



Review

Microbial assisted alleviation of nickel toxicity in plants: A review



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ABSTRACT

Nickel (Ni) is required in trace amounts (less than 500 $\mu\text{g kg}^{-1}$) in plants to regulate metabolic processes, the immune system, and to act as an enzymatic catalytic cofactor. Conversely, when nickel is present in high concentration, it is considered as a toxic substance. Excessive human nickel exposure occurs through ingestion, inhalation, and skin contact, ultimately leading to respiratory, cardiovascular, and chronic kidney diseases. Due to anthropogenic activities, the nickel concentrations in various environmental scenarios have progressively risen to levels as high as 26,000 ppm in soil and 0.2 mg L^{-1} in water; surpassing the established safety threshold limits of 100 ppm for soil and 0.005 ppm for surface water. Nickel is required by various plant species for facilitating biological processes; in the range of 0.01–5 $\mu\text{g g}^{-1}$ (dry weight). When present in excess, nickel toxicity in plants (10–1000 mg kg^{-1} dry weight mass) causes many disrupted metabolic processes; leading to lower growth, altered development, hindered seed germination, chlorosis, and necrosis. To tackle any metal-linked pollution issues, various remediation approaches are employed to remove heavy metals (especially nickel) and metalloids including physicochemical, and biological methods. Based on literature, the physicochemical methods are not commonly used due to their costly nature and the potential for producing secondary pollutants. Interestingly, bioremediation is considered by many practitioners as an easy-to-handle, efficient, and cost-effective approach, encompassing techniques such as phytoremediation, bioleaching, bioreactors, green landforming, and bio-augmentation. Operationally, phytoremediation is widely utilized for cleaning up contaminated sites. To support the phytoremediative processes, numerous nickel hyperaccumulating plants have been identified; these species can absorb from their surroundings and store high concentrations of nickel (through various mechanisms) in their biomass, thereby helping to detoxify nickel-contaminated soils via phytoextraction. The microbe-assisted phytoremediation further optimizes the nickel detoxification processes by fostering beneficial interactions between microbes and the nickel-hyperaccumulators; promoting enhanced metal uptake, transformation, and sequestration. Microbe-assisted phytoremediation can be categorized into four subtypes: bacterial-assisted phytoremediation, cyanoremediation, mycorrhizal-assisted remediation, and rhizoremediation. These diverse approaches are likely to offer more effective and sustainable remediative strategy to ecologically restore the nickel-contaminated environments.

Abbreviations: DWM, Dry Weight Mass; ACD, Allergic Contact Dermatitis; NRAMP, Natural Resistance-Association Macrophage Protein; ZIP, Zinc-Iron Permease; YSL, Yellow-Stripe 1-like; HMA, Heavy Metal ATPase; CDF, Cation Diffusion Facilitator; CAX, Cation exchanger proteins; ABC, ATP-binding cassette transporters; ROS, Reactive Oxygen Species; AO, Ascorbate Oxidase; POD, Peroxidase; CAT, Catalase; SOD, Superoxide Dismutase; GR, Glutathione Reductase; ETC, Electron Transport Chain; AMF, Arbuscular Mycorrhizal Fungi; H^+ -ATPase, Hydrogen Ion Proton ATPase; PM, Plasma Membrane; NA, Nicotinamide; IAA, Indole Acetic Acid; PGPB, Plant Growth-Promoting Bacteria; PGPR, Plant Growth Promoting Rhizobacteria; LMWOA, Low Molecular Weight Organic Acids.

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1. Introduction

Lithogenic and anthropogenic activities are continuously contaminating the biosphere with noxious gases, organic/inorganic chemicals, heavy metals/metalloids, pesticides, fungicides, excessive or long-term use of agrochemicals (e.g. superphosphate fertilizers, urea), and synthetic dyes (Adil et al., 2023; Clemens and Ma, 2016; Khaliq et al., 2024; Liu et al., 2012; Shaghaleh et al., 2024; Wang et al., 2020; Wei et al., 2024). These pollutants are irreversible and non-degradable, which induce notably negative impacts on the quality of soil and water reservoirs (Alamgir et al., 2024; Fayiga and Saha, 2016). Simultaneously, human population has also been exposed to environmental pollution, which may cause neurological disorders, instability, immune system suppression, induce cancer, skin diseases, and water or airborne diseases (Tan et al., 2010; Wu et al., 2023). Nowadays, heavy metal contamination in soil has become an important environmental and nutritional concern throughout the world. Approximately 0.5 million land sites in the European Union countries have been reported as uncontrolled contaminated sites, affecting a significant portion of agricultural land. The total area of contaminated land in the EU is substantial, with many of these sites impacting cultivable soil and agricultural productivity. In Greece, Portugal, Ireland, India, Poland, and North America, extensive agricultural lands have been reported to exhibit heavy metal-polluted soil. Literature reported that approximately 40% of fertile land in China has also been affected by heavy metal pollution (Qin et al., 2021; Wen et al., 2022).

Heavy metals or metalloids found in the periodic table with a relatively high atomic density greater than 4 g/cm^3 , about five times higher than water (Ejaz et al., 2023). The high atomic density of heavy metals makes the remediation process from soil very challenging. Unplanned industrialization and urbanization, irrigation practices, metal mining, industrial effluents, military explosives, automobiles, combustion processes, electroplating processes, etc., are major anthropogenic agents to accumulate heavy metals in soil and ultimately enter our food chain (Bauddh et al., 2015; Maurya et al., 2019; Rashid et al., 2023; Sharma et al., 2023; Singh et al., 2009; Willey, 2008). Heavy metals are categorized into three groups: toxic, precious, and radionuclide (Bishop, 2002). Certain heavy metals are essential for proper regulatory functioning of living cells, including zinc (Zn), iron (Fe), cobalt (Co), manganese (Mn), molybdenum (Mo), nickel (Ni), and copper (Cu). However, several metals or metalloids, especially cadmium (Cd), mercury (Hg), chromium (Cr), boron (B), aluminum (Al), lead (Pb), and arsenic (As) are toxic and potentially lethal to plant and animal cell physiology, considered as non-essential heavy metals (Rashid et al., 2023; Song et al., 2019; Tang et al., 2015; Tow et al., 2019; Van der Ent et al., 2013; Yong et al., 2010). The concentration of essential or non-essential heavy metals is important for plant cells in trace amounts (de Bang et al., 2021; Marschner, 2011). However, the occurrence of heavy metals in plant tissues above a certain threshold level can induce negative effects upon many essential physiological processes: photosynthesis, nutrient uptake, biosynthesis of hormones, and agglomeration of reactive oxygen species (ROS); and consequently lowering plant growth (Clemens and Ma, 2016; Gangwar et al., 2011; Kachenko et al., 2008; Kramer et al., 2000; Li et al., 2024; Sharma et al., 2016; Merian, 1984).

2. Nickel and its sources in the environment

Nickel, with the symbol "Ni" in the periodic table, has an atomic number of 28 and an atomic mass of approximately 58.69 at. mass units. Nickel exhibits several oxidation states, including -1 , $+1$, $+2$, $+3$, and $+4$. However, its most abundant oxidation state is $+2$ (Denkhaus and Salnikow, 2002). Nickel possesses a hard, cubic crystalline structure and silvery-white appearance. It is characterized by its ductility, corrosion resistance, and magnetic properties at temperatures below 345°C . Additionally, nickel is an excellent conductor of heat (Musiani et al., 2015).

It is a trace element, naturally present in ultramafic soil, released into the surroundings by natural processes and anthropogenic activities. Nickel occurs in atmosphere as particles ($0.1\text{--}0.2 \mu\text{m}$ diameter) and amalgamates with chlorides, sulfurs, and nitrites (Kabata-Pendias, 2000; Mustafa et al., 2023). Nickel and its salts occur naturally in the earth's crust at a concentration of $80 \mu\text{g g}^{-1}$. In ultramafic rocks, such as peridotite or serpentine soil, the abundance of nickel is estimated to be as high as $2000 \mu\text{g g}^{-1}$. Because of its chalcophilic characteristics, nickel is naturally found in association with sulfides, antimonides, and arsenides (Sigel et al., 2007). The concentration of nickel in soil ranges from 5 to $500 \mu\text{g g}^{-1}$ and can vary across different geographical areas. Moreover, its uptake in plant tissues has been reported between 0.5 and $5 \mu\text{g g}^{-1}$, with variations depending on the plant species. In animal tissues, nickel accumulation falls within the range of $0.1\text{--}5 \mu\text{g g}^{-1}$, while freshwater sources generally contain nickel concentrations ranging from 5 to $100 \mu\text{g L}^{-1}$ (Maurya et al., 2019; Schrenk et al., 2020).

2.1. Nickel concentration in air (airborne nickel)

Nickel and its compounds are constantly released into the atmosphere as a result of natural processes and human activities. Each year, approximately 8.5 million kg of nickel is discharged into the atmosphere through lithogenic sources, including waste incineration, windblown dust, and volcanic eruptions. Interestingly, anthropogenic emissions contribute to nickel release at a rate about five times higher than that of natural sources (Begum et al., 2022) shown in Fig. 1.

Nickel sulfate occurs in the ambient air, primarily due to its leachable nature. Approximately 20–80% of nickel sulfate emissions have been attributed to coal combustion, while around 90% of other nickel salts are released into the ambient air from oil combustion. Nickel oxides, sulfates, nitrates, and sulfide ores like pentlandite (FeNi_9S_8), as well as nickel species found in the garnierite zone (silicate-oxide), also play a role in air pollution. Each year, the input of nickel into the atmosphere amounts to approximately 150,000 to 180,000 metric tons, originating from both natural sources and human activities. These activities include industrial effluents, fossil fuel consumption, and the disposal of nickel compounds or alloys (Kasprzak et al., 2003).

2.2. Nickel levels in soil

Nickel is an essential trace element that occurs naturally in various forms, including inorganic metallic crystalline form, complexed organic or inorganic cations, water-soluble free ions, or metal-chelated complexes. In the Earth's geochemical makeup, nickel is normally found in combination with iron, sulfur, and cobalt. The deposition of nickel salts from the atmosphere to the soil occurs through different transferring processes like dew, fog, and rain. The estimated concentration of nickel in various soils falls within the range of 4–80 ppm. On average, nickel constitutes approximately 0.008% of the Earth's crust (Tian et al., 2012).

In naturally occurring soils, the concentration of nickel is typically around 50 mg kg^{-1} in sandstones or acidic igneous rocky soil. However, in argillaceous rocks (such as shales, siltstone, and mudstone) or basic rocks, the reported nickel concentration is approximately 500 mg kg^{-1} . In serpentine soils, the nickel content can be even higher, exceeding 1000 mg kg^{-1} (Kierczak et al., 2021; Reeves et al., 1996).

Nickel is introduced into water bodies through diverse natural and human activities. Mechanisms, including chemical weathering and direct leaching, may lead to a substantial increase in the dissolved nickel in water bodies (Friberg et al., 1979). Typically, the concentrations of nickel in seawater and drinking water were found to be $0.1\text{--}0.5 \mu\text{g L}^{-1}$ and $< 10 \mu\text{g L}^{-1}$ respectively. Drinking water generally serves as the primary source of nickel intake for humans (Sigel et al., 2007).

3. The role of nickel in biological systems

Nickel serves as an essential catalytic cofactor for enzymes in various

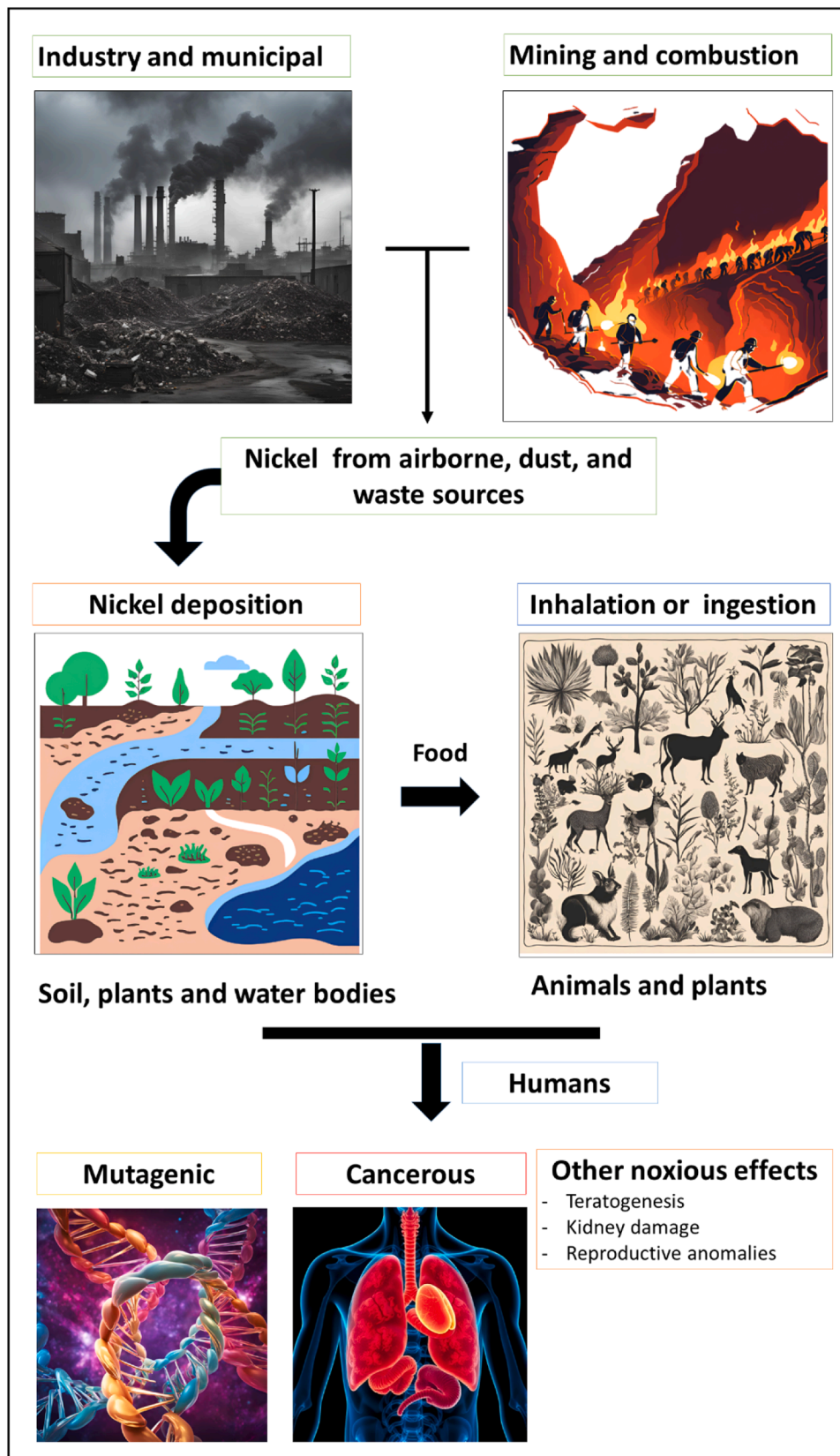


Fig. 1. Nickel sources and the different entry pathways into a biological system.

organisms from different kingdoms, including bacteria, fungi, animals, and plants, to regulate their cellular growth and metabolic processes (Denkhaus and Salnikow, 2002; Maroney, 1999; Zambelli and Ciurli, 2013). Nickel-dependent enzymes such as glyoxalases, hydrogenases, carbon monoxide dehydrogenases, methyl Co-A reductases, superoxide dismutase, and ureases play crucial roles in the biosynthesis of various metabolites (Macomber and Hausinger, 2011). As an essential micro-nutrient, nickel has been required by various plant species in the range of 0.01–5 $\mu\text{g g}^{-1}$ (dry weight) to enhance their growth and yield (Gajewska and Skłodowska, 2008; Parida et al., 2003). Within plants, nickel plays a critical role as a cofactor in nickel-based enzyme systems, known as metalloenzymes, such as urease which is responsible for converting urea nitrogen into NH_3 , which is vital for plant growth. Insufficient nickel levels in plants can result in leaf necrosis due to the accumulation of urea in plant tissues. Studies have demonstrated that barley cannot grow normally without a sufficient supply of nickel (Brown et al., 1987; Polacco et al., 2013). Plants absorb nickel from the soil through a combination of passive and active diffusion processes via the root system. It plays a crucial role in plant growth, seed germination, and fruit development (Aziz et al., 2015). In several leguminous plants, nickel serves as an enzyme catalyst essential for the biological nitrogen fixation processes (Chen et al., 2009; Welch, 1981).

In animals and humans, nickel is involved in the regulation of immune system. Its deficiency can result in reduced growth and reproductive abilities, as well as disruptions of the amino acid and lipid metabolisms and glucose pathways (Denkhaus and Salnikow, 2002). Microorganisms utilize nickel as a cofactor in several microbial enzymes. In microorganisms like *Bacillus pasteurii* and *Streptomyces* species, nickel has been found to regulate various cellular functions, including glycerol-1-phosphate dehydrogenase and quercetinase activity (Macomber and Hausinger, 2011).

Nickel compounds are used in many food and chemical industries and act as a catalyst in different processes i.e. hydrogenation of fats and margarines (Dohnalova et al., 2017). Moreover, it serves as a main component in electrochemical and electroplating industries, electronic instruments, production of Ni-Cd batteries, production of nickel-based alloys like stainless steel utensils, production of jewelry, coinage, and medical prostheses (Garrett, 2000). Nickel is found in natural foods and processed food, including cocoa powder, chocolate, dry fruits, green leafy vegetables, coffee, tea, cashews, kidney beans soybeans, etc. It is also used in many commercial items such as artificial jewelry, watches, eyeglasses, metallic frames, mobile phones, etc (Ricciardi et al., 2014). It serves various purposes in the food industry and functions as a catalyst in the hydrogenation process employed to produce margarine, potentially triggering allergic reactions in some individuals (Sharma, 2013). Lodyga-Chruscinska assessed nickel concentrations in 10 margarine brands available in the Polish market. They discovered that only 3 out of the 10 samples had nickel levels below the acceptable limit of 0.2 mg kg^{-1} (Łodyga-Chruścińska et al., 2012). Opting for a low-nickel diet can help to decrease nickel intake. Three types of nickel-dependent enzymes, such as hydrogenase, carbon monoxide dehydrogenase, and methyl coenzyme play essential roles in various industrial processes, including hydrogenation, desulfurization, and carbonylation (Evans, 2005; Harrop and Mascharak, 2005). Human activities, including solid waste incineration, mining, refining processes, and combustion of coal, residual, and fossil fuels, are the primary sources of atmospheric nickel emissions. These emissions consist of sulfides, oxides, metallic nickel, and silicates. Fossil fuel combustion is the main contributor to the presence of nickel-containing compounds in ambient air. Nickel concentrations in industrial areas range from 120 to 170 ng m^{-3} , while suburban areas have 6–17 ng m^{-3} (Cempel and Nickel, 2006; Denkhaus and Salnikow, 2002; Merian, 1984). Nickel production has been steadily rising due to the impacts of urbanization and industrialization. By 2012, global production had reached an impressive 1.76 million tons (Harasim and Filipek, 2015).

4. Nickel poisoning and its effects on human health

Nickel was categorized as a hazardous trace element and recognized as an acute toxic substance by numerous national and international organizations (Kumar et al., 2021). According to the International Agency for Research on Cancer (IARC), nickel compounds are classified as group 1 carcinogens, posing a significant risk to human health. Additionally, elemental nickel is considered a carcinogen in immuno-compromised individuals and falls under group 2B classification (Tian et al., 2012). Exposure to nickel toxicity can lead to detrimental impacts on multiple organs, including the cardiovascular, respiratory, immune, skin, and kidney systems. Nickel allergies are a significant concern, contributing to conditions like lung fibrosis, dermatitis, and various respiratory, cardiovascular, and chronic kidney disorders (Kasprzak et al., 2003). $\text{Ni}(\text{CO})_4$ represents an organic-nickel compound and is considered the most toxic form of nickel. Exposure to this compound can occur through inhalation, skin contact, or ingestion. Its fat-soluble nature enables it to permeate cell membranes via diffusion or calcium ion channels, leading to its accumulation in various body tissues (Duda-Chodak and Blaszczuk, 2008).

Nickel and its compounds are notorious allergens, detectable through atopy patch tests. The prevalence of nickel allergy is higher among females and young patients (under 18 years old) worldwide (da Rosa et al., 2015; Thyssen and Menné, 2010). It has been evident that allergic contact dermatitis (ACD) is induced by nickel as it stimulates T-cell T-cell-mediated response and appears as itchy skin rashes in susceptible patients (Boonstra et al., 2015). It was reported that nickel can stimulate the hypoxia state (oxygen deficiency) by its binding to an oxygen sensor instead of iron which may disrupt cellular growth or suppress apoptosis (Denkhaus and Salnikow, 2002).

5. Nickel Toxicity and Effects in Plants

Over recent years, there has been a growing global concern regarding the escalation of nickel contamination in soil and water. The levels of nickel in these environmental scenarios have progressively surged to levels as high as 26,000 ppm in soil and 0.2 mg L^{-1} in water, significantly surpassing the established threshold limits of 100 ppm for soil and 0.005 ppm for surface water (Chen et al., 2009). The degree of nickel toxicity in plants displays variation from one species to another. For instance, hypersensitive plant species show toxicity effects at levels exceeding $> 10 \text{ mg kg}^{-1}$ dry weight mass (DWM) of nickel. Slightly tolerant plant species, on the other hand, demonstrate toxicity symptoms at levels surpassing $> 50 \text{ mg kg}^{-1}$ DWM, while hyperaccumulator plants manifest these effects at levels greater than $> 1000 \text{ mg kg}^{-1}$ DWM (Belouchrani et al., 2016). Some morphological features associated with nickel toxicity in flowering plants are: lesser root growth, stunted development, chlorosis, necrosis, and reduced leaf area. Additionally, many physiological functionalities are also affected negatively, namely enzymatic activities, photosynthesis, morphogenesis, mineral nutrition and the production of reactive oxygen species (ROS) (Broadhurst and Chaney, 2016; Singh, 2005; Sujkowska-Rybikowska et al., 2022).

High levels of nickel can impair root morphology and function, leading to reduced root elongation, necrosis, and altered root architecture, which collectively diminish the plant's capacity for water and nutrient uptake (Mustafa et al., 2023). Additionally, nickel competes with essential nutrients such as calcium (Ca), zinc (Zn), magnesium (Mg), and iron (Fe) for uptake sites, leading to deficiencies of these nutrients and disrupting ion balance. Nickel also affects membrane permeability and the function of transport proteins like H^+ -ATPases, which are crucial for nutrient transport, thereby reducing the uptake of potassium (K), nitrate (NO_3^-), and phosphate (PO_4^{3-}) (Brown et al., 1987; Chen et al., 2009; Deng et al., 2018; Mustafa et al., 2023). Nickel disrupts physiological processes in plants by interacting with functional groups within proteins, leading to alterations in protein conformation

and functionality. Plant enzymatic activities have been disrupted by nickel (Fabiano et al., 2015). Moreover, in response to oxidative stress, plants activate their defensive mechanisms, increasing the activity of antioxidant enzymes such as glutathione reductase (GR), peroxidase (POD), catalase (CAT), superoxide dismutase (SOD), and ascorbate oxidase (AO) (Hasanuzzaman et al., 2020). The main cause of reduced cellular metabolism is the suppression of enzyme activities caused by metal ions (Seregin and Kozhevnikova, 2006). Nickel is thought to alter the various gas exchange (transpiration, stomatal openings) and photosynthetic processes. The extent of photosynthesis reduction has been associated with changes in chloroplast structure, disruption of the electron transport chain (ETC), limited CO₂ availability due to closed stomata, impairment in chlorophyll synthesis, and inhibition of key enzymatic processes in the Calvin cycle. These enzymes include Rubisco, 3-phosphoglycerate kinase, fructose-1,6-bisphosphatase, and aldolase, along with NAD- and NADP-dependent phospho-glyceraldehyde dehydrogenases (Seregin and Ivanov, 2001). Numerous studies have highlighted the impact of nickel toxicity, which predominantly leads to the inhibition of plant growth, suppression of root activity, and hindered seed germination. For instance, in the case of pigeon pea, exposure to a 1.5 mM nickel solution significantly hinders the process of seed germination (Rao and Sresty, 2000). Furthermore, shoot growth was influenced by a solution containing 0.2 mM of nickel. For *Nicotiana tabacum*, the roots exhibited a dark brown discoloration following a 7–10 day exposure to a solution containing 0.43 mM of nickel (Boominathan et al., 2004). The accumulated nickel affected plant biomass, leading to decreased leaf area (Ahmad and Ashraf, 2011). Nickel's toxicity reduced plant yield and reproductive capacity, mainly by physiological disruption and competing against the essential nutrients that are usually in limited supply (Ahmad et al., 2007).

6. Remediation Approaches for Nickel

Harnessing effective remediation strategies is essential to protect the environment for future generations (Clemens and Ma, 2016; Glick, 2010). Various biological and physicochemical approaches are employed to remediate and sequester heavy metals and metalloids. However, the intricate technical requirements and associated costs make the process of remediation a formidable task (Ahmad, 2019; Ahemad and Kibret, 2014; Ali et al., 2013; Sheoran et al., 2010). Although physicochemical methods like thermal treatment, landfilling, excavation, electro-reclamation, and leaching can deliver quick remedies, their efficacies are often limited, and incurring higher operational cost. Furthermore, these methods can lead to secondary pollution and have the potential to disrupt both the physicochemical and biological traits of the soil (Ali et al., 2013). Hence, these physicochemical approaches are not recommended for the secure extraction and sequestration of heavy metals (Lambert et al., 2000).

Biological remediation involves employing plants and/or microorganisms to eliminate harmful pollutants from the environment (Doty, 2008; Glick, 2010; Singh et al., 2009). This method is considered the most secure and operationally efficient approach for eliminating problematic metals. This strategy presents an environmentally friendly, economically viable, and naturally supported process with widespread public approval and attention (Doble and Kumar, 2005). Biological remediation technology includes a range of methods such as bioremediation, bioleaching, bioventing, bioreactors, land forming, bio-augmentation, composting, and bio-stimulation. Among these techniques, bioremediation has been widely used as the most efficient and cost-effective approach. It relies on solar energy and maintains the inherent characteristics of the soil (Beškoski et al., 2011; Boopathy, 2000; Vidali, 2001).

Bioremediation stands as an inventive and cost-efficient strategy to eliminate heavy metals and metalloids from soil-water ecosystems through living organisms. This approach can be categorized into two main branches: phytoremediation, which involves plant-based

bioremediation, and microbial bioremediation, which centers on the use of microorganisms (Guo et al., 2010). The synergistic utilization of both plants and microbes has significantly amplified the effectiveness of bioremediation (Hadi and Bano, 2010). The interactions observed between hyper-accumulating plants and metal-tolerant microbes have shown remarkable usefulness. A plethora of recent studies have highlighted the genetic capacity of both microbes and plants to gather and detoxify metals from polluted environments (Lyyra et al., 2007; Memon and Schröder, 2009; Pilon-Smits and LeDuc, 2009).

6.1. Phytoremediation - Green Technology

The term "phytoremediation" was initially used in the 1980s to describe the process of using various plant species for remediating contaminated sites. The term originates from the Ancient Greek word "phyto," which means plant, and the Latin word "remedium," which conveys the idea of restoring balance (Willey, 2008). Referred to as a green technology, this method serves as an environmentally friendly solution for the removal, degradation, or decontamination of toxic metals/metalloids, extremely volatile organic or inorganic foreign substances, and a multitude of other carcinogenic pollutants from the ecosystems (Kumar Yadav et al., 2018). Plant species are closely associated with soil microbes such as bacteria, arbuscular mycorrhizal fungi (AMF), protozoa, and algae; the effectiveness of the plant-microbe symbiosis generally vary along with soil properties and agronomic practices. These components collectively contribute to fostering the detoxification or sequestration of toxic pollutants by restoring plant growth under these unfavourable conditions (Vara Prasad and de de de Oliveira Freitas, 2003).

In plants, various mechanisms are involved in the uptake of contaminants and these are based on their distinct characteristics. Plants possess the capability to transform or degrade both organic and inorganic complex pollutants into less bioavailable forms within the rhizosphere, aided by rhizobacteria. This phenomenon is referred to as phytostimulation. Additionally, plants can directly facilitate the breakdown of organic toxic metals through their intrinsic enzymatic processes, which is known as phytodegradation. Certain plant species have potential to accumulate metal complexes within their tissues, eventually releasing these pollutants in volatile form, a process termed phytovolatilization (McCutcheon and Schnoor, 2003). In modern era, microbe-assisted phytoremediation has been widely used in fields because combination of plants and microbes incredibly enhances phytoremediation (Maurya et al., 2023).

6.1.1. Nickel Hyperaccumulating Plants

Certain plant species have the potential to accumulate metals within their shoot and root tissues, measured on a dry weight basis (Maestri et al., 2010; Van der Ent et al., 2013). Hyperaccumulators or metallophyte plants that have potential to uptake as much as 1000 ppm (0.1 %) for metals like nickel, lead, chromium, cobalt, and copper, and 10,000 ppm (1 %) for zinc and manganese, based on the dry weight of their shoots, when cultivated in metalliferous soil (Özyiğit and Doğan, 2014). Nickel is the most accumulated metal in a variety of hyper-accumulator plants. Approximately, over 350 taxa of nickel hyper-accumulators are reported (Van der Ent et al., 2013), while about 25 % of reported nickelophilous plants belong to Brassicaceae family (Prasad, 2005), specifically, genus *Alyssum* has a comprehensive diversity of nickelophilous plants (Rascio and Navari-Izzo, 2011) which can accumulate about 1000–38,000 ppm on a dry leaf matter basis (Reeves et al., 1999). Some well-known nickel hyper-accumulators are highlighted in Table 1. These hyper-accumulator plants offer an effective botanical resource to understand plant adaptive mechanisms to serpentine soils; these interesting genetic traits of certain species can be harnessed for bioremediation.

6.1.2. Nickel uptake Mechanisms in Plants

Similar to other living organisms, plants possess complex homeostasis mechanisms that maintain optimal concentrations of nickel ions within various cellular compartments. These mechanisms regulate the uptake, accumulation, trafficking, and detoxification of metal ions while simultaneously mitigating the adverse impacts stemming from exposure to non-essential metal ions (Clemens, 2001; Li and Zamble, 2009). Basic metal resistance mechanisms are ubiquitous in plants but metal hyper-accumulation is a complex and sporadic phenomenon. It is biggest task for scientists to understand nickel uptake and accumulation mechanisms from soil to translocate in shoot tissues, separation, and distribution in cellular compartments (Everhart et al., 2006). Several transporter proteins take participation in nickel uptake, transportation, and homeostasis mechanisms, including 1) cell membrane transporter proteins 2) vacuole membrane (tonoplast) transporters 3) vacuolar sequestration, and 4) endomembrane transporters (Maestri et al., 2010). Metal transporter proteins include 1) influx transporter protein families which comprise Zinc-Iron Permease (ZIP), Natural Resistance-Association Macrophage Protein (NRAMP), and Yellow-Stripe 1-like (YSL); 2) efflux transporter families such as Heavy Metal ATPase (HMA), Cation Diffusion Facilitator (CDF), Cation exchanger proteins (CAX) and ATP-binding cassette (ABC) transporters (Hall and Williams, 2003).

6.1.2.1. Nickel Uptake through the Roots. Plants can uptake nickel in the Ni²⁺ form by passive and active processes (Tack, 2010). Nickel is also highly reactive with organic acids and other dissolved organic substances that accelerate nickel desorption and dissolution in soils. Its availability in soil is potentially influenced by many factors, including soil redox potential, organic matter content, temperature, and pH (Fageria et al., 2002). Soil pH is a key factor and directly correlates with nickel uptake via roots such as nickel uptake capacity decreases as pH rises from 4.5 to 6.5 (Kabata-Pendias, 2000).

A large population of metal-resistance microorganisms present in the rhizosphere of hyperaccumulators has the potential to enhance the nickel uptake and increase plant biomass by adjusting the soil pH, producing organic substances such as metal-chelating agents, organic acids, and enzymes, protecting the plants against fungus and other microbes (Wenzel et al., 2003; Xiong et al., 2008). Plants also secrete certain chemicals, which are involved in the mobilization of nickel from soil to roots; including organic acids (malonic acid and oxalic acid), reductase enzymes, and metal chelating complexes akin to phytosiderophores (He et al., 2012). It was reported that by introducing *Microbacterium arabinogalactanolyticum* AY50922 to the soil, approximately 2.2–2.6 mg kg⁻¹ of nickel was extracted (Abou-Shanab et al., 2003). Another study discovered that *Synechroacter* sp. SRA1 and *Bacillus*

cereus SRA10 have the potential to promote beneficial plant growth-promoting bacteria (PGPB), leading to a significant enhancement in nickel accumulation in the root and shoot tissues of *Brassica juncea* when compared to control plants (Ma et al., 2011). Several studies showed that Plant Growth Promoting Rhizobacteria (PGPR) have potential to enhance the Ni availability to *Alyssum murale* by releasing non-soluble nickel in the soil. These bacteria produced indole-3-acetic acid (IAA), and siderophore compounds, and enhanced the phosphate solubilization which converts non-soluble Ni to a soluble form. Similarly, certain PGPB strains can protect plants from Ni toxicity, and promote root elongation and plant biomass by producing siderophores and 1-amino-cyclopropane-1-carboxylate (ACC) deaminase enzyme, which has the potential to suppress ethylene (plant hormone) production by hydrolysis of ethylene precursor ACC (Abou-Shanab et al., 2003; Idris et al., 2006).

In the roots, cell membrane acts as a barrier for nickel ions movement into cytosol via a variety of channels and transport proteins (Kabała et al., 2008). The hydrogen ion (proton) ATPase (H⁺-ATPase) is a membrane-bound enzyme involved in the uptake of nutrients via roots, expressed in the xylem, and transport of solutes in the phloem through generating a proton electrochemical gradient (Palmgren, 2001). Transportation of Ni into the xylem occurs by utilizing membrane channels and gradient pumps (Sheoran et al., 2010). The studies revealed that H⁺-ATPase enzyme activity accelerates or decelerates in roots significantly depending on the availability of metal concentration. For example, when *Cucumis sativus* seedlings treated with different heavy metals (Cu, Cd, and Ni) in different concentrations induced inhibitory effects on transporting and hydrolysis activities of H⁺-ATPase in plasma membrane (PM) (Janicka-Russak et al., 2008). Water soluble Ni can penetrate root symplast through the PM of endodermal root cells or it may penetrate to root apoplast via plasmodesmata. Mostly, symplast influx parameters have great importance in the uptake kinetics of trace elements due to the inability of the apoplastic metal ions to cross root casparian band (apoplastic barrier) and their translocation to shoots (Mukhopadhyay and Maiti, 2010; Peer et al., 2006).

6.1.2.2. Root to Shoot Nickel Translocation. In non-hyperaccumulator plants, Ni is absorbed from the soil and subsequently retained into the root cells. Plant employs detoxification mechanisms such as forming chelates in the cytoplasm or sequestering the Ni into vacuoles, as shown in Fig. 2. In paradox, hyperaccumulators possess the ability to absorb nickel from the roots' symplast into the xylem apoplast, and they efficiently transport nickel ions from the xylem to the shoots through transpiration-driven pumps (Maestri et al., 2010; Marschner, 2011). At molecular level, the mechanism and genetics basis of metal translocation into shoots is still unclear. However, in hyperaccumulators, a

Table 1
Nickel uptake and accumulation capacity in some nickelophilous plants.

Plant scientific name	Type of phytoremediation	Uptake capacity (mg kg ⁻¹)	Accumulation (dry weight)	References
<i>Alyssum argenteum</i>	Phytoextraction	29,400	Leaves	(Mengoni et al., 2003)
<i>Berkheya coddii</i>	Phytoextraction	1700	The upper epidermis of leaves	(Robinson et al., 2003)
<i>Leptoplaxemarginata</i>	Phytoextraction	34,400	Leaves	(Chardot et al., 2005)
<i>Alyssum inflatum</i>	Phytoextraction	3700	Leaves	(Ghaderian et al., 2007)
<i>Alyssum heldreichii</i>	Phytoextraction	1180	Leaves	(Bani et al., 2010)
<i>Pelargonium roseum</i>	Phytoextraction	20,055	Leaves	(Mahdieh et al., 2013)
<i>Alyssoides utriculata</i> L.	Phytoextraction	1065	Leaves and roots	(Roccoliello et al., 2015)
<i>Alyssum serpyllifolium</i>	Phytoextraction	7000	Leaves	(Morais et al., 2015)
<i>Alyssum obovatum</i>	Bioaccumulation	6008	Leaves	(Teptina and Paukov, 2015)
<i>Alyssum tortuosum</i> Willd.	Bioaccumulation	1789	Leaves	(Teptina and Paukov, 2015)
<i>Alyssum murale</i>	Phytoextraction	3600	Stem and leaves	(Broadhurst and Chaney, 2016)
<i>Isatis cappadocica</i>	Phytoextraction	5587	Shoots and leaves	(Çelik et al., 2018)
<i>Hybanthus austrocaledonicus</i>	Phytoextraction	3430–58 500	Leaves	(Paul et al., 2020)
<i>Thlaspi caerulescens</i>	Phytoextraction	5000	Leaves	(Fasani et al., 2023)
<i>Odontarrhena bertolonii</i>	Phytoextraction	3000	Leaves	(Colzi et al., 2023)
<i>Thlaspi triangulare</i>	Rhizofiltration	17000	Roots	(Fasani et al., 2023)

variety of plant metal transporter families, phytochelators/chaperons, and organic acids have been well documented. Such as nickel uptake and transport increased by chelation with citric acid in *Stackhousia tryoni*, *Datura innoxia*, *S. acuminata*, and *Alyssum bertolonii* (Bidwell et al., 2004; Callahan et al., 2008). Organic acids with free amino acids such as nicotinamine and histamine play a key role in metal accumulation because bivalent cations of organic acids and free amino acids form stable ligands which involved in Ni accumulation in plant tissues (Callahan et al., 2008).

Alyssum lesbiacum, characterized as a nickel hyperaccumulator, demonstrates a correlation with elevated tolerance to metals and enhanced translocation of metals into its shoots, which is closely linked to the presence of free histamine amino acids. In *Alyssum montanum* (non-hyperaccumulator), the transportation of histamine-chelated Ni into the xylem was 50 times faster (Krämer et al., 1996). Another chemical called nicotinamide (NA) is associated with iron homeostasis and tolerance to Zn and Ni. Studies have identified a positive correlation between Ni hyperaccumulation in *T. caerulea* with enhanced nicotinamide synthesis and NA-metal chelation (Vacchina et al., 2003). Following which, an important role was later observed for NA in Ni translocation (Callahan et al., 2008).

6.1.2.3. Distribution/ detoxification/ sequestration of Nickel. Several research studies have revealed a greater accumulation of Ni in the aerial parts of plants compared to their underground components (Bani et al., 2007; Broadhurst et al., 2004). Higher concentration of nickel is accumulated in the leaves compared to the stems within the aerial portions (Deng et al., 2016; Gramlich et al., 2011). Furthermore, the age of the plant could also influence the extent of nickel (Ni) accumulation (Bani et al., 2007; Chaney et al., 2007). Hyperaccumulators are generally much more efficient in detoxification and sequestration (Rascio and Navari-Izzo, 2011). In these plants, heavy metal detoxification occurs via compartmentalization, chelation, and sequestration of the metals by forming ligands, where the metal-ligand complex is transported to vacuoles and cell walls (metabolically inactive sub-cellular

compartments). In shoots, the sequestered metal is stored in apoplast or in different types of cells/tissues which include trichomes, mesophyll cells, epidermal cells, and cuticles (Bidwell et al., 2004; Freeman et al., 2004; Robinson et al., 2003). In epidermal cells, metal localization has been considered an important mechanism for Ni accumulation and tolerance (Kachenko et al., 2008). Following the complex formation, Ni is selectively sequestered within the vacuoles of epidermal tissues (Sharma et al., 2016). Furthermore, it has accumulated within the vacuoles of epidermal tissues in stems and leaves, as well as in trichomes (Broadhurst et al., 2004; Everhart et al., 2006). In Ni and Zn/Cd hyperaccumulating plants, cell walls may also play an important role in metal detoxification and it has been reported that about 60–70 % of accumulated Ni is distributed in the apoplast (Kramer et al., 2000).

Metal homeostasis and heavy metals detoxification in plants ultimately depend on the vacuolar sequestration (Martinoia et al., 2007). Vacuoles are supposed to be the principal storage site for metals and phytochelatin (PC)-metal complexes (Salt et al., 1995). When Ni compartmentation is compared between non-accumulating and hyper-accumulating plant species, it has been evident that the primary biochemical detoxification mechanism involves the Ni storage within the vacuoles of leaf cells (Kramer et al., 2000). The compartmentalization of metals in vacuoles is a very effective mechanism for metal dispersal and concentration within cell (Wu et al., 2010). In the tonoplasts, the active transport systems are involved in the sequestration of metal ions inside the vacuole. The process of sequestration is energized directly by ATP hydrolysis (Kramer et al., 2000; Martinoia et al., 2007). Tonoplast antiporters (CDF, CAX, and magnesium exchangers) and efflux transporters are involved in the distribution of metals in the vacuoles (Kobae et al., 2004; Persans et al., 2001). MTP1 tonoplast protein over-expression is linked with tolerance against Co, Cd, and Ni (Persans et al., 2001). Similarly, $\text{Ni}^{2+}/\text{H}^{+}$ antiport system has been identified in tonoplast of *A. lesbiacum* (Ingle et al., 2008). Proton pumps including V-ATPase and V-PPase are known to facilitate important processes supporting the metal tolerance mechanisms; these molecular pumps produce electrochemical gradient potentials across the tonoplast

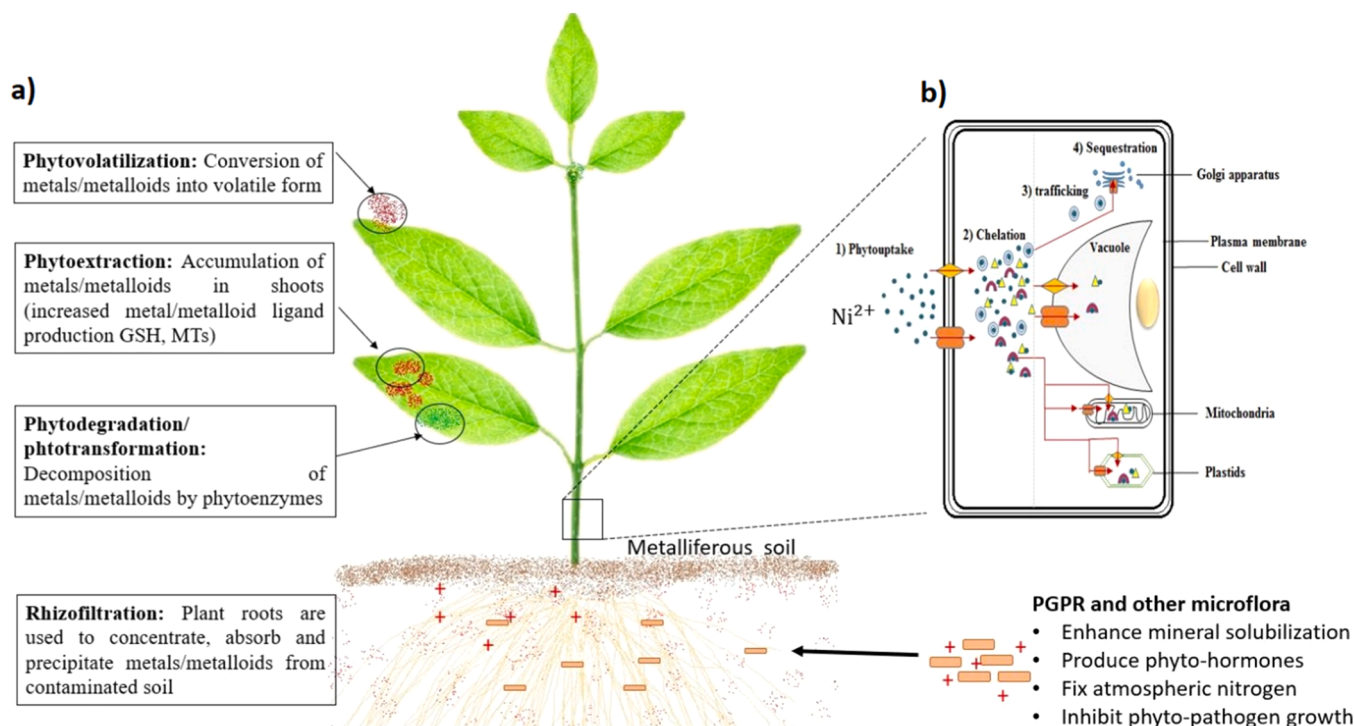


Fig. 2. Phytoremediation techniques and mechanisms. **a)** phytoremediation techniques, **b)** metal homeostasis mechanisms *in planta*. Nickel (Ni) ions enter into the plant cell via transporters (located in the tonoplast) and are chelated with phytochelators (PCs) and chaperones. These chelated complexes are involved in the trafficking of nickel to specific organelles via metal influx pumps, where the Ni detoxification or accumulation is accomplished via vacuolar sequestration.

and activate secondary transporters which act as H⁺-coupled carriers, including metal efflux transporters within plant cells (Kabała and Janicka-Russak, 2011).

6.1.2.4. Role of Transporter Proteins and Phytochelators in Nickel Hyperaccumulators. The binding of metal ions by ligands (metal chelation) affects the accumulation, transportation, and detoxification of heavy metals (Wu et al., 2010). Cellular damage induced by heavy metals has significantly reduced due to the inert nature of chelated metal ions. Metal ions tend to produce chelation with different ligands like amino acids, nitrogen and oxygen donor ligands, peptides, organic acids, metallothioneins (MTs), phytochelators (PCs), and other high molecular weight molecules (proteins, chaperones) (Clemens, 2001). Various types of metallochelators have been identified in plants, including phytochelatin, metallothioneins, amino acids, and organic acids.

Citrate is the major ligand for facilitating Ni entrapment in leaves of *T. goesingense* and *H. floribundus* (Kramer et al., 2000). Similarly, Ni-malate is associated with Ni accumulation in Ni hyperaccumulating *Phyllanthus serpentinus* and *P. douarrei* species (Deng et al., 2018). In *S. acuminata* latex, about 37–99 % of Ni form chelates with citric acid (Schauhlöffel et al., 2003). Another study has suggested that Ni becomes concentrated in the dermal leaf and stem tissues of *A. murale*, and majorly bound with malate and other low molecular weight organic acids (LMWOA) (McNear Jr et al., 2010). In plant sap and vascular tissues, nickel also binds with histidine, malate, and other low molecular weight compounds. Thus, Ni can be transported from roots to shoots (by forming a complex with His) and stored within the foliar dermal tissues (where Ni is complexed with malate and other low molecular weight organic acids or counter-ions) (McNear et al., 2010). The metal tolerance mechanisms have also been associated with the presence of cysteine-rich peptide ligands, specifically metallothioneins (MTs) and phytochelators (PCs) (Schat et al., 2002). For sequestration, Ni (II) binds with organic sulfur (R-SH) which acts as a functional group of the cysteine residues (Eapen and D'souza, 2005). These MT-metal complexes may be transported into vacuoles for long-term sequestration as they can produce glutathione (GSH) (Eapen and D'souza, 2005). When plants are exposed to heavy metal ions, phytochelators become activated which further bind with metals and promote metal storage in the vacuole (Rausser, 1995; Yang et al., 2001).

Specific nickel (Ni) transporters have not yet been identified in plants (Rascio and Navari-Izzo, 2011). However, a study has revealed that certain zinc/nickel (Zn/Ni) hyperaccumulating plants exhibit a preference for zinc (Zn) absorption over nickel (Ni). This observation suggested a shared transport system for the entry of zinc and nickel into the roots of these plants (Assunção et al., 2008). Moreover, various transporter proteins, including ZIP/NRAMP, are implicated in facilitating the translocation of metals into the shoots. However, for nickel (Ni) transportation, only the TjNRAMP4 transporter protein has been identified and reported in *Thlaspi japonicum* (Mizuno et al., 2005). Similarly, in *T. caerulescens*, TcYSL3 was also involved in translocation of Ni chelated complex via vascular loading and symplast (Gendre et al., 2007). At protein level, HMAs (heavy metal association domain) are involved in metal ions homeostasis and tolerance (Axelsen and Palmgren, 2001; Sun et al., 2014).

6.2. Microbes assisted remediation of Nickel

Before exploring microbe-assisted phytoremediation, it is crucial to recognize other methods used to enhance phytoremediation efficacy. Researchers have extensively employed various organic and inorganic compounds, including chelating agents, fertilizers, and soil amendments, aiming to augment the capability of plants in metal uptake and remediation (Abbott et al., 2018; Chen et al., 2020; Gul et al., 2020; Sani et al., 2023; Tang et al., 2015; Wei et al., 2024; Wong et al., 2020; Yin et al., 2024). While these additives can indeed enhance metal solubility

and availability for plant uptake, they often come with drawbacks such as potential ecological impacts, high costs, and dependency on external inputs. In contrast, microbial assistance presents a compelling alternative. Microbes leverage natural biological processes to not only facilitate metal uptake and promote plant growth but also offer a sustainable and eco-friendly solution. By harnessing the inherent abilities of microorganisms, we can minimize reliance on external inputs and mitigate environmental risks associated with chemical additives. This inherent eco-friendliness and self-sustainability position microbe-assisted phytoremediation as a preferred choice for long-term environmental management and sustainable agriculture practices.

Soil is a complex mixture of minerals, organic substances, and has diverse microbial biomass. Within the soil ecosystem, a variety of microbial genera coexist, contributing to the enhancement of plant growth, refinement of soil structure, and increased crop efficacy through the cycling of nutrients (Abbott et al., 2018; Ahemad, 2019; Ahemad and Kibret, 2014; Marschner, 2011). These microbes also generate various plant growth regulators, provide protection against opportunistic pathogens, and thereby reduce the incidence of different plant diseases. Additionally, microorganisms are actively involved in the remediation of various xenobiotic compounds and heavy metals (Glick, 2010). Moreover, these organisms have evolved different detoxifying mechanisms, including biomineralization, bioaccumulation, biosorption, and biotransformation (Gadd, 2000). Some bacterial strains have abilities to detoxify noxious compounds. For instance, *Xanthomonas maltophilia*, *Escherichia coli*, and *Pseudomonas putida* have been identified to catalyze the precipitation or reduction of highly mobile and relatively less hazardous compounds (Mitch, 2002). Most of the bacterial strains have multiple metal-resistance systems for their survival in extreme environments. A research study has demonstrated that all the rhizobacterial strains exhibit tolerance to numerous metal ions (Abou-Shanab et al., 2003). Similar studies were previously undertaken by other researchers, yielding consistent outcomes (Sabry et al., 1997). Moreover, various anaerobic microorganisms possess the capacity to independently detoxify several metal ions from the environment through their reduction to a lower redox state (Gadd, 2004).

Microorganisms are also involved in metal immobilization in different ways such as the accumulation of metal ions in their biomass or cell walls through intracellular sequestration or adsorption or precipitation (Fein et al., 2001; Leyval and Joner, 2001). Reportedly, when *Bacillus subtilis* and *Brassica juncea* were co-inoculated, it was noted that *Bacillus subtilis* offered protection to *Brassica juncea* against Ni toxicity. This safeguarding effect was attributed to the significant Ni accumulation capability of *Bacillus subtilis* (Zaidi et al., 2006). Ni resistance mechanisms in microorganisms were documented earlier, of which certain mechanisms could be exploited for the remediation of sites contaminated with selected hazardous metals. The screening of Ni-resistant microbes with the ability to immobilize Ni from polluted sites could have a substantial effect on environmental management (Puglisi et al., 2012). Furthermore, bacterial inoculants possessing metal immobilization capabilities along with plant growth-promoting (PGP) characteristics have introduced additional eco-friendly approaches for sustainable agriculture (Denton, 2007; Rajkumar and Freitas, 2008).

At genetic level, the *anik* locus is well characterized and recognized in *E. coli*, which transcribes 5 proteins, including NikA, B, C, D, and E, that have been found closed resemblance with periplasmic binding protein-dependent transport systems of gram-negative and positive species. The Nik operon has ATP-dependent ABC cassette proteins (Higgins, 2001). Sequence homology and phylogeny analysis identified a close relationship of Nik proteins with oligopeptide transporters (Dassa and Bouige, 2001). NikR is a unique class of nickel-binding regulatory proteins that control the Nik operon and are characterized as a nickel sensor. The Nik locus genes are suppressed under nickel availability. The NikR protein is encoded in the presence of nickel and transcribes DNA-binding proteins that inhibit the expression of Nik genes. Regulation of *nikR* expression also involves two promoters. The

first promoter is positioned upstream of the *nikA* gene, which serves as a Ni-binding site and governs the expression of genes that regulate microbial respiration and transition from aerobic to anaerobic phase. The second promoter is present at 51 base pairs upstream of the start site of *nikR* and partially auto-regulates the *nikR* expression. The expression of *Nik* locus is strictly regulated by global regulatory protein FNR (fumarate nitrate regulatory protein) under an anaerobic environment (Eitinger and Mandrand-Berthelot, 2000). Tetrameric *NikR* protein has four high affinity binding sites for nickel with additional lower affinity potassium binding sites. The *NikR* protein serves several regulatory functions in different microorganisms. For example, two transporters *NmtR* and *KmtR* belonged to the *ArsR-SmtB* metal-sensor transcriptional repressor family, and have been reported to regulate nickel and cobalt ions in *Mycobacterium tuberculosis* (Campbell et al., 2007; Cavet et al., 2002). However, certain bacterial species possess transporters specific to both nickel (Ni) and cobalt (Co). Apart from the *nikABCDE* system, additional nickel transporter proteins have also been identified in *Escherichia coli* (Navarro et al., 1993), these transport proteins belong to the *NiCoT* family that are conserved in eubacteria, archaea, and fungi, and some ABC transporters (Mulrooney and Hausinger, 2003; Rodionov et al., 2006). Interestingly, interruption of nickel uptake activity fails to completely block nickel accumulation and nickel-dependent enzyme activity. This indicates the presence of redundant nickel influx systems (Li and Zamble, 2009). The availability of complete genome sequences and advancements in omics techniques may facilitate the search for novel players in nickel-related processes in these microbes. Different types of bacteria have been discussed in context of their nickel homeostasis properties and potentials.

Microbe-assisted phytoremediation is a desirable, eco-friendly, and cost-effective approach to remediate heavy metal polluted soil-water ecosystems using plants and microbes. In soil, there is a huge variety of microbes, beneficial for plant growth and biomass including bacteria, fungi, algae, protozoa, and cyanobacteria. According to various soil microbiota, microbe-assisted phytoremediation is further subdivided into bacterial-assisted phytoremediation cyanoremediation, mycorrhizal-assisted remediation, and rhizoremediation.

6.2.1. Mechanisms involved in the microbe-assisted phytoremediation of Nickel

Microbe-assisted phytoremediation of nickel involves a complex interplay of biochemical and physiological mechanisms that enhance the bioavailability, uptake, and detoxification of nickel (Ni) in plants. These processes are facilitated by specific microbial activities in the rhizosphere and within plant tissues, ensuring effective remediation of nickel-contaminated environments (Ma et al., 2016; Mani and Kumar, 2014).

One of the key mechanisms is the microbial solubilization and mobilization of nickel in the rhizosphere. Certain bacteria, such as *Pseudomonas fluorescens* and *Bacillus subtilis*, secrete organic acids like citric acid, oxalic acid, and malic acid that chelate nickel ions, increasing their solubility and bioavailability for plant uptake (Becerra-Castro et al., 2011). For instance, in experiments involving *Brassica juncea*, the inoculation with *Bacillus subtilis* significantly enhanced nickel uptake due to increased solubilization in the rhizosphere (Zaidi et al., 2006). Similarly, siderophore-producing microbes, such as *Microbacterium liq-uefaciens*, mobilize nickel by altering soil chemistry and reducing nickel binding to organic matter or mineral surfaces (Abou-Shanab et al., 2003).

Microbes produce enzymes, such as phytases and reductases, which release nickel bound to soil particles and organic matter (Daunoras et al., 2024). Additionally, extracellular polymeric substances (EPS) produced by microbes stabilize nickel ions, preventing their leaching and maintaining their availability in the root zone (Li et al., 2024). Microbial metabolites, such as siderophores and chelators, also form stable complexes with nickel, facilitating its transport into plant root systems. In a study involving *Alyssum murale*, inoculation with

Microbacterium arabinogalactanolyticum increased nickel uptake from 8500 mg kg⁻¹ to 11,500 mg kg⁻¹, demonstrating the role of microbial chelation in enhancing phytoextraction (Abou-Shanab et al., 2003).

Plant growth-promoting microbes (PGPMs) like *Pseudomonas putida* and *Azospirillum brasilense* enhance root growth and development by producing phytohormones such as auxins, cytokinins, and gibberellins (Ahmad and Kibret, 2014; Ansari et al., 2023; Rothballer et al., 2003; Wong et al., 2020). These hormones stimulate root elongation and branching, thereby increasing the surface area available for metal uptake. For example, *Pseudomonas sp.* significantly enhanced root biomass and nickel uptake in *Alyssum murale*, a known hyperaccumulator plant (Ma et al., 2011). Furthermore, microbes producing 1-aminocyclopropane-1-carboxylate (ACC) deaminase alleviate ethylene stress in plants exposed to nickel toxicity, promoting healthier root systems (Gupta and Pandey, 2019).

Microbes contribute to the detoxification of nickel within plant tissues through processes such as compartmentalization and biotransformation (Li et al., 2024; Mustafa et al., 2023). For example, nickel ions are sequestered in vacuoles by forming complexes with phytochelatins (PCs) or metallothioneins (MTs), reducing their toxicity to plant cellular processes (Faizan et al., 2024). Certain microbes, such as *Psychrobacter sp.* and *Bacillus cereus*, have demonstrated the ability to convert toxic nickel forms into less harmful compounds, such as nickel sulfides, through biomineralization processes (Ma et al., 2009). In *Brassica juncea*, *Bacillus subtilis* SJ-101 not only facilitated nickel accumulation in shoots and roots but also protected the plants from nickel toxicity by promoting better biomass production and stress resilience (Zaidi et al., 2006).

Microbial activities significantly influence the physicochemical properties of soil, such as pH, redox potential, and organic matter composition, all of which directly affect nickel mobility and bioavailability. Microbes that produce organic acids, including citric acid, oxalic acid, and lactic acid, can lower the soil pH, thereby enhancing nickel solubility (Wei et al., 2024). This increased solubility allows for more efficient uptake of nickel by plant roots. For instance, studies have shown that inoculation with *Pseudomonas putida* can result in significant reductions in soil pH, facilitating the mobilization of nickel ions from less bioavailable forms (Becerra-Castro et al., 2011). Additionally, certain microbes influence the soil's redox potential by releasing reductive metabolites or altering oxygen availability (Rinklebe and Shaheen, 2017). This shift in redox conditions can convert nickel into forms that are either more soluble for plant uptake or less mobile, depending on environmental needs. For example, microbes such as *Geobacter* species can reduce nickel ions under anaerobic conditions, leading to the precipitation of nickel sulfides, which are less bioavailable and less toxic (Sitte et al., 2013). Microbes also promote nickel stabilization by facilitating its adsorption onto soil particles or through the formation of insoluble compounds. Some species produce extracellular polymeric substances (EPS), which create a sticky matrix that binds nickel ions to soil particles, preventing leaching into groundwater. Similarly, precipitation of nickel as hydroxides, phosphates, or sulfides by microbial metabolic activities significantly reduces environmental risks associated with nickel contamination (Gao et al., 2023). Furthermore, microbial contributions to soil organic matter decomposition enhance the availability of chelating agents, such as humic substances, which can bind nickel and modulate its mobility (Li et al., 2022). These interactions not only stabilize nickel in the soil matrix but also create a more favorable environment for plant-microbe interactions. For instance, it was reported that *Bacillus subtilis* released metabolites that facilitate both nickel adsorption and bioavailability; providing a balance between stabilization and uptake for phytoremediation (Zaidi et al., 2006).

Microbe-assisted phytoremediation of nickel involves a complex interplay of various mechanisms that enhance the efficiency of remediation processes. Chlorophyll fluorescence is a powerful tool used to assess the health and efficiency of the photosynthetic apparatus in plants

(Ma et al., 2021a; Ma et al., 2021b; Qin et al., 2023). Key chlorophyll fluorescence attributes include Fv/Fm (maximum quantum efficiency of PSII), Φ PSII (effective quantum yield of PSII), qP (photochemical quenching), qN (non-photochemical quenching), NPQ (non-photochemical quenching), Fo (minimal fluorescence), and Fm (maximum fluorescence) (Nabi et al., 2020). Beneficial microbes can mitigate nickel-induced stress, maintaining higher Fv/Fm values by protecting the photosynthetic machinery and ensuring better energy conversion efficiency in PSII. Microbial inoculants can enhance the effective quantum yield of PSII (Φ PSII) by promoting better nickel uptake and detoxification, ensuring more efficient use of absorbed light for photochemistry. By improving root health and nutrient uptake, microbes can maintain higher qP values under nickel stress, indicating more open PSII reaction centers available for photochemistry (Elbagory et al., 2022). Additionally, microbes can help plants better manage excess light energy, reducing photodamage through regulated non-photochemical quenching mechanisms, reflected in stable qN and NPQ values. Inoculated plants often exhibit lower Fo values under stress conditions, indicating less damage to the PSII reaction centers and better

overall health of the photosynthetic apparatus. Moreover, microbes can help in maintaining higher Fm levels by protecting PSII from nickel toxicity, ensuring efficient energy capture and transfer processes (Marchetto et al., 2024). Nickel hyperaccumulating plants treated with nickel-resistant *Psychrobacter* sp. exhibited improved chlorophyll content, protein synthesis, and biomass accumulation under nickel-contaminated conditions (Ma et al., 2010).

Microbes achieve these beneficial effects through various mechanisms, such as enhancing nutrient availability, producing growth-promoting substances, and modulating stress-responsive pathways. These interactions not only improve plant growth and nickel uptake but also safeguard the photosynthetic competence of plants, as evidenced by stable and improved chlorophyll fluorescence attributes.

Overall, the synergistic interactions between microbes and plants play a crucial role in enhancing the effectiveness and sustainability of nickel phytoremediation processes. Understanding these mechanisms is essential for the development of effective microbial inoculants and the design of optimized phytoremediation strategies for nickel-contaminated environments.

Table 2
Examples of PGPB-plant interaction in nickel phytoremediation.

PGPB(s)	Test Plant(s)	Change in Ni Concentration Due to Inoculation	Effects on Plant(s)	References
<i>Microbacterium arabinogalactanolyticum</i> <i>Sphingomonas macrogoltabidu</i> <i>Microbacterium liquefaciens</i> <i>Bacillus subtilis</i> SJ-101	<i>Alyssum murale</i> <i>Brassica juncea</i>	~8500 mg kg ⁻¹ → ~11,500 mg kg ⁻¹ 415 mg kg ⁻¹ (stem) → 736 mg kg ⁻¹ (stem) 290 mg kg ⁻¹ (roots) → 460 mg kg ⁻¹ (roots) 237 mg kg ⁻¹ (leaves) → 272 mg kg ⁻¹ (leaves)	Significantly increased Ni uptake in shoots Facilitated Ni accumulation; protected plants from Ni toxicity	(Abou-Shanab et al., 2003) (Zaidi et al., 2006)
<i>Pseudomonas</i> sp. 29 C, <i>Bacillus megaterium</i> 4 C	<i>Brassica juncea</i>	~140 mg kg ⁻¹ (roots) → ~175 mg kg ⁻¹ (roots) ~32 mg kg ⁻¹ (shoots) → ~38 mg kg ⁻¹ (shoots)	Enhanced shoots and root system, decreased Ni accumulation in plants	(Rajkumar et al., 2009)
<i>Psychrobacter</i> sp. SRA2 <i>Psychrobacter</i> sp. SRA1, <i>Bacillus cereus</i> SRA10	<i>Brassica juncea</i>	350 mg kg ⁻¹ → 520 mg kg ⁻¹ (SRA1) 350 mg kg ⁻¹ → 580 mg kg ⁻¹ (SRA10)	Enhanced biomass and Ni accumulation in plant tissues	(Ma et al., 2009)
<i>Pseudomonas</i> sp.	<i>Cicer arietinum</i>	~0.25 mg g ⁻¹ → ~0.39 mg g ⁻¹	Increased fresh and dry weight at 2 mM Ni concentration; protected plants against Ni toxicity	(Tank and Saraf, 2009)
<i>Paenibacillus macerans</i> NBRFT5, <i>Bacillus endophyticus</i> NBRFT4, <i>B. pumilus</i> NBRFT9	<i>Brassica juncea</i>	300 µg/plant → 950 µg/plant (combination of bacteria)	Facilitated Ni uptake	(Tiwari et al., 2012)
<i>Pseudomonas</i> sp. A3R3	<i>Alyssum serpyllifolium</i> , <i>Brassica juncea</i>	~85 mg kg ⁻¹ → ~115 mg kg ⁻¹	In <i>B. juncea</i> , significantly enhanced biomass; In <i>A. serpyllifolium</i> , increased Ni content under Ni stress	(Ma et al., 2011)
<i>Psychrobacter</i> sp. SRS8	<i>Ricinus communis</i> , <i>Helianthus annuus</i>	~325 mg kg ⁻¹ → ~500 mg kg ⁻¹ Approx. 250 mg kg ⁻¹ → Approx. 400 mg kg ⁻¹	Enhanced biomass, Ni accumulation, chlorophyll, and protein content	(Ma et al., 2010)
<i>Bacillus megaterium</i> SR28C	<i>Brassica juncea</i>	75 mg kg ⁻¹ (roots) → 90 mg kg ⁻¹ (SR12) 300 mg kg ⁻¹ (shoots) → 400 mg kg ⁻¹ (SR12)	Increased Ni accumulation by releasing Ni from non-soluble phases in the soil	(Rajkumar et al., 2013)
<i>Bornmuellera tymphaea</i> <i>Bornmuellera tymphaea</i>	<i>Noccaea tymphaea</i> <i>Alyssum murale</i>	320 mg kg ⁻¹ (roots) → 520 mg kg ⁻¹ (roots) 220 mg kg ⁻¹ (shoots) → 460 mg kg ⁻¹ (shoots)	39.9–79.6 % increase in Ni uptake after inoculation with PGPR	(A. Durand et al., 2016)
<i>Klebsiella pneumoniae</i>	<i>Juncus effusus</i>	69.5–11.5 mg kg ⁻¹ (Ni in root)	Promoted Ni transformation and exchangeable Ni content in the soil.	(Gao et al., 2022)
<i>Morganella morgani</i> <i>Anthyllis vulneraria</i>	<i>Arabidopsis thaliana</i>	0.01 mg kg ⁻¹ to 25 mg kg ⁻¹ in shoots	Improved nutrient availability and antioxidative enzyme activities	(Naqqash et al., 2024; Sujkowska-Rybkowska et al., 2022)
<i>Pseudomonas fluorescens</i> 20 <i>Pseudomonas fluorescens</i> 21 <i>Pseudomonas putida</i> 23 <i>Agrococcus terreus</i>	<i>Triticum aestivum</i> <i>Zea maize</i>	254 mg kg ⁻¹ (shoots) → 395 mg kg ⁻¹ (shoots) 0.125 mg kg ⁻¹ to less than 0.01 mg kg ⁻¹	Improved resistance to Ni toxicity, plant biomass and eliminated Ni phytotoxicity at full maturity. Increased the plant growth, nutrient uptake, and defense system. Decreased Ni uptake	(Shabayev and Ostroumov, 2023) (Shahzad et al., 2023)

6.2.2. Bacterial Assisted Phytoremediation

Among various bioremediation approaches, bacterial-assisted phytoremediation has garnered significant public interest (Kumar et al., 2019). This method involves the utilization of beneficial bacteria that not only aid in remediation, but also promote plant growth and development. These bacteria are referred to as plant growth-promoting bacteria (PGPB). A few bacterial-assisted phytoremediation trials are mentioned in Table 2.

In the presence of elevated levels of heavy metals, certain plant species are able to adapt biological to the unfavourable growth environment and continue to grow (Chaudhry et al., 2005; M. Li et al., 2024; Y. Li et al., 2024; Li and Zamble, 2009). Moreover, the remediation of contaminated soils is further hindered by their nutrient-deficient nature. Soil microbes are believed to positively influence plant health through mutualistic interactions. Microbes are highly susceptible to the effects of pollution, and contaminated soils often experience a depletion in both the diversity and abundance of microbial populations (Shi et al., 2002). Such bacteria are part of the soil's free-living microbiota, and they can be found in various ecological niches, including the rhizosphere, rhizoplane, histoplane, and phyloplane. PGPB is involved in nitrogen fixation, phosphorous, and iron solubilization, also produces plant growth hormones including auxins or IAA, cytokinins, gibberellins, and ethylene, protects plants from phytopathogens (Bashan et al., 2014). PGPBs are further classified into two categories based on their colonization area: Plant Growth Promoting Rhizobacteria (PGPR) and Plant Growth Promoting Endophytes (PGPE). In the following section, these two PGPBs are discussed in detail.

6.2.3. Plant Growth-Promoting Rhizobacteria

Microbial residents are integral and naturally interactive components of the soil's biota. When bacteria interact with plants in diverse ecological environments like the rhizosphere, they trigger a boost in plant growth by directly impacting plant metabolism and suppressing prevalent plant-harming pathogens found in the soil. Rhizobacteria colonization is of two types: 1) bacterial colonization within roots takes place in clusters along root tissues and/or the rhizoplane. The rhizoplane is the root surface where soil particles tightly adhere. Root tissues, on the other hand, are inhabited by specific microorganisms referred to as endophytes (Backer et al., 2018; Vacheron et al., 2013). 2) rhizosphere colonization refers to PGPR colonization in adjacent soil (Santoyo et al., 2021). The rhizosphere can contain up to 10^{11} bacterial CFU per gram of root (Egamberdieva et al., 2008) and over 30,000 prokaryotic species (Mendes et al., 2011). The diversity of rhizobacteria is vast, encompassing thousands of species. This intricate plant-associated PGPR community plays a vital role in maintaining plant growth and health (Berendsen et al., 2012). These PGPR encompass a wide range of genera, including *Arthrobacter*, *Kluyvera*, *Vibrio*, *Anabaena*, *Azotobacter*, *Staphylococcus*, *Bacillus*, *Serratia*, *Pseudomonas*, *Rhizobium*, *Enterobacter*, *Achromobacter*, *Azospirillum*, *Burkholderia*, *Flavobacterium*, *Phyllobacterium*, *Streptomyces*, *Azoarcus*, *Frankia*, *Clostridium*, *Microcoleus*, *Hydrogenophaga*, and *Acetobacter* (Bashan et al., 2008; Bashan and Holguin, 1998; Garbeva et al., 2001; Rothballer et al., 2003). Plant Growth Promoting Rhizobacteria (PGPR) is characterized by three inherent attributes including the organisms' capacity to establish root colonization, their ability to survive, multiply, and compete within microenvironments linked to the root surface, and their capability to enhance plant growth (Espinosa-Urgel, 2004; Gamalero et al., 2004).

A complex and dynamic microenvironment exists in the rhizosphere that promotes the growth of microorganism communities which ultimately possess the capacity to detoxify hazardous substances and establish a symbiotic relationship with roots (Alford et al., 2010). Rhizobacteria has been involved in metal mobilization for easy metal uptake by hyperaccumulator plants (Lebeau et al., 2008). On the other hand, the rhizosphere zone of hyperaccumulator plants also supports a variety of metal-resistant bacterial genera (Abouddrar et al., 2007). Moreover, they play an important role in regulating the metal

bioavailability of metallophytes (Whiting et al., 2001). Such as, nickel-resistant rhizosphere bacteria have been isolated from the shoots of *Alyssum murale* which is involved in the significant uptake of nickel into the shoots (Becerra-Castro et al., 2009). Biotic or abiotic stress through a minute change in the physicochemical and biological properties of rhizosphere may induce a negative impact on plant-microbe symbiosis. Plant growth-promoting rhizobacteria have received attention in the profitability of phytoremediation process; because they enhance metal tolerance and adequate biomass in plants (Aafi et al., 2012; De Maria et al., 2011; Ma and Wang, 2010). Phytoremediation and bio-augmentation have been used to describe rhizoremediation, in conjunction with PGPR (Kuiper et al., 2004).

PGPRs play a crucial role in nutrient cycling and plant growth regulation. They are involved in various activities, such as producing siderophores, fixing atmospheric nitrogen, generating phytohormones like gibberellins, cytokinins, and auxins, and facilitating the solubilization of minerals like phosphorus (Ahemad and Kibret, 2014; Yong et al., 2014). These actions enhance nutrient availability for plant growth and development. PGPRs also up-regulate ACC-deaminase, which reduces ethylene levels that are generally inhibitory to growth. Additionally, they contribute to biocontrol by depleting iron from the rhizosphere, producing chitinase enzymes to break down fungal cell walls, and competing for resources by binding with plant roots (Glick et al., 2007). Numerous reports have indicated that certain PGPR species exhibit notable resilience to elevated amounts of heavy metals and remain active in metalliferous soils (Afu et al., 1999). These naturally occurring rhizobacteria have the potential to support phytoremediation efforts via the up-regulation of metalliferous soil fertility, plant growth regulation by efficient uptake of nutrients and control of pathogenicity, and transformation of certain organics into biodegradation products (Kamnev et al., 1999).

Brassica juncea has been treated with *Azotobacter chroococcum*, *Bacillus megaterium*, and *Bacillus mucilaginosus* strains to increase phytoremediation potential of *Brassica juncea* grown on Pb–Zn mine tailings. It has been observed that these bacterial strains increased the plant growth and biomass, consequently enhancing plants' metal uptake capacity (Wu et al., 2006). Similarly, growth of *Brassica juncea* has been increased by the inoculation of *Bacillus subtilis* under Ni stress, which ultimately enhanced the production of phytohormone indole acetic acid (IAA) and solubilized the inorganic phosphates (Zaidi et al., 2006). The root-associated PGPB also has ACC-deaminase activity that provides a massive root system in metalliferous soils (Arshad et al., 2007). Elevated levels of ethylene, induced by metal toxicity and various stress factors, significantly inhibit root growth and differentiation. Bacterial ACC-deaminase plays an important role in mitigating this effect by reducing ACC levels through the conversion of its ethylene precursor ACC into alpha-keto butyric acid and ammonia (Glick, 2005). PGPR with ACC-deaminase activity leads to enhanced metal tolerance in Ni-tolerant *Thlaspi goesingense* (Idris et al., 2004). An investigative study has revealed that *Kluyvera ascorbata* has developed resistance to various heavy metals and has been observed to shield plants from nickel toxicity, without affecting the nickel uptake by seedlings (Dixit et al., 2015). The bacterium's ACC-deaminase activity might be linked to both the augmentation of plant growth and the escalation of Ni stress (Gupta and Pandey, 2019). Efficient Ni phytoextraction has been observed in the field experiments when a combination of hyperaccumulator plants *N. tymphaea* and *B. tymphaea* were treated with Ni resistant PGPR strain, which was isolated from the rhizosphere of these plants (Durand et al., 2016; Visioli et al., 2015).

6.2.4. Plant Growth Promoting Endophytes

Within the rhizosphere, several rhizobacteria and endophytic partnerships in bacteria-plant interactions participate in the breakdown of harmful substances. Endophytic bacteria are defined as beneficial plant growth-promoting microorganisms that reside within the internal tissues of plants without causing any harm to their host (Ryan et al., 2008).

The root serves as the main point of entry for endophytes. Numerous microscopic investigations validate this colonization pathway (Mengistu, 2020). Following their entry, endophytes may either remain localized within particular plant tissues, such as the root cortex or vascular tissues or establish themselves within the host's inner tissues through the transport of xylem/phloem sap or within the apoplast (Weyens et al., 2010). Endophytes have been reported in various herbaceous crop plants (Xia et al., 2022) different grass species (Dalton et al., 2004; Pašakinskienė et al., 2024; Zinniel et al., 2002), and woody tree species (Araújo et al., 2024; Cankar et al., 2005; Pandey et al., 2005). Generally, the most frequently encountered genera of cultivable endophytic species belong to *Burkholderiaceae*, *Enterobacteriaceae*, and *Pseudomonaceae* (Hossain et al., 2023). Plant-endophyte relationships are built upon the symbiotic, usually advantageous to both partners, interactions. In this dynamic relationship, plants provide habitat and nutrients to the endophytes, while endophytes reciprocate by generating metabolites that can improve plant growth through direct or indirect means (Tan and Zou, 2001). PGPEs act as biocontrol agents that safeguard plants from pathogens through multifaceted mechanisms. These mechanisms include resource competition for space and nutrients, the production of hydrolases, antibiosis, the breakdown of toxins produced by pathogens, and the synthesis of plant growth regulators such as auxins, cytokinins, and gibberellins. Additionally, PGPEs stimulate ACC-deaminase activity in response to increased ethylene stress (Glick, 2005; Weyens et al., 2009).

The phytoremediation of specific organic contaminants, such as trichloroethene (TCE), hinges on crucial factors, namely, transpiration rate and concentrations. In the process of removing TCE from soils, plants use a phytovolatilization mechanism (Ma and Burken, 2003). Phytoremediation involves the use of plants to establish ideal conditions for the microbial breakdown of pollutants and to facilitate the absorption of pollutants by the plants (Boominathan et al., 2004; Tamaoki et al., 2008). Hence, plants play a dual role in phytoremediation, providing optimal conditions for root-colonizing bacteria and offering a straightforward method for extracting pollutants (Suresh and Ravishankar, 2004). In last several decades, metal-resistant PGPEs have been frequently used in phytoremediation of metalliferous soils (Doty et al., 2003; Mastretta et al., 2006). Although an excess amount of heavy metals such as Ni is notorious for plant growth. Metal-resistant plant growth-promoting endophytic bacteria (PGPE) have been isolated from the root and shoot interiors of various metallophytes (Idris et al., 2004). This shows that PGPEs can tolerate high metal concentrations and assist in the translocation of metal ions within the plant. Furthermore, they have been reported to enhance plant growth through the production of siderophores, 1-aminocyclopropane-1-carboxylic acid (ACC) deaminase, indole-3-acetic acid (IAA), as well as the solubilization of phosphate (P), iron (Fe) (Rajkumar et al., 2009), biosurfactants and organic acids (Ma et al., 2016). While numerous studies have investigated the endophytic bacteria present in various metallophytes, only a limited number of experimental trials have been conducted to examine the role of Ni accumulation in plants with PGPE inoculation (Barzanti et al., 2007). Microbe-assisted phytoremediation can be enhanced through the genetic modification of plants and bacterial strains, a concept known as geno-remediation.

6.2.5. Advanced Mechanisms of Microbial Action

Recent studies have identified new mechanisms through which microbes help alleviate nickel phytotoxicity. Beyond traditional methods such as the production of siderophores and phytohormones, microbes have been found to induce systemic tolerance in plants. For instance, species like *Pseudomonas* and *Bacillus* can activate plant defense pathways via the production of signaling molecules like jasmonic acid and salicylic acid (Shi et al., 2024). These signaling molecules trigger antioxidant responses in plants, leading to the upregulation of stress-responsive genes, and enhancing the plant's ability to detoxify nickel through both enzymatic and non-enzymatic pathways (Naqqash

et al., 2024). Additionally, certain microbial communities (*Sporosarcina pasteurii* and *Bacillus megaterium*) have been discovered to engage in "chemo-attraction" of nickel ions, whereby microbial cells trap and compartmentalize the nickel within their biofilms or intracellular components (Gheethi et al., 2017; Phour et al., 2020; Shi et al., 2024). This biofilm-mediated immobilization offers a dual benefit: microbial protection against nickel toxicity and enhanced plant tolerance (Yousuf and Singh, 2024).

Microbial Synergy and Co-inoculation Strategies

Recent advancements have highlighted the importance of microbial consortia—combinations of bacteria and fungi—that act synergistically to enhance nickel tolerance in plants. Co-inoculation of beneficial microbes has been shown to provide superior protection against nickel stress compared to single inoculants. For example, co-inoculation with *Nitrosomonas*, *Pseudomonas*, *Penicillium*, *Bacillus*, *Xanthobacter*, *Flavobacterium*, and *Mycobacterium* can improve root growth, enhance metal sequestration, and reduce nickel uptake in plants (Sharma et al., 2023; Wu et al., 2024). The combined action of bacteria and fungi leads to more effective bioaccumulation and detoxification mechanisms, promoting healthier plant development in contaminated environments. Bioleaching with bio-surfactants (sugar esters) produced by *Burkholderia* sp. was conducted (Yang et al., 2016). The results demonstrated leaching efficiencies of 44.0 % for Zn, 52.2 % for Mn, and 37.7 % for Cd. Additionally, the presence of the surfactant enhanced carbon source consumption by *Aspergillus niger*, leading to improved nickel leaching (Dong et al., 2023).

Munoz et al. (Muñoz et al., 2006) explored the use of a microalgae-bacteria consortium for the remediation of Ni(II) and other heavy metals in wastewater, showing that metals were initially adsorbed onto cell surfaces, followed by a slower metabolically driven absorption. Another study reported that this consortium removed up to 62 % of nickel from industrial wastewater (Safonova et al., 2004). Microbial consortia can produce a range of beneficial metabolites, such as organic acids, which alter the rhizosphere pH and reduce the solubility of nickel, thus limiting its uptake by plants (Gadd, 2010). The role of mycorrhizal fungi in forming symbiotic relationships with plant roots has been particularly emphasized, as these fungi increase the surface area for nutrient absorption while reducing metal translocation to the shoots (Sharma et al., 2024). Some microbes not only detoxify nickel but may also help control microbial populations that could interfere with plant growth during phytoremediation (Parseghian et al., 2024; Rajabi et al., 2023). Additionally, the microbial synthesis of metal-organic nanostructures, such as bio-surfactants, nanoparticles, and metal-organic frameworks, may play a crucial role in enhancing the bioavailability of nickel, thereby improving its uptake in plants and contributing to more efficient nickel solubilization and sequestration (Moradi Alvand et al., 2019; Rajabi et al., 2017).

6.3. Gene-Targeted Bioremediation (Geno-Remediation)

The concept of geno-remediation originated from advanced research in phytoremediation, involving the stimulation of genes through safe biotechnological tools (Rafeeq et al., 2023). The potential of phytoremediation can be further enhanced by expressing selective metal-tolerant genes in transgenic plants and bacteria (Doty, 2008). The metal tolerance and accumulation capacity in plants could be increased by inducing genes that are involved in antioxidant enzymes, biosynthesis of glutathione (GSH), metallothioneins (MTs), and phytochelatins (PCs) (Mani and Kumar, 2014). Genetically, it was evident that the nutrient transporter proteins showed specificity towards Co(II) and Ni (II) can be induced in various bacterial strains (Deng et al., 2013; Zhang et al., 2007). Currently, it is possible to isolate metal defense genes from hyperaccumulators and introduce them into non-hyperaccumulators. Numerous bacterial, yeast, or fungal metal tolerance genes have been incorporated into plants to enhance phytoremediation potential. For

instance, the SAT (Serine Acetyl Transferase) gene was isolated from *T. goesingense* and expressed in *Arabidopsis*. The results showed that Ni tolerance increased by five times in shoots and 1.5 times in roots of *Arabidopsis* when grown under 100 mM Ni stress (Freeman et al., 2004). The bacterial ACC deaminase gene has also been introduced into plants to decrease ethylene production under stress conditions, ultimately leading to an increase in plant biomass (Stearns et al., 2005).

The *rcnA* system is a well-studied *E. coli* efflux pump for Ni(II) and Co (II) ions (Rodrigue et al., 2005). It is possible to disable genes that encode these efflux pumps, thereby trapping the imported metals inside the cytoplasm and preventing their exit through the cell membranes. Following these principles, an *E. coli* strain that accumulates cobalt has been engineered (Raghu et al., 2008). However, this strain had a significant drawback: bacteria could not be easily recovered from the decontaminated effluent. To overcome this challenge, a previously described bacterium capable of accumulating Ni and Co was engineered by incorporating a metal-inducible curli overproduction system (Raghu et al., 2008). The enhanced adhesive capacity of the engineered strain to inert surfaces facilitates its immobilization onto a solid support and subsequent removal from the decontaminated effluents. As a result, this strain could potentially serve as a promising candidate for utilization in an industrial-scale biofilter (Duprey et al., 2014). The findings from a series of experiments showed that endophytic bacteria can help to clean-up pollution. These bacteria can degrade harmful substances and resist or trap metals via degradation pathways and metal resistance/sequestration systems. They can make phytoremediation work better for different types of pollution, like TCE (trichloroethylene) (Weyens et al., 2015).

7. Challenges and Limitations

Phytoremediation and microbial methods offer promising solutions for environmental cleanup, but various environmental and biological factors often limit their effectiveness. One major challenge is the variability in environmental conditions, such as soil type, pH, temperature, and moisture content, which can significantly affect the growth and activity of plants and microorganisms involved in remediation. For instance, some plant species may be more tolerant to certain contaminants or environmental stressors than others, limiting the generalizability of these methods across different ecosystems. Additionally, the availability of nutrients and the presence of other pollutants can influence the ability of plants and microbes to effectively remove or stabilize contaminants like heavy metals, including nickel.

Another limitation lies in the slow rate of remediation and the long-term sustainability of these methods. Phytoremediation often requires extended periods to achieve substantial detoxification, which may not be feasible for sites with high contamination levels or urgent remediation needs. Similarly, microbial methods, while effective in reducing bioavailable nickel, may not be as efficient under extreme environmental conditions or at high contaminant concentrations. The complexity of microbial communities also poses challenges, as not all microbes have the same capacity for nickel uptake or transformation, making it difficult to predict outcomes. Moreover, the persistence of beneficial microbes in the field is a concern, as changes in environmental conditions can lead to the decline or loss of these populations, hindering the long-term effectiveness of microbial-assisted remediation strategies.

8. Conclusions and Future Perspectives

Nickel plays a crucial role in regulating key metabolic processes. However, when present in excess, its toxicity poses significant risks to both plant systems and human health. As Ni contamination in soils becomes more prevalent due to anthropogenic activities, effective remediation strategies are urgently required. This review has highlighted the negative effects of nickel toxicity on plant growth and metabolism, emphasizing the potential of harnessing microbial-assisted

phytoremediation in mitigating these emerging environmental pollution challenges.

Microbes play a pivotal role in nickel (Ni) remediation, particularly through their interactions with plants in phytoremediation processes. Plant growth-promoting bacteria (PGPB), such as *Microbacterium*, *Pseudomonas*, and *Bacillus* species, enhance the bioavailability of Ni and increase its uptake by plants. For instance, inoculation with *Microbacterium* strains led to a significant increase in Ni concentration in *Alyssum murale* from 8500 mg kg⁻¹ to 11500 mg kg⁻¹, highlighting their potential to increase Ni accumulation in shoots (Table 2). Similarly, *Bacillus subtilis* promoted Ni uptake in *Brassica juncea*, increasing its concentration in roots and stems, while also protecting the species from Ni toxicity (Table 2). This dual action of enhancing Ni uptake and providing biological buffering against toxicity is a common feature of these microbes. Additionally, *Pseudomonas* strains were able to improve plant biomass accumulation while reducing Ni phytotoxicity (Table 2). By facilitating metal solubilization and improving the adjacent soil properties, these microbes support the effectiveness of the phytoremediation efforts, contributing to better and plausibly sustainable Ni decontamination strategies.

Looking ahead, advancements in omics technologies—such as genomics, transcriptomics, proteomics, and metabolomics—are opening new avenues for gaining deeper insights into understanding the microbial-facilitated nickel stress alleviation. These technologies have enabled the identification of some key genes, regulatory networks, and metabolic pathways in both plants and microbes during exposure to high nickel levels. For example, transcriptomic studies have revealed plant genes related to metal chelation, antioxidative defense, and nutrient uptake, all activated by microbial interactions. Proteomic and metabolomic approaches have further elucidated how microbial consortia modulate plant metabolic profiles, leading to the production of critical metabolites like proline, glutathione, and ascorbate, which detoxify reactive oxygen species (ROS) generated under nickel stress. Moving forward, integrating these omics platforms will be essential in identifying novel plant-microbe interactions and improving the effectiveness and sustainability of phytoremediation.

In addition to omics technologies, gene editing tools such as CRISPR-Cas9 hold significant promise in advancing the understanding of microbial-assisted phytoremediation. Gene editing can be employed to enhance microbial resilience to high nickel concentrations or to engineer plants with enhanced metal-uptake capabilities. Targeted modifications in microbial genomes could also optimize the production of biosurfactants, siderophores, and organic acids, which facilitate nickel mobilization and uptake. Furthermore, systems biology approaches will provide a more comprehensive understanding of the complex interactions within plant-microbe-soil systems under nickel stress. By integrating multi-omics data, systems biology can help construct predictive models to fine-tune phytoremediation strategies for diverse environmental conditions. Emerging biotechnological applications, such as synthetic biology and nano-biotechnology, offer additional tools to enhance microbial-assisted remediation. Synthetic biology can be used to design custom microbial consortia tailored for specific soil types or contamination levels, while nano-biotechnology could deliver nano-scale amendments (nanobiochar, biogas digestates; nano-materials impregnated with suitable microbial consortia) that may increase nickel bioavailability to engineered microbes, accelerating the remediation process (Li et al., 2024; Sani et al., 2023, 2024; Visioli et al., 2015; Wu et al., 2024; Yang et al., 2016; Yin et al., 2024; Yousef and Singh, 2024).

Finally, field-scale trials and the integration of these technologies into sustainable agricultural practices are critical for translating lab-scale successes into real-world solutions. Future research must also address the socio-economic and regulatory aspects of implementing microbial-assisted phytoremediation. Assessing cost-effectiveness, public acceptance, and potential risks will be essential for the widespread adoption of these remediation strategies. By leveraging upon cutting-

edge technologies and fostering cross-disciplinary collaborations, we can better understand the scientific basis of phytoremediation of nickel-contaminated environments, ultimately contributing to better livability for humans and all other organisms.

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Data will be made available on request.

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