

عنوان مقاله:

Constructing barley PPIN using divergence time and interolog as two major evolutionary information

محل انتشار:

هشتمین همایش بیوانفورماتیک ایران (سال: 1397)

تعداد صفحات اصل مقاله: 1

نویسندگان:

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خلاصه مقاله:

Proteins perform their complicated functions by physical interaction with other proteins. Our knowledge about networks of protein-protein interactions was very limited until recently [1]. In the past 10 years, several high-throughput approaches have been developed. Two major high-throughput methods previously used to construct the interactomes were yeast two-hybrid system (Y2H) and affinity purification mass spectrometry (AP-MS) [2]. However, limitations of genome-scale experimental methods including taking a lot of time to do, needing hard work and high cost, has led to the development of bioinformatics-based approaches [3]. So according to lack of experimental PPI data specially for plants, we used interolog method (protein sequence similarity) and the evolutionary distances between barley and model organisms to construct barley PPIN. This method relied on an experimentally shown interaction of homologous proteins in other species [4]. The experimental PPI information was extracted from the Intact database. Inparanoid and Time Tree were used for identifying barley orthologous proteins and evolutionary age respectively. Our final constructed barley PPIN include 247,745 interactions in which 202996 PPIs were inferred from Homo sapiens and Saccharomyces cerevisiae. This PPIN provides valuable resources for the study of biological functions in barley.

کلمات کلیدی:

(Evolutionary distance, Interolog, Protein, protein interaction network (PPIN)

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