Environmental Dissemination of Antimicrobial Resistance in Rice Paddy Ecosystems Irrigated with Reclaimed Water

Afia Ibnath[1*], Mst. Abida Sultana[2], Ahsan Habib [3]

Abstract

Antimicrobial resistance (AMR) is often framed as a clinical crisis, yet increasingly, it seems difficult to ignore its environmental dimensions—particularly within agricultural systems that sit at the intersection of human activity and natural ecosystems. Rice paddies, with their water-intensive design and microbially rich environments, present a unique and somewhat underexplored setting where resistance may persist, evolve, and potentially circulate beyond field boundaries. This review attempts to bring together what is known—while also acknowledging what remains uncertain—about the dissemination of antibiotic resistance genes (ARGs) and antibiotic-resistant bacteria (ARB) in rice ecosystems irrigated with reclaimed wastewater. Drawing on recent studies, the evidence suggests that wastewater reuse does not simply introduce contaminants; it reshapes microbial communities and resistance dynamics in ways that are often gradual, context-dependent, and occasionally contradictory. The rhizosphere emerges as a particularly active zone, where dense microbial interactions may facilitate horizontal gene transfer, even as plants appear to exert selective filtering mechanisms. At the same time, agricultural practices—fertilization, compost application, and water management—seem to modulate these processes in complex ways.What becomes increasingly clear is that AMR in such systems cannot be understood in isolation. It is embedded within a broader soil–plant–water continuum, with implications that extend toward food safety, ecosystem stability, and public health. This review therefore highlights the need for integrated, One Health–oriented strategies to better understand and manage resistance in reclaimed water–irrigated agroecosystems.

Keywords

Antimicrobial resistance; Rice paddy ecosystems; Reclaimed wastewater; Antibiotic resistance genes; Soil microbiome; Rhizosphere dynamics; One Health

1. Introduction

The rapid escalation of antimicrobial resistance (AMR) is, increasingly, difficult to frame as anything less than a defining public health crisis of our time. Estimates suggesting up to 10 million annual deaths by 2050—alongside an economic burden approaching USD 100 trillion—are often cited, perhaps to the point of familiarity, yet they still convey an unsettling reality: the trajectory is not hypothetical; it is already unfolding (Ahmad et al., 2026; Zhu et al., 2019). What is becoming

Significance | Reveals how reclaimed water reshapes soil resistomes, linking agriculture, microbiomes, and public health through a One Health systems perspective.

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equally clear, however, is that the traditional clinical framing of AMR—focused primarily on hospitals and antibiotic misuse in medicine—captures only part of a far more complex system. There is, increasingly, a shift toward a broader ecological understanding, one that recognizes AMR as a phenomenon deeply embedded within interconnected human, animal, and environmental domains. This "One Health" perspective, now widely endorsed, positions environmental systems not merely as passive recipients but as active reservoirs and transmission pathways for antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs) (EFSA Panel on Biological Hazards, 2021; Wu et al., 2025).

Within this environmental context, agricultural systems—particularly those reliant on intensive irrigation—have emerged as critical interfaces where resistance can accumulate, persist, and potentially re-enter human exposure pathways. Among these systems, rice (*Oryza sativa* L.) cultivation stands out, not only because it feeds more than half of the global population but also because of its inherently water-intensive nature. Rice paddies are, in essence, engineered wetland ecosystems, characterized by prolonged flooding, fluctuating redox conditions, and complex microbial interactions. These unique features, while essential for crop productivity, may also inadvertently create conditions conducive to the persistence and exchange of resistance determinants (Duarte et al., 2022; Ondon et al., 2021).

At the same time, global freshwater scarcity—driven by climate variability, population growth, and urban expansion—has accelerated the adoption of reclaimed wastewater (RWW) as an alternative irrigation source. From a sustainability standpoint, this transition is both logical and necessary. Yet, it introduces a set of complications that are only now being fully appreciated. Conventional wastewater treatment plants (WWTPs), despite their effectiveness in removing organic pollutants and pathogens, were not originally designed to eliminate emerging contaminants such as antibiotics, ARB, or ARGs. As a result, treated effluents often retain a complex mixture of resistance determinants that are continuously discharged into receiving environments, including agricultural soils (Fahrenfeld et al., 2013; Phan et al., 2024).

In fact, WWTPs have been described—perhaps somewhat provocatively—as "genetic reactors," environments where dense microbial communities are exposed to sub-inhibitory concentrations of antibiotics, heavy metals, and other stressors. These conditions can promote horizontal gene transfer (HGT) through mobile genetic elements (MGEs) such as plasmids, integrons, and transposons (Gatica & Cytryn, 2013; Wang et al., 2014). Even after advanced treatment processes, ARGs associated with resistance to sulfonamides, tetracyclines, and macrolides frequently persist in effluents (Wu et al., 2025). When such water is used for irrigation, it introduces these genetic elements into the soil–plant continuum, raising questions about their fate, stability, and ecological impact.

Yet, the extent to which wastewater-derived resistance persists in agricultural soils is not entirely straightforward. Some studies suggest that introduced ARB may struggle to compete with native microbial communities, leading to limited long-term survival. Others, however, report substantial enrichment of the soil resistome under prolonged irrigation, in some cases increasing ARG abundance by several orders of magnitude (Williams-Nguyen et al., 2016; Phan et al., 2024). These discrepancies may reflect differences in soil type, irrigation regimes, climate conditions, and agricultural management practices, highlighting the need for context-specific investigations.

One particularly important interface within this system is the rhizosphere—the narrow region of soil influenced by plant roots. This zone is often described as a "hotspot" for microbial activity, driven by root exudates that provide carbon-rich substrates for microbial growth. It is also, crucially, a hotspot for gene exchange. Enhanced microbial density and metabolic activity can facilitate HGT, potentially accelerating the spread of ARGs within root-associated communities (Della-Negra et al., 2026; Xu et al., 2024). Evidence suggests that rice roots and surrounding soils frequently harbor detectable ARGs, while above-ground tissues, including leaves, may also contain measurable levels. Interestingly, the transfer of ARGs into edible grains appears more limited, and in some cases negligible, although the mechanisms governing this selective translocation remain poorly understood (Xu et al., 2024).

It is also important to recognize that antibiotic residues themselves are not the sole drivers of resistance dynamics in these environments. Co-selection mechanisms, particularly those involving heavy metals such as copper and zinc, play a significant role. Resistance genes for metals and antibiotics are often co-located on the same

MGEs, meaning that exposure to one selective pressure can indirectly maintain or enrich resistance to another (Rad et al., 2022; Zhu et al., 2019). In agricultural settings, this is further complicated by the widespread use of fertilizers and organic amendments. For example, nitrogen fertilization strategies have been shown to influence ARG abundance in reclaimed water–irrigated soils, with some studies indicating that nitrogen alone may reduce ARG levels more effectively than phosphorus or potassium inputs (Cui et al., 2022).

More subtly, there is emerging evidence that environmentally relevant concentrations of antibiotics may not uniformly suppress microbial processes. Instead, they can induce hormetic responses, where low concentrations stimulate microbial activity, including genes involved in nitrogen cycling such as nitrification and denitrification pathways (Yan et al., 2026). This suggests that the ecological impact of antibiotics in soil systems is not purely inhibitory but can involve complex, and sometimes counterintuitive, interactions.

From a public health perspective, the implications of these processes extend beyond the field. Human exposure to resistance determinants originating in rice paddy ecosystems can occur through multiple routes. Farmworkers, for instance, may be exposed through direct contact with contaminated water or soil, often over prolonged periods. Consumers may encounter ARGs indirectly through food consumption, although cooking practices may reduce viable ARB loads. Still, the potential for ARGs to integrate into the human gut microbiome—via horizontal gene transfer—remains an area of ongoing investigation (Kusi et al., 2022; Jadeja & Worrich, 2022).

Moreover, environmental dissemination pathways are not limited to direct human contact. Wildlife, insects, and even windborne dust can act as vectors, transporting resistance elements across spatial boundaries. This raises broader concerns about the mobility of AMR within agroecosystems and its capacity to transcend local environments (Selvarajan et al., 2023). In this sense, rice paddies irrigated with reclaimed water may serve not only as reservoirs but also as nodes within a larger network of resistance dissemination.

Taken together, these considerations underscore a central challenge: understanding AMR in rice paddy ecosystems requires an integrated, systems-level approach. It is not enough to quantify ARG abundance at a single point in time; rather, it is necessary to examine the interactions among water quality, soil processes, plant physiology, and agricultural management practices. Only by doing so can we begin to disentangle the pathways through which resistance emerges, persists, and potentially impacts human health.

This study, therefore, seeks to explore the environmental dissemination of antimicrobial resistance within rice paddy ecosystems irrigated with reclaimed water, focusing on the soil–plant–water continuum and the underlying mechanisms that govern resistance dynamics. In doing so, it aims to contribute to a more nuanced understanding of how sustainable water reuse practices intersect with the global challenge of antimicrobial resistance, an issue that, while complex, cannot be ignored.

2. Methods

2.1 Study Design and Conceptual Framework

This study adopts a narrative review approach to synthesize current knowledge on the environmental dissemination of antimicrobial resistance (AMR) within rice paddy ecosystems irrigated with reclaimed wastewater. Unlike systematic reviews that rely on strict inclusion criteria and quantitative synthesis, the narrative design allows for a more flexible, integrative exploration of complex and interdisciplinary evidence. This approach is particularly suited to topics such as AMR, where environmental, agricultural, and microbiological processes intersect in ways that are not always amenable to standardized comparison.

The conceptual framework of this review is grounded in the One Health perspective, recognizing that antimicrobial resistance is not confined to clinical settings but emerges from interconnected human, animal, and environmental systems (EFSA Panel on Biological Hazards, 2021; Wu et al., 2025). Within this framework, the soil–plant–water continuum in rice paddies is treated as a dynamic system through which antibiotic resistance genes (ARGs) and antibiotic-resistant bacteria (ARB) can circulate and evolve.

2.2 Literature Search Strategy

A comprehensive literature search was conducted to identify relevant studies addressing AMR dissemination in agricultural and aquatic environments, with a particular emphasis on rice paddy systems and reclaimed wastewater irrigation. Major electronic

databases—including Scopus, Web of Science, PubMed, and Google Scholar—were systematically searched for publications up to early 2026.

Search terms were developed iteratively to capture the breadth of the topic. Keywords included combinations of: “antimicrobial resistance,” “antibiotic resistance genes,” “reclaimed wastewater,” “treated wastewater irrigation,” “rice paddy soil,” “rhizosphere microbiome,” “horizontal gene transfer,” and “environmental resistome.” Boolean operators (AND/OR) were applied to refine search sensitivity and specificity. Reference lists of key articles were also manually screened to identify additional relevant studies, a process often necessary in narrative syntheses to avoid omission of influential work.

2.3 Study Selection and Inclusion Criteria

Given the narrative nature of the review, study selection followed a thematic relevance approach rather than rigid inclusion–exclusion thresholds. Studies were included if they addressed at least one of the following domains:

(i) occurrence and fate of antibiotics, ARB, or ARGs in soil or water systems,

(ii) impacts of reclaimed wastewater irrigation on microbial communities,

(iii) mechanisms of resistance dissemination, particularly horizontal gene transfer (HGT), and

(iv) ecological or public health implications within agroecosystems.

Priority was given to peer-reviewed articles, including experimental studies, field investigations, and high-quality review papers. Studies focusing on soil microbiome dynamics, nutrient cycling, and co-selection mechanisms (e.g., heavy metals) were also incorporated, as these processes are closely linked to resistome evolution (Rad et al., 2022; Zhu et al., 2019).

2.4 Data Extraction and Thematic Synthesis

Relevant information from selected studies was extracted and organized into thematic categories reflecting the structure of the review. These included:

(1) soil as a biodiversity habitat and resistome reservoir,

(2) bioactive compounds and intrinsic resistance,

(3) AMR reservoirs and dissemination pathways,

(4) planetary health implications, and

(5) management strategies and mitigation approaches.

Data were not quantitatively pooled; instead, findings were synthesized narratively to highlight patterns, inconsistencies, and emerging insights. Particular attention was given to the soil–plant–water continuum, the role of the rhizosphere as a hotspot for microbial interaction, and the influence of agricultural practices such as fertilization and wastewater reuse on resistance dynamics (Cui et al., 2022; Xu et al., 2024).

2.5 Integration of Tables and Comparative Analysis

To enhance clarity and facilitate comparison, key findings were systematically organized into four analytical tables (Tables 1–4). These tables summarize:

• The influence of irrigation and fertilization on the resistome

• taxonomic carriers and mechanisms of ARG transfer

• prevalence and geographic distribution of ARGs, and

• environmental stressors and mitigation strategies.

The tabulated data were used as a basis for cross-study comparison, allowing identification of consistent trends—such as the enrichment of ARGs under long-term wastewater irrigation—as well as context-dependent variations influenced by soil type, climate, and management practices (Phan et al., 2024; Della-Negra et al., 2026).

2.6 Limitations of the Methodological Approach

While the narrative review design enables a broad and integrative perspective, it also introduces certain limitations. The absence of formal meta-analytic procedures means that findings are interpreted qualitatively, potentially introducing subjective bias in study selection and interpretation. Additionally, variability in methodologies across primary studies—ranging from molecular detection techniques to field conditions—limits direct comparability.

Nevertheless, by synthesizing diverse lines of evidence

within a coherent conceptual framework, this approach provides a context-rich understanding of AMR dissemination in rice paddy ecosystems, highlighting both established knowledge and critical gaps for future research.

3.1 Soil as a Biodiversity Habitat in the Context of Soil Biota, AMR, and Planetary Health

3.1.1 Soil as a Living System and the Foundation of Planetary Health

Soil, despite often being treated as a passive substrate in agricultural discourse, is anything but inert. It is, in many respects, a living system—densely populated, metabolically active, and astonishingly complex. Within a single gram, one may find billions of microbial cells and an almost incomprehensible diversity of taxa, forming what is sometimes described as an "unseen majority." These microbial consortia are not merely present; they actively regulate biogeochemical cycles, including carbon sequestration and nitrogen transformation, processes that underpin the stability of terrestrial ecosystems. It is within this broader ecological framing that the concept of Planetary Health becomes particularly relevant, emphasizing that human well-being is deeply—and perhaps unavoidably—intertwined with the integrity of natural systems (Zhu et al., 2019; EFSA Panel on Biological Hazards, 2021). Yet, this intricate biological network is increasingly subjected to anthropogenic pressures. The growing reliance on reclaimed wastewater and organic amendments such as manure introduces not only nutrients but also a suite of emerging contaminants, including antibiotics and antibiotic resistance determinants. Over time, these inputs may subtly—but persistently—reshape the structure and function of soil microbial communities, raising concerns about long-term ecological stability (Phan et al., 2024; Wu et al., 2025). Figure 1 depicting the environmental dissemination of antimicrobial resistance across the soil–plant–water continuum in reclaimed wastewater–irrigated rice ecosystems, highlighting microbial, ecological, and human health linkages.

3.1.2 From Intrinsic Resistome to Anthropogenic Amplification

It is important, however, to distinguish between what might be termed the intrinsic soil resistome and the more recent, human-driven amplification of resistance. Soil microorganisms have, for millions of years, evolved mechanisms to resist naturally occurring antibiotics, using them as tools in ecological competition. In that sense, resistance itself is not new. What is new—and arguably more concerning—is the scale and intensity at which resistance genes are now being introduced and mobilized through human activity. The addition of clinically relevant antibiotics and antibiotic-resistant bacteria (ARB) into soil environments effectively transforms these ecosystems into what some researchers have described as "genetic reactors," where selective pressures favor the proliferation and exchange of resistance traits (Ahmad et al., 2026; Wu et al., 2025).

Under such conditions, horizontal gene transfer (HGT) becomes a central mechanism. Mobile genetic elements facilitate the movement of resistance genes across taxonomic boundaries, potentially accelerating the spread of antimicrobial resistance within soil microbiomes and beyond (Jadeja & Worrich, 2022). The consequences are not confined to microbial ecology alone; they extend to ecosystem functionality. For instance, elevated antibiotic concentrations have been associated with disruptions in nitrogen cycling, particularly through the suppression of nitrifying microorganisms, which may, in turn, reduce soil nitrogen-processing efficiency (Yan et al., 2026).

3.1.3 Soil Fauna as Mediators of Resistance Dynamics

An additional layer of complexity emerges when considering the role of soil fauna. Organisms such as earthworms and collembolans, often overlooked in discussions of AMR, harbor their own microbiomes and interact intimately with surrounding microbial communities. Interestingly, their role appears to be somewhat dualistic. On one hand, these organisms may act as vectors, facilitating the movement of resistance genes through soil layers and food webs. On the other, there is growing evidence that certain fauna—particularly earthworms—may exert a mitigating effect. Their gut environments can selectively suppress or degrade antibiotic-resistant bacteria, suggesting a form of biological filtration that may reduce the overall burden of resistance determinants in soil systems (Jadeja & Worrich, 2022; Phan et al., 2024).

3.1.4 Implications for One Health and Sustainable Soil Management

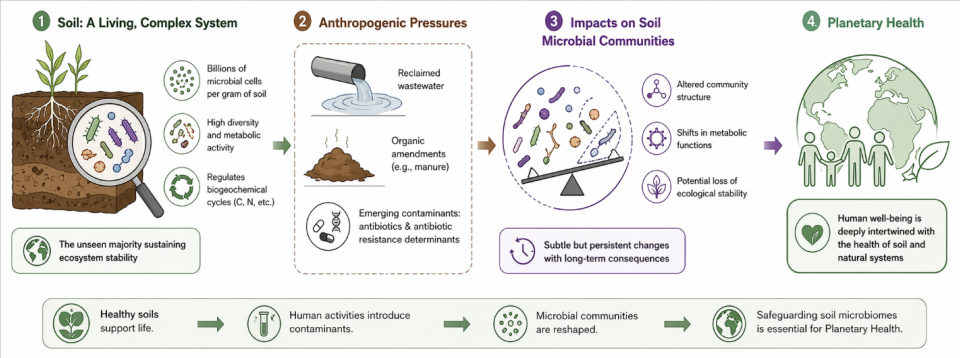

Figure 1: Hidden Resistome in Rice Paddies: How Reclaimed Water Irrigation Reshapes Soil Microbiomes and Amplifies AMR Risks. Soil is a dynamic, microbially rich ecosystem where reclaimed wastewater and agricultural inputs introduce antibiotics and resistance genes, subtly reshaping microbial structure and function. These interactions across the soil–plant–water continuum position rice paddies as critical nodes in the environmental dissemination of antimicrobial resistance, linking ecosystem integrity to human health..

Table 1. Effects of Irrigation Water Quality and Fertilization Regimes on Soil Resistome Dynamics in Agroecosystems. This table summarizes how reclaimed wastewater irrigation and different fertilization strategies influence ARG abundance and mobile genetic elements (MGEs) in soil systems. It highlights the dual role of nutrient inputs and irrigation sources in either suppressing or amplifying antimicrobial resistance within rhizosphere and bulk soils.

Reference	System/Matrix	Water Source	Fertilizer	Main ARG Class	Abundance Shift	MGE Status	Key Ecological Insight
Cui et al. (2022)	Tomato rhizosphere	Reclaimed wastewater (RWW)	N (NaNO)	Multidrug	24.06–73.09% decrease	Increased vs control	Nitrogen regulation reduces ARG burden in soil
Cui et al. (2022)	Tomato rhizosphere	RWW	P (CaMgOP)	Aminoglycoside	50.13–58.80% decrease	Variable	Soil pH and total N drive ARG variation
Cui et al. (2022)	Tomato bulk soil	RWW	P fertilizer	Sulfonamide	Up to 35.84% increase	Positive correlation	P fertilization may enrich ARGs in bulk soil
Cui et al. (2022)	Tomato rhizosphere	RWW	K (KSO)	Tetracycline	46.52–53.64% decrease	Moderate increase	KSO more effective than KCl
Xu et al. (2024)	Paddy soil	Paddy water	Swine compost	MLSB / Multidrug	Significant enrichment	Marker genes detected	Compost increases resistome load
Xu et al. (2024)	Rice roots	Paddy water	Swine compost	Beta-lactam	Substantial presence	intI1 / tnpA detected	Elevated HGT from soil to plant
Phan et al. (2024)	Spinach soil	Treated wastewater (TMW)	Antibiotic mixture	Multidrug	Highly diverse and elevated	9 MGEs detected	Residual antibiotics increase ARG diversity
Phan et al. (2024)	Radish rhizosphere	TMW	Antibiotic mixture	FCA resistance	Lower than bulk soil	Reduced HGT	Rhizosphere resilience moderates ARG spread
Della-Negra et al. (2026)	Loamy clay soil	Treated wastewater (TWW)	None	sul1	Significant increase	intI1 enrichment	Long-term TWW promotes ARG accumulation
Della-Negra et al. (2026)	Lettuce roots	Raw wastewater	None	ermB	Selective modulation	Barrier effect	Root microbiome limits AMR transfer

Taken together, these dynamics underscore the necessity of adopting a One Health perspective when addressing antimicrobial resistance in soil ecosystems. The soil–plant–water continuum is not an isolated system; rather, it functions as a conduit through which resistance can move between environmental reservoirs and human populations. Managing soil health, therefore, extends beyond agronomic productivity—it becomes a matter of public health relevance. Strategies such as precision fertilization, improved wastewater treatment technologies, and controlled reuse practices may offer pathways to mitigate these risks. Still, the challenge lies in balancing agricultural sustainability with the preservation of microbial integrity, ensuring that soil remains a resilient and functional component of the Earth system rather than a persistent source of resistance dissemination (EFSA Panel on Biological Hazards, 2021; Ahmad et al., 2026).

3.2 Soil as a Source of Bioactive Compounds in the Context of Soil Biota, AMR, and Planetary Health

3.2.1 Soil Biodiversity as a Reservoir of Bioactive Potential

It is tempting—perhaps too tempting—to think of soil merely as a substrate for plant growth. Yet, when examined more closely, it becomes evident that soil functions as a remarkably dynamic biochemical reservoir. Within its microscale heterogeneity exists a dense and metabolically versatile microbial community capable of producing an extraordinary diversity of bioactive compounds, many of which have historically underpinned antibiotic discovery. This immense biochemical potential, however, is not isolated from broader ecological processes. Rather, it is embedded within a system that regulates nutrient cycling, supports plant productivity, and ultimately sustains planetary health (Zhu et al., 2019; Ondon et al., 2021).

At the same time, this reservoir is increasingly influenced by anthropogenic pressures. The introduction of reclaimed wastewater, agricultural runoff, and manure amendments alters not only nutrient availability but also the chemical landscape of soil environments. These inputs may unintentionally reshape microbial metabolic pathways, influencing both the production and degradation of bioactive compounds. In this sense, soil is no longer just a source of beneficial metabolites—it is becoming a contested space where ecological function and anthropogenic disturbance intersect (Phan et al., 2024; Wu et al., 2025).

3.2.2 Bioactive Compounds, Resistome Evolution, and Selective Pressures

There is, however, an inherent paradox in the role of soil-derived bioactive compounds. Many antibiotics originate from soil microorganisms, functioning naturally as signaling molecules or competitive tools within microbial communities. This long evolutionary history has given rise to what is often described as the intrinsic resistome—a baseline level of resistance shaped by ecological interactions over geological timescales. Yet, the rapid influx of synthetic and clinical antibiotics into soil systems has disrupted this balance, amplifying resistance far beyond its natural context (Ahmad et al., 2026; Selvarajan et al., 2023).

Under these altered conditions, selective pressures intensify. Antibiotics, heavy metals, and other co-contaminants collectively drive the proliferation of resistance genes, often co-located on mobile genetic elements. Horizontal gene transfer (HGT) then facilitates their spread across diverse microbial taxa, effectively accelerating the evolution of the resistome. This process, while mechanistically fascinating, raises concerns about the long-term sustainability of soil ecosystems and their capacity to maintain essential functions (Jadeja & Worrich, 2022; EFSA Panel on Biological Hazards, 2021).

3.2.3 Agricultural Practices and the Modulation of Soil Bioactivity

Agricultural management practices further complicate this picture. Fertilization strategies, particularly the application of nitrogen, phosphorus, and potassium, do not merely influence crop yield—they also modulate microbial community structure and activity. Some evidence suggests that targeted fertilization approaches may mitigate the accumulation of antibiotic resistance genes in reclaimed water–irrigated soils, although the mechanisms remain incompletely understood (Cui et al., 2022). This introduces an important, if somewhat underexplored, possibility: that soil management practices could be strategically designed to preserve beneficial bioactivity while limiting the spread of resistance.

3.2.4 Toward Integrated Soil Stewardship

Ultimately, the role of soil as a source of bioactive compounds cannot be disentangled from its role in antimicrobial resistance dynamics. The same microbial

diversity that offers solutions—new antibiotics, novel metabolites—also harbors the capacity for resistance proliferation under selective pressure. This duality reinforces the need for a One Health perspective, where soil stewardship is recognized as integral to both environmental sustainability and global health. Managing this balance, admittedly, is not straightforward. It requires coordinated efforts across disciplines to ensure that soil remains a source of innovation rather than a reservoir of risk (EFSA Panel on Biological Hazards, 2021; Ahmad et al., 2026).

3.3 Antimicrobial Resistance (AMR) Reservoirs in the Context of Soil Biota and Planetary Health

3.3.1 Soil as a Dynamic Reservoir of Resistance

Soil, when viewed beyond its agronomic function, reveals itself as a remarkably dense and dynamic microbial habitat—arguably the most complex on Earth. Within this microcosm, vast and diverse microbial communities regulate essential biogeochemical cycles, quietly sustaining planetary habitability. It is precisely this richness, however, that makes soil both resilient and vulnerable. As agricultural systems increasingly rely on reclaimed wastewater and organic amendments, a subtle yet consequential shift is occurring: soil is becoming an active reservoir for antimicrobial resistance (AMR), rather than merely a passive recipient (Zhu et al., 2019; Ondon et al., 2021).

3.3.2 From Natural Resistome to Anthropogenic Amplification

There is, of course, a long-standing natural resistome within soil ecosystems—an evolutionary legacy shaped by microbial competition over millions of years. Yet, the introduction of anthropogenic pressures, particularly antibiotics and antibiotic-resistant bacteria (ARB), appears to have intensified this baseline in ways that are not entirely predictable. Under such conditions, soil environments may function as “genetic reactors,” where selective pressures and dense microbial interactions promote horizontal gene transfer (HGT) via mobile genetic elements such as plasmids and integrons (Ahmad et al., 2026; Phan et al., 2024). The extent of this transformation remains somewhat contested. While some studies report minimal disruption due to competitive microbial dynamics, others suggest that prolonged reclaimed wastewater irrigation can substantially enrich the soil resistome, in some cases by several orders of magnitude (Della-Negra et al., 2026).

3.3.3 Biological Mediators and Ecological Consequences

Adding further complexity, soil fauna contribute in ways that are not entirely linear. Organisms such as collembolans may facilitate the movement of resistance genes across trophic levels, effectively acting as vectors. Conversely, earthworms—perhaps unexpectedly—may exert a mitigating influence. Their gut-associated microbiomes have been shown to suppress certain antibiotic-resistant bacteria, suggesting a form of biological filtration that could reduce resistance burdens under specific conditions (Ondon et al., 2021; Phan et al., 2024).

3.3.4 Implications for One Health and Ecosystem Function

These intertwined processes ultimately reinforce the need for a One Health perspective. The soil–plant–water continuum represents not just an environmental interface but a pathway through which resistance can circulate across ecological and human systems. Moreover, antibiotic residues may disrupt key ecosystem functions, including nitrogen cycling, potentially diminishing soil nutrient efficiency (Yan et al., 2026). Addressing these challenges will require carefully balanced strategies—improving wastewater treatment, refining fertilization practices, and preserving microbial integrity—to ensure that soil remains a stabilizing force rather than a persistent reservoir of resistance (Ahmad et al., 2026; Zhu et al., 2019).

3.4 Planetary Health Implications in the Context of Soil Biota and Antimicrobial Resistance

3.4.1 Soil Integrity as a Pillar of Planetary Health

It is easy—perhaps misleadingly so—to reduce soil to its agricultural function, to think of it primarily as a medium that supports plant growth. Yet soil is better understood as a living, breathing interface between biological, chemical, and physical systems. Within a single gram exists an immense diversity of microorganisms whose collective activity regulates fundamental planetary processes, including carbon sequestration and nitrogen transformation. In this sense, soil does not merely support life—it helps sustain the conditions that make life possible. This perspective aligns closely with the concept of Planetary Health, where human well-being is inseparable from the stability of natural ecosystems (Zhu et al., 2019;

EFSA Panel on Biological Hazards, 2021).

However, this equilibrium appears increasingly fragile. The widespread use of reclaimed wastewater (RWW) and organic waste in agriculture introduces a complex mixture of antibiotics, resistant microorganisms, and chemical stressors into soil systems. While these practices are often promoted as sustainable solutions to water scarcity, they may simultaneously impose selective pressures that reshape microbial communities in ways that are not fully predictable (Phan et al., 2024; Wu et al., 2025).

3.4.2 Anthropogenic Pressures and Resistome Expansion

There is, undeniably, a natural baseline of resistance within soil ecosystems—the intrinsic resistome—formed through long evolutionary processes. Yet, the rapid influx of anthropogenic contaminants has shifted this balance. Soil environments, under these conditions, begin to resemble “genetic reactors,” where high microbial density and persistent selective pressures facilitate horizontal gene transfer (HGT) via mobile genetic elements such as plasmids and integrons (Ahmad et al., 2026; Ondon et al., 2021). This amplification of resistance is not merely a microbiological concern; it has broader ecological consequences.

For instance, antibiotic residues can interfere with microbial-mediated nutrient cycling, particularly nitrogen transformations. Disruptions to nitrification and denitrification processes may reduce soil nutrient efficiency, with cascading effects on plant productivity and ecosystem resilience (Yan et al., 2026). At a planetary scale, even modest perturbations in these cycles could accumulate, influencing broader biogeochemical stability.

3.4.3 Biological Intermediaries and Ecological Feedbacks

The role of soil fauna introduces an additional layer of complexity that is, perhaps, still underappreciated. Organisms such as collembolans and earthworms do not simply inhabit soil—they actively reshape it, both physically and biologically. Some fauna may inadvertently facilitate the spread of antimicrobial resistance by acting as vectors, transferring resistance genes through trophic interactions. Others, however, appear to contribute to mitigation. Earthworms, for example, have been observed to reduce the abundance of antibiotic-resistant bacteria through gut-associated microbial processes, suggesting a form of natural attenuation that may partially counterbalance anthropogenic inputs (Jadeja & Worrich, 2022; Della-Negra et al., 2026).

At the same time, abiotic stressors—such as heavy metals and residual agrochemicals—interact with biological processes, reinforcing selective pressures that sustain resistance traits. These co-selection mechanisms further complicate efforts to disentangle cause and effect within soil systems (Rad et al., 2022).

3.4.4 Toward a One Health Framework for Soil Stewardship

Taken together, these dynamics point toward a broader realization: soil is not an isolated component of the environment but a central node within the soil–plant–water–human continuum. The dissemination of antimicrobial resistance through this system underscores the urgency of adopting a One Health framework, where environmental management is directly linked to public health outcomes. Managing soil health, therefore, becomes more than an agronomic priority—it is a global imperative.

Moving forward, the challenge lies in balancing sustainability with precaution. Strategies such as advanced wastewater treatment, precision fertilization, and improved monitoring of resistance determinants may offer viable pathways. Yet, these approaches must be implemented with an awareness of ecological complexity, ensuring that interventions do not inadvertently exacerbate the very problems they aim to solve. In this context, preserving soil integrity is not simply about maintaining productivity—it is about safeguarding the ecological foundations upon which planetary health ultimately depends (Ahmad et al., 2026; Zhu et al., 2019).

3.5 Management Strategies and Future Research in the Context of Soil Biota, AMR, and Planetary Health

3.5.1 Reframing Soil Management Beyond Productivity

Soil, despite its frequent treatment as a static agricultural input, is perhaps better understood as a dynamic, living interface—one that mediates interactions between biological communities, chemical processes, and human interventions. Within this system, microbial diversity underpins essential functions such as nutrient cycling and organic matter turnover, quietly sustaining agricultural productivity and broader ecosystem stability. Yet, as reclaimed wastewater (RWW) and organic amendments

become more widely integrated into farming systems, particularly in water-intensive landscapes, this balance appears increasingly fragile. The introduction of antibiotics and antibiotic-resistant bacteria (ARB) into soil systems is not merely an environmental side effect; it is, increasingly, a defining challenge for sustainable land management (Zhu et al., 2019; Phan et al., 2024).

3.5.2 Mitigating Resistome Expansion Through Targeted Interventions

At the heart of this challenge lies the transition from the intrinsic resistome—long embedded within soil microbial ecology—to an anthropogenically amplified resistome shaped by continuous external inputs. Under these conditions, soil environments may function as "genetic reactors," where selective pressures promote horizontal gene transfer (HGT) via mobile genetic elements such as plasmids and integrons (Ahmad et al., 2026; Ondon et al., 2021). Addressing this requires interventions that are, admittedly, both technically robust and ecologically sensitive.

Improving wastewater treatment technologies is often presented as a primary solution. Advanced treatment processes, including membrane filtration and advanced oxidation, have shown promise in reducing antibiotic residues and resistance determinants before irrigation use. However, their implementation remains uneven, particularly in regions where water reuse is most critical (Duarte et al., 2022; Wu et al., 2025). Complementary to this, precision fertilization strategies—especially those optimizing nitrogen inputs—may help regulate microbial activity and limit the proliferation of antibiotic resistance genes (ARGs), although the mechanisms are not yet fully resolved (Rad et al., 2022; Yan et al., 2026).

3.5.3 Biological Mediation and Nature-Based Solutions

There is also growing interest in biological approaches to mitigation, though these remain, in some respects, exploratory. Soil fauna, particularly earthworms, appear to play a role that is more complex than previously assumed. While certain organisms may facilitate the spread of resistance through trophic interactions, others may contribute to attenuation. Earthworms, for example, have been observed to reduce the abundance of ARB through gut-associated microbial processes, suggesting a potential avenue for natural bioremediation (Jadeja & Worrich, 2022; Della-Negra et al., 2026). Whether such processes can be reliably harnessed at scale remains an open question.

3.5.4 Future Research Directions and One Health Integration

Looking forward, it becomes evident that addressing AMR in soil systems requires more than isolated technical fixes. There is a need for integrated research frameworks that link soil microbiology, agricultural practices, and public health outcomes. Long-term field studies, in particular, are essential to capture the cumulative effects of reclaimed water irrigation and management strategies on soil resistomes (Selvarajan et al., 2023; Phan et al., 2024). Additionally, improved monitoring tools—capable of tracking ARG dynamics across the soil–plant–water continuum—will be critical for risk assessment and policy development.

Ultimately, the management of soil in the age of antimicrobial resistance demands a One Health perspective. Soil health is no longer solely an agronomic concern; it is a shared environmental and public health responsibility. Balancing productivity with ecological integrity will require coordinated efforts, informed by both scientific insight and practical feasibility, to ensure that soil remains a resilient system rather than a persistent reservoir of resistance (EFSA Panel on Biological Hazards, 2021; Ahmad et al., 2026).

4. Integrated Dynamics of AMR Dissemination in Agro-Ecosystems

4.1 Irrigation, Wastewater Reuse, and Resistome Enrichment

The results collectively suggest that reclaimed wastewater irrigation does not simply introduce contaminants into agricultural systems—it reshapes microbial and genetic landscapes in ways that are both subtle and cumulative. Across multiple experimental and field-based studies, wastewater reuse emerges as a persistent driver of antimicrobial resistance (AMR) dissemination, particularly through the continuous input of antibiotics, antibiotic-resistant bacteria (ARB), and resistance genes (ARGs) (Christou et al., 2017a; Cacace et al., 2019). Interestingly, long-term irrigation with treated or untreated wastewater has been shown to alter soil physicochemical properties and microbial composition, thereby influencing ARG persistence (Ait-Mouheb et al., 2022; Bigott et al., 2022). While advanced reclamation technologies can reduce microbial loads, residual micropollutants often persist,

sustaining selective pressure within soil ecosystems (Christou et al., 2024). This aligns with broader regional analyses suggesting that wastewater reuse—particularly in Mediterranean agricultural systems—represents both a sustainability opportunity and a microbial risk pathway (Ait-Mouheb et al., 2018). The combined effects of irrigation source and fertilization strategies on ARG dynamics and mobile genetic elements are summarized in Table 1.

4.2 Fertilization Practices and Microbial Community Feedbacks

Fertilization strategies introduce an additional layer of control over resistome dynamics. As demonstrated in Table 1, nitrogen-based fertilization can significantly reduce ARG abundance under reclaimed water irrigation, whereas phosphorus inputs may promote selective enrichment of specific resistance classes (Cui et al., 2022). However, these effects are not purely chemical; they are mediated through shifts in microbial community structure. Soil microbial communities, particularly in the rhizosphere, exhibit strong feedback interactions with plant systems. Root-associated microbiota are known to respond dynamically to nutrient availability, influencing both microbial diversity and resistance gene exchange (Bever et al., 2012). This is further supported by studies showing that microbial diversity correlates with ecosystem functionality, including decomposition and nutrient cycling processes (Chiba et al., 2021). Consequently, fertilization strategies that maintain microbial diversity may indirectly suppress the dominance of ARG-carrying taxa.

4.3 Soil–Plant Continuum and ARG Transfer Pathways

The movement of resistance across the soil–plant continuum is neither uniform nor inevitable. Evidence indicates that while ARGs are readily detected in soils and root-associated microbiomes, their transfer into edible plant tissues is more restricted. As shown in Table 2, ARG abundance in crops such as rice grains or leafy vegetables is typically lower than in surrounding soils, suggesting the presence of plant-mediated filtering mechanisms (Xu et al., 2024; Cerqueira et al., 2019). At the same time, the rhizosphere acts as a critical interface where microbial exchange is intensified. Root exudates create nutrient-rich microenvironments that facilitate horizontal gene transfer (HGT), particularly during early plant growth stages (Della-Negra et al., 2025). However, plant genotype also plays a role. Recent work demonstrates that specific plant genes can shape microbiota composition, potentially influencing ARG distribution and persistence (Escudero-Martinez et al., 2022). This suggests that plant selection and breeding could emerge as indirect tools for AMR mitigation.

4.4 Microbial Carriers and Functional Trade-Offs

The taxonomic structure of soil microbiomes further clarifies how resistance is maintained and propagated. As detailed in Table 3, dominant phyla such as Proteobacteria and Actinobacteria frequently act as ARG carriers. These taxa are not incidental; they are deeply integrated into ecosystem processes, including nitrogen cycling and organic matter decomposition (Yan et al., 2026; Ondon et al., 2021). This dual functionality introduces a critical trade-off. For instance, certain Proteobacteria contribute to denitrification pathways while simultaneously harboring ARGs, creating a functional linkage between resistance dissemination and nutrient cycling (Yan et al., 2026). Moreover, environmental stressors—including antibiotics, heavy metals, and salinity—can co-select for resistance traits, reinforcing microbial adaptation under anthropogenic pressure (Rad et al., 2022). These findings suggest that efforts to control AMR must account for the ecological roles of microbial hosts rather than targeting resistance in isolation.

4.5 Environmental Distribution and Public Health Exposure

The geographic distribution of ARGs reflects a global footprint of antibiotic usage and environmental dissemination. As shown in Table 3, ARGs such as sul1, tetW, and mcr-1 are detected across diverse environmental matrices, including soils, wastewater effluents, and crops (Selvarajan et al., 2023). Urban and peri-urban agricultural systems, particularly those irrigated with reclaimed water, appear to function as key nodes in this network. In these systems, ARGs may spread beyond soil boundaries through aerosols, water runoff, and food consumption pathways (Wang et al., 2014; Jadeja & Worrich, 2022). The persistence of ARGs in wastewater and receiving environments further underscores the need for improved monitoring and regulatory frameworks, as emphasized in European water reuse policies (European Parliament, 2020).

Table 2. Environmental Prevalence, Distribution, and Transmission Risks of Antibiotic Resistance Genes Across Soil–Plant Systems. This table compiles the occurrence, abundance, and spatial distribution of ARGs across environmental matrices, including soil, crops, and wastewater. It emphasizes the variability of ARG transfer across the soil–plant continuum and associated public health implications.

Reference	Sample Matrix	Region	Antibiotic Class	ARGs	Abundance	Frequency	Health Implication
Wang et al. (2014)	Urban soil	Beijing, China	Tetracycline	tetG, tetW	10–5.3×10³	100% sites	Aerosol exposure risk
Wang et al. (2014)	Wetland soil	China	Sulfonamide	sulI, sulII	~10 copies/g	High correlation	Linked to pathogenic bacteria
Xu et al. (2024)	Rice grain	China	Aminoglycoside	strB	<0.3%	Compost-treated only	Soil-to-grain transfer risk
Xu et al. (2024)	Swine compost	Manure	Tetracycline	tetW	High	Dominant	Major external ARG source
Phan et al. (2024)	Spinach leaves	Mesocosm	Multiple	MDR	50–136 subtypes	High	Food chain exposure pathway
Ondon et al. (2021)	Phosphate soil	Residential	Tetracycline	tetM, tetO	10–10²	Increasing trend	Historical AMR rise
Ondon et al. (2021)	Feedlot soil	Farmland	Sulfonamide	sul1, sul2	10–10²	Moderate	Water contamination risk
Della-Negra et al. (2026)	Clay soil	France	Macrolide	ermB	Increasing	TWW only	Environmental adaptation
Selvarajan et al. (2023)	WWTP effluent	EU	Last-resort	mcr-1, blaKPC-3	High	Frequent	Spread to food systems
Kusi et al. (2022)	Mining water	China	Chloramphenicol	Multiple ARGs	10³–10¹	High	Metal-driven co-selection

Table 3. Taxonomic Distribution and Mechanistic Pathways of Antibiotic Resistance Gene Carriers in Soil Ecosystems. This table presents dominant microbial taxa associated with ARG carriage and their underlying transfer mechanisms, including horizontal and vertical gene transfer. It also links microbial ecological roles with resistance dissemination, highlighting functional trade-offs within soil microbiomes.

Reference	Habitat	Dominant Phylum	Dominant Family	Associated ARG	Transfer Mechanism	Ecological Role	Stability Insight
Cui et al. (2022)	Reclaimed soil	Actinobacteria	Nocardiaceae	Multidrug	Plasmid-mediated HGT	Dominant taxa	Reduced diversity under N fertilization
Cui et al. (2022)	Rhizosphere	Proteobacteria	Sphingomonadaceae	Aminoglycoside	Horizontal transfer	ARG host	High density near root exudates
Yan et al. (2026)	Paddy soil	Proteobacteria	Burkholderiales	Multidrug	Genetic linkage	Nitrogen cycling	Co-occurrence with N-cycle genes
Yan et al. (2026)	Paddy soil	Proteobacteria	Sulfuricella	nirS / nosZ	Co-localization	Denitrification	Adaptive advantage under antibiotic stress
Yan et al. (2026)	Paddy soil	Chloroflexi	Thermomicrobia	Multiple ARGs	Integron-mediated	N transformation	Increased diversity at low antibiotic levels

Phan et al. (2024)	Spinach soil	Pseudomonadota	Bradyrhizobium	MDR	Mobile elements	Nitrogen fixation	Strong ARG association
Phan et al. (2024)	Radish soil	Verrucomicrobiota	Unclassified	Tetracycline	Horizontal transfer	Dominant taxa	Correlated with ARG prevalence
Jadeja & Worrich (2022)	Polluted soil/air	Firmicutes	Bacillus	NDM-1	Aerosolization	Airborne spread	ARG dissemination via PM2.5
Della-Negra et al. (2026)	TWW soil	Ignavibacteria	Unclassified	sul1 / intI1	Vertical transfer	ARG carrier	Stimulated by nutrient inputs
Ondon et al. (2021)	Agricultural soil	Proteobacteria	Pseudomonadaceae	Multi-resistance	Co-selection	Pathogenic potential	Metal–antibiotic co-resistance

Table 4. Environmental Stressors and Integrated Mitigation Strategies Influencing Antimicrobial Resistance in Soil Systems. This table outlines key environmental drivers of AMR, including antibiotics, heavy metals, and agricultural inputs, alongside their ecological and biogeochemical impacts. It also summarizes emerging mitigation strategies and identifies critical research gaps for sustainable AMR management.

Reference	**Factor**	**Exposure**	**System**	**Microbial Effect**	**Biogeochemical Impact**	**Mitigation Strategy**	**Research Need**
Yan et al. (2026)	Antibiotics	0–100 µg/L	Paddy soil	Hormesis	Enhanced nitrification	Safe TMW reuse	Flux quantification
Yan et al. (2026)	NO dynamics	Low dose	Denitrifiers	nosZ increase	Reduced emissions	Targeted fertilization	Global validation
Phan et al. (2024)	Soil fauna	Organic input	Earthworms	ARG reduction	Lower dissemination	Biological filtering	Faunal diversity role
Phan et al. (2024)	Crop type	Spinach vs radish	Rhizosphere	Stability variation	Nutrient cycling	Crop selection	Filtering mechanisms
Cui et al. (2022)	Soil pH / TN	Variable	Tomato soil	Host shift	Soil quality change	Precision fertilization	Integrated NPK effects
Wu et al. (2025)	Herbicides	Glyphosate	Soil microbiome	Membrane disruption	Biogeochemical imbalance	Reduce chemical inputs	HGT facilitation study
Jadeja & Worrich (2022)	Heavy metals	Trace	Bacteria	Co-resistance	Synergistic selection	Metal control	Cross-resistance pathways
EFSA Panel (2021)	Composting	High temp	Manure	ARG reduction	Nutrient stabilization	Optimized composting	Airborne monitoring
Rad et al. (2022)	Salinity/heat	High	Coastal soil	ARG reduction	Metabolic shift	Saline treatment	Stress-response modeling
Wu et al. (2025)	Advanced WWTP	Tertiary	Wastewater	ARG removal	Pollution control	Membrane/UV	Risk quantification

4.6 Biological Mediation and Emerging Mitigation Pathways

Beyond chemical and physical drivers, biological processes offer both challenges and opportunities for AMR control. Soil fauna, for instance, play a complex role in resistance dynamics. As summarized in Table 4, organisms such as earthworms may reduce ARG abundance through gut-mediated microbial interactions, effectively acting as natural bioremediators (Phan et al., 2024). Simultaneously, emerging approaches such as microbiome engineering aim to restore ecological balance in disturbed soils. These strategies seek to manipulate microbial communities to suppress pathogenic or resistant taxa while enhancing beneficial functions (Darriaut et al., 2025). Early findings suggest that such interventions could mitigate microbial dysbiosis induced by wastewater irrigation, although large-scale validation remains limited.

4.7 Toward Integrated Management and Policy Frameworks

Taken together, the results highlight that AMR dissemination in agro-ecosystems is governed by interacting drivers rather than a single dominant factor. Effective mitigation therefore requires a multi-barrier approach that integrates technological, biological, and policy-based solutions. As indicated in Table 4, advanced wastewater treatment, precision fertilization, and biodiversity conservation represent complementary strategies for reducing ARG proliferation (Wu et al., 2025; EFSA Panel on Biological Hazards, 2021). At the same time, regulatory frameworks—such as those outlined by the European Union—are beginning to formalize safe water reuse practices, emphasizing risk-based monitoring and management (European Parliament, 2020). These policies, combined with scientific advances in soil microbiology and environmental engineering, provide a pathway toward sustainable agricultural systems that minimize AMR risks.

5.Integrating Soil Biota, AMR, and Planetary Health in Reclaimed Water Systems

5.1 Reclaimed Water Use: Between Necessity and Ecological Uncertainty

The expanding reliance on reclaimed wastewater (RWW) in agriculture, particularly in water-intensive systems such as rice paddies, presents a reality that is difficult to avoid—and perhaps equally difficult to fully understand. On one hand, it offers a pathway toward resource efficiency and climate resilience. On the other, it introduces a persistent influx of antibiotics, resistance genes, and microbial contaminants into already complex soil ecosystems (Larsson et al., 2018). The results synthesized here suggest that rice paddies do not passively receive these inputs; rather, they behave as biologically active systems where resistance dynamics are continuously negotiated.

As highlighted in Table 1, irrigation source and fertilization regimes collectively determine whether soils act as sinks or amplifiers of antimicrobial resistance (AMR). Nitrogen-based fertilization appears capable of suppressing ARG abundance, whereas organic amendments such as manure introduce substantial exogenous loads of resistance determinants (Cui et al., 2022; Insam et al., 2015). These contrasting outcomes emphasize that management practices, even seemingly routine ones, can significantly reshape resistome trajectories.

5.2 The Rhizosphere Paradox and Microbial Assembly Processes

A particularly intriguing pattern emerging from the results is what might be termed the “rhizosphere paradox.” The rhizosphere, enriched by root exudates, supports dense and metabolically active microbial communities that facilitate horizontal gene transfer (HGT). Yet, it also appears to exert a selective filtering effect. As shown in Table 2, dominant microbial groups—especially Proteobacteria—serve as key carriers of ARGs while simultaneously supporting essential ecosystem functions (Yan et al., 2026).This dual role may be partly explained by microbial community assembly processes. Soil microbial populations are not randomly structured; rather, they are shaped by both deterministic and stochastic factors, including nutrient availability and plant–microbe interactions (Bever et al., 2012). Interestingly, even small shifts in fertilization—such as phosphate inputs—can alter microbial community composition and, by extension, resistance gene distribution (Ikoyi et al., 2018). This suggests that the rhizosphere is not merely a passive interface but an actively regulated ecological niche.

5.3 Soil–Plant Transfer: Constraints, Pathways, and Risks

The movement of resistance across the soil–plant continuum remains a central concern for food safety. While ARGs are readily detected in soils and roots, their

transfer to edible tissues appears comparatively constrained. Data summarized in Table 3 indicate that ARG abundance in grains or edible plant parts is often significantly lower than in surrounding soils, pointing toward physiological and microbial barriers within the plant system (Xu et al., 2024). However, this apparent containment should be interpreted cautiously. The persistence of ARGs within the soil–plant continuum means that indirect exposure pathways—such as transfer to the human gut microbiome—remain plausible (Khan et al., 2016). Moreover, long-term trends suggest that resistance gene abundance in soils has been increasing since the pre-antibiotic era, reflecting cumulative anthropogenic pressures (Knapp et al., 2010). In this context, even low-level transfer may have long-term implications. As shown in Figure 2, ARGs persist within the soil–plant continuum, with constrained transfer to edible tissues but notable implications for indirect human exposure and long-term environmental accumulation.

5.4 Evolutionary and Genetic Dimensions of Resistance

From an evolutionary perspective, antimicrobial resistance is neither new nor entirely anthropogenic. Resistance mechanisms have existed for millions of years, serving as tools in microbial competition. Early evidence of plasmid-mediated resistance—even prior to widespread antibiotic use—underscores this point (Hughes & Datta, 1983). Yet, modern agricultural systems have amplified these mechanisms, accelerating the spread of resistance across taxa. Horizontal gene transfer plays a central role in this process. The movement of genetic material across species—and even across biological kingdoms—has been well documented (Hotopp et al., 2007). In soil systems, this transfer is facilitated by high microbial density and the presence of mobile genetic elements, effectively transforming soils into “genetic exchange hubs.” At the same time, resistance mutations and adaptive responses are often predictable, reflecting underlying evolutionary constraints (Knopp & Andersson, 2018).

5.5 Functional Trade-Offs and Ecosystem Implications

One of the more subtle, yet significant, insights from this study is the functional trade-off embedded within microbial systems. As shown in Table 2 and Table 4, many ARG-hosting microbes are also essential contributors to ecosystem services, including nitrogen cycling and organic matter decomposition. Disrupting these communities may therefore compromise soil functionality. Intriguingly, low concentrations of antibiotics may not suppress microbial activity entirely. Instead, they can induce hormetic responses, enhancing certain metabolic pathways (Yan et al., 2026). This creates a paradox: ecosystems may remain functionally stable while simultaneously accumulating resistance traits. Such dynamics complicate efforts to define “safe” thresholds for antibiotic contamination.

5.6 Soil Fauna and Ecosystem-Level Mitigation

Beyond microbial processes, soil fauna play an often-overlooked role in mediating AMR dynamics. As reflected in Table 4, organisms such as earthworms contribute to ecosystem services through bioturbation, nutrient cycling, and microbial regulation (Lavelle et al., 2006). Their ability to reduce ARG abundance through gut-associated processes suggests that biological interactions may provide natural mitigation pathways (Phan et al., 2024). At the same time, these organisms may also act as vectors, transporting resistance genes through trophic networks. This dual role reinforces the importance of maintaining biodiversity—not only for ecological resilience but also for resistance management.

5.7 Bioactive Compounds and the Soil Resistome

It is worth noting that soil is also a primary source of bioactive compounds, including antibiotics themselves. Historically, many clinically important antibiotics have been derived from soil microorganisms (Guzman et al., 2012). Advances in genomics and metabolomics continue to reveal untapped reservoirs of secondary metabolites within soil systems (Hautbergue et al., 2018). (Figure 3)

illustrates the dual role of soil as a source of antibiotics and a driver of intrinsic antimicrobial resistance evolution. However, this same capacity for bioactive compound production contributes to the intrinsic resistome. Resistance mechanisms, including modified target sites and enzymatic degradation, have evolved in parallel with antibiotic production (Lambert, 2005). This evolutionary interplay highlights the challenge of disentangling natural resistance from anthropogenic amplification.

5.8 Toward a One Health Framework

Ultimately, the findings converge on a central conclusion: antimicrobial resistance in agro-ecosystems cannot be addressed in isolation. It is a systems-level issue, spanning environmental, agricultural, and public health

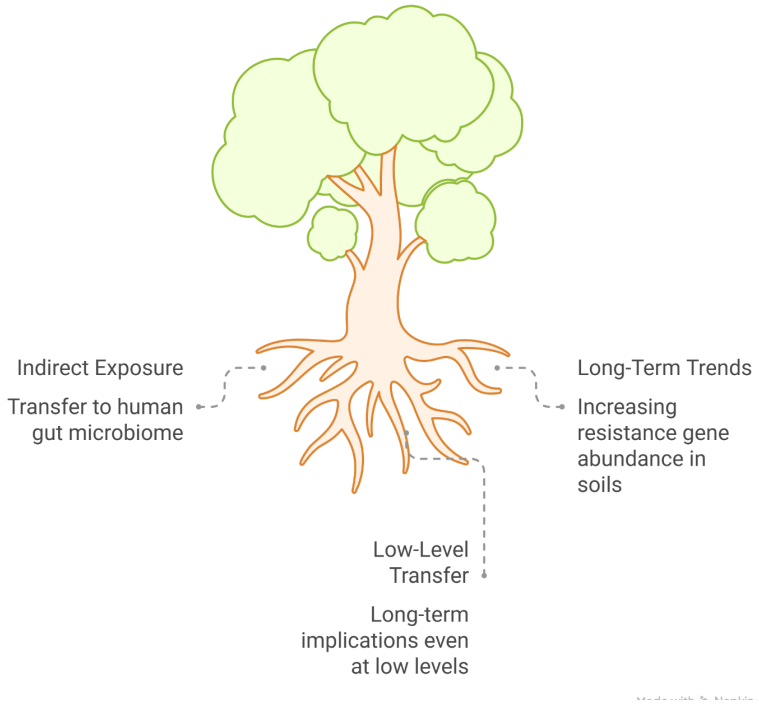

Figure 2: Persistence and Transmission Dynamics of Antibiotic Resistance Genes (ARGs) in the Soil–Plant Continuum. This schematic illustrates the persistence of antibiotic resistance genes (ARGs) within the soil–plant system, highlighting limited but detectable transfer from soil to plant tissues. While physiological and microbial barriers reduce ARG accumulation in edible parts, indirect exposure pathways—particularly via the human gut microbiome—remain plausible. The figure also emphasizes long-term trends of increasing ARG abundance in soils, underscoring cumulative environmental pressures and potential future risks.

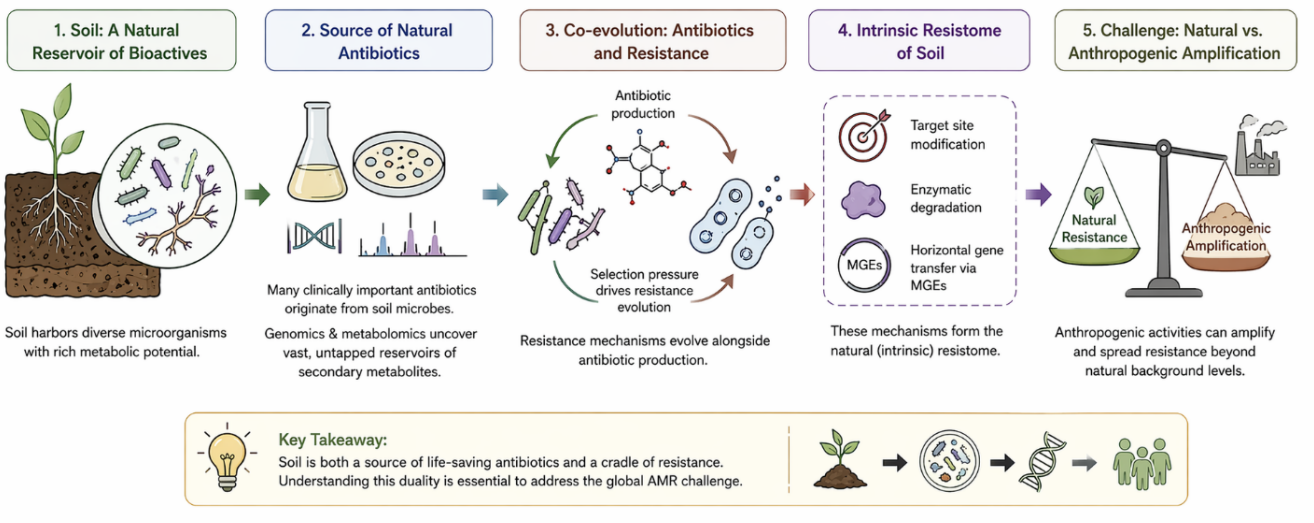

Figure 3: Soil's Double-Edged Role: From Antibiotic Discovery to the Evolution of the Intrinsic Resistome. Soil microbial communities serve as a rich reservoir of bioactive compounds, including many clinically important antibiotics, continuously revealed through genomics and metabolomics advances. Yet, this same system drives the co-evolution of resistance mechanisms, forming an intrinsic resistome that complicates the distinction between natural resistance and human-driven amplification.

domains. As emphasized in Tables 1–4, effective mitigation requires a multi-barrier approach combining technological innovation, ecological management, and policy intervention. Addressing critical knowledge gaps—particularly regarding environmental transmission pathways and long-term ecological impacts—remains essential (Larsson et al., 2018). At the same time, integrating soil health into broader One Health frameworks offers a pathway toward sustainable solutions.

5.9 Concluding Reflection

There is, perhaps, no simple resolution to the tensions described here. Soil systems demonstrate remarkable resilience, yet they are not immune to cumulative pressures. Reclaimed water irrigation represents both an opportunity and a challenge—one that demands careful, evidence-based management. If approached thoughtfully, leveraging both technological advances and ecological processes, it may be possible to balance productivity with safety. If not, the soil may gradually shift from a source of life-sustaining functions to a reservoir of resistance with far-reaching consequences.

6. Limitations of the study

This review, while aiming to provide a comprehensive and integrative perspective, is constrained by several methodological and evidence-related limitations. The narrative design, by its nature, does not employ formal meta-analytic techniques, which limits the ability to generate statistically robust effect estimates or directly compare outcomes across studies. Additionally, substantial heterogeneity exists among the included literature, spanning differences in experimental design, environmental conditions, analytical methods, and reporting standards, making cross-study synthesis inherently interpretive. Geographic bias is also evident, as much of the available research is concentrated in specific regions, potentially limiting global generalizability. Furthermore, many studies rely primarily on molecular detection of antibiotic resistance genes without assessing their functional activity or real-world transfer into human-associated microbiomes. Finally, the lack of long-term, longitudinal field studies restricts understanding of cumulative and temporal dynamics of AMR under sustained reclaimed wastewater irrigation conditions.

7. Conclusion

Antimicrobial resistance in reclaimed water–irrigated rice ecosystems emerge as a multifaceted, system-driven process shaped by microbial ecology, agricultural practices, and environmental pressures. These ecosystems function not only as reservoirs but also as active interfaces for resistance dissemination across the soil–plant–water continuum. While inherent resilience exists, the persistence and mobility of resistance elements underscore potential long-term risks to both ecosystem integrity and public health. Addressing these challenges requires integrated, One Health–oriented strategies that combine improved wastewater treatment, adaptive soil management, and robust monitoring frameworks, ensuring that sustainable agriculture does not inadvertently amplify the global burden of antimicrobial resistance.

Author Contributions

A.I. conceptualized and designed the study and led the overall manuscript development. A.I. and M.A.S. conducted the literature search, screening, and synthesis of evidence on antimicrobial resistance dissemination in rice paddy ecosystems. A.H. contributed to data interpretation, particularly in environmental pathways, soil–plant–water interactions, and One Health perspectives, and provided critical revisions to the manuscript. All authors contributed to drafting, reviewing, and final approval of the manuscript and agree to be accountable for all aspects of the work.

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