

## Exploring genetic basis for metal accumulation in plants

Qaisar Mahmood\*

Department of Environmental Sciences, COMSATS Institute of Information Technology, Abbottabad 22060, Pakistan

**Correspondence\***: mahmoodzju@gmail.com | +92-992383591 Ext. 312

Global developments interrelated with environmental issues produced systemic hazards entirely not on the single elements of that system (EEA, 2010). Similarly, environmental issues causes a systemic disturbance to environment by climatic change, reduction of natural resources, decline of biodiversity and the degradation of natural ecosystem (McMichael et al., 2009). The contamination of environment by the presence of toxic metals and organics is global in prevalence. The developed countries spent significant sum of their GDP on the clean up of the contaminated sites and environmental management. However, developing countries and under developed nations face serious financial crisis of resources to deal with such contaminants. Such critical condition demands effective low cost solutions to this menace. Phytoremediation has emerged a low cost solution to clean up metal and some organic pollutants where indigenous plant species are employed. Phytoremediation is being acknowledged as a cost effective technology for the removal, degradation and detoxification of hazardous chemicals from polluted soil, sediments and water bodies by using green plants (Clayton 2007). The choice of plant species involved in restoration of contaminated sites depends on a number of factors like plant habit, biomass production, root to shoot ratio, ethno botanical use, and post-harvest considerations etc. Phytoremediation is site specific treatment system that has an important interrelationship between plants roots, microorganisms of rhizosphere, metals and

soil. Integration of various bioinformatics tools and databases associated with biochemistry and the genetics of microbial degradation of chemicals have recently been discussed by Arora and Bae (2014). Such modern biotechnological and bioinformatics tools may be employed to improve phytoremediation of plants of interest. The use of bioinformatics tools for annotation of biodegradation related genes, predicted from the whole genomes of potential contaminant degrading bacteria may be quite beneficial. The automated Sanger sequencing method is referred to as first generation sequencing technology, and newer commercial sequencing methods from Roche/454, Illumina/Solexa, SOLiD/Life/APG, Helicos BioSciences, and the Polonator Instrument are often included in next-generation sequencing (NGS) technologies (Metzker, 2010). The field of bioremediation and biodegradation has entered into the (meta) omics era (from genomics to metabolomics) with recent advances in NGS. Many contaminant degrading bacterial genome sequences have been subjected to NGS technology and subsequent genes related to contaminant degradation have been identified by in silico prediction and annotation of metabolic pathways, to gain an holistic understanding of the metabolic network of an interesting bacterium (Lee et al., 2012). Further investigation on the genetic expression related to plant tolerance against toxic pollutants will be quite handy in efficient management of polluted sites.

## References

- Adriano, D. C., 2001. Trace element in Terrestrial Environments: Biochemistry, Bioavailability, and Risks of Metals, Chapter 6: Ecological and Health Effects of Chromium, 2nd Edition. Springer, p.333-337.
- EEA, 2010, The European environment — state and outlook 2010: synthesis, European Environment Agency, Copenhagen, Denmark.
- McMichael, A., Neira, M., Bertollini, R., CampbellLendrum, D. and Clayton LR (2007) Phytoremediation. Encyclopedia of plant and crop science. Taylor & Francis, London, UK.
- Arora PK, Bae H. Integration of bioinformatics to biodegradation. Biological Procedures Online. 2014;16:8.
- Metzker ML. Sequencing technologies—the next generation. Nature Reviews in Genetics. 2010;11:31–46.
- Lee SH, Jin HM, Lee HJ, Kim JM, Jeon CO. Complete genome sequence of the BTEX-degrading bacterium *Pseudoxanthomonas*

Citation: Mahmood, Q., 2017: Exploring genetic basis for metal accumulation in plants. *Bulletin of Environmental Studies* 2(1): xx-xx.

Copyright © 2017 Mahmood. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) or licensor are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.