PROTEOMIC CHARACTERIZATION OF SOYBEAN LEAF PROTEINS FROM CULTIVAR DT2000 WITH RUST-RESISTANT ABILITY IN VIETNAM

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TÓM TẮT:

Recently, proteomics has become one of the most promising and powerful tools for the proteome identification in plant cells. In this study, a proteomics approach was used to analyze and characterize soybean leaf proteins from a soybean rust (Phakopsora pachyrhizi Syd.) resistant soybean cultivar DT2000. Initially, nine-day-old leaf proteins were extracted from cultivar DT2000 and then separated by two-dimensional polyacrylamide gel electrophoresis (2DE). The collected protein spots were cut out, treated, trypsin-digested, and analyzed by using two-dimensional nano-liquid chromatography (LC) coupled online with tandem mass spectrometry. Results showed that 119 protein spots were found in 2DE gels. Of these, 35 leaf proteins were characterized from the cultivar DT2000. The identified proteins were classified into nine functional groups by Gene Ontology as follows: photosynthesis (29%), energy (17%), glycolysis (11%), storage (9%), metabolism (8%), transport (8%), transcription (8%), disease/defense (8%) and unknown (6%). Especially, out of 35 characterized proteins from the cultivar DT2000, three proteins related to the defense and disease resistance were discovered. The results of our study indicated that the 2DE combined with nanoLC and coupled with tandem mass spectrometry (ESI Q TRAP MSMS) analyze was a promising approach for the identification of soybean proteins