

Assessment of Tolerance and Bio-reductive Potential of Hexavalent Chromium (VI) to Trivalent Chromium (III) via Isolated Microorganisms from Contaminated Soil

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ABSTRACT

This study addresses the growing environmental concern of chromium contamination, particularly the toxicity of hexavalent chromium [Cr (VI)] in soil and aquatic systems. The primary objective of this study is to evaluate the mechanisms by which soil microorganisms tolerate and detoxify hexavalent chromium [Cr (VI)] and to assess their potential for sustainable bioremediation through bio-reductive transformation into the less toxic trivalent form [Cr (III)]. The research problem focuses on understanding how soil microorganisms tolerate and detoxify Cr (VI), a highly toxic, carcinogenic, and mobile form of chromium, and how these biological processes can be harnessed for sustainable bioremediation. The methodology of this study is based on a comprehensive review of existing literature focusing on the isolation, identification, and characterization of chromium-resistant microorganisms. Techniques such as 16S rRNA gene sequencing, Diphenylcarbazide (DPC) assays, and agar well diffusion methods have been analyzed to evaluate microbial resistance and reduction efficiency. Various microbial mechanisms, including biosorption, bioaccumulation, and biotransformation, are examined under different environmental conditions such as pH, temperature, and oxygen availability. Key findings reveal that several bacterial genera, including *Bacillus*, *Pseudomonas*, and *Streptomyces*, demonstrate high tolerance and efficiency in reducing Cr (VI) to Cr (III). Microbial detoxification occurs through enzymatic reduction, intracellular sequestration, efflux systems, and extracellular binding. Biosorption efficiencies exceeding 70–80% have been reported under optimal conditions. Overall, the study concludes that microbial bioremediation is a cost-effective, environmentally friendly, and efficient approach for mitigating chromium pollution and restoring ecosystem balance. This review provides a critical framework linking microbial physiology, enzymatic mechanisms, and environmental application, highlighting microbial bioremediation as a cost-effective and eco-friendly strategy while identifying future directions for improving field-scale implementation.

Keywords: Bioremediation, Bioaccumulation, Biosorption, Biotransformation

Introduction

The escalation of human-driven activities, including intensive agriculture with chemical fertilizers and pesticides alongside rapid industrial expansion, has significantly contributed to environmental pollution (Aktar et al., 2009; Upadhyay et al., 2017). Toxic heavy metals such as chromium, lead, cadmium, and arsenic are frequently detected at elevated concentrations in soils, particularly in mining regions (Upadhyay et al., 2017; Ladwani et al., 2012). The accumulation of these metals within biological systems leads to bio-magnification across trophic levels, adversely affecting ecosystem health, reducing soil fertility, and disrupting microbial populations (Ladwani et al., 2012). Chromium (Cr) is recognized as the seventh most abundant element in the Earth's crust in the modern era (McGrath and Smith, 1990; Cervantes et al., 2001). Among its various oxidation states, trivalent chromium [Cr (III)] and hexavalent chromium [Cr (VI)] are the most stable and commonly occurring forms. Cr (III) typically forms complexes with sulfates, hydroxides, and oxides and is commonly associated with organic matter in soil and aquatic systems, where it exhibits relatively low

mobility (McGrath and Smith, 1990; Cervantes et al., 2001). The natural concentration of chromium in the Earth's crust ranges from approximately 100 to 300 µg/g, while contaminated soils may contain concentrations ranging from 5 to 3000 µg/g (Shewry and Peterson, 1976; Aktar et al., 2009). Microorganisms, particularly rhizobacteria inhabiting the rhizosphere, play a crucial role in supporting plant growth under contaminated conditions. These microbes mitigate both biotic and abiotic stresses by enhancing nutrient availability through mineral solubilization and by producing compounds such as siderophores and phytohormones (e.g., indole-3-acetic acid and ethylene) (Upadhyay et al., 2017; Ahemad, 2015). Exposure to chromium species, especially Cr (III) and Cr (VI), negatively impacts microbial morphology, metabolic functions, and growth patterns (Ayele and Godebo, 2021; Ayangbenro and Babalola, 2017). Chromium is extensively utilized in various industrial sectors, including metallurgy, steel production, tanning, cement manufacturing, and textile dyeing, making these industries major contributors to chromium pollution. Both Cr (III) and Cr (VI)

are frequently released into aquatic systems through industrial discharge, where they persist due to their chemical stability (Ayele and Godebo, 2021; Choi et al., 2018; Kumar et al., 2019). Hexavalent chromium [Cr (VI)] is particularly hazardous and has been classified as a potent toxicant with carcinogenic, mutagenic, and nephrotoxic effects, posing serious risks to living organisms and the environment (Sen, M., and Dastidar, 2010; Rahman et al., 2015). Studies have demonstrated that Cr (VI) concentrations ≥ 0.2 mg/mL and Cr (III) concentrations ≥ 1.0 mg/mL can induce DNA damage, thereby inhibiting microbial growth (Bhupendra et al., 2021). This genotoxicity is associated with mechanisms such as Cr (III)-mediated DNA interstrand cross-linking, formation of Cr (III)-DNA mono-adducts, and protein–DNA cross-links (O’Brien et al., 2003; Macfie et al., 2010). Several microbial species, including *Streptomyces griseus*, *Streptomyces rimosus*, and other actinomycetes, have demonstrated significant capacity in reducing chromium, particularly in the detoxification of Cr (VI) from industrial effluents (Poopal and Laxman, 2009). Microbial remediation strategies, including the reduction of Cr (VI) to

less toxic forms, bioremediation processes, and detoxification of Cr (III), are considered effective and sustainable approaches for mitigating chromium contamination (Sharma et al., 2022). The reduction of Cr (VI) by microorganisms is often described using two kinetic models: a linear model representing the combined influence of major ions and an exponential model reflecting microbial reduction dynamics (Su et al., 2019). Various bacterial mechanisms involved in chromium detoxification include biotransformation, biosorption, and bioaccumulation, all of which contribute to the removal of Cr (VI) from contaminated environments (Srinath et al., 2002; Huang, et al., 2016). In addition to biological approaches, several physicochemical methods are employed for chromium removal from wastewater. These include ion exchange, electrocoagulation, membrane filtration, electrodialysis, adsorption, and chemical precipitation techniques (Fathima et al., 2005). However, a clear scientific gap exists in integrating enzymatic mechanisms with physiological responses and environmental applications. This review addresses these gaps by critically analysing microbial chromium

reduction mechanisms, physiological adaptations, and their implications for

Diverse Isolated Bacteria for Cr (VI) Reduction

Numerous investigations have explored chromium-resistant bacterial strains to evaluate their effectiveness in bioremediation of contaminated environments. In one such study, five bacterial strains capable of removing Cr (VI) were successfully isolated from contaminated soils and identified through 16S rRNA gene sequencing techniques (He et al., 2014). These isolates were cultivated in liquid broth media supplemented with optimized concentrations of potassium dichromate ($K_2Cr_2O_7$) to assess their chromium reduction efficiency (He et al., 2014). In another study, two bacterial isolates (IFR-2 and IFR-3) obtained from tannery effluents demonstrated significant control to transform toxic Cr (VI) into the less harmful Cr (III) form and molecular identification using 16S rRNA gene sequencing revealed these strains as *Pediococcus pentosaceus* and *Staphylococcus aureus* (Ilias et al., 2011). Similarly, five additional bacterial strains capable of Cr (VI) removal were isolated using the pour plate technique under alkaline conditions. Based on 16S rRNA gene sequence

sustainable remediation.

analysis, these strains were identified as *Lysinibacillus* sp. W3, *Oceanobacillus* sp. W4, *Sporosarcina saromensis* W5, *Pseudochrobactrum saccharolyticum* W1, and *Staphylococcus saprophyticus* W2. Among these, *P. saccharolyticum* W1, *Oceanobacillus* sp. W4, and *S. saromensis* W5 exhibited strong resistance and high Cr (VI) reduction potential (He et al., 2014). A broad spectrum of bacterial species, particularly from the genus *Pseudomonas*, including *Pseudomonas aeruginosa*, *P. synxantha*, *P. putida*, *P. ambigua*, *P. fluorescens*, *P. dechromaticans*, and *P. chromatophila*, have been widely reported to reduce Cr (VI) into Cr (III) (Thatheyus & Ramya, 2016). In addition, other bacterial genera such as *Acinetobacter* *woffii*, *Bacillus megaterium*, *Aeromonas dechromatica*, and *Escherichia coli* (ATCC 33456) have also demonstrated chromium-reducing abilities (Lowe et al., 2003). Certain bacteria, including *Shewanella oneidensis* and *Tepidibacillus decaturensis* sp. nov., are known to facilitate Cr (VI) reduction under microaerophilic conditions,

highlighting their adaptability in low-oxygen environments (Lowe et al., 2003),(Dong et al., 2016). Furthermore, several bacterial strains such as *Intrasporangium* sp. Q5-1, *Bacillus* sp. ES29, *Escherichia coli*, *Enterobacter cloacae*, and *Pseudomonas fluorescens* LB300 have been reported to effectively convert Cr (VI) to Cr (III) under both aerobic and anaerobic conditions (Yang et al., 2009),(Bopp et al., 1983). Among these, *Rhizobium pusense* LCC43 exhibited remarkable chromium tolerance up to 128 µg

mL⁻¹ and demonstrated a high Cr (VI) reduction efficiency ranging from 80% to 100%. This strain also showed the ability to produce exopolysaccharides, which may enhance its bioremediation efficiency (Rocha et al., 2022). Collectively, these findings suggest that such bacterial strains hold significant promise for application in the remediation of chromium-contaminated soils and environments (Rocha et al., 2022).

Table: Chromium-Reducing Bacteria and Their Functional Characteristics

Bacterial Strain	Source	Tolerance Level	Reduction Efficiency	Key Mechanism
<i>Pseudomonas aeruginosa</i>	Soil	High	Significant	Enzymatic reduction
<i>Bacillus subtilis</i>	Mining soil	Up to 900 mg/L	High	Multi-metal resistance
<i>Rhizobium pusense</i>	Contaminated soil	128 µg/mL	80–100%	EPS-mediated biosorption
<i>Shewanellaoneidensis</i>	Aquatic systems	Moderate	Efficient	Electron transport reduction
<i>Pediococcuspentosaceus</i>	Tannery effluent	Moderate	Effective	Industrial adaptation

Chromium Toxicity in Microorganisms

Chromium, a non-essential heavy metal, exhibits high toxicity toward microorganisms as well as plants, even at relatively low concentrations

(Cervantes et al., 2001). Elevated levels of hexavalent chromium [Cr (VI)] are particularly harmful, as most microorganisms are unable to

tolerate such conditions, resulting in inhibited growth and survival under stress (Yang et al., 2023). However, certain chromium-resistant microorganisms possess the ability to reduce toxic Cr (VI) into the less harmful trivalent form [Cr (III)], thereby mitigating its toxic effects (Yang et al., 2023). The presence of Cr (VI) in soil environments significantly suppresses microbial growth and metabolic activities, which are essential for maintaining nutrient cycling and soil health (Yang et al., 2023; Zhang et al., 2022). Chromium contamination also impacts microbial community structure by reducing population size, altering diversity, and affecting genetic composition (Zhang et al., 2022). Both Gram-positive and Gram-negative bacteria experience morphological changes when exposed to Cr (VI), indicating its broad-spectrum toxicity (Ayele & Godebo, 2021). At the cellular level, chromium interferes with multiple biological processes. It can damage nucleic acid structures, disrupt cell membrane integrity, and impair critical cellular functions. Additionally, chromium exposure inhibits enzyme activity and oxidative phosphorylation, induces lipid peroxidation, and disturbs osmotic balance, ultimately affecting microbial growth

and metabolism (Ayele & Godebo, 2021; (Ayangbenro & Babalola, 2017). Morphological abnormalities such as cell elongation and enlargement have also been observed, along with inhibition of cell division, which directly contributes to reduced microbial proliferation (Mishra & Bharagava, 2015). Cr (VI) readily penetrates microbial cell membranes, enhancing its intracellular toxicity. Once inside the cell, it induces DNA damage and is associated with carcinogenic, mutagenic, and oxidative stress-related effects, as well as alterations in gene expression (Bagchi et al., 2002). Furthermore, chromium contamination adversely influences soil microbial activity, leading to disruptions in organic carbon dynamics (Shi et al., 2002). Short-term exposure to Cr (VI) has been shown to inhibit key soil enzymes, including phosphatases and sulphatases, thereby reducing microbial functionality and population density (Speir et al., 1999). Additionally, Cr (VI) exposure triggers endoplasmic reticulum (ER) stress in microbial cells, which in turn activates stress-response pathways such as the protein kinase R-like endoplasmic reticulum kinase (PERK) signaling mechanism (Alvarez et al., 2021).

Chromium Transport and Accumulation by Microorganisms

In both prokaryotic and eukaryotic organisms, chromate ions are actively transported across cellular membranes through specific uptake systems (Cervantes et al., 2001; Alexander & Aaseth, 1995). Once chromium enters the microbial cell, hexavalent chromium [Cr (VI)] undergoes intracellular reduction to trivalent chromium [Cr (III)], typically via intermediate valence states such as Cr (V) and Cr (IV) (Arslan et al., 1987; Zayed et al., 1998). In yeast cells, chromium uptake occurs through multiple mechanisms, including passive diffusion and phagocytosis-like processes (Sun et al., 2022; Stout et al., 2009). Additionally, yeast exhibits bioaccumulation capabilities that facilitate the internal sequestration of heavy metals. After entering the intracellular environment, metal ions bind to proteins and low-molecular-weight peptides such as glutathione, metallothioneins, and phytochelatins. These interactions help sequester metals, reduce cytotoxicity, and prevent interference with essential metabolic pathways (Sun et al., 2022; Szczypka et al., 1996; Hall, 2002). In *Saccharomyces cerevisiae*,

sulfate transport systems play a significant role in chromium uptake. The high-affinity sulfate transporter genes Sul1 and Sul2 are regulated by transcriptional activators such as MET4 and MSN1, which coordinate sulfate assimilation pathways (Sun et al., 2022; Beyersmann & Hartwig, 2008). Due to structural similarity between chromate and sulfate ions, chromium can enter the cell via these sulfate transport mechanisms (Sun et al., 2022; Shanker et al., 2005). The intracellular accumulation and localization of chromium in bacterial cells have been investigated using advanced techniques such as transmission electron microscopy (TEM), which enables visualization of metal deposition and its effects on cellular structures (Bano et al., 2013). Heavy metals, including chromium, are highly persistent in the environment due to their non-degradable nature and long biological half-lives. Upon accumulation within cells, they can interfere with vital biomolecules such as proteins and nucleic acids, leading to cellular dysfunction (Bartlett, 1991). Hexavalent chromium [Cr (VI)]

is highly soluble and readily penetrates cell membranes, where it interacts with intracellular macromolecules, including proteins and DNA, resulting in toxic effects (Markiewicz et al., 2015). Within microbial cells, Cr (VI) is reduced

to Cr (III) through both enzymatic and non-enzymatic pathways. Although this reduction decreases its mobility, the resulting Cr (III) can still exert toxic effects within the cytoplasm (Cervantes et al., 2001).

Mechanisms Influencing Chromium Biosorption by Microorganisms

Microorganisms employ a variety of resistance strategies to cope with heavy metal stress, including active efflux of metal ions, intracellular sequestration, extracellular binding, and enzymatic reduction of metal species at the cell surface (Igiri et al., 2018). The biological removal of heavy metals by microbial systems generally occurs through two primary processes: bioaccumulation and biosorption, both of which are influenced by cellular metabolic activity (Hansda & Kumar, 2016; (Zabochnicka-Świątek & Krzywonos, 2014). Bioremediation of hexavalent chromium [Cr (VI)] in aqueous systems often involves both biosorption and bioreduction mechanisms. For instance, *Candida paurometabolum* has been reported to effectively remove chromium through biosorption, where the conversion of Cr (VI) to Cr (III) results in irreversible binding to the biomass (Prabhakaran & Subramanian, 2016). Unlike conventional physical adsorption

processes, biosorption is not highly exothermic; however, temperature variations can significantly influence the efficiency and rate of the process (Hlihor et al., 2015; Volesky, 2003). Environmental factors such as pH play a crucial role in chromium biosorption. At lower pH levels, microbial cells exhibit enhanced Cr (VI) uptake capacity, whereas higher pH conditions generally reduce biosorption efficiency. Typically, bacterial cell surfaces carry a net negative charge across a wide pH range, but this charge may decrease due to the binding of Cr (III), thereby influencing metal uptake dynamics (Prabhakaran et al., 2019). Under anaerobic conditions, enzymatic systems involving cytochromes—particularly cytochrome b and cytochrome c—facilitate electron transport processes that contribute to chromium reduction (Miransari, 2011; Li et al., 2018). Additionally, extracellular electron transfers mechanisms, often mediated by soluble electron shuttles,

further enhance the reduction of Cr (VI) outside the cells. Various functional groups present on microbial cell walls, including amine, carboxyl, hydroxyl, and phosphoryl groups, play a significant role in metal binding through electrostatic interactions during the biosorption process (Vijayaraghavan & Balasubramanian, 2015; Ansari et al., 2011). Experimental observations have shown that, at a biomass concentration of 3 g/L, bacterial systems can achieve biosorption efficiencies of up to 71.24% for Cr (VI) and 83.24% for Cr (III) (Saurav & Kannabiran, 2011). Microbial resistance to Cr (VI) toxicity also involves adaptive mechanisms such as reduced metal uptake, membrane-level

exclusion, biosorption, and the upregulation of genes associated with oxidative stress responses (Ahemad, 2014). Biosorption itself is primarily a passive physicochemical process, where heavy metal ions interact with microbial biomass and become immobilized, thereby reducing their bioavailability in the environment (Abbas et al., 2014). Importantly, biosorption does not require metabolic energy, as it relies on passive binding interactions between metal ions and cellular components. This process continues until an equilibrium is established between the concentration of metal ions in solution and those adsorbed onto the microbial surface (Abbas et al., 2014; Jobby et al., 2018).

Assessment of Physiological Modulation in Microorganisms under Different Cr (III) and Cr (VI) Treatments

Chromium toxicity in microorganisms has been extensively investigated and is known to induce a wide spectrum of physiological, biochemical, and molecular disturbances in bacteria, algae, and fungi (Cervantes et al., 2001; Wong & Trevors, 1988). The degree of toxicity varies considerably among species, reflecting differences in cellular structure and adaptive capacity. For example, *Chlorella vulgaris* demonstrates relatively high tolerance,

sustaining growth in chromium concentrations ranging from 45 to 100 ppm, whereas *Scenedesmus acutus* is highly sensitive, exhibiting complete growth inhibition at concentrations above 15 ppm (Cervantes et al., 2001; Travieso et al., 1999). Likewise, studies on algal species such as *Scenedesmus* sp. and *Selenastrum* sp. reveal that they can grow in the presence of Cr (III), but equivalent concentrations of Cr (VI) significantly suppress

growth, underscoring the greater toxicity and bioavailability of the hexavalent form (Cervantes et al., 2001; Brady et al., 1994). This heightened toxicity of Cr (VI) is primarily attributed to its structural similarity to sulfate ions, which allows it to enter microbial cells through sulfate transport systems (*Shanker et al., 2005*; *Ramírez-Díaz et al., 2008*). Once internalized, Cr (VI) undergoes intracellular reduction, a process that inadvertently generates reactive oxygen species (ROS), leading to oxidative stress and extensive cellular damage (Francisco et al., 2010; Reynolds et al., 2009).

At the cellular level, chromium exposure disrupts critical biomolecules, including nucleic acids, proteins, and lipids. DNA damage is particularly significant, as chromium induces mutations, strand breaks, and impaired replication processes, thereby compromising genetic stability (Bagchi et al., 2002; Kawanishi et al., 2002). Protein oxidation and enzyme inhibition further interfere with essential metabolic functions, reducing overall cellular efficiency (Ayele & Godebo, 2021; Ayangbenro & Babalola, 2017). In eukaryotic microorganisms such as *Saccharomyces cerevisiae*, chromium toxicity is more

pronounced under non-fermentable growth conditions, where it reduces oxygen consumption, disrupts mitochondrial activity, and induces petite mutations associated with defective energy metabolism (Cervantes et al., 2001; Henderson, 1989; Singh, 1987). Additionally, chromium exposure leads to oxidative damage of proteins, altering their structure and functionality (*Sumner et al., 2005*). Trivalent chromium [Cr (III)] also contributes to toxicity by forming stable complexes with phosphate groups in DNA, thereby interfering with transcriptional and replication processes (Kortenkamp, 1997).

Oxidative stress represents a central mechanism underlying chromium toxicity. The excessive generation of ROS not only damages cellular macromolecules but also affects membrane integrity and electron transport chains, ultimately impairing respiration and energy production (Francisco et al., 2010; Codd et al., 2001; Huser et al., 1998). Although microorganisms activate antioxidant defense systems—including enzymes such as superoxide dismutase, catalase, and peroxidases—to counteract ROS, these defenses are often insufficient under high chromium stress, leading

to cellular dysfunction and death. In addition to biochemical disruptions, chromium exposure induces morphological and metabolic changes, such as cell elongation, altered membrane permeability, and reduced nutrient uptake (Mishra & Bharagava, 2015; Henderson, 1989; Singh 1987). These changes reflect adaptive responses but also indicate severe physiological stress. At the community level, chromium contamination significantly alters microbial diversity and ecosystem dynamics. Sensitive species are often eliminated, while resistant populations become dominant, leading to shifts in microbial community structure and function (Zhang et al., 2022). Such changes can adversely affect ecological processes, including nutrient cycling, soil fertility, and overall environmental

health. Despite the extensive documentation of chromium-induced toxicity, most studies remain largely descriptive and fail to establish clear links between observed physiological effects and underlying molecular mechanisms. There is a notable lack of integration between classical microbiological observations and advanced molecular approaches, such as genomics, proteomics, and metabolomics. Therefore, future research should focus on bridging this gap by employing omics-based strategies to elucidate gene expression patterns, metabolic pathways, and regulatory networks involved in microbial adaptation and resistance to chromium stress. Such integrated insights are essential for developing more efficient and targeted bioremediation strategies.

Screening of Bacterial Isolates for Chromium(VI) Resistance

Numerous microbial species possess intrinsic chemical and enzymatic systems capable of reducing chromium, either through individual pathways or synergistic mechanisms (Ali et al., 2023). Bacterial genera such as *Pseudomonas*, *Bacillus*, *Leucobacter*, and *Streptomyces* have been reported to facilitate chromium reduction, often utilizing cofactors like NADH or NADPH during the process (Ali et al., 2023). Certain

bacterial strains also exhibit resistance to multiple heavy metals, including chromium (Cr), arsenic (As), nickel (Ni), and cadmium (Cd), highlighting their potential applicability in bioremediation strategies (Kumar & Saini, 2019). The ability of bacterial isolates to reduce Cr (VI) into less toxic forms is commonly assessed using analytical techniques such as the Diphenylcarbazide (DPC) method, which

quantifies the decline in Cr (VI) concentration (Marczenko & Balcerzak, 2000). Using this approach, *Bacillus subtilis* strain MNU16 demonstrated significant capacity to convert Cr (VI) into its less harmful form (Upadhyay et al., 2017; Zahoor & Reman, 2009). To evaluate resistance levels, the Agar Well Diffusion method has been widely employed. This technique was applied to *Bacillus subtilis* MNU16 to determine its tolerance against chromium exposure (Zahoor & Reman, 2009; Hassen et al., 1998). Further screening of this isolate against a range of heavy metals—including arsenic (As), iron (Fe), mercury (Hg), nickel (Ni), cadmium (Cd), copper (Cu), and chromium (Cr)—revealed that the strain could withstand chromium concentrations as high as 900 mg/L, indicating strong resistance capacity (Zahoor & Reman, 2009). For broader screening purposes, bacterial isolates are often exposed to different heavy metals prepared from their

Bioremediation of Chromium Pollution

Microorganisms present in soil, water, sludge, subsurface environments, and industrial residue play a crucial role in degrading harmful substances into environmentally safe or tolerable forms through the process of bioremediation

respective salts, such as $K_2Cr_2O_7$ for Cr (VI), $NaAsO_2$ for arsenic, $HgCl_2$ for mercury, $CdCl_2$ for cadmium, $FeCl_3$ for iron, and $Ni(NO_3)_2$ for nickel. These solutions are typically prepared in sterile distilled water and sterilized through autoclaving prior to experimental use (Hassen et al., 1998). Bacterial isolates obtained from chromite mining environments have demonstrated notable resistance to multiple heavy metals, including Cr, Cd, Pb, and As. These isolates were identified through 16S rRNA gene sequencing as *Bacillus fungorum* (AsS1M2), *Pseudomonas argentinensis* (CrS2C7), *Bacillus thuringiensis* (CdS2M1), and *Bacillus subtilis* (PbS1M1). Among these, *Pseudomonas argentinensis* exhibited the highest chromium removal efficiency, achieving approximately 73.4% reduction of Cr (VI) when treated with a 100 mg/L $K_2Cr_2O_7$ solution (Acharya et al., 2024).

(Sharma et al., 2022). Various bioremediation mechanisms—including bioaccumulation, biotransformation, biosorption, and bioleaching—are involved in the removal of chromium and other heavy metals from

contaminated industrial effluents (Sharma et al., 2022); Fernández et al., 2018).

Microorganisms can eliminate and utilize metal ions for their metabolic activities by transforming toxic compounds into simpler end products such as CO₂, CH₄, H₂O, and biomass through enzyme-mediated metabolic pathways (Ayele & Godebo, 2021; Grace Pavithra et al., 2019). Among these strategies, the biological reduction of toxic hexavalent chromium Cr (VI) to the less toxic trivalent form Cr (III) is considered one of the most effective detoxification approaches for chromium contaminated environments (Ayele & Godebo, 2021; Cervantes et al., 2001). Several studies have investigated the tolerance and bioremediation potential of different bacterial isolates, revealing diverse mechanisms of interaction with chromium ions (Pushkar et al., 2021; Zhu et al., 2019). Dominant bacterial groups identified from chromium-contaminated environments include Betaproteobacteria, Gammaproteobacteria, Firmicutes, and Alphaproteobacteria, all of which exhibit significant chromium tolerance and remediation

capabilities (Pushkar et al., 2021; He et al., 2016). For example, *Caldicellulosiruptor saccharolyticus* demonstrated complete reduction of 40 mg/L Cr (VI) at 70 °C within 12 hours under glucose-fermenting conditions, with the resulting Cr (III) precipitating on the cell surface (Bai et al., 2018; Li et al., 2018). Similarly, mesophilic and facultative anaerobic bacteria such as *Bacillus dabaoshanensis* have shown the ability to reduce Cr (VI) efficiently under moderate temperature conditions. Other microbial strains—including *Paecilomyces lilacinus*, *Aspergillus niger*, *Bacillus cereus* IST105, *Zobellella denitrificans*, and *Bacillus mycoides* 200AsB1—have been reported to remediate Cr(VI) through biosorption and bioaccumulation mechanisms (Bhattacharya et al., 2019). Furthermore, biosorption and bioaccumulation are key mechanisms responsible for the uptake of Cr (VI) by microbial cells, while biotransformation facilitates the conversion of toxic Cr (VI) into the less harmful Cr (III) form (Fernández et al., 2018; Singh & Singh, 2019).

Conclusion

Chromium contamination represents a persistent and critical environmental challenge due to its non-biodegradable nature, widespread industrial discharge, and severe toxicological effects on living systems. Among its various oxidation states, hexavalent chromium [Cr (VI)] is of particular concern because of its high solubility, mobility, and potent carcinogenic and mutagenic properties. The findings synthesized in this study clearly demonstrate that microorganisms possess remarkable adaptive capabilities that enable them to survive and function in chromium-stressed environments while simultaneously contributing to its detoxification. A wide range of bacterial genera, including *Bacillus*, *Pseudomonas*, *Streptomyces*, and others, exhibit significant resistance to Cr (VI) and are capable of reducing it to the less toxic trivalent form [Cr (III)]. This transformation occurs through diverse mechanisms such as enzymatic reduction, biosorption, bioaccumulation, intracellular sequestration, and efflux-mediated resistance systems. These processes not only decrease chromium toxicity but also limit its bioavailability and mobility in contaminated ecosystems. Environmental parameters such as

pH, temperature, oxygen availability, and biomass concentration play crucial roles in influencing the efficiency of these microbial processes. Despite the inherent toxicity of chromium, microorganisms employ complex physiological and molecular responses—including oxidative stress management, activation of resistance genes, and modification of cellular structures—to withstand metal-induced stress. The ability of these organisms to function under both aerobic and anaerobic conditions further enhances their applicability in diverse environmental settings. Importantly, microbial bioremediation emerges as a highly promising, eco-friendly, and cost-effective alternative to conventional physicochemical methods, which are often expensive and may generate secondary pollutants. However, to fully harness the potential of microbial systems, future research should focus on the exploration of novel chromium-resistant strains, genetic and metabolic engineering approaches, large-scale field applications, and the integration of microbial consortia for enhanced remediation efficiency. In conclusion, the microbial transformation of Cr (VI) to Cr (III) offers a

sustainable and efficient strategy for mitigating chromium pollution. Advancing our understanding of microbial mechanisms and

optimizing their application will be essential for developing robust, scalable, and environmentally sound remediation technologies in the future.

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