

Short Communication

Estimation of heterosis on CGMS based pigeonpea

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The term "pigeonpea" was coined by Barbados, where its seeds were considered an important pigeon-feed. Pigeonpea [*Cajanus cajan* (L.) Millspaugh], is the second most important pulse crop of India in area and production after chickpea. Pigeonpea belonging to the family *Fabaceae* with chromosome number $2n = 22$. The East Indies is the primary centre of origin for pigeonpea (Linnaeus 1937). Vavilov (1939) has also reported that India is the native of pigeonpea. The world's three primary regions for the production of pigeonpea are the Indian subcontinent, Eastern Africa, and Central America, in that order. Pigeonpea is cultivated in more than 25 tropical and sub-tropical countries, either as a sole crop or inter/mixed with cereals (sorghum, pearl millet, maize) and legumes (groundnut). Pigeonpea is differ from other legumes as it exhibits large variation (20-70%) in natural outcrossing, The out-crossing nature of pigeonpea has been explored for heterosis breeding using genetic male sterility (GMS) system reported by Reddy *et al.* (1978). In hybrid breeding technology, this significant proportion of natural outcrossing has been effectively utilized. In hybrid development programme to overcome the production constraints, an improved hybrid seed production technology based on more efficient cytoplasmic-genetic male-

ABSTRACT

Thirty-five hybrids generated from seven cytoplasmic male sterile lines and five fertility restorer lines were tested for determining heterosis. All studied traits except pod length, number of seeds per pod, and leaf area showed significant variations between the parents indicating a sufficient variability amongst the parents (lines and testers). The mean sum of squares of the hybrids suggested high heterosis for studied traits except for test weight and number of branches per plant. The findings showed noteworthy and affirmative relative heterosis for eaj hybrid. Top three hybrids *viz.* CMS GT 1615 A × GTR 105 (28.34% and 38.97%), CMS GT 1615 A × GTR 18 (24.36% and 34.66%) and CMS GT 1615 × GTR 23 (22.23% and 32.35%) identified for seed yield and its contributing traits on the basis of standard heterosis against standard checks GTH 1 and GT 101, respectively. These can be exploited commercially for heterosis breeding in pigeonpea.

Key words: CGMS, Cytoplasmic genic male sterility, Heterosis, Male sterility, Pigeonpea

sterility (CGMS) system was planned and achieved by integrating cytoplasm of wild relatives of pigeonpea with cultivated pigeonpea. The Line × Tester analysis helps in identifying superior parents and crosses which found the basic requirement for the success of any breeding programme. However, this investigation aims to know the extent of heterosis for seed yield and its contributing characters and further improvement of CMS lines and restorer lines.

The experimental material included five different restorers (GTR 18, GTR 23, GTR 37, GTR 92, and GTR 105), and seven cytoplasmic male sterile lines (CMS GT 301 A, CMS GT 307 A, CMS GT 1004 A, CMS GT 1402 A, CMS GT 1603 A, CMS GT 1604 A, and CMS GT 1615 A). The crossing work carried out at Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, during *kharif* 2019. The complete set of 49 genotypes comprising of 7 cytoplasmic male sterile lines, 5 diverse restorers, resultant 35 hybrid combinations and 2 checks *viz.*, GTH 1 and GT 101 were evaluated in a Randomized Block Design with three replications during *kharif* 2020. The observations were recorded based on five randomly selected competitive plants for various fourteen characters *i.e.*, plant height (cm), number

of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), seed yield per plant (g), biological yield per plant (g), harvest index (%), leaf area per plant (cm²), total protein content (%) and pollen fertility (%) in each replication for each genotype and the average value per plant was computed except for the phenological characters *viz.*, days to flowering and days to maturity which recorded on plot basis. The mean values of replication-wise for various characters were subjected to analysis of variance as per the procedure given by Panse and Sukhatme (1985).

Analysis of variance (table 1) for seed yield and its contributing traits except of pod length, number of seeds per pod, and leaf area, all the traits showed significant variations between the parents. This suggested that for the majority of the traits under study, there was a sufficient degree of variability in the parents (lines and testers). Analysis of variance for seed yield and its contributing traits except of pod length, number of seeds per pod, test weight, and leaf area, all of the traits mean sum of squares due to lines were significant. Analysis of variance for seed yield and its contributing traits except of plant height, number of branches per plant, number of pods per plant, length of pod, number of seeds per pod, seed yield per plant, and harvest index, the mean sum of squares provided by the testers was significant for all the traits. Analysis of variance for seed yield and its contributing traits except of test weight and the number of branches per plant, the mean sum of squares resulting from hybrids was significant for all the traits. Furthermore, for every feature except pod length, the mean sum of squares resulting from parent *vs.* hybrids was significant, indicating the presence of considerable heterosis for these traits. Analysis of variance for seed yield and its contributing traits except of test weight, seed production per plant, harvest index, number of branches per plant, number of pods per plant, pod length, and number of seeds per pod, mean sum of squares owing to line *vs.* tester significant for all the traits. The mean performance of parents and hybrids for quantitative and qualitative traits evinced that none of the females or males show consistent good performance for all the traits. Seed yield in female parents exhibited variation from 39.82 (CMS GT 1604 A) to 65.23 g (CMS GT 1615 A), whereas in male parents, it was varied from 44.83 (GTR 37) to 55.76 g (GTR 18). The variation for seed yield among the hybrids was from 64.29 (CMS GT 301 A × GTR 105) to 104.35 g (CMS GT 1615 A × GTR 105). Higher

seed yield obtained by parents *viz.* CMS GT 1615 A (65.23 g), CMS GT 1402 A (56.28 g), GTR 18 (55.76 g) and CMS GT 301 A (55.22 g). In hybrids, more seed yield obtained by CMS GT 1615 A × GTR 105 (104.35 g), CMS GT 1615 A × GTR 18 (101.11 g), CMS GT 1615 A × GTR 23 (99.38 g) and CMS GT 1603 A × GTR 92 (97.57 g).

The percentage change in the F_1 value over the mid-parent (relative heterosis), better parent (heterobeltiosis), and standard checks (GTH 1 and GT 101, standard heterosis) for various qualities indicates the amount of heterosis. The magnitude of heterosis observed in different characters varied from cross to cross.

All of the hybrids showed considerable and positive relative heterosis, according to Table 2 data. The range of relative heterosis was from 25.02 (CMS GT 301 A × GTR 105) to 103.10 per cent (CMS GT 1004 A × GTR 37). The estimated of heterobeltiosis revealed that thirty two hybrids possessed significant positive heterotic effect over its better parent. The variation range of heterobeltiosis was from 16.44 (CMS GT 301 A × GTR 105) to 95.14% (CMS GT 1004 A × GTR 37).

Six hybrids for GTH 1 and fourteen for GT 101 exhibited significant and positive standard heterosis. The standard heterosis ranged from -20.93 (CMS GT 301 A × GTR 105) to 28.34 per cent (CMS GT 1615 A × GTR 105) for GTH 1 and from -14.38 (CMS GT 301 A × GTR 105) to 38.97 per cent (CMS GT 1615 A × GTR 105) for GT 101. Three most positive heterotic crosses for GTH 1 and GT 101 in descending order were CMS GT 1615 A × GTR 105 (28.34% and 38.97%), CMS GT 1615 A × GTR 18 (24.36% and 34.66%) and CMS GT 1615 × GTR 23 (22.23% and 32.35%), respectively.

Table 3 showed that for seed yield per plant, the hybrid CMS GT 1615 × GTR 105 (28.24%) had the highest standard heterosis above GTH 1. For seed output per plant, all five hybrids exhibited positive heterobeltiosis. Significant heterosis was also demonstrated by the majority of these hybrids for the component traits, including as leaf area, harvest index, and pods per plant. Similar findings were also evident by the findings Wankhede *et al.* (2005), Ali *et al.* (2007), Chauhan *et al.* (2008), Patel and Tikka (2008), Acharya *et al.* (2009), Gite *et al.* (2009), Sarode *et al.* (2009), Gupta *et al.* (2011), Patel and Tikka (2014), Chethana *et al.* (2015) and Patel *et al.* (2020).

The current study showed heterosis for seed yield and its contributing characteristics. So, heterosis

Table 1. Analysis of variance showing mean sum of squares for different characters in pigeonpea

Source of variation	d.f.	Days to flowering	Days to maturity	Plant height	Number of branches per plant	Number of pods per plant	Pod length	Number of seeds per pod
Replications	2	1.82	1.43	7.30	1.55	31.86	0.07	0.03
Parents	11	271.33**	263.15**	369.39**	2.28*	774.19**	0.13	0.04
Lines	6	152.32**	159.08**	445.81*	2.96*	1050.17**	0.20	0.05
Testers	4	456.77**	425.00**	137.46	1.55	476.66	0.05	0.04
Lines vs Testers	1	243.59**	240.08**	838.56*	1.07	308.43	0.01	0.01
Parents vs Hybrids	1	1138.20**	979.98**	8143.48**	53.74**	155990.97**	2.27	1.06**
Hybrids	34	237.49**	218.92**	311.67*	0.84	1854.11**	0.15**	0.16**
Error	92	7.62	8.33	186.72	1.00	248.64	0.13	0.07

Table 1: Continue.....

Source of variation	d.f.	Test weight	Seed yield per plant	Biological yield	Harvest index	Leaf area	Protein content
Replications	2	0.18	0.39	378.83	1.85	5262.65	0.02
Parents	11	0.44*	160.32**	2771.87**	20.36**	48339.16	4.1**
Lines	6	0.40	238.25**	2478.95*	30.90**	12212.51	1.59**
Testers	4	0.60*	59.26	3108.87**	9.62	73221.21*	8.61**
Lines vs Testers	1	0.05	96.94	3181.46*	0.04	165564.92**	1.11**
Parents vs Hybrids	1	5.08**	30763.19**	150999.13**	836.26**	29152702.9**	18.56**
Hybrids	34	0.12	359.26**	2576.80**	8.67*	134104.08**	5.80**
Error	92	0.19	60.58	561.06	4.93	27927.15	0.08

*, ** Significant at 5 per cent and 1 per cent levels of significance, respectively

Table 2. Magnitude of heterosis for different thirteen characters in pigeonpea

Sr. No.	Characters	MP (Range)	No. of significant hybrids in desired direction for MP	BP (Range)	No. of significant hybrids in desired direction for MP	SH GTH 1 (Range)	No. of significant hybrids in desired direction for MP	SH GT 101 (Range)	No. of significant hybrids in desired direction for MP
1	Days of flowering	-22.67 to 7.38	20	-26.44 to 3.00	27	-13.81 to 27.28	5	-12.64 to 19.01	5
2	Days of maturity	-16.07 to 5.39	18	-19.92 to 3.53	24	-8.49 to 17.86	6	-7.66 to 18.92	5
3	Plant height	-2.88 to 28.54	0	-7.16 to 23.73	0	-5.64 to 21.44	0	-10.54 to 15.14	0
4	Number of branches per plant	1.66 to 36.92	20	-5.56 to 34.51	11	3.35 to 29.02	10	-3.14 to 20.93	1
5	Number of pods per plant	12.99 to 90.43	34	1.52 to 81.40	33	-24.55 to 20.29	6	-25.72 to 18.44	5
6	Pod length	-14.56 to 3.92	0	-17.68 to 1.92	0	-2.23 to 18.52	5	-12.00 to 6.67	0
7	Number of seed per pod	-3.51 to 21.37	6	-5.17 to 17.86	4	-11.22 to 14.61	1	-8.34 to 18.34	1
8	Test weight	-0.56 to 13.19	9	-2.19 to 12.14	1	0.15 to 8.99	5	4.14 to 13.33	27
9	Seed yield per plant	25.02 to 103.10	35	16.44 to 95.14	32	-20.93 to 28.34	6	-14.38 to 38.97	14
10	Biological yield per plant	5.35 to 55.93	32	-3.08 to 50.73	25	-27.84 to 3.64	0	-23.09 to 10.46	1
11	Harvest index	-3.61 to 63.79	33	-4.34 to 54.12	25	-5.34 to 27.76	16	-4.08 to 29.46	18
12	Leaf area	40.83 to 91.25	35	21.10 to 82.99	35	-7.84 to 21.52	17	-21.50 to 3.51	0
13	Protein content	-13.63 to 20.46	26	-18.91 to 14.65	14	-21.81 to 7.39	3	-18.06 to 12.54	6

MP:- Heterosis over mid parent, BP:- Heterosis over better parent, SH:- Heterosis over standard check GTH 1 and GT 101

Table 3. Best five high yielding hybrids with heterosis (%) over better parent and standard check and component traits showing significant standard heterosis

Sr. No.	Five best hybrids on the basis of seed yield	Mean seed yield per plant (g)	Heterosis (%) Over			Significant standard heterosis for component traits in desired direction
			MP	BP	Best SC	
1.	CMS GT 1615 A × GTR 105	104.35	84.89**	59.96**	28.34**	SP, TW, HI, LA
2.	CMS GT 1615 A × GTR 18	101.11	67.14**	55.00**	24.36**	PP, HI, LA
3.	CMS GT 1615 A × GTR 23	99.38	75.90**	52.35**	22.23**	BP, PP, HI, LA
4.	CMS GT 1603 A × GTR 92	97.57	97.44**	81.38**	20.00*	DM, PP, HI
5.	CMS GT 1603 A × GTR 105	96.21	89.70**	78.86**	18.33*	DE, DM, PP, HI

DF = Days to flowering; DM = Days to maturity; BP = Number of branches per plant; PP = Number of pods per plant; PL = Pod length; TW = Test weight; HI = Harvest index; LA = Leaf area; PC = Total protein content

breeding strategy should be applied extensively in Pigeonpea to achieve yield advantage. Top three hybrids *viz.* CMS GT 1615 A × GTR 105 (28.34% and 38.97%), CMS GT 1615 A × GTR 18 (24.36% and 34.66%) and CMS GT 1615 × GTR 23 (22.23% and 32.35%) found promising for seed yield and its contributing traits against standard checks GTH 1 and GT 101, respectively, suggesting for the direct commercial cultivation of hybrids after assessing their performance in a variety of environments in pigeonpea.

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