

REVIEW ARTICLE

Unravelling the Role of Rhizospheric Plant-Microbe Synergy in Phytoremediation: A Genomic Perspective

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Abstract: Background: Accretion of organic and inorganic contaminants in soil interferes in the food chain, thereby posing a serious threat to the ecosystem and adversely affecting crop productivity and human life. Both endophytic and rhizospheric microbial communities are responsible for the biodegradation of toxic organic compounds and have the capability to enhance the uptake of heavy metals by plants *via* phytoremediation approaches. The diverse set of metabolic genes encoding for the production of biosurfactants and biofilms, specific enzymes for degrading plant polymers, modification of cell surface hydrophobicity and various detoxification pathways for the organic pollutants, plays a significant role in bacterial driven bioremediation. Various genetic engineering approaches have been demonstrated to modulate the activity of specific microbial species in order to enhance their detoxification potential. Certain rhizospheric bacterial communities are genetically modified to produce specific enzymes that play a role in degrading toxic pollutants. Few studies suggest that the overexpression of extracellular enzymes secreted by plant, fungi or rhizospheric microbes can improve the degradation of specific organic pollutants in the soil. Plants and microbes dwell synergistically, where microbes draw benefit by nutrient acquisition from root exudates whereas they assist in plant growth and survival by producing certain plant growth promoting metabolites, nitrogen fixation, phosphate solubilization, auxin production, siderophore production, and inhibition or suppression of plant pathogens. Thus, the plant-microbe interaction establishes the foundation of the soil nutrient cycle as well as decreases soil toxicity by the removal of harmful pollutants.

Conclusion: The perspective of integrating genetic approach with bioremediation is crucial to evaluate connexions among microbial communities, plant communities and ecosystem processes with a focus on improving phytoremediation of contaminated sites.

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1. INTRODUCTION

Accumulation of both organic and inorganic pollutants like polycyclic aromatic hydrocarbons (PAHs), pesticides, polychlorinated biphenyls (PCB), explosives, metals, metalloids and radionuclides [1-3] in soil and water resources is a global concern. These contaminants possess serious threats to the living organisms and the environment owing to their toxicity and recalcitrant nature, thus remaining in the soil for a long period [4]. They can get access to groundwater and surface water by leaching, thus contaminating water bodies. Consumption of water contaminated with toxic pollutants causes various severe anomalies in living beings. Chemical pesticides have been reported to be toxic for humans, livestock, plants, soil microbes and other insects of the crop

fields [2]. For instance, the presence of hydrocarbons and heavy metals in soil adversely affects seed germination, plant growth [5-8], soil microbial population and activities [9, 10], and the ability of plants and microbes to absorb water and nutrients from soil. Furthermore, these organic contaminants even at very low concentrations can inhibit the growth activities of soil-associated microbes and upon access to the food chain, they could cause carcinogenicity in humans and animals [4, 10, 11]. Therefore, the removal of these toxic substances from the soil is critically important for sustainability in the environment [10, 12]. The traditional methods of remediating contaminated soil and water systems by chemical and physical methods are often very cost-intensive and destruct the natural environment. Thus, phytoremediation comes into play that is considered cost-effective, solar energy-driven, eco-friendly, and *in-situ* technology to clean up the contaminated soil and restore the degraded soil system [13].

Microbial population dwelling in the zone of rhizosphere and endosphere is capable of aiding in the development of

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the root system of plants growing under the stressed conditions, thereby resulting in greater efficiency of plants to mitigate the pollutants from soil [14, 15]. Rhizobacteria are recognized to colonize in the proximity of the root system, while the endophytes colonize the internal tissues of the plant root or shoot systems, without causing any pathogenicity to the host plants [4]. Endophytic bacteria have received substantial consideration to amend the proficiency of phytoremediation as they have an intimate connection with the host plant species and are conspicuous plant growth promoters and hence can lead to enhanced forbearance and removal of the pollutant from the environment [4, 16, 17]. Microbial-assisted phytoremediation is sustainable green technology by which plants and their associated rhizosphere/endophytic communities work together in the reclamation of degraded soils [14, 15, 18, 19].

In order to ameliorate the competence of hyperaccumulator plants to remove pollutants from the environment, there has been an emphasized research on the genetic perspectives of manipulating the genes from plants, microbes, endophytes and rhizospheric microorganisms [18, 19]. With the expression of specific bacterial genes in the transgenic plants, pollutants like mercury (Hg) and selenium (Se) can be converted into less toxic forms. Overexpression of mammalian genes encoding cytochrome P450s in plants is responsible for enhanced metabolism and elimination of a range of organic pollutants like herbicides from the polluted soil [20]. Phytoremediation efficiency is the consequence of synergistic interactions between the plant's system and surrounding microbial diversity. This technology has gained importance as a feasible remediation alternative due to its eco-friendly nature and cost-effectiveness but there is always uncertainty associated with phytoremediation that whether full or rapid soil remediation would happen or not under dynamic field conditions [21].

2. ROLE OF RHIZOSPHERIC AND ENDOPHYTIC MICROBES IN PHYTOREMEDIATION

The most predominant rhizospheric microbial communities include Firmicutes, Proteobacteria, Actinobacteria, *Bacillus*, *Pseudomonas* and *Arthrobacter* [22]. It is also well reported that certain heavy metal tolerant rhizobia are capable of carrying out symbiotic nitrogen fixation. Apart from this, the symbiotic association of leguminous plants and rhizobium is popularly known for detoxification of heavy metal contaminated sites [23, 24]. Metal-microbe interaction in the rhizospheric zone is dependent upon type and concentration of metal, physicochemical parameters of soil, diversity of rhizospheric microbes and their metabolic activity [24]. Rhizospheric microorganisms residing in the close vicinity of plant roots can alter the bioavailability of metals and organic contaminants by complexation, precipitation, acidification, chelation and redox reactions. Commonly, metal bioavailability is increased by the secretion of organic acids and metal-chelating compounds, favoring the adsorption of HMs by microbial/plant biomass in the rhizosphere [24].

Rhizospheric and endophytic microbial communities can also induce biofilm formation in the vicinity of roots of host plants. Biofilm formation by the microbes enhances their ability to survive in the presence of toxic pollutants [25, 26].

Microorganisms employ various molecular mechanisms like the expression of stress-responsive genes, production of reactive oxygen species (ROS) and synthesis of certain metabolites in response to a particular type of stress to combat various abiotic stresses such as salinity, drought, extreme temperatures, heavy metal toxicity and oxidative stress [27-31]. They also secrete a slimy substance called extracellular polymeric substance (EPS) composed of carbohydrates, lipopolysaccharides, glycoproteins, and soluble proteins that possess various functional groups that help to remove/sequester metal ions from the rhizosphere through biosorption process [25, 26]. The microbiome of the plant endosphere is significantly influenced by the particular species and genotype of the host plant [19]. It also influences the alteration of the endophytes dwelling in the stress environment of the soil. Moreover, endophytes can have more close interaction with the host plant as compared to rhizobacteria because they dwell inside the plant tissues [4, 19].

Madhaiyan *et al.* (2007) stated that endophytic bacterial species, *Methylobacterium oryzae* and *Burkholderia* sp. isolated from rice plants, can considerably reduce the toxicity and accumulation of Ni and Cd along with enhancement in plant growth in *Lycopersicon esculentum* (tomato) plants [32]. Wan *et al.* (2012) revealed that endophytes can also prevent metal-induced oxidative damage by modulating the activity of antioxidative enzymes and lipid peroxidation [33]. Sessitsch *et al.* (2012) used metagenomic analysis to find out the phytoremediation potential of certain endophytic bacteria, isolated from the roots of *Oryza sativa* plants (rice plants), that can degrade aromatic and aliphatic hydrocarbons [34]. Also, the genes encoding for the production of quorum sensing molecules, specific enzymes for degrading plant polymer and various detoxification pathways for the organic pollutants were identified. This metagenomic analysis decoded the information about various degradation genes that were found naturally in abundance even though the plant and endophytes were not subjected to a contaminated environment for the study [34]. This perhaps is indicative of the ability of endophytes possessing particular genes and enzymes for the breakdown of complex organic molecules which may be secreted by plant or present in the soil as organic contaminants. The endophytic microbes play key roles in reducing the phytotoxicity of toxic metal contaminants *via* intracellular accumulation, extracellular precipitation, metal chelation or biotransformation into less toxic forms [24, 35].

Additionally, certain reports also revealed about particular microbes that can degrade toxic organic contaminants which are recalcitrant in nature. In a study by Mitter *et al.* (2013), they reported the comparative genome analysis of *Burkholderia phytofirmans* PsJN, a natural plant growth-promoting endophyte, and eight other bacterial strains, and revealed that this strain has detoxification mechanisms for degrading hydrocarbon compounds such as phytosynthates. It possesses particular genes for alkane monooxygenase (alkB), and CYP450 alkane hydroxylase (AHs) enzymes employed in degrading particular organic contaminants [20]. Additionally, this strain PsJN possess several cell surface signaling and secretion systems that permit it to interact with a diversity of plant species which helps those plants to adapt to different stress conditions [20]. Thus, this strain plays a dual role in combating the stress as well as promoting the

expression of the γ -ECS gene isolated from bacterial source that encodes for glutamylcysteine synthetase enzyme *in planta* has been known to reduce oxidative stress in plants growing in contaminated soils. This gene also enhances the tolerance and accumulation of metals and herbicides in the plant species [50-52].

Some of the popular hyperaccumulator plants for which fortification protocols are pre-established include *Brassica juncea* (Indian mustard), *Lycopersicon esculentum* (tomato), *Helianthus annuus* (sunflower), and *Liriodendron tulipifera* (yellow poplar) [48, 49]. One of the hyperaccumulator plants *Brassica juncea* was genetically modified to overexpress the desired gene *E. coli* gshII that encodes glutathione synthetase (GS) in the cytosol of the plant cell in order to increase tolerance and accumulation of cadmium (Cd) and the production of phytochelatins and its precursor glutathione. The transgenic seedlings and mature plants with the expressed gene were able to exhibit improved accumulation of Cd as compared to wild type plants and could produce increased concentrations of phytochelatins, glutathione and non-protein thiols, Ca and S [53].

Some particular genes that have been introduced in *Arabidopsis thaliana* (Brassicaceae) include SMT (selenocysteine methyltransferase), LAC1 (secretory laccase), CdPCS1 (phytochelatin synthase), AsPCS1 and GSH1 (synthases) for enhanced phytovolatilization of Se, increased resistance to 2,4,6-trichlorophenol (TCP), increased accumulation of Cd and As and enhanced phytochelatin production, respectively [54-57].

There are certain examples of transgenic hyperaccumulator plants for effective phytoremediation, as tobacco plant was transformed with *CAX-2* gene from *A. thaliana* (involved in vascular transporters) to improve the accumulation of Ca, Mn and Cd from the contaminated soil [58]; *A. thaliana* was modified with gene *Glutathione-S-transferase* from tobacco to enhance tolerance towards Al and Cu [59]; tobacco and rice plants species have been genetically engineered to overexpress *Ferretin* gene from soybean to increase iron (Fe) accumulation in plant tissues [60]; Also, *B. juncea* (Indian mustard) have been transformed with a bacterial glutathione reductase by expressing the gene in cytosol and chloroplast to make the plant tolerant to higher levels of selenium [61].

Eapen & D'Souza (2005) have also reported that *A. thaliana* engineered with *ars C* and γ -ECS genes (from *E. coli*) can transport and reduce the oxyanion arsenate (high toxicity) to arsenite (less toxic) form, within shoot tissues, where thiol peptide complexes could sequester arsenite easily [48]. In order to achieve enhanced phytovolatilization of elemental Hg, *MerA* and *MerB* genes have been expressed in certain hyperaccumulator plants which eventually increased mercury tolerance and phytovolatilization potential by several folds [62, 63]. Also, overexpression of the ACC (1-aminocyclopropane-1-carboxylic acid) deaminase gene can lead to an enhanced accumulation of several heavy metals [48, 64].

5. GENOMIC PERSPECTIVE FOR ENHANCEMENT OF PHYTOREMEDIATION

Several plants have been characterized as phytoremediator plants for several pollutants and the genomes of these

plants are considered as models since they have been partially or fully sequenced. These model phytoremediators include *Thalpi caerulescens*, now called as *Nocca caerulescens* (Zn, Ni, and Cd hyperaccumulator), *Pteris vittata* (As hyperaccumulator), *Arabidopsis halleri* (Cd and Zn hyperaccumulator, rhizostimulation of PAHs), *Brassica juncea* (capable of detoxifying Pb, Cd, Ni, As, rhizostimulation of organophosphates) and some other plants species [65-67]. The knowledge of genomic sequences can be used to identify and characterize the key genetic determinants important for the phytoremediation potential of the particular plant species and manipulation of such sequences could be exploited to enhance the phytoremediation processes like phytostabilisation, phyto-transformation, phytoextraction, phytovolatilization, etc.

One such important and revolutionary technology of genome engineering is CRISPR (clustered regularly interspaced short palindromic repeats). This tool has the potential to enhance the targeted traits in plants. CRISPR technology could be used to transfer a target set of information which is desired to be integrated into the plant genome in a candid mode [68-70]. Moreover, two variant technologies of this ground-breaking genome editing tool, *i.e.* CRISPR-Cas9 and CRISPR-Cpf1 can be employed for generating knock-outs plants (removing a particular target gene from the plant genome), targeting transcriptional regulation or making gene-substitutions in the particular plant genome of interest [70, 71]. CRISPR systems can be established for enhancing phytoremediation by targeted engineering of mechanisms involved in the complexation, accumulation, volatilization and degradation of pollutants [69] (Fig. 1).

The main focus for enhanced phytoremediation of the contaminated soil is the expression of desired genes (through CRISPR) in order to increase the synthesis of metal-binding proteins such as metallothioneins (MT) and phytochelatins (PC), metal transporter proteins (from the MATE, CDF, HMA, ZIP and YSL families), plant growth hormones (like auxins, cytokinins, gibberellic acids), and root exudates [71]. Several studies since the early 2000s have revealed that particular plant and bacterial genes when integrated with the target plant genomes could enhance the phytoremediation ability. For example, expression of NAS1 gene (responsible for encoding the enzyme Nicotianamine synthase-1) in tobacco and *Arabidopsis thaliana* plants resulted in enhanced metal tolerance for Ni, Cd, Cu, Zn, Mn and Fe [72, 73]. Similarly, the overexpression of MT encoding genes like MT1, MT2 and MTA1 in tobacco, Arabidopsis and poplar plants have enhanced the ability to accumulate heavy metals like Cd, Cu and Zn [69, 74]. The gene MT2b is also involved in the up-regulation and down-regulation of genes associated with abscisic acid synthesis and is well reported to increase the accumulation of Pb by *H. incana* plant [69, 75, 76]. Apart from the role of a genomic perspective in phytoremediation by plants, the CRISPR technology can be applicable for competent PGPR microbes as well [77]. Various literature studies have been reported on the genes responsible for the synthesis of particular plant hormones [78], phosphate solubilization, Siderophore production [79], free nitrogen fixation, etc. [80], therefore manipulating these PGPR strains with these genes of interest could beneficially affect the ability of plant-microbe synergy to combat the abiotic stress of the pollutants (Table 1). Altogether the up-gradation in the

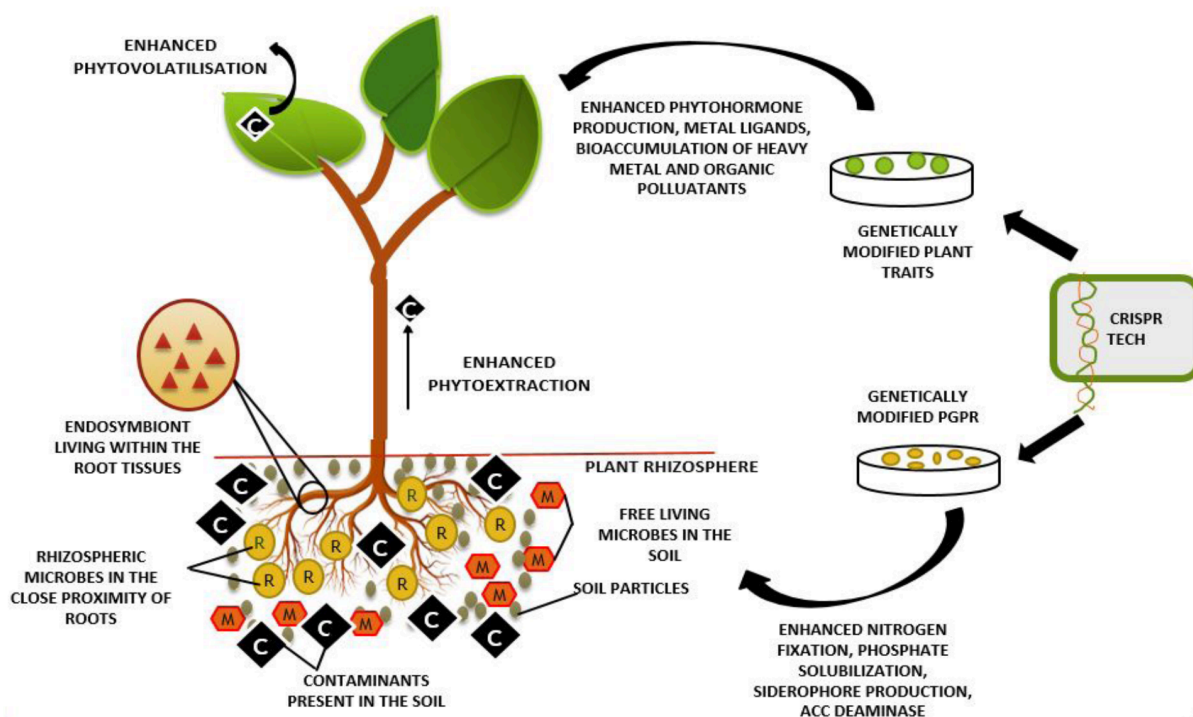


Fig. (1). The genomic perspective employing CRISPR technology in plant-microbe synergy for enhanced phytoremediation. (A higher resolution / colour version of this figure is available in the electronic copy of the article).

Table 1. Plant-microbe synergy for phytoremediation of organic and inorganic pollutants.

S. No.	Plants	Synergistic Microorganisms	Target Pollutant	Enhanced Effect on Phytoremediation	Refs.
1.	Poplar	<i>Pseudomonas putida</i> W619-TCE	TCE	Rapid TCE degradation	[4, 15]
2.	Yellow Lupine	<i>Bacillus cepacia</i> VM1468	TCE, Ni	Enhances degradation rate for TCE and increases Ni resistance in plants	[4, 15]
3.	<i>Triticum aestivum</i> (Wheat)	<i>Enterobacter</i> sp. 12J1 (endophyte)	Pyrene	Degrades pyrene and promotes plant growth by IAA and Siderophore production	[4]
4.	<i>Lycopersicon esculentum</i> (tomato)	<i>Methylobacterium oryzae</i> , <i>Burkholderia</i> sp.	Ni, Cd	Increases accumulation of Ni and Cd and simultaneously promotes plant growth	[32]
5.	<i>Populus deltoids</i>	<i>Agrobacterium radiobacter</i>	As	Increases phytoremediation and promotes plant growth by IAA and Siderophore production	[42]
6.	<i>Zea mays</i> (Maize)	<i>Microbacterium</i> sp., <i>Exophiala pisciphila</i>	Cr (VI)	Enhances phytoremediation and promotes plant growth, Reduces Cd phytotoxicity	[42, 30]
7.	<i>Spirulina platensis</i>	<i>Burkholderia</i> sp. D54	Pb, Cd, Zn, Cu	Increased uptake of metals and increased production of IAA, Siderophore, ACC deaminase, phosphate solubilization.	[43]

(Table 1) contd....

S. No.	Plants	Synergistic Microorganisms	Target Pollutant	Enhanced Effect on Phytoremediation	Refs.
8.	<i>Pteris vittata</i>	<i>Pseudomonas, Stenotrophomonas</i>	As	Enhanced phytoremediation, Siderophore production	[44]
9.	<i>Oryza sativa</i> (Rice)	<i>Bacillus aryabhatai, Pseudomonas stutzeri</i> A15	As	Alleviates As toxicity in rice, PGP properties	[45, 30]
10.	<i>Helianthus annuus</i> var (Sunflower)	<i>Pseudomonas fluorescens</i>	Pb	Increases phytohormone production, Siderophore and phosphate solubilization	[81]
11.	<i>P. trichocarpa</i> (Hybrid cottonwood)	<i>Pseudomonas</i> sp.	2, 4-dichlorophenoxyacetic acid, toluene, naphthalene	Enhances phytoremediation	[81]
12.	<i>Pisum sativum</i> (Pea) plants	<i>Pseudomonas putida</i> VM1441	Naphthalene (NAH)	40% higher degradation rate for NAH (a probable carcinogen)	[81]

plant-microbe synergy *via* genomic approaches would take phytoremediation to the higher levels, allowing the effective reclamation of the degraded natural soil systems in stipulated time frames.

CONCLUSION

The opportunities for exploiting plant-microbe synergy for remediation and detoxification of contaminated environment are numerous and diversified. The use of hyperaccumulators and other plants, along with their correlated rhizospheric microbiota and endophytes has an amplitude of potential to degrade toxic contaminants and enhance the uptake potential as well. From the genomic perspective, various approaches could be administered to produce transgenic plants and associated microbes that can degrade toxic pollutants like pesticides, polyaromatic hydrocarbons, and persistent organic pollutants or uptake heavy metals and radionuclides effectively, within a stipulated time frame. However, there are extensive possibilities for manipulation of the rhizospheric environment by engineering the plant metabolites as well as bacterial response mechanisms, as the majority of the plant-microbe interactions in this zone are complex, dynamic and influenced by a number of factors. The precedence of the CRISPR technology (targeting plants and PGPR) are vast and unexplored in the field of phytoremediation. In a similar way, the impediment associated with these genomic approaches to produce transgenic for phytoremediation should be assessed by conducting field trials to know their ecological impact. Hence, the advancement in the role of plant-microbe synergy would ameliorate the phytoremediation prospects as well as result in efficacious reclamation of the deteriorated soil and water systems.

CONSENT FOR PUBLICATION

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CONFLICT OF INTEREST

The authors declare no conflict of interest, financial or otherwise.

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