

## MALDI-TOF analysis of storage proteins from two Brazilian rice (*Oryza sativa*) cultivars

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**Approach:** Rice (*Oryza sativa*) has a grain with high content of carbohydrates, containing in addition proteins that have essential amino acids for the human diet. **Objectives:** a) Obtain reference grain proteome for two Brazilian cultivars, representatives of the *indica* and *japonica* subspecies; b) Compare the protein profile of the two cultivars; c) Determine the difference of the amino acid sequences of some peptides from the two genotypes. **Methods:** The total protein extracts of BRS Formoso (*indica* cultivar) and BRS Bonança (*japonica* cultivar) were separated with 2D-PAGE and protein spots were digested with trypsin and analyzed on MALDI-TOF MS. To map the position of these proteins in one gel for each cultivar, called "reference gels", three different experimental gels, on the pH range of 3-11, for each genotype, were analyzed. **Results:** A reference proteomic map was obtained for each cultivar, containing all protein spots detected on the cultivars. In the reference proteomic map of BRS Formoso, 92 spots were detected, from which 28 (30.7%) were analyzed for mass spectrometry (MALDI-TOF). From these, eight showed peptide sequences homologous to proteins described in the NCBI databank. In the reference map of BRS Bonança, 119 spots were detected, from which 40 (33.6%) were analyzed for mass spectrometry, and 19 spots showed peptide sequences homologous to proteins described at NCBI. Based on the reference proteomic map of both cultivars, it was possible to obtain a putative proteomic map of rice grain storage proteins for *indica* and *japonica*, resulting from the superposition of the maps. The proteomic map showed 96 spots, considering both differential and similar spots between the two cultivars. Interestingly, there were more differences than similarities between *indica* and *japonica*, and BRS Bonança showed a greater number of spots when compared to BRS Formoso. Forty seven proteins showed no similarity with protein sequences deposited in the NCBI, revealing the low representation of current proteomic databases for rice grain proteins. This work allowed the identification of storage proteins (28%); proteins associated with cell metabolism (16%); proteins involved in stock-storage of sugar in the form of starch (36%) and proteins with unknown functions (20%). **Conclusion:** There were marked differences between *indica* and *japonica* storage protein maps, which can be explored by rice breeding programs in order to increase the nutritional value of rice cultivars due to the differential content of essential amino acids. Supported by FINEP/MCT.