial stewardship programmes to oversee and manage AMR and promote evidence-based prescribing. To reduce the emission of antibiotics and drug resistant bacteria to the environment, agricultural practices should reduce the waste products released to the environment through management of livestock waste products, improve the outcome of treatment and quality of wastewater and good management of manure to be utilised as a fertiliser. It is necessary to further integrate healthcare, agriculture, and environmental sectors into one health strategy through the assistance of the population and education about the proper usage of antibiotics and hygiene. At the same time, new antimicrobials will require long term research and innovation to develop alternative treatments and sustainable agricultural practices to reduce the utilization of antibiotics without affecting productivity and ecosystem well-being.

List of Abbreviations

AMR - Antimicrobial Resistance

ARGs - Antibiotic Resistance Genes

HGT - Horizontal Gene Transfer

MGEs - Mobile Genetic Elements

ACKNOWLEDGMENTS

We are grateful to the Department of Research, Innovation and International Cooperation (RIIC), Babcock University, for their support.

Conflicts of Interest

The author declares no conflicts of interest.

Funding

The review article is self-sponsored

Ethical Statement

Ethical approval was not required for this study because it is a review article based solely on previously published literature and did not involve human participants, animal subjects, or unpublished personal data.

Data Availability Statement

No new data were generated or analysed in support of this review. All information discussed in this manuscript is derived from previously published studies cited in the reference list.

REFERENCES

1. Abate, T.A., & Birhanu, A.G. (2025). Antibiotic Use in Livestock and Environmental Antibiotic Resistance: A Narrative Review. Environmental health insights, 19, 11786302251357775. https://doi.org/10.1177/11786302251357775
2. Adefisoye, M.A., & Olaniran, A.O. (2022). Does Chlorination Promote Antimicrobial Resistance in Waterborne Pathogens? Mechanistic Insight into Co-Resistance and Its Implication for Public Health. Antibiotics.11(5):564. https://doi.org/10.3390/antibiotics11050564
3. Adefisoye, M.A., & Olaniran, A.O. (2023). Antimicrobial resistance expansion in pathogens: A review of current mitigation strategies and advances towards innovative therapy. JAC-Antimicrobial Resistance, 5(6), dlad127. https://doi.org/10.1093/jacamr/dlad127
4. Ahmed, S.K., Hussein, S., Qurbani, K., Ibrahim, R.H., Fareeq, A., Mahmood, K.A., & Shukur, F.O. (2024). Antimicrobial resistance: Impacts, challenges, and future prospects. Journal of Medicine, Surgery, and Public Health, 2, 100081. https://doi.org/10.1016/j.glmedi.2024.100081
5. Aijaz, M., Ahmad, M., Ansari, M.A., & Ahmad, S. (2023). Antimicrobial resistance in a globalized world: Current challenges and future perspectives. International Journal of Pharmaceutical & Drug Design, 1, 7–22.
6. Alabi, M.A., Chenia, H.Y., & Lin, J. (2025). Antibiotic use in livestock: A driver of resistance in Africa and the path to safer alternatives. MicrobiologyOpen, 14(6), e70122. https://doi.org/10.1002/mbo3.70122
7. Aslam, B., Khurshid, M., Arshad, M.I., Muzammil, S., Rasool, M., Yasmeen, N., Shah, T., Chaudhry, T.H., Rasool, M.H., Shahid, A., Xueshan, X., & Baloch, Z. (2021). Antibiotic resistance: One Health One World outlook. Frontiers in Cellular and Infection Microbiology, 11, 771510. https://doi.org/10.3389/fcimb.2021.771510
8. Baćmaga, M., Wyszkowska, J., & Kucharski, J. (2024). Response of Soil Microbiota, Enzymes, and Plants to the Fungicide Azoxystrobin. International journal of molecular sciences, 25(15), 8104. https://doi.org/10.3390/ijms25158104
9. Barrero-Canosa, J., Ebeling, J., Kenny, E.F., Marx-Stoelting, P., Paege, N., Feustel, S., & Leme, D.M. (2025). Human health risk assessment for microbial pesticides in the EU: challenges and perspectives. Environmental health: A global access science source, 24(1), 43. https://doi.org/10.1186/s12940-025-01196-1
10. Batuman, O., Britt-Ugartemendia, K., Kunwar, S., Yilmaz, S., Fessler, L., Redondo, A., Chumachenko, K., Chakravarty, S., & Wade, T. (2024). The Use and Impact of Antibiotics in Plant Agriculture: A Review. Phytopathology, 114(5), 885–909. https://doi.org/10.1094/PHYTO-10-23-0357-IA
11. Bava, R., Castagna, F., Lupia, C., Poerio, G., Liguori, G., Lombardi, R., Naturale, M.D., Mercuri, C., Bulotta, R.M., Britti, D., & Palma, E. (2024). Antimicrobial Resistance in Livestock: A Serious Threat to Public Health. Antibiotics (Basel, Switzerland), 13(6), 551. https://doi.org/10.3390/antibiotics13060551
12. Beutin, L., & Martin, A. (2012). Outbreak of Shiga toxin-producing Escherichia coli (STEC) O104:H4 infection in Germany causes a paradigm shift with regard to human pathogenicity of STEC strains. Journal of food protection, 75(2), 408–418. https://doi.org/10.4315/0362-028X.JFP-11-452
13. Bhat, B.A., Mir, R.A., Qadri, H., Dhiman, R., Almilaibary, A., Alkhanani, M., Mir, M.A. (2023). Integrons in the development of antimicrobial resistance: Critical review and perspectives. Frontiers in Microbiology, 14, 1231938.
14. Bougnom, B.P., Thiele-Bruhn, S., Ricci, V., Zongo, C., Piddock, L.J.V. (2020). Raw wastewater irrigation for urban agriculture in three African cities increases the abundance of transferable antibiotic resistance genes in soil, including those encoding extended spectrum β-lactamases (ESBLs). Science of the Total Environment, 698, 134201.
15. Brouwir, L., KleinJan, H., Balent, C., Quabron, G., Salmerón, I., Venditti, S., & Gritten, F. (2025). Fate and Removal of Antibiotics and Antibiotic Resistance Genes in a Rural Wastewater Treatment Plant: A Microbial Perspective of Nature-Based Versus Advanced Technologies. Microorganisms, 13(12), 2663. https://doi.org/10.3390/microorganisms13122663
16. Centers for Disease Control and Prevention. (2006). Update on multi-state outbreak of E. coli O157:H7 infections from fresh spinach (archived outbreak update).

17. Centers for Disease Control and Prevention. (2018). 2018 E. coli outbreak linked to romaine lettuce (archived outbreak investigation update).
18. Centers for Disease Control and Prevention. (2024). Salmonella outbreak linked to cucumbers (outbreak investigation summary and updates).
19. Chung P. Y. (2025). One Health strategies in combating antimicrobial resistance: a Southeast Asian perspective. Journal of global health, 15, 03025. https://doi.org/10.7189/jogh.15.03025
20. Craddock, H.A., Kearney, A., Fitzpatrick, F., Finn, C., Pryce, M.T., & Fitzgerald-Hughes, D. (2025). The challenge of reducing antimicrobial resistance (AMR) across the one health landscape: Diverse perspectives on AMR risks and their mitigation in sinks, drains, and wastewater. The Science of the total environment, 992, 179935. https://doi.org/10.1016/j.scitotenv.2025.179935
21. da Silva Souza, C.A., Gatica, E.A.T., da Silva, M.V., & de Souza, J.A. (2020). Occurrence of multiple antibiotic resistance in Enterococcus spp. isolated from soil used for agricultural purposes. International Journal of Antimicrobial Agents, 56(2), 106034.
22. Da Silva, R. A., Arenas, N. E., Luiza, V. L., Bermudez, J. A. Z., & Clarke, S. E. (2023). Regulations on the Use of Antibiotics in Livestock Production in South America: A Comparative Literature Analysis. Antibiotics (Basel, Switzerland), 12(8), 1303. https://doi.org/10.3390/antibiotics12081303
23. De Oliveira, D.M.P., Forde, B.M., Kidd, T.J., Harris, P.N.A., Schembri, M.A., Beatson, S.A., Paterson, D.L., & Walker, M.J. (2020). Antimicrobial resistance in ESKAPE pathogens. Clinical Microbiology Reviews, 33(3), e00181-19.
24. Despotovic, M., de Nies, L., Busi, S.B., & Wilmes, P. (2023). Reservoirs of antimicrobial resistance in the context of One Health. Current Opinion in Microbiology, 73, 102291.
25. Drechsel, P., Bartram, J., Qadir, M., & Medlicott, K.O. (2024). The challenge of supporting and monitoring safe wastewater use in agriculture in LMIC. npj Clean Water, 7, 67. https://doi.org/10.1038/s41545-024-00364-z
26. Duffey, M., Jumde, R. P., da Costa, R. M. A., Ropponen, H. K., Blasco, B., & Piddock, L. J. V. (2024). Extending the Potency and Lifespan of Antibiotics: Inhibitors of Gram-Negative Bacterial Efflux Pumps. ACS infectious diseases, 10(5), 1458–1482. https://doi.org/10.1021/acsinfecdis.4c00091
27. Elbehiry, A., Marzouk, E., Alzaben, F., Almuaither, A., Abead, B., Alamri, M., Almuzaini, A. M., & Abu-Okail, A. (2025). Emerging Technologies and Integrated Strategies for Microbial Detection and Control in Fresh Produce. Microorganisms, 13(7), 1447. https://doi.org/10.3390/microorganisms13071447
28. Enshaie, E., Nigam, S., Patel, S., & Rai, V. (2025). Livestock Antibiotics Use and Antimicrobial Resistance. Antibiotics (Basel, Switzerland), 14(6), 621. https://doi.org/10.3390/antibiotics14060621
29. European Food Safety Authority, & European Centre for Disease Prevention and Control. (2025). The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2022–2023. EFSA Journal, 23(3), e9237. https://doi.org/10.2903/j.efsa.2025.9237
30. Food and Agriculture Organization of the United Nations. (2024). The State of Food and Agriculture 2024: Value-driven transformation of agrifood systems. FAO. https://doi.org/10.4060/cd2616en
31. Food and Agriculture Organization of the United Nations. (2025a). New study projects a rise in global livestock antibiotic use. FAO.
32. Food and Agriculture Organization of the United Nations. (2025b). Better land, soil and water management key to feeding 10 billion people, FAO warns. https://www.fao.org/newsroom/detail/better-land--soil-and-water-management-key-to-feeding-10-billion-people--fao-warns/en
33. Galanakis C.M. (2024). The Future of Food. Foods (Basel, Switzerland), 13(4), 506. https://doi.org/10.3390/foods13040506
34. Gauba, A., & Rahman, K.M. (2023). Evaluation of antibiotic resistance mechanisms in Gram-negative bacteria. Antibiotics, 12(11), 1590.
35. Gens, K. D., Singer, R. S., Dilworth, T. J., Heil, E. L., & Beaudoin, A. L. (2022). Antimicrobials in Animal Agriculture in the United States: A Multidisciplinary Overview of Regulation and Utilization to Foster Collaboration: On Behalf Of the Society of Infectious Diseases Pharmacists. Open forum infectious diseases, 9(11), ofac542. https://doi.org/10.1093/ofid/ofac542

36. Gillieatt, B.F., & Coleman, N.V. (2024). Unravelling the mechanisms of antibiotic and heavy metal resistance co-selection in environmental bacteria. FEMS microbiology reviews, 48(4), fuae017. https://doi.org/10.1093/femsre/fuae017
37. Godijk, N.G., Bootsma, M.C.J., & Bonten, M.J.M. (2022). Transmission routes of antibiotic resistant bacteria: a systematic review. BMC infectious diseases, 22(1), 482. https://doi.org/10.1186/s12879-022-07360-z
38. Gomes, B., Dias, M., Cervantes, R., Pena, P., Santos, J., Vasconcelos Pinto, M., Viegas, C. (2023). One health approach to tackle microbial contamination on poultries—A systematic review. Toxics, 11, 374.
39. Gozzer, E., Becerra-Chauca, N., Abba-Aji, M., Wirtz, V. J., Cordoba, G., Canchihuamán, F., Nagassar, R. P., Yañez-Diaz, S., Brou, P. S., Delgado-Flores, C. J., & Fazaludeen Koya, S. (2025). Antimicrobial resistance interventions in Latin America and the Caribbean: a scoping review of reported interventions between 2018-2024. Antimicrobial resistance and infection control, 14(1), 137. https://doi.org/10.1186/s13756-025-01629-z
40. Gufe, C., Chari, T.A., Jambwa, P., Dinginya, L., Mahlangu, P., Marowero, S.T., … Machakwa, J. (2025). A review on the occurrence of antibiotic-resistant bacteria found in abattoir effluent from resource-limited settings: The necessity of a robust One Health framework. Sustainable Environment, 11(1). https://doi.org/10.1080/27658511.2025.2464419
41. Gurmessa, B., Pedretti, E.F., Cocco, S., Cardelli, V., & Corti, G. (2020). Manure anaerobic digestion effects and the role of pre- and post-treatments on veterinary antibiotics and antibiotic resistance genes removal efficiency. Science of the Total Environment, 721, 137532.
42. Hendiani, S., Carbajo, C., Caicedo, P.N.A., Verma, T., Hansen, M.F., Agbaje, O.B.A., Mulec, I.M., Burmølle, M., & Sand, K.K. (2025). Reconciling the role of mineral surfaces for bacterial evolution: Importance of minerals in the dissemination of antibiotic resistance. The Science of the total environment, 962, 178301. https://doi.org/10.1016/j.scitotenv.2024.178301
43. Ho, C.S., Wong, C.T.H., Aung, T.T., Lakshminarayanan, R., Mehta, J.S., Rauz, S., McNally, A., Kintses, B., Peacock, S.J., de la Fuente-Nunez, C., Hancock, R.E.W., & Ting, D.S.J. (2025). Antimicrobial resistance: a concise update. The Lancet. Microbe, 6(1), 100947. https://doi.org/10.1016/j.lanmic.2024.07.010
44. Ifedinezi, O.V., Nnaji, N.D., Anumudu, C.K., Ekwueme, C.T., Uhegwu, C.C., Ihenetu, F.C., Obioha, P., Simon, B.O., Ezechukwu, P.S., Onyeaka, H. (2024). Environmental Antimicrobial Resistance: Implications for Food Safety and Public Health. Antibiotics, 13, 1087. https://doi.org/10.3390/antibiotics13111087
45. Jian, Z., Zeng, L., Xu, T., Sun, S., Yan, S., Yang, L., Huang, Y., Jia, J., & Dou, T. (2021). Antibiotic resistance genes in bacteria: Occurrence, spread, and control. Journal of Basic Microbiology, 61(12), 1049–1070. https://doi.org/10.1002/jobm.202100201
46. Joseph, M.W., Moturi, W.N., & Ogendi, G.M. (2024). Assessment of veterinary antibiotic use and occurrence of veterinary antibiotics in livestock manure from farms in Rongai Sub-County, Kenya. Current World Environment, 19(2), 778–792. https://doi.org/10.12944/CWE.19.2.21
47. Kalli, M., Kontogiannatos, D., & Koi, A.M. (2025). Removal of antibiotic resistant bacteria and genes by conventional and nature-based municipal wastewater treatment systems. Environmental Processes. https://doi.org/10.1007/s40710-025-00779-x
48. Karwowska, E. (2024). Antibiotic Resistance in the Farming Environment. Applied Sciences, 14, 5776.
49. Kelbrick, M., Hesse, E., & O'Brien, S. (2023). Cultivating antimicrobial resistance: how intensive agriculture ploughs the way for antibiotic resistance. Microbiology, 169(9), 001384.
50. Kim, J., & Ahn, J. (2022). Emergence and spread of antibiotic-resistant foodborne pathogens from farm to table. Food Science and Biotechnology, 31, 1481–1499.
51. Krzemiński, P., Markiewicz, Z., & Popowska, M. (2020). Entry routes of antibiotics and antimicrobial resistance in the environment. In M.Z. Hashmi (Ed.), Antibiotics and Antimicrobial Resistance Genes: Environmental Occurrence and Treatment Technologies (pp. 1–26). Springer, Cham. https://doi.org/10.1007/978-3-030-40422-2_1
52. La Rosa, M. C., Maugeri, A., Favara, G., La Mastra, C., Magnano San Lio, R., Barchitta, M., & Agodi, A. (2025). The Impact of Wastewater on Antimicrobial Resistance: A Scoping Review of Transmission Pathways and Contributing Factors. Antibiotics (Basel, Switzerland), 14(2), 131. https://doi.org/10.3390/antibiotics14020131

53. Li, Z., Tang, J., Wang, X., Ma, X., Yuan, H., Gao, C., Guo, Q., Guo, X., Wan, J., & Dagot, C. (2025). The Environmental Lifecycle of Antibiotics and Resistance Genes: Transmission Mechanisms, Challenges, and Control Strategies. Microorganisms, 13(9), 2113. https://doi.org/10.3390/microorganisms13092113
54. Liao, H., Li, X., Yang, Q., Bai, Y., Cui, P., Wen, C., Liu, C., Chen, Z., Tang, J., Che, J., Yu, Z., Geisen, S., Zhou, S., Friman, V.P., & Zhu, Y.G. (2021). Herbicide Selection Promotes Antibiotic Resistance in Soil Microbiomes. Molecular biology and evolution, 38(6), 2337–2350. https://doi.org/10.1093/molbev/msab029
55. Lin, D., Xu, J. Y., Wang, L., Du, S., & Zhu, D. (2024). Long-term application of organic fertilizer prompting the dispersal of antibiotic resistance genes and their health risks in the soil plastisphere. Environment international, 183, 108431. https://doi.org/10.1016/j.envint.2024.108431
56. Liu, B., Shen, Z., Zhou, Q., Ren, J., Wang, H., Zhang, D., & Pan, X. (2025). Antibiotic resistance genes in the animal manure-amended soil-plant system: Occurrence, transmission, bacterial hosts, and human health risks. Ecotoxicology and Environmental Safety, 303, 118890. https://doi.org/10.1016/j.ecoenv.2025.118890
57. Liu, H., Zhang, Z., Li, X., Zhou, T., Wang, Z., Li, J., Li, Y., & Wang, Q. (2024). Temperature-phased anaerobic sludge digestion effectively removes antibiotic resistance genes in a full-scale wastewater treatment plant. The Science of the total environment, 924, 171555. https://doi.org/10.1016/j.scitotenv.2024.171555
58. Macesic, N., Uhlemann, A.C., & Peleg, A.Y. (2025). Multidrug-resistant Gram-negative bacterial infections. The Lancet, 405(10474), 257–272. https://doi.org/10.1016/S0140-6736(24)02081-6
59. Marano, R.B., Gupta, C.L., Cozer, T., Jurkevitch, E., & Cytryn, E. (2021). Hidden resistome: Enrichment reveals the presence of clinically relevant antibiotic resistance determinants in treated wastewater-irrigated soils. Environmental Science & Technology, 55(10), 6814–6827.
60. Markowicz, A., Bondarczuk, K., Cycoń, M., Sułowicz, S. (2021). Land application of sewage sludge: Response of soil microbial communities and potential spread of antibiotic resistance. Environmental Pollution, 271, 116317.
61. Marutescu, L.G., Jaga, M., Postolache, C., Barbuceanu, F., Milita, N.M., Romascu, L.M., Schmitt, H., de Roda Husman, A.M., Sefeedpari, P., Glaeser, S., Kämpfer, P., Boerlin, P., Topp, E., Gradisteanu Pircalabioru, G., Chifiriuc, M.C., & Popa, M. (2022). Insights into the impact of manure on the environmental antibiotic residues and resistance pool. Frontiers in microbiology, 13, 965132. https://doi.org/10.3389/fmicb.2022.965132
62. Massaccesi, L., Albini, E., Massacci, F.R., Giusepponi, D., Paoletti, F., Sdogati, S., Morena, F., Agnelli, A., Leccese, A., Magistrali, C.F., & Galarini, R. (2024). Impact of Soil Fertilization with Pig Slurry on Antibiotic Residues and Resistance Genes: A Longitudinal Study. Antibiotics (Basel, Switzerland), 13(6), 486. https://doi.org/10.3390/antibiotics13060486
63. Mbuthia, C.W., & Hoza, A.S. (2025). Wild birds as potential reservoirs of antimicrobial-resistant Escherichia coli: a systematic review. Frontiers in microbiology, 16, 1615826. https://doi.org/10.3389/fmicb.2025.1615826
64. Memesh, R., Yasir, M., Ledder, R.G., Zowawi, H., McBain, A.J., & Azhar, E.I. (2024). An update on the prevalence of colistin and carbapenem-resistant Gram-negative bacteria in aquaculture: an emerging threat to public health. Journal of applied microbiology, 135(1), lxad288. https://doi.org/10.1093/jambio/lxad288
65. Meradji, S., Basher, N.S., Sassi, A., Ibrahim, N.A., Idres, T., & Touati, A. (2025). The Role of Water as a Reservoir for Antibiotic-Resistant Bacteria. Antibiotics (Basel, Switzerland), 14(8), 763. https://doi.org/10.3390/antibiotics14080763
66. Mihrete, T.B., & Mihretu, F.B. (2025). Crop Diversification for Ensuring Sustainable Agriculture, Risk Management and Food Security. Global challenges (Hoboken, NJ), 9(2), 2400267. https://doi.org/10.1002/gch2.202400267
67. Mohammed, E.A.H., Kovács, B., Kuunya, R., Mustafa, E.O.A., Abbo, A.S.H., & Pál, K. (2025). Antibiotic Resistance in Aquaculture: Challenges, Trends Analysis, and Alternative Approaches. Antibiotics (Basel, Switzerland), 14(6), 598. https://doi.org/10.3390/antibiotics14060598

68. Murray, L.M., Hayes, A., Snape, J., Kasprzyk-Hordern, B., Gaze, W.H., & Murray, A.K. (2024). Co-selection for antibiotic resistance by environmental contaminants. npj antimicrobials and resistance, 2(1), 9. https://doi.org/10.1038/s44259-024-00026-7
69. Mustapha, A., Allamin, I.A., Ismail, H.Y., Eze, U.A., Ibrahim, M.M., Bello, R.Y., & Faruq, A.U. (2021). Environmental contribution to antimicrobial resistance: A largely ignored global health issue. The Proceedings of the Nigerian Academy of Science, 14(2), 61–80.
70. Ni, B., Xiao, L., Lin, D., Zhang, T. L., Zhang, Q., Liu, Y., Chen, Q., Zhu, D., Qian, H., Rillig, M.C., & Zhu, Y.G. (2025). Increasing pesticide diversity impairs soil microbial functions. Proceedings of the National Academy of Sciences of the United States of America, 122(2), e2419917122. https://doi.org/10.1073/pnas.2419917122
71. Nickodem, C.A., Tran, P.Q., Neeno-Eckwall, E., Congdon, A.G., Sanford, G.R., Silva, E.M., & Hite, J.L. (2025). Soil management strategies drive divergent impacts on pathogens and environmental resistomes. Scientific reports, 15(1), 43215. https://doi.org/10.1038/s41598-025-27157-9
72. Obijianya, C. C., Yakamercan, E., Karimi, M., Veluru, S., Simko, I., Eshkabilov, S., & Simsek, H. (2025). Agricultural Irrigation Using Treated Wastewater: Challenges and Opportunities. Water, 17 (14), 2083. https://doi.org/10.3390/w17142083
73. Olanrewaju, O.S., & Bezuidenhout, C.C. (2025). Harnessing beneficial bacteria to remediate antibiotic-polluted agricultural soils: integrating source diversity, bioavailability modulators, and ecological impacts. Frontiers in microbiology, 16, 1635233. https://doi.org/10.3389/fmicb.2025.1635233
74. Oliveira, M., Antunes, W., Mota, S., Madureira-Carvalho, Á., Dinis-Oliveira, R. J., & Dias da Silva, D. (2024). An overview of the recent advances in antimicrobial resistance. Microorganisms, 12(9), 1920. https://doi.org/10.3390/microorganisms12091920
75. Ortega-Pozo, J.L., Alcalá, F.J., Poyatos, J.M., & Martín-Pascual, J. (2022). Wastewater reuse for irrigation agriculture in Morocco: Influence of regulation on feasible implementation. Land, 11(12), 2312
76. Ouoba, L. I. I., Treilles, M., Noumedem, R. N. G., Keck, N., Kiptiness, J. K., Diallo, A. A., Mouillé, B., Gourlaouen, M., Kimani, T., Obonyo, M., Niang, M., Dsani, E., Latronico, F., Garcia, A. D., Kabali, E., Song, J., & Shamsuddin, M. (2025). Building capacities in Sub-Saharan African countries for antimicrobial resistance surveillance in the food and agriculture sectors using the FAO ATLASS tool. Frontiers in veterinary science, 12, 1607013. https://doi.org/10.3389/fvets.2025.1607013
77. Paidi MK, Satapute P, Haider MS, Udikeri S.S, Ramachandra YL. (2021). Mitigation of organophosphorus insecticides from environment: Residual detoxification by bioweapon catalytic scavengers. Environmental Research 200:111368.
78. Pandey, S., Doo, H., Keum, G. B., Kim, E.S., Kwak, J., Ryu, S., Choi, Y., Kang, J., Kim, S., Lee, N.R., Oh, K.K., Lee, J.H., & Kim, H.B. (2024). Antibiotic resistance in livestock, environment and humans: One Health perspective. Journal of animal science and technology, 66(2), 266–278. https://doi.org/10.5187/jast.2023.e129
79. Patra, M., & Dubey, S. K. (2024). Understanding the spread of antibiotic resistance in vegetables cultivated with sewage sludge: Implications for food safety and human health. Environmental Systems Research, 13, 21. https://doi.org/10.1186/s40068-024-00347-6
80. Patra, M., Pandey, B., & Dubey, S. K. (2024). Prevalence of diverse antimicrobial resistance genes and bacteria in sewage treatment plant-derived sludge environment. FEMS microbes, 5, xtae004. https://doi.org/10.1093/femsmc/xtae004
81. Patyra, E., Osiński, Z., & Kwiatek, K. (2024). Residues of veterinary antibiotics in solid natural and organic fertilizers-method development and sample analysis. Environmental science and pollution research international, 10.1007/s11356-024-33956-w. Advance online publication. https://doi.org/10.1007/s11356-024-33956-w
82. Pinho, J.O., Plácido, A.I., Monteiro, A., Nogueira, R., Oliveira, P.A., Coelho, A.C., Figueiras, A., Roque, F., & Herdeiro, M.T. (2025). Evaluation of guidelines on antimicrobials use in food-producing animals: a systematic review. One health outlook, 7(1), 39. https://doi.org/10.1186/s42522-025-00160-w
83. Punch, R., Azani, R., Ellison, C., Majury, A., Hynds, P.D., Payne, S.J., & Brown, R.S. (2025). The surveillance of antimicrobial resistance in wastewater from a One Health perspective: A global scoping and temporal review (2014–2024). One Health, 21, 101139.

https://doi.org/10.1016/j.onehlt.2025.101139

84. Roy, S., Dumont, M.G., Bradley, J.A., & Hernández, M. (2025). Microbial interactions between climate warming and antimicrobial resistance threaten soil carbon storage and global health. The ISME journal, 19(1), wraf220. https://doi.org/10.1093/ismejo/wraf220
85. Sassi, A., Basher, N.S., Kirat, H., Meradji, S., Ibrahim, N.A., Idres, T., & Touati, A. (2025). The Role of the Environment (Water, Air, Soil) in the Emergence and Dissemination of Antimicrobial Resistance: A One Health Perspective. Antibiotics (Basel, Switzerland), 14(8), 764. https://doi.org/10.3390/antibiotics14080764
86. Shafiq, M., Obinwanne Okoye, C., Nazar, M., Ali Khattak, W., & Algammal, A.M. (2025). Ecological consequences of antimicrobial residues and bioactive chemicals on antimicrobial resistance in agroecosystems. Journal of advanced research, 74, 99–120. https://doi.org/10.1016/j.jare.2024.10.013
87. Sharifmand, M., Sepehr, E., Rasouli-Sadaghiani, M., Asri-Rezaei, S., & Rengel, Z. (2024). Antibiotics pollutants in agricultural soil: Kinetic, sorption, and thermodynamic of ciprofloxacin. Heliyon, 10(18), e37035. https://doi.org/10.1016/j.heliyon.2024.e37035
88. Shawver, S., Ishii, S., Strickland, M. S., & Badgley, B. (2024). Soil type and moisture content alter soil microbial responses to manure from cattle administered antibiotics. Environmental science and pollution research international, 31(18), 27259–27272. https://doi.org/10.1007/s11356-024-32903-z
89. Shawver, S., Wepking, C., Ishii, S., Strickland, M.S., & Badgley, B. (2021). Application of manure from cattle administered antibiotics has sustained multi-year impacts on soil resistome and microbial community structure. Soil Biology and Biochemistry, 157, 108252. https://doi.org/10.1016/j.soilbio.2021.108252
90. Shen, L.Q., Lin, D., Ye, Y.Q., Liu, Y., Ni, B., Wu, D., Wang, L., & Zhu, D. (2025). Combined pesticide pollution enhances the dissemination of the phage-encoded antibiotic resistome in the soil under nitrogen deposition. Proceedings of the National Academy of Sciences of the United States of America, 122(40), e2516722122. https://doi.org/10.1073/pnas.2516722122
91. Slobodiuk, S., Niven, C., Arthur, G., Thakur, S., Ercumen, A. (2021). Does Irrigation with Treated and Untreated Wastewater Increase Antimicrobial Resistance in Soil and Water: A Systematic Review. International Journal of Environmental Research and Public Health, 18, 11046.
92. Sorinolu, A.J., Tyagi, N., Kumar, A., Munir, M. (2021). Antibiotic resistance development and human health risks during wastewater reuse and biosolids application in agriculture. Chemosphere, 265, 129032.
93. Ste Marie, J., Mays, C., Guo, B., Radniecki, T.S., Waite-Cusic, J., & Navab-Daneshmand, T. (2025). Longitudinal replicated metagenomic analysis of biosolids-amended soils reveals enrichment of ARGs, virulence factors, and ESKAPE pathogens. npj antimicrobials and resistance, 3(1), 96. https://doi.org/10.1038/s44259-025-00166-4
94. Tayeb, S. M., Alharbi, J. A., Alattas, B. B., Alotaibi, D. M., Althibaiti, N. M., Alharbi, J. F., SafirAldeen, A. E., Alqurashi, I. R., & Wali, S. M. (2025). Promising Future of Novel Beta-Lactam Antibiotics Against Bacterial Resistance. Drug design, development and therapy, 19, 9185–9197. https://doi.org/10.2147/DDDT.S551862
95. Totaro, V., Guido, G., Cotugno, S., De Vita, E., Asaduzzaman, M., Patti, G., Segala, F. V., Putoto, G., Frallonardo, L., Farkas, F. B., Lakatos, B., Veronese, N., Locantore, P., Di Gennaro, F., & Saracino, A. (2025). Antimicrobial Resistance in Sub-Saharan Africa: A Comprehensive Landscape Review. The American journal of tropical medicine and hygiene, 113(2), 253–263. https://doi.org/10.4269/ajtmh.25-0035
96. Trinchera, M., De Gaetano, S., Sole, E., Midiri, A., Silvestro, S., Mancuso, G., Catalano, T., & Biondo, C. (2025). Antimicrobials in livestock farming and resistance: Public health implications. Antibiotics, 14(6), 606. https://doi.org/10.3390/antibiotics14060606
97. Trotta, V., Baaloudj, O., & Brienza, M. (2024). Risks associated with wastewater reuse in agriculture: Investigating the effects of contaminants in soil, plants, and insects. Frontiers in Environmental Science, 12, 1358842. https://doi.org/10.3389/fenvs.2024.1358842
98. Truchado, P., Gil, M. I., López, C., Garre, A., López-Aragón, R. F., Böhme, K., & Allende, A. (2021). New standards at European Union level on water reuse for agricultural irrigation: Are the Spanish wastewater treatment plants ready to produce and distribute reclaimed water within the minimum quality requirements? International journal of food microbiology, 356, 109352.

https://doi.org/10.1016/j.ijfoodmicro.2021.109352

99. Van Laere, Y., Fraiture, M.A., Gobbo, A., De Keersmaecker, S.C.J., Marchal, K., Roosens, N.H.C., & Vanneste, K. (2025). Assessing the authenticity and purity of a commercial Bacillus thuringiensis bioinsecticide through whole genome sequencing and metagenomics approaches. Frontiers in microbiology, 16, 1532788. https://doi.org/10.3389/fmicb.2025.1532788
100. Wachino J. I. (2025). Horizontal Gene Transfer Systems for Spread of Antibiotic Resistance in Gram-Negative Bacteria. Microbiology and immunology, 69(7), 367–376. https://doi.org/10.1111/1348-0421.13222
101. Wallinga, D., Smit, L. A. M., Davis, M. F., Casey, J. A., & Nachman, K. E. (2022). A Review of the Effectiveness of Current US Policies on Antimicrobial Use in Meat and Poultry Production. Current environmental health reports, 9(2), 339–354. https://doi.org/10.1007/s40572-022-00351-x
102. Wang, G., Gao, X., Cai, Y., Li, G., Ma, R., & Yuan, J. (2024). Dynamics of antibiotic resistance genes during manure composting: Reduction in herbivores manure and accumulation in carnivores. Environment international, 190, 108900. https://doi.org/10.1016/j.envint.2024.108900
103. Wang, J., Wang, L., Zhu, L., Wang, J., & Xing, B. (2022). Antibiotic resistance in agricultural soils: Source, fate, mechanism and attenuation strategy. Critical Reviews in Environmental Science and Technology, 52(6), 847–889. https://doi.org/10.1080/10643389.2020.1835438
104. Wang, L., Gu, X., Hui, K., Yu, T., Yuan, Y., Chen, G., & Tan, W. (2025a). Interactions between antibiotic resistance genes and soil environmental factors: Coupling, antagonism, and synergism. Emerging Contaminants, 11(4), 100578. https://doi.org/10.1016/j.emcon.2025.100578
105. Wang, Y., Liu, Q., Ran, H., Peng, P., Wang, Y., Peng, G., Wu, Y., & Wen, X. (2025b). Residual ciprofloxacin in chicken manure inhibits methane production in an anaerobic digestion system. Poultry science, 104(1), 104539. https://doi.org/10.1016/j.psj.2024.104539
106. Wasan, H., Singh, D., Reeta, K.H., & Gupta, Y.K. (2023). Landscape of push funding in antibiotic research: Current status and way forward. Biology, 12(1), 101. https://doi.org/10.3390/biology12010101
107. Woolhouse M.E.J. (2024). One Health approaches to tackling antimicrobial resistance. Science in One Health, 3, 100082. https://doi.org/10.1016/j.soh.2024.100082
108. World Health Organization. (2023). Antimicrobial resistance (Fact sheet).
109. World Health Organization. (2024). Supporting countries with national action plan implementation and monitoring.
110. Wu, R., Fang, J., Yang, Y., Liu, L., Liu, H., & Du, S. (2025). Transmission pathways and intrinsic mechanisms of antibiotic resistance genes in soil-plant systems: A review. Environmental Technology & Innovation, 37, 103985. https://doi.org/10.1016/j.eti.2024.103985
111. Xie, Y., Srivastava, I. M., Jing, F., Ma, C., Wu, X., Chen, Y., Du, Y., Low, X. C., Ping, Y., Pan, J., Gupta, A., Graves, N., & Mo, Y. (2025). One health perspective of antibiotic resistance in enterobacterales from Southeast Asia: a systematic review and meta-analysis. Scientific reports, 16(1), 1694. https://doi.org/10.1038/s41598-025-31195-8
112. Yordanova, R., Platikanova, M., & Hristova, P. (2024). The use of antibiotics in food animals: A threat to human health. Journal of IMAB – Annual Proceeding (Scientific Papers), 30(2), 5495–5499. https://doi.org/10.5272/jimab.2024302
113. Zalewska, M., Bła˙zejewska, A., Czapko, A., Popowska, M. (2021). Antibiotics and antibiotic resistance genes in animal manure–consequences of its application in agriculture. Frontiers in Microbiology, 12, 610656.
114. Zhang, X., Li, X., Wang, Y., Zhang, T., & Li, A. (2022). Occurrence and distribution of antibiotic resistance genes in reclaimed water irrigation systems and their potential risks. Journal of Hazardous Materials, 424, 127265.
115. Zhang, Y., Cheng, D., Zhang, Y., Xie, J., Xiong, H., Wan, Y. (2021). Soil type shapes the antibiotic resistome profiles of long-term manured soil. Science of the Total Environment, 786, 147361.
116. Zhang, Y., Hao, X., Thomas, B. W., McAllister, T.A., Workentine, M., Jin, L., Shi, X., & Alexander, T.W. (2023). Soil antibiotic resistance genes accumulate at different rates over four decades of manure application. Journal of Hazardous Materials, 443, 130136. https://doi.org/10.1016/j.jhazmat.2022.130136

117. Zhao, B., Zhang, R., Jin, B., Yu, Z., Wen, W., Zhao, T., Quan, Y., & Zhou, J. (2025a). Sludge water: a potential pathway for the spread of antibiotic resistance and pathogenic bacteria from hospitals to the environment. Frontiers in microbiology, 16, 1492128. https://doi.org/10.3389/fmicb.2025.1492128
118. Zhao, P., Ma, M., Hu, Y., Wu, W., & Xiao, J. (2022). Comparison of international standards for irrigation with reclaimed water. Agricultural Water Management, 274, 107974.
119. Zhao, Y., Li, L., Huang, Y. (2025b). Global soil antibiotic resistance genes are associated with increasing risk and connectivity to human resistome. Nature Communications, 16, 7141. https://doi.org/10.1038/s41467-025-61606-3
120. Zhou, G., Wang, Q., Wang, Y., Wen, X., Peng, H., Peng, R., Shi, Q., Xie, X., & Li, L. (2023). Outer Membrane Porins Contribute to Antimicrobial Resistance in Gram-Negative Bacteria. Microorganisms, 11(7), 1690. https://doi.org/10.3390/microorganisms11071690