SELECTION PRACTICE AMONG AND WITHIN SOME WHEAT CROSSES

BY

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B.Sc. Agric. Sci. (Agronomy) Fayoum University, 2006
M.Sc. Plant Molecular Biology, Mediterranean Agronomic Inst.
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ABSTRACT

Grain yield is a genetically complex trait and greatly influenced by various environmental conditions. Four field experiments in RCBD with three replications were executed. In the 1st and 2nd seasons, the experiments were carried out at the Experimental Farm of the Fac. of Agric., Fayoum Univ. at Demo. The 1st experiment was designed to study thirty six wheat genotypes (*Triticum aestivum*. L) of hybrid origin in their F4 generation and subjected to selection among and within them. In addition to these genotypes there were four check parental varieties. In the 2nd experiment the wheat selected genotypes became thirty eight together with the same parental varieties were evaluated and selection was again practiced. In the 3rd season, two experiments were executed at two different locations, Demo and Basyounya, Fayoum Governorate. In this last season the selected promising lines together with the four check varieties, were sown at two different sowing dates with the aim to evaluate their performance and phenotypic stability. Results revealed that mean square values were highly significant for all studied traits in all seasons, indicating the presence of sufficient variability among the investigated genotypes and gave opportunities for wheat improvement. In the second season, C.V % and SE values became lower than the corresponding values in the 1st season , particularly for the traits PH, NTT, NFT, GWS, GYP and BYP. CV% and SE values at Basyounya location were lower than those of Demo location for the traits PH, NTT, NFT, GWS and HI. On the other hand, Demo exhibited lower CV % and SE values than those of Basyounya for other traits like GYP, BYP and NSM.

Great correspondence was observed between genotypic coefficients of variation and phenotypic coefficients of variation in every one of the traits. The coefficients of variation were high for NFT, GS, GWS, GYP, NSM, GY, HI. In addition to, Moderate were recorded for HD and SL in the all seasons, and low ones were obtained for DPM in all seasons. Heritability was greater than 80% for all studied traits and the genetic advance as a percent of mean (GAM %) ranged from 12.22 (SS) to 77.00 (GY) in the 1st season and from 15.42

& 12.69 (DPM) to 112.07 & 68.35(GYP) in 2nd and 3rd seasons, respectively.

Correlation coefficients of trait pairs obtained under both sowing dates and / or both locations revealed that BYP, GS, NFT, SY and BYF did not show any significant relations under late sowing. Likewise, NSM, SS at Demo and NFT at Basyounya showed non-significant coefficients. GYP, clarified its strong relations with NFT, GS, HGW, BYP, BYF and GYF. In addition, BYP, showed considerable association with PH, NTT, NFT, GS, GWS, GYP, BYF and GYF.

Stepwise results revealed that the relative contributor traits in the total variation of grain yield were GYP (48.1%), HI (20.6%), GFP (3.2%) and PH (2.5%), at early Basyounya location. However, at early Demo location, were GFP (31.4%), GYP (28.5%), NFT (2.9%) and GWS (2.9%). At late Basyounya, the effective traits were GYP (93.5%), NFT (0.7%) and HI (0.6%), however, at late Demo were GYP (82.9%) and HI (4.9%). The other variables were not included in the model due to their low relative contributions.

Seven stability measures i.e., β_i, S^2d_i, δ_i^2, R^2_i, RD_i, RHD_i, RDD_i, and CV_i were used to identify stable genotypes with consistent yielding performance across the testing environments. Genotypes G2-7, G1-5 short, G2-5, G6-4 and G6-7 short were identified as the most stable genotypes by stability measures of β_i, S^2d_i, δ_i^2 and R^2_i. However, G1-2, G1-3, G3-8, G4-3 and Sakha93 were identified as stable genotypes by CV_i, RD_i , RD_i and RHD_i. Regression coefficient parameter (β_i), relative deviation (RD_i), Half sum of RD_i, RDD_i (RHD_i) and coefficient of variability (CV_i) showed highly significant positive perfect correlation. which indicating that these parameters were equivalent for genotypes stability purposes.

Key words: *Bread wheat, Genotypes, Sowing dates, Locations, Yield and yield components, Genetic parameters, correlation, Stepwise regression, Phenotypic stability.*