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## Leaf and Root Proteome Analysis of Sorghum in Response to Lead Stress

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### [Introduction]

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. Several investigations have postulated that plants respond to any type of stress condition via rapid alterations in gene expression and protein synthesis. Therefore, 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.

### [Material and Method]

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.

### [Result and Discussion]

The present study aimed to identify differentially accumulated proteins (DAPs) involved in Pb stress in Sorghum bicolor seedlings. After 15 days of Pb exposure, the total protein of the fresh leaves and roots was extracted and analyzed using label-free quantitative proteomics techniques. The results revealed that the growth inhibition induced by Pb depended on the degree of heavy metal concentration. The quantitative proteome analysis led to the identification of 1392 proteins, of which 627 were differentially modulated in response to Pb stress. Of the identified 627 proteins, a total of 383 proteins were specific to leaf proteins, and 244 proteins were specific to root proteins. The DAVID Bioinformatics analysis showed that the proteins with increased abundance were mainly associated with energy metabolism, detoxification and stress defense and protein metabolism, whereas the proteins related to the cell growth/division, intracellular traffic and photosynthesis were downregulated. 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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