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ENVIRONMENTAL GENETICS OF MICROBIAL ADAPTATION TO HEAVY METAL-CONTAMINATED INDUSTRIAL ECOSYSTEMS

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ABSTRACT

Background: Heavy metal contamination in industrial ecosystems leads to severe environmental stress affecting microbial diversity, genetic adaptation and ecosystem stability. Microorganisms from polluted habitats develop mechanisms of resistance allowing them to survive in the presence of toxic metals.
Objective: The study was conducted to investigate environmental genetics of microbial adaptation and to identify heavy metal resistance genes in contaminated industrial ecosystems.
Methodology: Samples of soil and wastewater were collected from three industrial sites contaminated with lead (Pb), cadmium (Cd) and chromium (Cr). Physicochemical analysis, microbial isolation, metagenomic sequencing and bioinformatics analyses were used to evaluate microbial diversity and resistance-associated genetic pathways.
Findings: The results indicated high concentrations of Cr (145–180 mg/kg), Pb (67–120 mg/kg) and Cd (7–19 mg/kg) in the sampling sites. Metagenomic analysis revealed dominant metal-resistant taxa, including Pseudomonas spp. (28%), Bacillus spp. (22%), and Acinetobacter spp. (16%). Highly contaminated samples showed significant enrichment of resistance genes including czcA, merA and arsB. Heavy metal concentration was strongly positively correlated (r=0.82) with resistance gene abundance.
Conclusion: The current study demonstrates that industrial heavy metal pollution drives microbial genetic adaptation via specific resistance mechanisms, suggesting the potential for resistant microbial communities in sustainable bioremediation applications.

KEYWORDS: Heavy metals, environmental genetics, microbial adaptation, metagenomics, resistance genes, industrial pollution, bioremediation.

1 INTRODUCTION

1.1 Environmental Pollution by Heavy Metals

The rapid industrialization and urbanization have resulted in heavy-metal pollution, which has become a serious environmental and public health concern. Industries such as mining, electroplating, battery manufacturing, textile processing, tanning and metallurgy discharge large quantities of toxic metals into the soil as well as water ecosystems [1]. Heavy metals are not biodegradable and remain in the environment for a long time, leading to bioaccumulation and biomagnification in food chains [2]. Some of the most dangerous pollutants are lead (Pb), cadmium (Cd), mercury (Hg), chromium (Cr) and arsenic (As) which are extremely toxic even at low concentrations [3]. Lead exposure interferes with neurological and developmental processes; cadmium causes renal dysfunction and skeletal damage. Chromium and arsenic are known carcinogens, and mercury disrupts aquatic ecosystems and neurological functions [4].

1.2 Microbial Survival in Toxic Ecosystems

Microorganisms living in polluted industrial ecosystems are subjected to a strong selective pressure exerted by high concentrations of toxic metals. Despite such harsh conditions, microbial communities have remarkable adaptive capabilities through physio-biochemical and genetic modifications [5]. Heavy metal stress induces oxidative damage, membrane disruption and inactivation of enzymes which compel the microbes to evolve protective mechanisms for their survival [6]. Adaptive responses include activation of efflux pumps, enzymatic detoxification and intracellular sequestration and biofilm formation [7]. Exposure to toxic contaminants is constantly promoting the evolutionary selection of resistant microbial populations that are capable of tolerating extreme environmental conditions. Such adaptations are involved in microbial community restructuring and redirected ecosystem functions in industrially polluted habitats [8].

1.3 Environmental Genetics and Adaptation

Environmental genetics is important to understand the adaptation of microbes under heavy metal stress. Resistance mechanisms are primarily regulated by specific genes and operons regulating metal transport, detoxification and oxidative stress responses [9]. Genes such as czcA, merA and arsB are generally associated with resistance to cadmium, mercury and arsenic respectively. Horizontal gene transfer via plasmids, transposons and integrons allows for rapid dissemination of resistance determinants within microbial populations [10]. These mobile genetic elements accelerate microbial evolution and permit adaptation to changing environmental conditions. Metagenomics and next-generation sequencing technologies have enhanced the ability to detect functional resistance genes and microbial interactions in contaminated ecosystems [11].

1.4 Research Gap

Although several studies have examined microbial resistance to heavy metals, few genomic studies have integrated industrial ecosystems that combine physicochemical characteristics and microbial genetic adaptation. In most of the previous studies, environmental pollution or microbial diversity were studied separately, and there was no comprehensive analysis of the interaction between gene and environment [12]. Hence, there is a growing need to integrate environmental chemistry, microbial ecology and genomics to better understand adaptation mechanisms in polluted ecosystems.

1.5 Objectives

The present study aims to analyze the microbial diversity in heavy metal contaminated industrial ecosystems, to identify resistance genes, to evaluate the adaptive genetic mechanisms, and to assess the ecological significance and bioremediation potential of resistant microbial communities.

2 RELATED WORK

2.1 Heavy Metal Toxicity in Industrial Ecosystems

Heavy metal contamination of terrestrial and aquatic ecosystem is one of the serious concerns among industrial activities. During ore extraction and waste disposal processes, mining industries release significant concentrations of arsenic (As), cadmium (Cd) and mercury (Hg) in the environment, which results in persistent environmental toxicity [1]. Electroplating industries generates chromium (Cr), nickel (Ni) and lead (Pb) rich effluents which affects the soil chemistry and microbial diversity [2]. Likewise, textile and tannery industries discharge untreated wastewater containing chromium compounds, dyes and toxic organic pollutants into nearby ecosystems adversely affecting microbial and plant communities [3]. Battery manufacturing industries contribute a significant amount of lead and cadmium contamination that builds up in the sediments and groundwater systems [4]. These contaminants exert a powerful selective pressure on environmental microorganisms inducing oxidative stress, DNA damage and enzymatic inhibition in microbial populations.

2.2 Microbial Genetic Adaptation Mechanisms

Microorganisms develop genetic and biochemical mechanisms of adaptation in response to heavy metal stress to survive in contaminated ecosystems. Efflux transport systems such as czcA and copA genes actively pump out toxic metal ions from microbial cells, thus reducing the toxicity inside [5]. Intracellular sequestration and detoxification of metals shown in table 1 is enabled by metallothionein proteins and bioaccumulation pathways. Biofilm formation also enhances the resistance of microorganisms by creating extracellular matrices that protect against toxic exposure [6]. Genetic mutations and activation of oxidative stress defense genes such as sodA and katG are involved in cellular protection under metal-induced reactive oxygen species (ROS) stress [7]. Mobile genetic elements such as plasmids, transposons and integrons are important contributors to horizontal gene transfer and rapid dissemination of resistance genes among microbial communities living in polluted environments [8].

Table.1. Microbial Adaptation Mechanisms in Heavy Metal-Contaminated Ecosystems

Adaptation Mechanism	Function	Representative Genes
Efflux transport	Metal ion export	*czcA, copA*
Bioaccumulation	Intracellular sequestration	*smtA*
Oxidative stress defense	ROS neutralization	*sodA, katG*
Horizontal gene transfer	Resistance dissemination	Plasmid-borne genes

2.3 Metagenomics in Environmental Genetics

Recent advances in metagenomics and next generation sequencing technologies have greatly improved our understanding of microbial adaptation in polluted ecosystems. Functional genomics identifies metabolic pathways associated with resistance, while comparative metagenomics gives insights into microbial diversity, gene abundance and ecological interactions under heavy metal stress [6]. These molecular approaches are useful in the development of sustainable bioremediation strategies and environmental monitoring systems.

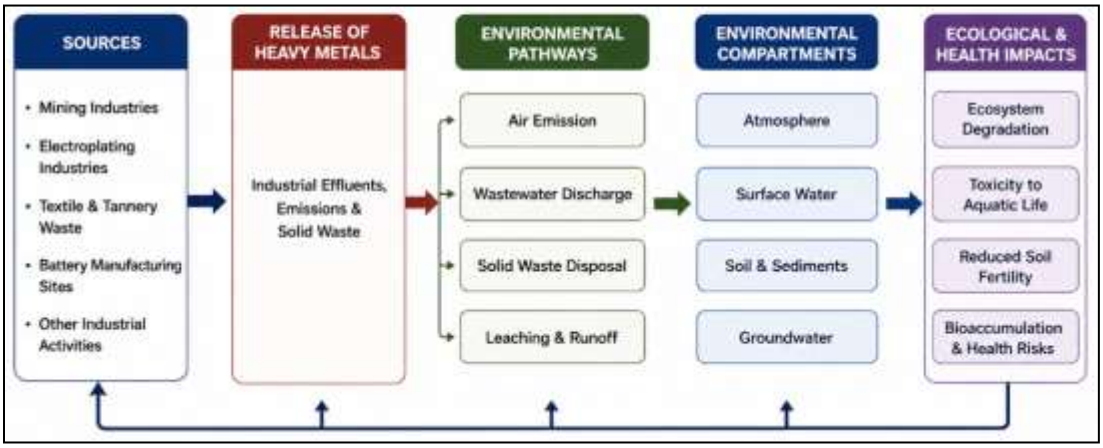

Figure.1. Sources and pathways of heavy metal contamination in industrial ecosystems

Figure 1 shows the main sources and environmental pathways of heavy metal contamination in industrial ecosystems. Industrial sectors such as mining, electroplating, textile processing, tannery operations, battery manufacturing release toxic metals like lead (Pb), cadmium (Cd), mercury (Hg), chromium (Cr) and arsenic (As). These contaminants are released into the environment via industrial effluents, air emissions, solid waste disposal and discharge of wastewater. Accumulation of heavy metals in soil, surface water, groundwater and plants leads to ecological degradation, toxicity to aquatic organisms, reduced soil fertility, bioaccumulation and serious human health risks in contaminated ecosystems.

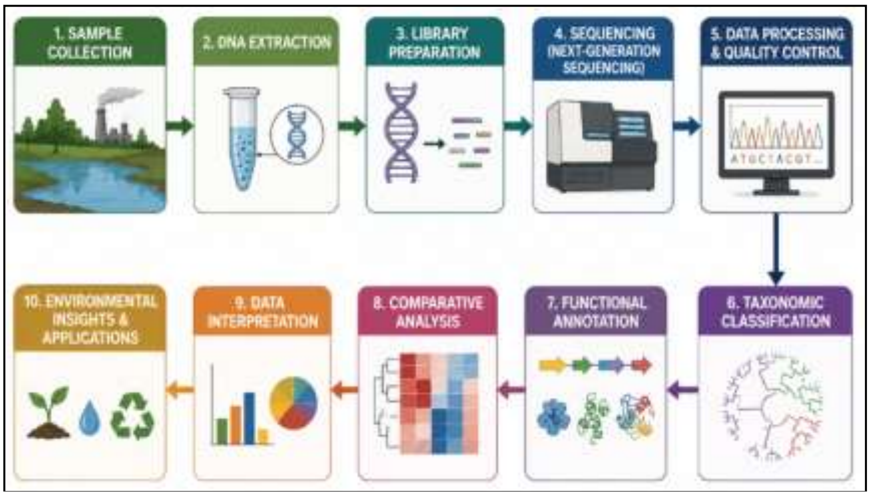

Figure.2. Metagenomic workflow for environmental microbial analysis

Figure 2. Metagenomic workflow for environmental microbial analysis in ecosystems contaminated with heavy metals. The first step is to collect environmental samples (soil or wastewater) and then isolate and purify DNA. Microbial communities and functional genes are identified by next generation sequencing of extracted microbial DNA. The sequences were analyzed by bioinformatics methods for sequence assembly, taxonomic classification, gene annotation and comparative metagenomics. The workflow helps to identify heavy metal resistance genes, microbial diversity and adaptive metabolic pathways. This integrated approach gives a comprehensive insight into microbial ecology, environmental genetics and bioremediation potential of the contaminated industrial ecosystem.

3 MATERIALS & METHODS

3.1 Study Area Description

The study was conducted in three industrially contaminated regions characterized by intensive anthropogenic activities and elevated heavy metal pollution. Site A was located near an electroplating industrial zone where chromium (Cr) and nickel (Ni) contamination was predominant due to metal finishing operations shown in table 2. Site B represented a textile and tannery wastewater discharge area contaminated mainly with lead (Pb) and cadmium (Cd). Site C was situated near an abandoned mining region with high arsenic (As) and mercury (Hg) accumulation. The study areas experienced tropical climatic conditions with annual temperatures ranging from 24–36°C and average rainfall between 800–1100 mm, which influence contaminant mobility and microbial activity [18].

Table.2. Characteristics of Sampling Sites

Sampling Site	Industrial Activity	Major Contaminants
Site A	Electroplating	Cr, Ni
Site B	Textile industry	Pb, Cd
Site C	Mining area	As, Hg

3.2 Sample Collection

Samples of soil and waste water were collected from contaminated industrial ecosystems during pre-monsoon season. Surface soil samples (0–15 cm) were taken with sterile stainless-steel augers and wastewater samples were collected in sterilized polypropylene containers. To ensure reproducibility, triplicate samples were collected from each site. All samples were transported to the laboratory at 4°C under refrigerated conditions and processed within 24 hours using sterile handling procedures to minimize cross-contamination [12].

3.3 Physicochemical Analysis

The physicochemical properties including pH, electrical conductivity (EC), organic matter content and heavy metal concentrations were determined using standard laboratory protocols. The soil pH and EC were determined using the digital pH and conductivity meters as shown in table 3. The Heavy metals concentrations were determined by Atomic Absorption Spectroscopy (AAS) after acid digestion of samples. Organic matter content was determined using the Walkley-Black method.

Table 3. Physicochemical Parameters and Analytical Methods

Parameter	Method Used	Instrument
pH	Electrometric	pH meter
Electrical conductivity	Conductometric	EC meter
Metal analysis	Atomic absorption spectroscopy	AAS
Organic matter	Walkley-Black method	Laboratory analysis

3.4 Microbial Isolation and Identification

Heavy metal resistant microbial populations were isolated using culture-dependent methods on nutrient agar and selective media with varying concentrations of heavy metals. Morphological characterization of diverse bacterial colonies was done based on colony colour, shape, texture and Gram staining properties. Biochemical tests and microscopic examination were used for the preliminary identification of resistant strains [15].

3.5 DNA Extraction and Sequencing

Genomic DNA was extracted from microbial communities in soil and wastewater using a commercial environmental DNA isolation kit. Agarose gel electrophoresis and spectrophotometric analysis were used to confirm DNA quality and concentration. The 16S rRNA gene was PCR amplified using universal bacterial primers . Microbial diversity and heavy metal resistance genes studied by high-throughput sequencing and shotgun metagenomic analysis. [20].

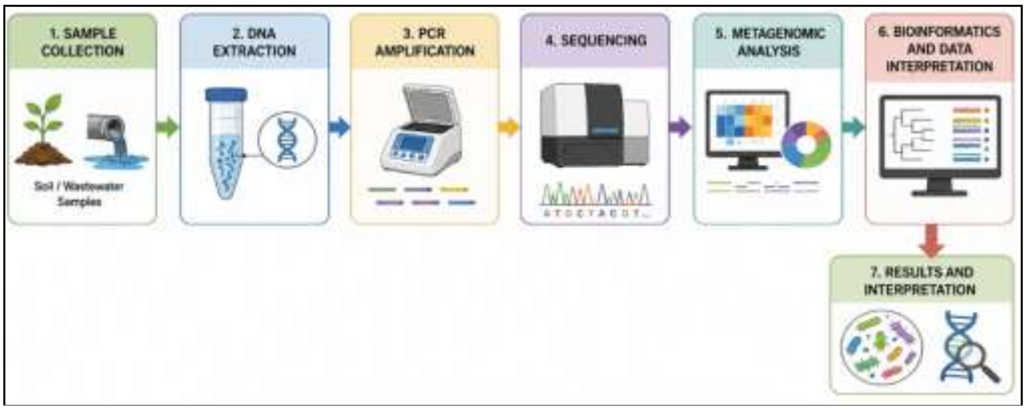

Figure.3. Experimental workflow for microbial genomic analysis

The experimental workflow used for the microbial genomic analysis is depicted in Figure 3 . It includes the collection of environmental samples, DNA extraction, PCR amplification, sequencing, metagenomic analysis and interpretation of bioinformatics to identify microbial diversity and resistance genes .

3.6 Bioinformatics and Statistical Analysis

QIIME2 and MEGA softwares were used for quality filtering of raw sequencing data and assembly into sequences for taxonomic classification. Functional gene annotation and diversity analyses were performed to evaluate the mechanisms of microbial adaptation Alpha diversity indices such as the Shannon and Simpson indices were calculated to measure microbial richness. Statistical analysis and correlation studies were performed using R software and SPSS, to determine the relations between the heavy metal concentrations and the genetic diversity of microbes.

4 RESULTS & DISCUSSION

The present study assessed heavy metals contamination, microbial diversity and genetic adaptation mechanisms in industrial ecosystems by physicochemical and metagenomic analyses. The concentrations of heavy metals varied greatly among the industrial sites, affecting the composition of the microbial community and the abundance of resistance genes. Metagenomic sequencing identified a prevalence of bacterial taxa resistant to heavy metals and functional genes involved in detoxification and metal transport. Further correlation analysis showed significant correlations of the environmental pollution levels with the adaptive responses of the microbes, which highlighted the ecological significance of microbial evolution in contaminated industrial ecosystems.

4.1 Heavy Metal Concentration Analysis

The concentration of heavy metals was found to vary considerably among the studied industrial sites. Site C showed the highest concentrations of chromium (180 mg/kg) and lead (120 mg/kg), indicating severe contamination associated with mining activities (table 4). Higher levels of cadmium were recorded at site B due to discharge from the textile industries . Moderate chromium contamination was observed at site A associated with electroplating activities .

Table.4. Heavy Metal Concentrations across Industrial Sites

Site	Pb (mg/kg)	Cd (mg/kg)	Cr (mg/kg)
Site A	85	12	145
Site B	67	19	98
Site C	120	7	180

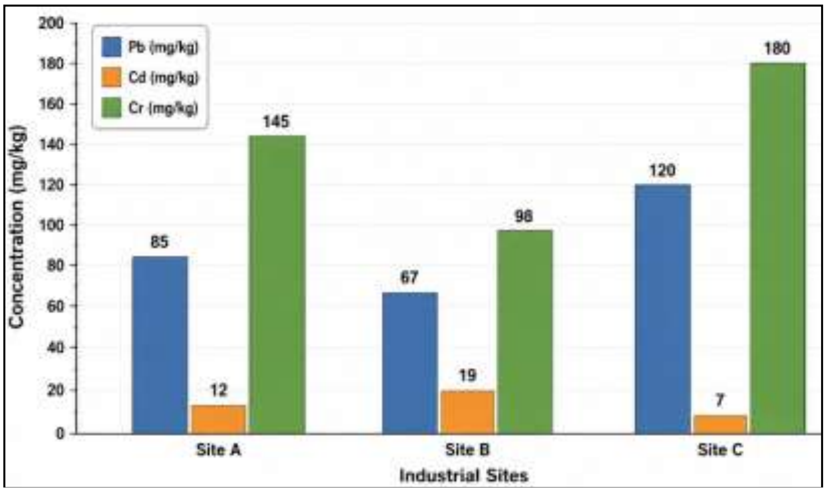

Figure.4. Comparative Heavy Metal Concentrations across Industrial Sites

Figure 4 presents the relative distribution of the concentrations of lead (Pb), cadmium (Cd) and chromium (Cr) among the studied industrial sites. The graphical representation demonstrated the highest contamination levels in the mining associated areas indicating increased environmental risk and selective pressure on resident microbial communities.

4.2 Microbial Diversity and Community Structure

Metagenomic analysis demonstrated high variation of microbial diversity in contaminated ecosystems. Proteobacteria and Firmicutes were the most prevalent bacterial phyla in highly polluted samples. Microbial taxa resistant to metal stress were able to adaptively survive under conditions of heavy metal stress. Diversity indices showed that microbial richness was lower in highly contaminated sites than in moderately polluted sites.

Table.5. Dominant Heavy Metal-Resistant Microbial Taxa

Microbial Taxa	Relative Abundance (%)	Resistance Characteristic
Pseudomonas spp.	28	Chromium resistance
Bacillus spp.	22	Cadmium tolerance
Acinetobacter spp.	16	Multi-metal resistance

The relative abundance of Pseudomonas spp. was the highest, showing the strong capacity of the chromium resistance, as shown in Table 5. Bacillus spp. showed significant cadmium tolerance, while Acinetobacter spp. showed resistance to multiple heavy metals, indicating adaptive evolution in the context of industrial contamination.

4.3 Detection of Heavy Metal Resistance Genes

Functional metagenomic analysis identified several heavy metal resistance genes involved in detoxification, metal transport and stress response mechanisms (Table 6). We found that genes associated with efflux systems and arsenic detoxification were highly abundant in contaminated samples.

Table.6. Heavy Metal Resistance Genes and Functional Roles

Gene	Metal Resistance	Functional Role
czcA	Zn/Cd/Co	Efflux transport
merA	Mercury	Detoxification
arsB	Arsenic	Arsenic resistance

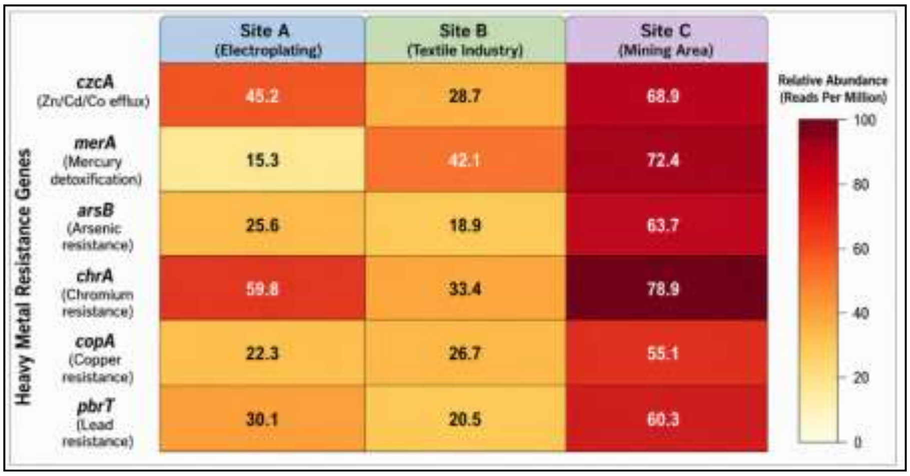

Figure.5. Heatmap of Heavy Metal Resistance Gene Abundance

Figure 5 Distribution of heavy metal resistance genes. The distribution of heavy metal resistance genes obtained by metagenomic sequencing. The sites with high contamination levels showed higher expression levels of czcA, merA and arsB genes, which suggests that microbes have developed specific resistance pathways to adapt.

4.4 Correlation Between Pollution and Genetic Adaptation

Statistical analysis showed strong positive correlations between heavy metal concentration and resistance gene abundance ($r = 0.82$, $p < 0.05$). Enhanced contamination levels led to selective pressure and an improved microbial adaptation and transmissibility of resistance genes through horizontal gene transfer mechanisms.

4.5 DISCUSSION

The results show that heavy metal pollution has a profound effect on microbial ecology and environmental genetics in industrial ecosystems. High concentrations of chromium, cadmium and lead exerted strong selective pressure, favoring the adaptive evolution of resistant microbial populations. The prevalence of Pseudomonas spp., Bacillus spp. and Acinetobacter spp. is indicative of their ecological significance in contaminated environments. Functional resistance genes like czcA, merA and arsB confirmed the role of genetic adaptation in the microbial survival in toxic stress conditions.

Horizontal gene transfer via plasmids and mobile genetic elements likely facilitated the rapid dissemination of resistance determinants within the microbial communities. Similar results were found in recent metagenomic studies of industrially polluted ecosystems . The mechanisms of microbial adaptation observed indicate potential applications of resistant bacterial communities in sustainable bioremediation technologies. Furthermore, knowledge about the genetic response of microbes to heavy metal stress is useful for environmental monitoring, restoration of ecosystems and for taking long-term measures for ecological sustainability.

5 CONCLUSION

The present study showed that heavy metal contamination could significantly change microbial ecology and community structure in industrial ecosystems. Strong environmental stress and selection of resistant microbial populations were caused by high concentrations of lead (Pb), cadmium (Cd), chromium (Cr) and arsenic (As). Metagenomic and physicochemical analysis showed the dominance of adapted microbial taxa such as

Pseudomonas spp., Bacillus spp. and Acinetobacter spp. with specialized resistance mechanisms to survive under toxic conditions.

Functional resistance genes czcA, merA and arsB were present, indicating genetic adaptation through efflux transport, detoxification and arsenic resistance pathways. Moreover, horizontal gene transfer and mobile genetic elements probably contributed to the spread of resistance determinants among microbial communities living in contaminated industrial environments.

The study also pointed to the utility of metagenomic methods for understanding microbial diversity, functional genomics and environmental adaptation mechanisms. Correlation analyses revealed significant positive correlations between heavy metal concentrations and the abundance of resistance genes, suggesting that pollution drives selective evolutionary pressure on microbial ecosystems.

In general, the findings underline the ecological relevance of microbial adaptation in polluted environments and endorse the application of resistant microbial communities in sustainable bioremediation and environmental restoration strategies. Environmental chemistry, microbial ecology, and genomics provide a comprehensive framework for monitoring and managing industrial contamination.

6. Future Scope

Further research should be directed towards sophisticated genomic and biotechnological approaches to increase the efficiency of microbial remediation in heavy metal polluted ecosystems. The CRISPR-based microbial engineering can be explored to modify the resistance genes and improve the metal detoxification potential of the environment-beneficial microbes. Synthetic biology approaches may also further enable the development of engineered microbial consortia with enhanced bioremediation potential and environmental adaptability. Long-term ecological monitoring studies are essential to understand the persistence, evolution and ecological impact of resistance genes in industrial ecosystems in the context of changing environmental conditions. "Continuous monitoring would be helpful in assessing the recovery and sustainability of ecosystems post remediation practices".

Furthermore, the predictive modeling of microbial adaptation, resistance gene distribution, and contamination risk assessment can be improved by AI-assisted environmental genomics and machine learning-based bioinformatics tools. The integration of multi-omics technologies, environmental sensors and computational approaches could offer better insights into the functioning of ecosystems and help design effective and eco-friendly remediation strategies for industrially contaminated environments.

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