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Proteome Changes of Sorghum Leaves in Response to Lead Stress using Gel-free Proteomics

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[Introduction]

The heavy metal lead (Pb) is a significant threat to human health, agricultural production and ecological safety. The mechanism of Pb uptake, accumulation and tolerance in Sorghum has not been reported and the molecular mechanism of Pb tolerance and accumulation is still not clear. Thus, there is a need to investigate the proteins and metabolic pathways associated with Pb tolerance and accumulation. One strategy could be to use proteomics to study the physiological process of adaptation to Pb stress in Sorghum.

[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 leaves were harvested and performed morpho-physiological analysis, and the proteome analysis were performed using gel-free proteome techniques.

[Results and Discussion]

The present study aimed to identify differentially accumulated proteins (DAPs) involved in Pb stress in *S. bicolor* seedlings leaves. After 15 days of Pb exposure, the total protein of the fresh leaves was extracted and analyzed using gel-free quantitative proteomics techniques. The results revealed that the growth inhibition induced by Pb depended on the degree of heavy metal concentrations. Using iTRAQ LC-MS/MS, we identified a total of 2000 proteins was identified with ≥ 2 peptide match without filtering the proteomics data sets. Among these 2000 proteins, a total of 627, 698, and 675 proteins were identified in control, 500 μ M Pb and 1000 treated samples in sorghum, whereas 525 proteins were commonly identified in all the treatments. Functional analysis indicated that the number of proteins associated with translation, protein folding and degradation, and stress and defense in response to lead stress. Protein-protein interaction analyses highlighted an energy metabolism centered sub-network that synergistically responded to Pb stress. Taken together, our results provide essential reference protein and gene information for future molecular studies into the tolerance and accumulation of Pb in Sorghum.

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