



Genome-wide Modulation in Transcriptome of Rice Root During Heavy Metal Toxicity

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ABSTRACT: Heavy metal pollution is one of the greatest ecological problems on the Earth. It has been reported that increase in concentration of heavy metals such as arsenic (As), cadmium (Cd), chromium (Cr) and lead (Pb) in the soil and water results in the growth inhibition, toxicity and enhanced accumulation in plant parts as well as causes severe human health hazards. Numerous studies have been carried out to study biochemical and molecular processes involved in uptake and translocation of specific heavy metals from soil by plants which suggested that most of the physiological and molecular processes affected by different heavy metals are similar to those affected by other abiotic stresses. To identify common and unique responses by different metals, a comparative analysis of oxidative stress and modulation in root transcriptome under exposure to different heavy metals [As(V), Cd, Cr(VI) and Pb] in rice have been carried out in hydroponic condition. We observed that root tissue shows variable responses for antioxidant enzyme system for different heavy metals. Genome-wide expression analysis suggested variable number of genes differentially expressed in root in response to As(V), Cd, Pb and Cr(VI) stresses. In addition to unique genes, each heavy metal modulated expression of a large number of common genes. Our study advances the knowledge about specific responses, genes and networks involved during heavy metal stress which might be responsible for heavy metal accumulation, responses, tolerance and detoxification. © 2016 iGlobal Research and Publishing Foundation. All rights reserved.

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