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Comparative proteome analysis of rice leaves in response to high temperature

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Abstract

The productivity of rice has been influenced by various abiotic factors including temperature which cause to limitations to rice yield and quality. Rice yield and quality are adversely affected by high temperature globally. In the present study, four Korean four cultivars such as Dongan, Ipum, Samkwang, Chucheong were investigated in order to explore molecular mechanisms of high temperature at seedling stage. Rice seedlings grown at 28/20°C (day/night) were subjected to 7-day exposure to 38/28°C for high-temperature stress, followed by 2-D based proteomic analysis on biological triplicates of each treatment. The growth characteristics demonstrated that Dongan is tolerant while Ipum is sensitive to high-temperature stress. High temperature has an adverse effect in the seedling stage both in high temperature sensitive and tolerant cultivar. Two-dimensional gels stained with silver staining, a total of 722 differential expressed protein spots (≥ 1.5 -fold) were identified using Progenesis SameSpot software. However, a total of 38 differentially expressed protein spots were analyzed by LTQ-FT-ICR MS. Of these, 9 proteins were significantly increased while 10 decreased under high-temperature treatment. Significant changes were associated with the proteins involved in the carbohydrate metabolism, photosynthesis, and stress responses. Proteome results revealed that high-temperature stress had an inhibitory effect on carbon fixation, ATP production, and photosynthetic machinery pathway. The expression level of mRNA is significantly correlated with the results obtained in the proteome investigation. Taken together, these findings provide a better understanding of the high-temperature resistance by proteomic approaches, providing valuable insight into improving the high-temperature stress tolerance in the global warming epoch.

Keywords: heat stress; leaves; proteome; rice

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