GENE EXPRESSION IN SOME GENOTYPES OF *Helianthus annuus* L. UNDER SALT STRESS CONDITIONS

By

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B.Sc., Agric. Sc. (Genetics), Ain Shams University., Egypt, 2003
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ABSTRACT

Mokhtar Said Moktar. Gene Expression in Some Genotypes of *Helianthus annuus* L Under Salt Stress Conditions, Unpublished P.H.D. Thesis, Department of Genetics, Faculty of Agriculture, Ain-Shams University, 2018.

Sunflower (*Helianthus annuus* L.) belongs to the family *Asteraceae* and is amongst the significant oilseed crops grown for edible oil in the world. Sunflower oil is being ranked fourth after palm, soybean and canola oils. In the present investigation, we sought to assess the genetic diversity among fourteen Egyptian genotypes of sunflower using the fluorescence-based AFLP (F-AFLP) and evaluation of yield-related traits. The genome coverage was assessed using *in-silico* PCR analysis and the real-time PCR technique (qPCR) was used to determine gene expression of some salt-related genes. The analysis of variance for yield-related traits indicated that there were significant differences among genotypes for all studied traits ($p\leq 0.01$). The total numbers of amplicons produced by the six primers combinations of F-AFLPs were 1007 polymorphic bands, with 97.42% polymorphic percentage. As for the molecular markers-associated traits, 73 markers were observed related to morphological and yield components traits. The results of *in-silico* analysis revealed that F-AFLPs exhibited the highest chromosomal coverage (0.055%) and targeted 1378 genes with the average area (75kb) covered by the F-AFLPs. The statistical correlation of the euclidean distances matrix found lowest to the genetic distance based on the 1007 amplicons 0.15, and highly correlated to the genetic distance matrix 0.55. Concerning the outlier's AFLP loci (73 loci), our findings confirm that the genetic variation within the population was more significant than the variation among populations. In the context, seven genotypes out of the fourteen were tested under greenhouse conditions on different salt stress concentrations at 4000 and 6000 ppm NaCl. We can point out that, S_{10} genotype was considered as the most sensitive genotype, while S_3

genotype was considered as salt tolerant one based on the combined results of estimated agronomic traits such as plant height, number of leaves/ plant, root length and plant dry weight. To explorer the genetic factors behind the improved salt tolerance in selected sunflower genotypes, gene expressions of *CDPKs* and *P5CS* genes were estimated using real time qRT-PCR and showed substantial differentiation between the two aforementioned contrasting genotypes regarding salt tolerance.

Key words: Sunflower (*Helianthus annuus* L.), F-AFLP, *in-silico* PCR analysis, Salt Stress, qRT-PCR, outlier's loci.

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