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Identification of Differentially Accumulated Proteins Involved in Regulating Lead Stress in Sorghum Seedling Roots

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[Introduction]

Roots are important organs in plants that uptake water and nutrients from soil, and perceive and transduce various soil signals to shoots, which induce a suite of physiological, morphological, and molecular responses in the whole plant. Lead (Pb) is one of the most hazardous pollutants of the environment that is an ecological concern due to its impact on human health and the environment. In the present investigation, a high throughput proteome technique was performed to explore the differentially expressed proteins that are potentially involved in different level of Pb stress. Our results from the proteome level provide new evidence for further understanding the molecular mechanisms of the plant abiotic stress response.

[Materials and Methods]

Seeds of *Sorghum bicolor* L. (BTX 623) were surface sterilized, placed in petri dishes containing two layers of filter papers moistened with de-ionized water. For Pb-treatment experiments, three replicates each consisting of seven seedlings were included for both control and Pb treatment. After 5 days of Pb-treatment, the seedling roots were harvested and performed morpho-physiological analysis, and the proteome analysis were performed using gel-free proteome techniques.

[Results and Discussion]

In this study, we aimed to identify differentially accumulated proteins (DAPs) involved in Pb stress responses in *S. bicolor* L. Elevated Pb concentration provoked notable reduction of interacting ions uptake in the roots of sorghum seedlings. For proteomics analysis, a total of 1190 proteins was identified with ≥ 2 peptide match without filtering the LC-MS/MS proteomics data sets of which 1190 proteins, a total of 465, 413, and 312 proteins were identified in control, 500 μ M and 1000 μ M Pb treated samples, whereas 230 proteins were commonly identified in all the treatments. Totally, 96 DAPs were identified that are responsive to Pb stresses in roots that mainly involved in energy metabolism, detoxification and stress defense, and protein metabolism. Taken together, the present study may provide new insights into the molecular mechanisms of plant response to Pb stress at the protein level in sorghum.

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