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Proteomic Approach to Analyzing Flooding Stress in Soybean (*Glycine max* (L.) Merr.)

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Objectives

The analysis of stress-responsiveness in plant is an important route to the discovery of genes conferring stress tolerance and their use in breeding programs. Comparative proteomics of seed of soybean have been used to identify specific tissue-expressed proteins. Also, we focus on proteomics as a tool for gene discovery in relation to flooding tolerance.

Material and Methods

Six varieties of soybean were used for this experiment. Seed storage proteins were examined by two-dimensional gel electrophoresis according to the protocol of O'Farrell (1975).We tried to identify the proteins that formed peptide bands in 2-DE gel by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF/MS).

Results and Discussion

Protein extracts were first prepared from soaked seed and the proteins were visualized with two-dimensional electrophoresis (2-DE). After visual comparison, the proteins spots that were differentially expressed in infected plant tissues were cut from gels and analyzed by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF/MS). Over 100 protein spots were reproducibly resolved in the two-dimensional gels from seeds. The patterns of the gels were different and little correlation among the proteins could be observed. Some proteins that were only expressed in seeds were chosen for identification by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF/MS) and peptide mass fingerprint database searching. Soaked seed proteome were also compared, with the finding that less then half of the proteins expressed in non-soaked were also expressed. Some selected flooding tolerance protein spots were identified.

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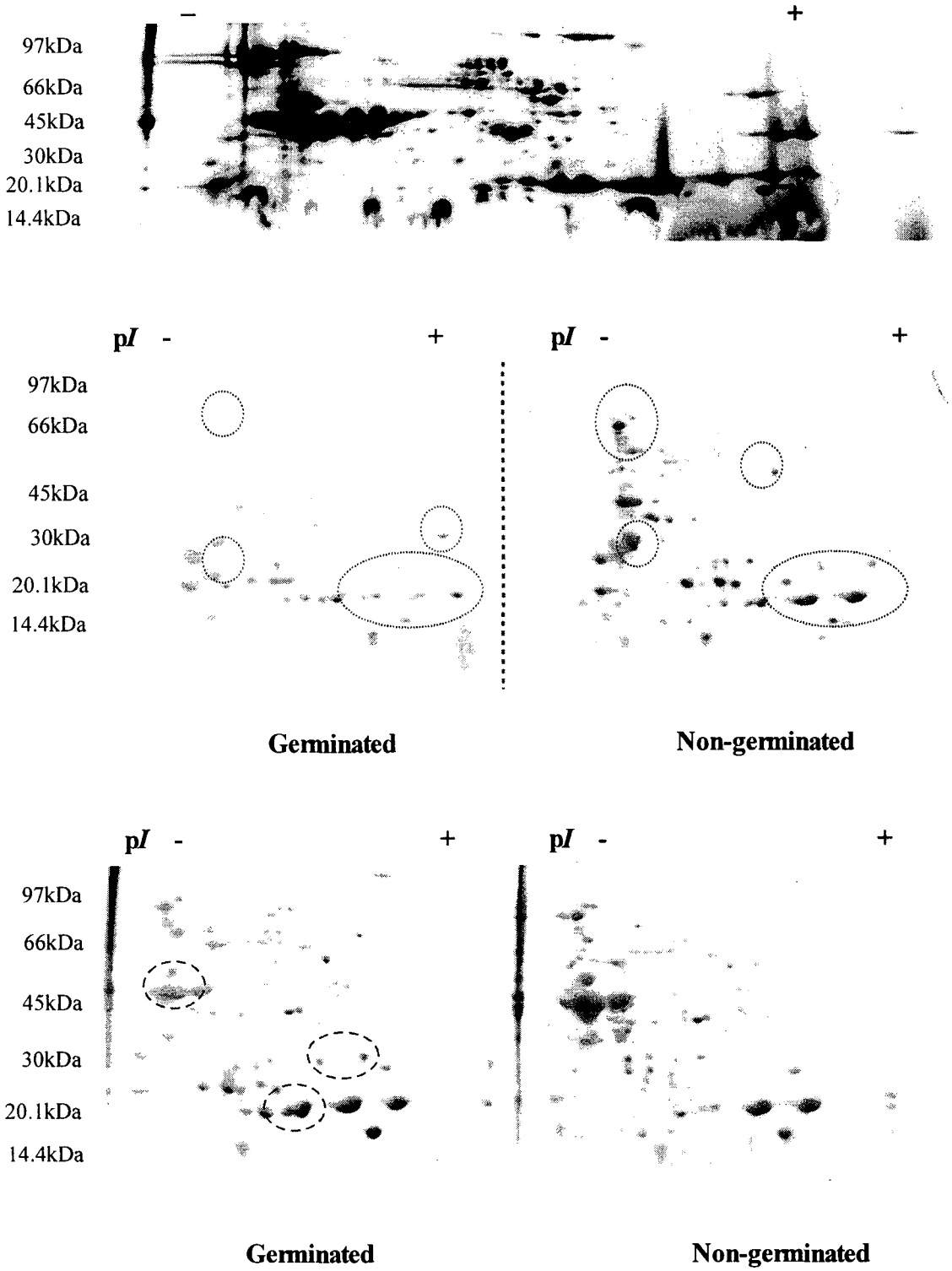

Figure 1. 2D gels of germinated and non-germinated soybean in flooded and non-flooded conditions.