

عنوان مقاله:

Genome-Wide Identification and Functional Analysis of Genes Expressed in salt tolerance of Barley

محل انتشار:

سومین کنگره بین المللی و پانزدهمین کنگره ملی ژنتیک ایران (سال: 1397)

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خلاصه مقاله:

In recent years, an explosion has been made in advancing high tech techniques to achieve and demonstrate different aspects of the gene. Use these new technologies has made it possible to identify new connections between genes with higher resolution. The microarray is a tool for measuring and gaining information from the expression of genes. Barley is a plant that is resistant to non-biological stresses. So it can be used as a robust model plant for studies. In this study, salinity-tolerant genes were collected through two methods including microarray and resource review. Then, for each category, the gene network was reconstructed by the string software. By drawing on protein-protein interactions with Cytoscape software and using computational algorithms defined candidate genes. For each of the identified genes, promoter analysis was performed with plant care. It was found that most genes were candidates for the heat shock proteins such as HSP70, HSP70-15, and functional proteins such as SBPASE, P5CS1. The promoter analysis of the dominant commonality between these genes was mostly responsive to methyl jasmonate and temperature and photosynthesis. Which indicates that jasmonic acid plays a special role in non-biological stresses, especially salinity.

کلمات کلیدی:

Gene network, Barley, salt tolerance, promoter analysis

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