Indian J. Genet., **62**(4): 334-335 (2002)

Short Communication

Components of variation over locations in maize (*Zea mays* L.)

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(Received: April 2001; Revised: November 2002; Accepted: November 2002)

Maize (*Zea mays* L.) is the principal food crop of Himachal Pradesh covering an area of about 0.31 million hectares in *kharif* season with an average yield of 19.9 q/ha, national average 17.21 q/ha but lower than U.S.A. in the world and China in Asia 1999 [1] challenging the maize breeders to develop suitable maize varieties/hybrids best suited under wide range of growing conditions. To achieve this goal, a breeder has to employ an efficient breeding programme which inturn will depend upon the information on different components of variation/gene action.

The 66 single crosses, 12 parents and 3 checks (EHB-1520, KH-101, PSCL-3436) were evaluated in a simple lattice design (9 × 9) of Federer [2] with two replications in two environments: (*i*) Research Farm of CSK HPKV, Palampur, Kangra (32°6′ N latitude, 76°3′ longitude, 1290.8m elevation, high rainfall up to 3000mm) (*ii*) Research Farm of CSK HPKV, Bajaura, Kullu (31°8′ N latitude, 77°E longitude, 1090m elevation, low rainfall up to 1000mm). In both the environments, each plot consisted of 5 rows of 5 m length. Row-to-row and plant-to-plant distances were kept 75 and 20 cm, respectively. Both the experiments were conducted under rainfed, conditions during *kharif* 1998 with all other recommended agronomic practices. The data were recorded on plot basis for phonological traits. For other characters observations were recorded on 10 randomly selected plants. The mean values pooled over the environments were used for standard statistical analysis. The genetic components of variation were calculated as per the method proposed by Hayman [3].

Estimates of genetic components of variation and other estimates derived from them for yield and its contributing traits have been presented in Table 1. The magnitude of t^2 values for majority of the traits indicated the validity of most of the assumptions underlying diallel analysis. The significant values of (1-b) indicated the non-allelic interactions for phonological, yield and most of its contributing traits. However few characters *viz.*, ear height, kernel rows/ear and 100-seed weight exhibited significant regression coefficient values (b) coupled with significant values of (1-b), probably indicated the presence of complementary type of interactions.

Dominance component (H1) was observed to be significant for all the traits thereby, indicating, the predominance of dominance effects. The KD/KR ratio was greater than unity for all the traits except days to 75 per cent silking and car circumference thereby, further confer mining the preponderance of dominant genes. The positive and negative genes in the parents were distributed unequally for all the traits as was evident from the ratio $H_2/4H_1$. The average degree of dominance $(H_1/D)^{1/2}$ revealed high overdominance for most of the important character including harvest index. Earlier, Sanjay Swarup [4], Turgut *et al.* [5] and Joshi *et al.* [6] had reported non-additive gene action for yield and yield contributing traits in maize.

Besides getting information on gene action, the other advantage of Hayman approach over combining ability is that, one can get information on heritability estimates (narrow sense). High heritability (> 30%) was observed only for plant height and ear height. Low to medium heritability was recorded for most of the characters including grain yield. From the present study, it is concluded that very few characters like plant height and ear height, which exhibited high heritability, could safely be subjected to any selection method for effecting desirable genetic improvement. Altinbas [7], Ismail [8], Dass *et al.* [9] and Mathur *et al.* [10] have also reported the similar results for gene action and heritability for different yield and yield related traits. Since, majority of the traits exhibited low heritability values coupled with preponderance of dominant effects, suggested the heterotic breeding in the present material.

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Table 1. Estimate of components of variation for different yield and yield-contributing traits pooled over two environments

	Characters													
Component	Days to 75% silking	Days to 75% pollen shedding	Plant height	Ear height	Days to 75% maturity	Ear length	Ear circumference	Kernel rows/ ear	Kernels / row	Shelling percentage	100-seed weight	Grain yield	Biological yield	Harvest index
D	0.00	0.54	137.39*	99.27*	0.22	0.65*	0.02	0.59*	1.21	1.85*	1.28*	16.26	490.68*	8.56*
	±00.34	±00.30	±20.35	±12.46	±00.20	±00.16	±00.04	± 0.14	±00.96	± 0.69	±00.55	±18.12	±127.81	±02.74
H_1	2.59*	2.69*	270.11	156.92*	1.45*	1.55*	0.43*	1.50*	11.10*	5.85*	7.14*	519.17*	1779.92*	44.79*
	±00.68	±00.60	±40.72	±24.92	±00.39	±00.31	±00.09	± 0.29	±01.91	± 1.38	±01.10	±36.25	±255.69	±05.48
H_2	2.36*	2.18*	198.57*	107.57*	1.14*	1.23*	0.40*	1.26*	9.93*	5.57*	6.44*	468.14*	1416.37*	35.56*
	±00.57	±00.50	±33.87	±20.73	±00.33	±00.26	±00.07	± 0.24	±01.59	± 1.15	±00.91	±30.16	±212.69	±04.56
$(H_1/D)^{1/2}$	-	-	1.40	1.26	-	1.55	-	1.59	-	1.78	2.36	-	1.90	2.29
$H_2/4H_1$	0.23	0.20	0.18	0.17	0.20	1.20	1.23	0.21	0.22	0.24	0.23	0.23	0.20	0.20
H^2_{ns}	-	14.40	46.97	54.26	6.30	27.29	2.03	25.78	8.17	17.12	12.57	3.07	29.60	22.47
KD/KR	-	2.05	2.85	2.69	1.97	2.19	-	1.12	1.38	1.17	1.22	1.25	2.22	2.35
B	–0.04	0.10	0.63*	0.60*	0.12	0.16	0.14	0.39*	0.25	0.58*	0.47*	0.25	0.47	0.16
	±00.09	±00.21	±00.17	±00.15	±00.37	±00.19	±00.12	± 0.10	±00.21	±00.24	±00.21	± 0.17	±00.21	±00.18
1-b	1.04*	0.90*	0.37	0.40*	0.89*	0.84*	0.86*	0.61*	0.75*	0.42	0.54*	0.75*	0.53*	0.84*
t^2	27.36*	1.79	0.93	1.80	0.26	2.78	13.68*	13.29*	1.59	0.05	0.79	3.81	0.62	3.01

*Significant at $P \leq 0.05$

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