

Abstract

Herbal fennel, fragrant, two-year-old or perennial, is one of the most important and most used herbs of apiaceae family, which is mainly cultivated in order to use its essential oil in various industries. Water deficit stress is one of the most important abiotic stresses which adversely affect crop quality and quantity. Therefore, assessment of the molecular mechanism of sensitivity and tolerance to water deficit stress has special importance in fennel. In this study, during the two growing years (2014-2015), the stability of 19 fennel populations including 15 domestic populations and 4 external populations was evaluated in a randomized complete block design in two control and limited irrigation conditions with three replications in the Agricultural Research Station, University of Tabriz. Analysis of variance revealed a significant difference between two irrigation conditions and evaluated populations for some studied traits. As well as the population \times conditions and population \times years interactions effect was significant for all traits. Based on the morphological and physiological traits and indice of drought tolerance, Gaziantep, Khorshidabad, and Karaj were assigned as drought-sensitive populations; and Birjand, Germany11486, and Tatmaj were assigned as drought-tolerant populations; were selected for proteome analysis. The protein profiles of fennel leaves were compared using a PEG-fractionation method. Using a gel-free/label-free proteomic technique, 149, 96 and 89 proteins in Gaziantep, Khorshidabad, and Karaj; and 87, 150, 146 and 144 proteins in Birjand, Germany11486, and Tatmaj were uniquely identified in drought-sensitive and -tolerant populations, respectively. By PEG-fractionation, a total of 170 and 135 proteins were identified in drought-sensitive Gaziantep and drought-tolerant Birjand, respectively. Gel-free/label-free proteomic analysis of developing fennel seeds at the milky, hard and mature stages were performed under normal irrigation and water deficit stress conditions. A total of 137 and 106 proteins in the seed of drought-tolerant Gaziantep and a total of A total of 134 and 92 proteins were identified under normal irrigation and water deficit stress conditions, respectively. Notably, the abundance of copper/zinc superoxide dismutase was significantly increased in drought-tolerant Birjand under water deficit stress. Under water deficit stress, the abundance of glycolysis-related proteins were decreased in sensitive populations; however, they were increased in tolerance populations. In addition, cobalamin-independent methionine synthase was decreased and increased in drought-sensitive and -tolerant genotypes, respectively. These results suggest that cobalamin-independent methionine synthetase is involved in the tolerance of drought-tolerant fennel leaf under water deficit stress. Beta-glucosidase was decreased and increased in seeds of drought-sensitive and -tolerant populations, respectively. Proteins are associated with an increase in the synthesis of beta-glucosidase during water deficit stress, with the tolerance of plants against these stresses and is a factor in increasing plant tolerance to stress. Totally, preservation of relevant water statues by morpho-physiological changes, supporting natural cellular metabolism, and changes in energy and antioxidant defense relate proteins were the main factors for adaption and water deficit stress tilrance of fennel.

Keywords: Fennel, Water deficit stress, Tolerant indice, Proteome



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Thesis Submitted in Partial Fulfillment of the Requirements for PhD degree in the field of agricultural engineering, the trend of Biotechnology

Title

Evaluation and proteome analysis of sensitive and tolerant populations of *Foeniculum vulgare* Mill. under water deficit stress

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January 2018