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Genome-wide transcriptome analysis reveals that chromium stress signalling controls the expression of genes in glutathione metabolism in rice

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Widespread use of chromium (Cr) contaminated fields due to careless and inappropriate management practices of effluent discharge, mostly from industries related to metallurgy, electroplating, production of paints and pigments, tanning, and wood preservation elevates its concentration in surface soil and eventually food chain becomes contaminated due to accumulation in edible plant parts and causes several health hazards in humans as well as animals. In contrast to other heavy metals like cadmium, lead, mercury and arsenic, Cr has received little attention from plant scientists. Since Cr (VI) causes toxic effects directly or indirectly sodeciphering the detoxification mechanism is often desirable to counteract such issues. Transcriptomics analysis revealed that the expression of several genes was modulated in roots by Cr (VI). Most of the genes differentially expressed were related to glutathione metabolism, transport, and signal-transduction pathways. However, somewhat unexpectedly, up-regulation of phytochelatin synthase was not detected in our transcriptome analysis suggesting that PCs are not involved in Cr (VI) detoxification. This might be due to their nonresponsive behaviour to Cr (VI) stress, which is in agreement with previous report. On the contrary, in our study it is clear that glutathione plays an important role for detoxification of Cr-stress. Simultaneous analysis of microarray and metabolite content also suggested that sucrose degradation pathway was modulated in Cr stress response involving three main fermentation pathways operating as a rescue mechanism when respiration is arrested. In the subsequent study we identified two root specific Tau class GSTs (OsGSTU30 and OsGSTU41) which specifically up-regulated when exposed to Cr (VI). Over expressing these two OsGSTs in S. pombe resulted in an enhanced resistance to Cr (VI) and OsGSTs-expressing yeast accumulated larger amounts of Cr (VI) than the vector control. Similarly, the transgenic yeasts also showed higher GST enzyme activities. Inhibition of glutathione biosynthesis by exogenous application of buthionine sulfoximine (BSO) abolishes the protective effect of OsGSTs against Cr (VI) stress which suggests a possibility that specific Tau class of GSTs are conserved in rice for binding with Cr (VI) and its homeostasis and detoxification.

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