

Differential expression of proteins of rice plants (*Oryza sativa* L.) submitted to water stress

Koshino, L.L.N.¹ ; Rangel, P.H.N.²; Guimarães, C.M.²; Ferreira, M.E.^{3,4} and Mehta, A.³

¹Universidade de Brasília; ²Embrapa Arroz e Feijão; ³Embrapa Recursos Genéticos e Biotecnologia; ⁴Universidade Católica de Brasília

The genetic basis of plant tolerance to abiotic stresses such as drought is still poorly understood. Drought tolerance is a complex trait controlled by multiple loci. Genomic technology can certainly provide new insights on the expression of genes associated with the control of drought tolerance. The objective of this study was to analyze the differential expression of proteins of rice (*Oryza sativa* L.) plants submitted to water stress. In Brazil, rice is cultivated in non-irrigated areas where water is provided by natural rainfall in the rainy season (upland rice) or in intensively prepared soil with artificial irrigation (irrigated rice). Upland rice provides about 40% of the rice produced in the country. A major constraint to upland rice production is its yield variation, which is primarily due to short periods of drought stress ("veranico") during the rainy season. Increasing cost of water for irrigation represents a challenge for breeding programs to develop varieties which are more efficient in water usage. In this study, the variety of upland rice Três Meses Antigo received adequate water supply until 30 days after emergence and was then submitted to two treatments: treatment 1 - maintenance of adequate soil moisture during the plant life cycle; treatment 2 - application of only 50% of water in relation to treatment 1. Thirty days after the beginning of the water stress period, leaves were harvested and submitted to protein extraction. The proteins obtained were separated by bidimensional gel electrophoresis and visualized after silver staining. The results revealed a total of approximately 200 proteins ranging from 10 to 100 kDa and in pH from 4 to 8. Overall, a higher number of proteins was observed in treatment 1, indicating a repression of protein synthesis due to water stress. The comparison of the protein profile of treatment 1 in relation to treatment 2 revealed six major differentially expressed proteins in treatment 2, including three up- and three down-regulated. These differentially expressed proteins in the water stressed conditions are currently being identified by mass spectrometry in order to study their association with drought tolerance.

Aknowledgements: financial support provided by PADCT (projeto 68076/02) e Embrapa Macroprograma 1 (projeto 010220201).