

## Large Scale Gene Expression Analysis towards Understanding the Roots Response to Drought Stress in Wheat

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**Abstract:** Root is an important part of plant architecture that significantly affects the growth, biomass production and the final yield of plants [1]. The impressive role of root in enhancing drought tolerance has been reported in many researches [2, 3]. However, limited information on the genes function in root features is available in wheat. Here, the responsive genes to drought stress were studied in root by using high-throughput microarray analysis. The available data at ArrayExpress Dataset were retrieved from an experiment conducted on 18-day old wheat seedlings of three different genotypes under both normal and drought stress conditions. The analysis was carried out by using FlexArray software version 1.6.3 and robust multiarray average algorithm (RMA) was used for normalization, background correction and expression value calculation. To select responsive genes, P-value was adjusted at false discovery rate of <0.05. Singular Enrichment Analysis (SEA) and EC pathways on specific responsive genes were conducted by using AgriGo tools (<http://bioinfo.cau.edu.cn/agriGO/>) and David (<https://david.ncifcrf.gov/>) database, respectively. The identified 3298 up-regulated genes in root against drought stress were mainly involved in metabolic process, catalytic activity, binding, cell, cell part and organelle categories. Interestingly, we deduced also death process in root tissues in response to drought stress. Programmed cell death has been detected in primary roots under the salt treatment in wheat [4]. Thereby, pathway analysis indicated that glutathione transferase, peroxidase and sucrose-phosphate synthase, ADP-glucose pyrophosphorylase, aminolevulinic acid dehydratase and wpk4 protein kinase have immense roles in root tissues against drought stress. Glutathione transferase is an enzyme involved in various physiological processes such as primary metabolisms, secondary products, signaling mechanisms following exposure to UV light and presumably played a major role in plant growth and development and even in biotic and abiotic stresses [5]. These results help to uncover genetic response to drought stress in root.

**Keywords:** Drought stress; Ontology; Pathway; Wheat

### References

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