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Investigating the association between the flooding tolerance genes of soybean by pathway analysis and network analysis

Li-Hsin Jhan, Mu-Chien Lai, Chung-Feng Kao

National Chung Hsing University, Taichung, Taiwan

Abstract

Under the extreme climate conditions, the events of crop damage are increasing. There is an urgent need to breed stress-tolerant varieties. Flooding stress on different growth stages of soybean can negatively affect seed germination, plant growth, flowering, yield and quality. These impacts are linked with the ability of plant adaptation or tolerance to flooding stress, which involves with complex physiological traits, metabolic pathways, biological processes, molecular components and morphological adaptations. However, investigating mechanisms of flooding stress tolerance is time-consuming. In the present study, we conducted systems biology approaches to identify pathways and network hubs linking flooding stress tolerance. We previously identified 63 prioritied flooding tolerance genes (FTgenes) of soybean from multiple dimensional data sources using large-scale data mining and gene prioritization methods. We conducted competitive (using hypergeometric test) and self-contained (using SUMSTAT) approaches of gene-set enrichment analysis, using gene ontology (GO) database, and found 20 significantly enriched pathways by hypergeometric test and 20 significantly enriched pathways by SUMSTAT. These GO pathways were further compared to seven candidate pathways that identified by gene regulatory pathway databases collected from NCBI PubMed. The FTgenes were found being resist flooding stress in these significantly enriched pathways, which form a module through a closely linked pathway crosstalk network. The module was associated to ethylene biosynthesis, jasmonic acid biosynthesis, abscisic acid biosynthesis, and phosphorylation pathway. The systems biology methods may provide novel insight into the FTgenes and flooding stress tolerance.

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Biography:

Li-Hsin Jhan is a Master student in the Department of Agronomy at National Chung Hsing University (Taiwan). He majors in bioinformation and biostatistics. In the past three years, he made efforts at studying abiotic stress of soybean using systems biology methods to explore mechanisms of flooding stress tolerance.

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