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Transcriptomic profiling of the maize (*Zea mays* L.) to drought stress at the seedling stage

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Abstract

The development and productivity of maize (*Zea mays* L.) is frequently impacted by water scarcity, and consequently to increased drought tolerance in a priority target in maize breeding programs. To elucidate the molecular mechanisms of resistance to drought stress in maize, RNA-seq of the public database was used for transcriptome profiling of the seedling stage exposed to drought stress of three levels, such as moderate, severe drought stress and re-watering. *In silico* analysis of differentially expressed genes (DEGs), 176 up-regulated and 166 down-regulated DEGs was detected at moderated stress in tolerance type. These DEGs was increasing degradation of amino acid metabolism in biological pathways. Six modules based on a total of 4,771 DEGs responses to drought stress by the analysis of co-expression network between tolerance and susceptible type was constructed and showed to similar module types. These modules were discriminated yellow, greenyellow, turquoise, royalblue, brown4 and plum1 with 318, 2433, 375, 183, 1405 and 56 DEGs, respectively. This study was selected 30 DEGs to predicted drought stress response gene and was evaluated expression levels using drought stress treated sample and re-watering sample by quantitative Real-Time Polymerase Chain Reaction (qRT-PCR). 23 genes was shown increasing with drought stress and decreasing with re-watering. This study contribute to a better understanding of the molecular mechanisms of maize seedling stage responses to drought stress and could be useful for developing maize cultivar resistant to drought stress.

Keywords: maize, drought stress, differentially expressed genes, seedling stage, transcriptome.

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