seed yield. For fruiting branches, high BP heterosis was associated with high inbreeding depression in most of the crosses, the exception being AL 15 × T 21 (DT × IDT) which has high BP heterosis but very low inbreeding depression. In five out of nine cross combinations, T 21 × AF 239, AL 15 × AF 354, AL 15 × AF 239, AL 201 × AF 354, and AF 98 × AF 239, low or negative BP heterosis was associated with very low inbreeding depression for pods plant^{-1}. Two crosses, AF 98 × AL 201 and AF 98 × T 21, having high heterosis for pods plant^{-1} exhibited very low inbreeding depression. The reverse was the case in cross AF 98 × AL 15. Most of the cross combinations did not show vigor in F_1 generation. High heterosis was associated with high inbreeding depression for plant height in crosses AL 15 × AF 201, AF 98 × AL 15, and AL 15 × AF 239, whereas high heterotic cross AF 98 × AL 201 did not show high inbreeding depression. However, four cross combinations (T 21 × AF 239; AL 201 × AF 354; AL 15 × T 21 and AF 98 × AF 239) having either low or negative heterosis for plant height showed high inbreeding depression.

The present study indicates that, in general, cross combinations involving parents of different growth habit expressed high heterosis and low inbreeding depression while the cross combinations involving parents of similar growth habit (DT × DT or IDT × IDT) exhibited very low heterosis over BP and high inbreeding depression for most of the traits. Out of the nine cross combinations studied, the cross AF 98 × AL 201 (DT × IDT) seems to be promising. It expressed high BP heterosis and very low inbreeding depression for most of the characters.

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Nature of Resistance to Phytophthora Blight in Pigeonpea—Breeding Implications

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Among the fungal pathogens of pigeonpea, phytophthora blight (PB) caused by *Phytophthora drechsleri* f. sp *cajani* is second only to fusarium wilt in incidence (Kannaiyan et al. 1984). The severity and importance of this pathogen prompted this study of the genetic nature of resistance to this disease.

Twelve-day-old seedlings of parents, F_1s, F_2s, and backcrosses (BCs) of eight crosses (six between susceptible × resistant and two between susceptible parents) were screened against P_3 isolate of PB under artificially created epiphytotic conditions in greenhouses at ICRISAT Asia Center (IAC), Patancheru, India (Gupta 1995). Seedlings were scored on a visual rating scale of 1–5 (modified after Singh et al. 1992), where plants with a score of 1–4 were considered resistant, and those with a score of 5, susceptible. Chi-square test was used to test the fit of expected segregation ratios. The mean disease score (Table 1) for every generation of susceptible × resistant crosses, was also subjected to scaling test and generation mean analysis (Mather and Jinks 1982). A sequential model-fitting approach, using the weighted least square technique, was adopted to find out the best-fit model.

Results indicated the monogenic dominant nature of resistance in the resistant parent. Results also revealed the presence of some minor genes in the expression of resistance. The generation mean analysis indicated the presence of interallelic interactions in all crosses except ICPL 84023 × KPBR 80-2-1, where an additive dominance model was found to be adequate (Table 2). In UPAS 120 × KPBR 80-2-1, however, no model was found to be a best fit with the original data. Therefore, log (natural) transformation was used, and the model was tested on transformed values. Overdominance was observed in all crosses except UPAS 120 × KPBR 80-2-1

Table 1. Mean disease score (X) and number of plants screened in six generations of six crosses (susceptible × resistant) of pigeonpea, ICRISAT Asia Center, India, 1994.

	Crosses											
	UPAS 120 × KPBR 80-2-1		Pant A-3 × KPBR 80-2-1		ICPL 84023 × KPBR 80-2-1		ICPL 87119 × KPBR 80-2-1		ICPL 90005 × KPBR 80-2-1		ICPL 90035 × KPBR 80-2-1	
Generation	Mean (X) ± SE	No. of plants	Mean (X) ± SE	No. of plants	Mean (X) ± SE	No. of plants	Mean (X) ± SE	No. of plants	Mean (X) ± SE	No. of plants	Mean (X) ± SE	No. of plants
P_1	4.85±0.13	193	4.77±0.17	185	4.79±0.17	186	4.74±0.18	189	4.87±0.11	163	4.86±0.10	164
P_2	2.04±0.13	195	2.04±0.13	195	2.04±0.13	195	2.04±0.13	195	2.04±0.13	195	2.04±0.13	195
F_1	2.34±0.11	12	1.62±0.15	13	1.85±0.14	20	1.28±0.09	18	2.56±0.12	18	2.45±0.07	9
F_2	2.31±0.18	390	2.56±0.25	387	2.67±0.23	366	2.39±0.21	373	2.52±0.16	379	2.94±0.14	377
BC_1P_1	3.42±0.16	12	3.62±0.20	42	2.94±0.28	17	3.64±0.22	25	3.34±0.16	18	3.16±0.31	19
BC_1P_2	1.22±0.18	14	1.17±0.17	12	1.75±0.15	16	1.15±0.14	14	2.06±0.10	18	1.28±0.14	18

P_1 = First (female) parent, susceptible to phytophthora.
P_2 = Second (male) parent, resistant to phytophthora.
BC_1P_1 = $F_1 \times P_1$.
BC_1P_2 = $F_1 \times P_2$.

Table 2. Estimates of parameters in six crosses (susceptible × resistant) of pigeonpea, ICRISAT Asia Center, India, 1994.

	Crosses					
Parameters	UPAS 120 × KPBR 80-2-1	Pant A-3 × KPBR 80-2-1	ICPL 84023 × KPBR 80-2-1	ICPL 87119 × KPBR 80-2-1	ICPL 90005 × KPBR 80-2-1	ICPL 90035 × KPBR 80-2-1
Variance components						
E	0.03	0.05	0.04	0.04	0.03	0.02
D	-0.14	-0.10	-0.06	-0.21	-0.03	-0.42
H	0.08	-0.13	-0.14	0.04	-0.04	0.68
Degree of dominance H/D	0.78	1.17	1.49	0.43	1.14	1.27
Heritability						
Broad sense	62.65	64.00	61.28	81.63	43.75	75.00
Narrow sense	54.47	35.16	25.47	73.09	29.66	37.53
Heterosis						
Better parent	14.71	-20.59	-9.31	-37.25**	25.49*	20.10
Mid parent	-32.08**	-52.42**	-45.82**	-62.24**	-25.90**	-28.99**
Inbreeding depression	1.28	-58.02	-44.30	-86.70	1.56	-20.00
Significant scales	BC	B	–	AB	AC	BD
Best-fit model (based on weighted least square analysis)	mdhjl (transformed)	mdhj	mdh	mdhj	mdi	mdhil

* $P = 0.05$ and ** $P = 0.01$.
K at 30% = 1.16.

and ICPL 87119 × KPBR 80-2-1, where partial dominance was evident (Table 2). Heritability estimates were generally high and environmental variance was low. The resistance in the present material seems to be conditioned by an ontogenic effect also. The present resistant gene designated as pd_3 seems to be durable as well as different from that reported earlier (pd_1) by Sharma et al. (1982).

Since resistance has been found to be dominant it is easier to transfer to an otherwise susceptible variety through backcrossing. In order to transfer some of the minor genes, the F_1 between susceptible and resistant parents can be backcrossed to resistant parent, and plants with higher levels of resistance can be selected and used for crossing with recurrent parent to retain desirable features, other than resistance. A modified backcross method of breeding can also be adopted where F_1 is backcrossed, once or more than once, to the susceptible parent, and the resultant progenies from BC_1s or BC_ns are routed through typical pedigree method of breeding. Dominance of resistance to PB can also be utilized through a pedigree breeding program, where a large proportion of plants would be resistant in the F_2 generation.

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Effect of Different Crossing Procedures on Pod and Seed Set in Pigeonpea

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Pigeonpea flowers show parentheses cleistogamy which may result in self- or cross-pollination. The estimates of natural crossing vary between 2% and 70% depending on environmental conditions (Reddy 1990). Artificial crossing in pigeonpea is difficult because of the high percentage of flower drop. This paper reports the results of different times of emasculation and pollination during Oct–Dec 1994 and Feb–Mar 1995.

Four improved lines, ICPL 151, UPAS 120, Pant A-3, and ICPL 84023, were crossed in diallele fashion to produce six crosses. Two times were chosen for emasculation and pollination: 0730–1100 and 1500–1800. This resulted in four combinations; (a) evening emasculation-morning pollination, (b) morning emasculation-morning pollination, (c) morning emasculation-evening pollination, and (d) evening emasculation-evening pollination.

A total of 1482 crosses were attempted, i.e., 393 in method a, and 1089 in method b. In methods c and d pod set was less than 1.6% and therefore, these results are not presented. Overall pod set success rate was 9.5%. Morning emasculation followed by immediate pollination gave the highest pod set (12.1%). Pod set was greater in Oct–Dec as compared to Feb–Mar. Different cross combinations gave different percentage of pod set. UPAS 120 × ICPL 84023 gave the highest percentage of pod set (18.8%).

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