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Genetic analysis in maize *(Zea mays* L.)

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SUMMARY

Based on genetic distance and clustering pattern, the eight diverse inbred lines were crossed in a half diallel to estimate the combining ability and component analysis, showed presence of additive and non-additive gene effects with preponderance of latter. The mean degree of dominance indicated over dominance for all the traits. The distribution of genes with positive and negative effects was symmetrical and one to six dominant genes governed the inheritance of grain yield. The narrow sense heritability was low for all traits except for ear diameter and day to maturity. The predominance of non-additive genetic variation (over-dominance) and low narrow sense of heritability for majority of character may prove useful in hybrid breeding programme.

Key words : Maize, Combining ability, Heterosis, Heritability

Hybrid development is an evolutionary process emphasizing development and identification of simple hybrid types as a short-tem objective with gradual shift towards producing more diversified types to cater to various specialized uses. Success depends on the availability of genetically superior source germplasm to develop hybrids. Genetically diverse and productive lines play vital role in a successful breeding programme. The component analysis, besides providing necessary information on the type of gene action governing the yield components, also determines the nature and magnitude of genetic variation present in the population and helps in planning efficient breeding methodology. The present study in an attempt to gather information on gene action and other parameters of genetic variation in yield traits of maize.

MATERIALS AND METHODS

Fifty-five inbred lines derived from broad based heteroic Populations were evaluated to assess genetic divergence. Multivariate analysis by means of Mahalanobis D^2 statistics was performed to quantify divergence in the inbreds. Eight genetically diverse inbred lines *viz*., (M_9 x CM 601) S_6-7-8-⊗-#, Across 8331 S_5-3-3-⊗-#. AB(w)S_5-3-2-⊗-#, M_9-S_6-11-1-⊗-#, (CM400 x CM300)-S_5-⊗-#, Jogia local S_6-2-1-⊗-#, Pant 7421-S_6-194-3-⊗-# and CM601-S_5-8-7-⊗-# selected on D^2 values were planted to make all possible crosses, excluding reciprocal. Twenty eight F_1's, eight parental lines and four hybrids were used as checks were planted in RBD with three replications. Mean of quantitative traits for each entry for all replications were measured. The graphical analysis was performed based on the variance and co-variance values following the procedures given by Jinks and Hayman (1953) and Hayman (1954). Variance components were calculated as per Hayman (1954). Combining ability analysis followed Griffings (1956) Methods 2, Model 1.

RESULTS AND DISCUSSION

Based on Mahalanobis D^2 values the fifty-five inbred lines were grouped into five clusters (Table 1). Clusters were not formed according to geographical distribution/ origin of the source genotypes. The clustering pattern reflected the presence of genetic diversity in the inbred lines and also revealed that there was no correlation between genetic diversity and geographical diversity from cluster I, III and V. Hence, crossing among selected inbred lines from different clusters was suggested to produce hybrids for exploitation of heterosis considering the intra and intercluster distances (Table 2) the higher inter cluster distances (D = 1.886) was observed between cluster I and IV indicating wide genetic diversity between these two groups. Cluster III showed high statistical distance.

Mean squares due to general combining ability and specific combining ability (Table 3) were highly significant for all the characters indicating that both additive as well as non-additive gene actions were involved in the control of these characters.

Non-significant value of t^2 for most of the characters indicated the validity of hypothesis of the diallel analysis (Table 4). The estimates of both additive (D) and

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