



Large Scale Gene Expression Analysis towards Understanding the Crown Response to Cold Stress in Barley

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Abstract: Abiotic stresses such as heat and cold substantially affect crop production. They change the expression of many genes related to different biological and physiological processes [1]. Barley is the fourth most cultivated cereals and a model plant in genetics and genomic studies [2]. Crown tissue has the most impact on survival and re-establishment of the whole barley plant when exposed to cold stress [3]. Here, the responsive genes to cold stress in crown were studied in barley by using high-throughput microarray analysis. The data (E-GEOD-10329) were obtained from ArrayExpress Dataset and analyzed by using FlexArray software version 1.6.3. The analysis was conducted by using robust multiarray average algorithm (RMA) for normalization, background correction and expression value calculation. To identify responsive genes, P-value was adjusted in false discovery rate of <0.05. Therefore, Singular Enrichment Analysis (SEA) and EC pathways on specific responsive genes were implemented by AgriGo tools (<http://bioinfo.cau.edu.cn/agriGO/>) and David (<https://david.ncifcrf.gov/>) database, respectively. Above all, the 356 up-regulated genes in crown tissue were mainly involved in developmental processes, cellular processes, metabolic processes, binding and catalytic activity. Catalytic activity known as important part of a molecular function that has a various role against abiotic stresses especially osmotic stress [4]. Moreover, pathway analysis according to David database represented that sucrose synthase and xyloglucan xyloglucosyl transferase have impressive roles in crown tissue toward cold tolerance. Sucrose metabolism has important roles in development and stress response [5]. These results help to gain holistic approach about genetic response to cold stress in crown tissue.

Keywords: Abiotic stresses; functional categories; Gene expression; Microarray

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