OPEN ACCESS

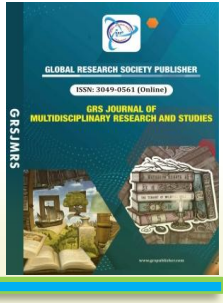
GRS Journal of Multidisciplinary Research and Studies

Abbreviate Tittle- GRS J Mul Res Stud

ISSN *(Online) - 3049-0561*

https://grspublisher.com/journal-details/GRSJMRS

Vol-2, Iss-11 (Nov- 2025)



Ecological Review on Heavy Metal Interactions with Bacterial Dynamics of Soil

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Article History

Received: 10.10.2025

Accepted: 03.11.2025

Published: 17.11.2025

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Abstract: The growing exploitation of natural resources is increasing the human-induced pressure on soil. Industrial, metallurgical, and mining operations release excessive amounts of heavy metals into the soil. Waste and wastewater from various facilities also contribute to contamination. These metals accumulate in the soil and can disrupt the bacterial community, which is an essential indicator of soil health. Modern molecular genetic tools, such as shotgun sequencing and met barcoding of standard DNA markers are widely used to study soil bacterial diversity. This review summarizes recent research on how heavy metals affect soil bacterial communities using metagenomics approaches. Studies from the past decades consistently reveal that heavy metal pollution generally harms bacterial diversity and alters community structure. Several factors also influence metal toxicity, such as soil salinity, pH, ecosystem type, the presence of plant roots, and other soil characteristics. The paper further highlights potential future directions for research in this field.

Keywords: *Heavy metal, Soil, bacteria, pollution, biodiversity.*

Cite this Article

Md. M. Rahman, Md. E. Ahmed, A. Kumar3 Md. A. Rahman, M. Hasan. Chowdhury, Ecological Review on Heavy Metal Interactions with Bacterial Dynamics of Soil (2025) *GRS Journal of Multidisciplinary Research and Studies, Vol-2(Iss-11).50-56*

Introduction

Soil is an essential component of terrestrial ecosystems. It provides a wide range of functions, such as food production, climate and water regulation, energy provision and is the habitat for various life forms [1]. Soil bacterial communities are essential for nutrient cycling, maintaining soil fertility, and storing carbon, all of which are crucial for the ecological functioning of soils [2]. The diversity of bacterial species in soil is a crucial feature. It plays a significant role in determining the soil's ability to resist and recover from disturbances [3]. According to modern understanding, high biodiversity helps maintain ecological functions because having more species increases the likelihood that the ecosystem can continue to function even if some species are lost or affected by stress. Among all environments, soil likely hosts the greatest bacterial diversity. It is estimated that a single gram of soil may contain around 10 billion bacterial cells and thousands of different bacterial phyla [4]. Different environmental factors can affect the composition and diversity of soil bacterial communities. Soil can retain a wide range of pollutants, including heavy metals (HMs), pesticides, hydrocarbons, and their by-products [5]. Human activities like mining and metallurgical processes are the primary causes of heavy metal pollution in soils. These metals can spread from mining and smelting sites to nearby agricultural lands [6]. The over application of pesticides can lead to higher concentrations of heavy metals in agricultural soils. Likewise, the excessive use of fertilizers can further raise the accumulation of these metals in farmland [7]. The mobility of metal contaminants in soil can be affected by its pH. In addition, soil moisture plays a role in determining how these metals disperse [8]. Soil pH can impact how metal contaminants move within the soil. Additionally, the level of soil moisture influences the spread of these metals [9]. A major feature of soil bacterial communities is their biodiversity. This biodiversity is defined by richness, which refers to the number of operational taxonomic units in the community, and by diversity, which reflects how evenly these operational taxonomic units are represented and distributed. Typically, the Chao index quantifies community richness, while the Shannon index measures diversity. Assessing the biodiversity of soil bacterial communities is a key approach to evaluating soil health. Modern molecular biology techniques are commonly used to analyze the structure and diversity of these communities, either partially or comprehensively. Partial community analysis relies on polymerase chain reaction (PCR) methods, using total DNA or RNA extracted directly from soil as a template. The resulting PCR products can then be examined through clone libraries, DNA microarrays, genetic fingerprinting, or combinations of these techniques. Comprehensive community analysis involves sequencing the 16S rRNA gene, as well as full bacterial genome sequencing, metagenomics, proteomics, and [10,11]. The development of next-generation sequencing (NGS) has transformed our knowledge of bacterial communities across different environments. Metagenomics allows for the extraction of genomic DNA directly from environmental samples, eliminating the need to culture organisms in the lab. This approach enables genomic analysis of the entire bacterial community, avoiding the necessity of isolating and culturing individual bacteria to classify them within their communities [12]. Therefore, the aim of this review is to examine recent studies focused on the effects of heavy metals, introduced into soil through human activities, on prokaryotic soil communities.

Bacterial Community Dynamics in Metal Contaminated Soil

In recent years, heavy metal contamination in soil has become a global concern because of its severe toxicity. These metals are non-biodegradable and tend to accumulate in the environment over long periods [13]. Heavy metal pollution creates stress in the soil environment, leading to significant changes in bacterial community composition. The diversity and population of sensitive bacteria tend to decline, whereas resistant species adapt more easily and become dominant, resulting in a distinct microbial structure. Continuous heavy metal exposure influences both bacterial biomass and metabolic activity. The most frequently encountered toxic metals and metalloids include mercury (Hg), lead (Pb), cadmium (Cd), copper (Cu), chromium (Cr), manganese (Mn), zinc (Zn), and arsenic (As). Among these, Zn, Mn, and Cu serve as essential micronutrients for plants, while Hg, Pb, Cd, Cr, and As have no known biological function. The diversity and abundance of sensitive soil bacteria can decrease, resistant bacteria can easily adapt and increase in abundance, thereby forming a specific structure of the bacterial community [14]. Heavy metal contamination constantly affects bacterial biomass and activity [15]. The most common toxic metals and metalloids are mercury (Hg), lead (Pb), cadmium (Cd), copper (Cu), chromium (Cr), manganese (Mn), zinc (Zn) and arsenic (As, metalloid). Among them, Zn, Mn and Cu perform the function of microelements in plants, while functions have not been shown for Hg, Pb, Cd, Cr and As [7]. Effects of metal pollution on soil bacteria are shown in Figure 1.

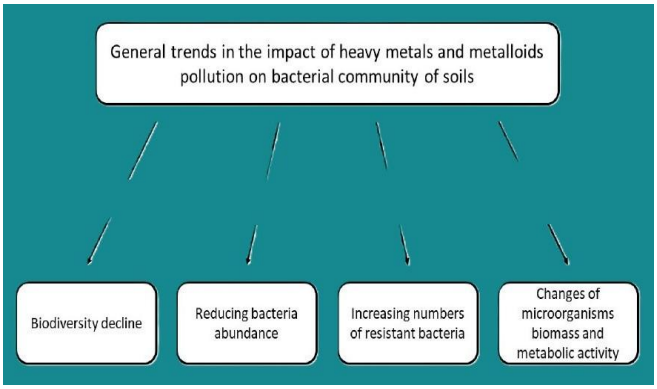

Figure 1. Effect of metal pollution on soil bacteria

Physicochemical Controls on Heavy Metal Release and Movement in Soils

Heavy metals (HMs) can be present in several forms, including free metal ions, exchangeable ions, soluble complexes, and metals incorporated into other compounds. These different chemical forms determine their bioavailability and thus their impact on bacterial communities. Studies have shown that copper and zinc salts (such as sulfates and nitrates) can alter the composition of soil bacterial communities. For instance, the phyla Chloroflexi, Planctomycetes, Patescibacteria, and Latescibacteria were found in higher abundance in soils treated with nitrate salts compared to sulfate-enriched soils, whereas Bacteroidetes and Proteobacteria were less abundant. Moreover, in soils containing both metals, the relative abundance of Proteobacteria, Actinobacteria, and Firmicutes was significantly higher than in the control soil. Studies have shown that treating soil with nanoscale zero-valent iron increases the relative abundance of the Verrucomicrobia phylum, while reducing the proportion of Bacilli and particularly Actinobacteria. The bioavailability and toxicity of nanosized iron are strongly influenced by soil pH and organic matter content. At low pH levels, iron nanoparticles dissolve more rapidly; in contrast, high pH slows dissolution, and organic matter lessens toxicity by neutralizing reactive oxygen species formed through Fenton-like reactions. Ma et al. [16] also examined the interaction between soil pH and heavy metals/metalloids (Cd, Pb, Cu, Cr, Zn, Sb, and As) in acidic and neutral soils from an antimony (Sb) mine in Lengshuijiang, China. They found that bacterial communities responded differently under varying pH conditions. In acidic soils, Zn and Pb showed a stronger correlation with bacterial community composition, while in neutral soils, Sb, As, and Cr were the dominant influencing factors. The main bacterial phyla identified-Acidobacteria, Proteobacteria, Chloroflexi, and Actinobacteria—accounted for about 89.89% of all bacteria. Among them, Acidobacteria was most abundant, comprising an average of 37.28% in acidic soils and 22.92% in neutral ones. Most bacterial taxa showed positive correlations with heavy metals in both soil types. In acidic soils, genera such as Rhodobium, Sphingopyxis, Streptomyces, Burkholderia, Mucilaginibacter, Phenylobacterium, Flavobacterium, and Arthrobacter were positively associated with metals like Sb, As, Cd, and Zn. In neutral soils, genera including Gaiella, Arthrobacter, Nitratireductor, Iamia, Chryselinea, Rhodobium. Researchers observed that the abundance of arsBCR genes increased with higher As concentrations, while the acr3 gene was absent in the upper soil layer (0–20 cm). Genes responsible for As oxidation and arsenate respiration accounted for 17.86–20.45% and 11.44-14.76%, respectively, of the total gene pool. Therefore, soil bacterial communities not only alter their composition in response to heavy metals and metalloids—favoring taxa that are resistant and can adapt to such contamination—but also play an active role in pollutant remediation. They do so by mediating redox reactions through enzymatic activity, influencing solubility and bioavailability, and contributing to processes such as adsorption, leaching, mineralization, and intracellular accumulation. Research on soils with varying levels of arsenic (As) contamination indicated that metallic arsenic is the primary factor influencing the abundance of arsenic transformation genes. However, other metals and metalloids, including Pb, Cu, Zn, and Cd, along with soil pH in abandoned gold mine tailings, also affected microbial dynamics. The highest microbial diversity was found in soils with medium to high As levels. Mercury (Hg) has been shown to significantly alter soil bacterial community structure, decrease microbial diversity, and exhibit strong toxicity toward soil bacteria. Importantly, the specific form of mercury plays a crucial role in determining its impact. Frossard et al. [17] demonstrated that the bioavailable and particularly water-soluble form of mercury exerts a greater influence on bacterial communities than total mercury content in contaminated soils, often leading to reduced biodiversity. A study conducted in China on soils from regions with a 600-year history of mercury mining revealed mercury concentrations ranging from 0.27 to 52.4 mg/kg, with most samples exceeding 0.6 mg/kg. The total bacterial abundance decreased as total mercury levels rose and showed a negative correlation with methylmercury concentrations in paddy soils. Overall, factors such as soil acidity, metal oxidation state, and the chemical form of metals or metalloids influence their solubility, bioavailability, and consequently, their toxicity, microbial diversity, and community structure. Conversely, heavy metal stress promotes the proliferation of resistant bacterial taxa

that possess metal-metabolizing enzyme genes and contribute to pollutant remediation through mechanisms like redox transformations, adsorption, intracellular accumulation, and modification of solubility or bioavailability. Both chemical and biological soil properties, along with the duration of exposure, play key roles in shaping the biological activity and toxicity of metals and metalloids toward soil bacterial communities.

Environmental Setting, Heavy Metal Stress and Exposure Time in Shaping Microbial Communities

The composition of soil bacterial communities is strongly shaped by both the type of ecosystem and the level of heavy metal contamination [18]. In a study of soils chronically contaminated with lead (Pb) across different ecosystems—including deciduous forests, coniferous forests, and hydromorphic soils—the dominant bacterial phyla identified were Acidobacteria, Actinobacteria, Verrucomicrobia, Chloroflexi, Planctomycetes, Bacteroidetes, and Gemmatimonadetes. Soils from coniferous forests contained a lower proportion of Acidobacteria and Proteobacteria compared to deciduous and hydromorphic soils, but had a higher abundance of Actinobacteria (18%) versus 12% and 8% in the other two ecosystems, respectively. In all soil types, Proteobacteria and Chlamydiae were more prevalent in heavily polluted samples, whereas Verrucomicrobia decreased with increasing lead levels. Similarly, in cadmium- and zinc-contaminated mangrove sediments from Kerala, India, Proteobacteria, Bacteroidetes, Firmicutes, Acidobacteria, and Actinobacteria were dominant [19]. Proteobacteria represented the majority of sequences (53.59–75.99%), mainly within the Gammaproteobacteria and Deltaproteobacteria classes. At the genus level, Anaeromyxobacter, Geobacter, Pseudomonas, Candidatus Solibacter, and Pelobacter were most abundant. Functional metagenomic analysis revealed a high prevalence of genes associated with resistance to cobalt, zinc, and cadmium. Another experiment conducted with soil microcosms artificially contaminated with cadmium ($CdCl_2$, 50 mg/kg) and hydrocarbons (phenanthrene and n-octadecane, 1000 mg/kg) demonstrated that the bacterial community exhibited functional resilience, returning to its initial abundance within 90 days [20]. Another study demonstrated that increasing heavy metal concentrations led to a decline in bacterial richness while simultaneously increasing diversity, as measured by the Chao and Shannon indices, respectively [21]. In soils contaminated with Pb, Cd, and Zn, the combined effects of different HM fractions were shown to alter bacterial richness, diversity, and community structure over long-term exposure. Acid-soluble Pb was identified as the main factor shaping the bacterial community. The dominant bacterial phyla in chronically contaminated soils were Bacteroidetes, Acidobacteria, Chloroflexi, Proteobacteria, and Actinobacteria, collectively comprising over 85% of the total bacterial population. Sensitive taxa, including Marmoricola, Nocardioides, and Gibberella, were proposed as bioindicators of soil pollution by these metals. Molecular analyses of soils from Picher, an abandoned mining town in Oklahoma, USA, revealed that bacterial abundance negatively correlated with Pb, Cd, Zn, and Mg concentrations [9]. While overall diversity indices showed no correlation with the concentrations of Al, Pb, Zn, and Cd, individual correlations were observed for seven phyla (Acidobacteria, Actinobacteria, Bacteroidetes, Chloroflexi, Planctomycetes, Proteobacteria, and Verrucomicrobia), linking specific HM concentrations to bacterial abundance. Similarly, Song et al. [22] reported that bacterial biomass in Chinese rice field soils declined with increasing concentrations of Cd, Cu, and Zn in both short- and long-term experiments. Copper had the strongest impact on both bacterial biomass and community composition, with synergistic effects observed among metals, particularly between Cu and Cd. In six rice fields contaminated with antimony (Sb) and arsenic (As), bacterial community structure was most strongly influenced by nitrate levels and the content of As, Sb, and Fe(III) [23]. Dominant genera included Bradyrhizobium, Bryobacter, Candidatus Solibacter, Geobacter, Gemmatimonas, Haliangium, and Sphingomonas, which were strongly associated with As and Sb fractions and likely capable of metabolizing these metalloids. Overall, As and Sb had a greater impact on bacterial diversity than soil physicochemical properties, suggesting that the observed microbiome composition was largely shaped by long-term exposure to Sb and As contamination. A study of agricultural and mining soils with high arsenic content in Guanajuato, Mexico [24], revealed that bacterial communities were primarily dominated by Proteobacteria, Acidobacteria, and Actinobacteria. Proteobacteria was the most abundant phylum, representing 39.6% of sequences in agricultural soils and 36.4% in mining soils. Acidobacteria accounted for 11.6% and 24.2%, while Actinobacteria made up 19.0% and 14.2% in agricultural and mining soils, respectively. The study also highlighted the widespread presence of the genus Bradyrhizobium and uncultivated members of the Rhodospirillaceae family. Bacterial isolates capable of arsenic reduction were obtained from mine soils containing 39 mg/kg As (compared to 15 mg/kg in agricultural soils), all belonging to the genera Bacillus and Williamsia. These microorganisms reflect the adaptation of the bacterial community to high arsenic levels and can influence its bioavailability, mobility, and soil content. In the Hengshi River Basin of the Dabaoshan Mining District (Guangdong, China), agricultural soils irrigated with acid mine drainage (AMD) exhibited severe pollution. Soil pH dropped to 4.3–5.5 under AMD irrigation, compared to 6.5 in the control plot, while concentrations of SO_4^{2-} and heavy metals such as Cu (43.56–249.89 mg/kg), Pb (43.79–144.50 mg/kg), Zn (70.33–293.06 mg/kg), and Cd (0.34–2.91 mg/kg) increased significantly [6]. Microbiome analysis showed dominance of Acidobacteria, Proteobacteria, and Chloroflexi, which together accounted for over 70% of sequences. Acidobacteria were the most abundant phylum (29–38%) in contaminated soils, whereas the control plot was dominated by Chloroflexi (29%) and Proteobacteria (24%), with a lower proportion of Acidobacteria. Among archaea, Crenarchaeota (62–86%), Euryarchaeota (8.9–31%), and Parvarchaeota (3.8–6.5%) dominated contaminated areas. The reference plot also showed prevalence of these three phyla, but in different proportions: Euryarchaeota 48%, Crenarchaeota 34%, and Parvarchaeota 19%. At the phylum and class level, bacterial taxa such as Acidobacteria, Deltaproteobacteria, and Ktedonobacteria, along with the archaeal phylum Crenarchaeota, dominated AMD-contaminated soils. At lower taxonomic levels, heavily polluted sites were enriched in Koribacteraceae, Acidobacteriales, and Solibacteriales, whereas the control site was dominated by Methanosarcinales, Methanocella, and Nitrososphaerales. Heavy metals such as Cu, Pb, and Zn were positively correlated with Acidobacteria and Crenarchaeota, but negatively with Proteobacteria and Euryarchaeota, while Cd showed a strong correlation with Methanoregula. The dominance of Acidobacteria in contaminated soils suggests that chronic AMD irrigation creates

ecological niches favorable to acidophilic bacteria. In archaea, AMD exposure shifts dominance from Euryarchaeota to Crenarchaeota. Fajardo et al. [13] demonstrated that exposure to heavy metals (HMs) in contaminated soils induces stress in bacterial communities, leading to shifts in their composition, with different bacterial groups responding variably to pollution. In a 160-day study of soils exposed to high concentrations of Pb, Zn, and Cd, the HM mixture exerted selective pressure on the microbiome, causing substantial changes over time. Phyla such as Proteobacteria, Actinobacteria, Verrucomicrobia, and Bacteroidetes showed clear declines after incubation, indicating high sensitivity, while Firmicutes proved to be the most HM-resistant phylum, increasing in relative abundance under HM exposure. Conversely, Lin et al. [25] observed that in heavily contaminated rice field soils on China's east coast, Proteobacteria abundance was higher than in less polluted soils, whereas Verrucomicrobia, Firmicutes, and Chloroflexi were significantly reduced. Resistance to HM contamination varied across phyla: Proteobacteria, Acidobacteria, and Bacteroidetes were more resilient in areas with high, medium, and low contamination, respectively. Alpha diversity was higher in soils with high, medium, or no HM contamination compared to soils with low HM levels. Vanadium's inhibitory effects on bacterial richness and diversity were also reported [5]. Long-term exposure (240 days) to vanadium caused initially distinct bacterial communities to converge, dominated by Proteobacteria, Acidobacteria, and Actinobacteria, particularly bacteria capable of tolerating or reducing vanadium toxicity [26]. High cadmium concentrations similarly reduced bacterial richness and diversity [27], although in some cases, bacterial diversity remained stable, likely because Cd levels were insufficient to suppress activity, with the Chao index positively correlating with total and bioavailable soil Cd [14]. Short-term mercury exposure (30 days) had little effect on bacterial community structure or activity [28], but long-term Hg pollution significantly altered community composition and diversity. Interestingly, bacterial abundance and Shannon diversity were higher in areas with medium and high Hg contamination than in low-pollution sites, indicating adaptation to prolonged Hg exposure. Mercury bioavailability can increase when humic and fulvic acids are added, which reduces bacterial diversity [29]. Higher Hg levels were associated with increased relative abundance of Firmicutes, Bacteroidetes, Chitinophagaceae, Ferruginibacter, Sphingobacteriaceae, Pedobacter [30]. A study of uranium tailings soils in southern China [31] found that uranium concentrations in contaminated samples exceeded 40 mg/kg, nearly ten times higher than in uncontaminated soils. Comparison of bacterial community structures across different depths (0–15, 15–30, and 30–45 cm) revealed similar phylum-level compositions at all depths. The five dominant phyla were Actinobacteria (14.4–60.7%), Proteobacteria (29.9–49.6%), Planctomycetes, Acidobacteria, and Firmicutes. At the genus level, Robiginitalea, Microlunatus, Alicyclobacillus, and Azorhizobium were more abundant in uranium-contaminated soils, suggesting better adaptation to radioactive environments. The study also showed that alpha diversity was lower in uranium-contaminated soils, indicating fewer bacterial phyla, while beta diversity increased with soil depth, reflecting greater differences in species composition between contaminated and uncontaminated soils. Most dominant genera, including Azorhizobium, Chelativorans, Variovorax, Delftia, and Citrobacter, belonged to Proteobacteria, highlighting this phylum's adaptability and potential for uranium remediation. Overall, Proteobacteria, Acidobacteria, and Actinobacteria dominate polluted soils across ecosystems, with Bacteroidetes, Firmicutes, and Chloroflexi also representing significant portions of the community. Heavy metal and metalloid contamination strongly influences bacterial community structure, with dominance of these taxa likely linked to resistance and adaptability. Typically, high heavy metal levels reduce alpha diversity [6,21,31], although some studies report increased [25,28] or unchanged [14] species richness, possibly due to moderate heavy metal concentrations stimulating resistant bacteria without severely affecting sensitive taxa. Additionally, some heavy metals lead to a more even distribution of taxa (Shannon index) in moderately or highly polluted areas [28]. The effects of heavy metal contamination are highly time-dependent. Short-term mercury exposure (30 days) did not alter bacterial community structure [28], whereas 90-day experiments with soil microcosms contaminated with hydrocarbons and cadmium showed succession, with sensitive bacterial populations initially declining and later recovering, while resistant species displayed opposite dynamics [20]. In contrast, long-term exposure (160 days) to heavy metals reduced the abundance of Proteobacteria, Actinobacteria, Verrucomicrobia, and Bacteroidetes, indicating that these phyla require extended periods to adapt and dominate under heavy metal stress [13]. Similarly, vanadium exposure over 240 days led to convergence of bacterial communities and dominance of Proteobacteria, Acidobacteria, and Actinobacteria [5]. Long-term HM exposure, especially mercury, substantially reshapes soil bacterial communities [28], whereas short-term studies may be affected by methodological limitations, as extracellular bacterial DNA can persist in soil, potentially distorting results in metagenomic PCR analyses [30].

Effects of Heavy Metals on Rhizospheric Bacterial Community

Soil bacterial population, bacterial diversity, soil respiration as well as total nitrogen, available nitrogen mostly influenced negatively [32-35]. A study of bacterial communities in the rhizosphere of nickel hyperaccumulator plants (Odontarrhena chalcidica, O. smolikana, O. rigida, and Noccaea ochroleuca) in Albania identified 14 bacterial phyla. Proteobacteria showed a negative correlation with magnesium and nickel, Acidobacteria positively correlated with Ni, Gemmatimonadetes negatively correlated with Fe, Ca, N, C, and organic carbon, Chloroflexi positively correlated with Mg, and Bacteroidetes negatively correlated with Mg and Pb. In these rhizospheres, Proteobacteria dominated, with Acidobacteria and Actinobacteria also forming significant portions. Notably, Proteobacteria and Actinobacteria favor organic carbon-rich soils typical of the rhizosphere, while Acidobacteria benefit from elevated pH levels. Unexpectedly, Chloroflexi had an average relative abundance of only 7.8%, despite being common in chemically extreme soils and dominant in nickel mine dump samples. Similarly, it was previously found to be the most abundant phylum in the rhizosphere of O. chalcidica on ultrabasic soils in Greece [37]. The effect of cadmium pollution on bacterial community composition was also examined by planting Robinia pseudoacacia and inoculating soils with rhizobia [38]. Overall, soil conditions exerted greater selective pressure on bacterial communities than plants, and bacterial diversity decreased with increasing contamination in both rhizosphere and bulk soil. The rhizospheric bacterial community of Elsholtzia haichowensis, a plant widely recognized as an indicator of elevated copper levels in China, was investigated in copper-contaminated soils [39]. Soil

samples were collected from areas near copper mines with varying Cu contamination and from a non-metallic reference site. Contaminated soils contained Cu concentrations ranging from 502 to 2760 mg/kg and Zn concentrations from 127 to 2100 mg/kg. The highest alpha diversity indices were observed in the rhizosphere of E. haichowensis or in bulk soils of the non-metallic area, whereas the lowest diversity was found in heavily polluted non-rhizospheric soils. Across all soils, archaeal alpha diversity was significantly lower than bacterial diversity. Environmental factors influenced microbial community structure in the order of soil pH > heavy metals > nitrogen > soil texture. Heavy metals, particularly Cu and Zn, but also Cr, Ni, and Cd, explained most of the variation, highlighting their strong effect on microbial communities. The study also showed that rhizosphere soils had higher bacterial abundance than non-rhizosphere soils, likely due to root exudates from the host plant stimulating bacterial growth, activity, and turnover [41].

Prospects of Research

Research has demonstrated that bacterial taxa are highly interconnected, forming a single ecological network composed of clusters [42]. These clusters likely contribute to soil fertility, nutrient cycling, and other sustainable ecological functions [43]. The stability of such clusters is probably linked to the fact that constituent bacteria occupy specific ecological niches and are metabolically interdependent. For instance, taxa within certain clusters have been shown to correlate closely with soil pH, moisture levels, macro-ecosystem type, and the availability and composition of organic and inorganic substrates [42]. These findings suggest that metagenomic analysis of soil bacterial communities can help identify sensitive taxa, which may serve as environmental indicators of heavy metal pollution and soil ecosystem disturbances. Detailed study of such indicator taxa and clusters could enable the development of rapid and efficient metagenomic approaches for assessing soil ecological health, sustainability, productivity, and contamination levels. Another promising area of research is rhizosphere-mediated bioremediation of heavy metal pollution. Unlike organic pollutants, heavy metals are not biodegradable but can be stabilized or extracted by plants [44]. Rhizospheric bacteria influence HM transformation by modifying soil pH, releasing chelating agents, and altering redox potential [45]. They also enhance plant growth by secreting hormones and improving nutrient availability [46]. Plants capable of heavy metal hyper accumulation, such as the Ni-hyper accumulators described earlier, are of particular interest for bio extraction and phytomining applications [47]. While bacteria can alter heavy metal oxidation states, mobility, and intracellular accumulation, heavy metals that do not form volatile compounds cannot be removed solely by microbial activity; plant participation is essential. Therefore, the development of sustainable, cost-effective biotechnologies for heavy metal remediation requires identifying and studying heavy metal-hyper accumulator plants and ensuring optimal functioning of their rhizosphere. Using effective hyper accumulators not only allows heavy metal phytoextraction from soils but also enables phytomining of valuable metals.

Conclusion

Soil contamination with heavy metals represents a major challenge for modern society, particularly for agriculture, which depends heavily on soil health. Investigating soil bacterial communities is now a common approach to assess the negative impacts of human activity. However, the effects of pollutants on bacterial taxonomic composition and diversity are difficult to determine definitively. This is largely because soil is an extremely heterogeneous environment, influenced by numerous factors such as pH, texture, organic matter content, moisture, temperature, and vegetation. Experimental design also plays a key role, as results often differ between long-term field studies and short-term laboratory experiments. Several studies have shown that soil bacteria can adapt to long-term pollutant exposure, while acute, short-term exposure tends to reduce bacterial richness and diversity. Prolonged heavy metal exposure can lead to tolerance within the bacterial community: sensitive bacteria die off, and resistant taxa survive under stress**.** Consequently, soil bacteria can adjust to long-term heavy metal pollution by altering community structure and composition while maintaining functional diversity and ecological roles. Interestingly, low concentrations of heavy metals such as Zn, Cu, Cd, and Hg can even stimulate bacterial abundance and diversity. The toxicity of a given metal largely depends on its dose, as seen with Fe, Ni, and Cd, which show only weak correlations with bacterial diversity. The resilience of soil bacterial communities may be explained by functional redundancy: functions lost from sensitive species can be compensated by resistant species already present in the soil in smaller numbers. Additionally, bacteria can adapt to environmental changes through gene modifications, increasing their resistance to pollutants. Overall, soil bacterial communities are highly complex and finely regulated, simultaneously sensitive to pollution yet capable of remarkable adaptation and restoration of both structure and function under adverse conditions.

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