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.

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-$\otimes$-#, Across 8331 S$_5$-3-3-$\otimes$-#. AB(w)S$_5$-3-2-$\otimes$-#, M$_9$-S$_6$-11-1-$\otimes$-#, (CM400 x CM300)-S$_5$-$\otimes$-#, Jogia local S$_5$-2-1-$\otimes$-#, Pant 7421-S$_6$-194-3-$\otimes$-# and CM601-S$_5$-8-7-$\otimes$-# selected on D^2 values

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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

Table 1 : Composition of clusters based on D^2-Statistics of fifty-five inbred lines of maize

Clusters	No. of inbred lines included	Line included in clusters with their pedigree
I	9	CM601–S_5–1–8–⊗–#, CM601–S_5–2–2–⊗–#, CM300–S_5–1–⊗–#, AB(w)–S_5–3–2–⊗–#, AB(w)–S_5–4–2–⊗–#, M_9 X CM601–S_6–2–⊗–#, X_1–S_5–10–1–⊗–#, Across 8331–S_5–76–1–⊗–#, Pant 7421– S_6–107–1–⊗–#
II	16	CM601–S_5–2–3–⊗–#, CM601–S_5–87–⊗–#, AB(w)–S_5–4–3–⊗–#, M_9–S_5–2–1–⊗–#, M_9–S_5–62–2–⊗–#, M_9 X CM601–S_5–1–⊗–#, X_1–S_5–9–3–⊗–#, Across 8331–S_5–18–1–⊗–#, Across 8331–S_5–63–1–⊗–#, M_9 X CM400–S_5–14–2–⊗–#, Pant 7421– S_5–76–1–⊗–#, Pant 7421–S_6–133–3–⊗–#, Pant 7421–S_6–166–1–⊗–#, Pant 7421–S_6–194–3–⊗–#, Pant 7421–S_6–228–1–⊗–#, Pant 7421–S_6–238–2–⊗–#
III	9	CM601–S_5–14–1–⊗–#, CM601–S_5–14–2–⊗–#, CM601–S_5–14–3–⊗–#, M_9–S_6–11–1–⊗–#, AB(w)–S_5–5–2–⊗–#, M_9–S_5–37–2–⊗–#, Across 8331–S_5–71–1–⊗–#, Jogia local–S_6–2–1–⊗–#, Pant 7421– S_6–22–1–⊗–#
IV	11	M_9–S_6–36–1–⊗–#, M_9–S_6–37–1–⊗–#, M_9–S_5–37–3–⊗–#, M_9 X CM601–S_6–7–8–⊗–#, Across 8331–S_5–3–2–⊗–#, Across 8331–S_5–68–1–⊗–#, M_9 X CM400–S_6–2–1–⊗–#, M_9 X CM400–S_6–14–1–⊗–#, Jogia local–S_6–78–⊗–#, Jogia local–S_6–78–⊗–#, CM400 X CM300–S_5–⊗–#, Pant 7421– S_6–93–1–⊗–#
V	10	CM601–S_5–1–2–⊗–#, CM601–S_5–2–8–⊗–#, AB(w)–S_5–4–4–⊗–#, M_9 X CM601–S_6–6–8–⊗–#, Across 8331–S_5–3–3–⊗–#, Jogia local–S_6–12–1–⊗–#, Jogia local–S_6–72–1–⊗–#, Jogia local–S_6–72–2–⊗–#, Jogia local–S_6–75–⊗–#, Pant 7421– S_6–129–1–⊗–#

Table 2: Intracluster (in both) and inter-cluster average D^2 and D value (in parenthesis) per cent the inbred lines in maize

Clusters	I	II	III	IV	V
I	1.317 (1.147)	2.287 (1.512)	3.294 (1.814)	3.560 (1.886)	1.807 (1.344)
II		1.334 (1.154)	2.832 (1.682)	1.991 (1.411)	1.980 (1.407)
III			1.544 (1.242)	2.075 (1.440)	1.797 1.340
IV				1.167 (1.080)	2.091 (1.446)
V					1.037 (1.018)

Table 3: Analysis of variance for combining ability in maize

Source	d.f.	Mean squares							
		Days to 75% tassel	Days to 75% silk	Days to maturity	Plant height	Ear length	Ear diameter	Kernel rows per ear	Grain yield per plant
GCA	7	7.87**	7.94**	20.33**	214.09**	2.37**	0.35**	2.04**	135.29**
SCA	28	10.09**	12.33**	8.67**	126.45**	3.98**	0.42**	4.02**	301.88**
Error	10	0.73	1.08	0.80	10.89	0.70	0.02	0.25	7.64

** indicates significant of value at P =0.01

dominance (H_1) effects of gene were significant for ear length and ear diameter whereas only dominant effect for days to 75 per cent tassel, days to 75 per cent silk, days to maturity, plant height, kernel rows per ear and yield per plant. It reflected that both additive and non additive gene effect accounted for the expression of these characters but their relative magnitude varied considerably.

Mean degree of dominance $(H_1/D)^{0.5}$ indicated over dominance for all the characters (Table 5) positive and significant h^2 values for all the characters also confirmed importance of dominance gene action. Since $H^2/4H_1$ values for days to 75 per cent tassel, days to 75 per cent silk, ear length, kernel rows per ear and yield per plant

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Table 5: Comparative evaluation of the results on gene action and average degree of dominance							
Character	Variance component analysis			Combining ability analysis		Average degree of dominance	
	D	H_1	H_2	GCA	SCA	Wr-Vr	$(H_1/D)^{1/2}$
Days to 50% tassel	NS	HS	HS	HS	HS	OD	OD
Days to 75% silk	NS	HS	HS	HS	HS	OD	OD
Days to maturity	NS	HS	HS	HS	HS	OD	OD
Plant height	NS	HS	HS	HS	HS	OD	OD
Ear length	HS	HS	HS	HS	HS	OD	OD
Ear diameter	HS	HS	HS	HS	HS	OD	OD
Kernel per row	NS	HS	HS	HS	HS	OD	OD
Yield per plant	NS	HS	HS	HS	HS	OD	OD

N.S.-Non significant

were approximately 0.25, it indicated equal distribution of increasing and decreasing alleles in the parents. Other values were far from expected value 0.25 showing unequal distribution of positive and negative alleles for different characters in the parents. The computed value h^2/H_2 ranged from 0.06 to 5.88 for different characters suggesting that there were 1-6 dominant genes or group controlling these characters.

The ratio of total number of dominant to recessive alleles in the parents was estimated by the ratio $\sqrt{4DH}$ 1 + F / $\sqrt{4DH}$ 1 - F Closer ratio to unity implies equality of number of dominant and recessive alleles in the parents. This ratio was close to unity in case of plant height, kernel rows per ear and yield per plant which exhibited symmetrical distribution of dominant and recessive alleles in the parents for these traits. This ratio was much greater than unity for days to 75 per cent tassel, days to 75 per cent silk, days to maturity, ear length and ear diameter denoting excess of dominant genes in the parents. The F value for three traits were negative coupled with high magnitude of standard error and positive estimates were for rest other traits showed excess of dominant alleles.

The significant negative values of the correlation co-efficient (r) between the parental measurement (Vr) and parental order of dominance (Wr + Vr) indicated that positive genes for expression in plant height, ear length, ear diameter kernel rows per ear and yield per plant were mostly dominant. The estimates of heritability in the narrow sense was observed to be quite low for all the characters except for ear diameter and days to maturity which indicated that major part of the phenotypic variability for most of the traits was due to dominance.

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The result indicated that the parents with genetically diverse origin should be used for heterosis breeding. The preponderance of non-additive genetic variance (over dominance) for eight characters including grain yield and low heritability in narrow sense for majority of the character may prove useful in hybrid breeding programme of maize.

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