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GENETICAL ANALYSIS OF SOME ECONOMIC TRAITS IN FLAX (Linum usitatissimum L.)

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ABSTRACT:

: The main objectives of the present study are to evaluate six different flax genotypes [P1 (Giza 8), P2 (Sakha 2), P3 (Sakha 4), P4 (Ilona), P5 (S. 22) and P6 (Sakha 3)] and their F1 crosses (including the reciprocal crosses) under three different nitrogen levels (30, 45 and 60 kg Nitrogen/faddan). Data were recorded on days to maturity, seed yield per plant (gm), seed index, straw yield/plant and oil %. The magnitude of both general and specific combining abilities were estimated for all traits, but gene action effects and genetically graphical analysis were done only for the two later traits. The obtained data revealed that the most desirable and/or highest mean performances for all parents and crosses were defined in all traits studied under the three nitrogen levels and their combined data. The mean squares associated with general (G.C.A) and specific (S.C.A) combining ability effects were found to be highly significant for most studied traits in the three nitrogen levels and their combined data, this mean the importance role of both (G.C.A) and (S.C.A) effects controlling in the inheritance of all traits, but the first one were the greatest one. Based on the combined data, the best general combiners were detected in the parental cultivar Ilona (P4) for days to maturity; in Sakha 2 (P2) for straw yield/plant, seed index and seed yield per plant and in S. 22 (P5) for oil %. Also, based on the combined data of specific combining ability, the most desirable and/or highest values were defined in five crosses (P3 x P4, P3 x P5, P2 x P1, P4 x P6 and P6 x P4) for straw yield/plant, and in two crosses (P1 x P3 and P4 x P1) for oil %. The analysis of gene action effects for straw yield/plant and oil % showed that the additive variances (D) and dominance components (Ĥ1) were significant for the two traits studied in the three nitrogen fertilizing levels. Also, the ratios of recessive and dominant genes for both traits were markedly differed in each parents under the different nitrogen levels. Degrees of partial dominance, complete dominance and over dominance effects were also sharply differed under the three nitrogen levels for both traits. In general, the third nitrogen level (60 kg N/faddan) gave the highest and/or the most desirable mean performances and different genetic components for most studied traits. 60 and 30 kg N/faddan gave the maximum gain for straw yield and oil %, respectively.

Key words: Flax breeding, combining abilities and gene action analysis.

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ESTIMATION OF GENETIC VARIANCE COMPONENTS FOR YIELD AND PROTEIN CONTENT FOR SOME NEW GENOTYPES IN MAIZE

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ABSTRACT:

Increasing grain protein concentration in maize (Zea mays L.) has not been a major focus of most breeding programs, which mainly focus on yield, maturity, and resistance to stress. The objectives of this research work are: (1) Evaluation of the non selected and selected H.S families(the original 100 H.S tested and the 20 % H.S selected) in two locations i.e., Gemmeiza and Sids Agricultural Research Stations, three maize population's i. e., Pool – 15 – 67 CIMMYT, Composite – 45 and Gemmeiza yellow. (2) Evaluation of the original populations and the first cycles of selection (C0 and C1) of all studied populations in two sowing dates (early and late) at University of Menoufiva Agriculturally Research Farm. (3) Determine the efficiency of the modified ear – to – row method for improving the yielding ability and protein content of the three maize populations. Considerable amount of genetic variations existed between all maize families within each studied population. At the same time, the mean squares of Genotype x location interaction were highly significant for all studied traits of each population separate. It indicated that the behavior of all traits were obviously differing from location to another. For all studied maize populations, the estimates of genotypic variances for grain yield/plant and protein content traits represented in the main and major partition of the phenotypic variances which reflected high estimates of heritability in broad senses. Increasing and/or decreasing rates of all studied traits due to selection showed that the Ear $\hat{a} \in \hat{a}$ to $\hat{a} \in \hat{a}$ row selection method was effective in this concern. The data showed that the improved one cycle in 1st sowing date (C1D1) had the highest mean values of all studied traits such as protein content and grain yield/plant traits except the days of 50 % silk trait for all studied maize populations. Generally, the improved half-sib maize families of Gemmeiza Yellow population had the higher mean value of protein content % (13.925), while Composite-45 population during the 1st sowing date had the highest mean value of grain yield / plant compared to the other studied maize populations (232 gm).

Key words: Maize (Zea Mays L.), Genetic Variance, Genotypes, Phenotypes, Heritability.