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Proteomic changes in leaves of sorghum exposed to copper stress in sorghum

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Abstract

Copper (Cu) is very toxic to plant cells due to its inhibitory effects on many physiological and biochemical processes. In spite of its potential physiological and economic significance, molecular characterization after Cu stress has so far been grossly overlooked in sorghum. To explore the molecular alterations that occur in response to copper stress, the present study was executed in ten-day-old Cu-exposed leaves of sorghum seedlings. The growth of shoots was markedly reduced, and ionic alterations were prominently observed in the leaves when the seedlings were exposed to different concentrations (0, 100, and 150 μM) of CuSO_4 . Using two-dimensional gels with silver staining, 643 differentially expressed protein spots (≥ 1.5 -fold) were identified as either significantly increased or reduced in abundance. Of these spots, a total of 24 protein spots (≥ 1.5 -fold) from Cu-exposed sorghum leaves were successfully analyzed by MALDI-TOF-TOF mass spectrometry. Of the 24 differentially expressed proteins from Cu-exposed sorghum leaves, a total of 13 proteins were up-regulated, and 11 proteins were down-regulated. The abundance of most identified protein species, which function in carbohydrate metabolism, stress defense, and protein translation, was significantly enhanced, while that of another protein species involved in energy metabolism, photosynthesis and growth and development were severely reduced. The resulting differences in protein expression patterns together with related morpho-physiological processes suggested that these results could help to elucidate plant adaptation to Cu stress and provide insights into the molecular mechanisms of Cu responses in C_4 plants. The over-expression of GAPDH plays a significant role in assisting *Sorghum bicolor* to attenuate the adverse effects of oxidative stress caused by Cu, and the proteins involved in resistance to stress helped the sorghum plants to tolerate high levels of Cu.

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