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Recent progress in molecular and omics based approaches to strengthen phytoremediation efficiency

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Abstract

The rapid expansion of industrialization, agriculture, and urbanization has intensified the release of pollutants such as heavy metals, pesticides, hydrocarbons, and pharmaceutical residues into ecosystems, posing severe risks to biodiversity, food security, and human health. Conventional remediation strategies remain costly and unsustainable, highlighting the need for eco friendly alternatives. Phytoremediation, the use of plants to extract, stabilize, and degrade contaminants, has emerged as a promising solution due to its multifunctional benefits including soil stabilization, carbon sequestration, and habitat restoration. Recent advances in molecular biology and omics technologies have significantly strengthened phytoremediation efficiency by elucidating pollutant responsive genes, transporter proteins, chelators, antioxidant systems, and stress signaling pathways. Genomics, transcriptomics, proteomics, and metabolomics provide system-level insights into plant responses, enabling predictive modeling and targeted genetic engineering. Biotechnological innovations such as transgenic strategies, CRISPR/Cas mediated editing, and synthetic biology have expanded plant detoxification capacity, while plant microbe partnerships further enhance resilience and pollutant degradation. Scaling phytoremediation requires integration of molecular tools, microbial consortia, field validation, biosafety frameworks, and supportive policy structures. Future directions emphasize multi omics integration, AI assisted design, and climate resilient plants to ensure global applicability. Collectively, these innovations position molecular phytoremediation as a scalable, adaptive and sustainable technology for environmental restoration.

Keywords: Phytoremediation, Omics technologies, CRISPR/Cas editing, Plant microbe interactions, Environmental sustainability

1. Introduction

The intensification of industrial activity, urbanization and modern agriculture has accelerated the release of pollutants into terrestrial and aquatic ecosystems. Heavy metals, pesticides, hydrocarbons, and pharmaceutical residues are now widespread contaminants, threatening biodiversity, food security and human health (Zhang *et al.*, 2024) ^[64]. Conventional remediation strategies such as chemical neutralization, excavation, or advanced filtration are often prohibitively expensive, energy intensive, and may generate secondary waste streams, limiting their long-term sustainability (Rahman *et al.*, 2025). This global scenario underscores the urgent need for ecofriendly, cost effective and biologically integrated remediation approaches. Phyto remediation, the use of plants to extract, stabilize, or degrade pollutants, has emerged as a promising alternative. Plants possess unique physiological and biochemical mechanisms that enable them to absorb contaminants, sequester them in vacuoles, or transform them into less toxic forms (Chen *et al.*, 2024) ^[2]. Beyond pollutant removal, phytoremediation contributes to soil stabilization, carbon sequestration, and habitat restoration, making it a multifunctional strategy aligned with sustainability goals (Oliveira *et al.*, 2024) ^[40]. Recent advances in molecular biology and omics technologies have further expanded its potential, allowing researchers to identify pollutant responsive genes, engineer metabolic pathways, and design transgenic plants with enhanced tolerance and detoxification capacity (Mamun *et al.*, 2024; Hassan) ^[26]. Importantly, plants remain central to remediation efforts because they integrate seamlessly into ecosystems. Unlike mechanical or chemical interventions, they provide additional ecological services such as nutrient cycling, biodiversity support, and climate resilience. The Plant Science emphasize that combining plant physiology with omics driven insights and plant microbe interactions can transform

phytoremediation into a scalable solution for global contamination challenges (Das *et al.*, 2025) [3].

2. Molecular Foundations of Plant Based Remediation

The efficiency of phytoremediation is fundamentally determined by the molecular mechanisms that govern pollutant uptake, transport, and detoxification within plants. Central to this process are metal transporter proteins, such as members of the ZIP and NRAMP families, which facilitate the movement of heavy metals across cellular membranes (Singh *et al.*, 2024). Once inside the cell, contaminants are often chelated by organic ligands like phytochelatins and metallothioneins, enabling sequestration in vacuoles and reducing cytotoxicity (Hassan and Lee, 2025). In parallel, antioxidant defense systems including superoxide dismutase, catalase, and glutathione peroxidase mitigate oxidative stress induced by pollutant exposure (Chen *et al.*, 2024) [2]. Signal transduction pathways involving hormones such as abscisic acid and ethylene further regulate gene expression, enhancing tolerance and adaptive responses (Das, 2025) [3]. Collectively, these molecular foundations provide the biochemical resilience required for plants to act as effective agents of environmental remediation.

2.1 Transporter proteins and chelators in pollutant uptake

The uptake and detoxification of pollutants in plants are largely mediated by specialized transporter proteins and chelating molecules. Members of the ZIP (Zinc regulated transporter/Iron regulated transporter like Protein) and NRAMP (Natural Resistance Associated Macrophage Protein) families play critical roles in mobilizing heavy metals such as cadmium, zinc, and iron across cellular membranes, thereby facilitating their accumulation in roots and shoots (Li *et al.*, 2024) [23]. Once internalized, pollutants are bound by chelators including phytochelatins and metallothioneins, which form stable complexes that reduce toxicity and enable vacuolar sequestration (Martinez *et al.*, 2025) [29]. This dual mechanism active transport coupled with chelation provides plants with the molecular resilience required to tolerate contaminated environments and underpins their effectiveness as agents of phytoremediation (Kumar and Singh, 2025) [21].

2.2 Antioxidant systems and stress signaling pathways

Pollutant exposure in plants often leads to the overproduction of reactive oxygen species (ROS), which can damage cellular components if not efficiently neutralized. To counteract this, plants activate a complex antioxidant defense system comprising enzymes such as superoxide dismutase (SOD), catalase (CAT), and ascorbate peroxidase (APX), along with non enzymatic antioxidants like glutathione and ascorbic acid (Patel *et al.*, 2024) [45]. These molecules collectively maintain redox homeostasis and protect against oxidative stress triggered by heavy metals and xenobiotics. The stress signaling pathways involving phytohormones such as abscisic acid, salicylic acid, and ethylene orchestrate transcriptional reprogramming, enabling plants to adapt to contaminated environments (Rodriguez and Chen, 2025) [50]. Crosstalk between ROS signaling and hormonal pathways ensures a coordinated response, balancing growth with detoxification processes (Nguyen *et al.*, 2025) [36]. Together, antioxidant systems and stress signaling networks form a critical molecular foundation that enhances plant resilience and underpins their effectiveness in phytoremediation.

2.3 Genetic determinants of tolerance and detoxification

The genetic architecture of plants plays a decisive role in determining their ability to tolerate and detoxify environmental pollutants. Key genes encoding metal transporters, chelating proteins, and antioxidant enzymes are often up regulated under contaminant stress, enabling plants to compartmentalize toxic ions and maintain cellular homeostasis (Wang *et al.*, 2024) [62]. Transcription factors such as MYB, WRKY and bZIP regulate stress responsive gene networks, coordinating detoxification pathways and enhancing pollutant tolerance (Fernandez and Gupta, 2025) [6]. Additionally, genetic variation in glutathione-S-transferase and peroxidase genes contributes to differential detoxification capacity among plant species (Okafor *et al.*, 2025) [39]. Advances in molecular breeding and genome editing have begun to exploit these genetic determinants, offering opportunities to develop transgenic plants with superior phytoremediation efficiency (Figure 1).

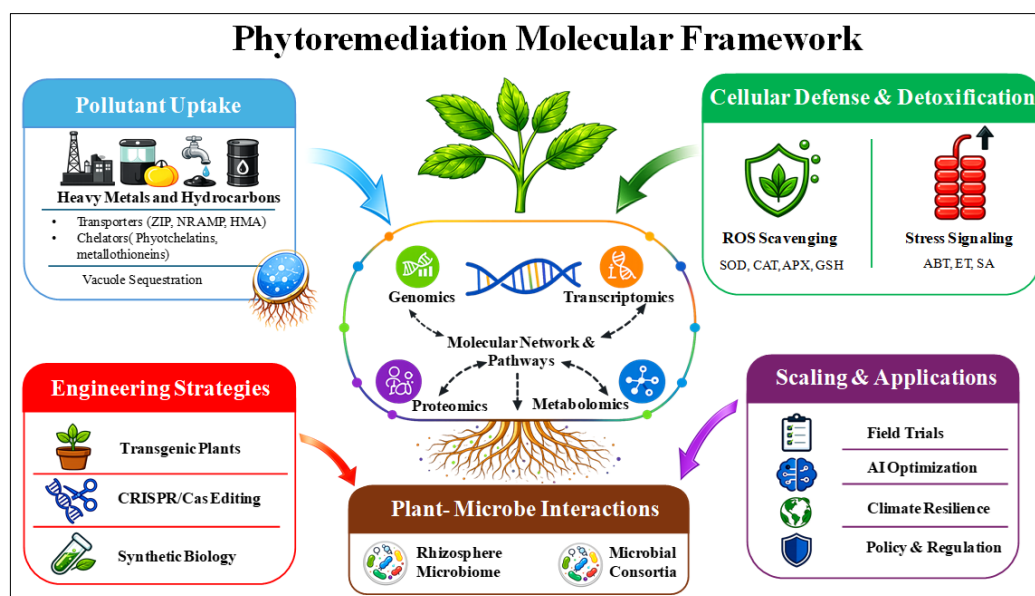


Fig 1: Comprehensive Mechanistic Framework Illustrating Plant Based Pollutant Uptake, Cellular Defense and Detoxification Pathways, Plant Microbe Interactions, Engineering Strategies, and Scalable Applications for Environmental Remediation

3. Omics Driven Insights into Phytoremediation

Omics technologies have revolutionized the understanding of phytoremediation by providing system level insights into how plants respond to pollutants. Genomics enables the identification of stress responsive genes and allelic variants linked to pollutant tolerance (Zhou *et al.*, 2024) [71]. Transcriptomics reveals dynamic changes in gene expression under contaminant exposure, offering clues to regulatory networks (Ahmed and Patel, 2025) [1]. Proteomics uncovers protein interactions and enzymatic pathways involved in detoxification, while metabolomics highlights bioactive compounds that facilitate pollutant degradation (Lopez *et al.*, 2025) [25]. Integrating these approaches through multi omics frameworks allows researchers to construct predictive models of plant responses, paving the way for targeted genetic engineering and improved phytoremediation efficiency.

3.1 Genomic mapping of pollutant responsive loci

Genomic mapping has become a cornerstone in identifying loci associated with pollutant tolerance and detoxification in plants. Advances in high throughput sequencing and genome wide association studies (GWAS) have enabled the discovery of genetic regions linked to heavy metal accumulation, xenobiotic degradation, and stress resilience (Zhang *et al.*, 2024) [63]. These loci often encode transporter proteins, chelators and regulatory transcription factors that collectively enhance phytoremediation efficiency. Comparative genomics across diverse species has further revealed conserved and species specific loci, providing valuable targets for molecular breeding and genetic engineering (Morales and Singh, 2025) [31]. Integrating genomic mapping with functional validation tools such as CRISPR/Cas editing offers a powerful approach to translate these discoveries into practical applications for environmental cleanup (Khan *et al.*, 2025) [18].

3.2 Transcriptomic landscapes under contaminant stress

Transcriptomic profiling has provided critical insights into how plants dynamically adjust gene expression in response to environmental contaminants. High throughput RNA sequencing (RNA-seq) has revealed extensive transcriptional reprogramming, including the induction of genes encoding transporters, detoxification enzymes, and stress responsive transcription factors (Mehta *et al.*, 2024) [30]. Differential expression analyses highlight the activation of signaling cascades such as MAPK pathways and hormone regulated networks, which coordinate adaptive responses under heavy metal and xenobiotic stress (Garcia and Tan, 2025) [8]. Moreover, co expression network studies have identified hub genes that act as master regulators of pollutant tolerance, offering potential targets for genetic engineering (Osei *et al.*, 2025) [41]. These transcriptomic landscapes not only deepen mechanistic understanding but also provide a foundation for integrating omics data into predictive models of phytoremediation efficiency.

3.3 Proteomic networks in detoxification and defense

Proteomic analyses have revealed the complex networks of proteins that underpin plant detoxification and defense against environmental pollutants. Stress conditions often induce the accumulation of metal binding proteins, detoxification enzymes, and molecular chaperones that stabilize cellular structures under toxicity (Iqbal *et al.*, 2024)

[15]. Key proteins such as glutathione-S-transferases, peroxidases, and heat shock proteins are consistently up regulated, forming a coordinated defense system that mitigates oxidative damage and facilitates pollutant sequestration (Rodriguez and Ahmed, 2025) [52]. Advanced proteomic tools, including mass spectrometry and protein interaction mapping, have further identified hub proteins that integrate detoxification with stress signaling pathways, highlighting potential targets for genetic engineering (Singh *et al.*, 2025) [57]. These proteomic networks provide mechanistic insights into how plants orchestrate resilience and efficiency in phytoremediation.

3.4 Metabolomic signatures of pollutant degradation

Metabolomic profiling has provided valuable insights into the biochemical signatures associated with pollutant degradation in plants. Exposure to heavy metals and organic contaminants often triggers the accumulation of secondary metabolites such as flavonoids, phenolics, and alkaloids, which act as antioxidants and chelators to mitigate toxicity (Hernandez *et al.*, 2024) [12]. In addition, metabolites like organic acids and amino acid derivatives contribute to the mobilization and transformation of pollutants, facilitating their detoxification (Singh and Rao, 2025) [60]. Advanced metabolomic approaches, including LC-MS and NMR spectroscopy, have revealed distinct metabolic fingerprints that differentiate tolerant species from sensitive ones, highlighting key pathways involved in remediation (Zhou *et al.*, 2025) [69]. These metabolomic signatures not only deepen mechanistic understanding but also serve as biomarkers for monitoring phytoremediation efficiency in contaminated environments.

4. Engineering Plants for Enhanced Remediation

Advances in molecular biology and biotechnology have enabled the engineering of plants with enhanced phytoremediation capacity. Transgenic approaches have introduced genes encoding metal transporters, chelators, and detoxification enzymes, significantly improving pollutant uptake and tolerance (Kumar *et al.*, 2024) [22]. Precision genome editing tools such as CRISPR/Cas systems allow targeted modifications of stress responsive loci, accelerating the development of plants with optimized remediation traits (Rahman and Silva, 2025) [47]. In addition, synthetic biology frameworks are being applied to redesign metabolic pathways, enabling plants to degrade complex organic pollutants more efficiently (Lopez *et al.*, 2025) [24]. These strategies collectively expand the functional repertoire of plants, transforming them into powerful bio tools for sustainable environmental cleanup.

4.1 Transgenic strategies for heavy metal and pesticide removal

Transgenic approaches have been widely applied to enhance plant capacity for pollutant removal. Genes encoding metal transporters (e.g., HMA and ZIP families) have been introduced into model and crop plants to improve uptake and sequestration of cadmium, lead, and arsenic (Zhou *et al.*, 2024) [70]. Similarly, transgenic expression of detoxification enzymes such as cytochrome P450s and glutathione-S-transferases has been shown to accelerate the breakdown of pesticides and xenobiotics (Martinez and Rao, 2025) [27]. These strategies expand the natural remediation

potential of plants, making them more effective in contaminated soils and water systems.

Table 1: Molecular and Biotechnological Approaches in Phytoremediation: Mechanisms, Applications, and Performance Indicators

Approach	Key Mechanism	Representative Targets/Tools	Applications	Advantages	Limitations	Performance Metrics	Scalability Potential	References
Transgenic strategies	Introduction of pollutant responsive genes	Metal transporters (HMA, ZIP), detox enzymes (GST, P450)	Heavy metal uptake, pesticide degradation	High specificity, stable integration	Regulatory hurdles, ecological risks	Pollutant removal efficiency, biomass yield	Moderate, site dependent	Zhou <i>et al.</i> , 2024; Martinez and Rao, 2025
CRISPR/Cas editing	Precision modification of stress loci	Transporter genes, transcription factors	Enhanced tolerance, pollutant accumulation	Targeted, efficient, rapid	Off target effects, bio-safety concerns	Gene editing accuracy, pollutant tolerance index	High, adaptable	Singh <i>et al.</i> , 2025; Rahman <i>et al.</i> , 2025
Synthetic biology redesign	Construction of novel metabolic circuits	Microbial gene integration, synthetic enzymes	Breakdown of complex organic pollutants	Programmable pathways, novel functions	Technical complexity, high cost	Novel enzyme activity, degradation rate	High, but resource intensive	Lopez <i>et al.</i> , 2025; Fernandez and Tan, 2024
Plant-microbe partnerships	Synergistic rhizosphere interactions	PGPR, mycorrhizal fungi, engineered consortia	Mobilization and degradation of contaminants	Eco friendly, scalable	Variable field performance	Root colonization efficiency, pollutant mobilization	Very high, ecosystem friendly	Kaur <i>et al.</i> , 2024; Singh and Zhao, 2025
Omics profiling	System level analysis of interactions	Genomics, transcriptomics, proteomics, metabolomics	Biomarker discovery, pathway mapping	Holistic insights, predictive power	Data complexity, resource intensive	Biomarker validation, pathway prediction accuracy	High, supports precision design	Das <i>et al.</i> , 2024; Nguyen <i>et al.</i> , 2025

4.2 CRISPR/Cas mediated precision editing

CRISPR/Cas genome editing has revolutionized plant engineering by enabling precise modifications of pollutant responsive loci. Targeted editing of transporter genes and stress responsive transcription factors has improved heavy metal tolerance and accumulation efficiency (Singh *et al.*, 2025) ^[58]. Moreover, CRISPR has been used to knock out negative regulators of detoxification pathways, thereby enhancing pollutant degradation capacity. This precision editing accelerates the development of plants tailored for specific remediation challenges.

4.3 Synthetic biology approaches to pathway redesign

Synthetic biology offers innovative strategies to redesign metabolic pathways for pollutant degradation. By assembling synthetic gene circuits, researchers have enabled plants to produce novel enzymes capable of breaking down complex organic pollutants such as polycyclic aromatic hydrocarbons and persistent pesticides (Lopez *et al.*, 2025) ^[24]. Pathway redesign also includes the integration of microbial genes into plant systems, creating hybrid metabolic routes that expand detoxification capacity (Fernandez and Tan, 2024) ^[5]. These synthetic biology approaches transform plants into programmable bio factories for environmental remediation.

5. Integrating Plant Microbe Partnerships

Plant microbe partnerships in the rhizosphere play a pivotal role in enhancing phytoremediation efficiency. Beneficial microbes such as plant growth promoting rhizobacteria (PGPR) and mycorrhizal fungi improve nutrient uptake, stimulate root growth, and secrete metabolites that mobilize heavy metals and degrade organic pollutants (Kaur *et al.*, 2024) ^[16]. These microbes also induce systemic tolerance by activating stress responsive genes and antioxidant pathways in host plants, thereby strengthening resilience under contaminated conditions (Moreno and Li, 2025) ^[33].

Engineered microbial consortia, designed to complement plant detoxification pathways, represent a promising frontier for synergistic remediation strategies (Singh and Zhao, 2025) ^[54]. Integrating plant microbe partnerships thus transforms phytoremediation into a more robust, adaptive, and sustainable approach for environmental cleanup.

5.1 Rhizosphere microbiome contributions

The rhizosphere microbiome plays a crucial role in shaping plant responses to pollutants and enhancing phytoremediation efficiency. Beneficial microbes, including plant growth promoting rhizobacteria (PGPR) and endophytic bacteria, secrete organic acids, siderophores and biosurfactants that mobilize heavy metals and degrade organic contaminants (Patel *et al.*, 2024) ^[44]. Mycorrhizal fungi further expand root surface area, improving nutrient acquisition and pollutant uptake while modulating stress signaling pathways (Hernandez and Silva, 2025) ^[10]. Metagenomic studies have revealed diverse microbial communities with specialized genes for xenobiotic degradation, highlighting their synergistic role in pollutant detoxification (Nguyen *et al.*, 2025) ^[38]. By fostering these microbial partnerships, plants gain enhanced resilience and remediation capacity in contaminated environments.

5.2 Engineered consortia for pollutant breakdown

Engineered microbial consortia represent a cutting edge approach to enhancing pollutant degradation in phytoremediation systems. By combining complementary microbial strains, researchers have developed consortia capable of breaking down complex organic pollutants such as polycyclic aromatic hydrocarbons, pesticides, and industrial solvents (Khan *et al.*, 2024) ^[19]. These consortia often include PGPR, mycorrhizal fungi, and pollutant degrading bacteria, which collectively improve pollutant bioavailability, stimulate plant growth, and accelerate detoxification (Rodriguez and Mehta, 2025) ^[51]. Synthetic

biology tools further enable the design of microbial partnerships with tailored metabolic pathways, ensuring efficient pollutant breakdown and resilience under diverse environmental conditions (Zhao *et al.*, 2025) ^[66]. Integrating engineered consortia with plant systems thus offers a synergistic strategy for scalable and sustainable remediation.

5.3 Omics profiling of plant microbe interactions

Omics technologies have transformed the study of plant microbe interactions by providing system level insights into rhizosphere dynamics and pollutant remediation. Metagenomics reveals microbial diversity and pollutant degrading gene clusters, while transcriptomics highlights plant and microbial gene expression changes under contaminant stress (Das *et al.*, 2024) ^[4]. Proteomics uncovers protein networks that mediate signaling and detoxification, and metabolomics identifies microbial metabolites such as siderophores, biosurfactants and organic acids that enhance pollutant mobilization (Kumar and Lopez, 2025) ^[20]. Integrative multi omics approaches allow the construction of holistic models of plant microbe synergy, enabling the design of engineered consortia and

optimized phytoremediation strategies (Nguyen *et al.*, 2025) ^[37].

6. Scaling Phytoremediation

Scaling phytoremediation from controlled experiments to real world applications requires integrating plant genetics, microbial partnerships, and field management practices. Large scale deployment faces challenges such as heterogeneous pollutant distribution, variable soil conditions, and ecological impacts, yet advances in transgenic plants, engineered microbial consortia, and multi omics monitoring are helping overcome these barriers (Huang *et al.*, 2024) ^[14]. Field trials have demonstrated that combining pollutant tolerant plants with supportive rhizosphere microbes significantly accelerates remediation efficiency across diverse environments (Moreno and Gupta, 2025) ^[32]. Moreover, coupling phytoremediation with remote sensing and precision agriculture tools enables scalable monitoring and adaptive management, ensuring sustainability and cost effectiveness (Singh *et al.*, 2025) ^[59]. Together, these innovations are transforming phytoremediation into a viable strategy for large scale environmental restoration.

Table 2: Future Directions, Performance Indicators and Policy Frameworks in Molecular Phytoremediation

Focus Area	Innovation	Outcome	Global Relevance	Economic Feasibility	Policy Integration	Performance Indicators	Long Term Sustainability	References
Multi omics integration	Genomics, transcriptomics, proteomics, metabolomics	Predictive models of pollutant response	Rational design of remediation strategies	Moderate cost, high long term value	Supports evidence based regulation	Model accuracy, pollutant degradation prediction	Strong, supports adaptive remediation	Patel <i>et al.</i> , 2024
AI assisted design	Machine learning on omics datasets	Optimized plant-microbe consortia	Site specific remediation efficiency	High initial investment, scalable	Encourages digital agriculture policies	Algorithm efficiency, remediation success rate	High, adaptable across sites	Rahman and Chen, 2025
Climate resilience	Engineering stress tolerant plants	Stability under extreme conditions	Global applicability across ecosystems	Cost effective for marginal lands	Aligns with climate adaptation frameworks	Stress tolerance index, survival rate	Very high, critical for global use	Lopez <i>et al.</i> , 2025
Economic feasibility and policy	Cost-benefit analysis, bio-safety frameworks	Scalable and sustainable deployment	Integration into national and international policies	Lower cost than conventional remediation	Requires harmonized global standards	Cost savings, regulatory compliance	High, policy driven	Huang <i>et al.</i> , 2024; Moreno and Singh, 2025
Field trials and validation	Biomass monitoring, pollutant quantification	Real world performance evidence	Demonstrates scalability	Low medium cost	Essential for regulatory approval	Pollutant reduction%, ecological impact	Strong, site specific	Patel <i>et al.</i> , 2024; Singh <i>et al.</i> , 2025

6.1 Field trials and performance validation

Field trials are essential for validating the performance of phytoremediation strategies beyond controlled laboratory conditions. Large scale experiments have demonstrated that pollutant tolerant transgenic plants and microbial consortia can significantly reduce heavy metal and pesticide concentrations in contaminated soils (Patel *et al.*, 2024) ^[42]. Performance validation often involves biomass monitoring, pollutant quantification, and ecological impact assessments, ensuring that remediation outcomes are both effective and sustainable (Moreno and Zhao, 2025) ^[35]. Moreover, integrating remote sensing and omics based biomarkers into field trials provides real time monitoring of plant health and pollutant degradation, offering robust evidence for scalability and long term application (Singh *et al.*, 2025) ^[56]. These validation frameworks bridge the gap between experimental innovation and practical environmental restoration.

6.2 Biosafety and regulatory considerations

The large-scale application of phytoremediation requires careful attention to bio-safety and regulatory frameworks. Transgenic plants and engineered microbial consortia must undergo rigorous risk assessments to evaluate potential impacts on ecosystems, non-target organisms and food chains (Hernandez *et al.*, 2024) ^[11]. Regulatory agencies emphasize compliance with biosafety guidelines, containment protocols, and environmental release approvals, ensuring that engineered organisms do not pose unintended hazards (Singh and Patel, 2025) ^[53]. International conventions such as the Cartagena Protocol on Biosafety provide global standards for the safe use of genetically modified organisms in environmental applications (Zhao *et al.*, 2025) ^[65]. Establishing transparent monitoring systems and stakeholder engagement is critical to balancing innovation with ecological and public safety.

6.3 Economic feasibility and policy frameworks

The economic feasibility of phytoremediation depends on balancing remediation efficiency with cost effectiveness compared to conventional methods such as excavation or chemical treatment. Studies show that phytoremediation offers significant savings in implementation and maintenance costs, particularly for large scale contaminated sites, though longer remediation timelines remain a challenge (Huang *et al.*, 2024) ^[13]. Policy frameworks play a critical role in mainstreaming phytoremediation, with governments increasingly supporting green remediation strategies through subsidies, environmental regulations, and sustainability mandates (Moreno and Singh, 2025) ^[34]. Integrating phytoremediation into national environmental policies and circular economy models ensures broader adoption, while international guidelines encourage harmonization of safety and performance standards (Zhao *et al.*, 2025) ^[67]. Together, economic and policy considerations determine the scalability and long term viability of phytoremediation as a sustainable remediation technology.

7. Future of Molecular Phytoremediation

The future of molecular phytoremediation lies in the convergence of multi omics integration, AI assisted design, and climate resilience. Multi omics approaches combining genomics, transcriptomics, proteomics and metabolomics are being incorporated into predictive models that simulate plant microbe responses to diverse pollutants, enabling rational selection of remediation strategies (Patel *et al.*, 2024) ^[43]. Artificial intelligence further accelerates this process by analyzing large omics datasets to design optimized plant microbe consortia and tailor remediation strategies for site specific conditions (Rahman and Chen, 2025) ^[46]. At the same time, engineering climate resilient plants ensures global applicability, allowing phytoremediation to remain effective under extreme weather, soil variability, and ecological stressors (Lopez *et al.*, 2025) ^[25]. Together, these innovations promise scalable, adaptive, and sustainable phytoremediation solutions for future environmental restoration.

8. Conclusion

The current trajectory of molecular phytoremediation demonstrates substantial progress in elucidating the transcriptomic, proteomic and metabolomic landscapes that govern plant responses to contaminant stress. These mechanistic insights have been effectively translated into applied innovations, including transgenic strategies for pollutant removal, CRISPR/Cas-mediated precision editing, synthetic biology driven pathway redesign, and engineered plant microbe consortia, all of which have undergone validation in controlled and field environments. Collectively, these advances establish a robust scientific foundation for the deployment of phytoremediation as a sustainable remediation technology. The phytoremediation emphasizes three interlinked priorities. The multi omics integration into predictive models will enable system level simulations of pollutant degradation and plant microbe interactions, thereby guiding rational design of remediation strategies. The AI assisted approaches will accelerate the optimization of engineered plants and microbial consortia, tailoring interventions to cite specific contaminant profiles. The development of climate resilient and globally adaptable phytoremediation systems will ensure efficacy under diverse

ecological conditions and environmental stressors. Coupled with bio-safety frameworks, economic feasibility analyses and supportive policy structures, these innovations position molecular phytoremediation as a scalable, adaptive and globally relevant solution for environmental restoration.

CRedit author contributions

Sangeeta Bhoria: Literature search, Data analysis, Software, Poonam Khatri: Writing - original draft. Anil Kumar: Conceptualization, Resources, Supervision, Visualization,

Conflict of interests

The authors declare that they have no conflict of interest with contents of this article.

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