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Review

Impact of Abiotic Stressors on Soil Microbial Communities: A Focus on Antibiotics and Their Interactions with Emerging Pollutants

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Abstract: Soil is a complex and dynamic ecosystem containing a diverse array of microorganisms, and plays a crucial and multifaceted role in various functions of the ecosystem. Substantial fluctuations in the environmental conditions arise from diverse global changes. The microbial shifts in the soil in concordance with the changing environmental factors, or a combination of these factors, are of high significance. Exploring the contribution of global change drivers to the microbial community to improve the predictions of the response of the microbial community to the functioning of the ecosystem is of prime importance. Promoting the health of soil microorganisms maintains the overall health and fertility of the soil, which in turn supports the health of terrestrial ecosystems and agricultural systems. The current review aims to assemble different abiotic factors or stressors that exist in the environment that affect the microbial community. More focus will be given to one of the stressors—antibiotics, a recent emerging pollutant. The effects on the soil microbial community and the future of soil health due to the presence of antibiotics will be addressed. The scope of the interaction of antibiotics with other pollutants like plastics and heavy metals (HMs) will be examined.

Keywords: soil microbial communities; abiotic stressors; antibiotic pollution; emerging pollutants; soil health

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1. Introduction

Soil is a critical component crucial for plant nutrition, nutrient cycling, water purification, biodiversity conservation, carbon sequestration, and regulation of climate [1,2]. It serves as a source and depot of beneficial microorganisms, pathogens, and total diversity of microbes [3]. The interconnectedness of soil, animals, humans, plants, and microbiomes is now understood to be more intricate than previously known. Hence, soil serves as the cornerstone of the holistic health of the environment [4]. In addition to providing several ecosystem services like maintaining plant production and water quality, healthy soil also regulates the decomposition and recycling of soil nutrients and absorbs greenhouse gases from the environment [5,6].

In recent decades, publications with the word "soil health" have exponentially increased [7]. It is an inherent property of soil, where soil microorganisms drive the metabolism and transformation processes of harmful substances and biological elements [6]. These processes play a vital role in the functioning of the soil–microorganism–plant–animal ecosystem and ultimately affect human health. Along with key challenges, including climate change, environmental degradation, and global food security, maintaining healthy soil is critical to

life, emphasizing the significance of soil health research. There are various soil qualities that benefit agroecosystems, such as water and nutrient cycling, suppression of plant pathogens, pollution reduction, and biodiversity. The biological (microorganisms, flora and fauna), physical (aggregation, porosity, texture), and chemical (pH, soluble salts, cation exchange capacity) indicators that link these functions are used to rate soil health [8] (Figure 1).

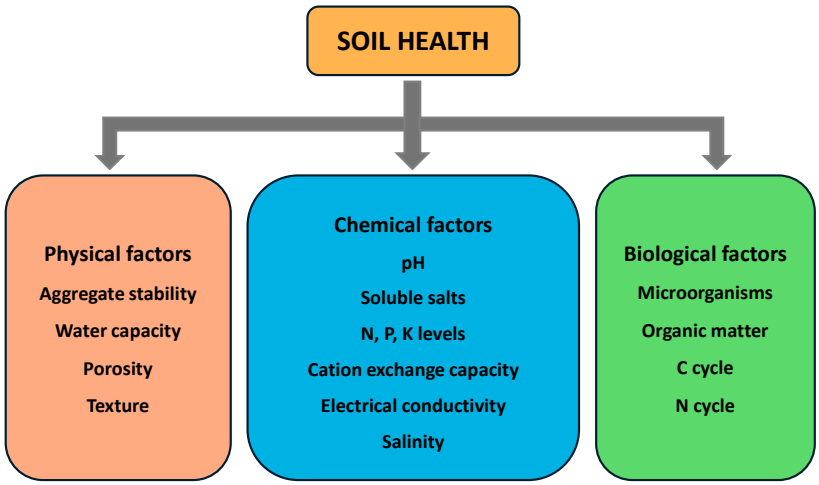


Figure 1. Factors contributing to soil health.

Soil microbial diversity is a biological indicator of soil health. A major part of soil fertility, plant health, and plant nutrition are contributed by it [9]. Microorganisms living in the soil are abundant and highly diverse, with estimates of up to 10^9 cells and 10^4 species per gram of soil [10,11]. The biological activities inside the soil are an important element shaping the function and structure of the soil. Soil microorganisms play a vital role in regulating soil nutrient cycle and plant productivity. These microbes release nutrients, mainly, N, P, and S, after mineralization of organic matter (OM). This adds to the health of the soil and, in turn, the sake of the whole ecosystem. Their action and diversity are thus the primary determinants of soil health [6,12]. Because soil biological health is so sensitive to various environmental effects, it is a major component of agricultural output, and it has become a worldwide concern [13].

The soil microbiota is of great importance in maintaining the balance of the ecosystem. There is an increased research interest in determining soil microbial biomass, diversity, and composition in ecosystem functioning due to its ability to change soil quality following a land-use change [14]. The soil microbiome field is now focusing on revealing the interactions between microorganisms and their environment and their underlying mechanisms. Numerous biotic and abiotic factors alter the functions and composition of soil microbial communities, which in turn impact the quality of their environment [15]. Many environmental conditions impact microbial communities, and the interactions between microbial communities and environmental factors serve as indicators of the composition [16]. This ecosystem is more vulnerable to alterations in environmental conditions than any other ecosystem. Moreover, these factors can also be indirectly influenced because of various anthropogenic activities. In the context of global climate change and agricultural modernization, it is crucial to gather different elements affecting the soil microbiota to conserve and utilize them effectively for the well-being of the whole ecosystem. We aim to examine various environmental abiotic factors and stressors affecting the soil microbial community structure and its composition and suggest areas for further research. In addition, recent studies have an intense focus on the consequences of antibiotics on the soil microbiota in the frame of One-health. Soil, as a direct receptor of antibiotics in the veterinary and

agricultural areas, has received very little attention. Thus, this review also examines various studies in this area and identifies existing research gaps.

2. Survey Methodology

A random search was conducted on Scopus on the topic "the environmental factors affecting soil microorganisms". On analyzing the results, 698 documents published from 2000 to 2023 were found (Figure 2). Moreover, the number of research studies has shown to be doubled when comparing the years 2020 (73 papers) and 2023 (139 papers). This indicates the importance of focusing more on studies in this field. Relevant papers were also searched for using the Google Scholar search engine and to broaden the searched field. Initially, the phrase "environmental factors affecting soil microbiome" was used for the search. Various factors were noted, and each factor (e.g., pH, temperature, elevation, etc.) was searched for in combination with "soil microbial community" for relevant articles. The search on "antibiotics" along with the previous phrase generated a limited number of articles, whereas a search on "plastic interaction on antibiotics" displayed an escalation of published documents (195 articles) in the past 3 years, of which only a few studies have concentrated on its influence on soil microbiomes. Our interest via this review is to draw attention to "antibiotics" as an emerging environmental concern to examine their effects on the soil microbiome, and to identify and address the research gaps related to the field. The findings illustrated in Figure 2 are based on document analysis from 2000 to 2023, which highlights the significant interest of scientists in understanding the alterations happening to the microbiota due to various environmental stressors to mitigate their impact on the agricultural sector and living beings.

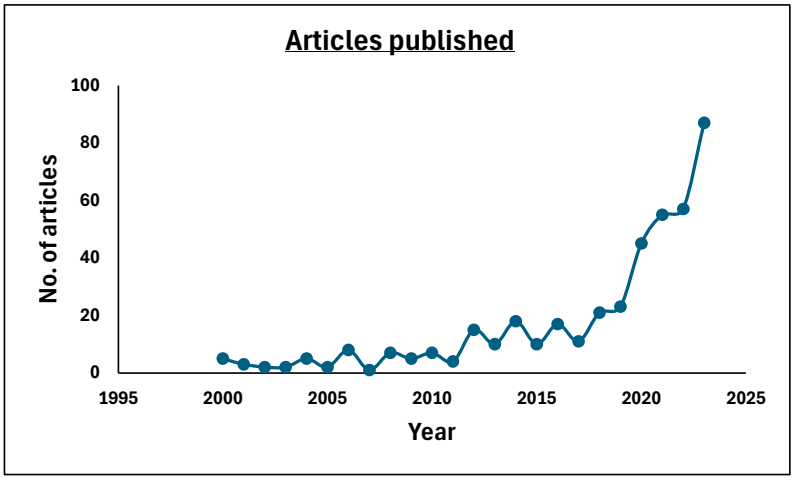


Figure 2. Results generated on Scopus on analyzing the documents from the year 2000 to 2023 on the topic "environmental factors affecting soil microorganisms".

3. Soil Microbiome and Its Importance

The soil microbiota contains crucial components of the ecosystem that contribute to different ecosystem services, and hence, they directly and indirectly influence the health of plants and animals [17]. The extreme heterogeneity of soil environmental circumstances contributes to the rich diversity of soil microbial communities. Numerous different microbial habitats with distinctive microbial assemblages can be found in a single soil [18].

Soil lodges different microorganisms, like archaea, bacteria, protists, actinomycetes, nematodes, protozoa, fungi, and viruses [19]. The most prevalent and varied microorganisms in soil are fungi and bacteria, which have a high degree of environmental adaptation [20,21]. *Azotobacter* are free-living nitrogen-fixing bacteria, whereas *Rhizobium* species are known to

fix nitrogen in legumes [20]. Anaerobic, anoxygenic facultative cyanobacteria; green sulfur bacteria; and phototrophic sulfide-oxidizing purple bacteria are a few bacteria involved in the sulfur cycle. Phosphorus-soluble microorganisms like *Pseudomonas*, *Rhizobium*, *Aspergillus*, *Bacillus*, *Penicillium*, arbuscular mycorrhizal fungi (AMF), and actinomycetes are also embedded in the soil [22]. Acidobacteria is the second most abundant type of bacteria and plays a crucial role in the soil carbon cycle. Proteobacteria and AMF are the microbes related to C cycling [21]. These soil microorganisms are involved in various reactions, such as biodegradation, biomass decomposition, antibiotic production for pathogen defense, nutrient uptake, maintenance of soil structure, and stress tolerance in the soil [23]. The richness of bacteria and archaea can vary significantly depending on the soil [24]. The abundance of living organisms in the soil is provided in Figure 3.

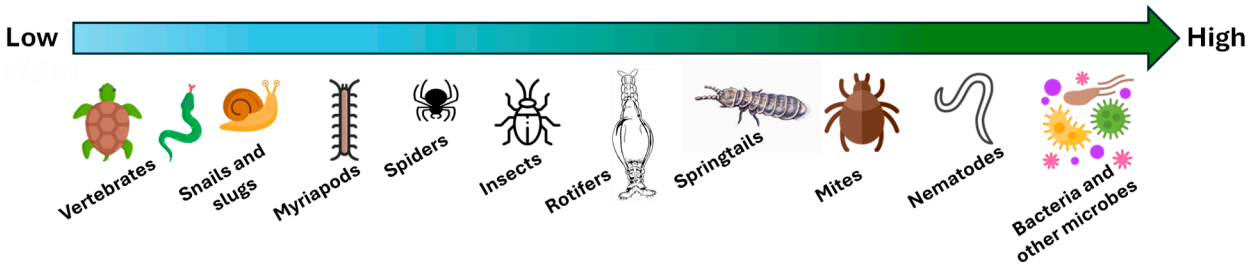


Figure 3. The abundance and diversity of common living organisms found in the soil.

4. Abiotic Factors Shaping the Soil Microbiome

In the soil, microbiomes respond to and interact with various environmental variables, resulting in alterations in the structure and composition of the microbial community. These serve as indicators of the composition and operation of the ecosystem. An array of abiotic factors, including plant species, soil type, soil properties, moisture content, climate, and management practices, collectively shape the microbial populations within the rhizosphere and soil of agroecosystems [16]. Various environmental abiotic factors affecting the soil microbial structure, community, composition, and diversity are shown in Table 1.

Table 1. List of selected studies on environmental abiotic factors shaping the soil microbiome.

Factors Affecting Microbial Community	Comments	References
Temperature	Directly or indirectly affect microbial community, complexity, community composition, stability of their interaction, and nutrient cycling (C, P, K, N).	[25–29]
Seasonal dynamics	Microbial diversity, composition, and function display variations based on the seasons.	[30–34]
Aeration	Varied according to the soil depth and properties; oxygenation of soil rhizosphere enhanced soil health and optimized soil microbiome.	[35,36]
Elevation	Soil properties, climatic conditions, etc., play a dominant role in structuring bacterial communities along the elevational gradient.	[37–40]
Soil physical properties (soil type, texture, clay content, grain content)	Soil type resulting from land use management practices influence the structure and composition of microbial communities.	[41–43]

Table 1. *Cont.*

Factors Affecting Microbial Community	Comments	References
Saline alkali degradation/restoration	Saline and alkali degradation has a negative effect on bacterial and fungal community structure; soil amendments increased the abundance of bacteria.	[44,45]
Light	Important effects on the microbial community structure and interaction; light structures the phototrophic, bacterial, and fungal communities at the soil surface.	[46–48]
Soil water content (rainfall, precipitation, moisture etc.)	Modulates microbial abundance and biodiversity.	[49–54]
Soil pH	Universal factor directly affecting soil microbial diversity, activity, and community composition.	[55–58]
Soil chemical properties (pH, NO_3^--N, available phosphorus, C:N:P)	Governs the bacterial and fungal community distribution and composition.	[50,59–61]
Soil salinity (assessed as electrical conductivity (EC))	Salinity stress in different saline habitats induces various responses in the soil microbial community and microbial functional genes due to the alterations in soil properties (i.e., low water availability and ionic toxicity).	[62–65]
Soil depth	Soil microbial diversity decreased with depth in soils.	[66–71]
Soil nutrient availability	Enriched various microbial taxa and communities and their interconnections across soil depth.	[67,72,73]

Most of the physico-chemical properties and the above-ground plant attributes govern the soil microbiome. The structure and composition of soil microbial taxa are influenced by plant diversity. The significant resistance of soil microbial and fungal communities (e.g., during drought) has been improved by the increased availability of soil resources along the plant diversity gradient [74]. In addition, the plant root and associated microbiome is considered a holobiont, which forms an ecosystem unit. Plant roots can interact with the microorganisms in the rhizosphere by secreting various chemical compounds. Various interactions that occur between them may be synergistic or antagonistic, or show metabolic cooperation with various signaling responses and microbial dysbiosis [75,76]. Thus, this communication between the plant and the microbiome is known to be an integral element of the ecosystem [77,78].

The soil archaeal and bacterial diversity decrease with soil depth [66,69], while fungal taxa vary with respect to soil depth [68]. It was found that the depth of the soil has a higher impact on the sulfur biological cycle and microbial communities than the salinity factor [70]. Root morphological traits like surface area, diameter, and length were major factors explaining the variations in rhizosphere soil fungal and bacterial communities in alpine ecosystems [72]. The ratios of fungi to bacteria and Gram-positive to Gram-negative bacteria are expected to respond to fine root traits that are linked to root quality [73]. A recent study in the Arctic tundra provided new insights into the relationships between rhizosphere microbial communities and fine root traits and was useful for predicting the abundance of major microbial groups [74]. Thus, understanding the root microbial interplays and their symbiotic relationships is important to understanding the future ecosystem.

Seasonal dynamics change the physicochemical properties of soil, which in turn affect the microbial diversity, composition, and functions [30,31]. The diversity of the fungal community showed more seasonal variability than the diversity of the bacterial community. For instance, the seasons (spring, summer, autumn, and winter) and habitats (rhizosphere

and bulk soil) of two temperate forests situated in Dongling mountain, Beijing, had significant effects on microbial composition, which ultimately affects the biogeochemical cycles [34]. This study identifies that the functional groups in fungi are more susceptible to environmental seasonal variations than the bacteria. In an experimental setup of mesotopic grassland in UK, unlike the fungal communities, drought-induced alterations in the plant community have a long-lasting impact on the bacterial community [31]. An examination of bulk soil from six forest stands in Zhuyu Bay, Jiangsu, revealed higher diversity in spring than in summer and autumn, where *Proteobacteria* and *Ascomycota* were the dominant bacterial and fungal phyla across all the stand soils [33]. More insights into the alteration in the microbial community concurrent to seasonal variations help us to understand the impact of global climate change on soil.

Environmental factors like soil carbon and nitrogen content critically affect the bacterial community distribution in the alpine–tundra ecosystem along elevations on Changbai Mountain in China [39]. More than 75% of the bacterial genomes from each of the Changbai Mountain soils belong to the major phyla, which include *Acidobacteria*, *Alphaproteobacteria*, *Actinobacteria*, *Betaproteobacteria*, and *Gammaproteobacteria*. The distinct responses of the fungal, bacterial, and archaeal communities to soil nutrients in the alpine ecosystem of the Eastern Tibetan Plateau demonstrated the metabolic diversity of the microbial taxa *proteobacteria* and *acidobacteria* [59]. The ecological and soil resource stoichiometry (C:N, N:P, C:P ratios) is reflected in the microbial structure and diversity. The findings show that variations in the availability of C, N, and P as well as C:N:P ratios due to land use can modify the makeup of bacteria in the soil [60]. Low C:N, N:P, and C:P ratios, which frequently characterize ideal circumstances for bacterial-dominated communities, high P availability, and decreased soil organic matter, contribute to the pinnacle of bacterial diversity.

Mountains, which are integral components of the terrestrial ecosystem, are ideal places to study the impacts on microbial distribution patterns over short geographic distances. The microbial responses and the structural and functional patterns in the mid-subtropical forest ecosystems in Wuyi Mountain of China are mainly due to the influence of climatic factors on the plant diversity along the elevation gradient [77]. Prior studies indicate that shifts in soil properties like soil pH, total phosphorus, and organic carbon are major factors that govern microbial distribution along the elevational gradient. Alterations in the soil physicochemical properties induced by climatic change along the elevation were important factors in determining the plant-associated microbial communities in the terrestrial forest. The abundance of the fungal community in the rhizosphere decreased with an increase in elevation [78]. The specific microbial N-cycling genes varied along the elevation gradient of the Tibetan grassland due to the variations in the soil, vegetation, and climatic conditions [40]. The elevation gradient is thus an important factor necessary to be considered, especially for mountain ecosystems that harbor complicated soil properties and abundant biodiversity [37,38].

Soil bacterial alpha diversity and community composition are mainly due to alterations in the pH, whereas fungal shifts along the elevation are mainly due to the soil organic matter (SOM) and nutritional status along the elevational gradient [55,79]. Narrow pH ranges are required for the optimal growth of bacteria; thus, pH has a strong influence on bacterial community distribution compared to that of the fungal community, which supports the growth discovered in [55,79] and a wider pH range [55]. Bacterial communities and phylogenic diversities were significantly correlated with salt content and soil pH in saline soils in Northwest China [80]. Increased soil pH due to bamboo forest expansion has increased the soil bacterial and fungal diversity [48,81]. The bacterial distribution in the lake sediments across the Tibetan Plateau is driven by soil pH. For instance, the lake sediments revealed high relative abundances of *Gammaproteobacteria* and *Deltaproteobacteria*,

with *Bacteroidetes* and *Firmicutes* being the most common phylum [82]. Another factor is aeration, which determines the soil oxygen content. Studies indicate that the aeration in the vicinities of the rhizosphere enhanced the physico-chemical properties of the soil and the richness of the soil microbiome, ensuring soil health [35,36]. This resulted in different patterns in the diversity and richness of bacteria and fungi when investigated with three different aeration treatment methods. Temperature plays a critical role in mediating and accelerating important metabolic cycles, as well as controlling the growth and activity of soil microbes. Studies elucidated that the soil microbial diversity decreased under the influence of elevated temperature. *Acidobacteria*, *Planctomycetes*, *Bacteroidetes*, and *Verrucomicrobia* are a few of the soil microbes whose response declined with elevating temperatures, except *Firmicutes*, which showed a significant abundance under high temperatures. In comparison to forest, grassland, tundra, and farmland ecosystems, wetlands are more sensitive to elevated temperature [28]. Variations in root exudation rates and exudate compositions due to a warming effect have been found to induce noteworthy changes in rhizosphere soil and resulted in a decreased complexity of rhizosphere bacterial and fungal community networks [83]. However, the increase in air temperature in the maritime Antarctic has positive effects on soil bacterial diversity [84].

Soil moisture content is another factor that controls nutrient transformation and oxygen diffusion, which in turn modulates soil microbial diversity [49]. Reduced precipitation decreases microbial stability [84]. On the other hand, the presence of continuous water in soil negatively impacts the hydro-physical properties of the soil and thus the soil microbiome [49]. Investigations are being carried out to explore the prokaryotic community distribution in the riparian soils in the fluctuating water zones of the Three Gorges reservoir in China [53]. While the relative abundance of *Firmicutes* and *Thermotogae* increased from upstream to downstream, the dominating phyla, *Proteobacteria*, *Chloroflexi*, and *Planctomycetes*, decreased.

The hydrological changes subjected to flooding events in the Lower Missouri River Floodplain (MRF) resulted in the most prevalent bacterial phyla, *Proteobacteria*, *Actinobacteria*, and *Acidobacteria* [50]. Stamou et al. [85] studied the response of associated patterns of soil microbial communities after recurrent rainfall events and found that the precipitation altered the soil microbial community and abundance significantly. The rainfall on the grave soil reduced the microbial community processes in the Qinghai–Tibet Plateau. As an outcome of both moderate and heavy rains, distinct successions of grave soil bacterial community structure and dominant taxa, including *Chloroflexi* and *Acidobacteria*, were identified [86]. The effect on the microorganism abundance and the decomposition rates in the Misty Forest in northeastern China [54] were determined, and it was found that the absence of precipitation had sporadic effects on the soil biological processes. Related studies are critical to understand the microbiome abundance in the context of global climatic changes.

Soil salinity is another key factor that governs microbial and fungal diversity and structure. In the Gurbantunggut Desert ecosystem in China, the significance of salinity in microbial community diversity and composition was examined [65]. This shows that the microbial taxa *Proteobacteria*, *Bacteroidetes*, *Actinobacteria*, and *Halobacteria* have a propensity for high-salinity niches, and they could serve as possible indicators for a community that can withstand high salinity. Six bacterial phyla with high abundance was detected after the restoration of saline–alkaline soil through soil amendments [45]. The microbial diversity tended to decrease as the EC increased. In particular, the fungal community was less susceptible to EC variations than the bacterial community [5]. The microbial community shows bacterial dominance in saline soil, as they are capable of adapting to those conditions. Availability of nutrients is another major factor affecting plant community diversity. Microbial biomass is significantly controlled by the availability of soil nutrients in the topsoil and subsoil [61]. A phytoremediation model of planting salt-tolerant legumes

along a coastal saline ecosystem improved the soil nutrient content and greatly altered the soil diazotrophic, bacterial, and fungal communities, and enriched different microbial taxa across soil depths [72]. Microbial community response to soil nutrient availability through mulching measures in the Loess Plateau was examined [71].

The study on the dynamics of rhizosphere-inhabiting microbes of rice plants revealed the presence of *Verrucomicrobia*, *Proteobacteria*, and *Gemmatimonadetes* [41]. Growing corn or maize for five years altered the composition of the Ultisol soil type's bacterial community and the Mollisol soil type's fungal community, but did not influence the Inceptisol soil type's microbial composition [87]. Notable differences in the microbial structure and composition were recorded in bare sandy land and three forest lands in China [88]. While soil fungal alpha diversity stayed constant, soil bacterial alpha diversity increased dramatically with the formation of a sand-fixing forest. The top eight phyla were *Armatimonadetes*, *Bacteroidetes*, *Actinobacteria*, *Gemmatimonadetes*, *Verrucomicrobia*, *Chloroflexi*, and *Proteobacteria*.

The soil microbial and plant compositions are significantly different in shaded and non-shaded areas. The effects of light on microbial communities were investigated in Shanxi Province, which receives plenty of solar radiation [48]. Unlike bacterial communities, fungal community structure is influenced by photosynthetic active radiation (PAR) [46]. Light structures the photosynthetic fungal and bacterial community on the soil surface, similar to the inner bulk soil [47]. Light radiation altered the plant growth-promoting rhizobacteria and microbial community [89].

The longevity and efficiency of soil ecosystems are thus determined by the complex interactions among these abiotic variables. Understanding and management of abiotic factors can improve soil microbial populations, increasing global environmental sustainability, agricultural productivity, and nutrient cycling. In addition, abiotic stresses occur due to various environmental pressures. Some stresses can be categorized as anthropogenic, and their effects are profoundly increasing day by day.

5. Abiotic Stressors Influencing the Soil Microbiome

Abiotic stressors are specific abiotic factors that mostly result in detrimental effects on the soil microbiota. These factors or stressors arise due to climatic shifts or anthropogenic activities. Various climatic changes (like drought, storm, flood), habitat degradation (deforestation, land conversion, urbanization, etc.), and soil contaminants like heavy metals (HMs), antibiotics, plastics, pesticides, fertilizers, etc., that impose negative impacts on the soil microbiome have been discussed. Different stresses cause changes in the root morphology of plants, oxygenation and nutrient availability within the soil, physico-chemical properties, etc. Moreover, these factors are interconnected. The impact on one factor may have either a positive or a negative influence on the others, thereby resulting in changes in the architecture of the soil microbiome [90]. The environmental abiotic stressors that affect the microbial community structure or its biodiversity are listed in the table below (see Table 2).

Table 2. List of selected studies on abiotic stresses shaping the soil microbiome.

Abiotic Stressors Influencing Microbial Community	Remarks	References
Drought/water stress	Significantly altered microbial community composition and diversity, enriched the genes controlling biogeochemical cycles and metabolism.	[91–94]
Flood/submergence	Dynamic distribution of nutrients and microorganisms.	[94–96]

Table 2. *Cont.*

Abiotic Stressors Influencing Microbial Community	Remarks	References
Storm/hurricane	Physico-chemical and community changes after storm; other run-off components during storm impacted the soil microbiome.	[97–99]
Wildfire	The impact of fire and recovery may vary from days to months to year. Microbial communities vary in burned and unburned areas.	[100–104]
Habitat degradation (deforestation, land conversion, urbanization)	Degradation of natural habitats, reducing biodiversity and altering ecosystem structure and function.	[105–107]
Restoration of degraded areas	Enhanced the soil fertility and the soil microbial properties; increased generalist microbes.	[105,108]

Extreme weather events, especially drought, affect the soil environment, soil microorganisms, plant morphology, and plant physiology [109]. A combination of drought stress with microbial properties, after long-term drought events, influences the contribution of carbon to SOC (soil organic carbon). The results of these microbial shifts were indicated in such a way that it was evident that the bacterial necromass C contributed more to SOC than the fungi in the subsoil, while the opposite was true in the topsoil. This highlights the importance of SOC prediction for future climate change. An in situ experimental drought across UK grasslands displayed the resistance of dominant bacterial and fungal taxa against drought [93]. The genes controlling metabolism, enzymatic activities, and soil properties were altered with stress [92,93]. An abundance of *Actinobacteria* and *Ascomycota* was observed under increased drought stress in Jilin Province, China. A drought-tolerant group like *Actinobacteria* and *Streptomyces* has higher microbial diversity in the farms of China [80]. Drought-induced Scot pine tree death in Switzerland decreased copitrophic bacterial taxa, while the oligotrophic taxa increased [110].

During a flood, the distribution of nutrients, water, microorganisms, etc., is more dynamic. The highest relative abundance of *Acinetobacter* was observed after the flood season at Zipingpu Reservoir, located in the upstream of the Min River, Southwest China. The survival and the relative abundance of this denitrifying bacteria played a crucial role in the restoration of the reservoir after the flood [95]. *Proteobacteria*, *Actinobacteriota*, and *Cyanobacteria* were the dominant phyla in the water column, while *Proteobacteria*, *Actinobacteriota*, *Chloroflexi*, and *Acidobacteriota* were the dominant phyla in the sediment observed under extreme flood conditions in Poyang Lake, the largest freshwater lake in China [96].

Global changes in the climate have increased the frequency of storms and hurricanes. This has resulted in the mixing of soil and alterations in the structure and composition of soil life. Storms in a Mediterranean holm oak forest resulted in a decrease in symbiotrophic and ectomycorrhizal community composition and an increase in plant pathogens in the gaps created by treefall [98]. The succession of bacterial communities in White Clay Creek (Chester Co., PA, USA) was considered following Tropical Storm Lee and Hurricane Irene in the year 2011 [99]. A transient microbial shift was identified on Okinawa Island, Japan, as a response to its significant recovery after three days of storm events [97].

Land desertification and reforestation have distinct impacts on microbial biodiversity and community structure. For instance, desertification in Brazilian semi-arid regions resulted in a significant loss of microbial biodiversity [105], whereas reforestation increased the number of biomarkers and bacterial alpha diversity [106]. Implementation of various restoration practices like terracing, cover crops, and grazing exclusion has shown an enhancement in soil fertility and restored microbial properties [105]. The functional characteristics of soil

microorganisms have not been consistently impacted by urbanization. However, older urban parks have higher levels of carbon degradation genes, while reference forests have higher levels of other functional genes. This implies that microbe-provided ecosystem services could be able to withstand the effects of urbanization [107]. Long-term monitoring is needed to understand the full-length restoration of the microbial properties.

Soil erosion due to natural processes takes away the topsoil, moving its nutrients, disrupting soil ecosystem functions and services, and depleting soil productivity, whereas deposition increases soil nutrients and ecosystem services [111,112]. A study on Mollisol soil in Heshan Farm, Heilongjiang Province, Northeast China, revealed that erosion had negative effects on the microbial community, complexity, and stability, whereas deposition increased the bacterial co-occurrence network [113]. The composition of bacteria increased with soil deposition, and the functional expression of the bacterial population was altered [114].

The shift in land use patterns and changes in the climate have resulted in the occurrence of frequent and severe wildfires. They are unpredictable disturbances that modify the soil microbiome and biogeochemical processes depending on their severity and impact [101,102]. Australia, the area most prone to forest fires, has an ecosystem that has fire adaptation systems and promotes rapid recovery [103]. Another frequent area of wildfires, the boreal forest in the permafrost region of Canada, highlights the bacterial fitness in the fire-prone area and its C and N cycling ability [104]. Immediately following the fire, a short-lived shift in the microbial community led to fungi predominating over Gram-positive bacteria [100]. A loss of ectomycorrhizal fungi and less tolerant microbial taxa followed severe burns in the coniferous forests in Colorado and Wyoming, USA, whereas viruses remained active post-fire and influenced vital cycling processes [102]. Based on intermediate and long-term analysis, the rhizosphere prokaryotic communities of the holm oak forest recovered after the wildfire but have not reached the conditions prior to the burns. Long-term persistence of three microbial biomarkers—*Arthrobacter*, *Blastococcus*, and *Massilia*, which possess remarkable resilience—were identified in the rhizosphere soil of a Mediterranean holm oak forest [115]. A high-intensity fire decreased the richness of microbes for N-fixation, while low-intensity fires significantly enhanced the abundance of ammonia-oxidizing archaea [116]. However, long-term monitoring and research are required to understand the post-wildfire impacts and recovery for the soil microbiota.

6. The Impact of Various Materials on Soil Microorganisms

Anthropogenic stress alters and regulates several genes that affect metabolites, enzyme activity, and soil characteristics. The studies on the soil contaminants that influence soil microbiomes are listed in Table 3.

Table 3. List of selected studies addressing the impact of soil contaminants on soil microbiomes.

Soil Contaminants	Remarks	References
Plastic (microplastics (MPs)/nanoplastics)	Influence on the bacterial community depends on the characteristics (size, type, composition, concentration) of the MPs.	[117–122]
Antibiotics	Abundance of the bacterial community composition and functions altered.	[93,123–126]
Heavy metals	Spatial distribution of the microbiome varies in accordance with the land use types and revegetation. Heavy metals, nutrients, and antibiotics directly/indirectly affect the ARGs and variations in bacteria.	[127–131]
Biocides	Shifts in the bacterial–fungal community and functionalities.	[132–136]
Manufactured nano materials (MNOs) (nanosensors, nanopesticides, nanofertilizers)	Various MNOs may have negative, positive, or neutral effects on the soil microbiota.	[137–140]

6.1. Nanomaterials

With the development of nanotechnology, manufactured nanomaterials (MNOs) added for various purposes enter the soil as contaminants. Nanomaterials (NMs) demonstrated that they could manage soil contamination, regulate the soil rhizosphere community, tolerate the abiotic stresses of plants, and improve agricultural production [137,140]. The introduction of nanoparticles modulates the activity of the soil microbiota and affects it negatively in rare cases [141]. A study on the effect of silver nanoparticles (AgNP) on the wheat rhizosphere microbiome demonstrated that the larger particles of AgNP boosted the beneficial plant growth-promoting bacteria (nitrogen-fixing, protease, urease, and lignin-degrading bacteria), while the smaller particles promoted the growth of harmful microbiota [138]. The concentration of titanium dioxide (TiO_2) influenced the microbial structure and composition in the rhizosphere of one of the medicinal plants, named ginseng. Additionally, it also altered the cooperative and competitive relationships among the soil microorganisms, impacting the overall soil health and plant growth [142]. Metal nanoparticles (Me-NPs) can affect the soil microbiome directly or indirectly, through particle–microbe interaction, increased toxicity, or decreased nutrient absorption. The consequences of its presence have been examined by da Silva Júnior et al. [139]. Nevertheless, further research needs to be carried out in this direction so that the active compounds from nanotechnology can be used effectively without interfering with the soil microbiome.

6.2. Plastics

The indiscriminate use of plastics has posed a great threat to the environment and the biosphere. MPs formed by the degradation of plastics are of great concern to the environment. Besides the effect of MPs on soil physico-chemical properties, they also alter the microbial community structure and diversity (e.g., microbial abundance, functional diversity, genetic diversity, etc.). In addition, MPs provide a niche for microbial colonization. When the population and number of species increase, the physical proximity decreases, thereby enhancing the antibiotic-resistant gene (ARG) transmission frequency among the bacteria. Microorganisms attach to the surface of MPs by producing extra polymeric substances (EPSs) (composed of lipids, nucleic acids, polysaccharides, and proteins) to form biofilm. The possible mechanisms of ARG enrichment have been reviewed in detail by Liu et al. [110]. However, the information on MP selective enrichment of bacteria is still in its infancy.

Smaller-size biodegradable MPs cause adverse effects compared to conventional MPs [120]. The effects of biodegradable plastics are similar to those of conventional plastics, suggesting that even biodegradable ones are not environmentally friendly [118]. The size of micro (nano)plastic plays a crucial role in determining the soil microbial community. MNPs 0.5 and 5 μm in size significantly lowered the soil microbial biomass and relative richness of *Rhizomicrobium* [119]. The plastic residues induced metabolic alterations and significant changes in the microbial community structure in three types of soils (farmland, woodland, and wetland). As a result, the amount of *Bryobacter* in soil samples increased. The abundance of *Propionibacteriales* decreased in both farmland and woodland soils, regardless of the type of plastic residues added. In contrast, in wetland soils, the abundance of *Propionibacteriales* increased after exposure to plastic residues [117]. This study also showed that soil ecosystems are more vulnerable to biodegradable plastic polylactic acid than they are to nonbiodegradable plastic polyethylene (PE). The microbial community structure and abundance in the cinnamon soil collected from Weiming Lake, China, was altered after amendments with three different MPs (microsphere PP, MPs (membranous PE, fibrous polypropylene (PP)). The microbial community structure was considerably changed by the MPs, particularly in terms of the enrichment of Acidobacteria and Bacteroidetes and the loss of *Deinococcus-Thermus* and *Chloroflexi*, while *Streptomyces*, *Mycobacterium*, *Nocardia*, *Aeromicrobium*, *Janibacter*, and

Arthrobacter were more prone to inhabiting the MPs [122]. Bacterial species like *Amycolatopsis*, *Nocardia*, *Sinomonas*, *Burkholderia*, and *Bradyrhizobium* and fungal species like *Exophiala* and *Cladophialophora* increased in the presence of plasticizer-containing MPs, except for a decrease observed for one archaeal taxon, *Candidatus nitrosocosmicus* [121]. More research is required to understand the potential impacts of MPs on soil and whether these changes upset nutritional status and crop productivity.

6.3. Biocides

Biocides are substances added to protect against a broad spectrum of microbial activity in building materials during storage or application. The use of these substances has increased over time due to various developments. Even though these substances do not directly affect the physico-chemical properties, they significantly create shifts in the bacterial–fungal community and functionality patterns. Active bacteria were more sensitive to these substances than fungi [135]. The effects of 20 commercially available pesticides on the N-cycle-related functions of microbes and microbial communities were investigated in three contrasting Australian agricultural soils, which resulted in a significant impact on the nitrifier community [143]. Inhibitory effects on the abundance of ammonia-oxidizing microorganisms (AOMs) were also determined in various studies [132–134,136]. Moreover, these substances have led to the emergence of biocide-resistant bacteria and biocide-resistant genes (BRGs), which may contribute to cross-resistance.

6.4. Heavy Metals

The dispersion of heavy metals (HMs) has been contaminating various systems on Earth. Investigation of the spatial distribution of HMs and the roles of soil microbial communities during revegetation in different areas of Pb-Zn tailings in northern Guangdong Province, China, displayed dominant genera shift from *Weissella* (44%) to *Thiobacillus* (17%) and then to *Pseudomonas*, and were identified as Pb remediation bacteria [129]. The influence of HMs on soil microbial community under different land use types was examined in Dading Village, Guizhou Province, China. This shows that the Actinobacteria, Proteobacteria, and Acidobacteria were the most dominant groups of bacteria, while *Verrucomicrobiota* and *Firmicutes* demonstrated robust resistance to the HM cadmium (Cd), with *Verrucomicrobiota* exhibiting particularly noteworthy tolerance to the HM mercury (Hg) [131]. Microbial community structure in different land use types in the Yellow River Delta under HM soil contamination was evaluated, and the dominant phyla were *Actinobacteria*, *Chloroflexi*, and *Proteobacteria*. The phyla *Actinobacteriota* and *Chloroflexi* were shown to be positively associated with arsenic (As), nickel (Ni), copper (Cu), zinc (Zn), and cadmium (Cd), indicating a potential resistance to these heavy metals. The results also showed that total nitrogen (TN), total phosphorus (TP), pH, Ni, and As had the largest influence on the microbial community structure in the Yellow River Delta's surface soils [130]. The concurrent presence of HMs and antibiotics (of two commonly used feed additives in the farming industry) in the soil induced the synergetic resistance of both of the microbiota. High cadmium and sulfadiazine (SDZ) concentrations increased the abundance of mobile genetic elements (MGEs) [128]. Addressing the interconnected challenges of HM contamination, heavy metal-resistant genes (HMRGs), and antibiotic resistance is crucial for safeguarding public health, preserving the efficacy of antibiotics, and protecting the environment.

6.5. Antibiotic Storm: Emerging Trends

Antibiotics have revolutionized modern medicine by treating various infections. They are also present in the soil naturally, as they are produced by soil microbes. However, the widespread use and misuse of the compound in the agricultural and veterinary fields beyond intended therapeutic purposes has created a myriad of risks and challenges in the

environment. Residues from antibiotic manufacturing, improper disposal of unused medications, agricultural runoff, and animal industry promote the proliferation of antibiotic-resistant strains, thereby posing a serious threat to the environment and global health security. For example, SDZ and oxytetracycline (OTC) in bacterial communities and the abundance of ARGs were determined in soil collected from Jinan, China, with the latter showing more significance in increasing the abundance of bacterial communities and ARGs [126]. The ARG profiles in eight different lands in China with different utilization patterns revealed the richness of ARGs in parks, farmlands, vegetable cultivation soils, and residential areas [93]. The bacterial community composition and function were altered on ARG amendments, and these were intensified by the tetracycline contamination of the soil [144]. Furthermore, research conducted in the vicinity of a smelting plant in Henan Province, China, demonstrated a complex linkage between bacterial community composition, eight HM concentrations, and ARG abundance in the soil [125]. Research has shown that antibiotics, heavy metals (HMs), and nutrients directly or indirectly influence the persistence of antibiotic resistance genes (ARGs) and their variation levels in bacteria [127].

Antibiotic pollution and its potential risks have gained scientific and public attention globally. There is widespread concern regarding the spread of ARGs because they persist in the environment for a long time. HMs are also widely used in animal feed to ensure optimum growth. Once in the soil, they interact with the soil microbes and modify their structure and functions. On analyzing the documents generated during the past 5 years, an upward trend was observed in the recent publications of antibiotics, especially in combination with plastics and HMs (Table 4). This leads to the emergence of the cross-resistance of microorganisms. More studies are to be conducted in these areas to address the threats posed by "plastics," "heavy metals," and "antibiotics."

The abiotic stress caused by natural pressures may be recovered over time. But it is important to assess the stress caused intentionally and tackle the problems associated with it, as they may persist for a long period of time once they get into the environment, especially in the soil.

Table 4. Number of documents by year produced on antibiotics in combination with heavy metals, plastics, and biocides during the years 2019–2023.

Documents by Year	Antibiotics and Heavy Metals	Antibiotics and Plastics	Antibiotics and Biocides
2019	341	252	111
2020	386	290	110
2021	524	414	148
2022	610	439	163
2023	616	597	152

7. Distribution of Antibiotics in the Soil

Scientists focusing on accurate quantification of antibiotics present in the soil and the method of their transformation in the soil voiced their concerns and issued warnings. The range of antibiotic concentrations in soil was reported to range from minimal concentrations in nanograms to milligrams per kg. ARGs and related MGEs can spread among bacteria even at very low antibiotic concentrations in the soil (less than the minimum inhibitory concentration (MIC)). For example, tetracyclines, fluoroquinolones, and sulfonamides, with their corresponding ARGs and multi-drug resistance genes, were found in higher amounts in agricultural soil after the application of manure or wastewater [145]. The two main sources of antibiotic contamination in agricultural soil are sewage sludge and livestock manure, in addition to bio-solids and municipal wastewater. In addition, the reckless disposal of antibiotics from houses, hospitals, and pharmaceutical industries significantly

contributes to their presence in the environment [146]. Figure 4 illustrates various sources and pathways of antibiotic contamination.

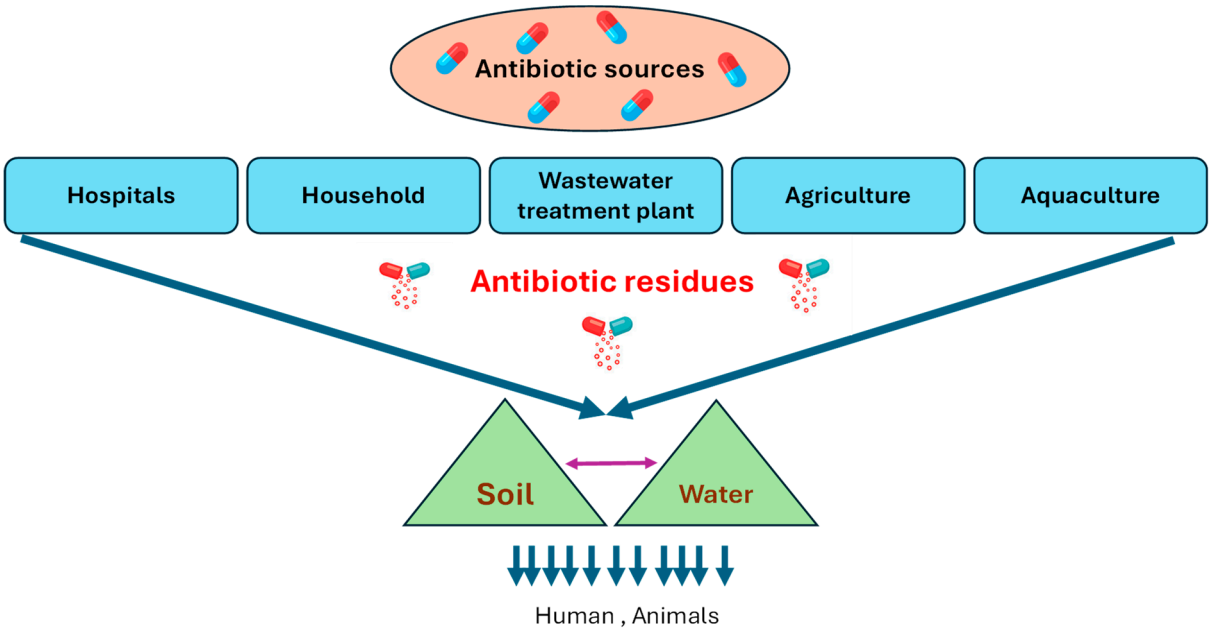


Figure 4. Major sources and pathways of antibiotic contamination release residues into soil and water, increasing pollution risk. The potential movement between these ecosystems highlights the interconnectedness of these ecosystems and the risk of antibiotic pollution in both environments.

7.1. Factors Affecting the Distribution of Antibiotics

The differences in antibiotic distribution could be attributed to various factors, such as land management, amounts of fertilizers applied and application methods, density of cultivation, or climatic factors (mean annual precipitation (MAP), mean annual temperature (MAT)), soil properties (total N, SOC, pH, HMs, pH)) [106]. Many studies have reported the effects of soil parameters on antibiotic concentrations in soil, like the sorption coefficient (K_{oc}) [146], OM content [147,148], temperature [149], O2 status [150], water content, and soil texture [149]. The distribution in environmental matrices (solids or water) is also determined by their physicochemical characteristics, which include their molecular size, shape and structure, solubility, and hydrophobicity. Soil depth is another factor that determines the distribution of these compounds, indicating the easy accumulation and persistence of these substances in the deep soil.

7.2. Fate and Degradation of Antibiotics

The non-volatile nature (because of low vapor pressure) and high polarity of these substances prevent their escape from these matrices. The long-term presence of antibiotics in the environment even at low levels (ng/L to µg/L (water) and low medium µg/kg for sediments) can produce harmful effects, leading to bioaccumulation and long-term ecological disruption [150]. Thus, accumulation takes place when the input is higher than the dissipation.

7.2.1. Half-Lives, Rate of Degradation, and Mobility of Antibiotics

Several factors, including sorption, sequestration, and intrinsic stability, influence the dissipation of half-lives of antibiotics. The interaction of antibiotics with the soil solid phase via biotransformation and sorption reactions generally determines the fate of antibiotics. The rate of degradation of these chemicals in the soil ranges between <1 and 3466 days [146]. There is a considerable tendency for many antibiotics to bond with

soil particles. The adsorption performance of antibiotics is affected by the adsorption coefficient (K_d) value, acid dissociation constant (pKa) value, and octanol–water partition coefficient (log K_{ow}) value. There have been reports of distribution coefficients (K_d solid) for tetracycline, enrofloxacin, and tylosin that are as high as 2300, 6310, and 128 L/kg, respectively [146]. The ability of antibiotics to adsorb from the liquid to solid phase and their hydrophobicity is expressed as log K_{ow}. Low adsorption potential is given by $K_{ow} < 2.5$, while high adsorption potential is given by $K_{ow} > 4$. But $2.5 < \log K_{ow} < 4.0$ indicates medium adsorption. The polarity parameter of antibiotics with a certain degree of dissociation in solution is represented as the acid dissociation constant (pKa) value [151].

One of the most crucial parameters for determining the dispersion of antibiotics in the environment and their degree of exposure is the sorption coefficient (K_{oc}). Antibiotics that have low degradation in soil and are non-mobile have higher values of K_{oc} (e.g., >4000 L/kg). These are very persistent in the soil, as the DT50 > 60 days (i.e., the time required for the degradation of 50% of an initial dose). Low persistent antibiotics, on the other hand, have low K_{oc} (for example, <15 L/kg) and are readily degraded (DT < 5 days). A few antibiotics, like macrolides, fluoroquinolones, sulfonamides, and tetracyclines, bind strongly to soil to form stable residues [146].

Recent models use degradation rates (DT50) and soil water-partitioning approaches (K_d in L/kg) to understand the degradation and mobility of antibiotics in the soil. K_d is equal to Q_i/C_i, where Q_i (expressed in mg/kg ds soil) is the content of substance "i" in the soil and C_i (expressed in mg/L) is its equivalent concentration in the solution. Since the OM, especially the SOC, plays a significant role in the binding of antibiotics, the K_d value is often normalized based on the SOC, with $K_{oc} = K_d\ f_{oc} - 1$, where f_{oc} is the fraction of soil organic carbon. The log K_{oc} of different non-ionic organic adsorbents is often correlated with the *n*-octanol/water distribution coefficient (K_{ow}) and is compound-specific [152].

7.2.2. Degradation Pathways of Antibiotics

Antibiotics can undergo biological and non-biological degradation processes. Biological degradation involves the action of microbes, plants, and algae, while non-biological degradation encompasses hydrolysis (cleavage of chemical bonds with the help of water), photolysis (breakdown by UV radiation from sunlight), oxidative degradation (involves oxidation reactions by oxidizing agents), and ionizing radiation degradation. Beta lactams are more susceptible to hydrolysis than macrolides and sulfonamides [153]. Quinolones and tetracycline can be subjected to photo-degradation [154]. But this type of degradation may be limited because of low light penetration. Macrolides, fluoroquinolones, and tetracyclines have high DT50 or half-life values showing longer persistence [146]. Furthermore, hydrolysis and photo-degradation are considered the most essential abiotic degradation factors of antibiotics. Other processes in the soil environment include sorption or desorption, plant uptake (as plants can absorb antibiotics from soil), transformation or degradation, particle-facilitated transport surface runoff, and vertical percolation into the groundwater (leaching) [155,156]. The fate of antibiotics is summarized in Figure 5.

The rate of sorption of antibiotics is given in the decreasing order tetracyclines > quinolines > macrolides > chloramphenicol > sulfonamides [156]. The sorption and desorption reactions of antibiotics in the soil depend upon the pH, water solubility, chemical speciation, polarity, dissolved organic carbon (DOC), charge of compounds, fertilization history, and presence of other solutes. For example, sorption of ciprofloxacin was not affected, unlike sulfonamides, after irrigation with untreated wastewater [157]. A few antibiotics, like sulfonamides, undergo leaching, while most of the fraction remains on the soil surface [158]. However, the uptake of plants cannot be considered a common degradative pathway.

Some recalcitrant antibiotics, like sulfonamides (e.g., sulfamethoxazole (SMX)), which are discarded at higher concentration in nature, are stable at higher temperatures. However, UV/hydrogen peroxide, fenton, ozone, and UV/persulfate-mediated advanced oxidation showed good efficiency for sulfonamide degradation [159].

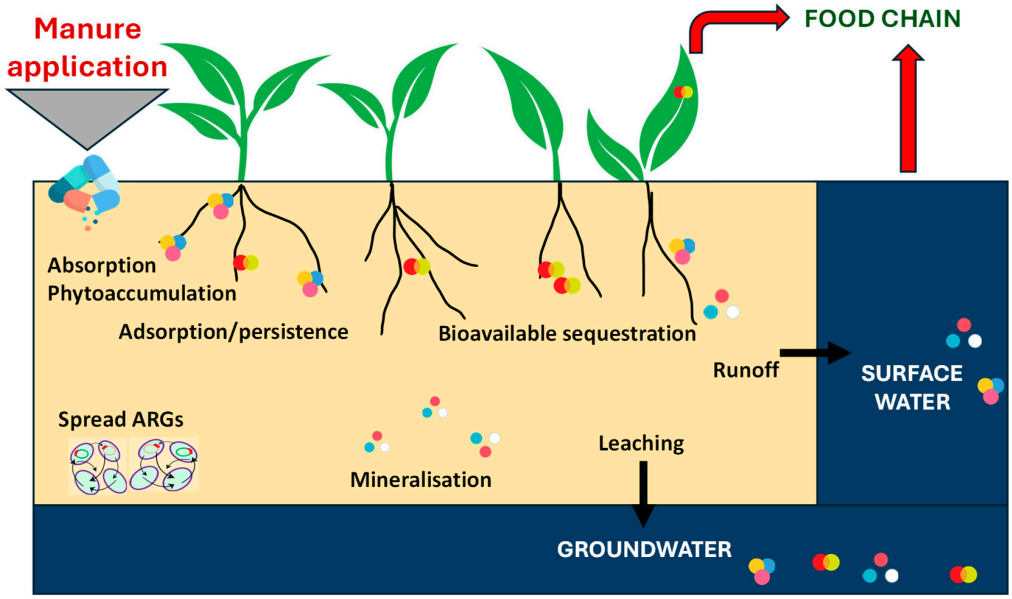


Figure 5. Fate of antibiotics in the soil, depicting the cycle of antibiotics in different environmental compartments through the application of manure.

7.2.3. Degradation by Microorganisms

Microbial degradation of antibiotics may be by the utilization of growth substrates or by co-metabolism. Pure bacterial culture does not readily consume antibiotics but does uptake carbon-energy sources for metabolism. Microorganisms may be capable of hydrolyzing or modifying the structure of antibiotics due to the presence of certain degradative enzymes like β-lactamase, macrolide passivase, chloramphenicol-inactivating enzymes, and aminoglycoside-modifying enzymes [160]. Antibiotics were reported to be degraded by a few microbes, such as *Acinetobacter* sp. [161], *Bacillus* sp. [162], *Burkholderia* sp. [163], *Escherichia* sp. [161,164], *Klebsiella* sp. [164], *Bradyrhizobium* sp. [165], and *Stenotrophomonas* sp. [166]. Moreover, two bacterial strains, *B. cereus* and *B. pumilus*, belonging to Bacillus, were able to degrade penicillin V potassium (PVK), and B. subtilis was involved in the removal of cefalexin (10.62%), amoxicillin (22.59%), and ampicillin (25.03%) [167]. Up to 82.31 $\pm$ 0.62% tetracycline (TC) and up to 79.20 $\pm$ 0.32% OTC are degraded by a novel bacterium *Burkholderia cepacia* [168]. But trimethoprim, tetracycline, and CIP fail to stimulate the activation of bacterial genes responsible for degradation, leading to their low biodegradability [169]. Table 5 provides a list of a few microbial degrading capacities of antibiotics.

Moreover, the environmental conditions and the presence of other substances may interfere with the degradation processes. For example, soil contaminants like HMs, antibiotics, plastics, pesticides, fertilizers, etc., impose negative impacts on the soil microbiome, thus affecting the degradation process. Long-term antibiotic usage can result in the emergence of ARGs and the proliferation of resistant bacteria. According to Cheng et al. [170], the concentration of antibiotics increases the abundance of ARGs. Multiple elements, such as geographic location, composition of microbial communities, presence of MGEs, type and concentration of antibiotics, soil characteristics (including pH, moisture, nutrient levels, and temperature), as well as anthropogenic pollutants like PAHs, HMs, and pesticides, can influence soil resistomes and consequently impact the elimination of antibiotics from the environment [171].

Microorganisms identified in Qatari ecosystems have shown promise for bioremediation applications in the field of agriculture [172]. However, during antibiotic degradation by a microbe, there is a high possibility for horizontal transfer of the gene from donor to the recipient normal bacteria, resulting in the spread of ARGs. Thus, this strategy, which is thought to be good, makes the condition even worse. The era of advanced biotechnology should open research to overcoming the limitations of microbial antibiotic degradation [173]. The potential toxicity of antibiotics should not be disregarded, even if observed quantities of the drugs in soil or water rarely equal or surpass the EC50 values [174]. The EC50 represents the concentration of a drug required to inhibit 50% of maximal cell growth. It serves as an indicator of a drug's potency and aids in identifying the most promising drug candidates [175]. Analyzing the presence of antimicrobial chemicals in soil samples thus becomes critical for determining the potential effects on human and animal health as well as on the environment.

Table 5. Microbial degrading capacity of antibiotics.

Microorganism	Degraded Antibiotics	% of Degradation	References
Acenitobacter sp.	Sulfathiazole (Sulfonamide)	45–67%	[161]
Bacillus sp.	Ceftiofur (Cephalosporin)	>50%	[162]
Escherichia sp.	Sulfapyridine (sulfonamide)	66–72%	[161]
Klebsiella sp. *Escherischia* sp.	p-Nitroaromatic antibiotic chloramphenicol (CAP)	10.5%–45% 95%	[164]
Bradyrhizobium sp.	Ciprofloxacin	70%	[165]
Strenotrophomonas sp.	Tetracycline	11.11%	[166]
Bacillus sp.	Penicillin Cefalexin Ampicillin Amoxicillin	68% 10.62% 22.59% 25.03%	[167]
Burkholderia sp.	Tetracycline Methoprim, ciprofloxacin	82.31 ± 0.62% 79.2 ± 0.32%	[168]

7.3. Antibiotic Resistance

The ability of microorganisms to resist the inhibitory effect of antibiotics is known as antibiotic resistance. Even though antibiotic resistance is ancient, various human activities have brought its prevalence to the environment. The majority of MGEs did not carry ARGs in the antibiotic era. ARGs can be spread through numerous routes, including horizontal gene transfer (HGT) and vertical gene transfer (VGT). VGT is the generation-to-generation transfer of the genetic material [176,177]. HGT is the most frequent way to acquire foreign DNA material. Bacteria acquire this genetic material through three main pathways: (i) conjugation (cell-to-cell contact), (ii) transformation (incorporation of the naked DNA), and (iii) transduction (mediated by phage) [177]. The spread of ARGs in this mechanism is mediated by MGEs like insertion sequences, integrons, transposons, plasmids, etc. In addition, prokaryotes can also develop resistance by mutation through changes in antimicrobial target, efflux mechanisms, or the modulation of metabolic pathways. However, it is important to note that once a microorganism becomes resistant to a particular antibiotic, the same mechanism of resistance could also lead to resistance against other antibiotics (cross-resistance), or potentially make the microorganism more susceptible to different antibiotics (collateral sensitivity). De novo mutations (point mutations, deletions,

insertions, etc.) and genetic recombination via ARG exchange between bacteria also contribute to multidrug resistance (MDR) [178]. Human activities lead to selective pressures and enhance the dissemination of ARGs among microbial populations, leading to the evolution of "superbugs," thus making them ineffective in the treatment of diseases caused by these superbacteria [176] (Figure 6). According to the World Health Organization (WHO), AMR (antimicrobial resistance) is one of the top global public health hazards [177]. By 2050, it is expected to cause over 10 million deaths annually and cost more than USD 100 trillion globally [179].

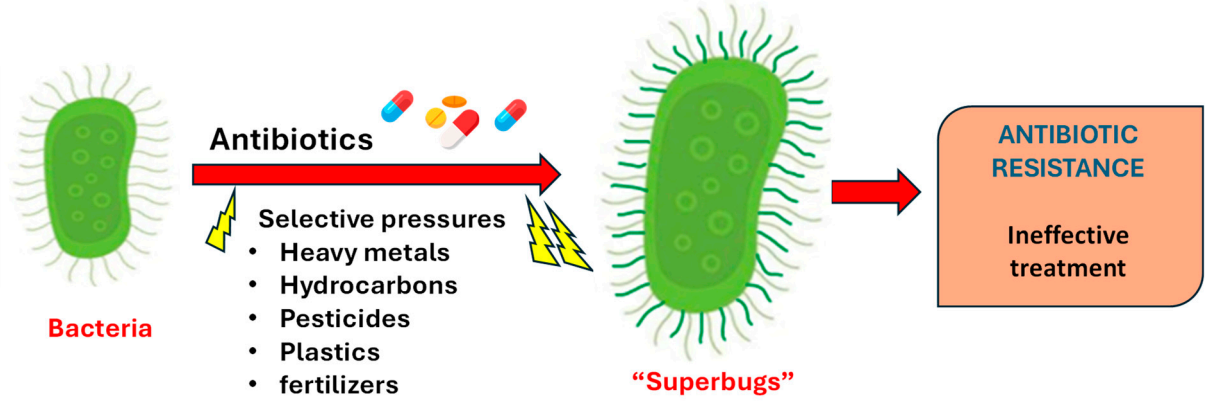


Figure 6. Antibiotic use leads to ineffective treatments. The evolution of bacteria into "superbugs" takes place through repeated antibiotic exposure (indicated by the red arrow). The lightning symbols represent the emergence of resistance mechanisms through their interaction with other pollutants, ultimately leading to antibiotic resistance and ineffective treatments.

ARGs demonstrate significant diversity due to their ability to transfer between different microorganisms. The genetic plasticity of bacteria enables them to adapt to a variety of environmental stressors, such as the existence of antibiotic compounds that could endanger them [179]. The structural families involved in veterinary and human medicine are almost similar. Thus, these antibiotics are thought to selectively affect human commensal and pathogenic bacteria because they have similar basic chemical molecular structures and modes of action.

7.3.1. Antibiotic Resistance Genes (ARGs)

ARGs have been present in soil since ancient times, prior to the selective pressure exerted by manmade antibiotics. ARGs native to the soil originate from the soil microorganism. As described previously, ARGs can be transferred between microorganisms via HGT, facilitating the rapid spread of resistant genes. The bacteria that are carrying ARGs thus become resistant and can survive antibiotic treatments, providing a competitive advantage over non-resistant strains. This leads to the selection and proliferation of resistant bacteria. These can also acquire resistance to multiple antibiotics, making them multidrug resistant. ARGs are present in soil, water, the human gut, etc. These act as reservoirs for ARGs, facilitating the spread of pathogenic bacteria. The presence of ARGs in pathogens can lead to infections that are difficult to treat with the available antibiotics, posing a risk to human health. Even in soil with fewer or no human disturbances (e.g., permafrost, Antarctica, Qinghai–Tibet Plateau), the resistance genes for vancomycin, β-lactam, and tetracycline were detected [180]. In 24 pristine forest soils in China, seven different types of ARGs were found, with the most common types being quinolones, β-lactam, sulfonamides, aminoglycosides, and multidrug and macrolide–lincomycin–streptomycin B (MLSB) resistance genes [181]. Polar sediments contained thirty types of ARGs resistant to β-lactam, tetracyclines, aminoglycosides, quinolones, and macrolides [182]. β-lactamase, aminoglycoside,

MLSBs, tetracycline resistance genes, and FCAs (quinolone, florfenicol, chloramphenicol, amphenicol, and fluoroquinolone resistance genes) dominated in the relatively ancient Qinghai–Tibet plateau wetlands [1]. However, the presence of antibiotics in the soil enhances the selection pressure and thereby increases the acquired resistance among clinically important pathogens as well as commensal bacteria. Depending on the kind of soil, several elements have an impact on the profiles of ARGs. Selective pressure on soil resistomes can be applied by microbial community structure, soil physicochemical parameters (pH, humidity, nutrition, and temperature), antibiotic type and concentration, PAHs, pesticides, and HMs (Figure 6).

Additionally, the pattern of ARGs can be impacted by various pollutants/contaminants present in the soil. PAHs found in soils, such as naphthalene, phenanthrene, pyrene, and benzopyrene, increased the expression of ARGs [183]. HMs such as Cu, Cd, and Zn have a major impact on ARGs. This positive link between HMs and ARGs exerts selective pressure on the metal-resistant genes (MRGs), because the ARGs and MRGs are situated in the same DNA region [184]. Antibiotics interact with HMs and promote the transmission of ARGs by co-selection. Together, antibiotics and pesticides put microbes under selective pressure, which results in the development of pesticide–antibiotic cross-resistance [185]. Research indicates that soils are also hotspots for plastics, which leads to the cross-resistance of microorganisms.

7.3.2. Factors Driving the ARG Pattern

Soil pH, moisture, temperature, and nutrient levels play crucial roles in shaping the profiles of ARGs in different geographical locations and soil types. Soil pH influences ARG diversity and composition, with neutral pH promoting higher diversity (the ideal pH of soil microorganisms remains closer to neutral pH). Moisture levels correlate positively with ARG richness, potentially due to increased microbial biomass. Nutrients like potassium and phosphorus also affect ARG abundance, with varying effects depending on the nutrient type. Soil temperature negatively correlates with ARG abundance, with high temperatures reducing microbial community diversity and thus ARG abundance [180].

Meteorological parameters, especially precipitation, have significant effects on ARGs. Rainfall increases the abundance (with a contribution of 16.34% ARGs), diversity, and composition of ARGs, likely due to the dissemination of ARGs from airborne particles to soil, bacterial blooms, and the promotion of MGEs [186]. Variations in local air temperature influence the abundance of ARGs across the four seasons [187]. As temperatures rise, the transmission of high-risk ARGs to human pathogens may increase, resulting in elevated ARG levels and posing significant risks to public health. Thus, a clear understanding of the factors that enrich ARGs and enhance their dissemination is necessary in the context of climate change, especially global warming, which is a critical environmental challenge in the world today. Therefore, comprehending these factors is vital for addressing this pressing issue and mitigating potential risks.

7.4. Impact of Antibiotics on Soil Health

Microorganisms in the soil are essential for maintaining soil health and quality, including the degradation of OM, nutrient release, improvement in the structure and fertility of the soil, and biological control agents. They ensure the provision of ecosystem services to maintain good quality and fertility of the soil [146]. Soil is also considered a natural reservoir for many ARG-harboring bacteria. Being a complex matrix, it is challenging to distinguish the sources of ARGs and the practices impacting the ecosystem with the risks associated with ARGs. Consequently, the ecological function of soil is changing, such as the activity of enzymes that turn over C, N, and P; nitrification; denitrification; reduction of sulfate and iron; and methanogenesis [188].

ARGs in agricultural soil enter the food chain, creating an important route for dissemination to humans. Manure, biosolids (often used in irrigation and fertilizing agricultural fields), sludge, and wastewater effluents are major sources of antibiotics and other pollutants that are added to agricultural soil. Incomplete metabolized antibiotic residues enter the environment and enhance the antibiotic content in nature. The increased exposure of soil to antibiotic activity inhibits or affects the composition of the soil microbial community. Common agricultural practices adopted nowadays, mainly to increase crop yield, have led to the selection of antibiotic-resistant bacteria (ABR) and the alteration of microbial characteristics [146]. Additionally, different types of pollutants end up in the soil through disposal. This allows ARGs to interact with other pollutants, exerting tremendous selection pressure. Interactive effects like antagonism, synergism, and additivity could influence the potential effects and degradation capabilities of these substances in the environment. Thus, soil becomes an important medium for various mechanisms to take over and spread ARGs rapidly.

7.5. Soil Resistance and Human Health

The soil microbiota is thought to constitute a reservoir of resistance genes that can be exchanged with clinical pathogens. Clinical cases of resistant infections may be closely correlated with soil antibiotic resistance. Using a functional metagenomic screening of bacteria that live in soil, it was possible to identify resistance cassettes in multidrug-resistant bacteria from soil and those in human pathogens from clinical settings, with a high nucleotide identity (>99%), suggesting that these microorganisms have recently undergone horizontal gene transfer. For instance, Class 1 integrons, which contain the gene *IntI1*, play a crucial role in the integration of numerous ARGs at the same genomic locus, resulting in multidrug resistance in bacterial genomes. *IntI1* is considered a potential marker of anthropogenic pollution [189]. Integrons have been identified as common carriers of various ARGs in both natural and anthropogenically affected environments. Manure applications significantly increase soil *IntI1.* Thus, a global expansion of antibiotic-resistant infections, or "superbugs," is expected when many ARGs from bacterial genomes make their way into plasmids.

There is an immediate necessity to oversee antibiotic usage in both human healthcare and animal agriculture. The presence of antibiotics in the soil led to concern from and warnings by scientists focusing on the accurate quantification of antibiotics and the method of their transformation in soil. Research on the effects of manure antibiotics on the environment and human health is urgently needed. Key areas include understanding the fate of different antibiotics in manure, their uptake by plants grown in manure-treated soil, the stability of antibiotics in cooked food, and their potential to cause antibiotic resistance or adverse health reactions in humans. To accomplish this, modern analytical techniques are required, like high-performance liquid chromatography with tandem mass spectrometry (HPLC/MS) [190]. The assessment of soil microbial diversity has been achieved through historical, yet still relevant, methods based on partial (indirect) community studies. Examples of these methods include fingerprints (e.g., terminal restriction fragment length polymorphism (t-RFLP), single-strand conformation polymorphism (SSCP), amplified ribosomal DNA restriction analysis (ARDRA), and electrophoresis in gradient denaturing gels (DGGEs) [190]. However, the impact of antibiotics is underestimated, and more studies are yet to be conducted. Initially, thorough assessments should be conducted to monitor antibiotic consumption across various sectors and assess resistance levels nationwide. The likelihood of substances biodegrading is known to increase with bacterial community diversity, and this is a crucial factor to consider when testing antibacterial compounds and analyzing test outcomes. As soil microorganisms are sensitive to exposure and respond faster to contaminants and pollutants, they are a good indicator of soil quality. To assess

microbial diversity, 16S rRNA gene sequencing is used, as are changes in phospholipid fatty acids (PLFAs) found in the soil [191]. Subsequently, informed by these investigations and contemporary scientific insights, it is imperative to promptly establish and enforce more robust legislation, regulations, and standards to govern antibiotic usage effectively.

8. Conclusions

Changes in environmental factors directly and/or indirectly affect the soil microbial structure, its metabolic functions, and enzyme activities. In addition, soil is under increased environmental stress, which is mostly linked to inflation in human activity and global climate change. The recent unchecked use and application of antibiotics in healthcare and animal husbandry is one of the activities that have led to the emergence of these compounds as a major contaminant of the soil. Persistent exposure of these compounds in the soil can lead to long-term detrimental effects on microbial communities and soil biodiversity. If this trend continues, antibiotic resistance can cause health risks in living beings and thus affect ecosystem stability. This highlights the importance of safeguarding soil biodiversity and health for future generations.

The recent and rapid advances in metagenomic analyses have enabled scientists to carry out various investigations on the aspects that shape the microbial ensemble. More studies on microbial community shifts, especially during antibiotic resistance, may therefore pave the way for the formulation of the best management practices for different agro-ecosystems. Agricultural soils need special attention because they are influenced by various anthropogenic activities and are recognized as the largest reservoirs of ARGs through activities with antibiotics, pesticides, HMs, plastics, etc. Researchers are exploring ways to maintain a healthy microbial community to improve agricultural sustainability and fulfill the need for beneficial outputs. Future studies should provide information on more interactions between different pollutants/contaminants present in the soil. As these contaminants share their MGEs, the dissemination of the resistant genes becomes much easier. Further investigations should also focus on the impact of antibiotics in combination with other abiotic factors or stressors, especially among rising concerns like plastics and heavy metals.

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