

Application of Proteome Approach of Biotic Stress-responsive Proteins in Bread Wheat (*Triticum aestivum* L.)

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Proteomic techniques that allow the identification and quantification of stress-related proteins, mapping of dynamics of their expression and post translational modifications represent an important approach in the research of plant stresses. Biotic stress is one of the major stresses limiting crop productivity and the geographical distribution of many important crops worldwide. To gain a better understanding of the biotic stress responses at molecular level in dry land cereal grains, wheat (*Triticum aestivum* L.), we carried out a comparative proteomic investigation and identification of the biotic stress responses proteins in different wheat cultivars as two Korean: Keumgang, Jinpum; two Chinese: China-108, Yennon-78 and two Japanese: Norin-61, Kantou-107. Among 217 protein spots reproducibly detected from six gels, some were up regulated and few others were down regulated at least at one time. After tryptic digestion, MALDI-TOF/MS analysis and database searching of some of the identified proteins indicated that the proteins are known to be involved in several biotic stress related functions as disease associate with pathogens. Mass spectrometry analysis allowed the identification of 185 differential expressed proteins with isoforms including well known biotic stress responsive proteins. Keumgang (13%), Jinpum (8%), China-108 (14%), Yeonnon-67 (11%), Norin-61 (22%) and Kantou-107 (32%) were identified as biotic stress responses proteins directly coupled to disease and pathogen infection on wheat. The Japanese wheat cultivar “Kantou-107” showed more biotic stress related proteins than other cultivars. Nevertheless, our study provides new insights into identification of biotic stress responses protein in wheat and demonstrates the advantages of proteomic analysis.

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