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REVIEW

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Unraveling antibiotic resistance dynamics at the soil–plant interface under climate change for One Health

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Abstract

Antibiotic resistance genes (ARGs) naturally serve ecological and adaptive functions in microorganisms, yet human activities have disrupted this balance, accelerating their enrichment and spread in the soil–plant system. As a key ARG transmission interface across One Health sectors, the soil–plant system warrants greater attention. This review synthesizes emerging evidence on the distribution and transmission of resistomes in the rhizosphere, phyllosphere, and endosphere, revealing the potential risk of soil–plant ARGs to human, animal, and plant health. However, major gaps remain, particularly in horizontal and vertical ARG transmission associated within the plant endosphere and across plant generations. Moreover, we summarize key factors shaping soil–plant ARG dynamics, including soil conditions, plant evolution and traits, and anthropogenic influences. Among these, climate change emerges as a global, long-term, and largely irreversible driver, altering soil properties, plant physiology, and microbial activity through drastic environmental shifts. We discuss the risks of climate-driven ARG dissemination and its broader ecological and agricultural implications. Addressing these challenges requires advanced monitoring methods, integrated data sources, and policy innovations. In this review, we highlight climate change as an emerging driver of ARG selection and dissemination, emphasizing its impact on soil–plant resistome and the need for future One Health research on climate-driven resistome shifts.

Keywords Plant resistome, Antibiotic resistance gene, Climate change, One Health, Plant microbiome

Introduction

The resistome, encompassing all antibiotic resistance genes (ARGs) within a given environment, has gained significant attention because antibiotics and ARGs are emerging environmental contaminants [1, 2]. The soil–plant system, as a vital interface connecting human, animal, and environmental health, serves as a key reservoir of ARGs [3, 4]. The interconnected ecological network in the soil–plant system comprises soil, plant (rhizosphere, phyllosphere, and endosphere), and associated microorganisms, including bacteria, fungi, viruses, protozoa, etc. [5]. This system acts as a dynamic interface where ARGs persist, evolve, and transfer at the human-animal-environment nexus, posing serious health risks [4, 6]. Thus, a deeper understanding of the soil–plant systems within

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a One Health context—an integrated approach that recognizes the interconnectedness of human, animal, and environmental health and promotes cross-sector collaboration to prevent and respond to shared health threats—is crucial for mitigating the spread of ARGs [7].

ARGs are specific genes that encode proteins allowing bacteria to resist antibiotics [8]. They occur naturally in microorganisms as a defense strategy against environmental threats and as part of their metabolism, enabling adaptation to diverse ecological niches [9–11]. Strong selection pressures allow ARGs to persist in the soil–plant system, further contributing to their dissemination across different One Health sectors [12]. However, anthropogenic activities (such as manure application, wastewater irrigation, pesticide application, and post-harvest management) have indirectly shaped indigenous or directly introduced, selected, and enriched ARGs in the soil–plant system [3, 13–15]. Clinically, the spread of ARGs (e.g., those conferring resistance to beta-lactams, aminoglycosides, vancomycin, and tetracycline) from the soil–plant system to humans and animals can lead to treatment-resistant infections; while non-clinically, the accumulation of ARGs in the environment can disrupt ecological balances and affect agricultural productivity [4, 11, 16, 17].

Our understanding of plant resistomes has advanced in recent years; studies have revealed that diverse clinically and non-clinically relevant ARGs are present across various soil–plant niches, including the rhizosphere, phyllosphere, and even endosphere [4, 18, 19]. However, they are colonized by specifically adapted microbial communities, and accordingly, harbor ARGs of different compositions and abundances [20]. Researchers have found key microbial taxa as hosts of ARGs, highlighted how important environmental factors and plant traits shape resistome composition, and demonstrated the evidence of ARG transfer from the soil–plant resistome to human microbiomes [3, 21]. However, the influence of climate change—a global-scale, long-term, and largely irreversible environmental factor—on the behavior of plant resistomes remains largely understudied. Unlike conventional factors that influence ARG persistence in relatively stable conditions, climate change influences ARG dynamics through both direct and indirect pathways [22–24]. Climate change modifies environmental conditions, affects soil and plant performance, altering microbial communities and interactions, further shaping the dynamics of soil–plant resistomes [25, 26]. Such changes may exacerbate the dissemination of ARGs, heightening risks across human, animal, and environmental sectors.

This review aims to provide insights into the distribution, dissemination pathways, risks, and influencing factors of antibiotic resistance in the soil–plant system. By framing climate change as an emerging driver of ARG selection and dissemination, we aim to provide a comprehensive understanding of how this global challenge might affect the soil–plant resistome dynamics and inspire future research on climate-driven changes in the soil–plant resistome with a One Health perspective.

Distribution and transmission of ARGs in the soil–plant system

Soil serves as a reservoir of ARGs, with environmental filtering, niche differentiation, and antagonism between bacteria and fungi shaping microbial communities and promoting the persistence and dissemination of ARGs [27, 28]. Antibiotic resistance, the ability of microorganisms to survive antibiotics that normally inhibit or kill them, arises either from inheritance, genetic mutations, or horizontal gene transfer (HGT) [8, 29, 30]. Within the soil matrix, the rhizosphere provides a favorable environment for ARG proliferation and transmission [3]. As a unique, nutrient-rich interface between plant roots and soil, the rhizosphere harbors a high-density microbial community with distinct taxonomic composition compared to microbiomes in other plant-associated niches [5]. In the rhizosphere, microorganisms compete for abundant root exudates, and these intense microbial interactions enhance HGT [31]. Various bacterial orders, such as *Burkholderiales*, *Bacillales*, and *Enterobacteriales*, have been identified as potential ARG carriers in this zone [4], and a substantial proportion of antibiotic resistant bacteria (ARBs) found here exhibit resistance to multiple antibiotic classes [32]. Moreover, millions of years of plant–microbe co-evolution revealed a species-specific rhizosphere microbiome and resistomes across ~ 500,000 plant species, resulting in distinct ARG profiles and transfer potentials across diverse plant rhizospheres [20, 33]. HGT is the movement of genetic material between organisms without inheritance from parent to offspring, primarily facilitated by mobile genetic elements (MGEs) [34]. Conjugation (direct cell-to-cell transfer via plasmids), transformation (uptake of free DNA from the environment), and transduction (gene transfer mediated by bacteriophages) are the primary mechanisms of HGT facilitating ARG transmission among diverse microorganisms [35, 36]. Key rhizosphere colonizers such as Proteobacteria, Actinobacteria, and Firmicutes often harbor plasmids carrying ARGs, enabling ARG transmission into plant tissues [37, 38]. For example, soil *Bacilli* species can acquire exogenous genomic and plasmid DNA, potentially integrating free DNA fragments containing ARGs, thereby increasing the risk of ARG dissemination [39]. In addition, soil viruses also play a significant role as ARG carriers, with 16 unique ARGs detected in the soil

viromes [40, 41], and bacteriophages further potentiate ARG spread through transduction, shuttling resistance determinants between phylogenetically distant hosts [40, 41].

The below-ground rhizosphere can host up to 10^{10} cells per gram of soil, whereas the above-ground phyllosphere, exposed to air and harsh conditions, harbors only 10^5 to 10^9 cells per cm^2 on leaf surfaces [42, 43]. However, its global surface area is estimated to exceed 10^9 km^2, making it an expansive and significant microbial niche [42], along with its associated resistomes. The phyllosphere of plants exhibits a high diversity of ARGs but low overall abundance [44]. Studies have documented the presence of approximately 11 to 242 distinct ARGs in the phyllosphere of crops, including maize, endive, lettuce, arugula, and *Brassica chinensis* L. [38, 45–49], and non-crop plants including *Sphagnum*, *Chlorophytum comosum* and *Musa acuminata* [11, 50] (Table 1). Although bacterial diversity in the phyllosphere is low, plasmid transfer rate may still be high, as the specific mechanism remains unclear [51, 52]. Beyond bacterial hosts, increasing evidence suggests protists may serve as ARG vectors in the phyllosphere [53]. Recent research revealed that protists in the vegetable phyllosphere can harbor opportunistic pathogens carrying multiple ARGs [53]. This expands our understanding of phyllosphere resistomes and highlights the need for increased attention to phyllosphere protists as potential reservoirs and vectors of ARGs. Critically, a significant proportion of phyllosphere ARGs originate from soil ARGs or bioaerosols [54]. From a broader perspective, this underscores the necessity to evaluate plant surfaces not as isolated niches but as dynamic ARG filters across ecosystems.

Beyond the well-studied rhizosphere and phyllosphere, the plant endosphere constitutes a comparatively less-studied yet critical frontier in ARG dissemination. The plant endosphere microbiome harbors endogenous ARGs that are naturally prevalent with the plant microbiome [7]. In wild legumes, diverse ARGs have been detected in root nodules, with some bacterial isolates that exhibit high resistance to antibiotics such as ampicillin, chloramphenicol,

Table 1 The ARG numbers and dominant ARG types in the rhizosphere, phyllosphere, and endosphere of plants

Host species	Position	ARG types	Dominant ARG subtypes	Methodology	Refs
Coriandrum sativum, Cichorium endivia, Lactuca sativa, Brassica chinensis L.	Rhizosphere soil	61–73	Aminoglycoside, Beta-lactam, macrolide–lincosamide–streptogramin B (MLSB), and Multidrug	High-throughput quantitative PCR (HT-qPCR)	[38]
	Root endosphere	16–57	Aminoglycoside and Multidrug		
	Leaf endosphere	11–18	Multidrug and MLSB		
Zea mays	Phyllosphere	124	Multidrug, Beta-lactams and Chloramphenicol	HT-qPCR	[45]
Triticum aestivum	Phyllosphere	104	Aminoglycoside, Fluoroquinolones, Sulfonamide, and Multidrug	HT-qPCR and metagenomic analysis	[44]
Lactuca sativa	Phyllosphere	134	Aminoglycoside and Multidrug	HT-qPCR	[46]
Eruca sativa	Rhizosphere	1599	Fluoroquinolone, MLSB, and Aminocoumarin	Metagenomic analysis and cultivation	[47]
	Phyllosphere	2185	Fluoroquinolone, Chloramphenicol, and MLSB		
Brassica chinensis L.	Phyllosphere	82	Aminoglycoside, Beta-lactams, and Multidrug	HT-qPCR	[49]
Lactuca sativa	Rhizosphere	92	Aminoglycoside, MLSB, and Multidrug	HT-qPCR	[48]
Chlorophytum comosum	Phyllosphere	240	Multidrug and MLSB	Metagenomic analysis and cultivation	[50]
Musa acuminata	Phyllosphere	242			
Sphagnum	Phyllosphere (of gametophytes)	943	MLSB, Fluoroquinolone, and Tetracycline	Metagenomic analysis	[11]
Oryza sativa	Endosphere (seed)	99	Aminoglycoside, Multidrug, and Tetracycline	HT-qPCR	[57]
Solanum lycopersicum	Endosphere (xylem)	60–105	Aminoglycoside, Beta-lactam, Chloramphenicol, and Multidrug	Metagenomic analysis and single-cell raman spectroscopy	[19]
Malus domestica	Endosphere (fruit)	132	Fluoroquinolones, Polymyxin, Mupirocin, and Multidrug	Metagenomic analysis	[15]

and streptomycin [9, 55]. Apples harbor indigenous, low-abundance, and versatile resistomes, influenced by post-harvest transportation [15]. In the crop endosphere, genera such as *Enterobacter*, *Acinetobacter*, *Pseudomonas*, and *Staphylococcus* often carry ARGs [56]. Notably, emerging evidence showed that ARGs are prevalent in various endospheric niches, including the xylem and seeds [19, 57, 58], revealing new pathways for ARG migration within the plant. Li et al. found that the majority of the xylem microbiome originated from the soil, with ARG abundance 2–6 times higher in the xylem than the rhizosphere, suggesting soil-to-phyllosphere ARBs migration via the xylem and stem [19]. Beyond vegetative organs, recent studies highlight seeds as potential vectors for ARG vertical transmission. ARGs have been detected in seeds and subsequently in the progeny rhizosphere [57, 58], emphasizing the potential risk of seeds as long-term ARG reservoirs. However, the mechanisms of ARG transmission in the endosphere and vertical inheritance between plant generations require further investigation. Overall, the soil–plant system functions as a multilayer ARG reservoir and exchange hub, bridging human, animal, and environmental health within the One Health framework (Fig. 1).

Risk of antibiotic resistance gene dissemination in the soil–plant system

(1) Potential human and animal exposure risk

The dissemination of ARGs in the soil–plant system poses significant risks to human and animal health through various pathways. At the molecular level, ARGs can move from the soil-plant system to the animal microbiome when animals get in contact with soil or plants carrying these genes [3, 59]. The microbiome of fruits and vegetables often contains intrinsic ARGs, which can be enriched under antibiotic or pesticide pressure and become more abundant due to contamination from manure or wastewater [60]. Consequently, fresh produce may act as a reservoir for antibiotic-resistant bacteria, underscoring the significant role that diet plays in the transmission of antibiotic resistance genes from food to humans [21]. A metagenomic analysis revealed a strong connection between the high-risk ARGs in human feces and the park environment

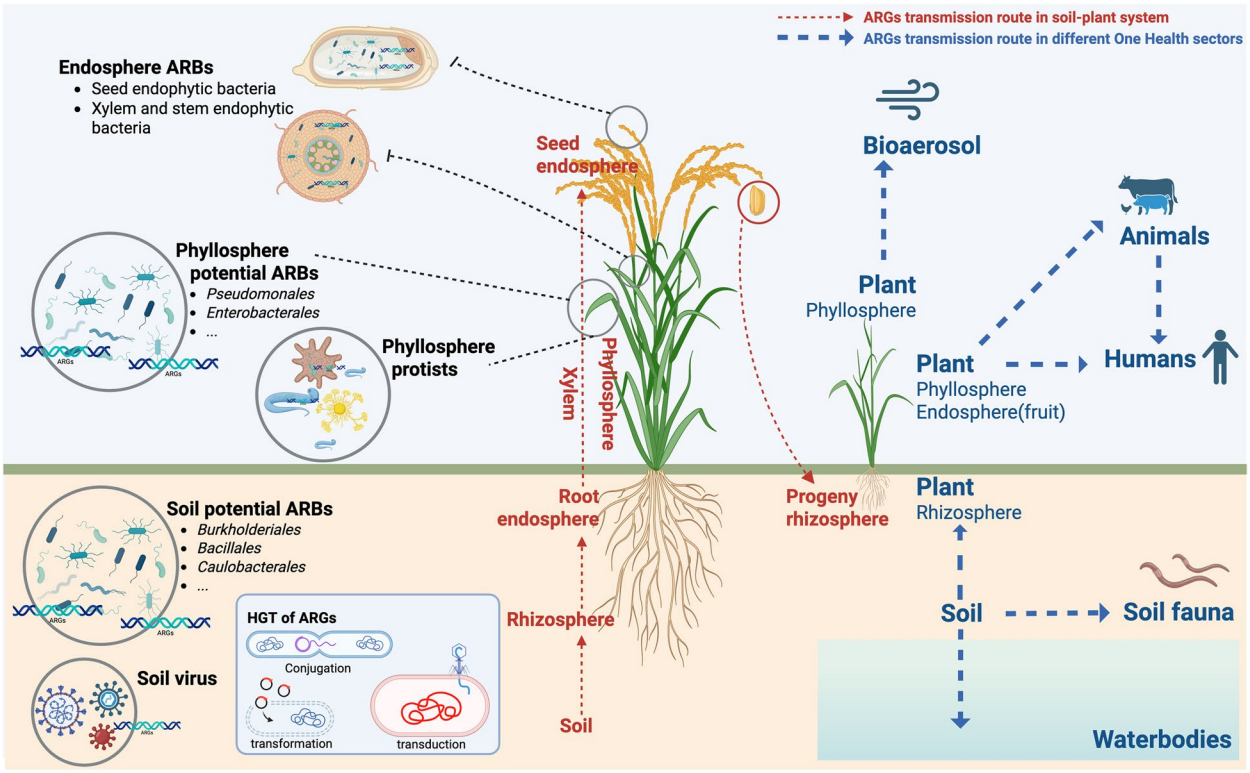


Fig. 1 Schematic of the distribution and transmission of ARGs in the soil–plant system in the context of One Health framework. Left: illustration of ARG distribution and transmission processes within the soil–plant system, including rhizosphere, phyllosphere, and plant endosphere compartments. A detailed inset highlights key HGT mechanisms—conjugation, transformation, and transduction—that operate broadly within this system. Right: representation of the soil–plant system as a central interface for ARG dissemination across human, animal, and environmental health sectors under the One Health framework. ARBs, antibiotic resistant bacteria; ARGs, antibiotic resistance genes; HGT, horizontal gene transfer. Created with https://www.BioRender.com/

resistomes, suggesting potential high-risk ARGs transmission between humans and the environment [61]. More importantly, foodborne pathogens, such as *Campylobacter* spp., *Bacillus cereus*, *Staphylococcus aureus* and *Enterococcus* spp., may gain antibiotic resistance via horizontal or vertical gene transfer leading to hard-to-treat human infections [62, 63]. Likewise, phytopathogens, such as *Agrobacterium* and *Erwinia* species, can acquire ARGs and cause human and animal diseases, further extending the health risks of plant-associated microbes [64]. Trophic transmission is another key route, where ARGs move up the food chain through the consumption of plant products [56, 65]. In bayberry orchard ecosystems, ARG levels increased along the soil-bayberry-fruit fly food chain, driven mainly by increasing antibiotic and pesticide concentrations [13]. Metagenomic evidence supports the risk of ARGs spreading from produce-associated microbes to the human gut microbiome [65, 66]. Moreover, global travel and trade can carry ARGs on plant products across regions, further exacerbating the worldwide spread of resistance [3, 64]. These interconnected pathways highlight the critical need for monitoring and control strategies to prevent the spread of antibiotic resistance through the soil–plant continuum to humans and animals.

(2) Potential plant health risk

In nature, ARGs are survival strategies evolved by microorganisms, including those within the plant microbiome, and play a dual role in plant-microbiome interaction [67]. On one hand, plant-derived antimicrobial compounds selectively enrich ARG-harboring microbiota, particularly beneficial symbionts like *Pseudomonas* spp. that antagonize pathogens while maintaining intrinsic resistance profiles [10]. However, this adaptive advantage becomes a disadvantage under anthropogenic disturbances, as dysbiosis weakens microbial biocontrol functions [5]. This is particularly likely to happen under climate change conditions, which involve drastic environmental changes such as high temperatures, drought, and floods. Crucially, the transfer of resistance traits from non-pathogenic bacteria to plant pathogens can enhance pathogen virulence, posing new challenges for plant health management [52, 68–70]. Although the influence of ARGs on plant health is recognized, our understanding remains incomplete. Further studies are needed to elucidate the dual role of ARGs in maintaining plant microbiome homeostasis and resilience under environmental pressures.

Factors affecting antibiotic resistance genes in the soil–plant system

(1) Soil factors

Both abiotic and biotic factors shape ARG distribution, abundance, and mobility within the soil, ultimately affecting their transfer to plants. Abiotic factors include soil type, pH, heavy metals, microplastics, herbicides, and pesticides [71–74]. According to a global analysis, soil nutrients accounted for 7% of the variability in ARG abundance [75]. The variable soil pH affects the soil ARG profiles by influencing the assembly of microbial communities, and alter the antibiotics sorption and desorption on soil particles [71]. Additionally, soil moisture conditions and drying-rewetting cycles can enhance plasmid conjugation, further promoting ARG transfer in soil microbiomes [76]. Heavy metals apply selective pressure on metal resistance genes in soil bacteria, which often co-occur with ARGs [73]. Similarly, increased pesticides contribute to ARG accumulation, evolution and HGT [77]. These multiple pollutant inputs from human activities demand further investigation and consideration in practical applications.

Interactions between soil fungi and bacteria, such as competition for nutrients and mutualistic associations, also influence community composition and can indirectly affect ARG dynamics by altering bacterial abundance and activity [23, 27]. In addition, their hyphal networks can facilitate microbial dispersal, potentially affecting ARG transmission [78]. Other biotic factors, such as pathogen invasion and soil fauna activities, also significantly impact soil resistomes [79, 80]. A metagenomic analysis revealed that the invasion of pathogen *Ralstonia solanacearum* led to ARG enrichment by activating the ARG-rich taxa to restrict the biotic stress [80]. This pathogen-ARG interaction underscores the need to integrate soil-borne disease ecology into One Health risk assessments, as agricultural intensification escalates both pathogen outbreaks and antibiotic resistance co-selection. Concurrently, soil fauna modulates soil ARG profiles through their physical activities, including burrowing, gut digestion, and mucus release [81, 82]. However, burrowing halts when soil dries, because earthworm movement is constrained by hydromechanical conditions sensitive to climate [83]. Despite this, burrowing can still reduce the relative abundance of ARGs by loosening soil structure and increasing oxygen content, which inhibits anaerobic ARBs [84]. In addition, the gut of earthworms, collembolans, and nematodes can serve as ARG reservoirs, manure application significantly stimulated HGT in earthworm guts [79, 85, 86]. Nevertheless, critical knowledge gaps remain regarding how soil fauna influence ARG transmission and distribution beyond their physical activities, especially at the soil–plant interface.

(2) Plant factors

Throughout their evolution, plants have developed diverse interactions with microbes, leading to specialized microbial communities that influence ARGs

accumulation and transmission [20, 33]. These evolutionary shifts have likely shaped specialized microbial communities, contributing to ARG accumulation in both phyllosphere and rhizosphere [44, 87]. Fungal endophytes can also shape plant-associated microbiomes and thus indirectly influence ARG distribution [26], though their role remains largely underexplored. Besides, other factors influencing the plant microbial community also indirectly shape the soil–plant resistomes. Plant-associated traits, such as species, genotype, and nutrient composition, play pivotal roles in determining microbial diversity and activity, which in turn affect ARG dynamics [18, 38, 44]. In vegetables, plant species strongly influence ARG abundance and distribution [38]. Xiang et al. found that host gene variation altered phyllosphere resistomes by modulating *Pseudomonas* spp. through plant-derived metabolite DIMBOA-Glc (2,4-dihydroxy-7-methoxy-1,4-benzoxazin-3-one glucoside) [44]. A multi-generation study showed that approximately 60% of ARGs associated with beneficial microbiomes, linking ARG enrichment to host plant life strategies [87]. Thus, the long evolutionary history of plants, in combination with their current traits, shapes the dynamics of plant-associated resistomes in a way that must be considered when analyzing ARGs in the soil–plant system.

Root exudates were also important factors in shaping the rhizosphere microbiome and indirectly shaping the plant resistomes [5]. A metabolome analysis showed that tomato defensive root exudates reduced ARG abundance by selectively shaping rhizosphere microbial communities [88]. Conversely, high-molecular-weight root exudates can trap antibiotic compounds and boost the expression of specific tetracycline resistance genes [89]. Additionally, rhizosphere metabolic processes may interact with phyllosphere microbial communities, potentially influencing phyllosphere microbiome and resistomes [5, 54], though this remains a topic requiring further investigation.

(3) Anthropogenic influence

Anthropogenic activities are a major contributor to the input and dissemination of ARGs in the soil–plant system, which accounts for 58% of soil ARG variability globally [1, 75, 90]. Agricultural practices, such as manure application, irrigation of reclaimed wastewater, pesticide and herbicide application, post-harvest management, and breeding strategies strongly shape the abundance and diversity of ARGs [15, 77, 91]. For instance, poultry and swine manures exerted greater selection pressure on soil resistomes than cattle manure, and combining manure and antibiotics can enhance the HGT of ARGs [91]. Herbicide can promote antibiotic resistance by increasing cell membrane permeability and plasmid conjugation frequency [14]. Post-harvest handling, storage, and transportation, can affect the composition of bacterial communities and their ARGs by altering the environmental conditions [15, 92]. Intensive breeding often reduces microbial diversity, favoring the proliferation of copiotrophic bacteria [93], may influence plant-associated resistomes. Additionally, targeted breeding can modify plant–microbe interactions, further shaping the soil–plant resistome.

Beyond these direct anthropogenic influences, recent advances have further highlighted the multifaceted impact of anthropogenic inputs. The application of organic fertilizers increased bacteria-virus interactions, raising the potential for ARG exchange between viruses and their microbial hosts [40]. Additionally, microplastics, a byproduct of human activities, act as ARG vectors, facilitating their transport and exchange within the soil–plant continuum [94]. Greater microplastic diversity correlates with higher ARG abundance and richness, and other global changes, such as fungicide use and reduced plant diversity, further amplify ARG proliferation [95].

While anthropogenic activities directly introduce or select ARGs in the soil–plant system, climate change, another consequence of human activity, emerges as the second most influential driver of global soil ARG distribution [75]. Climate change acts as a global-scale, long-term, and largely irreversible driver that modifies the environmental conditions governing ARG persistence, transfer, and evolution [22, 96]. Unlike antibiotics, pesticides, and microplastics, which exert selective pressure or serve as direct ARG carriers, climate change influences ARG dynamics indirectly by altering environmental conditions that affect the soil and plant microbiomes [22, 24]. Studies indicate that global warming accelerates HGT and heightens health risks associated with ARGs [24]. Free-air CO_2 enrichment experiments revealed that elevated CO_2 levels can suppress certain ARG hosts, reducing their relative abundance, while paradoxically increasing overall ARG levels by shifting bacterial composition and modifying bacteria-fungi interactions [25, 26]. However, research on the effects of global change on the soil–plant resistome remains limited, and its long-term ecological consequences are largely unexplored. Addressing the links between climate change and antibiotic resistance requires greater attention and integrated governance to address One-Health issues.

Impact of climate change on antibiotic resistance dissemination in the soil–plant system

Climate change can influence ARG dissemination both directly and indirectly. Directly, thawing cryospheric regions may release ancient and active ARGs, posing potential risks to Arctic soils and vegetation [97–99].

Although their current spread is constrained by limited dispersal with mainly vertical transfer, continued warming may enhance their mobility and ecological impact, warranting further investigation. Indirectly, climate change modifies environmental conditions that regulate soil–plant microbiome activity, affecting ARG persistence and mobility [22, 96]. Rising temperatures, altered precipitation patterns, and increased CO_2 levels change soil properties, plant physiological performance, and microbial activities [100], which in turn influence soil–plant resistomes. For example, a five-year climate warming experiment showed that major categories of antibiotics, including aminoglycoside, beta-lactam, MLSB, and multidrug resistance were enriched in forest soil under climate warming [23]. Higher temperatures increase membrane fluidity, induce stress responses (SOS), and enhance transposase and conjugative plasmid activity, leading to more efficient HGT of ARGs [101–103]. Although direct evidence remains limited, warming may also enhance virus-mediated ARG transfer via prophage activation and SOS response [104]. Increased CO_2 concentrations reshaped rhizosphere microbial communities by modifying soil and plant carbon-to-nitrogen ratios, as well as increasing cell membrane permeability, therefore indirectly selecting specific ARGs [25]. Studies revealed that elevated CO_2 reduced the relative abundance of soil ARGs, *sul2*, *tetG*, and *intl1* by inhibiting the ARG's hosts [25], while beta-lactamase genes in the rice seed endosphere increased under the same conditions [26]. Changes in precipitation, flooding, and drought, affect soil properties and plant growth [96], but their impact on soil–plant resistomes remains unexplored. Soil moisture can facilitate the activity of MGEs by enhancing microbial biomass and activity, potentially increasing ARG dissemination among bacteria [105, 106]. Although the number of soil resistome studies under climate change is growing, research on plant-associated resistomes remains in their early stages, and the influence of long-lasting climate change on soil–plant resistomes remains largely unexplored. Future research should also investigate fungal communities' roles in ARG dissemination within the soil–plant system. Given their influence on plant–microbe interactions and microbial network structure [107], fungi may be an overlooked yet significant factor in climate-driven resistome dynamics.

Beyond the effects on microbiome activities, climate change triggers cascading ecological consequences that may amplify ARG transmission risks [108]. For example, the frequent use of reclaimed water due to global water supply shortage from climate change increase the likelihood of ARG entering the soil and crops through irrigation [109]. More importantly, climate-induced crop yield reductions can push farmers toward agricultural intensification, leading to increased fertilizer, herbicide, and pesticide use [108, 110, 111]. This, in turn, disrupts soil microbial diversity, potentially shifting ARG hosts from rare species to dominant taxa, thereby enhancing ARG persistence and mobility within microbial communities [14]. With climate change accelerating at an unprecedented rate, the soil–plant system risks becoming a

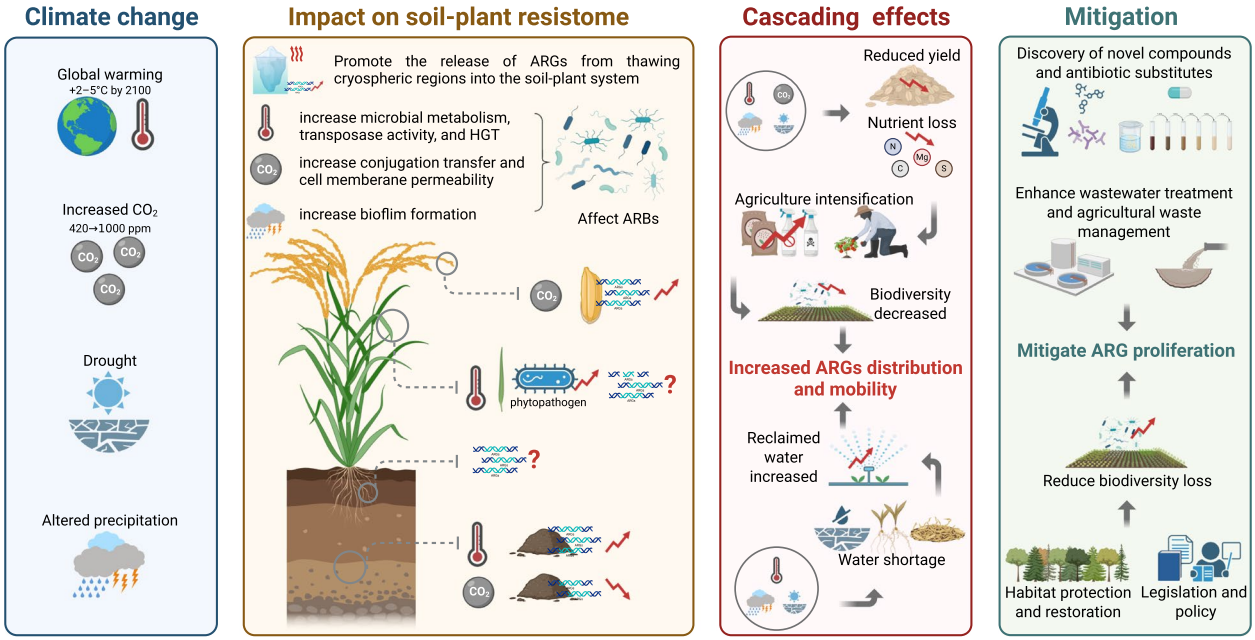


Fig. 2 Schematic of how climate change would affect the ARGs in the soil–plant system. Created with BioRender.com

critical amplifier and evolutionary hotspot for ARG accumulation and dissemination (Fig. 2).

To address this emerging threat, several strategies are essential. First, the discovery of novel compounds or antibiotic substitutes (vaccines, phytochemicals, antimicrobial peptides, probiotics, etc.) is crucial to counteract the increasing prevalence of resistant pathogens [62]. Second, promoting sustainable agricultural practices to include enhanced wastewater treatment and agricultural waste management, especially under climate change. Finally, we should prioritize conserving microbial diversity in soil–plant system to curb the possible proliferation potential of resistant strains. Implementing these strategies is crucial to mitigate ARG proliferation and preserving microbiome stability in the face of climate change.

Conclusion and future perspective

Substantial progress has been made in elucidating the distribution, transmission, and risk associated with soil–plant resistomes. Available data confirms that diverse ARGs are present and actively exchanged across soil, rhizosphere, phyllosphere, and plant endosphere. The soil–plant system serves as a critical interface for ARG dissemination at the convergence of human, animal, and environmental health, which aligns with the One Health framework. This interconnectivity underscores the potential for soil–plant ARGs to influence broader public and ecosystem health. Key factors, including soil biotic/abiotic factors, plant traits, and anthropogenic activities, play pivotal roles in shaping, selecting, and enriching ARGs in the soil–plant system. However, climate change introduces additional complexity by altering environmental conditions that govern microbial community dynamics, thereby intensifying the potential for ARG dissemination across One Health sectors.

Given the global-scale, long-term, and largely irreversible implications of climate change, further research is crucial to elucidate how climate-driven processes reshape soil–plant resistome and influence global antibiotic resistance management. This field must be driven by advanced methods for monitoring and assessing ARG dynamics, supported by complementary data sources as well as policy advancement. (1) Decipher key ARG hosts (e.g., multidrug-resistant *Pseudomonas* and *Enterobacter* strains) and their climate-responsive genomic traits to identify high-risk microbiota signatures. To overcome current limitations in ARG detection, multi-omics approaches such as metagenomics and transcriptomics, as well as emerging microbial bioelectronic sensors offer transformative potential [112]. (2) Develop AI-driven "Climate-ARG" predictive models that integrate environmental parameters and climate forecasts to predict ARG-climate synergies. Using machine learning models, high-risk combinations of ARGs and climate factors can be identified, enabling proactive monitoring and mitigation strategies. (3) Implement actionable strategies, such as regulating manure application in flood-prone zones, establishing ARG monitoring in agricultural runoff, and mandating risk assessments of wastewater reuse under extreme weather conditions. Importantly, the link between ARG dissemination and climate change should be formally integrated into climate adaptation frameworks, such as the IPCC's health chapters and One Health policies. Altogether, combining real-time sensing, predictive modeling, and actionable policy frameworks will strengthen One Health strategies for ARG control in the soil–plant system under future climate scenarios.

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Authors' contributions
X.Y.Li. and Y.G.Z. contributed to the conception and design of the review. X.Y.Li. drafted the manuscript and prepared the figures. S.B., W.A.W., X.Y.Lin, G.B., and Y.G.Z. substantively revised the manuscript. All authors read and approved the final version.

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Data availability
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Declarations

Ethics approval and consent to participate
Not applicable.

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Competing interests
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