Indian J. Genet., **58**(4): 525-527 (1998)

Short Communication

COMBINING ABILITY STUDIES FOR YIELD AND ITS COMPONENTS IN CLUSTERBEAN

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(Received: November 22, 1996; accepted: November 14, 1998)

Six homozygous but highly diverse and well adapted genotypes of clusterbean (*Cyamopsis tetragonoloba* L. Taub.) were crossed in a half diallel fashion to obtain 15 F_1 crosses. In *Kharif*, 1990, the parents and 15 F_1 s were raised in a randomised complete block design with three replications at CCS Haryana Agricultural University, Hisar. Each parent and F_1 was sown in a single row of 2.8 m length spaced 45 cms and plants spaced to 10 cm distance. All recommended cultural practices and plant protection measures were adopted to raise a good crop. Data on days to first flowering, days to maturity, plant height (cm), number of branches, clusters and pods per plant, pod length (cm), seeds per pod and seed yield per plant(g) were recorded on five random and competitive plants in each of parents and F_1s. The combining ability analysis was carried out following Method 2, Model 1 of Griffing [1].

The mean squares due to general combining ability (g.c.a.) and specific combining ability (s.c.a) were significant for all the characters studied, indicating the importance of both additive and non-additive components of genetic variance controlling these traits. Similar results in clusterbean have also been reported earlier [2, 3].

The estimates of g.c.a. effects (Table 1) showed that, parents CP 68 and HG 79-1-5 were superior for grain yield and most of other traits. Genotype HG 75 was also found good general combiner for seed yield and other component traits except that it was late in flowering and maturity. Parents HG 75 and CP 68 showed higher *per se* performance for grain yield per plant, whereas parent HG 79-1-5 was the poor performer. Thirteen out of 15 crosses occupied the first five ranks for six major characters (Table 2). The four top ranking crosses for seed yield per plant also figured in the top five, for pod and cluster number, indicating a close association between pod and cluster number with seed yield. Such observations have earlier been reported in guar [4, 5]. Of these 13 crosses, 7 crosses were between high ×

Table 1. G.C.A. effects for seed yield and component characters in guar

Parents	Days to first flowe-ring	Days to matu-rity	Plant height	Branches per plant	Clusters per plant	Pods per plant	Pod length	Seeds per pod	Seed yield per plant
HG 75	2.13*	4.24*	1.69*	0.690*	4.66*	8.33*	−0.068*	−0.198*	0.32*
CP 68	−3.55*	−5.29*	−18.81*	0.525*	4.39*	9.41*	−0.113*	−0.034	1.76*
PLG 85	−1.31*	−2.30*	−7.97*	−0.556*	−5.07*	−13.42*	−0.073*	0.009	−2.28*
FS 277	2.13*	4.02*	22.62*	−0.484*	−4.74*	−9.45*	0.099*	0.107*	−0.24
HG 314	2.32*	2.65*	11.04*	−0.472*	−5.74*	−8.06*	0.061*	−0.149*	−0.83*
HG 79-1-5	−1.72*	−3.32*	−8.56*	0.297*	6.51*	13.19*	0.094*	0.266*	1.26*
S.E. (GI)	0.08	0.13	0.23	0.014	0.17	0.49	0.016	0.023	0.13
S.E.(GI-GJ)	0.13	0.20	0.36	0.021	0.27	0.76	0.025	0.036	0.21

*Significant at P = 0.05

Table 2. Best five crosses based on *per se* performance, s.c.a effect and g.c.a status of their parents.

Character	Cross	Mean	sca effect	gca status of parent P_1	gca status of parent P_2
Seed yield/ plant (g)	CP 68 × HG 79-1-5	25.82	10.36*	High	High
	CP 68 × FS 277	18.60	4.65*	High	Low
	HG 75 × FS 277	16.57	4.06*	High	Low
	CP 68 × HG 314	14.92	1.55*	High	Low
	HG 75 × HG 79-1-5	14.21	0.19	High	High
No. of pods/plant	CP 68 × HG 79-1-5	158.87	50.26*	High	High
	HG 75 × HG 79-1-5	117.27	9.74*	High	High
	CP 68 × FS 277	107.87	21.10*	High	Low
	HG 75 × FS 277	106.00	21.12*	High	Low
	FS 277 × HG 79-1-5	105.07	15.32*	Low	High
No. of clusters/plant	CP 68 × HG 79-1-5	48.67	16.81*	High	High
	HG 75 × HG 79-1-5	39.13	7.01*	High	High
	HG 75 × CP 68	28.53	−1.47*	High	High
	CP 68 × FS 277	24.93	4.33*	High	Low

(*Cont. on next page*)

	HG 75 × FS 277	24.00	3.13*	High	Low
Days to maturity	CP 68 × HG 79-1-5	107.47	0.73	High	High
	PLG 85 × HG 79-1-5	108.73	–0.99*	High	High
	CP 68 × PLG 85	109.80	2.05*	High	High
	HG 314 × HG 79-1-5	114.27	–0.41	Low	High
	CP 68 × FS 277	114.33	0.26	High	Low
Days to flowering	CP 68 × HG 79-1-5	37.93	0.03	High	High
	PLG 85 × HG 79-1-5	38.33	–1.81*	High	High
	CP 68 × PLG 85	38.47	0.14	High	High
	HG 75 × PLG 85	43.93	–0.07	Low	High
	FS 277 × HG 314	45.07	–1.56*	Low	Low
Branches/ plant	HG 75 × CP 68	9.73	0.133*	High	High
	HG 75 × HG 79-1-5	10.27	0.431*	High	High
	CP 68 × HG 79-1-5	10.67	0.661*	High	High
	CP 68 × FS 277	2.67	–0.061	High	Low
	HG 75 × HG 314	2.60	– 0.253*	High	Low

*Significant at P = 0.05

low, 5 between high × high and only one cross involved low × low g.c.a. parents. The large number of high × low g.c.a. crosses figuring in top ranks for different characters is of immense interest, as such combinations may result in desirable transgressive segregants, if the additive effects of one parent and complementary epistatic effects in the cross act undirectionally and maximize the expression of the character under selection. Thus crosses CP 68 × HG 79-1-5 (High × High), CP 68 × FS 277 (high × Low) and HG 75 × FS 277 (high × Low) may be further exploited for harnessing the available heterosis for pod and cluster number and earliness in flowering and maturity in evolving the ideal genotype in guar.

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