Differentially Expressed Genes under water scarcity in the root of Wheat

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Abstract

Wheat (Triticum aestivum L.) is one of the most important crops in the world. Water scarcity strongly affects the growth of cereal crops and productivity. Approximately 88% of Iran is located in arid and semi-arid regions, therefore the assessment of water deficiency hazard controls on wheat cultivation is critical.
The study is aimed at identifying the genes involved in mitigation and decreasing the impacts of drought on wheat. Finally, the expression profiles of the wheat transcriptome in normal and dehydration conditions were investigated using the available RNA sequencing (RNA-Seq) data and then validated by quantitative real-time polymerase chain reaction (qRT-PCR) to obtain the stress-responsive candidate genes.

Keywords: Wheat, Dehydration, RNA-Seq, Root

Introduction

Wheat (*Triticum aestivum* L.) is the most widely cultivated staple food crop in many countries including Iran. Water deficit limits crop growth and development.

In the present study, RNA sequencing (RNA-Seq) technology, were used to identify water deficit responsive differentially expressed genes (DEGs) in wheat roots. GO (Gene Ontology) analysis showed that these DEGs were significantly enriched in biological processes.

Based on the transcriptome results and GO analyses candidate genes and their related signaling pathways were identified to be associated with wheat roots response to water deficit.

Materials and Methods

Total RNA was extracted from the root, using TRIzol reagent (Invitrogen) according to the manufacturer's instructions. RNA was purified and concentrated using an RNeasy column (Qiagen). RNA integrity and purity were assessed using a NanoDrop 2000 Spectrophotometer, an Agilent 2100 Bioanalyzer.RNA samples were sent to StarSEQ® GmbH (packages), Germany (https://www.starseq.com) for library construction and sequencing. Libraries were sequenced on an Illumina Next Seq 500/High generating 2x150 bp paired-end reads. In this study, RNA sequencing (RNA-seq) analysis were performed to identify the transcriptional changes and the differentially expressed genes (DEGs) involved in the response to water deficiency in the root.
Gene Ontology (GO) enrichment analysis were performed with Web Gene Ontology Annotation Plot (WEGO) tool. The criteria to identify the putative differentially expressed transcript were false discovery rate (FDR)≤ 0.01 and fold change (FC)≤ 2 or ≥ -2. The GO annotation was downloaded from ensembl plants (https://plants.ensembl.org).GO analysis showed that genes were defined in three major categories: Molecular Function (MF), Cellular Component (CC), and Biological Process (BP).

Discussion, Conclusion and Suggestions

From the 504 total genes selected, the 51genes were DEGs, between normal and dehydration conditions, that highlighted i9 molecular function and 60 biological processes GO terms. The genes are involved in ornithine-oxo-acid transaminase activity, transaminase activity, transferase activity, calmodulin-binding, arginase activity, agmatinase activity, glycerol kinase activity, vitamin B6 binding, pyridoxal phosphate binding in roots were significantly enriched in the set of upregulated genes.

Results

GO enrichment analysis of up-regulated of DEGsis suggested that there are several pathways related to defense response, response to stress, response to biotic stimulus, arginine catabolic process, and immune response in dehydration conditions compared to normal.
Additionally, the sets of DEGs are identified that may be related to mitigation or dehydration tolerance in the root.

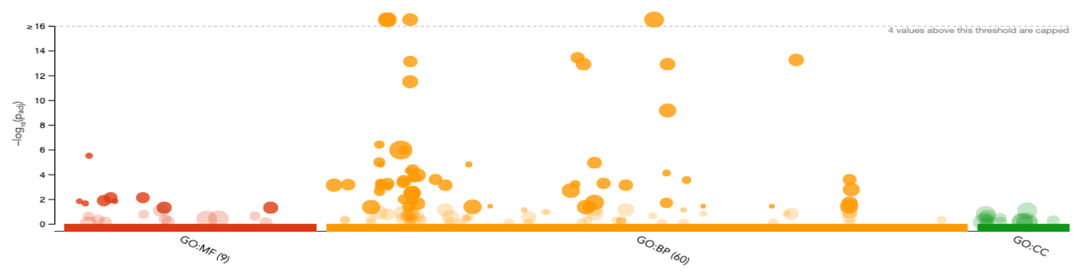

Figure 1. Histogram of GO terms assigned to DEGs in the roots

The DEGs are categorized into three main groups: cellular component (CC), molecular function (MF), and biological processes (BPs).

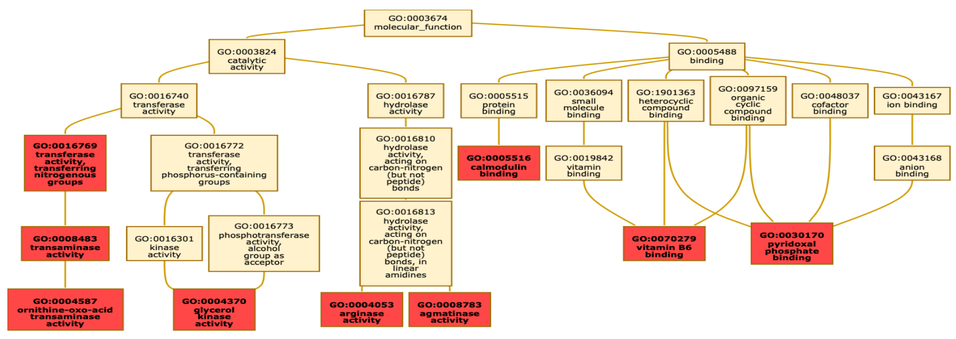

Figure 2. Molecular Function (MF) GO terms diagram

Themolecular function (MF) of up-regulated root genes in dehydration conditions compared to normal. GO terms as nodes in the graph and the relations between the terms as edges (more ontology information at Gene Ontology Overview).

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