Proteome of rice roots treated with exogenous proline

ABSTRACT

Proteomic analysis was conducted to identify the rice root proteins induced by exogenous proline and their involvement in root growth. Proteins were extracted from the root tissues grown under two conditions, T1 (control) and T2 (10 mM proline), and profiled by twodimensional polyacrylamide gel electrophoresis. Seventeen of 30 differentially expressed proteins were identified by mass spectrometry. Proline-treated rice roots showed upregulation and down-regulation of nine and eight proteins, respectively, when compared to those in the control. Among the differentially expressed proteins, the down-regulation of glutathione reductase and peroxidase could be involved in the regulation of cellular hydrogen peroxide and reactive oxygen species levels that modulate the root cell wall structure. Differentially expressed proteins identified as pathogenesis-related proteins might be related to stress adaptive mechanisms in response to exogenous proline treatment. In addition, differentially expressed protein identified as the fructose-bisphosphate aldolases and cytochrome c oxidase might be associated with energy metabolism, which is needed during root developmental process. This is the first attempt to study the changes in rice root proteome treated with proline. The acquired information could open new avenues for further functional studies on the involvement of proline in modulating root development and its relation to stress adaptation of plants.

Keyword: Proline; Protein; Rice; Root