



Molecular Genetic Studies on Some Barley Entries for Drought Tolerance

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Abstract : Five barley lines with different reaction for drought tolerance were hybridization using half diallel analysis without reciprocals to produce F1 hybrids. All genotypes (5 Parents and their 10 F1 crosses) were estimated on the farm of (Nubaria, Beheira governorate under normal and water deficit conditions) for knowing the genetic behavior responsible for drought stress tolerance based on studying morphological and physiological traits beside appreciation DNA-fingerprinting using (RAPD-PCR) through five primers for the five parents and the best five crosses revealed from the highest calculated data resulting from the genetic parameters of the aforementioned traits under drought stress conditions compared with the control treatment. Plant height, days to maturity, grain yield/plant, maximum root length, number of roots/plant, relative water content, osmotic pressure and canopy temperature traits were the most measurements calculated under both treatments in all genotypes of barley based on genetic parameters such as mean performances, analysis of variance, heterosis over better-parents, combining ability effects with both types in addition to tolerance indices. From the previous results can be seen that the entries ; (P1, P2, P1 X P2, P1 X P3, P1 X P4, P2 X P4, P2 X P5) considered as the most desirable genotypes for drought stress tolerance where they achieved the highest values and detected significant and highly significant positive values of heterosis over better-parent, GCA and SCA effects in all traits under both treatments of irrigation beside exhibited highly data of tolerance indices especially (MP, GMP, YSI, DTI, YI) and lowest data of (DSI, YR) respectively. Five different primers were recorded total of 43 reproducible amplification products, where 30 of them were polymorphic bands with (69.76 %) polymorphism and 13 fragments were monomorphic. The genetic similarity ranged from 54.50 to 95.20%, with an average of 74.85%. Cluster analysis divided the ten barley entries into two main clusters. The first cluster contained the hybrid H3 (P1 X P4) only, while the second cluster divided into two sub-clusters; the first sub-cluster contained the genotype H5 (P2 X P5) only, while the second sub-cluster contained the other entries, respectively.

Keywords: Barley, Drought stress, GCA, SCA effects, Half Diallel analysis, DNA – RAPD markers.