

Proteomic Analysis of Alfalfa Seeds in Response to Boron Deficiency and Toxicity Reveals Effects on Seed Yield and Quality

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Alfalfa (*Medicago sativa* L.) is one of the most important legume forage in the world because of its good quality characteristics and high adaptability, but its seed production is a complicated process that is strongly influenced by the environment and agronomic practices. Improving the seed yield is critical for the commercial development of alfalfa. Boron (B) has been recognized as an essential element for increasing seed yield and yield components in alfalfa. However, the specific functions and molecular mechanisms for B in alfalfa seeds are not clear. To investigate this question, proteomic and physiological studies were carried out on mature seeds obtained from plants grown under B deficiency (0%) and toxicity (1.6%). A combination of two-dimensional electrophoresis (2DE) and mass spectrometry (MS) approaches was used to investigate expressed proteins. 12 differentially expressed proteins were successfully identified in B deficient seeds, and 7 proteins were up-regulated while 5 proteins were down-regulated. 11 differentially expressed proteins were successfully identified in B toxic seeds, and 7 proteins were up-regulated while the others were down-regulated. The identified proteins were grouped into different categories of biological process according to GO and KEGG pathway enrichment analyses. Then the genes of selected proteins were analysed by quantitative RT-PCR. The result of this work might be helpful to understand the basic molecular mechanism of alfalfa seeds in response to B stress, and give insight into potential strategies for improving seed yield, quality and stress tolerance in alfalfa grown for seed production.

Keywords: Alfalfa; Seed; Boron; Proteomics; Deficiency; Toxicity