

## EXPRESSION PROFILES OF DROUGHT INDUCED WRKY TRANSCRIPTION FACTORS IN SOME SUNFLOWER CULTIVARS; MICROARRAY DATA ANALYSIS

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### ABSTRACT

Drought or water scarcity is an unbalanced state between the water availability in soil and its physiological demand by plant. Drought stress significantly inhibits the plant growth and development, and reduces the crop productivity as well as it is predicted to become more severe in years to come. Sunflower is mainly regarded as an oil crop able to grow under water-scarce conditions. However, not all sunflower genotypes are homogeneous in water usage regimes under water available and scarce conditions. Thus, this study aimed to analyze the gene expression profiles of drought induced *WRKY* transcription factors (TFs) in eight sunflower (*Helianthus annuus*) cultivars such as Inedi, Melody, Tekny, SF028, SF107, SF109, SF193 and SF326. Two different drought stress scenarios such as Fixed Duration Stress (FDS; 7days/0-0.57 FTSW) and Fixed Intensity Stress (FIS;  $\geq 7$ days/0-0.09 FTSW) were implemented to understand the *WRKY*s-drought relationship in sunflower plants. Sunflower Affymetrix microarray with 96 samples, including 32423 probesets were retrieved from NCBI GEO Data Sets (access. GSE25719). For array analyses, sunflower cultivars were grown in pots filled with 15 L of substrate, including 50% clay loam, 40% potting soil and 10% sand in greenhouse at 17°C/night and 20-25°C/daylight temperatures. 96 pots were arranged in six blocks, each containing 16 plants with eight treatment and eight control groups. All pots were daily watered and three times fertilized for 25 days before drought stress treatment. A total of 18 putative *WRKY* TFs were analyzed in eight drought-induced sunflower cultivars. Hierarchical clustering analysis demonstrated that expression profiles of *WRKY4* (Heli013712 and Heli000574) and *WRKY30* (Heli009222) TF genes show more divergence from others. Besides, SF028 (FIS), SF107 (FIS), SF326 (FIS) and Tekny (FDS) cultivars demonstrated more similar clustering pattern. Revealing the gene expression profiles of *WRKY* TFs in various sunflower cultivars under different water regimens will provide valuable insights to elucidate the drought-induced transcriptional regulatory elements or mechanisms in plants, with purposes of enhancing the crop productivity and yield.

**Key Words :** Water scarcity, FDS, FIS, genotype, *WRKY*, cultivar