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Transcriptome -wide modulation combined with morpho-physiological analyses of Typha orientalis roots in response to lead challenge

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Abstract

Lead (Pb) is a common pollutant in many environments, including in the soil, water, and/or air. Typha orientalis Presl, a large emergent aquatic plant, has been reported to function as a Pb-tolerant and Pb-accumulating plant; however, very little molecular information regarding the tolerance of T. orientalis towards Pb is known. In this study, Pb accumulation and key factors involved in the Pb stress response at different Pb concentrations were investigated. Pb was primarily accumulated in the roots and was mainly located in the cell wall and membrane systems. Differentially expressed genes (DEGs) were identified in T. orientalis roots after Pb exposure via RNA-seq analyses. In the 0.10 mM and 0.25 mM Pb2+-treated groups, a total of 3275 DEGs were detected relative to the control. Many of these genes were associated with oxidation-reduction processes, metal transport, protein kinase/phosphorylation, and DNA binding transcription factors, which were shown to be Pb-responsive DEGs. Mapping Kyoto Encyclopedia of Genes and Genomes (KEGG) database, "phenylpropanoid biosynthesis" was analyzed as the major pathway of the important modules of overlapping DEGs of 0.10 mM and 0.25 mM Pb2+ treatments. Furthermore, a lead response gene named ToLR1 with unknown function was of particular interest. The full-length of ToLR1 sequence was cloned using rapid amplification of cDNA ends (RACE) and overexpressed in Arabidopsis thaliana, which resulted in enhanced resistance to Pb stress. This is the first report providing genomic information detailing Pb responsive genes in T. orientalis. Moreover, this study provides novel insights into the molecular mechanisms underlying the response of T. orientalis and other accumulators towards Pb stress. The key genes identified in this study may serve as potential targets for genetic engineering targeting phytoremediation.

Key words: Pb stress; RNA sequencing; RT-qPCR; ToLR1; Transcriptomics; Typha orientalis

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