

## Identification and Validation of UGE1 Candidate Gene Associated to Drought Stress in Plants by Gene Expression Analysis

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**Abstract:** Drought stress is one of main challenges in crop production [1]. The research was performed to identify and validate Uge1 genes involved in drought stress using gene expression data analysis which was downloaded from NCBI database. We considered three datasets related to three plants, barley, tomato, and soybean, to start the analysis of gene expression data [2,3]. Data analysis indicated that there are 258 genes in which at least two datasets had a significant change to drought stress (Fold Change > 2 and p-value < 0.05). 18 common genes were identified which were regulatory factors based on plant database. We chose Uge1 gene to validate. We studied the expression of this gene in three plants (barley, soybean, and tomato) under five drought stress levels (10, 15, 20, 25, and 30 percent). It was conducted based on completely randomized factorial design. The first factor of drought stress had 5 irrigation levels of 10, 15, 20, 25 and 30% of field capacity, and the second factor included 3 different plants of barley, tomato and soybean [4,5]. After treatment of drought stress on seedling stage, the leaf tissue of plants was excised for RNA extraction. Gene expression was determined by RealTime PCR [6]. According to the results, for Uge1 gene expression, the highest and the lowest expression values were observed in tomato and soybean, respectively. In drought stress factor, maximum and minimum gene expression values were observed in the levels of 25% and 10%, respectively. This experiment was carried out at Institute of Biology and Technology in University of Zabol.

**Keywords:** RT-PCR; Uge1; Drought stress; Gene expression

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