Short Communication



Analysis of gene effects for yield and yield attributing traits in interspecific crosses of pigeonpea [*Cajanus cajan* (L.) Millsp]

Jogendra Singh and G. C. Bajpai

Department of Genetics and Plant Breeding, G.B. Pant University of Agril. & Technology, Pantnagar 263 145 (Received: January 2004; Revised: January 2005; Accepted: January 2005)

Pigeonpea [*Cajanus cajan* (L.) Millsp] is an important legume suited for cultivation in subtropical and tropical regions. Wild species, *Cajanus scarabaeoides* possesses pod borer tolerance, earliness, high protein content, which may be transferred in cultivated lines. To provide estimate of different non-allelic gene actions operating in the inheritance of quantitative traits, the present study in *Cajanus cajan* × *Cajanus scarabaeoides* crosses was carried out to investigate genetics of seed yield and its contributing traits through generation mean analysis.

Six generations viz., P1, P2, F1, F2, BC1 and BC₂ of each of three crosses viz., UPAS-120 \times C. scarabaeoides, PA 134 × Cajanus scarabaeoides and ICPL 84023 × C. scarabaeoides were grown in compact family block design with three replications following 60 cm × 15 cm spacing on ridge at Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar during kharif 2001. Each parent and F1 generation was sown in one row, backcross and F₂ in three rows of 3 m length. Data on 5 randomly selected plants in the parents and F1, 10 plants in BC_1 and BC_2 and 20 plants per plot in F_2 were used to record observations on plant height, days to 50% flowering, days to maturity, primary branches per plant, biological yield per plant, pods per plant, 100-seed weight and seed yield per plant. Data were subjected to scaling test [1] and in case of significance of scaling tests, analyzed for gene effects and interactions [2].

The scaling tests indicated presence of epistatic/digenic interactions for plant height, primary branches per plant, biological yield per plant, 100-seed weight and seed yield per plant in the cross UPAS-120 \times *C. scarabaeoides*, whereas, primary branches per plant, biological yield per plant, 100-seed weight and seed yield per plant in the cross PA 134 \times *C. scarabaeoides* and for days to 50% flowering, primary branches per plant and 100-seed weight in the cross ICPL-84023 \times *C. scarabaeoides*.

The results of generation mean analysis (Table 1) revealed that additive (d) gene effect was significant for plant height, days to 50% flowering, primary branches per plant, biological yield per plant, 100-seed weight and seed yield per plant. However, dominance (h) gene effect was significant in the cross PA 134 \times *C. scarabaeoides* for biological yield per plant and in the cross UPAS-120 \times *C. scarabaeoides* for seed yield per plant. Earlier Saxena *et al.* [3] reported role of additive gene effects in early pigeonpea. However, importance of both additive as well as non-additive gene action has been reported in past in the inheritance of yield and yield traits in pigeonpea [4-7].

Epistatic interactions (i, j and 1) were significant in the cross UPAS-120 \times C. scarabaeoides for seed vield per plant and dominance \times dominance (1) interaction for biological yield per plant. The magnitude of the additive \times additive (i) and dominant \times dominant (1) interactions were more than the magnitude of additive × dominance (j) for seed yield/plant as also evidenced by duplicate type of epistasis. Dominance × dominance (1) interaction was significant in the crosses, UPAS-120 \times C. scarabaeoides and PA-134 \times C. scarabaeoides for biological yield per plant and in cross ICPL-84023 × C. scarabaeoides for 100-seed weight. It is obvious that non-fixable gene effects (h) and (1) were higher than the fixable (d) and (i) in these crosses for all the characters, indicating greater role of non-additive gene effects in the inheritance of yield and yield attributing traits in interspecific crosses of pigeonpea. Duplicate gene action was observed for all the characters excluding days to 50% flowering, which indicated hinderance in selection improvement. Thus being interspecific crosses restricted recurrent selection by intermating desirable segregants will break undesirable linkages and further selection will be useful in combining desirable traits of Cajanus scarabaeoides into UPAS-120, PA-134 and ICPL-84023 cultivated lines of pigeonpea.

Cross	Scale						Туре
	(m)	(d)	(h)	(i)	(j)	(I)	of inte- rac-
							tion
		Plan	t height (cm)				
UPAS-120 \times C. scarabaeoides	334.64±137.30	58.47±2.64**	-561.03±280.98	-179.08±137.28	-32.20±26.63	390.40±146.04	D
		Days to	50% flowering				
ICPL-84023 × C. scarabaeoides	68.22±15.89*	-7.92±0.98**	38.58±36.39	10.99±15.86	7.63±8.04	26.56±21.38	С
		Primary	branches/plant				
UPAS-120 × C. scarabaeoides	27.43±13.25	8.73±1.21**	-33.85±32.93	-9.89±13.19	-18.10±8.99	19.46±20.21	D
PA-134 \times C. scarabaeoides	30.78±9.86*	6.98±1.12**	-21.68±23.11	-15.33±9.79	-3.69±5.64	2.50±14.22	D
ICPL-84023 × C. scarabaeoides	14.63±10.22	1.63±0.79	12.50±23.66	4.87±10.19	10.27±5.49	15.40113.84	С
		Biologic	al yield/plant (g)				
UPAS-120 \times <i>C. scarabaeoides</i>	655.03±24.60	154.38±23.38*	1240.44±517.84	-364.60±233.43	-189.37±101.03	905.58±318.43	* D
PA-134 \times C. scarabaeoides	508.34±122.43	* 86.15±12.70*	*-893.49±265.65*	-253.69±121.77	-79.80±46.33	661.89±170.74	* D
		100-s	eed weight (g)				
UPAS-120 × C. scarabaeoides	4.47±1.09*	3.07±0.13**	-4.03±2.57	0.66±1.09	-1.79±0.63	2.60±1.52	D
PA-134 \times <i>C. scarabaeoides</i>	4.65±1.87	3.15±0.10**	-5.72±4.29	0.27±1.87	-3.23±0.96*	5.23±2.50	D
ICPL-84023 × C. scarabaeoides	9.78±2.97	3.25±0.13**	-15.9±16.29	-4.79±2.97	-2.89±0.93	9.49±3.38*	D
		Seed	yield/plant (g)				
UPAS-120 \times <i>C. scarabaeoides</i>	40.27±5.79**	14.24±2.14*	-84.60±14.37**	-20.19±5.38*	-22.94±5.21*	56.52±9.69**	D
PA-134 \times C. scarabaeoides	18.39±11.05	7.89±1.93	-33.82±24.89	-1.27±10.89	-10.19±5.93	32.31±15.48	D

Table 1. Estimates of gene effects for yield and yield attributing traits in interspecific crosses of pigeonpea

P = 0.05 and 0.01 respectively; D = Duplicate, C = Complementary

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