

Antimicrobial Resistance in Agricultural Soils: Environmental Pathways, Drivers, Risks, and Mitigation Strategies—A Review

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ABSTRACT

Antimicrobial resistance (AMR) is increasingly recognized as a critical environmental, medical, and veterinary concern. Agricultural soils play a pivotal role in this dynamic, receiving antibiotics, antibiotic-resistant bacteria (ARB), and antibiotic-resistance genes (ARGs) via livestock manure, wastewater irrigation, sewage sludge, contaminated fertilizers, and agricultural runoff. While resistance genes occur naturally in soil microbial communities, modern agricultural practices accelerate their abundance, persistence, mobility, and potential transfer to human and animal pathogens. This integrative review synthesizes peer-reviewed literature published primarily between 2010 and 2026 to examine the sources, environmental behavior, drivers, and mitigation strategies of soil-based AMR. Findings indicate that repeated application of contaminated manure substantially increases ARG levels, while untreated wastewater irrigation consistently drives ARB and ARG introduction into cropland. Conversely, the impact of treated wastewater varies depending on treatment efficiency, irrigation intensity, and soil characteristics. Horizontal gene transfer—driven by mobile genetic elements like plasmids and integrons—serves as the main vehicle transferring resistance between environmental organisms and clinical pathogens. Mitigation strategies including composting, anaerobic digestion, advanced wastewater treatment, antimicrobial stewardship, and biochar amendments show promise, though their efficacy depends heavily on environmental context. Ultimately, agricultural soil must be addressed as an active, dynamic component within the One Health AMR framework rather than a passive reservoir. Future efforts should prioritize standardized environmental surveillance, quantitative risk assessment, longitudinal field studies, and integrated interventions that combine reduced antimicrobial use with targeted pollution control and sustainable soil management.

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INTRODUCTION

Antimicrobial resistance (AMR) occurs when microorganisms develop the capacity to survive exposure to antimicrobial agents that would normally inhibit or kill them. Although antimicrobial resistance is often discussed primarily in relation to clinical infections, resistance is fundamentally an ecological and evolutionary phenomenon that occurs across human, animal, and environmental systems. Resistance genes existed in microbial communities long before the modern antibiotic era. For example, metagenomic evidence from ancient permafrost

demonstrated resistance genes associated with β -lactam, tetracycline, and glycopeptide antibiotics in microbial communities approximately 30,000 years old (D'Costa et al., 2011). Thus, human use of antibiotics did not create resistance itself; rather, contemporary antimicrobial use and environmental pollution can strongly alter the abundance, distribution, selection, and dissemination of existing and newly evolved resistance determinants.

The environmental dimension of AMR has gained increasing scientific attention because microorganisms and resistance genes can circulate among humans, animals, plants, soil, water, and other environmental compartments. Larsson and Flach (2022) emphasized that the environment can function simultaneously as a reservoir, evolutionary arena, transport medium, and transmission pathway for antibiotic resistance. The environmental contribution to AMR is therefore not limited to the passive accumulation of resistant organisms; environmental conditions can influence selection, persistence, horizontal gene transfer, and movement of resistance determinants between microbial populations.

Agricultural soils are particularly important in this context. Soil receives substantial quantities of organic amendments and irrigation water, making it an interface where human, animal, plant, and environmental microbial communities interact. Livestock manure may contain antibiotic residues, ARB, and ARGs resulting from antimicrobial use in animal production. When manure is applied to agricultural land, these contaminants can enter soil microbial communities and potentially persist or disseminate. A meta-analysis of 94 studies found that application of antibiotic-contaminated manure increased total ARG abundance by an average of 591% and mobile genetic element abundance by 351% relative to unamended soils (Zhang et al., 2022).

Wastewater represents another important pathway. In regions affected by water scarcity, wastewater is increasingly reused for agricultural irrigation. This practice can provide water and nutrients but may simultaneously introduce resistant bacteria, resistance genes, antibiotics, metals, and other contaminants into agricultural ecosystems. A systematic review of 26 studies found consistent evidence that untreated wastewater irrigation increased ARB and ARGs in agricultural soils, whereas evidence concerning treated wastewater was substantially more heterogeneous (Slobodiuk et al., 2021).

The soil-plant interface is especially significant because crops can provide a potential bridge between environmental resistance and human exposure. ARGs and resistant bacteria may occur in the rhizosphere and on plant surfaces, and some evidence indicates that agricultural practices can facilitate the movement of resistance determinants within soil-plant systems (Xiao et al., 2023). This raises questions concerning the potential contribution of agricultural environments to food-associated exposure to antimicrobial resistance.

At the molecular level, the problem is further complicated by horizontal gene transfer. Resistance genes can be carried by plasmids, transposons, integrons, and other mobile genetic elements that facilitate their movement between bacterial cells. Research has demonstrated substantial overlap between resistance genes found in soil bacteria and those present in human pathogens, providing evidence that environmental resistomes can contain genes with clinical relevance (Forsberg et al., 2012).

The environmental dimension of AMR has consequently become a central component of the One Health framework. The United Nations Environment Program (UNEP) identifies agriculture, pharmaceutical manufacturing, healthcare, and poorly managed sanitation and wastewater systems as major environmental sources associated with AMR. The 2026 Quadripartite biennial report from the World Health Organization (WHO), Food and Agriculture Organization (FAO), UNEP, and World Organization for Animal Health (WOAH) likewise emphasizes stronger integration of environmental considerations into national AMR responses.

Despite the growing literature, important uncertainties remain. Studies differ considerably in the ARGs examined, analytical methods used, soil characteristics, antimicrobial compounds considered, experimental duration, and definitions of environmental risk. Moreover, the detection of an ARG in soil does not necessarily demonstrate that it will reach a human pathogen or cause a clinical infection. Environmental risk depends on multiple bottlenecks, including gene mobility, host compatibility, ecological selection, transmission opportunities, and the eventual exposure of susceptible hosts (Martínez et al., 2015).

Therefore, a synthesis that integrates the major environmental pathways, mechanisms, risks, and mitigation strategies is needed.

Accordingly, this review addresses the following research questions:

1. What are the major sources and environmental pathways through which antimicrobial resistance enters agricultural soils?
2. What biological and environmental mechanisms contribute to the persistence and dissemination of ARB and ARGs in agricultural soils?
3. How can agricultural soils and soil-plant systems contribute to the wider environmental circulation of antimicrobial resistance?
4. What mitigation strategies have demonstrated potential for reducing antimicrobial residues, ARB, and ARGs in agricultural systems?
5. What major scientific gaps should be addressed to improve environmental AMR surveillance and risk management?

RESEARCH METHODOLOGY

Research Design

This study employed an integrative literature review design. An integrative review was selected because the objective was not to calculate a single pooled effect size but to synthesize findings from different types of evidence, including experimental studies, field studies, systematic reviews, meta-analyses, environmental microbiology studies, and reports from international organizations.

The review focused on the environmental dimensions of AMR associated with agricultural soils and the soil-plant system. Particular attention was given to antibiotic residues, ARB, ARGs, mobile genetic elements (MGEs), horizontal gene transfer, manure application,

wastewater irrigation, sewage sludge, composting, anaerobic digestion, biochar, and antimicrobial stewardship.

Relevant literature was identified through searches of major scientific literature sources and publisher databases, including PubMed, ScienceDirect, Nature Portfolio, and multidisciplinary academic search platforms. Additional authoritative evidence was obtained from the WHO, FAO, UNEP, and WOAHA.

Search terms were combined using Boolean operators and included:

- “antimicrobial resistance” AND agricultural soil;
- “antibiotic resistance genes” AND soil;
- “antibiotic resistance” AND manure;
- “antibiotic resistance genes” AND wastewater irrigation;
- “antimicrobial resistance” AND crops;
- “soil resistome” AND agriculture;
- “horizontal gene transfer” AND soil;
- “ARGs” AND composting;
- “biochar” AND antibiotic resistance genes.

The literature search emphasized publications from 2010 to 2026, while earlier foundational studies were retained when necessary to explain the biological origins or mechanisms of environmental antibiotic resistance.

Inclusion and Exclusion Criteria

Studies were included when they:

1. examined antimicrobial or antibiotic resistance in soil, agricultural environments, plants, manure, wastewater, sludge, or related environmental compartments;
2. investigated ARGs, ARB, antimicrobial residues, resistomes, or mobile genetic elements;
3. addressed environmental pathways, mechanisms, ecological effects, or mitigation;
4. were published in peer-reviewed journals or by authoritative scientific organizations; and
5. provided sufficient methodological or conceptual information to support interpretation.

Studies focusing exclusively on clinical treatment outcomes without an environmental component were excluded. Duplicate publications, non-scientific opinion pieces, and sources without sufficient methodological or evidentiary information were also excluded.

Data Analysis

The selected literature was organized thematically into five major categories:

1. Sources and pathways of environmental contamination;
2. Mechanisms of resistance persistence and dissemination;
3. Soil-plant and food-chain implications;
4. Environmental and ecological risk; and
5. Mitigation and management strategies.

Findings were compared qualitatively, with attention to areas of agreement, conflicting evidence, methodological limitations, and knowledge gaps.

RESULTS

Agricultural Soil Is Both a Reservoir and an Active Ecological Compartment

The literature indicates that agricultural soil should not be considered simply a passive repository for resistance genes. Soil contains highly diverse microbial communities capable of producing, acquiring, maintaining, and exchanging resistance determinants. Natural soil resistomes contain numerous resistance genes, some of which are evolutionarily ancient (Allen et al., 2010; D'Costa et al., 2011).

However, anthropogenic activities can modify the structure and abundance of environmental resistomes. Forsberg et al. (2012) identified resistance genes in soil bacteria that were highly similar to resistance determinants found in human pathogens. The presence of such genes does not mean that all environmental ARGs represent an immediate public-health threat, but it demonstrates that soil microbial communities can contain resistance determinants with the potential for transfer between bacterial populations.

The environmental risk therefore depends not only on the abundance of ARGs but also on their genetic context, host organisms, mobility, expression, and proximity to pathogenic bacteria. This distinction is important because the mere detection of a resistance gene cannot be equated with a clinically meaningful resistance event.

Manure Application Is a Major Agricultural Pathway

Livestock production is a major source of antimicrobial residues and resistance determinants entering agricultural environments. Animals receiving antibiotics may excrete unmetabolized antimicrobial compounds as well as resistant bacteria and ARGs. Manure subsequently becomes an important vector for transferring these contaminants to soil.

Zhang et al. (2022) conducted a meta-analysis of 94 studies involving 640 observations and reported a mean increase of 591% in total ARG abundance following application of antibiotic-contaminated manure. Mobile genetic elements increased by approximately 351%. Particularly large increases were observed for sulfonamide, aminoglycoside, and tetracycline resistance genes.

These findings suggest that manure application can alter the selective environment of agricultural soils. Antibiotic residues may exert selection pressure, while resistant microorganisms introduced through manure may compete with or exchange genes with indigenous soil bacteria.

However, the effect is not uniform. Soil pH, organic carbon, texture, temperature, moisture, microbial community composition, manure characteristics, antibiotic concentration, and application history can influence the persistence and behavior of resistance determinants (Zhang et al., 2022).

Wastewater Irrigation Creates an Important Soil-Water Interface

Wastewater reuse is increasingly relevant in water-scarce agricultural regions. From an agricultural perspective, treated wastewater may provide an alternative source of irrigation water and nutrients. From an environmental microbiology perspective, however, wastewater can also transport antibiotics, ARB, ARGs, pathogens, and other contaminants into agricultural fields.

The strongest evidence concerns untreated wastewater. Slobodiuk et al. (2021) reviewed 26 studies and found that nine of ten studies with appropriate comparison groups reported increased ARB or ARG abundance in soils irrigated with untreated wastewater. Evidence from treated wastewater was more variable: six studies reported positive associations, while six reported mixed or negative findings.

This variation indicates that “treated wastewater” should not be treated as a single environmental category. Treatment technology, treatment intensity, hydraulic conditions, microbial removal efficiency, antibiotic degradation, sludge management, and post-treatment contamination can all affect the resulting AMR profile.

Recent evidence reinforces this concern. Chen et al. (2024), using metagenomic analysis of paddy soils, reported that long-term irrigation with municipal-treated wastewater increased the number and abundance of ARGs, although no detrimental effects on rice growth and grain quality were detected in the studied system.

Thus, agricultural wastewater reuse may be feasible under controlled conditions, but its AMR implications require site-specific monitoring rather than assumptions that conventional treatment completely eliminates resistance-related risks.

Soil-Plant Transfer Represents a Potential Exposure Pathway

The rhizosphere provides a biologically active interface between soil microorganisms and plants. Roots release organic compounds that influence microbial growth and community composition, while soil microorganisms can colonize plant surfaces and internal tissues.

Xiao et al. (2023) concluded that agricultural practices can contribute to the dissemination of ARGs in soil-plant systems and identified multiple factors influencing the movement and distribution of resistance determinants. These include antibiotic residues, soil properties, plant species, microbial community structure, and environmental conditions.

The potential transfer of ARGs or ARB to crops is particularly relevant for vegetables consumed raw or minimally processed. However, a critical distinction must be made between detection and demonstrated human-health risk. Detection of an ARG on a crop does not establish that the gene will enter a human pathogen or that it will be expressed in a clinically relevant organism.

Nevertheless, agricultural crops can form part of the environmental pathway connecting soil and human populations, supporting the need for integrated monitoring.

Horizontal Gene Transfer Is a Central Mechanism

The environmental dissemination of resistance is not driven solely by the movement of resistant bacteria. ARGs can move horizontally among microorganisms through transformation, transduction, and conjugation.

Mobile genetic elements are especially important because plasmids, transposons, and integrons can facilitate movement of resistance determinants between bacteria. Castañeda-Barba et al. (2024) identified plasmids as a major molecular mechanism connecting resistance reservoirs across human, animal, and environmental habitats.

Sub-inhibitory concentrations of antibiotics and other pollutants can potentially modify bacterial physiology and influence horizontal gene transfer. Larsson and Flach (2022) emphasized that environmental antibiotic pollution can contribute not only to persistence and transmission but also to evolutionary processes associated with resistance.

Co-selection represents another important mechanism. Metals, biocides, and antibiotics may interact because resistance determinants can be genetically linked or because different selective pressures can favor bacteria carrying multiple resistance traits. Agricultural soils receiving repeated inputs of manure, wastewater, pesticides, metals, and other chemicals may therefore create complex selective environments.

Environmental Conditions Determine Resistance Persistence

The fate of antibiotics and ARGs in soil depends heavily on environmental conditions.

Important factors include:

- soil pH;
- organic carbon;
- clay and silt content;
- moisture;
- temperature;
- redox conditions;
- microbial community composition;
- antibiotic physicochemical properties;
- manure characteristics;
- frequency of amendment application; and
- interactions with metals and other contaminants.

Antibiotics may undergo adsorption, degradation, transformation, or sequestration in soil. ARGs may persist within viable bacterial cells or extracellular DNA. Their persistence therefore cannot be predicted solely from the persistence of the corresponding antibiotic.

Zhang et al. (2022) found significant relationships between ARG abundance and several environmental variables, including soil properties, antibiotic concentrations, temperature, and mobile genetic elements.

This finding reinforces the need to consider AMR as a dynamic ecological process rather than as a simple contamination problem.

Composting and Anaerobic Digestion Can Reduce Resistance but Do Not Guarantee Elimination

Treatment of manure before agricultural application is a potentially important control point.

Aerobic composting can reduce antibiotic residues and ARGs through heat generation, microbial succession, degradation of antibiotics, and changes in microbial community structure. Liu et al. (2021) emphasized that the fate of ARGs during composting depends on temperature, moisture, aeration, substrate composition, microbial succession, and other operating conditions.

Similarly, Allegrini and Zabaloy (2024) reviewed evidence concerning anaerobic digestion and concluded that anaerobic digestion can significantly reduce ARG loads under appropriate conditions, although treatment outcomes vary and complete elimination cannot be assumed.

This finding is important for agricultural management because poorly controlled treatment may merely redistribute resistance determinants rather than eliminate them.

Sewage Sludge Represents Another Potential Source

Wastewater treatment concentrates microorganisms and contaminants in sewage sludge. Consequently, sludge can contain antibiotics, ARB, ARGs, and other pollutants.

Wang et al. (2023) reviewed treatment and disposal processes for sewage sludge and concluded that anaerobic digestion, composting, drying, pyrolysis, constructed wetlands, and other approaches can influence the fate of resistance determinants, but their effectiveness differs among processes and operating conditions. The authors also identified risk assessment of sludge-amended soils as an important research gap.

This is particularly relevant where treated sludge is used as a soil amendment. Resource recovery may provide agricultural benefits, but the environmental safety of such practices requires resistance-specific assessment.

Biochar Is an Emerging Mitigation Strategy

Biochar has attracted attention as a soil amendment capable of influencing contaminant mobility, microbial communities, and the environmental behavior of antibiotics and ARGs.

A 2026 meta-analysis by Wu et al. synthesized evidence across soil, plant, and manure systems and reported reductions of antibiotic concentrations of approximately 35.0% in soil, 59.1% in plants, and 47.9% in manure following biochar application. The study also reported reductions in ARG abundance, although the magnitude varied among environmental compartments and experimental conditions.

Potential mechanisms include adsorption of antimicrobial compounds, modification of soil physicochemical properties, changes in microbial community composition, and suppression of horizontal gene transfer. However, biochar should not yet be considered a universally applicable solution. Its effectiveness depends on feedstock, pyrolysis conditions, biochar properties, soil characteristics, contaminant type, application rate, and environmental aging.

DISCUSSION

The findings demonstrate that agricultural soils occupy a strategically important position in the environmental AMR network. Three conclusions are particularly important.

First, AMR in agricultural soil is a pollution and ecological-management problem as well as a microbiological problem. Agricultural practices can introduce antibiotics, resistant bacteria, and ARGs into soils through multiple pathways. Manure and wastewater are particularly important because they simultaneously introduce microbial populations and selective chemical pressures.

Second, the presence of an ARG should not automatically be interpreted as equivalent to clinical risk. Environmental resistomes are naturally diverse, and many resistance genes may have little probability of reaching human pathogens. Risk is better conceptualized as a sequence of events:

source → environmental persistence → selection → gene mobility → host acquisition → pathogen acquisition → human/animal exposure → clinically relevant infection.

At every stage, biological and ecological bottlenecks can reduce the probability of a clinically important outcome. Martínez et al. (2015) therefore argued that environmental resistance genes should be evaluated according to their likelihood of entering pathogens and their potential consequences rather than simply according to their abundance.

Third, agricultural AMR management should prioritize prevention at source rather than relying exclusively on downstream remediation. If antimicrobial use in livestock and crop production generates unnecessary environmental contamination, end-of-pipe treatment alone is unlikely to provide a complete solution.

The One Health Framework Is particularly appropriate because agricultural resistance is connected to veterinary antimicrobial use, human sanitation, wastewater management, food production, environmental microbiology, and public health. Recent international policy documents increasingly recognize this interconnectedness. The 2026 Quadripartite report identifies stronger surveillance, multisectoral coordination, investment, and environmental integration as continuing priorities in global AMR action.

Implications for Agricultural Management

The evidence supports a hierarchy of interventions:

- The first intervention should be reducing unnecessary antimicrobial exposure in livestock, aquaculture, and crop production. Responsible antimicrobial stewardship can decrease both direct antimicrobial pollution and the selective pressure favoring resistant microorganisms.
- Recent One Health stewardship literature emphasizes that antimicrobial stewardship must extend beyond clinical medicine to include veterinary and environmental systems (James et al., 2026).
- Manure should not automatically be regarded as a harmless organic fertilizer. Where animals have received antimicrobials, manure can represent a concentrated source of resistance determinants.
- Appropriate composting, anaerobic digestion, storage, and treatment should therefore be incorporated into agricultural waste-management systems.
- Wastewater reuse should be accompanied by AMR-sensitive treatment and monitoring. Conventional wastewater treatment can reduce microbial loads but may not completely eliminate ARGs or resistant organisms. The appropriate level of treatment should therefore depend on the intended use and local environmental conditions.

Environmental surveillance should move beyond measuring only antibiotic concentrations. Monitoring should include:

- clinically important ARGs;
- mobile genetic elements;
- resistant bacterial hosts;
- antimicrobial residues;
- relevant pathogens;
- environmental parameters; and
- potential exposure pathways.

Metagenomic and quantitative PCR approaches provide opportunities for high-resolution surveillance, but standardization is necessary before data can be compared reliably across countries and environments.

Directions for Future Research

- Different studies use different ARG targets, normalization methods, sampling designs, and analytical platforms. Consequently, comparisons across studies are difficult. Future research should establish standardized indicators that combine ARG abundance, mobility, host association, and clinically relevant resistance phenotypes.
- Many experimental studies are short-term and laboratory-based. Agricultural soils, however, are exposed repeatedly over years or decades. Longitudinal field studies are

needed to determine whether ARGs accumulate, stabilize, or decline following repeated manure or wastewater application.

- The detection of resistance genes does not necessarily establish human-health risk. Future studies should connect environmental concentrations with exposure pathways and probability of transmission to clinically relevant organisms.
- The environmental AMR literature is concentrated in particular regions, especially China, Europe, and North America. Agricultural systems in low- and middle-income countries are comparatively underrepresented despite potentially important exposure pathways involving untreated wastewater, limited sanitation, intensive livestock production, and informal agricultural practices.

Temperature, precipitation, flooding, drought, and extreme weather events can alter microbial communities and pollutant transport. Climate-related changes may therefore modify AMR dissemination through agricultural landscapes. UNEP has emphasized that climate and environmental degradation can interact with the development and spread of AMR. Future research should investigate AMR under realistic climate scenarios rather than treating environmental conditions as static.

CONCLUSION

Antimicrobial resistance in agricultural soils represents an important and increasingly recognized environmental challenge. The evidence reviewed in this study demonstrates that agricultural soils can function simultaneously as reservoirs, selection environments, and transmission interfaces for antibiotic resistance.

Manure application, wastewater irrigation, sewage sludge, agricultural runoff, and other anthropogenic inputs can introduce antibiotics, ARB, and ARGs into soil. Once introduced, resistance determinants may persist or disseminate depending on soil properties, microbial community structure, environmental conditions, antimicrobial concentrations, and the presence of mobile genetic elements. Horizontal gene transfer provides an important mechanism through which resistance determinants can move between environmental microorganisms and potentially clinically relevant bacteria.

The evidence is strongest for the association between untreated wastewater or antibiotic-contaminated manure and increased environmental resistance. However, substantial uncertainty remains concerning the clinical significance of many environmental ARGs and the extent to which environmental reservoirs contribute directly to human infections. Consequently, environmental AMR research should move from simple detection and abundance measurements toward quantitative assessments of mobility, host association, transmission probability, and human or animal exposure.

Mitigation should follow a prevention-oriented hierarchy. Responsible antimicrobial use, improved manure management, effective wastewater treatment, controlled sludge application,

environmental surveillance, and targeted soil-management practices should be implemented together. Emerging technologies such as biochar show considerable promise, but they should complement rather than replace source control and antimicrobial stewardship.

Ultimately, agricultural soil should be incorporated explicitly into AMR management under a One Health framework. Protecting the effectiveness of existing and future antimicrobials requires not only responsible use in hospitals and farms but also control of the environmental pathways through which resistance can persist and circulate. Future research should prioritize standardized surveillance, long-term field experiments, quantitative environmental risk assessment, and integrated interventions that connect agricultural productivity with environmental and public-health protection.

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