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Assessing Matrix Assisted Laser Desorption/ Ionization-time of flight-Mass Spectrometry(MALDI-TOF/MS) as a means of Rapid Embryo Protein Identification in Rice (*Oryza sativa* L.)

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Objectives

In the present study, as a first step to rice grain proteome analysis, we attempt to identify rice embryo proteins by peptide mass fingerprinting using MALDI-TOF/MS. The usefulness and pitfalls of this method in the identification of rice embryo proteins is discussed.

Material and Methods

Rice seed embryos were used in this study. 2-DE was performed as described by O'Farrell with slight modifications. Molecular masses of all tryptic peptides were determined with a TofSpec-2E"MALDI-TOF-MS (Micromass, Manchester, UK) equipped with a 337 nm nitrogen laser.

Results and Discussion

Mass spectrometry is a most prevalent technique to identify rapidly a number of proteins in proteome analysis. Rice embryo proteins were separated by two-dimensional gel electrophoresis (2-DE). A total of 105 spots were digested with trypsin and the resultant peptides were analyzed by matrix assisted laser desorption/ionization-time of flight-mass spectrometry (MALDI-TOF-MS). Raw mass spectra were fully-automatically processed and searched with selected monoisotopic masses against SWISS-PROT/TrEMBL and NCBInr databases. High quality mass spectra were obtained from 53 spots, of which 36 spots were identified including 29 not registered in databases. Fifty percent of the rice embryo proteins resolved in 2-DE could not be identified, indicating more efficient sample preparation techniques need to be developed in the future. At least four to five matching peptides were found to be essential for unambiguous identification of rice embryo proteins; peptide matching of less than four lead to ambiguous results. The suitability of peptide mass fingerprinting method as a means of rapid embryo protein identification in rice was discussed.

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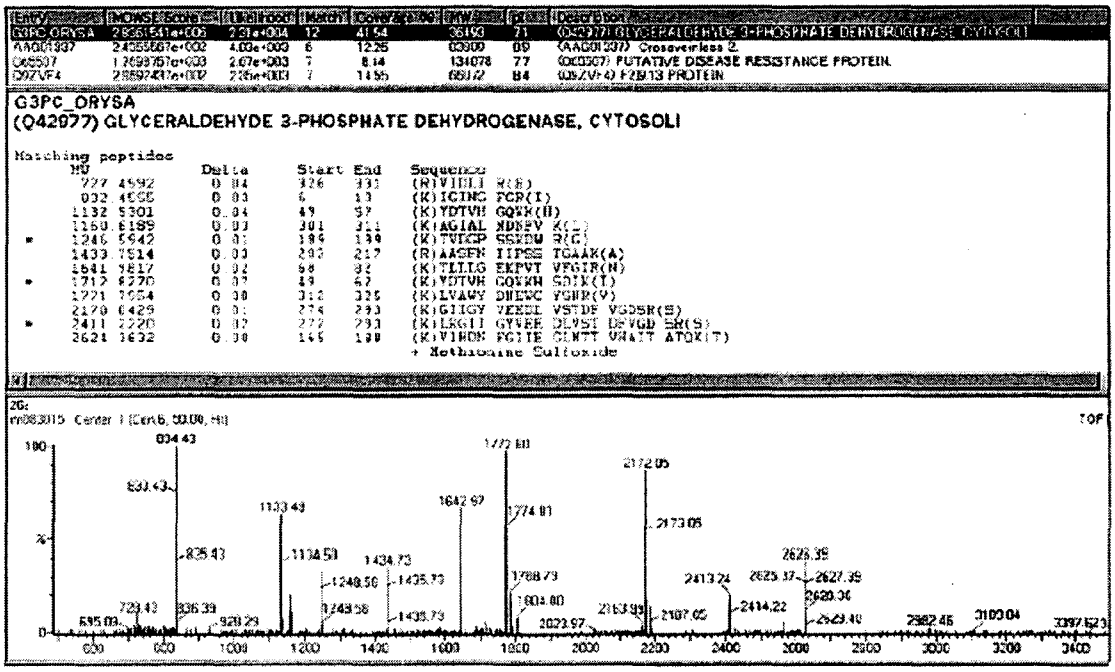

Figure 1. Peptide mass fingerprinting and database search results of spot No. 26

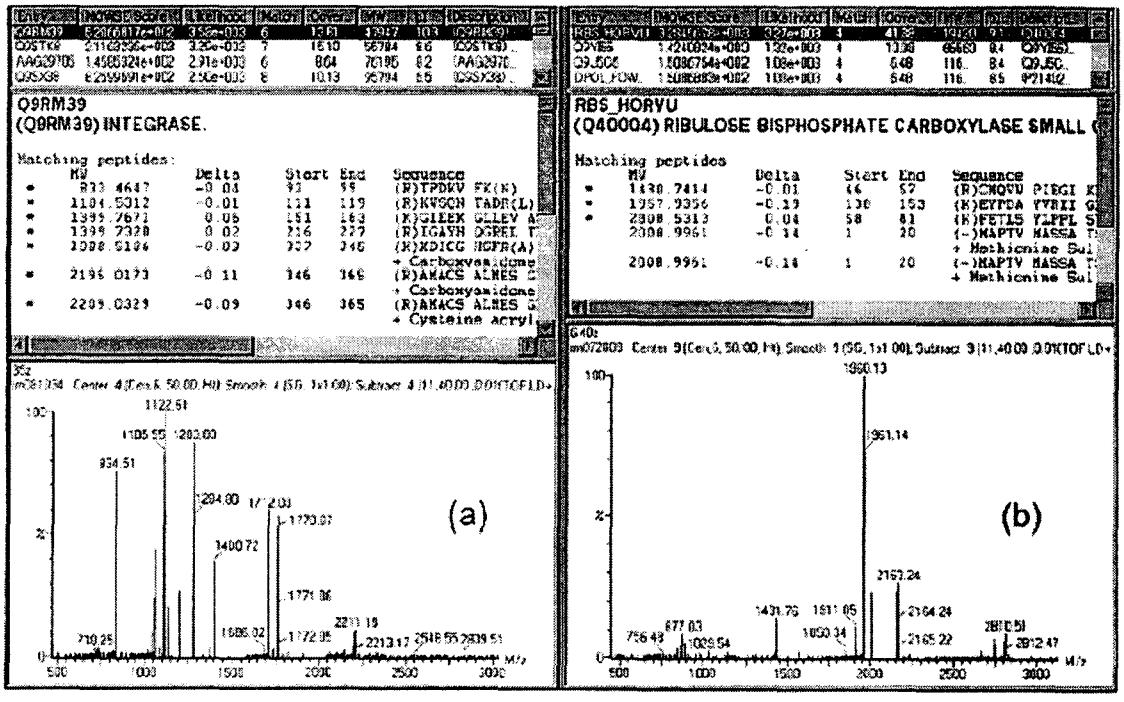

Figure 2. Peptide mass fingerprinting and database search results of spot Nos. (a) 35 and (b) 40. Both spots were observed in the 35 kDa region on 2-DE gel.