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ROLE OF GENETIC DIVERSITY FOR EXPLOITING THE HETEROSIS IN PIGEONPEA [*CAJANUS* CAJAN (L.) MILLSP.]

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ABSTRACT

Fifteen pigeonpea genotype consisting of seven male parents, four male sterile and four maintainer were evaluated for 17 traits to quantify the genetic diversity existing among them by using Mahalanobis statistic. All the genotypes were grouped in to 4 clusters comprising the 4 genotype in each cluster except cluster-I having the 3 genotype only. The genotype placed in the one cluster either having the similar genetic background or belong to the similar geographical area. The maximum contribution towards divergence was observed by pollen viability test (41.90 %), followed by grain yield (29.52 %), 100-seed weight (10.48 %), grain/pods (5.71 %) and days to maturity as well as plant height contributed (2.86 %). Among all the crosses only three cross combination namely, ICP-2043A/DA-11, H-28A/ MAL-28 and H-28A/IPA-203 have shown positive and significant standard heterosis for most of the yield and yield attributing traits, suggesting that these cross combination may be exploited to developed the hybrid using CGMS system in pigeonpea for obtaining higher grain yield owing to the diverse genetic back ground of the parental lines.

INTRODUCTION

In the recent past, emphasis is given on developing hybrids in pigeonpea [*Cajanus* cajan (L.) Millsp.]. Heterosis is expressed in three ways, depending on the criteria used to compare the performance of a hybrid. The three ways are: mid parent, better parent and standard variety heterosis. However, from the plant breeder's viewpoint, better parent (heterobeltiosis) (Fanseco and Peterson, 1968) and/or standard variety (standard heterosis) are more effective. The hybrid technology, based on cytoplasmic genetic male-sterility (CGMS) system, has given an opportunity of achieving the long-cherished goal of breaking yield barriers and represent a single greatest applied achievement in the discipline of genetics. Pigeonpea is a partially often cross pollinated crop and the plants express strong heterosis in their F_1 hybrids. These led to the conclusion of the presence of significant heterosis in pigeonpea, which could be exploited commercially by developing F_1 hybrids. Solomon *et al*. (1957) were the first to reported hybrid vigour in pigeonpea in ten inter-varietal crosses. Saxena (2007) reported that CGMS based pigeonpea hybrids gave 50-100% yield advantage over the popular variety. Thus, main objective of this investigation was to estimate the extent of heterosis for seed yield and its component characters and to isolate better crosses for further study by using CGMS lines. Genetic diversity is an important factor and also prerequisite in any hybridization programme. Hybrids between genetically diverse parents manifest greater heterosis than those closely related parents (Arunachalam, 1981). Genetic diversity determine the cause of heterosis in hybrids using CGMS lines, there is a great need to estimates the genetic divergence, which is understood either to be due to crossing of distantly related CGMS lines with pollinator lines or due to heterotic effect of cytoplasm and fertility restorer gene interaction. Mahalanobis (1936) generalized distance (D^2) has been very often used by crop breeders to measure the nature and magnitude of diversity. In view of these, the present study undertaken in fifteen genotypes is an attempt to ascertain the nature and magnitude of genetic diversity and to identify suitable donors having wider genetic base in pigeonpea.

MATERIALS AND METHODS

The present study comprised of four genetic male sterile lines (female) viz., ICP-2043A, ICP-2092A, HY-4A and H-28A and seven testers (males) viz., Bahar, NDA-1, P-9, MAL-13, DA-11, MAL-28 and IPA-203. The crossing programme was carried out in line x tester fashion at Tirhut College of Agriculture, Dholi during kharif 2010-11. Eleven parents along with their 28 hybrids were sown in a randomized block design with three replications during kharif 2011-12. Each entry was sown in two rows of 3 meters length with a spacing of 70 x 30cm row to row and plant to plant. Observations on five randomly selected competitive plants were recorded for days to 1st flowering, days to 50 per cent flowering, days to last flowering, days to maturity, plant height, number of primary branches/ plant, number of secondary branches/plant, leaf area (cm^2), number of pods/plant, pod bearing zone (cm), pod length (cm), pod width (cm), number of grains/pod, 100-seed weight (g), harvest index (per cent), pollen viability (per cent) and grain yield (kg/ha). The data were subjected to analysis of variance for various character, mean performance of parent and their crosses and heterosis as per method given by Kempthorne (1957) and Singh and Narayanan (1997).

Table 1: Analysis of variance for 17 characters in pigeonpea

Sl.No.	Characters	Mean sum of Squares Replication(df=2)	Treatments(df=38)	Error(df=76)
1.	Days to 1st Flowering	48.85	30.02**	13.07
2.	Days to 50% Flowering	7.15	32.87**	10.61
3.	Days to Last Flowering	28.06	56.11**	10.41
4.	Days to Maturity	7.96	87.42**	20.87
5.	Plant Height (cm)	323.60	672.15**	121.27
6.	No. of Primary branches/plant	62.13	13.55**	3.70
7.	No. of Secondary branches/plant	12.16	40.77**	5.38
8.	Leaf Area (cm^2)	0.09	9.23**	0.95
9.	No. of Pods/Plant	2401.10	35455.51**	2828.41
10.	Pod Bearing Zone (cm)	7.02	83.06**	6.51
11.	Pod Length (cm)	0.18	0.34**	0.06
12.	Pod Width (cm)	0.001	0.010**	0.0004
13.	No. of Grains/Pod	0.05	0.19**	0.03
14.	100-Seed Weight (g)	0.11	4.06**	0.32
15.	Harvest Index (%)	5.51	66.16**	3.00
16.	Pollen Viability test (%)	5.37	1738.67**	9.31
17.	Grain Yield (Kg/ha)	16798.62	2586319.73**	40434.47

**significant at P= 0.01

Table 2: Number and name of genotypes in different cluster

Cluster	No. of genotypes	Genotype
I	3	P-9, DA-11, IPA-203
II	4	MAL-13, MAL-28, Bahar, NDA-1
III	4	ICP-2043B, H-28B, ICP-2092B, HY-4B
IV	4	ICP-2092A, H-28A, ICP-2043A, HY-4A

Table 3: Inter and intra cluster distance

Cluster	I	II	III	IV
I	46.07	582.07	128.47	63.36
II		28.41	406.55	592.57
III			77.21	158.05
IV				0.00

Table 4: Independent character contribution towards divergence

Sl.No.	Source	Times Ranked1st	Contribution (%)
1.	Days to 1st Flowering	0	0.00
2.	Days to 50% Flowering	0	0.00
3.	Days to Last Flowering	0	0.00
4.	Days to Maturity	3	2.86
5.	Plant Height (cm)	3	2.86
6.	No. of Primary branches/plant	0	0.00
7.	No. of Secondary branches/plant	0	0.00
8.	Leaf Area (cm^2)	0	0.00
9.	No. of Pods/Plant	1	0.95
10.	Pod Bearing Zone (cm)	0	0.00
11.	Pod Length (cm)	1	0.95
12.	Pod Width (cm)	0	0.00
13.	No. of Grains/Pod	6	5.71
14.	100-Seed Weight (g)	11	10.48
15.	Harvest Index (%)	5	4.76
16.	Pollen Viability test (%)	44	41.90
17.	Grain Yield (Kg/ha)	31	29.52

RESULTS AND DISCUSSION

Appraisal of Table 1, it is obvious that all the characters have shown highly significant differences among the genotypes.

In present study attempted were made to group the different pigeonpea variety on the basis of D^2 and provide information for characters, which contributes most to the D^2 value, besides the efforts have also been made to link divergence to source of origin of different lines and their impact, if any, on expression of heterosis.

The 15 pigeonpea genotypes under study constellated in to four clusters. Cluster-I consisted of three genotypes namely, P-9, DA-11 and IPA-203; cluster-II four genotypes viz., MAL-13, MAL-28, Bahar and NDA-1; cluster-IV comprised of four maintainer lines *i.e.* ICP-2043 B, H-28 B, ICP-2092 B and HY-4 B, while in cluster-IV all male sterile lines were placed.

The maximum intra cluster distances were observed in cluster-III followed by cluster-II, while cluster-IV had intra cluster distance zero may be due to the similar source of cytoplasmic genetic male sterility as evident from the Table 3; suggesting that the genotypes placed in the same cluster are either having the same genetic back ground or may belong to be same geographical area. The inter cluster distance indicated that cluster-IV has the longest distance from the cluster-II followed by cluster-II from cluster-I, than cluster-III from cluster-II, cluster-IV from cluster-II, cluster-III from cluster-I and cluster-IV from cluster-I. Incidentally cluster-IV comprised of all the four CGMS line used under study, which are believed to have similar source of male sterility thus genetic behaviour especially in relation to sterility mechanism is of common in nature. Cluster-I comprising three genotypes all having the common parent owing to this, they may be placed in same cluster. Cluster-II also having the all four genotypes comprising almost similar genetic back ground as well as belongs to the similar geographical area. The inter cluster distances are very higher in magnitude indicating, that the genotypes are used in the study having the diverse genetic base. It is thus, evident that different genotypes have grouped themselves both on the basis of their origin and genetic constitution evolved through identical selection pressure. Hence, it may be concluded that the clustering pattern is influenced by the parent involved and habit (pollen viability test) of genotype than geographical origin. Murthy and Arunachalam (1966) reported that genetic drift and selection in different environments could cause greater

Table 5: Cluster mean for 17 characters in pigeonpea

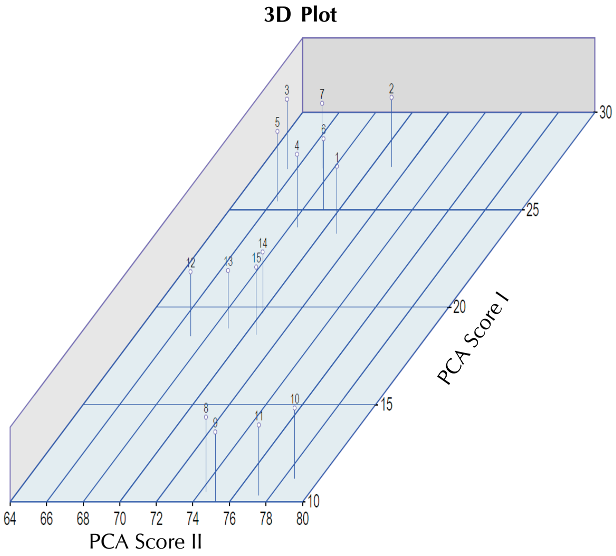
Sl. No.	Character	Days to 1st Flowering	Days to 50 % Flowering	Days to Last Flowering	Days to Maturity (cm)	Plant Height Branches	No. of primary Branches	No. of Secondary (cm²)	Leaf Area Plant	No. of pods/ Zone	Pod Bearing (cm)	Pod Length (cm)	Pod Width (cm)	No. of Grains/ Pod	100Seed Weight (g)	Harvest Index (%)	Pollen Viability test	Grain Yield (Kg/ha)
1.	Cluster-I	151.56	183.11	219.11	246.56	230.99	11.08	16.83	13.00	429.17	34.86	5.43	0.74	3.68	12.26	15.32	86.44	1873.66
2.	Cluster-II	153.00	189.58	220.33	255.17	211.84	10.71	18.45	14.45	399.32	33.91	5.59	0.81	3.76	12.19	12.88	85.08	1623.50
3.	Cluster-III	151.75	182.75	217.67	247.42	209.88	9.98	19.50	11.69	135.49	25.98	5.40	0.78	3.88	11.38	0.94	9.17	97.50
4.	Cluster-IV	150.58	181.00	215.08	241.00	188.92	11.22	19.68	12.31	303.61	26.18	5.36	0.77	3.87	11.88	12.68	67.25	694.83

diversity than geographic distance.

In addition to classify the genotype into cluster based on the genetic divergence, the amount of contribution made by 17 traits towards divergence was also estimated the maximum contribution towards divergence was observed by pollen viability test (41.90 %), followed by grain yield (29.52 %), 100-seed weight (10.48 %), grain/pods (5.71 %) and days to maturity as well as plant height contributed (2.86 %) as evident from the Table 4. Hence, the present study clearly indicated the influence of the parent and their habit in the clustering pattern. Similar result was also obtained by Singh and Gumber (1996). The above mentioned characters are important in this respect for the variety under consideration and they have proved most useful for studying divergence among them.

Cluster 1st has shown the highest character mean for plant height, pod/plant, pod bearing zone, 100-seed weight, pollen viability and grain yield; cluster 2nd exhibited highest character mean for days to 1st flowering, days to 50 % flowering, days to last flowering, days to maturity, leaf area, pod length, pod width and harvest index; cluster 3rd shown highest character mean for grains/pod, whereas, cluster-IV exhibited highest character mean for primary and secondary branches/ plant as per Table 5. Hence, it is obvious from the result obtained that, to enhance the number of primary and secondary branches genotype of cluster-IV may be used as one of the parent in the crossing programme, to enhance the number of grains/pod genotype belong to cluster-III may be used as the parent, for enhancing the pods/plant, pod bearing zone, 100-seed weight and grain yield, the genotype present in the cluster-I may be used as one of the parent in pigeonpea improvement programme.

Standard heterosis for days to 1st



PCA-I = X-axis; PCA-II = Y-axis
Figure 6.a: Cluster plotting of 3 D Plot

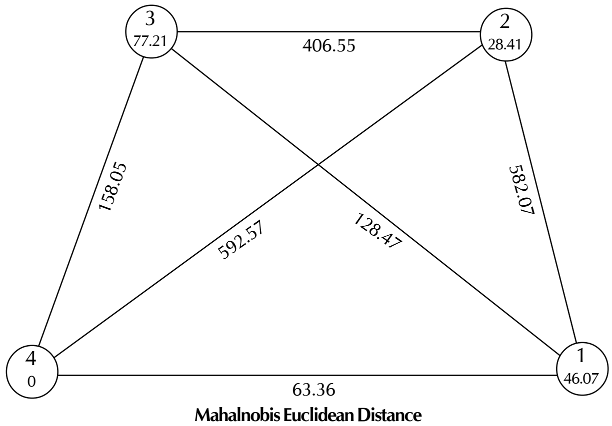


Figure 6.b: Cluster diagram (not to the scale)

flowering, days to 50 % flowering, days to last flowering and days to maturity traits, none of the cross combination had shown significant superiority for earliness than the standard variety P-9 as evident from the Table 7(a).

Standard heterosis for plant height ranged from -17.48 (ICP-2043A/MAL-28) to 15.13 (HY-4A/MAL-28). Negative and significant heterosis over standard variety was found in the crosses viz., ICP-2043A/MAL-28, ICP-2043A/Bahar, ICP-2092A/Bahar, ICP-2043A/ IPA-203, H-28A/MAL-13, H-28A/ Bahar and ICP-2092A/NDA-1. The negative heterosis is desirable to develop dwarf high yielding genotype of pigeonpea. Similar results were also obtained by Pandey (2004) and Chandirakala *et al.* (2010).

Standard heterosis of primary branches/plant ranged from -13.16 (HY-4A/MAL-28) to 59.91 (ICP-2043A/DA-11). Positive and significant heterosis over standard variety were recorded for hybrids viz., ICP-2043A/DA-11, HY-4A/MAL-13, ICP-2043A/P-9, ICP-2043A/ MAL-13, ICP-2092A/P-9, HY-4A/Bahar, H-28A/IPA-203, ICP-2043A/NDA-1, HY-4A/ NDA-1, ICP-

Table 6 a: Heterosis for Mid-Parent, Better Parent (BP) and Standard Heterosis (SH) in percentage for different characters in Pigeonpea

Sl. No.	Crosses	Characters Days to 1st Flowering			50% Flowerings			Last Flowerings		
		SH	MP	SH	MP	BP	BP	SH	MP	BP
1	ICP 2043A/Bahar	0.11	-2.15	1.11	-0.18	-3.14*	1.65	0.15	-0.91	0.46
2	ICP 2043A/NDA-1	-5.02**	-7.64**	-3.55	-2.58*	-6.48**	0.37	-1.75	-3.43**	-0.76
3	ICP 2043A/P-9	2.01	1.33	1.33	0.09	-0.55	-0.55	1.46	1.07	1.08
4	ICP 2043A/MAL-13	-0.56	-0.67	-2	-0.55	-1.63	-0.73	0.15	-0.61	0.16
5	ICP 2043A/DA-11	-2.46	-3.1	-3.1	1.39	1.3	0.18	0.46	-0.15	0.31
6	ICP 2043A/MAL-28	-0.67	-1.76	-0.88	0.18	-2.12	1.28	1.3	0.61	1.23
7	ICP 2043A/IPA-203	1.43	-0.43	2	0.09	-1.96	0.92	1.52	0.15	2.15
8	ICP 2092A/Bahar	-0.87	-2.58	0.06	-1.07	-3.49*	1.28	0.69	0	1.38
9	ICP 2092A/NDA-1	-0.76	-2.97	1.33	-0.8	-4.27**	2.75	-0.76	-2.09	0.62
10	ICP 2092A/P-9	1.44	1.33	1.33	2.29	2.2	2.2	0.15	0.15	0.16
11	ICP 2092A/MAL-13	4.25*	3.56	3.32	3.10*	2.54	3.48*	1.15	0.76	1.54
12	ICP 2092A/DA-11	1.22	1.11	1.11	2.86*	2.39	2.2	1.76	1.53	2
13	ICP 2092A/MAL-28	0.11	-0.44	0.45	0.36	-1.42	2.02	2.45*	2.13	2.77**
14	ICP 2092A/IPA-203	0.44	-0.87	1.56	2.44	0.89	3.85**	0.38	-0.6	1.38
15	HY-4A/Bahar	-2.04	-2.14	1.33	-2.83*	-4.19**	0.55	3.04**	2.57*	3.99**
16	HY-4A/NDA-1	0.43	0	4.44*	-0.79	-3.24*	3.85**	4.30**	3.13*	5.98**
17	HY-4A/P-9	-0.44	-2.14	1.33	-0.45	-1.44	0.55	5.74**	5.50**	5.98**
18	HY-4A/MAL-13	-1.21	-3.64	-0.22	-0.72	-1.26	0.73	5.03**	4.87**	5.67**
19	HY-4A/DA-11	0.87	-0.86	2.66	2.64*	1.08	3.12*	3.82**	3.82**	4.30**
20	HY-4A/MAL-28	-1.74	-3	0.45	-2.32	-3.01*	0.37	0.99	0.91	1.54
21	HY-4A/IPA-203	-2.69	-3.21	0.23	-0.8	-1.25	1.65	4.70**	3.91**	5.98**
22	H-28A/Bahar	1.19	0.43	3.77*	-0.27	-2.09	2.75	0.38	-0.3	1.08
23	H-28A/NDA-1	1.29	0	4.44*	0.88	-2.05	5.13**	3.03**	1.64	4.45**
24	H-28A/P-9	2.2	1.31	3.11	1.28	0.72	1.83	5.06**	5.06**	5.06**
25	H-28A/MAL-13	3.21	1.53	3.33	1.54	1.45	2.57	3.44**	3.04*	3.84**
26	H-28A/DA-11	4.40*	3.49	5.32**	3.48**	2.36	3.48*	2.07	1.83	2.3
27	H-28A/MAL-28	2.63	2.18	3.99*	0.45	-0.71	2.75	0.46	0.15	0.77
28	H-28A/IPA-203	-0.54	-0.87	1.56	0.18	-0.71	2.2	-1.44	-2.41*	-0.46

Table 6 a: Cont......

SI.No	Crosses	Days to Maturity			Plant Height (cm)			No. of Primary Branches/plant		
		MP	BP	SH	MP	BP	SH	MP	BP	SH
1	ICP 2043A/Bahar	0.87	-2.58	3.28*	-16.47**	-20.89**	-16.07**	37.70**	29.23*	22.81*
2	ICP 2043A/NDA-1	-1.66	-5.61**	1.37	-4.63	-7.47	-1.83	31.83*	28.74*	28.33**
3	ICP 2043A/P-9	1.45	0.82	0.82	-2.18	-4.99	0.81	41.53**	38.01**	37.98**
4	ICP 2043A/MAL-13	0.41	-1.34	0.96	-1.1	-6.71	-1.02	40.06**	35.24*	37.98**
5	ICP 2043A/DA-11	1.31	1.24	0.14	-8.91*	-9.53	-2.09	71.21**	68.31**	59.91**
6	ICP 2043A/MAL-28	0.81	-1.33	1.78	-16.37**	-22.22**	-17.48**	37.01**	33.85*	27.19**
7	ICP 2043A/IPA-203	3.16*	0.26	4.92**	-17.09**	-18.23**	-13.24**	12.31	9.68	9.39
8	ICP 2092A/Bahar	-1.66	-4.26**	1.5	-7.49	-9.33*	-13.98**	42.91**	37.89*	14.19
9	ICP 2092A/NDA-1	0.99	-2.29	4.92**	-4.86	-9.00*	-9.19*	2.64	-8.8	-9.04
10	ICP 2092A/P-9	2.66	2.45	2.87	8.80*	3.96	3.96	47.94**	31.29*	31.32**
11	ICP 2092A/MAL-13	4.05**	3.07*	5.47**	5.89	4.23	-1.96	33.22*	17.19	19.56*
12	ICP 2092A/DA-11	1.44	0.68	1.09	-5.88	-13.08**	-6.5	45.08**	33.76*	22.81*
13	ICP 2092A/MAL-28	4.30**	2.92	6.12**	10.79**	10.70*	1.02	35.65*	25.81	14.04
14	ICP 2092A/IPA-203	0.47	-1.57	3.01	-3.71	-9.34*	-6.46	12.54	0	-0.26
15	HY-4A/Bahar	-1.69	-2.45	3.42*	1.9	-2.84	-7.82	47.84**	40.38**	30.09**
16	HY-4A/NDA-1	0.39	-1.02	6.29**	11.82**	4.12	3.9	31.00*	26.39	26.05**
17	HY-4A/P-9	1.34	-0.79	3.55*	14.42**	6.44	6.44	14.72	10.53	10.53
18	HY-4A/MAL-13	-1.52	-2.49	1.78	13.66**	8.82*	2.36	49.25**	42.41**	45.35**
19	HY-4A/DA-11	-4.17**	-6.68**	-2.6	6.15	-4.46	2.77	6.18	5.68	-2.02
20	HY-4A/MAL-28	-3.10*	-3.67*	0.54	-4.27	-6.99	15.13**	-5.26	-6.31	-13.16
21	HY-4A/IPA-203	-1.96	-2.09	2.46	0.36	-7.97*	-5.04	22.8	18.48	18.16
22	H-28A/Bahar	-2.16	-3.74*	2.05	-5.29	-6.13	-10.94**	17.91	16.9	-0.88
23	H-28A/NDA-1	-2.28	-4.46**	2.6	-1.94	-5.18	-5.38	19.81	10.85	10.53
24	H-28A/P-9	0.88	-0.4	2.19	6.75	3.12	3.13	16.46	7.6	7.63
25	H-28A/MAL-13	-0.13	-0.27	2.32	-5	-5.43	-11.04**	5.48	-3.44	-1.49
26	H-28A/DA-11	0.75	-1.07	1.5	-5.62	-11.92**	-5.26	15.23	10.83	1.75
27	H-28A/MAL-28	1.6	1.33	4.51**	2.59	1.52	-5.38	12.33	8.71	-1.49
28	H-28A/IPA-203	-2.31	-3.27*	1.23	0.09	-4.75	-1.72	14.42	5.87	5.53

*significant at P = 0.05, **significant at P = 0.01

Table 6b: Heterosis for Mid-Parent, Better Parent (BP) and Standard Heterosis (SH) in percentage for different characters in Pigeonpea

Sl. No.	Crosses	Characters No. of Sec. Branches/plant			Leaf Area (cm²)			No. of Pods/plant		
		MP	BP	SH	MP	BP	SH	MP	BP	SH
1	ICP 2043A/Bahar	-4.13	-9	18.72	-28.76**	-31.65**	-32.99**	9.67	-23.04*	-21.60*
2	ICP 2043A/NDA-1	31.38**	28.55**	75.28**	-39.83**	-43.86**	-41.61**	25.51*	-16.32	3.19
3	ICP 2043A/P-9	20.00*	6	38.29**	-35.35**	-38.56**	-38.54**	20.37	-15.07	-15.07
4	ICP 2043A/MAL-13	-3.86	-14.83	11.09	-24.19**	-30.44**	-24.96**	90.51**	51.71**	5.24
5	ICP 2043A/DA-11	36.91**	27.67**	66.54**	-16.28**	-17.75**	-23.21**	61.08**	10.02	23.57*
6	ICP 2043A/MAL-28	38.90**	37.17**	78.93**	-16.26**	-24.46**	-15.40*	60.82**	11.93	17.41
7	ICP 2043A/IPA-203	-9.68	-14.5	11.55	-18.48**	-19.07**	-26.06**	31.74*	-9.43	-0.69
8	ICP 2092A/Bahar	-9.03	-11.42	9.59	-13.49*	-19.12**	-20.73**	0.77	-33.81**	-32.57**
9	ICP 2092A/NDA-1	-26.25**	-29.67**	-4.11	-13.69*	-21.46**	-18.32**	-12.36	-44.82**	-31.95**
10	ICP 2092A/P-9	17.78	6.5	31.77*	-15.66**	-21.87**	-21.90**	68.76**	11.35	11.34
11	ICP 2092A/MAL-13	-3.29	-12.3	8.48	-12.07*	-21.28**	-15.11*	96.02**	43.16**	-0.69
12	ICP 2092A/DA-11	18.01	12.83	39.60**	-16.54**	-20.15**	-25.47**	12.43	-27.79**	-18.89
13	ICP 2092A/MAL-28	16.81	15.21	46.58**	-4.65	-16.03**	-5.99	25.49	-18.14	-14.13
14	ICP 2092A/IPA-203	-1	-3.87	18.02	-11.28	-14.25*	-21.68**	38.31**	-10.69	-2.06
15	HY-4A/Bahar	2.95	-0.69	25.24	16.97**	3.53	1.46	53.48**	1.63	3.53
16	HY-4A/NDA-1	33.39**	28.39**	75.02**	0.42	-13.34*	-9.93	27.59*	-19.12*	-0.25
17	HY-4A/P-9	11.54	0	26.09*	-8.62	-19.83**	-19.85**	46.35**	-2.65	-2.65
18	HY-4A/MAL-13	-11.41	-20.34*	0.46	1.51	-13.72*	-6.93	67.42**	23.58*	-14.27
19	HY-4A/DA-11	-16.11	-20.52*	0.26	0.37	-9.23	-15.26*	42.16**	-8.02	3.32
20	HY-4A/MAL-28	16.91	16.41	48.08**	4.56	-12.49*	-1.97	48.29**	-2.5	2.27
21	HY-4A/IPA-203	17.2	12.76	42.20**	9	-0.48	-9.05	41.50**	-7.94	0.96
22	H-28A/Bahar	-4.42	-8.63	17.42	13.28*	8.96	6.79	88.91**	21.74*	24.02*
23	H-28A/NDA-1	2.63	-0.32	35.88**	-3.38	-9.62	-6.06	49.43**	-7.46	14.13
24	H-28A/P-9	39.68**	24.20*	59.62**	-9.1	-13.41*	-13.43*	115.08**	39.19**	39.19**
25	H-28A/MAL-13	29.60**	15.57	48.52**	1.53	-6.61	0.73	139.54**	70.57**	18.33
26	H-28A/DA-11	17.66	10.49	42.00**	20.02**	18.22**	10.36	45.13**	-8.42	2.86
27	H-28A/MAL-28	45.92**	45.18**	86.56**	-19.17**	-26.92**	-18.18**	91.14**	22.38**	28.37**
28	H-28A/IPA-203	36.11**	29.78**	66.80**	-4.36	-4.79	-12.99*	97.36**	25.16**	37.25**

Table 6b: Cont.........

No.	Characters	Pod Bearing Zone (cm)			Pod Length (cm)			Pod Width (cm)		
		MP	BP	SH	MP	BP	SH	MP	BP	SH
1	ICP 2043A/Bahar	29.37**	23.29**	23.30**	1.31	-2.98	0.37	1.66	0	17.14
2	ICP 2043A/NDA-1	23.72**	6.17	34.29**	0	-4.39	-0.74	3.54	-1.27	11.43
3	ICP 2043A/P-9	36.77**	30.34**	30.35**	-2.56	-5.11	-5.18	20.81**	13.92**	28.57
4	ICP 2043A/MAL-13	26.43**	16.50*	25.22**	7.78*	2.59	7.58	-2.77	-8.55**	17.14
5	ICP 2043A/DA-11	34.46**	22.16**	35.48**	0.13	-2.82	-2.22	-4.41*	-8.44**	2.86
6	ICP 2043A/MAL-28	22.61**	16.44*	17.31*	-2.2	-5.24	-4.25	-22.43**	-22.92**	-11.43
7	ICP 2043A/IPA-203	-2.64	-15.82**	4.58	-0.44	-3.37	-2.77	1.04	0	15.71
8	ICP 2092A/Bahar	31.99**	22.54**	22.53**	-0.28	-5.36	-2.03	5.15**	4.08*	21.43
9	ICP 2092A/NDA-1	20.85**	1.35	28.21**	9.05**	3.32	7.39	5.93**	0.42	14.29
10	ICP 2092A/P-9	18.53**	10.04	10.03	13.35**	9.37*	9.43*	8.44**	1.67	15.71
11	ICP 2092A/MAL-13	3.65	-6.86	0.1	8.38*	2.23	7.21	-0.98	-6.32**	20
12	ICP 2092A/DA-11	-3.48	-14.45*	-5.13	6.90*	2.82	3.51	12.91**	7.50**	22.86
13	ICP 2092A/MAL-28	13.70*	5.2	5.99	7.40*	3.11	4.25	-2.08	-2.08	11.43
14	ICP 2092A/IPA-203	6.06	-10.4	11.31	11.80**	7.53*	8.32*	4.15*	3.72	20
15	HY-4A/Bahar	43.97**	28.21**	28.21**	-14.39**	-15.53**	-10.17*	5.74**	5.31**	22.86
16	HY-4A/NDA-1	27.42**	3.04	30.35**	-10.43**	-11.47**	-5.91	15.72**	9.05**	25.71
17	HY-4A/P-9	41.57**	26.07**	26.06**	-1.7	-4.63	1.48	8.61**	1.23	17.14
18	HY-4A/MAL-13	67.18**	44.33**	55.13**	-5.83	-6.49	0.55	0.78	-4.09*	22.86
19	HY-4A/DA-11	24.36**	5.97	17.53*	-8.10*	-10.54**	-4.81	-6.09**	-11.11**	2.86
20	HY-4A/MAL-28	30.70**	16.01*	16.89*	-0.77	-3.24	2.96	1.04	0.41	15.71
21	HY-4A/IPA-203	30.52**	6.28	32.05**	-4.88	-7.42*	-1.48	1.86	1.65	17.14
22	H-28A/Bahar	54.07**	37.61**	37.60**	2.19	1.41	6.65	6.52**	0	17.14
23	H-28A/NDA-1	11.25	-9.8	14.1	14.74**	14.07**	19.96**	20.47**	20.47**	22.86
24	H-28A/P-9	25.96**	12.5	12.5	13.13**	10.38**	16.08**	4.94*	3.72	5.71
25	H-28A/MAL-13	43.74**	24.45**	33.75**	5.75	5.63	11.09**	0	-10.04**	15.71
26	H-28A/DA-11	9.81	-6.17	4.07	5.15	2.93	8.13*	12.50**	11.98**	15.71
27	H-28A/MAL-28	27.93**	13.89*	14.74*	-1.61	-3.52	1.48	5.49**	0	14.29
28	H-28A/IPA-203	13.43*	-7.39	15.06*	-0.48	-2.58	2.4	7.66**	1.65	17.14

*significant at P = 0.05, **significant at P = 0.01

Table 6c: Heterosis for Mid-Parent, Better Parent (BP) and Standard Heterosis (SH) in percentage for different characters in Pigeonpea

S.No No.	Crosses	Charcters No. of Grains/pods MP	BP	SH	100-Seed wt. (g) MP	BP	SH
1	ICP 2043A/Bahar	-0.44	-4.24	-1.57	-8.88*	-18.44**	-9.63*
2	ICP 2043A/NDA-1	3.93	-0.83	3.66	-10.70**	-13.61**	-19.09**
3	ICP 2043A/P-9	2.68	0	0	-4.52	-10.44*	-10.47*
4	ICP 2043A/MAL-13	6.54	4.59	-0.78	-4.79	-14.64**	-5.74
5	ICP 2043A/DA-11	0.45	-1.75	-2.61	2.84	2.49	-9.63*
6	ICP 2043A/MAL-28	-0.46	-0.92	-6.01	6.55	1.51	-1.77
7	ICP 2043A/IPA-203	1.42	-1.83	-6.79	-18.91**	-30.46**	-14.86**
8	ICP 2092A/Bahar	-4.64	-5.04	-1.57	3.01	-2.34	8.28*
9	ICP 2092A/NDA-1	2.93	2.5	7.05	-9.22*	-11.79**	-12.42**
10	ICP 2092A/P-9	2.56	0.84	4.44	-12.20**	-12.50**	12.50**
11	ICP 2092A/MAL-13	5.36	-0.84	2.61	-10.07**	-14.58**	-5.66
12	ICP 2092A/DA-11	2.15	0	3.66	-9.49*	-14.57**	-15.12**
13	ICP 2092A/MAL-28	5.73	0.84	4.44	-10.31**	-11.48**	-12.08**
14	ICP 2092A/IPA-203	22.17**	13.45**	17.49**	-20.23**	-27.77**	-11.57**
15	HY-4A/Bahar	-1.24	-3.25	3.66	-11.67**	-18.54**	-9.71*
16	HY-4A/NDA-1	-0.41	-1.63	5.22	-6.76	-6.82	-12.67**
17	HY-4A/P-9	-4.2	-7.32*	-0.78	-3.64	-6.73	-6.76
18	HY-4A/MAL-13	10.53**	2.44	9.66*	-9.61**	-16.50**	-7.77
19	HY-4A/DA-11	-2.95	-6.5	0	-14.25**	-16.73**	-22.04**
20	HY-4A/MAL-28	3.9	-2.44	4.44	-6.6	-8.12	-11.15**
21	HY-4A/IPA-203	-4	-12.20**	-6.01	-13.40**	-23.61**	-6.42
22	H-28A/Bahar	3.45	1.69	4.44	2.24	-0.99	9.71*
23	H-28A/NDA-1	12.82**	10.00**	14.88**	5.25	0.11	3.97
24	H-28A/P-9	14.41**	13.91**	14.10**	0.36	-1.49	2.28
25	H-28A/MAL-13	8.68*	4.39	3.66	8.80**	5.56	16.55**
26	H-28A/DA-11	14.04**	14.04**	13.05**	8.33*	0.16	3.97
27	H-28A/MAL-28	0.9	-1.75	-2.61	-2.47	-5.8	-2.2
28	H-28A/IPA-203	0.93	-4.39	-5.22	-11.15**	-17.91**	0.51

Table 6c: Cont.......

S.No No.	Crosses	Charcters Harvest Index (%) MP	BP	SH	Pollen Viability Test (%) MP	BP	SH	Grain Yield (Kg/ha) MP	BP	SH
1	ICP 2043A/Bahar	118.24**	16.55	-13.19	14.91**	-35.77**	-37.29**	74.34**	-7.74	-34.73**
2	ICP 2043A/NDA-1	178.39**	49.91**	-1.24	62.14**	-9.56**	-9.92**	223.54**	70.37**	32.42**
3	ICP 2043A/P-9	63.03**	-14.35	-14.32	5.34	-41.27**	-41.27**	45.35**	-24.32**	-24.32**
4	ICP 2043A/MAL-13	113.26**	13.77	-13.87	26.57**	-29.57**	-28.18**	243.76**	83.34**	13.59
5	ICP 2043A/DA-11	116.46**	15.19	-9.08	58.60**	-11.72**	-10.32**	242.02**	80.93**	28.79**
6	ICP 2043A/MAL-28	115.10**	14.92	-14.88	66.22**	-7.87**	-2.38	247.09**	83.12**	37.08**
7	ICP 2043A/IPA-203	59.75**	-15.06	-31.96**	-13.71**	-52.22**	-48.81**	57.98**	-16.7	-36.90**
8	ICP 2092A/Bahar	79.83**	-4.39	-28.81**	-18.55**	-54.47**	-55.56**	68.38**	-11.38	-37.31**
9	ICP 2092A/NDA-1	174.21**	46.92**	-3.21	5.71	-41.04**	-41.27**	79.18**	-6.12	-27.03**
10	ICP 2092A/P-9	119.27**	14.8	14.83	55.16**	-13.49**	-13.49**	171.92**	41.02**	41.02**
11	ICP 2092A/MAL-13	107.19**	10.05	-16.69	16.08**	-35.41**	-34.13**	205.77**	62.07**	0.41
12	ICP 2092A/DA-11	98.29**	5.07	-17.08*	-28.42**	-60.16**	-59.52**	63.87**	-13.78	-38.63**
13	ICP 2092A/MAL-28	66.32**	-11.55	-34.50**	-12.16**	-51.31**	-48.42**	87.63**	-1.53	-26.28**
14	ICP 2092A/IPA-203	70.44**	-9.76	-27.73**	-40.47**	-67.04**	-64.68**	46.49**	-23.16*	-41.79**
15	HY-4A/Bahar	82.51**	-1.51	-26.66**	60.44**	-10.98**	-13.09**	131.78**	23.33*	-12.75
16	HY-4A/NDA-1	89.53**	3.25	-31.96**	14.39**	-36.65**	-36.90**	68.78**	-10.68	-30.58**
17	HY-4A/P-9	45.64**	-22.88**	-22.89**	33.33**	-26.19**	-26.19**	50.08**	-21.56*	-21.55**
18	HY-4A/MAL-13	96.96**	6.15	-19.62*	46.48**	-19.07**	-17.46**	143.65**	30.75*	-18.99*
19	HY-4A/DA-11	70.28**	-8.5	-27.79**	-24.38**	-58.20**	-57.54**	72.93**	-8.02	-34.53**
20	HY-4A/MAL-28	105.64**	11.01	-17.81*	49.66**	-17.60**	-12.70**	197.45**	57.75**	18.08*
21	HY-4A/IPA-203	59.57**	-14.34	-31.40**	27.27**	-30.00**	-25.00**	104.05**	8.14	-18.08*
22	H-28A/Bahar	74.88**	-6.01	-29.99**	40.22**	-22.76**	-24.61**	126.15**	20.66*	-14.64*
23	H-28A/NDA-1	88.54**	2.25	-32.64**	19.57**	-34.26**	-34.52**	88.60**	0.06	-22.23**
24	H-28A/P-9	52.70**	-19.39*	-19.39*	71.84**	-5.56	-5.56	194.56**	54.27**	54.27**
25	H-28A/MAL-13	98.52**	6.58	-19.28*	14.18**	-37.35**	-36.11**	196.82**	59.77**	-1.01
26	H-28A/DA-11	94.62**	4.19	-17.76*	32.38**	-27.34**	-26.19**	182.74**	50.79**	7.34
27	H-28A/MAL-28	192.54**	57.30**	16.46	72.60**	-5.62*	0	301.07**	113.24**	59.63**
28	H-28A/IPA-203	138.91**	27.78**	2.31	80.34**	-1.48	5.56	344.57**	136.21**	78.93**

*significant at P = 0.05, **significant at P = 0.01

2043A/Bahar, ICP-2092A/DA-11 and ICP-2092A/MAL-13.

Standard heterosis for number of secondary branches/plant ranged from - 4.11 (ICP-2092A/NDA-1) to 86.56 (H-28A/MAL-28). Positive and significant heterosis over standard variety were recorded for the hybrid namely, H-28A/MAL-28, ICP-2043A/MAL-28, ICP-2043A/NDA-1, HY-4A/NDA-1, H-28A/IPA-203, ICP-2043A/DA-11, H-28A/P-9, H-28A/ MAL-13, HY-4A/MAL-28, ICP-2092A/MAL-28, HY-4A/IPA-203, H-28A/DA-11, ICP-2092A/DA-11, ICP-2092A/P-9, H-28A/NDA-1, ICP-2092A/P-9 and HY-4A/P-9, suggesting that to have the higher number of primary and secondary branches/plant the above crosses may be exploited. The results are corroborating with the findings of Rajesh *et al.* (2005), Patel and Tikka (2008) and Chandirakala *et al.* (2010) for number of branches/plant.

Standard heterosis of number of pods/plant ranged from - 32.57 (ICP-2092A/Bahar) to 39.19 (H-28A/P-9). Positive and significant heterosis over standard variety was recorded for hybrids namely, H-28A/P-9, H-28A/IPA-203, H-28A/MAL-28, H-28A/Bahar and ICP-2043A/DA-11. These crosses may be further advanced to develop genotype with higher number of pods/plant. Venkateswarlu *et al.* (1981), Singh *et al.* (1983), Narladkar and Khapre (1996), Patel and Tikka (2008), Rajesh *et al.* (2005) and Chandirakala *et al.* (2010) also reported standard heterosis for pods/plant.

Standard heterosis for pod bearing zone ranged from -5.13 (ICP-2092A/DA-11) to 55.13 (HY-4A/MAL-13). Most of the genotypes exhibited positive and significant heterosis over standard variety except namely, ICP-2092A/DA-11, ICP-2092A/MAL-13, H-28A/DA-11, ICP-2043A/IPA-203, ICP-2092A/MAL-28, ICP-2092A/IPA-203, ICP-2092A/P-9, H-28A/P-9 and H-28A/NDA-1.

Standard heterosis of pod length ranged from -10.17 (HY-4A/Bahar) to 19.96 (H-28A/ NDA-1). Positive and significant heterosis over standard variety was obtained in six hybrids namely, H-28A/NDA-1, H-28A/P-9, H-28A/MAL-13, ICP-2092A/P-9, ICP-2092A/IPA-203 and H-28A/DA-11. This finding is in agreement of Patel and Tikka (2008).

Standard heterosis for grains/pod ranged from - 6.79 (ICP-2043A/IPA-203) to 17.49 (ICP-2092A/IPA-203). Positive and significant standard heterosis was obtained in ICP-2092A/IPA-203, H-28A/NDA-1, H-28A/P-9, H-28A/DA-11 and HY-4A/MAL13 cross combinations. This finding is also corroborated with Yadav and Singh (2004), Rajesh *et al.* (2005) and Patel and Tikka (2008).

Standard heterosis for 100-seed weight ranged from -22.04 (HY-4A/DA-11) to 16.55 (H-28A/MAL-13. Only four hybrids had shown positive and significant standard heterosis viz., H-28A/MAL-13, ICP-2092A/P-9, H-28A/Bahar and ICP-2092A/Bahar to develop the bold seeded genotype, above cross may further advanced and tested. Singh *et al.* (1989), Rangaswamy *et al.* (1991), Deshmukh *et al.* (2001), Rajesh *et al.* (2005) and Patel and Tikka (2008) also recorded standard heterosis for 100-seed weight.

Grain yield is a complex character. The range of standard heterosis varied from - 41.79 (ICP-2092A/IPA-203), to 78.93 (H-28A/IPA-203). Out of 28 hybrids only 8 hybrids exhibited positive and significant heterosis over standard variety viz; H-28A/IPA-203, H-28A/ MAL-28, H-28A/P-9, ICP-2092A/P-9, ICP-2043A/MAL-28, ICP-2043A/NDA-1, ICP-2043A/DA-11 and HY-4A/MAL-28 appear to be promising in desirable direction for seed yield. These crosses could be considered for exploitation of hybrid vigour through the use of genetic male sterile lines in pigeonpea for enhancing the yield potential. Pandey (2004), Patel and Tikka (2008) and Chandirakala *et al.* (2010) also observed standard heterosis for grain yield.

Among all the crosses only three cross combination namely, ICP-2043A/DA-11, H-28A/ MAL-28 and H-28A/IPA-203 have shown positive and significant standard heterosis for most of the yield and yield attributing traits; suggesting that these cross combination may be exploited to develop the hybrid using CGMS system in pigeonpea for obtaining higher grain yield owing to the diverse genetic back ground of the parental lines.

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