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Proteome characterization reveals the role of pollen and pistil of W22 (ga1; Ga1) in maize

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Abstract

The first key point to the successful pollination and fertilization in plants is the pollen pistil interaction, referring to the cellular and molecular levels, which mainly play active roles in limiting gene flow among maize populations and between maize and teosinte. This study was carried out to identify proteins and investigate the mechanism of gametophytic factors using protein analysis. W22 (ga1); which didn't carry a gametophytic factor and W22 (Ga1), a near iso-genic line were used for the proteome investigation. SDS-PAGE was executed to investigate proteins in the pollen and pistil of W22 (ga1) and W22 (Ga1). A total of 44 differentially expressed proteins were identified in the pollen and pistil on SDS-PAGE using LTQ-FTICR MS. Among the 44 proteins, a total of 24 proteins were identified in the pollen of W22 (ga1) and W22 (Ga1) whereas 20 differentially expressed proteins were identified from the pistil of W22 (Ga) and W22 (Ga1). However, in pollen, 2 proteins were identified only in the W22 (ga1) and 12 proteins only in the W22 (Ga1) whereas 10 proteins were confirmed from the both of W22 (ga1) and W22 (Ga1). In contrary, 10 proteins were appeared only in the pistil of W22 (ga1) and 7 proteins from W22 (Ga1) while 3 proteins confirmed in the both of W22 (ga1) and W22 (Ga1). Moreover, the identified proteins were generally involved in hydrolase activity, nucleic acid binding and nucleotide binding. These results help to reveal the mechanism of gametophytic factors and provide a valuable clue for the pollen and pistil research in maize. In addition, it might provide a comprehensive insight on the proteins that were involved in the regulation of pollen-pistil interaction.

Keywords: maize; pollen; pistil; gametophytic factors; proteomics

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