

Review on Bioremediation of Metal Contaminated Soils

Yamini Agrawal¹, Isha Gunwal² and Payal Mago^{1*}

¹Shaheed Rajguru college of Applied Sciences for Women, University of Delhi, New Delhi, India

²Sri Aurobindo College, University of Delhi, New Delhi, India

*Corresponding author: Payal Mago, ShaheedRajguru college of Applied Sciences for Women, University of Delhi, New Delhi, India, Tel: 9711169572; E-mail: payal500@hotmail.com

Received date: June 17, 2020; Accepted date: July 01, 2020; Published date: July 08, 2020

Copyright: © 2020 Yamini A, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Abstract

Rapidly increasing population and industrialization are the major factors in environmental degradation. Development of eco-friendly approach to reduce environmental contamination is an issue in great demand. The challenge is to build up a cost-effective and safer technology for cleaning up of contaminated environments. Bioremediation is promising new technology to decontaminate polluted surroundings. Heavy metals are the major toxic non-biodegradable environmental pollutant and their cleanup from environment is a chief concern. Several conventional physical and chemical technologies have already been employed for their removal but majority of them are not very flourishing in terms of their cost and efficacy. Therefore, we present a review on status of studies employing biological materials (microbes and plants) for heavy metal removal and recovery.

Keywords: Microbial remediation; Phytoremediation; Heavy metals; Metagenomics

Introduction

Modern lifestyle, population rise, industrial activities and urbanization has largely elevated the release of large amounts of metal contaminants (such as arsenic, cadmium, copper, lead, mercury, nickel, zinc, etc.) into the environment. Landfill, mining industries and refineries are the potential contamination sites containing large amount of inorganic toxic waste that impose huge threat to human life and environment. Continued exposure and accumulation of these heavy metals deleteriously affect the biota by creating oxidative stress in the body, impairing significant biological functions which could ultimately lead to cell death [1]. There is, therefore, an urgent need to hunt environment friendly measures for these accumulated heavy metals at contamination sites. Bioremediation of metal polluted sites using plants and microbes is one such cost effective alternate, having potential to refurbish metal contaminated environments. However, there is a limited understanding of microbial metabolism of accumulated metals at such sites that restricts its precise implementation. Progress in research projects are therefore in demand to understand the molecular mechanism of microbes (culturable as well as non-culturable) in bioremediation and to evaluate their remediation potency using genome-enabled experimental techniques. Application of genome-scale microbial models to bioremediation has become quite feasible these days due to the complete genome sequencing of microorganisms that aid in providing visions on genes related to the microbial sensitivity towards metal contaminants in the soil. Further, microbial diversity analysis using metagenomics approaches would provide data related to community composition, relative abundance of microbes at the specific habitat (such as contaminated soil) that would be helpful in designing potential bioremediation strategies at a particular site.

International Status of Bioremediation of Metal Contaminated Soils

Heavy metal pollution is a major environmental problem worldwide. A lot of research therefore has focused on bioremediation strategies to overcome this issue. Leading researchers in this field are OlubukolaOlurantiBabalola and group from Florida. They have been interested in understanding the plant-soil microbe interactions, rhizospheremetagenomics, symbiosis and aspects of stress tolerance with intend to provide effective biocontrol products. For this, they have surveyed various mining sites for heavy metal pollutants and revealed the strategies adopted by bacteria to resist these heavy metals [2]. Microbial biosorbents based strategy for bioremediation of hazardous metals was further introduced [3]. D. Huguenot and group from France provided the comparative account of bioremediation strategies for contaminated environment. They have established that the collective utilization of plant and bacteria was the most helpful alternative for the management of the polluted soil, in comparison to natural attenuation, bioaugmentation or phytoremediation strategies alone [4]. Further, various bioremediation strategies: bioleaching, bioimmobilization and bioaugmentation- assisted phytoextraction for copper-contaminated soils have also been described by their research group [5]. Jae-Seong So and group from Korea were involved in bioremediation of heavy metals using isolated bacteria, bacterial mixtures and microbially induced calcite precipitation method [6-8]. Their results show that the use of bacterial mixtures and microbially induced calcite precipitation based sequestration of soluble heavy metals via coprecipitation with calcite would be useful for toxic heavy metal bioremediation from the contaminated environment. A. Sumiahadi and group from Turkey and Indonesia have emphasized on phytoremediation technology [9]. They have tested plant physiology with heavy metal in artificial contaminated soil [10]. KawtarFikri-Benbrahim and group from Morocco have explored Rhizobium-legume symbioses as an effective tool to refurbish heavy metal contaminated soils [11,12]. Matthias Kästner and group from Germany provided the valuable contribution to the assessment of potential remediation action at polycyclic aromatic hydrocarbons

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].

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

bioremediation technology and mechanism of heavy metal uptake by microorganisms with the information pertaining to sources and effects of various heavy metals on plants and human health. They also reported some potential species of microorganisms and plants which are commonly used for heavy metal removal [27]. A study conducted on samples of sewage, sludge and industrial effluents from sewage treatment plants at Karnal, Panipat and electroplating industry at Sonapat indicated the potential of fungi as biosorbent for removal of heavy metals from wastewater and industrial effluents containing higher concentration of heavy metals [28]. The biosorption ability of bacterial strain *Bacillus thuringiensis* OSM29 recovered from rhizosphere of cauliflower grown in soils irrigated by metal contaminated water, near Aligarh, North India was examined. It was observed that the metal biosorbing ability of *B. thuringiensis* OSM29 was fairly rapid which could be an advantage for large scale treatment of contaminated sites [29]. Further, a study on isolation of heavy metal tolerant microbes from sewage water collected from different localities (domestic, industrial and agricultural sites) of Jabalpur, Madhya Pradesh, India recommended that isolated *Bacillus* sp. has the properties to resist a wide range of heavy metals and antibiotics [30]. All these studies have reflected the widened research and development scope of microbes as potential agent for bioremediation of heavy metals polluted environment. However, so far genome wide diversity analysis of microbes has not been performed for any contaminated site in India, to select a better and specific target agent.

Conclusion

As it will be clear from above mentioned research status that so far utilization of genomic tools in bioremediation is naïve, quite a few studies from India and abroad have explicitly utilized genome-wide approaches to decipher molecular basis of microbial mechanisms in bioremediation. Also there is a lack of implementation in confident designing of bioremediation strategies for metal contaminated sites. Therefore studies exploring the remediation capacity of heavy metals by microbial remediation and phytoremediation processes are much desirous.

References

- Gaur N, Kukreja A, Yadav M, Tiwari A (2017) Assessment of phytoremediation ability of *Coriander sativum* for soil and water co-contaminated with lead and arsenic. *Biotech* 7:196.
- Fashola MO, Ngole-Jeme VM, Babalola OO (2016) Heavy metal pollution from gold mines: environmental effects and bacterial strategies for resistance. *Int J Environ Res Public Health* 13: 1047.
- Ayangbenro AS, Babalola OO (2017) A new strategy for heavy metal polluted environments: A review of microbial biosorbents. *Int J Environ Res PubHealth* 14:94.
- Agnello AC, Bagard M, van Hullebusch ED, Esposito G, Huguenot D (2016) Comparative bioremediation of heavy metals and petroleum hydrocarbons co-contaminated soil by natural attenuation, phytoremediation, bioaugmentation and bioaugmentation-assisted phytoremediation. *SciTotal Environ* 563:693-703.
- Cornu JY, Huguenot D, Jezequel K, Lollier M, Lebeau T (2017) Bioremediation of copper-contaminated soils by bacteria.
- Kang CH, Han SH, Shin YJ, Oh SJ, So JS (2014) Bioremediation of Cd by microbially induced calcite precipitation. *ApplBiochemBiotechnol* 172:1929-193.
- Kang CH, Oh SJ, Shin YJ, Han SH, Nam IH, et al. (2015) Bioremediation of lead by ureolytic bacteria isolated from soil at abandoned metal mines in south korea. *EcolEng* 74:402-407.

8. Kang CH, So JS (2016) Heavy metal and antibiotic resistance of ureolytic bacteria and their immobilization of heavy metals. *EcolEng* 97:304-312.
9. Sumiahadi A, Acar R (2018) A review of phytoremediation technology: Heavy metals uptake by plants. *Earth Environ Sci* 142:012-023.
10. Sumiahadi A, Dursun S, Acar R (2017) Investigation of pea tolerance to chromium in artificially polluted soil. The fourth international conference on sustainable agriculture and environment, Surakarta, Indonesia.
11. Lebrazi S, Kawtar FB (2015) Environmental stress conditions affecting the N₂ fixing rhizobium-legume symbiosis and adaptation mechanisms. *African J Microbiol Res* 8:4053-4061.
12. Lebrazi S, Kawtar FB (2018) Rhizobium-legume symbioses: Heavy metal effects and principal approaches for bioremediation of contaminated soil.
13. Rein A, Adam IKU, Miltner A, Brumme K, Kästner M, et al. (2016) Impact of bacterial activity on turnover of insoluble hydrophobic substrates (phenanthrene and pyrene)-model simulations for prediction of bioremediation success. *J Hazard Mater* 306: 105-114.
14. Kästner M, Miltner A (2016) Application of compost for effective bioremediation of organic contaminants and pollutants in soil. *ApplMicrobiolBiotechnol.* 100:3433-3349.
15. Trellu C, Miltner A, Gallo R, Huguenot D, van Hullebusch ED, et al. (2017) Characteristics of PAH tar oil contaminated soils-black particles, resins and implications for treatment strategies. *J Hazard Mater.* 327:206-215.
16. Liu SH, Zeng GM, Niu QY, Liu Y, Zhou L, et al. (2017) Bioremediation mechanisms of combined pollution of PAHs and heavy metals by bacteria and fungi: A mini review. *BioresourTechnol* 224:25-33.
17. Daquiado AR, Kuppusamy S, Kim SY, Kim JH, Yoon YE, et al. (2016) Pyrosequencing analysis of bacterial community diversity in long-term fertilized paddy field soil. *App Soil Ecol* 108: 84-91.
18. Kuppusamy S, Thavamani P, Megharaj M, BokLee Y, Naidu R (2016) Pyrosequencing analysis of bacterial diversity in soils contaminated long-term with PAHs and heavy metals: Implications to bioremediation. *J HazardMater* 317:169-179.
19. Das S, Pettersson BM, Behra PR, Ramesh M, Dasgupta S, et al. (2015) Characterization of three *Mycobacterium spp.* with potential use in bioremediation by genome sequencing and comparative genomics. *Genome BiolEvol* 7:1871-1886.
20. Rahman SF, Kantor RS, Huddy R, Thomas BC, van Zyl AW, et al. (2017) Genome-resolved metagenomics of a bioremediation system for degradation of thiocyanate in mine water containing suspended solid tailings. *Microbiol* 6: e446.
21. Lasa A, Romalde JL (2017) Genome sequence of three *Psychrobacter sp.* strains with potential applications in bioremediation. *Genomics Data* 12:7-10.
22. Hassan I, Eastman AW, Weselowski B, Mohamedelhassan E, Yanful EK, et al. (2016) Complete genome sequence of *Arthrobacter sp.* strain LS16, isolated from agricultural soils with potential for applications in bioremediation and bioproducts. *Genome Announ* 4: e01586.
23. Méndez V, Hernández L, Salvà-Serra F, Jaén-Luchoro D, Durán RE, et al. (2018) Complete genome sequence of the hydrocarbon-degrading strain *Achromobacter sp.* B7, isolated during petroleum hydrocarbon bioremediation in the valparaiso region, chile. *Microbiol Res Announ* 7: e01326.
24. Scheibe TD, Mahadevan R, Fang Y, Garg S, Long PE, et al. (2009) Coupling a genome-scale metabolic model with a reactive transport model to describe in situ uranium bioremediation. *Microbial Biotechnol* 2: 274-286.
25. Basha SA, Rajaganesh K (2014) Microbial bioremediation of heavy metals from textile industry dye effluents using isolated bacterial strains. *Int J CurrMicrobiol App Sci* 3:785-794.
26. Dixit R, Wasiullah, Malaviya D, Pandiyan K, Singh UB, et al. (2015) Bioremediation of heavy metals from soil and aquatic environment: An overview of principles and criteria of fundamental processes. *Sustainability* 7: 2189-2212.
27. Yadav KK, Gupta N, Kumar V, Singh JK (2017) Bioremediation of heavy metals from contaminated sites using potential species: A review.
28. Joshi PK, Swarup A, Maheshwari S, Kumar R, Singh N (2011) Bioremediation of heavy metals in liquid media through fungi isolated from contaminated sources. *Indian J Microbiol* 51:482-487.
29. Oves M, Khan MS, Zaidi A (2013) Biosorption of heavy metals by *Bacillus thuringiensis* strain OSM29 originating from industrial effluent contaminated north indian soil. *Saudi J Biological Sci* 20:121-129.
30. Gupta MK, Kiran K, Amita S, Shikha G (2014) Bioremediation of heavy metal polluted environment using resistant bacteria.