



## HETEROSIS FOR SEED YIELD AND ITS RELATED TRAITS IN PIGEON PEA USING CYTOPLASMIC GENIC-MALE STERILITY SYSTEM

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**Abstract-** Exploitation of heterosis through the cultivation of hybrid cultivars is one of the landmark achievements of plant breeding. Heterosis breeding has been extensively used for improving yield potential in most of the crops through development of hybrids. Hence, an attempt was made in this study to assess 48 F<sub>1</sub> hybrids derived by crossing 3 cytoplasmic male sterile lines with 16 genotypes of pigeonpea to identify the best heterotic combinations to achieve a quantum jump in yield. The results showed that a wide range of variation in the estimates of heterobeltiosis and standard heterosis in positive and negative direction was observed for seed yield per plant as well as remaining ten traits. In case of seed yield per plant, heterobeltiosis ranged from -84.46% to 25.26% and standard heterosis varied from -84.18% to 22.46%. The cross NDACMS 1-3A x NDA 1 showed highest mean performance (63.00g) for seed yield per plant and it also exhibit 25.26% and 22.46% heterobeltiosis and standard heterosis, respectively. The crosses NDACMS 1-3A x NDA 1, NDACMS 1-2A x NDAGC 35, NDACMS 1-6A x NDA 1, NDACMS 1-2A x NDA 7-14, NDACMS 1-6A x BHUA 8-2 and NDACMS 1-2A x NDA-selection showing high mean performance and significant heterosis for seed yield per plant and its important components like primary & secondary branches per plant, pods per plant, seeds per pod, biological yield per plant and harvest index were most promising combinations and need to be tested on large scale for their feasibility of commercial utilization.

**Keywords-** Pigeonpea, line x tester analysis, gene effects, heterosis, quantitative traits

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### Introduction

Pulses are the important crops which provide high value food and nutritional security for abolishing starvation of poor people. They play a vital role in improving soil fertility and conserve natural resources which are essential for sustainable agriculture. Their deep penetrating root system enables them to do relatively better under low soil fertility and low moisture conditions. The multiple uses and roles in sustainable agriculture make pulses a favorite crop of marginal farmers. Among the various pulses grown, pigeonpea [*Cajanus cajan* (L.) Millsp.] is the most important pulse crops of the semi-arid tropics of the world. It is a rich source of protein, carbohydrate, vitamins, lipids and certain minerals. In fact, this crop has diversified uses such as food, feed, fodder and fuel.

The annual demand for pulses is increasing by 3 per cent [1]. Since the demand for pigeonpea is ever increasing and area available for expansion is limited, research now needs to focus on the genetic enhancement of yield through novel genetic approaches like hybrid technology. Hybrid provides better opportunity to break the yield barrier of conventional varieties and have already been successfully used in rice, maize, pearl millet and sorghum. The success of heterosis breeding in any crop mostly depends on the availability of sta-

ble and viable cytoplasmic genetic male sterility (CGMS) system and the information on various genetic aspects are essential. Pigeonpea being often cross pollinated crop (20-70 % out-crossing) in nature provides an opportunity to breed commercial hybrids [2].

Knowledge of genetic inheritance of yield and related traits plays an important role in deciding breeding strategies and methodologies for any crop improvement programme. However, unfortunately, relatively less effort has been made to understand the genetics of important traits in pigeonpea compared to other economically important crops. Both additive and non-additive gene effects have been reported in pigeonpea which is crucial in determining yield [3]. 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 [4]. Further, fertility restoration in cytoplasmic genetic male sterility based hybrids is also critical as it governs the viability of hybrid system.

Pigeonpea has been considered technically suitable for heterosis breeding due to predominance of non-additive genetic variance for the traits like grain yield and other important yield components. Keeping in view, present experiment has been undertaken to identi-

fy the out yielding effects of hybrids for various agronomic traits and their possible exploitation for commercial use.

## Materials and Methods

### Experimental Details

The parental material comprised with 3 CMS lines were crossed with 16 genotypes in a line x tester mating design in 2010-11. The resultant 48 hybrids along with their parents and standard check variety (NDA 2) were evaluated in a randomized block design with three replications at Research Farm of Genetics and Plant Breeding, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad (U.P.) during next crop growing season. Geographically this experimental site is situated between 26.47 °N latitude, 82.12 °E longitudes and at an altitude of 113 m above the mean sea level. The soil type of experimental site was sandy loam, rich in potash and low in organic carbon, nitrogen and phosphorus. The seeds of each entry were sown on 25<sup>th</sup> July, 2011 in single row plots of 4 m length with intra-row and inter-row spacing of 25 cm and 75 cm, respectively. Recommended cultural practices were followed to raise a good crop stand.

### Data Collection

The observations were recorded on five randomly selected competitive plants of a genotype in a plot in each replication for eleven characters viz., days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height (cm), pods per plant, seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%).

### Statistical Analysis

The per cent increase or decrease of  $F_1$  hybrids over better parent as well as standard variety was calculated to estimate possible heterotic effects for above mentioned parameters [5]:

$$\text{Heterobeltiosis} = \frac{\bar{F}_1 - \bar{BP}}{\bar{BP}} \times 100$$

$$\text{Standard heterosis} = \frac{\bar{F}_1 - \bar{SV}}{\bar{SV}} \times 100$$

Where,

$$\bar{F}_1 = \text{Mean of } F_1, \bar{BP} = \text{Mean of better - parent},$$

$$\bar{SV} = \text{Mean of standard variety or check variety}$$

Deviation of  $F_1$  from its either of the parental values was interpreted by [6] depicting type of gene action operating for controlling the trait. The 't' test was applied to determine significant difference of  $F_1$  hybrid means from respective mid parent and better parent values using formulae as reported by [7].

### Results and discussion

The analysis of variance [Table-1] revealed that the mean squares due to testers emerged highly significant for days to maturity, seeds per pod, 100-seed weight and biological yield per plant and significant for seed yield per plant, pods per plant and secondary branches per plant, indicating importance of general combining ability and additive gene effects in expression of seven out of eleven characters. However, variances due to lines were highly significant for days to 50% flowering and days to maturity while remaining nine characters showed non-significant variances due to lines. The mean squares due to lines x testers interactions, representing importance of specific combining ability and non-additive gene effects, were highly significant for all the 11 characters under study. The above discussion suggests importance of both additive and non-additive gene effects represented by general and specific combining ability variances, respectively, for most of the characters except days to 50% flowering, plant height, primary branches per plant and harvest-index for which only non-additive gene effects were important. The importance of additive as well as non-additive gene effects with predominance of non-additive gene effects in inheritance of seed yield and yield components of pigeonpea has also been reported earlier [8-15, 18-22].

**Table 1-** Analysis of variance following line x tester mating design for 11 characters in pigeon pea

Characters	Sources of variation				
	Replications	Lines	Testers	Lines x Testers	Error
d.f.	2	2	15	30	94
Days to 50 % Flowering	3.444	594.80**	72.18	49.90**	5.189
Days to Maturity	4.382	516.34**	94.26**	30.20**	6.566
Plant Height (cm)	0.0285	44.55	1228.94	812.28**	1.87
Primary Branches/ Plant	0.0108	0.0705	1.266	0.9817**	0.3114
Secondary Branches/ Plant	2.465	4.616	22.52*	10.71**	0.8039
Pods/ Plant	7.741	279.56	11043.77*	4435.53**	30.76
Seeds/ Pod	0.1692*	0.1901	0.4588**	0.1691**	0.044
100 Seed Weight (g)	0.0254	1.01	14.02**	2.179**	0.0274
Seed Yield/ Plant (g)	0.7759	110.51	1421.44*	685.03**	2.893
Biological Yield/ Plant (g)	7.052	410.81	10325.58**	2861.66**	45.39
Harvest Index (%)	0.3514	114.55	423.93	229.19**	0.2741

\*,\*\* significant at 5% and 1% probability levels, respectively

The exploitation of heterosis for developing high yielding commercial hybrids in pigeonpea has been found highly fruitful in spite of its often cross-pollinated nature because significant heterosis is encountered in  $F_1$  hybrids and successful and economical technology for commercial hybrid seed production is available. In present

study, the estimates of heterosis over better-parent and standard variety (NDA 2) were calculated for 48  $F_1$ 's to assess their genetic potential as breeding material were presented in [Table-2] (a&b). The salient results obtained on different aspects are summarized below:

**Table 2a-** Extent of per cent heterobeltiosis (BPH) and standard heterosis (SH) for 11 characters in pigeon pea

SNo	Crosses	Days to 50 % Flowering		Days to Maturity		Plant Height (cm)		Primary Branches/ Plant		Secondary Branches/ Plant	
		BPH	SH	BPH	SH	BPH	SH	BPH	SH	BPH	SH
1	NDA CMS 1-2 A x NDA 1	-2.95*	-2.95*	-3.43**	-2.53**	-10.97**	-19.85**	3.57	8.75	7.82	10.55*
2	NDA CMS 1-3 A x NDA 1	-4.54**	-4.54	-4.22**	-3.32**	-10.47**	-13.78**	13.33	6.25	22.69**	11.81*
3	NDA CMS 1-6 A x NDA 1	0.91	0.91	-2.10*	-0.66	-18.82**	-22.93**	-10.67	-16.25*	6.94	-2.53
4	NDA CMS 1-2 A x NDA 3	0	-4.54**	-2.12	-1.99*	2.59**	-7.61**	-7.14	-2.5	4.12	6.75
5	NDA CMS 1-3 A x NDA 3	2.85*	-1.81	-2.92**	-2.79**	-5.48**	-8.98**	2.74	-6.25	20.89**	8.65
6	NDA CMS 1-6 A x NDA 3	-0.46	-1.36	-3.28**	-1.86*	-14.12**	-18.48**	31.88**	13.75	8.65	-15.19**
7	NDA CMS 1-2 A x NDAGC 33	-2.49	-11.34**	1.7	-4.39**	-14.52**	-22.57**	-15.18*	-10.94	8.02	10.76*
8	NDA CMS 1-3 A x NDAGC 33	1.43	-3.4	4.23**	-1.73	-5.87**	-9.36**	-2.5	-2.5	-6.1	-15.61**
9	NDA CMS 1-6 A x NDAGC 33	-5.49**	-6.35**	-3.80**	-2.39**	-5.45**	-10.25**	-7.5	-7.5	0.24	-10.13*
10	NDA CMS 1-2 A x NDAGC 35	1.17	-1.59	-0.27	-1.73	8.79**	-2.37**	-2.38	2.5	-13.99**	-11.81*
11	NDA CMS 1-3 A x NDAGC 35	-1.17	-3.85	-1.35	-2.79**	2.06**	-1.71**	20.55*	10	7.98	-2.95
12	NDA CMS 1-6 A x NDAGC 35	-1.14	-2.04	-3.80**	-2.39**	-13.82**	-18.20**	26.81**	9.38	23.60**	-6.65
13	NDA CMS 1-2 A x NDA 98-2	-1.38	-2.72*	-0.67	-1.73	-20.55**	-23.83**	0	5	3.7	6.33
14	NDA CMS 1-3 A x NDA 98-2	0.23	-1.13	0	-1.06	2.63**	-1.17	14.59	7.5	-9.32	-15.19**
15	NDA CMS 1-6 A x NDA 98-2	-3.89**	-4.76**	-2.36**	-0.93	-30.18**	-33.06**	-0.07	-6.25	-4.13	-10.34*
16	NDA CMS 1-2 A x NDA 98-7	-6.19**	-7.26**	-2.17*	-3.86**	7.30**	-3.70**	-2.38	2.5	0.41	2.95
17	NDA CMS 1-3 A x NDA 98-7	-0.69	-1.81	-1.08	-2.79**	-11.85**	-15.11**	24.66**	13.75	6.52	0
18	NDA CMS 1-6 A x NDA 98-7	0	-0.91	-2.10*	-0.66	4.37**	-0.93	5.26	-6.25	-5.62	-11.39*
19	NDA CMS 1-2 A x NDA 96-6	-0.47	-4.54**	-1.34	-1.86*	-16.71**	-19.74**	16.07*	21.88**	-8.44	-6.12
20	NDA CMS 1-3 A x NDA 96-6	0.24	-3.85	-1.74	-2.26*	4.16**	0.38	15.58	11.25	28.64**	15.61**
21	NDA CMS 1-6 A x NDA 96-6	2.29	1.36	0.52	1.99*	0.85	-2.81**	29.87**	25.00**	45.24**	28.69**
22	NDA CMS 1-2 A x NDA Selection	-5.49**	-2.49	-0.94	-1.46	1.60*	-8.81**	16.07*	21.88**	-19.75**	-17.72**
23	NDA CMS 1-3 A x NDA Selection	-5.49**	-2.49	2.54**	1.99*	-11.95**	-15.21**	-1.85	-10.44	-6.9	-16.33**
24	NDA CMS 1-6 A x NDA Selection	-1.98	1.13	0.13	1.6	-4.30**	-9.15**	21.74*	5	2.82	-23.21**
25	NDA CMS 1-2 A x NDA 7-14	-6.96**	-9.07**	-2.28*	-3.19*	2.30**	-3.81**	-31.82**	-6.25	7.81	16.46**
26	NDA CMS 1-3 A x NDA 7-14	1.62	-0.68	0.54	-0.4	-7.87**	-11.28**	-21.82**	7.5	-4.3	3.38
27	NDA CMS 1-6 A x NDA 7-14	-0.46	-1.36	-1.57	-0.13	-1.95**	-6.92**	-25.45**	2.5	-4.3	3.38
28	NDACMS 1-2 A x BHUA8-2	-8.80**	-3.63**	-2.87**	-1.06	2.06**	-8.40**	-5.95	-1.25	1.98	8.44
29	NDACMS 1-3 A x BHUA8-2	-6.44**	-1.13	-2.74**	-0.93	-21.90**	-24.79**	13.01	3.13	-10.22*	-4.54
30	NDACMS 1-6 A x BHUA8-2	-4.08**	1.36	0	1.86*	-11.85**	-16.32**	24.64**	7.5	1.98	8.44
31	NDACMS 1-2 A x Azad	-4.75**	-4.54**	-2.94**	-3.32**	-1.64*	-11.72**	7.14	12.5	3.29	5.91
32	NDACMS 1-3 A x Azad	-2.94*	-2.72	-2.40**	-2.79**	-5.78**	-9.27**	14.11	4.13	9.55	-1.54
33	NDACMS 1-6 A x Azad	-0.23	0	-1.7	-0.27	7.35**	1.90**	44.93**	25.00**	64.97**	37.13**
34	NDACMS 1-2 A x ICP 3372	-4.74**	-13.38**	1.15	-6.52**	-8.52**	-17.90**	8.33	13.75	-7.41	-5.06
35	NDACMS 1-3 A x ICP 3372	-2.38	-7.03	1.55	-4.26**	-33.96**	-36.41**	-13.22	-20.81**	-14.07**	-18.42**
36	NDACMS 1-6 A x ICP 3372	-2.52	-3.40**	-4.59**	-3.19**	-8.54**	-13.18**	18.06*	6.25	13.33**	7.59
37	NDACMS 1-2 A x ICP 2934	-7.07**	-1.59	-2.73**	-0.66	12.24**	0.73	3.15	8.31	-2.97	3.38
38	NDACMS 1-3 A x ICP 2934	-10.92**	-5.67	-5.73**	-3.72**	0.45	-3.27**	20.96*	10.38	11.54**	18.84**
39	NDACMS 1-6 A x ICP 2934	-0.43	5.44**	0.65	2.79**	2.65**	-2.55**	19.57*	3.13	4.95	11.81*
40	NDACMS 1-2 A x Amar	6.98**	-2.72*	2.27*	-4.26**	-10.48**	-19.65**	-19.44**	-9.38	-8.44	-6.12
41	NDACMS 1-3 A x Amar	-1.43	-6.12	3.24**	-2.66**	1.99**	-1.78**	13.33	27.50**	17.84**	5.91
42	NDACMS 1-6 A x Amar	-0.92	-1.81	-3.41**	-1.99*	-15.76**	-20.04**	-5.56	6.25	15.82*	-13.50**
43	NDACMS 1-2 A x NDA 8-6	-6.74**	-9.07**	-2.04*	-3.99**	-5.08**	-12.17**	-1.19	3.75	-2.47	0
44	NDACMS 1-3 A x NDA 8-6	-1.16	-3.63	-0.54	-2.53**	-18.73**	-21.73**	17.81*	7.5	21.13**	8.86
45	NDACMS 1-6 A x NDA 8-6	5.95**	4.99**	0.92	2.39**	-10.36**	-14.91**	20.55*	10	25.60**	9.70*
46	NDACMS 1-2 A x NDAW 1003-13	-1.38	-2.72*	-3.95**	-3.06**	-11.67**	-20.72**	-12.2	-7.81	0.82	3.38
47	NDACMS 1-3 A x NDAW 1003-13	-3.68**	-4.99	-3.69**	-2.79**	-15.17**	-18.31**	-9.59	-17.50*	-24.88**	-32.49**
48	NDACMS 1-6 A x NDAW 1003-13	-0.46	-1.36	-2.75**	-1.33	-15.22**	-19.52**	12.32	-3.13	0.28	-25.11**
	Mean heterosis (%)	0.06		0.04		-0.12		12.75		13.92	
	No. of crosses with significant positive heterosis	3	2	24	5	14	1	15	5	12	10
	No. of crosses with significant negative heterosis	18	26	4	27	32	43	5	4	5	14
	Range of heterosis	-17.9	-18.82	-9.96	-9.31	-46.2	-38.31	-76.75	-48.31	-89.85	-69.62

\*, \*\* significant at 5% and 1% probability levels, respectively

**Table 2b-** Extent of per cent heterobeltiosis (BPH) and standard heterosis (SH) for 11 characters in pigeon pea

SNo	Crosses	Pods/ Plant		Seeds/ Pod		100 Seed Weight (g)		Seed Yield/Plant (g)		Biological Yield/ Plant (g)		Harvest Index (%)	
		BPH	SH	BPH	SH	BPH	SH	BPH	SH	BPH	SH	BPH	SH
1	NDA CMS 1-2 A x NDA 1	-13.22**	-9.32**	-12.24*	4.88	-2.37	-23.73**	-19.12**	-20.93**	9.54**	-15.96**	-27.57**	-5.89**
2	NDA CMS 1-3 A x NDA 1	11.97**	13.30**	-2.78	28.05**	7.55**	-15.98**	25.26**	22.46**	14.38**	-7.39**	1.83	32.32**
3	NDA CMS 1-6 A x NDA 1	-2.74	-1.59	-5.77	19.51**	-5.69**	-8.33**	10.91**	13.42**	1.14	4.1	-16.11**	9.00**
4	NDA CMS 1-2 A x NDA 3	-53.98**	-51.91**	-10.91	19.51**	-4.16**	-31.57**	-51.72**	-57.63**	8.56**	-16.40**	-55.67**	-49.28**
5	NDA CMS 1-3 A x NDA 3	-17.05**	-22.44**	9.09	46.34**	1.47	-27.55**	-0.32	-11.77**	-4.16	-22.40**	3.90*	13.74**
6	NDA CMS 1-6 A x NDA 3	-40.90**	-51.86**	-9.09	21.95**	-30.73**	-32.67**	-57.93**	-56.98**	-27.17**	-25.04**	-42.87**	-42.56**
7	NDA CMS 1-2 A x NDAGC 33	-15.23**	-11.42**	-7.14	18.90**	17.55**	-17.44**	4.29	-8.49**	16.52**	-5.75*	-15.09**	-2.86
8	NDA CMS 1-3 A x NDAGC 33	4.57	-2.23	-24.07**	0	24.14**	-12.81**	-3.72	-14.77**	-3.44	-21.82**	-0.4	9.03**
9	NDA CMS 1-6 A x NDAGC 33	-0.78	-19.18**	-4.76	21.95**	-19.02**	-21.29**	-21.88**	-20.12**	-29.73**	-27.67**	11.15**	10.46**
10	NDA CMS 1-2 A x NDAGC 35	-4.09	0.23	-8.16	9.76	28.69**	-8.33**	17.50**	3.1	-2.1	-24.89**	8.61**	37.35**
11	NDA CMS 1-3 A x NDAGC 35	-78.54**	-79.64**	-18.52**	7.32	14.06**	-18.76**	-77.96**	-80.49**	24.77**	1.02	-84.74**	-80.70**
12	NDA CMS 1-6 A x NDAGC 35	-79.41**	-80.45**	-20.67**	0.61	-11.65**	-14.13**	-82.32**	-81.92**	-22.83**	-20.57**	-82.03*	-77.28**
13	NDA CMS 1-2 A x NDA 98-2	-77.77**	-76.77**	-25.02**	-2.44	6.78**	-18.61**	-77.83**	-80.54**	-0.95	-23.87**	-77.66**	-74.44**
14	NDA CMS 1-3 A x NDA 98-2	-72.92**	-74.68**	-9.26	19.51**	10.42**	-15.83**	-71.34**	-74.63**	-5.97	-23.87**	-69.55**	-66.67**
15	NDA CMS 1-6 A x NDA 98-2	-66.24**	-72.50**	-1.59	28.05**	-22.38**	-24.56**	-69.85**	-69.17**	-55.90**	-54.61**	-31.61**	-32.03**
16	NDA CMS 1-2 A x NDA 98-7	-76.08**	-72.18**	0	19.51**	-24.59**	-26.04**	-75.42**	-72.21**	-18.16**	-28.40**	-70.03**	-61.19**
17	NDA CMS 1-3 A x NDA 98-7	-14.10**	-0.09	-18.52**	7.32	-21.21**	-22.73**	-21.88**	-11.68**	-29.71**	-38.51**	11.01**	43.72**
18	NDA CMS 1-6 A x NDA 98-7	-17.41**	-3.94	-13.46**	9.76	-8.40**	-10.16**	-7.54**	4.54	-30.54**	-28.50**	12.97**	46.26**
19	NDA CMS 1-2 A x NDA 96-6	-71.73**	-70.45**	-1.96	21.95**	-9.79**	-17.86**	-66.61**	-68.67**	4.09	-12.52**	-68.68**	-64.17**
20	NDA CMS 1-3 A x NDA 96-6	-67.09**	-69.23**	-12.96**	14.63*	-23.01**	-29.89**	-69.37**	-71.26**	7.49*	-9.66**	-71.49**	-68.16**
21	NDA CMS 1-6 A x NDA 96-6	-62.20**	-67.27**	-8.65	15.85*	-27.54**	-29.57**	-70.80**	-70.14**	-11.81**	-9.22**	-70.53**	-67.08**
22	NDA CMS 1-2 A x NDA Selection	7.44*	12.27**	-14.29**	9.76	-21.00**	-21.92**	4.95	7.13**	-0.63	-13.98**	5.69**	24.64**
23	NDA CMS 1-3 A x NDA Selection	-8.85**	-14.77**	-10.56*	17.80**	-19.35**	-20.29**	-22.85**	-21.25**	-15.72**	-27.04**	-8.47**	7.94**
24	NDA CMS 1-6 A x NDA Selection	24.22**	1.18	-12.38*	12.2	-14.96**	-15.96**	-0.39	1.86	-20.34**	-18.01**	5.38**	24.27**
25	NDA CMS 1-2 A x NDA 7-14	-14.36**	8.45**	-2.04	17.07**	8.39**	-8.70**	-3.6	19.77**	-4.93*	-4.1	1.4	24.94**
26	NDA CMS 1-3 A x NDA 7-14	-66.22**	-57.23**	1.85	34.15**	9.89**	-7.43**	-60.65**	-51.11**	20.46**	21.52**	-67.34**	-59.76**
27	NDA CMS 1-6 A x NDA 7-14	-70.64**	-62.82**	0	26.83**	2.46*	-0.41	-63.69**	-54.89**	-33.43**	-31.48**	-46.68**	-34.31**
28	NDACMS 1-2 A x BHUA8-2	-80.02**	-76.50**	8.16	29.27**	-0.96	-17.37**	-77.78**	-73.23**	8.26**	-4.1	-79.46**	-72.05**
29	NDACMS 1-3 A x BHUA8-2	-82.66**	-79.60**	-0.46	31.10**	-0.96	-17.37**	-80.61**	-76.63**	-17.15**	-26.61**	-76.59**	-68.14**
30	NDACMS 1-6 A x BHUA8-2	-28.40**	-15.77**	-1.92	24.39**	-5.06**	-7.72**	-8.32**	10.47**	-32.15**	-30.16**	16.24**	58.20**
31	NDACMS 1-2 A x Azad	-21.40**	-17.86**	2.04	21.95**	-3.25**	-23.12**	-5.31	-16.91**	-7.92**	2.2	-28.89**	-18.65**
32	NDACMS 1-3 A x Azad	-17.68**	-23.03**	1.85	34.15**	3.68**	-17.61**	5.03	-7.03**	-2.81	7.86**	-21.27**	-13.81**
33	NDACMS 1-6 A x Azad	-73.63**	-78.52**	-3.85	21.95**	-23.63**	-25.77**	-77.79**	-77.28**	35.88**	50.81**	-84.83**	-84.92**
34	NDACMS 1-2 A x ICP 3372	-24.53**	-21.14**	1.89	31.71**	-36.78**	-37.10**	-30.72**	-32.39**	-15.16**	-24.60**	-21.63**	-10.34**
35	NDACMS 1-3 A x ICP 3372	-59.08**	-61.74**	-13.61**	13.78*	-41.90**	-42.19**	-69.49**	-70.23**	-36.30**	-43.39**	-52.08**	-47.35**
36	NDACMS 1-6 A x ICP 3372	1.21	-17.56**	-0.94	28.05**	-31.17**	-31.52**	-19.99**	-18.18**	-31.90**	-29.90**	6.30**	16.78**
37	NDACMS 1-2 A x ICP 2934	-81.59**	-80.76**	4.76	34.15**	-46.97**	-47.19**	-84.46**	-84.18**	7.04*	-16.54**	-85.49**	-81.04**
38	NDACMS 1-3 A x ICP 2934	-70.26**	-72.20**	4.91	38.17**	-35.30**	-35.57**	-73.02**	-72.53**	12.12**	-9.22**	-76.86**	-69.75**
39	NDACMS 1-6 A x ICP 2934	-66.66**	-72.84**	-4.76	21.95**	-44.25**	-44.48**	-78.68**	-78.20**	-2.92	-0.07	-83.30**	-78.18**
40	NDACMS 1-2 A x Amar	-30.19**	-27.05**	8.17	37.20**	28.89**	-16.76**	-6.43*	-17.90**	16.77**	-3.92	-25.24**	-14.48**
41	NDACMS 1-3 A x Amar	-21.97**	-27.05**	4.17	37.20**	20.15**	-16.76**	-7.25*	-17.90**	17.08**	-3.66	-22.13**	-14.76**
42	NDACMS 1-6 A x Amar	0.17	-18.41**	5.77	34.15**	-13.63**	-16.05**	-0.6	1.65	-7.89**	-5.20*	7.94**	7.27**
43	NDACMS 1-2 A x NDA 8-6	-71.94**	-70.68**	4	26.83**	-1.9	-21.95**	-63.73**	-68.17**	10.11**	-15.52**	-67.19**	-62.30**
44	NDACMS 1-3 A x NDA 8-6	-15.85**	-21.32**	-1.85	29.27**	9.28**	-13.06**	-6.20*	-16.97**	-16.46**	-32.36**	6.92**	22.86**
45	NDACMS 1-6 A x NDA 8-6	5.25	-8.91**	-9.62	14.63*	-35.14**	-36.95**	-25.36**	-23.67**	-37.98**	-36.16**	3.97*	19.46**
46	NDACMS 1-2 A x NDAW 1003-13	-22.74**	-19.26**	2.04	21.95**	10.25**	-30.06**	-17.15**	-27.30**	-25.81**	-43.08**	12.01**	28.14**
47	NDACMS 1-3 A x NDAW 1003-13	-37.39**	-37.95**	-1.85	29.27**	2.81*	-28.77**	-31.43**	-39.30**	-29.48**	-42.90**	-2.78	6.43**
48	NDACMS 1-6 A x NDAW 1003-13	-13.02**	-13.81**	-1.44	25.00**	-13.43**	-15.86**	-9.77**	-7.73**	-32.08**	-30.09**	32.90**	32.08**
Mean heterosis (%)		-31.14		0.12		-2.31		-28.13		0.54		-25.91	
No. of crosses with significant positive heterosis		3	3	0	38	16	0	3	5	14	3	14	20
No. of crosses with significant negative heterosis		38	40	13	0	27	47	36	39	24	37	30	27
Range of heterosis		82.66-24.22	-94.06	25.02-9.09	-48.78	-75.86	-47.19	-109.72	-106.64	-91.78	-105.42	-117.39	-143.12

\*, \*\* significant at 5% and 1% probability levels, respectively



Early maturing hybrids are generally preferred therefore, negative heterosis for days to 50% flowering is considered as useful parameter. The heterosis for this trait over better-parent (BP) ranged from -10.92 per cent (NDACMS 1-3 A x ICP 2934) to 6.98 per cent (NDACMS 1-2 A x Amar); however, over standard variety (NDA 2) ranged from -13.38 per cent (NDACMS 1-2 A x ICP 3372) to 5.44 per cent (NDACMS 1-6 A x ICP 2934). Eighteen hybrids exhibited negative and significant heterosis over BP and the best five hybrids were NDACMS 1-3 A x ICP 2934, NDACMS 1-2 A x BHUA 8-2, NDACMS 1-2 A x ICP 2934, NDACMS 1-2 A x NDA 7-14 and NDACMS 1-2 A x NDA 8-6. Twenty-six crosses showed negative and significant heterosis over standard variety and best five among were NDACMS 1-2 A x ICP 3372, NDACMS 1-2 A x NDAGC 33, NDACMS 1-2 A x NDA 7-14 and NDACMS 1-2 A x NDA 8-6. These findings were in closely agreement with the findings of several earlier workers [11-14].

The heterosis for days to maturity ranged from -5.73 per cent (NDACMS 1-3 A x ICP 2934) to 4.23 per cent (NDACMS 1-6 A x NDAGC 33) over better parent, whereas it ranged from -6.52 per cent (NDACMS 1-2 A x ICP 3372) to 2.79 per cent (NDACMS 1-6 A x ICP 2934) over standard variety. Out of forty-eight hybrids, twenty-four crosses exhibited negative and significant heterosis over BP and best five among them were NDACMS 1-3 A x ICP 2934, NDACMS 1-6 A x ICP3372, NDACMS 1-2 A x NDAW 1003-13, NDACMS 1-3 A x NDA 1 and NDACMS 1-6 A x NDAGC 35. Twenty-seven crosses possessed negative and significant heterosis over SV and the best five hybrids possessing superior negative heterosis over SV were NDACMS 1-2A x ICP 3372, NDACMS 1-2 A x NDAGC 33, NDACMS 1-3 A x ICP 3372, NDACMS 1-2 A x Amar and NDACMS 1-2 A x NDA 8-6. [16] reported that most of the promising hybrids depicted significant negative heterosis for days to 50% flowering and days to maturity, thereby suggesting that high yield in hybrids can be achieved along with early flowering and maturity.

Plant height is desirable character in pigeonpea for achieving high yield as vigour in plant height may lead to increase biomass as well as source-sink capacity for obtaining optimum yield. The heterobeltiosis for plant height ranged from -33.96 per cent (NDACMS 1-3 A x ICP 3372) to 12.24 per cent (NDACMS 1-2 A x ICP 2934). The standard heterosis varied from -36.41 per cent (NDACMS 1-3 A x ICP 3372) to 1.90 per cent (NDACMS 1-6 A x Azad). The positive and significant value of heterobeltiosis was noted for fourteen crosses and best five among these crosses were NDACMS 1-2 A x ICP 2934, NDACMS 1-2 A x NDAGC 33, NDACMS 1-6 A x Azad, NDACMS 1-2 A x NDA 98-7 and NDACMS 1-6 A x NDA 98-7. Out of 48 crosses, only one cross, NDACMS 1-6 A x Azad exhibited significant and positive heterosis over SV. Similar findings were also reported by [12-15, 17-21].

More primary and secondary branches per plant are believed to be closely associated with high seed yield per plant resulting high productivity. Heterobeltiosis for primary branches per plant ranged from -31.81 per cent (NDACMS 1-2 A x NDA 7-14) to 44.93 per cent (NDACMS 1-6 A x Azad). The positive and significant estimates of heterosis over standard variety were exhibited by five hybrids which were NDACMS 1-3 A x Amar, NDACMS 1-6 A x Azad, NDACMS 1-6 A x NDA 96-6, NDACMS 1-2 A x NDA Selection and NDACMS 1-2 A x NDA 96-6.

The magnitude of heterobeltiosis for secondary branches per plant varied from -24.88 per cent (NDACMS 1-3 A x NDAW 1003-13) to

64.97 per cent (NDACMS 1-6 A x Azad). The estimates of heterosis over standard variety ranged from -32.49 per cent (NDACMS 1-3 A x NDAW 1003-13) to 37.13 per cent (NDACMS 1-6 A x Azad). Over standard variety, ten crosses showed positive and significant heterosis. Based on magnitude of heterosis over SV, the best five cross combinations were NDACMS 1-6 A x Azad, NDACMS 1-6 A x NDA 96-6, NDACMS 1-3 A x ICP 2934, NDACMS 1-2 A x NDA 7-14 and NDACMS 1-3 A x NDA 96-6.

The heterosis for pods per plant over BP ranged from -82.66 per cent (NDACMS 1-3 A x BHUA 8-2) to 24.22 per cent (NDACMS 1-6 A x NDA Selection). The heterosis over standard variety varied from -80.76 per cent (NDACMS 1-2 A x ICP 2934) to 13.30 per cent (NDACMS 1-3 A x NDA 1). Out of 48 hybrids, only three hybrids, NDACMS 1-3 A x NDA 1, NDACMS 1-2 A x NDA Selection and NDACMS 1-2 A x NDA 7-14 exhibited positive and significant heterosis over SV. The undesirable negative and significant estimates of heterobeltiosis and standard heterosis for pods per plant were exhibited by 38 and 40 crosses, respectively.

The hybrids with positive heterosis for number of seeds per pod are desirable to increase the yield. The heterobeltiosis for seeds per pod ranged from -25.02 per cent (NDACMS 1-2 A x NDA 98-2) to 9.09 per cent (NDACMS 1-3 A x NDA 3) while standard heterosis varied from -2.44 per cent (NDACMS 1-2 A x NDA 98-2) to 46.34 per cent (NDACMS 1-3 A x NDA 3). None of the 48 crosses registered significant positive heterobeltiosis for seeds per pod while 38 crosses recorded positive and significant standard heterosis. The best five crosses in respect of standard heterosis were NDACMS 1-3 A x NDA 3, NDACMS 1-3 A x ICP 2934, NDACMS 1-2 A x Amar, NDACMS 1-3 A x Amar and NDACMS 1-3 A x NDA 7-14. These findings were closely agreement with [9,12, 13,15,21,23].

For 100-seed weight, the heterosis over BP ranged from -46.97 per cent (NDACMS 1-2 A x ICP 2934) to 28.89 per cent (NDACMS 1-2 A x Amar). The heterosis over standard variety varied from -47.19 per cent (NDACMS 1-2 A x ICP 2934) to 0.41 per cent (NDACMS 1-6 A x NDA 7-14). None of the 48 hybrids exhibited positive and significant heterosis over SV. Heterosis with respect to 100-seed weight in positive and negative direction have also been reported by several earlier researchers [12-14, 17-21].

Yield is a complex trait and end product of a number of components most of which are under polygenic control. All changes in yield must be accompanied by changes in one or more of the components have been pointed out by Grafius (1959). For seed yield per plant, the heterosis over better-parent varied from -84.46 per cent (NDACMS 1-2 A x ICP 2934) to 25.26 per cent (NDACMS 1-3 A x NDA 1). Three crosses, NDACMS 1-3 A x NDA 1, NDACMS 1-2 A x NDAGC 35 and NDACMS 1-6 A x NDA 1 exhibited positive and significant heterosis over BP. The standard heterosis for seed yield per plant ranged from -84.18 per cent (NDACMS 1-2 A x ICP 2934) to 22.46 per cent (NDACMS 1-3 A x NDA 1). Out of 48 cross combinations, only five crosses, namely, NDACMS 1-3 A x NDA 1, NDACMS 1-2 A x NDA 7-14, NDACMS 1-6 A x NDA 1, NDACMS 1-6 A x BHUA 8-2 and NDACMS 1-2 A x NDA Selection showed positive and significant standard heterosis. The undesirable negative and significant estimates of heterobeltiosis and standard heterosis for seed yield per plant were possessed by 36 and 39 crosses, respectively. These findings were in close agreement with the findings of earlier workers [8-21, 23-24].

The heterosis for biological yield per plant ranged from -55.90 per cent (NDACMS 1-6 A x NDA 98-2) to 35.88 per cent (NDACMS 1-

6A x Azad) over BP and from -54.61 per cent (NDACMS 1-6 A x NDA 98-7) to 50.81 per cent (NDACMS 1-6 A x Azad) over SV. Out of 48 cross combinations, desirable positive and significant heterosis was exhibited by fourteen crosses over better-parent and three crosses over standard variety. The best five crosses exhibiting positive and significant heterobeltiosis were NDACMS 1-6 A x Azad, NDACMS 1-3 A x NDAGC 35, NDACMS 1-3 A x NDA 7-14, NDACMS 1-3 A x Amar and NDACMS 1-2 A x Amar, while the three crosses having positive and significant standard heterosis for seed yield plant were NDACMS 1-6A x Azad, NDACMS 1-3 A x NDA 7-14 and NDACMS 1-3 A x Azad.

The heterobeltiosis for harvest-index varied from -85.49 per cent NDACMS 1-2 A x ICP 2934) to 32.90 per cent (NDACMS 1-6 A x NDAW 1003-13). Out of 48 hybrids, twenty hybrids showed positive and significant heterosis over standard variety and best five among were NDACMS 1-6 A x BHUA 8-2, NDACMS 1-6 A x NDA 98-7, NDACMS 1-3 A x NDA 98-7, NDACMS 1-2 A x NDAGC 35 and NDACMS 1-3 A x NDA 1. The significant positive and negative heterosis for harvest-index was also reported by [15,18,20,21,23, 24].

### Conclusion

On the basis of overall consideration it may be concluded that both type of gene effect with preponderance of non-additive gene effect were important for inheritance of all the traits studied. Estimates of heterosis revealed that heterobeltiosis for seed yield per plant, ranged from -84.46% to 25.26% and standard heterosis varied from -84.18% to 22.46% and the cross NDACMS 1-3 A x NDA 1 showed highest mean performance (63.00g), heterobeltiosis (25.26%) and standard heterosis (22.46%). The most desirable crosses showing high mean performance and significant heterosis seed yield per plant and some of its components were NDACMS 1-3 A x NDA 1, NDACMS 1-2 A x NDAGC 35, NDACMS 1-6 A x NDA 1, NDACMS 1-2 A x NDA 7-14, NDACMS 1-6A x BHUA 8-2 and NDACMS 1-2 A x NDA-selection were most promising combinations and need to be tested on large scale for their feasibility of commercial utilization.

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