

Review on Bioremediation of Metal Contaminated Soils

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Rapidly increasing population and industrialization are the major factors in environmental degradation.

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polluted sites with investigation of insoluble hydrophobic substrates turnover in the environment catalysed by microorganisms [13], role of composting processes in effective treatment of soil pollutants [14], and analysis of tar oil contaminated soil characteristics for effective treatment plan [15]. Guangming Zeng and group from China have reviewed the list of bacterial and fungal species that can tolerate polycyclic aromatic hydrocarbons and heavy metal combined pollution. They provided insights on bioremediation mechanisms by microbes under such contaminated environments [16].

bioremediation technology and mechanism of heavy metal uptake by microorganisms wiof di"

All the above mentioned research groups are extensively working on development of bioremediation strategies for decontaminating the polluted environment. However, they have not yet utilized genomics approach for exploring microbial diversity at the contaminated site. Genome-wide DNA sequencing is a potent technique to study diversity, distribution and composition of microbial community which has aided in providing some novel postulates with respect to microbial catabolic potential, metal tolerance, enzymatic activity, phylogenetic profile in long term polluted environments [17,18]. Genome sequencing and comparative genomics enabled the identification of potential genes for biodegradation of aromatic compounds and copper homeostasis in non-pathogenic *Mycobacterium* spp. and suggested the role of this group of *Mycobacterium* spp. in bioremediation as well as the evolution of copper homeostasis within the *Mycobacterium* genus [19]. Genome-based analysis resolved the metagenomics of a bioremediation system for degradation of thiocyanate in mine water containing suspended solid mineral tailings. The results from this investigation have provided novel insights into the community composition of the industrially relevant community, giving potential for improved process control [20]. Genome sequences of three *Psychrobacter* sp. strains made it possible to identify the genes related to mercury detoxification, heavy metals and antibiotic resistance, showing their potential applications in bioremediation [21]. Further, complete genomic sequences of bacteria *Arthrobacter* sp. strain LS16, *Achromobacter* sp. B7 provided potential for their applications in bioremediation and bioproducts [22,23]. The increasing availability of microbial genome sequences involved in processes important in bioremediation may provide a good approach to develop models that can be truly predictive for evaluating the probable response of subsurface microorganisms to possible bioremediation approaches prior to implementation [24].

National Status of Bioremediation of Metal Contaminated Soils

Many research groups from India are working on bioremediation of heavy metal contaminated environment. One of the research group conducted study to assess the phytoremediation potential of *Coriander sativum* for heavy metals lead and Arsenic contaminated soil, collected from an industrial area of Govindpura, Bhopal, Madhya Pradesh [1]. Basha and Rajaganesh studied the textile industry dye effluents from Komarapalayam, Tamil Nadu for bacterial bioremediation of heavy metals [25]. Another research group investigated the abilities of microorganisms and plants in terms of tolerance and degradation of heavy metals. They have also discussed the advances in remediation technologies and strategies to explore these immense and valuable biological resources for the bioremediation. Genetic and molecular basis of metal tolerance in microbes were conferred with special reference to the genomics of heavy metal accumulator plants and the identification of functional genes involved in tolerance and detoxification [26]. A review by Yadav et al. describes about

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