

## Proteome analysis of roots of sorghum under copper stress

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### Abstract

*Sorghum bicolor* is considered as copper-tolerant species. The present study was conducted to understand the copper tolerance mechanism in Sorghum seedling roots. Morphological and effects of Cu on other interacting ions were observed prominently in the roots when the plants were subjected to different concentrations (0, 50, and 100  $\mu\text{M}$ ) of  $\text{CuSO}_4$ . However, the morphological characteristics were reduced by Cu stress, and the most significant growth inhibition was observed in plants treated with the highest concentration of  $\text{Cu}^{2+}$  ions (100  $\mu\text{M}$ ). In the proteome analysis, high-throughput two-dimensional polyacrylamide gel electrophoresis coupled with MALDI-TOF-TOF mass spectrometry was performed to explore the molecular responses of Cu-induced sorghum seedling roots. In two-dimensional silver-stained gels, a total of 422 differentially expressed proteins ( $\geq 1.5$ -fold) were identified using Progenesis SameSpot software. A total of 21 protein spots ( $\geq 1.5$ -fold) from Cu-induced sorghum roots were analyzed by mass spectrometry. Of the 21 differentially expressed protein spots from Cu-induced sorghum roots, a total of 10 proteins were up-regulated, and 11 proteins were down-regulated. The abundance of the most identified protein species from the roots that function in stress response and metabolism was significantly enhanced, while protein species involved in transcription and regulation were severely reduced. The results obtained from the present study may provide insights into the tolerance mechanism of seedling roots in Sorghum.

**Keywords:** Cu stress, root, metal uptake, proteome changes, sorghum

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