

## Heterosis and Combining Ability Study in Hybrids Developed from A<sub>2</sub> Cytoplasm of *Cajanus scarabaeoides* in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]

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**ABSTRACT:** The twenty-eight CGMS based pigeonpea [*Cajanus cajan* (L.) Millsp.] hybrids were examined in the experiment, which involved mating four CMS lines with seven restorer lines in a line by tester mating design evaluated to study heterosis and the combining abilities of hybrids and parents, along with two checks; GT 104 and GTH 1. The mean sum of squares resulting from genotypes was significant for all traits, in accordance with the analysis of variance. It indicates that the parents utilized in hybridization have an appropriate amount of variation. Five cross combinations, viz., GNP 3A × GNPR-20-18, GNP 3A × GNPR-20-10, GNP 4A × GNPR-21-23, GNP 1A × GNPR-20-18, and GNP 4A × GNPR-21-29, manifested significant and positive heterobeltiosis as well as significant standard heterosis over checks GT 104 and GTH 1. The presence of both additive and non-additive gene effects was found by means of combining ability analysis. With the exception of days to 50% flowering, days to maturity, and primary branches per plant, which showed a preponderance of non-additive genetic variation for the inheritance of these traits, the ratio of  $\sigma^2_{gca}/\sigma^2_{sca}$  demonstrated that all the characters under consideration showed less than unity. Among parents, GNP 3A and GNPR-20-18 were trustworthy general combiners for yield and other yield related traits among lines. The crosses GNP 4A × GNPR-21-23 and GNP 4A × GNPR-21-29 were found promising hybrids having significant *sca* effects for seed yield per plant. From the overall study, the crosses GNP 3A × GNPR-20-18, GNP 3A × GNPR-20-10, and GNP 4A × GNPR-21-23 showed higher *per se* performance along with significant and positive heterobeltiosis, standard heterosis, and a high *sca* effect for seed yield per plant, which suggested that these hybrids may be used for commercial cultivation. Hybrids with greater *sca* estimations were the consequence of average × average, good × average, good × good, and average × good general combiners.

**Keywords:** Pigeonpea, Cytoplasmic male sterile hybrids, heterosis and combining ability.

### INTRODUCTION

The pigeonpea is cultivated for both food and trade in the drought-prone and semi-arid tropics, formerly considered an orphan crop, has over time become a lifeline for millions of poor farmers. The genome size of the pigeonpea, having  $2n = 2x = 22$  diploid chromosomes and a cross-pollinated rate ranging from 20–70%, is 833.07 Mb (Varshney, 2015). It is always cultivated as an annual crop and belongs to the short-lived perennial Fabaceae family. India is thought to be the pigeonpea's centre of origin due to the natural genetic variety exhibited in the local germplasm and the presence of the plant's wild relatives there (Van der Maesen, 1980). It has been grown on 5.4 million hectares of land worldwide, producing 4.49 million tonnes per year (Simion, 2022). Around 75% of the world's pigeonpea production is produced in India,

which is also the leading producer. In India, total area coverage and production of pigeonpea were 4.80 million hectares and 4.32 million tons, respectively with 900 kg per ha productivity. Implementing heterosis and hybrid vigour in pigeonpea can increase yield because of the significant additive and non-additive gene activity in heterosis breeding (Saxena and Sharma 1990a). Since pigeonpea undergoes a significant amount of natural out-crossing (20–70%), non-additive genetic diversity can be exposed through the creation of heterotic hybrids (Saxena *et al.*, 1990b). This amount of out-crossing was discovered to be adequate for producing F<sub>1</sub> hybrid seeds as well as maintaining male-sterile lines. Numerous insects (Onim, 1981) mediate the out-crossing in this crop; wind has little impact on the process (Kumar and Saxena, 2001). In order to increase the yield, an

alternative breeding strategy called heterosis breeding was used. The main factors hindering the development of hybrids in legumes crops are low male to female pollen dispersal (low out-crossing rates), which is primarily caused by flower morphology and/or low insect pollinator participation; unstable male sterility systems; and a lack of excellent maintainers and restorers. These factors restrict the utilisation of heterosis in breeding for legumes and render large scale hybrid seed production in the majority of edible legumes crops neither efficient/easy nor economically feasible. In pigeonpea, a complete male sterility system, an effective mass pollen transmission mechanism, hybrid vigour, and a large scale seed production system are necessary for economically viable hybrid technology. Due to the accessibility of and consistency under a range of agro-climatic conditions, good maintainers and fertility restorers, the A2 (*C. scarabaeoides*) and A4 (*C. cajanifolius*) systems, which were developed through crosses between wild relatives and forms of pigeonpea and cultivated types, shown potential (Saxena and Nadarajan, 2010). A hybrid GTH-1 with early maturation was made utilising A2 cytoplasm and released by SDAU, Sardarkrushinagar for commercial cultivation in Gujarat state. The concern of whether hybrid technology might be used to satisfy all of our domestic pigeonpea demands has been investigated. Though the challenge is significant, it is not unresolved. The choice of production location is crucial even when seed production is not any longer a problem.

## MATERIALS AND METHODS

**Plant Material and Experimental Detail.** Four cytoplasmic sterile lines (GT 288A, GNP 1A, GNP 3A and GNP 4A) were crossed with seven restorer lines of pigeonpea during *kharif* 2021. At the Pulses and Castor Research Station, NAU, Navsari, a total of 28 F1s were developed and assessed alongside their parents and checks, GT 104 and GTH 1, during the following growing season, *kharif* 2022. A randomised complete block design involving three replications was used to set up the experiment. On July 23, 2022, seeds for each entry were planted individually in plots with a single row and a length of 3 m, with a space between plant and inter row of 20 cm and 90 cm, correspondingly. The recommended packages of practices were followed as per the recommendation to raise a healthy crop.

**Measurement of Growth Characteristics.** Five competing plants were chosen at random, and the polygenic characters were noted for each plant. *i.e.* plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), 100 grain weight (g), pollen fertility (%), Seed yield per plant (g). The phenological characters were recorded as visual assessment on plot basis *viz.* Days to 50% flowering and days to maturity. Harvest Index was calculated by using following formula [(Economic yield/Biological yield) × 100]. By multiplying the nitrogen content % by a factor of 6.5, the protein

content was determined using the micro-Kjeldahl technique (Stoskopf, 1985).

**Statistical Analysis.** The experimental data were collected by averaging mean values over each plot's randomly chosen plants, and they were then statistically analysed. In accordance with Panse and Sukhatme (1967), the experiment's design undergoes an analysis of variance. According to Kempthorne's (1957) technique, the combining ability study was carried out for a line by tester mating design.

## RESULTS AND DISCUSSION

The analysis of variance (Table 1 and 2) revealed that variances due to tester, parents, hybrids, parents *vs* hybrids and check *vs* rest of genotypes were significant for all the traits except seeds per pod. Variance due to line was significant for all the characters. Additionally, interactions and the mean sum of squares resulting from the lines x tester were shown to be highly significant for each of the twelve characters.

### Estimation of Heterobeltiosis and Standard Heterosis

On the basis of better parent heterosis, 20 crosses were found to be significant positive for seed yield per plant while on the basis of standard heterosis, 8 and 16 crosses were significant positive for seed yield per plant over standard checks GT 104 and GTH 1 (Table 3). In Table 6 shown that best performing cross according to standard heterosis *i.e.*, GNP 3A × GNPR-20-18 also had significant positive heterosis for seed yield per plant (Ashutosh *et al.*, 2017; Puttawar *et al.*, 2018; Patel *et al.*, 2020 and, Aarif *et al.*, 2022, and its component characters *viz.*, plant height, primary branches per plant, pods per plant, pod length, 100 grain weight, pollen fertility, harvest index, protein content indicating the presence of combination breeding as a result of cumulative effects of component characters. Others four cross combinations *viz.*, GNP 3A × GNPR-20-10, GNP 4A × GNPR-21-23, GNP 1A × GNPR-20-18 and GNP 4A × GNPR-21-29 manifested significant and positive heterobeltiosis as well as significant standard heterosis over checks GT 104 and GTH 1.

**General Combining Ability (GCA) and Specific Combining Ability (SCA).** An overall appraisal of *gca* effects revealed that among the female parents, GNP 3A and among the males, GNPR-20-18 were identified to be good general combiners for seed yield per plant and other yield attributing traits. and one or more component characters and were therefore highlighted as an important source of desirable genes for accumulating a greater yield either directly or indirectly through different component characters. The female parent GNP 1A was also good general combiner for days to 50 % flowering, days to maturity, and other yield component characters like 100 grain weight and pollen fertility. Similarly, female parent GT 288A was also found good general combiners for days to 50 % flowering, days to maturity and harvest index. while, the female parent GNP 4A was good general combiner for primary branches per plant and protein content. Male parent GNPR-20-22 was found to be good general combiner

for primary branches per plant, pod length, 100 grain weight and pollen fertility. The male parent GNPR-20-10 was good combiner for pod length, pollen fertility and protein content. Such parents could be utilized in a later breeding programme to increase pigeonpea production. Furthermore, it was found that parents possessing various general combining abilities for the same trait displayed differences in their offspring, proving that each male and female line has a unique genetic makeup and the capacity to pass on its traits to offspring. In general, it was evident from the Table 5 that parents which were good combiners for seed yield per plant were also good combiners for its component traits. It was also highlighted that, in a large number of instances, these parental contributions had also led to hybrids displaying beneficial heterosis for a variety of characters. According to the estimations of *sca* effects (Table 6), not any hybrid consistently outperformed the others in all attributes. Nine of the 28 hybrids that were studied had notable positive *sca* effects on the number of seeds produced per plant. The hybrids GNP 4A × GNPR-21-23, GNP 4A × GNPR-21-29 and GNP 3A × GNPR-20-10 were considered as best specific cross combinations as they depicted highest significant positive *sca* effects for seed yield per plant and it was also supported by previous workers in pigeonpea (Srivarsha *et al.*, 2017; Marawar *et al.*, 2018; Patel *et al.*, 2018; Patel *et al.*, 2020; and Chandra *et al.*, 2021). Among these hybrids, hybrid GNP 4A × GNPR-21-23 also had significant and desirable *sca* estimates for plant height, primary branches per plant, pods per plant and harvest index. The hybrid GNP 4A × GNPR-21-29 also recorded significant and desirable *sca* estimates for the characters plant height, pods per plant, 100 grain weight and protein content. As for days to 50% flowering, pods per plant, pod length, 100 grain weight, harvest index, and protein content, the hybrid GNP 3A × GNPR-20-10 likewise showed substantial and good *sca* effects. The fact that not necessarily both parents in a cross with a high *sca* effect also had demonstrates the importance of intra- and inter-allelic interactions.

Although strong heterotic response and high *sca* effects of crosses usually work together in the same direction, these effects may also be accompanied by poor and/or average *gca* effects of the parents.

The hybrids with high *sca* effects for seed yield per plant usually noticed positive *sca* effects for the majority of the yield-contributing traits, nevertheless those might not necessarily have higher *sca* effects for those traits. This suggested that the cumulative impact of the various yield components may result in high *sca* effects for seed yield and, consequently, high heterotic effects as well.

The best performing five hybrids for seed yield per plant viz., GNP 4A × GNPR-21-23 (average × average), GNP 4A × GNPR-21-29 (average × average), GNP 3A × GNPR-20-10 (good × average), GNP 3A × GNPR-20-18 (good × good) and GNP 1A × GNPR-20-18 (average × good) also had significant positive *sca* effects and high heterotic response over better parent and standard check hybrid.

**Estimates of Genetic Components.** The ratio of GCA to SCA variance ( $\sigma^2_{gca}/\sigma^2_{sca}$ ) was found less than unity (Table 4) for plant height, pods per plant, pod length, seeds per pod, 100 grain weight, pollen fertility, seed yield per plant, harvest index and protein content indicating the pre-dominance of non-additive nature of genes governing the various characters and more than one (unity) for days to 50 % flowering, days to maturity and primary branches per plant indicating the preponderance of additive nature of genes governing the characters. For each character, the additive and dominance variances (Table 4) were estimated. Days to 50 % flowering, days to maturity, and the primary branches per plant all showed additive variance that was greater than dominance variance, suggesting that these traits may be more responsive to selection. All of the traits, with the exception of those already stated, exhibited more dominant variance than additive variation, hence improving such characters would be accomplished by heterosis breeding.

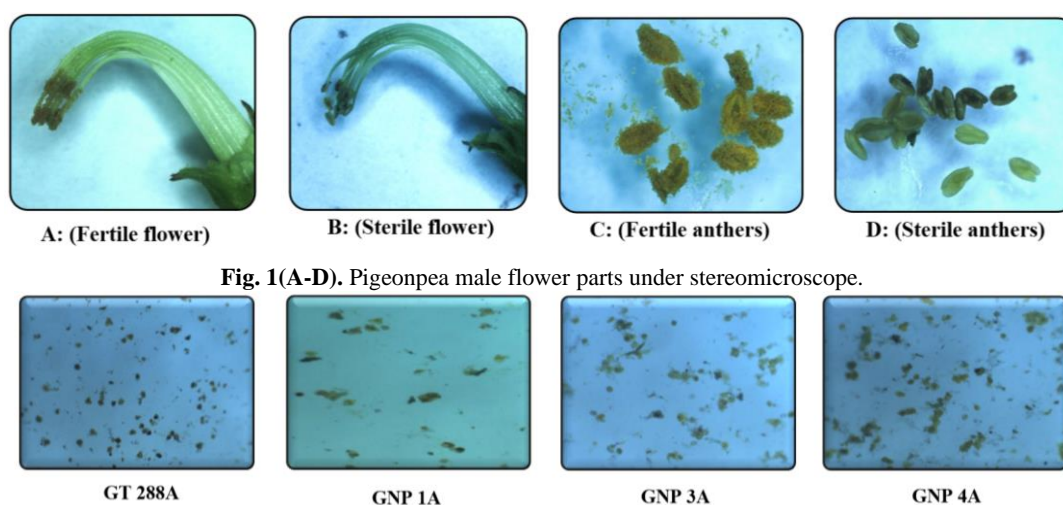
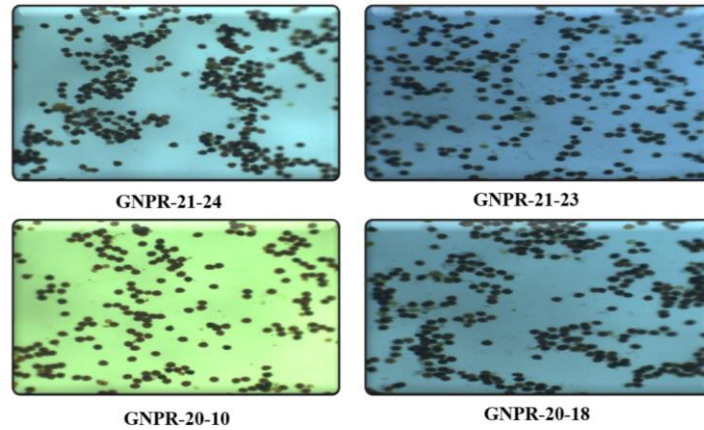
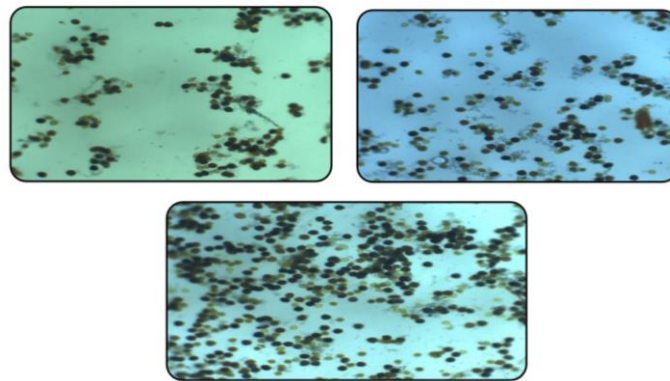


Fig. 2. Pollen study of all pigeonpea male sterile lines *i. e.* GT 288A, GNP 1A, GNP 3A and GNP 4A under stereomicroscope.



**Fig. 3.** Pollen study of best identified pigeonpea restorer lines *i. e.* GNPR-21-24, GNPR-21-23, GNPR-20-10 and GNPR- 20-18 under stereomicroscope.



**Fig. 4.** Pollen study of best pigeonpea hybrids *i. e.* GNP 3A x GNPR-20-18, GNP 3A x GNPR-20-10, GNP 4A x GNPR-21-23 under stereomicroscope.

**Table 1: Analysis of variance for combining ability following line x tester mating design for 12 quantitative characters in pigeonpea.**

Source of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	100 grain weight (g)	Pollen fertility (%)	Seed yield per plant (g)	Harvest index (%)	Protein content (%)
Replications	2	0.84	0.50	50.66	0.17	431.49	0.04	0.01	0.80	5.20	84.22*	127.61**	0.04
Genotypes	40	126.38**	307.00**	522.91**	42.88**	2877.10**	0.33**	40	0.88**	3.99**	80.94**	292.60**	122.11**
Parents	10	133.45**	390.55**	1022.2**	23.47**	834.42**	0.73**	10	0.37**	4.68**	21.58**	151.28**	88.39**
Hybrids	27	69.86**	167.37**	174.09**	44.44**	2095.65**	0.10**	27	0.18**	2.84**	59.20**	279.52**	81.14**
Parents vs Hybrids	1	720.08**	2718.68**	5762.67**	133.65**	49012.84**	0.31**	1	4.57**	26.06**	909.43**	2308.88**	1215.96**
Check vs Rest of genotypes	1	74.07**	173.99**	118.72	8.67*	1144.46*	0.55**	1	12.28**	3.89**	112.22**	91.80*	588.34**
Error	80	1.61	3.23	61.49	1.95	198.78	0.01	80	0.07	0.29	2.11	19.42	11.84

\*, \*\* Significant at 5 percent and 1 percent levels of significance, respectively.

**Table 2: Analysis of variance for combining ability following line x tester mating design for 12 quantitative characters in pigeonpea.**

Source of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	100 grain weight (g)	Pollen fertility (%)	Seed yield per plant (g)	Harvest index (%)	Protein content (%)
Replications	2	0.84	0.50	50.66	0.17	431.49	0.04	0.01	0.80	5.20	84.22*	127.61**	0.04
Line effect	3	540.14**	1394.56**	229.69*	287.32**	6741.92**	0.17**	0.44**	7.85**	95.61**	1184.44**	58.52**	19.39**
Tester effect	6	14.50**	11.33**	209.71**	31.70**	1179.93**	0.17**	0.11	4.53**	60.67**	164.91**	128.58**	7.37**
Line x Tester effect	18	9.93**	14.85**	152.95**	8.20**	1626.51**	0.06**	0.16**	1.44**	52.64**	166.9**	69.09**	12.22**
Error	54	1.88	3.14	58.06	2.07	159.87	0.01	0.07	0.28	2.71	23.26	14.81	0.02

\*, \*\* Significant at 5 percent and 1 percent levels of significance, respectively.

**Table 3: Range of heterobeltiosis (H1) and standard heterosis (GT 104 and GTH 1) as well as number of crosses with significant heterotic effects for various characters in pigeonpea.**

Sr. No.	Characters	Range of heterosis (%)			Number of crosses with significant heterosis					
		Heterobeltiosis (%)	Standard heterosis 1 (%)	Standard heterosis 2 (%)	H1 (%)		GT 104 (%)		GTH 1 (%)	
					+Ve	-Ve	+Ve	-Ve	+Ve	-Ve
1.	Days to 50% flowering	-7.73 to 3.93	-14.68 to -1.39	9.22 to 26.24	3	4	0	27	28	0
2.	Days to maturity	-8.29 to 4.91	-12.18 to 0.59	3.23 to 18.24	8	11	0	22	28	0
3.	Plant height	-3.17 to 14.52	-5.98 to 11.18	-0.67 to 17.46	8	0	4	0	14	0
4.	Primary branches per plant	74.24 to 756.06	-71.95 to 37.8	-5.74 to 363.11	24	0	2	13	24	0
5.	Pods per plant	-18.22 to 89.39	-18.39 to 89.01	-0.53 to 8.81	20	0	14	0	13	0
6.	Pod length	-4.62 to 7.18	-16.22 to -5.86	1.20 to 13.71	4	7	0	28	25	0
7.	Seeds per pod	-1.72 to 25.86	-45.19 to -29.81	-13.64 to 10.61	14	0	0	28	1	2
8.	100 grain weight	-11.36 to 43.79	-36.9 to 2.37	-22.82 to 25.2	19	1	0	27	3	6
9.	Pollen fertility (%)	-25.00 to -0.52	-30.61 to -7.96	-16.29 to 11.02	0	26	0	28	13	4
10.	Seed yield per plant	22.34 to 285.9	-45.65 to 71.45	-0.90 to 212.58	20	0	8	10	16	0
11.	Harvest index (%)	-36.15 to 14.49	30.95 to 134.79	18.17 to 111.87	0	14	27	0	23	0
12.	Protein content (%)	-20.38 to 17.26	-21.99 to 14.89	-22.25 to 14.51	11	11	9	11	9	11

**Table 4: GCA variance, SCA variance, ratio of GCA and SCA variance, additive variance and dominant variance for 12 quantitative characters in pigeonpea.**

Sr. No.	Characters	GCA variance ( $\sigma^2$ GCA)	SCA variance ( $\sigma^2$ SCA)	$\sigma^2$ GCA/ $\sigma^2$ SCA	Additive variance ( $\sigma^2$ A)	Dominance variance ( $\sigma^2$ D)
1.	Days to 50% flowering	16.21**	2.77**	5.85	64.82	11.09
2.	Days to maturity	41.70**	3.87**	10.76	166.81	15.5
3.	Plant height	4.05*	30.49**	0.13	16.18	121.94
4.	Primary branches per plant	9.17**	2.08**	4.4	36.68	8.34
5.	Pods per plant	141.48**	475.91**	0.3	565.92	1903.64
6.	Pod length	0.01**	0.02**	0.38	0.03	0.07
7.	Seeds per pod	0.01**	0.03**	0.21	0.03	0.13
8.	100 grain weight	0.29**	0.38**	0.75	1.15	1.54
9.	Pollen fertility (%)	1.55**	16.84**	0.09	6.18	67.36
10.	Seed yield per plant	30.77**	49.16**	0.63	123.1	196.64
11.	Harvest index (%)	1.48**	19.08**	0.08	5.93	76.34
12.	Protein content (%)	16.21**	2.77**	5.85	64.82	11.09

\*, \*\* Significant at 5 percent and 1 percent levels of significance, respectively.

**Table 5: General combining ability effect of parents for different characters in pigeonpea.**

Sr. No.	Parents	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	100 grain weight (g)	Pollen fertility (%)	Seed yield per plant (g)	Harvest index (%)	Protein content (%)
Lines													
1	GT288A	-4.02**	-7.98**	3.18	-4.68**	-22.00**	-0.03	-0.08	0.07	0.50	-10.09**	2.35*	-0.35**
2	GNP 1A	-4.74**	-6.07**	2.31	-1.10*	-2.42	-0.11**	-0.11	0.79**	2.75**	0.16	-1.02	-1.13**
3	GNP 3A	4.12**	7.21**	-1.68	3.66**	21.57**	0.10**	0.21*	-0.18	-1.08*	7.97**	0.02	1.12**
4	GNP 4A	4.64**	6.83**	-3.81	2.12**	2.85	0.04	-0.02	-0.68**	-2.17**	1.96	-1.35	0.36**
	SE(g)	0.39	0.55	2.42	0.43	4.35	0.04	0.08	0.16	0.45	1.36	1.06	0.12
Testers													
1	GNPR-20-10	0.12	0.83	3.31	0.67	10.61	0.10*	-0.16	-0.26	2.18**	2.34	-1.66	1.36**
2	GNPR-20-18	-1.05*	0.17	7.03*	1.76**	-8.44	0.13**	0.09	1.08**	-1.77**	5.38**	-3.63*	-0.56**
3	GNPR-20-22	2.04**	-0.33	0.39	2.36**	-13.46*	0.12*	-0.06	0.66**	3.56**	-0.21	2.59	0.25
4	GNPR-21-23	-0.88	-1.33	-0.11	-0.45	5.21	-0.02	0.06	-0.32	0.58	0.94	5.75**	-0.22
5	GNPR-21-24	0.29	0.83	-4.07	-1.39*	9.71	-0.13**	-0.07	-0.52*	-2.64**	-4.00*	-1.71	-0.23
6	GNPR-21-29	-0.96	1.00	-1.48	-1.13	5.14	-0.04	0.09	-0.23	-0.40	1.04	0.87	0.46**
7	GNPR-21-30	0.45	-1.17	-5.06	-1.83**	-8.77	-0.16**	0.04	-0.42	-1.51*	-5.48**	-2.21	-1.07**
	SE(g)	0.52	0.73	3.20	0.57	5.76	0.05	0.11	-0.26	0.59	1.80	1.40	0.16

\*, \*\* Significant at 5 percent and 1 percent levels of significance, respectively.

**Table 6: Specific combining ability effect of parents for different characters in pigeonpea.**

Sr. No.	Crosses	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	100 grain weight (g)	Pollen fertility (%)	Seed yield per plant (g)	Harvest index (%)	Protein content (%)
1	GT 288A × GNPR-20-10	-1.66	-1.00	-0.96	0.61	-0.42	-3.26**	-0.16	-1.57	1.01	-0.73	-0.65	19.37**
2	GT 288A × GNPR-20-18	1.51	1.28	-0.16	-0.62	-1.56	-4.44**	0.40	-3.40**	4.30**	-2.44*	-2.68**	-26.13**
3	GT 288A × GNPR-20-22	-1.55	-0.19	-0.24	1.11	-1.35	0.36	-0.82	0.63	-1.08	1.46	1.46	10.42**
4	GT 288A × GNPR-21-23	2.14*	1.44	-2.57*	-2.17*	-2.57*	-0.84	-1.15	0.32	-1.28	0.86	0.86	-7.82**
5	GT 288A × GNPR-21-24	-1.44	-3.28**	0.79	-0.04	2.00*	3.76**	2.39*	1.97	-1.28	2.32*	2.67**	9.51**
6	GT 288A × GNPR-21-29	1.40	0.14	0.99	0.73	1.76	0.77	0.40	1.33	-6.1**	0.83	-3.59**	-10.15**
7	GT 288A × GNPR-21-30	-0.39	1.60	2.16*	0.37	2.13*	3.65**	-1.04	1.03	1.11	2.38*	1.94	4.8**
8	GNP 1A × GNPR-20-10	-0.75	-1.23	0.97	0.63	1.71	-0.15	-0.79	-0.91	-1.20	-1.06	-2.21*	-35.73**
9	GNP 1A × GNPR-20-18	0.30	-0.26	0.94	0.04	2.30*	0.45	-0.24	1.74	3.25**	2.05*	2.43*	-27.41**
10	GNP 1A × GNPR-20-22	-2.75**	-2.37*	0.05	0.37	1.13	-1.20	-0.57	-1.86	0.46	0.25	-0.18	-1.95
11	GNP 1A × GNPR-21-23	1.78	0.23	1.20	0.30	-3.22**	0.21	3.97**	2.52*	-3.40**	-0.36	-1.46	21.53**
12	GNP 1A × GNPR-21-24	1.14	2.35*	0.18	-0.87	-2.79**	-0.63	-2.23*	-1.49	4.71**	-1.76	-0.56	15.83**
13	GNP 1A × GNPR-21-29	-1.07	-1.40	-1.12	-0.66	-0.03	0.46	1.57	-1.21	4.39**	2.10*	1.58	18.37**
14	GNP 1A × GNPR-21-30	1.35	2.67**	-2.22*	0.19	0.90	0.86	1.42	1.22	1.21	-1.22	0.40	9.36**
15	GNP 3A × GNPR-20-10	3.22**	0.44	1.01	-1.37	2.16*	2.67**	0.60	2.44*	-2.96**	2.48*	2.06*	5.27**
16	GNP 3A × GNPR-20-18	0.06	-0.86	1.15	3.17**	2.58*	4.44**	-0.62	0.90	4.02**	2.29*	1.41	13.72**
17	GNP 3A × GNPR-20-22	0.80	2.88**	0.05	-0.71	0.28	-1.28	1.26	-0.38	-2.99**	0.92	-0.79	-15.4**
18	GNP 3A × GNPR-21-23	-3.10**	-2.33*	-0.81	-1.98	-1.63	1.25	-1.72	-1.94	-0.87	-2.43*	-2.37*	20.83**
19	GNP 3A × GNPR-21-24	1.32	3.05**	0.49	3.44**	2.38*	-2.20*	-0.40	1.72	3.15**	2.15*	-0.54	26.88**
20	GNP 3A × GNPR-21-29	1.22	-0.37	-2.07*	-1.41	-4.45**	-0.87	0.71	-3.34**	1.74	-5.73**	2.01*	-24.12**
21	GNP 3A × GNPR-21-30	-3.52**	-2.81**	0.17	-1.13	-1.34	-4.01**	0.16	0.60	-2.09*	0.31	-1.78	-27.18**
22	GNP 4A × GNPR-20-10	-0.81	1.79	-1.02	0.13	-3.45**	0.74	0.35	0.04	3.15**	-0.70	0.80	11.08**
23	GNP 4A × GNPR-20-18	-1.87	-0.16	-1.93	-2.59*	-3.32**	-0.44	0.46	0.76	-11.57**	-1.91	-1.15	39.82**
24	GNP 4A × GNPR-20-22	3.51**	-0.33	0.15	-0.77	-0.07	2.12*	0.13	1.65	1.90	-0.09	-0.49	6.92**
25	GNP 4A × GNPR-21-23	-0.81	0.65	2.18*	3.85**	7.41**	-0.62	-1.09	-0.61	3.95**	4.07**	2.97**	-34.53**
26	GNP 4A × GNPR-21-24	-1.02	-2.12*	-1.46	-2.53*	-1.60	-0.93	0.24	-2.21*	2.84**	-2.70**	-1.57	-52.21**
27	GNP 4A × GNPR-21-29	-1.55	1.63	2.20*	1.33	2.72**	-0.37	0.46	3.21**	-0.03	2.80**	0.00	15.9**
28	GNP 4A × GNPR-21-30	2.56*	-1.47	-0.11	0.57	-1.69	-0.50	-0.54	-2.85**	-0.23	-1.47	-0.56	13.02**

\*, \*\* Significant at 5 percent and 1 percent levels of significance, respectively.

**Table 7: Best heterotic crosses and their performance for seed yield per plant and related parameters in pigeonpea.**

Best crosses (P <sub>1</sub> × P <sub>2</sub> )	Mean yield per plant (g)	Batter parent heterosis (%)	Standard Heterosis (%)		Significant standard heterosis of other traits in desired direction
			GT 104	GTH 1	
GNP 3A × GNPR-20-18	48.37	285.90**	71.45**	212.58**	DF, DM, PH, PBP, PP, PL, GW, PF, HI, PC
GNP 3A × GNPR-20-10	45.87	265.96**	62.59**	196.42**	DF, PH, PBP, PP, PL, HI, PC
GNP 4A × GNPR-21-23	42.87	242.02**	51.96**	177.04**	DF, DM, PBP, PP, PL, PF, HI
GNP 1A × GNPR-20-18	39.88	218.22**	41.38**	157.76**	DF, DM, PH, PBP, PP, PL, GW, PF, HI
GNP 4A × GNPR-21-29	39.43	214.63**	39.78**	154.85**	DF, PH, PBP, PP, PL, HI, PC

\*, \*\* Significant at 5 percent and 1 percent levels of significance, respectively.

DF = Days to 50 % flowering, DM = Days to maturity, PH = Plant height, PBP = Primary branches per plant, PP = Pods per plant, PL = Pod length, SPP = Seeds per pod, GW = 100 grain weight, PF = Pollen fertility, SYPP = Seed yield per plant, HI = Harvest index, PC = Protein content

## CONCLUSIONS

In order to potentially increase production through the creation of hybrid cultivars in pigeonpea, heterosis breeding has been employed extensively. The estimates of heterosis for seed yield per plant showed that the five hybrids viz., GNP 3A × GNPR-20-18, GNP 3A × GNPR-20-10, GNP 4A × GNPR-21-23, GNP 1A × GNPR-20-18 and GNP 4A × GNPR-21-29 based on superior parent, standard heterosis, and *per se* performance, were deemed to be the most promising. Both additive and non-additive gene effects, with non-additive gene effects predominant, had an impact on the inheritance of seed yield and its constituent parts. On the basis of general combining ability the most promising parents identified was GNP 3A, among CMS lines and GNPR-20-18 among R lines.

## FUTURE SCOPE

Out of 28 hybrids evaluated, 9 hybrids showed significant positive *sca* effects for seed yield per plant. Among them best cross combinations viz., GNP 4A × GNPR-21-23, GNP 4A × GNPR-21-29 and GNP 3A × GNPR-20-10 which had high estimates for parents and good *sca* effects may be considered for commercial exploitation of hybrids.

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