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**Abstract:** Rice (*Oryza sativa* L.) is the most important cereal crop in Asia, and is considered as a model cereal plant for genetic and molecular studies. Proteome analysis provides information to predict the translation and relative concentration of gene products, including the extent of modifications. Proteomic analysis provides a broad view of plant responses to stress at the level of proteins. In the present study one dimensional gel electrophoresis was used to identify proteins altered in rice tissue in response to different drought stress regimes. Proteomic approach has increased in sensitivity and power as a result of improvements in two-dimensional polyacrylamide gel electrophoresis (2DE), protein detection and quantification, fingerprinting and partial sequencing of proteins by mass spectrometry (MS), bioinformatics, and methods for gene isolation. The present study was undertaken to analyze the protein profile changes in Birsa- Dhan 101 under different regimes of drought stress. Proteins were extracted from rice tissue at different hours after stress treatment and recovery. The proteins were precipitated in acetone and were separated by one dimensional gel electrophoresis followed by silver staining. Gradient –SDS / PAGE was also done to monitor low molecular weight proteins. Additional experiments like staining with Propidium Iodide and chlorophyll analysis were also done. Many changes related to drought stress in the morphology were observed. Propidium Iodide staining and chlorophyll analysis determined how the drought is affecting the plant tissue and with the onset of stress. The chlorophyll content was also found to be decreasing. Few protein changes were also observed in the shoot samples.

**Description:** Proteomic analysis of rice (*Oryza sativa* L.) under different stress and recovery phases of drought

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