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Exploitation of heterosis in hybrids developed using cytoplasmic genetic male sterility (CGMS) system in pigeonpea [*Cajanus cajan* (L.) Millspaugh]

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Abstract

To ascertain heterosis forty hybrids were developed from fourteen parents in a line x tester mating design during *kharif*, 2017-18 and tested in a Randomized Block Design with three replications during *kharif*, 2018-19. The analysis of variance revealed that the mean sum of squares due to lines were significant for all characters except number of seed per pod and 100 seed weight, whereas the mean sum of squares due to testers were significant for all characters except number of seed per pod and seed yield per plant. This indicates the presence of sufficient amount of variability in parents utilized for hybridization. The mean sum of squares due to lines vs testers was significant for all characters except days to flowering, days to maturity, plant height, number of seed per pod and 100 seed weight. The mean sum of squares due to parents vs hybrids as well as due to hybrids were significant for all characters. The analysis of variance further revealed that the significant difference was found among lines, tester and hybrids for all the characters. This indicates that there is good chance of exploit the heterosis from present investigation. The estimates of heterosis showed that the five hybrids CMS GT 1603 A x GTR 23, CMS GT 288 A x GTR 55, CMS GT 1603 A x GTR 97, CMS GT 1616 A x GTR 55 and CMS GT 1616 A x GTR 97 were found the most promising on the basis of per se performance, standard heterosis, mid parent heterosis and better parent heterosis. Therefore, it needs to be exploited in future breeding programme.

Keywords: Cytoplasmic genetic male sterility system, Heterobeltiosis, Line x tester mating design, Mid parent heterosis, Pigeonpea, Standard heterosis

Introduction

The term 'pigeonpea' was coined by Barbados, where its seeds were considered an important pigeon-feed (Gowda *et al.*, 2011) [8]. 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 $2n = 2x = 22$. The East Indies is the primary center of origin for pigeonpea (Linnaeus, 1937) [15]. Vavilov (1939) [31] reported that India is the native of pigeonpea. The Indian sub-continent, Eastern Africa and Central America, are the world's three main pigeonpea producing regions, respectively. It 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 an often cross-pollinated crop with 25-70 % natural out-crossing reported from different locations (Saxena *et al.*, 1990) [27]. This considerable amount of natural out crossing has been used efficiently in hybrid breeding technology. The availability of male sterility system, exhibiting large variation in natural out crossing with precise selection of pollen fertility restorers recognized as an important tool for genetic improvement of yield and may serve as a major fruitful technique to break existing yield barriers through heterosis breeding.

Both additive and non-additive gene effects have been reported in pigeonpea which is crucial in determining yield (Saxena & Sharma, 1990) [26]. The highly sensitive nature towards major abiotic stresses, pleiotropic effects of genes and physiological changes make it complicated to infer the inheritance of yield and its component traits (Byth *et al.*, 1981) [5].

Commercial exploitation of heterosis has been possible in crops like sorghum and cotton either through male sterility systems or through hand pollination. Until recently, hybrid vigour in pigeonpea could not be used to enhance its genetic yield potential due to lack of stable male sterility systems. A successful search for easily identifiable and stable genetic male sterility at different institutions in India has paved the way for commercial exploitation of hybrid vigour in pigeonpea.

Appreciable genetic diversity is the backbone of any successful hybrid development programme. The choice of parents to be incorporated in hybridization programme is a crucial step for breeders, particularly if the aim is to improve the complex quantitative characters such as yield and its components. The use of parents of known superior genetic worth ensures much better success. It requires extensive and detailed genetic assessment of existing germplasm as well as newly developed promising genotype, which could be used in future breeding programme or could be directly released as a cultivar after thorough testing.

Material and Methods

The experimental materials for the present investigation were generated using ten cytoplasmic male sterile (A) lines (CMS GT 1001 A, CMS GT 1002 A, CMS GT 1003 A, CMS GT 1402 A, CMS GT 301 A, CMS GT 307 A, CMS GT 1616 A, CMS GT 288 A, CMS GT 1603 A and CMS GT 1602 A) as female parents and four fertility restoration (R) lines (GTR 97, GTR 55, GTR 23 and GTR 18) as male parents by using line x tester mating design as suggested by Kempthorne (1957) during *kharif* 2017-18. The complete set of 55 genotypes comprising 10 male sterile (A) lines, 4 male fertile (R) lines, resultant 40 hybrids and 1 standard check variety (GT 103) were evaluated in a Randomized Block Design (RBD) with three replications at the Department of Seed Technology, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat during *kharif* 2018-19. The observations were recorded based on five randomly selected competitive plants for various thirteen 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 (%), total protein content (%) and leaf area per plant (cm²) 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 replication wise mean values for all the traits were subjected to analysis of variance technique suggested by Snedecor and Cochran (1967) [29] and reviewed by Panse and Sukhatme (1978) [20] to determine significance differences among genotypes.

Results and Discussion

The analysis of variance was performed to test the differences among parents and hybrids for all thirteen characters were presented in Table 1. The analysis of variance revealed that the mean sum of squares due to lines were significant for all characters except number of seed per pod and 100 seed weight. The mean sum of squares due to testers was significant for all characters except number of seed per pod and seed yield per plant. These indicate the existence of considerable variation in line and tester under study. The mean sum of squares due to line vs tester were found significant for the number of branches per plant, number of pods per plant, pod length, seed yield per plant, biological yield per plant, harvest index, total protein content and leaf area per plant. The mean sum of squares due to hybrids as well as parents vs hybrids were found significant for all the traits under present investigation. These indicate that, there should be possibility to get the substantial amount of heterosis for different characters under present investigation.

Presence of sufficient variability among the genotypes exhibited through highly significant differences among

themselves for all the traits studied. Mean performance of seed yield per plant varied from 20.16 (CMS GT 288 A) to 69 (CMS GT 1402 A), 49.96 (GTR 97) to 60.23 (GTR 55) and 31.33 (CMS GT 1002 x GTR 18) to 91.23 (CMS GT 1603 A x GTR 23) in female parents, male parents and hybrids, respectively. Total five hybrids *viz.*, CMS GT 1603 A x GTR 23 (91.23%), CMS GT 288 A x GTR 55 (86.70%), CMS GT 1603 A x GTR 97 (86.26%), CMS GT 1616 A x GTR 55 (86.06%) and CMS GT 1616 A x GTR 97 (84.73%) were found out yielded than the check variety GT 103 for seed yield per plant.

The phenomenon of heterosis has provided the most important genetic tools in improving seed yield of crop plants. Identification of specific parental combination capable of producing the highest level of heterotic effects in F₁ has immense value for commercial exploitation of heterosis. The magnitude of various heterotic effects and number of hybrids exhibiting significant heterosis in desired direction for all thirteen traits were presented in Table 2.

The estimates of mid parent heterosis for seed yield per plant ranged from -47.23 (CMS GT 1402 A x GTR 55) to 115.67 (CMS GT 288 A x GTR 55). Out of forty hybrids, as many as fourteen hybrids registered significant positive mid parent heterosis. Out of which, the best three hybrids CMS GT 288 A x GTR 55 (115.67%), CMS GT 1603 A x GTR 97 (104.50%) and CMS GT 1603 A x GTR 23 (94.73%) were found promising for seed yield per plant and its contributing characters like number of branches per plant, number of pods per plant and pod length. For days to flowering and days to maturity, hybrids CMS GT 301 A x GTR 55, CMS GT 301 A x GTR 18, CMS GT 307 A x GTR 18 and CMS GT 1616 A x GTR 23 were found significant negative mid parent heterosis.

The heterosis over better parent for seed yield per plant varied from -50.58 (CMS GT 1402 A x GTR 55) to 72.65 (CMS GT 1603 A x GTR 97). Among forty hybrids under study, ten hybrids registered significant positive heterobeltiosis. The best three hybrids CMS GT 1603 A x GTR 97 (72.65%) followed by CMS GT 1603 A x GTR 23 (53.85%) and CMS GT 288 A x GTR 55 (43.94%) were reported significant for seed yield per plant and its contributing characters like number of branches per plant, number of pods per plant, pod length, 100 seed weight and biological yield per plant. In case of days to flowering total seven hybrids registered significant negative heterobeltiosis, out of which the best three hybrids were CMS GT 1603 A x GTR 18, CMS GT 1616 A x GTR 23 and CMS GT 301 A x GTR 18. For days to maturity, hybrid CMS GT 307 A x GTR 23 was found significant negative heterobeltiosis.

The standard heterosis over check variety GT 103 for seed yield per plant varied from -56.80 (CMS GT 1002 A x GTR 18) to 25.78 (CMS GT 1603 A x GTR 23). Total five hybrids *viz.*, CMS GT 1603 A x GTR 23 (25.78%), CMS GT 288 A x GTR 55 (19.53%), CMS GT 1603 A x GTR 97 (18.93%), CMS GT 1616 A x GTR 55 (18.66%) and CMS GT 1616 A x GTR 97 (16.82%) out of forty hybrids recorded significant positive standard heterosis over check variety GT 103 for seed yield per plant. Their superiority seems to have resulted from significant values of their standard heterosis for yield contributing characters like number of branches per plant, number of pod per plant, number of seeds per pod, 100 seed weight, biological yield per plant and leaf area per plant. Top five promising hybrids for seed yield per plant and its contributing traits in pigeonpea were presented in Table 3. In relation with days to flowering and days to maturity total seven hybrids were found significant negative standard

heterosis, out of which the best three hybrids were CMS GT 288 A x GTR 23, CMS GT 1616 A x GTR 23 and CMS GT 307 A x GTR 18.

As observed in the present investigation, several workers have also reported the presence of considerable degree of heterosis for seed yield in pigeonpea, these were Narladkar and Khapre (1994) [17], Aghav *et al.* (1997) [2], Hooda *et al.* (1999) [10], Khorgade *et al.*, (2000) [12], Pandey and Singh (2002) [19], Lohithaswa and Dharmaraj (2003) [16], Phad *et al.* (2003) [24], Pandey (2004) [18], Yadav and Singh (2004) [33], Wankhede *et al.* (2005) [32], Baskaran and Muthiah (2006) [4], Ali *et al.* (2007) [3], Patel and Tikka (2008), Acharya *et al.* (2009), Kumar *et al.* (2009), Sarode *et al.* (2009), Chadirakala *et al.* (2010), Shoba and Balan (2010), Gupta *et al.* (2011), Lay *et al.* (2011), Patel and Tikka (2014^a) [22], Patel and Tikka

(2014^b) [23], Chethana *et al.* (2015) [7] and Soni *et al.* (2017) [30].

Conclusion

Heterosis breeding has been used comprehensively in potential yield enhancement through development of hybrid cultivars in pigeonpea. Heterosis for seed yield per plant and yield contributing characters were clearly revealed in the present investigation. The estimates of heterosis for seed yield per plant showed that the five hybrids viz., CMS GT 1603 A x GTR 23, CMS GT 288 A x GTR 55, CMS GT 1603 A x GTR 97, CMS GT 1616 A x GTR 55 and CMS GT 1616 A x GTR 97 were found the most promising on the basis of *per se* performance, standard heterosis, mid parent heterosis and better parent heterosis. Thus, these hybrids could be selected for enhancement of productivity in pigeonpea.

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

Sources 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	7.46	25.95	596.64	1.23	173.24	0.01	0.12
Parents	13	153.51**	242.00**	1510.03**	17.75**	2270.61**	0.45**	0.08
Lines	9	195.11**	320.57**	1875.50**	11.08**	2931.88**	0.50**	0.09
Testers	3	76.52**	86.97**	864.05**	29.39**	346.27**	0.35**	0.07
Lines vs Testers	1	10.05	0.00	158.73	42.88**	2092.18**	0.30*	0.01
Parents vs Hybrids	1	68.34*	1660.07**	5064.49**	363.73**	18797.14**	6.64**	0.33*
Hybrids	39	125.10**	184.82**	1196.99**	46.12**	1654.72**	0.47**	0.10**
Error	106	14.87	17.03	132.93	2.35	64.55	0.05	0.05

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

Table 1: Continues.....

Sources of variation	d.f	100 seed weight	Seed yield per plant	Biological yield per plant	Harvest index	Total protein content	Leaf area per plant
Replications	2	0.30	84.86	169.42	6.62	0.28	221893.04
Parents	13	0.50*	536.73**	7792.41**	635.91**	0.49**	16297983.68**
Lines	9	0.35	667.40**	9561.08**	583.34**	0.38**	17732895.55**
Testers	3	1.02**	64.51	648.94*	116.81**	0.80**	11361014.31**
Lines vs Testers	1	0.27	777.37**	13304.81**	2666.36**	0.50*	18194684.90**
Parents vs Hybrids	1	5.46**	1062.53**	13124.44**	2179.67**	0.68*	44469089.43**
Hybrids	39	1.17**	908.21**	10420.20**	258.16**	3.53**	101652701.03**
Error	106	0.24	35.37	218.92	20.48	0.11	1031149.61

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

Table 2: Magnitude of heterosis for different thirteen traits in pigeonpea.

S. No.	Characters	MP (Range)	No. of significant hybrids in desired direction for MP	BP (Range)	No. of significant hybrids in desired direction for BP	SH (Range)	No. of significant hybrids in desired direction for SH
1	Days to flowering	-11.27 to 16.64	07	-8.86 to 23.83	07	-10.14 to 11.55	09
2	Days to maturity	-6.15 to 14.19	06	-4.17 to 21.26	01	-9.47 to 8.48	10
3	Plant height	-9.47 to 23.77	03	-5.07 to 32.47	00	-23.35 to 5.17	18
4	Number of branches per plant	-20.29 to 72.32	22	-29.55 to 66.00	18	-32.38 to 29.52	07
5	Number of pods per plant	-23.58 to 129.40	27	-29.34 to 72.07	19	-39.13 to 20.77	05
6	Pod length	-6.50 to 26.52	26	-10.95 to 25.10	13	-20.40 to 6.09	00
7	Number of seeds per pod	-7.02 to 13.51	06	-11.67 to 10.91	01	-8.62 to 10.34	01
8	100 seed weight	-10.11 to 29.15	13	-11.41 to 28.15	05	-12.24 to 12.30	04
9	Seed yield per plant	-47.23 to 115.67	14	-50.58 to 72.65	10	-56.80 to 25.78	05
10	Biological yield per plant	-59.16 to 105.89	24	-59.69 to 97.54	12	-70.33 to 21.26	09
11	Harvest index	-66.63 to 50.01	04	-69.71 to 8.37	00	-54.44 to 69.43	07
12	Total protein	-16.92 to	08	-17.73 to	04	-15.80 to	06

	content	27.06		24.01		25.88	
13	Leaf area per plant	-80.40 to 104.57	17	-80.75 to 83.96	10	-87.12 to 20.67	08

MP :- Heterosis over mid parent, BP:- Heterosis over better parent, SH:- Heterosis over standard check variety GT 103

Table 3: Top five promising hybrids for seed yield per plant and its contributing traits in pigeonpea.

S. No.	Hybrids	Mean performance of seed yield per plant (gm)	MP	BP	SH	Significant and desirable heterosis over standard check variety GT 103 for contributing traits
1	CMS GT 1603 A x GTR 23	91.23	94.73**	53.85**	25.78**	NBP, NPP, NSP, 100 SW, BYP
2	CMS GT 288 A x GTR 55	86.70	115.67**	43.94**	19.53**	NBP, NPP, 100 SW, BYP
3	CMS GT 1603 A x GTR 97	86.27	104.50**	72.65**	18.93**	NBP, NPP, 100 SW, BYP, LAP
4	CMS GT 1616 A x GTR 55	86.07	34.13**	26.38**	18.66**	NBP, NPP, 100 SW, BYP
5	CMS GT 1616 A x GTR 97	84.73	43.53**	24.42**	16.82 *	NBP, NPP, BYP, LAP

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

MP :- Heterosis over mid parent, BP:- Heterosis over better parent, SH:- Heterosis over standard check variety GT 103, NBP:- Number of branches per plant, NPP:- Number of pods per plant, NSP:- Number of seeds per pod, 100 SW:- 100 seed weight (gm), BYP:- Biological yield per plant (gm), LAP:- Leaf area per plant (cm²).

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