

عنوان مقاله:

Functional Annotation of Two Hypothetical Proteins Reveals Valuable Proteins Involved in Response to Salinity: An in silico Approach

محل انتشار:

مجله منابع ژنتیک, دوره 5, شماره 2 (سال: 1398)

تعداد صفحات اصل مقاله: 11

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خلاصه مقاله:

Through the exponential development in the specification of sequences and structures of proteins by genome sequencing and structural genomics approaches, there is a growing demand for valid bioinformatics methods to define these proteins function. In this study, our objective is to identify the function of unknown proteins from UCB-1 pistachio rootstock and specify their classification using bioinformatics tools. In previous research, we recognized 5 HPs in proteomic profile of the University of California at Berkeley I pistachio rootstock leaf under salinity stress. Two of them had 2.95 and 2.29-fold up-regulation under salinity stress. In this study, the probable function and characterization of these HPs were recognized using different statistical methods and programs. According to our analyses, these HPs have similarities with reverse transcriptase enzyme as well as helicase enzyme and some responsive proteins to salt stress. These observations suggest a close relationship between the overexpression of these enzymes and plant responses to salinity stress. These stress-responsive proteins could provide a novel plant defense strategy in response to salinity.

کلمات کلیدی:

Hypothetical protein, UCB-1 pistachio rootstock, Response to salinity, Reverse transcriptase enzyme

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