



Research Article

Estimation of Heterosis, Combining ability and Gene action in Pigeonpea [*Cajanus cajan* (L.) Millsp.]

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(Received: 13 Mar 2014; Accepted: 26 Apr 2014)

Abstract

Eight cytoplasmic-genetic male sterile lines with A₂ (*Cajanus scarabaeoides*) and A₄ (*Cajanus cajanifolius*) cytoplasm were crossed with 10 testers in a line × tester design. Resultant 80 experimental hybrids were evaluated along with parents and check (Maruti) in lattice design with two replications. Combining ability analysis evinced predominance of non-additive gene effects for 10 characters indicating relevance of heterosis breeding for improving yield attributes. The *gca* effects of parents revealed that ICPA-2078, GT-308A, PKV-TATA, ARCCV-2 and GPHR-08-11 were good general combiners for seed yield and its direct components. The estimates of *sca* effects revealed that nine experimental hybrids had significant, desirable and positive *sca* effects for seed yield. The cross combination ICPA-2092 × VIPUL, ICPA-2078 × BSMR-856 and ICPA-2078 × ARCCV-2 were good specific combiners for number of secondary branches, number of pods per plant, seed yield per plant. These parental combinations are being used for exploitation of hybrid vigour.

Key words: Pigeonpea, Combining ability, heterosis, hybrids, Line X Testers

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is a short lived perennial shrub belonging to the economically most important tribe Phaseoleae and the *subtribe* *Cajaninae*. In India it is one of the very important grain legume and occupies second position in area and production next to chickpea. It is grown in an area of 3.90 m ha with an annual production of 2.89 m tonnes. In Karnataka, among different crops, pigeonpea occupies second place in area (5.97 Lakh ha) and ranks second in production (3.14 Lakh tonnes) with a productivity of 467 kg/ha. (Anon., 2011).

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 and six hybrids *viz.*, ICPH 8, COPH 1, COPH 2, PPH 4, AKPH 4104 and AKPH 2022 have been released for cultivation (Bajpai *et al.*, 2003).

In GMS system, it is an obligate practice to rogue out 50 per cent of fertile plants. This is laborious and time consuming job, adding to the production cost of seeds. Due to the limitation of large-scale

hybrid seed production in GMS-based hybrids, the development of cytoplasmic-nuclear male-sterility (CMS) became imperative. So far, seven different such CMS systems have been identified in pigeonpea with varying degrees of success (Saxena *et al.*, 2010). Of these, A₂ and A₄ systems derived from crosses involving wild relatives of pigeonpea and cultivated types have shown promise because of their stability under various agro-climatic-ecological conditions and availability of good maintainers and fertility restorers (Saxena and Nadarajan, 2010). Exploitation of heterosis depends much on general and specific combining ability effects. Therefore, present study was undertaken to estimate combining ability for seed yield and other traits in pigeonpea using cytoplasmic genic male sterile lines derived from A₂ and A₄ cytoplasm. An attempt was made to assess the combining ability involving 8 CGMS lines and 10 diverse testers crossed in line × tester design in pigeonpea.

Material and Methods

The experimental material comprised of five CMS lines developed from ICRISAT *viz.*, ICPA-2043, ICPA-2078, ICPA-2047, ICPA-2048-4 and ICPA-2092 derived from *Cajanus cajanifolius* with A₄ cytoplasm (Saxena *et al.* 2005) and three CMS lines procured from Gujarat Agricultural University *Viz.* GT-288A, GT-307A and GT-308A derived from *Cajanus scarabaeoides* with A₂ cytoplasm (Tikka *et al.* 1997) and ten diverse testers *viz.*, AKT-8811, PKV-TARA, VIPUL,

TARA, BSMR-856, ARCCV-2, PT-4-31, PT-0012, GRG-333 and GPHR-08-11 maintained at ARS, Gulbarga. The crosses were made in a line x tester mating design during *Kharif* 2011-12 and evaluated the hybrids during *Kharif*-2012-13 at Agricultural Research Station, Gulbarga.

A total of eighty experimental hybrids, eight females, ten males along with check variety Maruti were grown in a lattice design with two replications. Each genotype was sown in two rows of 4.0 meter length with the spacing of 90 x 30 cm. Recommended agronomical practices were adopted for optimum crop growth including population. Observations on five randomly selected competitive plants were recorded for days to 50% flowering, days to maturity, plant height(cm), number of primary & secondary branches/plant, pod bearing length (cm), number of pods/plant, 100 seed weight (g), seed yield/plant (g). The data was subjected to analysis of variance (Panse and Sukhatme, 1967) and combining ability analysis (Kempthorne, 1957) using Windostat version 8.5.

Results and Discussion

Analysis of variance revealed that the ratio of variance due to *GCA* to *SCA* was less than unity for all the characters (Table-1) indicating that these traits may be under the influence of non additive gene action and these characters are more likely to be improved through heterosis breeding. The above findings are in agreement with the earlier reports of Sunil Kumar *et.al.* (2003), Sekhar *et.al.* (2004), Sameer Kumar *et.al.* (2009), Beekham and Umaharan (2010), Shobha and Balan (2010), Sony Tiwari (2010), Meshram *et.al.* (2013) and Chethana *et.al.* (2013).

Analysis of variance for combining ability revealed that mean squares due to females were significant for all the characters while mean squares due to males were significant for characters *viz.*, days to 50% flowering, number of secondary branches/plant, pod bearing length (cm) and 100 seed weight. The mean squares due to line x tester interaction were significant only for number of secondary branches, number of pods per plant and seed yield/plant. Thereby it is suggested that the variation in hybrids in respect of seed yield may strongly influenced by the lines. The mean squares due to lines were larger in magnitude for most of the important yield attributes than testers indicating greater diversity amongst the lines as compared to testers (Table-2 & 3).

The analysis of variance for combining ability showed that mean squares due to general and specific combining ability effects indicating involvement of both additive and nonadditive gene action. The mean sum of squares due to lines x testers interactions were highly significant for seed

yield and its component characters that indicated the importance of *sca* variance, and consequently the non-additive genetic variation in the inheritance of these characters (Table- 2). These results were in agreement with the findings of Khorgade *et al.* (2000), Sunil Kumar *et al.* (2003) and Sekhar *et al.* (2004). Vaghela *et al.*(2009), Sameer Kumar *et al.* (2009) Bharate *et al.* (2011) for seed yield/plant and other important yield attributes *viz.*, pod bearing length, number of pods per plant and 100 seed weight. Preponderance of non-additive genetic variance suggested the relevance of heterosis breeding in pigeonpea.

Per cent contribution of line, testers and line x testers to the crosses (Table 3) revealed that a greater contribution of lines to the performance of crosses was observed for days to 50% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, number of pods per plant, seed yield/plant and seed yield/hectare while, the contribution of testers to the performance of crosses were found to be higher only for 100 seed weight indicating the significant contribution of maternal parents with more favorable alleles. The contribution of lines and testers were found equally important for the development of the yield and its attributing characters. This showed that average general combiner could give high heterotic performance and could be effectively used in heterosis breeding programmes. Similar results were also reported by Pandey and Singh (2002), Meshram *et.al.* (2013) and Chethana *et.al.* (2013).

The nature and magnitude of combining ability effects helps in identifying superior parents and their utilization in breeding programme. Character wise estimation of *gca* effects of lines and testers are presented in Table 3. The *gca* effects of parents revealed that ICPA-2078, GT-308A, ARCCV-2 and GPHR-08-11 were good general combiners for seed yield and its direct components (shown in Table 4). ICPA-2043, ICPA-2092 and BSMR-856 were good general combiners for seed yield, line GT-288A and tester GRG-333 for days to 50 % flowering, line GT-288A and tester PKV-TARA for days to maturity, line ICPA-2048-4 and tester PT-0012 for plant height, line ICPA-2048-4 and tester ARCCV-2 for both primary and secondary branches/plant, line GT-288A and tester PKVTARA for pod bearing length, line ICPA-2078 and tester PKVTARA for number of pods/plant, line ICPA-2078 and tester PT-4-31 for good general combiner for 100 seed weight.

The top three crosses exhibiting high specific combining ability effects along with their *Per se* performance, standard heterosis and *gca* status of the parents (Table 5) indicated that the cross combinations ICPA-2092 x VIPUL, ICPA-2078 x BSMR-856 and ICPA-2078 x ARCCV-2 were

good specific combiners for seed yield per plant, number of secondary branches and number of pods per plant. These parental combinations can be used for exploitation of hybrid vigour. The cross combination ICPA-2078 x AKT-8811 was good specific combiner for days to 50% flowering and maturity as it was showing highly significant negative *sca* effect this is very much suitable in dry land (rainfed) condition because it has advantage of escaping terminal moisture stress. The crosses ICPA-2092 x AKT-8811 and GT-288A x TARA for plant height, ICPA-2048-4 x GPHR-08-11 for both primary and secondary branches, GT-288A x PKV-TARA for pod bearing length, ICPA-2078 x ARCCV-2 for number of pods per plant, ICPA-2048-4 x TARA for 100 seed weight were found to be useful.

The estimates of *sca* effects revealed that 9 experimental hybrids had significant, desirable and positive *sca* effects for seed yield/hectare. Among these, three best crosses were selected on the basis of *per se* performance for ascertaining their association with *sca* effects of seed yield per plant and its attributes. All the crosses selected on the basis of *per se* performance possessed significantly desirable *sca* effects for seed yield per plant and other important yield attributing characters *viz.*, secondary branches, number of pods per plant, seed yield per plant. All these crosses showed significant positive *sca* response to pods per plant and 100 seed weight indicating its direct effect for increasing seed yield.

Out of three crosses showing high mean and significant positive *sca* effects for grain yield, two crosses ICPA-2078 x ARCCV-2 and ICPA-2092 x VIPUL involved high × high and low × low *gca* parents respectively and the remaining cross ICPA-2078 x BSMR-856 with high × low *gca* effects of parents. These results were also in conformity with those of Baskaran and Muthiah (2007), Meshram *et.al* (2013) and Chethana *et.al* (2013). Better performance of hybrids involving high × low or low × low general combiners indicated dominance × dominance (epitasis) type of gene action. The crosses showing high *sca* effects involving one good general combiner indicated additive × dominance type gene interaction which exhibit the high heterotic performance for yield and yield related traits.

The above results suggested that the crosses having high mean performance, positive *sca* effects for seed yield and their significant response to other related traits had necessarily involved both or at least one parent as good combiner which could be commercially exploited for heterosis by taking advantage of high degree of natural out crossing in pigeon pea.

Acknowledgments

Sincere thanks to National Food Security Mission, New Delhi and ICRISAT for having provided seed materials and financial support.

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Table 1. Variance due to GCA, SCA and their proportion in Pigeonpea

Characters	Variance due to GCA	Variance due to SCA	GCA :SCA
Days to 50 per cent flowering	0.4229	1.7608	1:4.164
Days to maturity	0.4108	6.2622	1:15.244
Plant height (cm)	1.4706	24.3191	1:16.537
Primary branches	0.188	0.7681	1:4.086
Secondary branches	0.0798	4.0128	1:50.286
Pod bearing length (cm)	1.367	5.919	1:4.330
No. of pods/plant	12.6781	833.1884	1:65.719
100 seed weight (g)	0.0269	0.1712	1:6.364
Seed yield/ plant (g)	0.6038	80.4664	1:133.267

Table 2. ANOVA for combining ability in respect of 9 characters in Pigeonpea (*Cajanus cajan* L.)

Source of variation	DF	DFF	DM	PHT	PB	SB	PBL	NPPP	SW	SYPP
Females	7	193.91**	272.592**	1077.778**	124.37*	49.99**	850.09**	8367.81**	9.06**	669.55**
Males	9	89.20**	46.97	138.24	9.76	20.50*	122.11*	3040.33	7.66**	126.53
Females x Males	63	14.89	29.02	131.64	6.52	10.74*	52.19	1770.51**	0.65	192.61**
Error	79	11.37	16.50	83.00	4.98	2.72	64.03	104.14	0.31	31.68

*, ** – Significant at 5% and 1% levels, respectively

DF= Degree of freedom, DFF= Days to 50 % flowering, DM= Days to maturity, PHT= Plant height (cm), PB = No. of Primary branches, SB= No. of Secondary branches, PBL = Pod bearing length (cm), NPPP= No. of pods/ plant, SW = 100-Seed weight (g), SYPP= Seed yield/ plant.

Table 3. General combining ability effects for parents in respect of 9 characters in Pigeonpea (*Cajanus cajan* L.)

ENTRIES	DFF	DM	PHT	PB	SB	PBL	NPPP	SW	SYPP
Lines									
ICPA-2043	-2.19 **	-2.21 *	-6.37 **	-0.14	-0.28	-0.64	1.02	-0.15	-1.3
ICPA-2078	-0.39	2.24 *	-9.94 **	-3.92 **	-1.68 **	5.32 **	37.53 **	1.21 **	6.94 **
ICPA-2047	3.36 **	4.19 **	7.06 **	1.51 **	1.62 **	-7.14 **	-17.42 **	-0.08	-7.04 **
GT-288 A	-6.49 **	-7.81 **	2.36	-3.17 **	-2.38 **	11.08 **	-19.67 **	-0.47 **	-5.20 **
ICPA-2048-4	1.71 *	2.09 *	11.22 **	2.71 **	1.44 **	-3.93 *	-16.02 **	-0.09	-4.10 **
ICPA-2092	1.81 *	1.34	-5.84 **	1.52 **	1.98 **	-6.67 **	4.38	-0.92 **	0.27
GT-307A	0.46	0.69	4.01	2.33 **	-0.3	-3.08	-10.73 **	0.74 **	0.94
GT-308A	1.76 *	-0.56	-2.49	-0.85	-0.4	5.06 **	20.92 **	-0.24	9.50 **
CD@5%	2.11	2.5	5.7	1.39	1.03	5.01	6.38	0.34	3.52
CD@1%	2.8	3.37	7.57	1.85	1.37	6.65	8.48	0.46	4.68
Testers									
AKT-8811	-1.56	-2.08 *	-4.33	-0.04	1.33 **	0.19	1.49	-0.61 **	2.29
PKV-TARA	-1.93 *	-2.52 *	1.56	-0.12	-0.21	5.73 **	19.42 **	-0.51 **	0.58
VIPUL	-0.49	-1.14	-2.94	-1.35 *	0.19	1.51	-2.51	0.36 *	1.39
TARA	-0.31	0.79	-0.48	0.28	-0.44	1.12	-10.01 **	-0.22	-2.47
BSMR-856	3.13 **	-0.21	-2.6	-0.24	2.00 **	-4.36 *	17.74 **	-0.95 **	1.35
ARCCV-2	5.01 **	3.23 **	1.56	1.65 **	0.96 *	-1.87	12.30 **	-0.41 **	3.26 *
PT-4-31	-0.99	1.11	-0.69	-0.27	-1.29 **	-2.98	-22.01 **	0.96 **	-3.67 *
PT-0012	-0.81	0.67	5.67 *	0.71	-1.23 **	0.45	-13.57 **	0.91 **	-3.72 **
GRG-333	-2.62 **	-0.83	-0.17	-0.39	-0.15	0.67	-7.95 **	0.78 **	-2.44
GPHR-08-11	0.57	0.98	2.42	-0.24	-1.16 **	-0.46	5.11 *	-0.30 *	3.43 *
CD@5%	2.36	2.84	6.37	1.56	1.15	5.6	7.14	0.38	3.94
CD@1%	3.13	3.77	8.47	2.07	1.53	7.44	9.48	0.51	5.23

DF= Degree of freedom, DFF= Days to 50 % flowering, DM= Days to maturity, PHT= Plant height (cm), PB = No. of Primary branches, SB= No. of Secondary branches, PBL = Pod bearing length (cm), NPPP= No. of pods/ plant, SW = 100-Seed weight (g), SYPP= Seed yield/ plant.



Table 4. Percent contribution of Lines, Testers and Line X Testers to crosses in Pigeonpea

SOURCE OF VARIATION	DFE	DM	PHT	PB	SB	PBL	NPPP	SW	SYPP
Lines	43.81	45.88	44.17	63.60	28.89	57.56	29.66	36.57	26.10
Testers	25.91	10.16	7.28	6.42	15.23	10.63	13.86	39.80	6.34
LinesX Testers	30.28	43.96	48.55	29.99	55.88	31.81	56.48	23.62	67.56

DF= Degree of freedom, DFF= Days to 50 % flowering, DM= Days to maturity, PHT= Plant height (cm), PB = No. of Primary branches, SB= No. of Secondary branches, PBL = Pod bearing length (cm), NPPP= No. of pods/ plant, SW = 100-Seed weight (g), SYPP= Seed yield/ plant.

Table 5. Comparison of top three best crosses selected on the basis of specific combining ability effects for different characters

Charact ers	Crosses	SCA effects	GCA effects of Parents and Status			Standard heterosis	<i>per se</i>	Significant SCA effects for other traits
			P1	P2	Status			
DFF	GT-288A X TARA	-5.19	-6.49	-0.31	H X L	-13.61	82.5	PHT, NPPP
	ICPA-2078 X AKT-8811	-5.04	-0.39	-1.56	L X L	-8.38	87.5	
	GT-308A X PT-4- 31	-4.76	1.76	-0.99	H X L	-5.24	90.5	-
DM	GT-308A X BSMR-856	-11.19	-0.56	-0.21	L X L	-78.3	129.5	NPPP,SYPP, SYPH
	GT-308A X GRG- 333	-11.07	-0.56	-0.83	L X L	-8.19	129	SB
	ICPA-2078 X AKT-8811	-10.12	2.24	2.08	H X H	-6.41	131.5	DFE
PHT	ICPA-2092 X AKT-8811	16.8	-5.84	-4.33	L X L	13.3	167.5	NPPP
	GT-288A X TARA	15.74	2.36	-0.48	L X L	20.74	178.5	NPPP
PB	ICPA-2048-4 X GPHR-08-11	3.41	2.71	-0.24	H X L	56.32	18.5	SB,NPPP, SYPP, SY/PT,SYPH
	GT-288A X BSMR-856	7.3	-2.38	2	L X H	20.75	16.5	NPPP, SYPP, SY/PT,SYPH
SB	ICPA-2092 X VIPUL	5.24	1.98	0.19	H X L	24.41	17	NPPP, SYPP, SY/PT,SYPH
	GT-308A X GRG- 333	4.46	-0.4	-0.15	L X L	-1.21	13.5	DM
	GT-288A X PKV- TARA	14.21	11.08	5.73	H X H	103.27	67.75	-
NPPP	ICPA-2078 X ARCCV-2	63.35	37.53	12.3	H X H	50.29	255.5	SYPP
	ICPA-2043 X GPHR-08-11	52.54	1.02	5.11	L X H	18.24	201	SYPP, SY/PT,SYPH
	ICPA-2078 X BSMR-856	51.41	37.53	17.74	H X H	46.47	249	DM, SYPP
SW	ICPA-2048-4 X TARA	1.28	-0.09	-0.22	L X L	24.39	11.17	-
	GT-308A X GPHR-08-11	1.15	-0.24	-0.3	L X L	20.55	10.82	-
	ICPA-2078 X VIPUL	1.08	1.21	0.36	H X H	43.1	12.85	-
	ICPA-2078 X BSMR-856	26.74	6.94	1.35	H X L	39.68	71.41	DM,NPPP
SYPP	ICPA-2092 X VIPUL	16.19	0.27	1.39	L X L	6.09	54.23	SB,NPPP, SYPP, SY/PT,SYPH
	ICPA-2078 X ARCCV-2	15.9	6.94	3.26	H X H	22.23	62.48	NPPP

DF= Degree of freedom, DFF= Days to 50 % flowering, DM= Days to maturity, PHT= Plant height (cm), PB = No. of Primary branches, SB= No. of Secondary branches, PBL = Pod bearing length (cm), NPPP= No. of pods/ plant, SW = 100-Seed weight (g), SYPP= Seed yield/ plant(g).