Journal of Food Legumes 25(3): 231-233, 2012

Short communication

Combining ability studies in pigeonpea [*Cajanus cajan* (L.) Millsp.] hybrids

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(Received: March 31, 2012; Accepted: July 04, 2012)

ABSTRACT

Twelve cytoplasmic genetic male sterile lines were crossed with 5 restorer lines in Line x Tester design. The resultant 60 hybrids were evaluated along with their parents and the standard checks (JKM 189 and TJT 501) during ***Kharif*** **2010. Combining ability analysis revealed predominance of non-additive gene effect for all the characters indicating relevance of heterosis breeding for improving the yield and its attributes in pigeonpea. The lines ICPA 2086, ICPA 2089, ICPA 2052, Asha and GT 101 were good general combiner for seed yield and crosses ICPA 2086 x Asha, ICPA 2089 x JKE 114 and GT 33 x JKM 189 showed higher sca effect for seed yield/plant. Besides ICPA 2079 x ASHA, ICPA 2086 x JKE 114, ICPA 2047 x JKE 114 were the top most heterotic hybrids for seed yield/plant. These crosses also manifested high and significant standard heterosis for pods/ plant and 100 seed weight.**

Key words: CGMS lines, Combining ability, Pigeonpea

Pigeonpea [*Cajanus cajan* (L.) *Millasp*] is the second important pulse crop of india which has diversified uses as food, feed, fodder and fuel. It has been recognized as a valuable source of protein for the vegetarians in their daily diet. Exploitation of hybrid vigour or heterosis has been successfully attempted in a number of crops to break the yield ceiling. Among pulses, pigeonpea has the highest out crossing of about 20-25%, which gives the ample opportunity for exploitation of heterosis. The development of hybrid pigeonpea using cytoplasmic genetic male sterility is very much required to break the yield platue of this crop .Looking into availability of several CMS lines, identification of better restorers for exploiting full heterosis is essential. Therefore, this study has been aimed to evaluate the restorer lines suitable for agro-ecological conditions of Madhya Pradesh.

The experiment materials for the present investigation were generated using twelve Cytoplasmic genetic male sterile (‘A’) lines which were used as female parents (lines)for developing hybrids using five fertility restorers (R) as male parents (testers) following Line x Tester mating design (Kempthorne 1957). The complete set of (60 crosses and 17 parent) were evaluated in a randomized block design with two replications at Zonal Agriculture Research Station, Khargone (M.P.) during *Kharif* 2009-10. Each hybrid and parent was grown in a twin row plot of 4 m length, spaced 75 cm apart and intra row spacing was 25 cm. The recommended packages of practices were followed to raise a good crop. The observations were recorded on individual plant for days to 50% flowering, days to maturity, plant height (cm), primary branches/plant, stem girth (cm), pods/plant, clusters/plant, pods/cluster, pod length (cm), fruiting branch length (cm), 100-seed weight (g), seed yield/plant (g) and harvest index (%). The combining ability and heterosis were estimated as per cent increase or decrease in the mean value of F1 hybrids over mid parent and better parent (heterobeltiosis) for each character.

The analysis of variance for combining ability and the estimate of variance component indicated that the mean sum of square due to lines were significant for all the characters (Table 1 and 2) indicating significant contributions of lines towards gca variance components for all the character. The mean sum of squares due to testers were also highly significant for all the characters, except seeds/pods suggesting larger contribution of tester towards gca variance component.

The variance estimates due to lines were highly significant for all the characters except grain yield, pods/plant and pod length. Variance estimates due to testers were also significant for 100-seed weight and seed yield/plant, which indicated greater variation among testers for those traits.

The mean sum square due to female x male interaction were highly significant for all the characters which indicated the importance of sca variance and consequently, the non-additive genetic variation in the inheritance of the characters studied. This was further substantiated by less than unity ratio of $ä^2$ gca /$ä^2$ sca. Preponderance of non-additive genetic variance suggested the relevance of heterosis breeding in pigeonpea.

Nature and magnitude of combining ability effect helps in identifying the best parent and their utilization in the breeding programme. Based on the estimates of general combining ability effect, the parents were classified as good and poor combiners for thirteen traits (Table 2). Among females, ICPA 2052 was the good general combiner for days to 50% flowering, days to maturity, pods/plant, pods/cluster, pod length (cm), fruiting branch length, seed yield/plant (g) and harvest index. Hence, female ICPA 2052 may be considered

Table 1. Combining ability variance for seed yield and its attributes in pigeonpea

Source of variance	D. f	Days to 50 % flowering	Days to maturity	Plant height	Primary branches	Stem girth	Pods/plant	Clusters/ plant	Pod/ clusters	Pod length	Fruiting branch length	100-seed weight	Seed yield / plant	Harvest index
Replication	1	3.7	807.5**	193.7**	584.9**	0.2	12378.4**	12037.314**	17.721**	3.089	193.248**	0.315	7803.132**	39.281**
Crosses	59	78.0**	143.7	243.2**	8.0**	1.5	6413.4**	1101.847**	0.525	0.392	10.583**	3.393**	771.379**	16.837**
Lines	11	227.5**	210.3**	390.1**	8.0**	4.7**	6078.8**	566.559**	0.528	0.508	15.437**	7.617**	834.734**	28.308**
Tester	4	132.8	1074.9**	1254.5**	27.9**	1.2	21946.3**	537.313**	0.318	0.934	17.669**	11.252**	1530.778**	5.849**
L x T	44	35.6*	58.7**	142.3**	7.1**	0.9	5813.7**	34942.035**	0.603	0.358	9.928**	2.009**	774.160**	16.881**
Error	64	8.7**	62.7	124.8**	4.9**	0.6	4176.5**	121.773**	0.410	0.059	3.783**	0.204	130.105**	7.672**

Table 2. General combining ability effects (GCA effect) variance for seed yield and its attributes in lines and testers

Lines/ tester	Days to 50 % flowering	Days to maturity	Plant height	Primary branches	Stem girth	Pods / plant	Cluster / plant	Pod / cluster	Pod length	Fruiting branch length	100 seed weight	Seed yield / plant	Harvest index
Lines													
GT 33	-1.208	-1.967	-8.818*	1.526*	-0.052	-44.488**	2.596	-0.415*	0.252**	-2.443**	0.033	4.336	1.669
• ICPA 2042	-2.408*	2.733	-1.550	0.787	1.194**	-5.489	-5.435	0.122	-0.179*	0.827	-0.158	-6.647*	0.893
• ICPA 2043	-3.008**	-1.067	-0.834	0.285	-0.313	-12.240	-5.666	0.031	0.452**	0.627	-0.62**	-11.51**	2.004*
• ICPA 2047	0.592	9.033**	-1.985	1.309	1.518**	14.071	2.945	0.008	-0.095	-1.883**	0.723	-6.544*	-0.015
• ICPA 2048	1.492	3.433	0.908	0.514	-0.563	-18.460	-18.936**	0.465*	-0.27**	-0.523	0.323*	3.458	-0.295
• ICPA 2050	-4.408**	-0.767	-6.117	-0.098	0.161	-31.500	-5.226	-0.082	0.242**	0.027	-0.487	7.433	1.888*
• ICPA 2052	14.192**	3.633	-2.950	-0.370	0.056	8.681	-1.566	0.078	-0.28**	2.157**	0.053	-8.303	-2.763**
• ICPA 2078	0.292	3.433	-0.484	-0.224	-0.241	-6.229	8.535*	-0.342	-0.062	0.007	1.053**	-5.679	-1.050
• ICPA 2079	-2.608*	-2.567	8.716*	-1.065	-0.513*	4.671	7.695*	-0.020	-0.018	0.427	0.672**	-5.193	1.738
• ICPA 2086	-1.708	-7.567**	-3.650	-1.137	-0.513*	25.131	4.464	0.024	-0.052	-0.133	1.183**	17.226	-0.039
• ICPA 2089	-0.508	-3.367	2.582	-0.704	-0.616**	27.414	0.171	0.202	0.122	-0.193	-1.77**	13.536	-2.080*
• ICPA 2098	-0.708	-4.967*	14.183**	-0.825	-0.117	38.440	15.615	-0.070	-0.098	1.107	-0.98**	-2.106	-1.950*
Tester													
JKM 189	-0.208	-1.742	-4.128	-0.436	0.230	30.944*	3.979	0.122	-0.27**	-0.103	-0.30**	1.341	-0.219
TJT 501	-3.750**	-5.700**	-1.490	-0.404	-0.275*	8.000	-0.710	0.028	0.004	-0.032	-0.225*	-3.175	-0.384
GT 101	2.292**	3.758*	-1.406	-0.893*	-0.166	-39.241**	-12.192*	*0.089*	0.281**	1.326**	-0.25**	-11.12**	0.291
JKE 114	0.000	-5.992**	-5.520*	-0.134	-0.013	-23.244	0.374	*-0.138*	0.032	-0.112	1.217**	2.265	-0.412
Asha	1.667**	0.675	12.545**	1.868**	0.223	23.561	8.549*	*-0.101*	-0.045	-1.078**	-0.43**	10.694**	0.725
SE for gca line	0.932	2.505	3.532	0.703	0.237	20.437	3.490	0.203	0.077	0.615	0.143	3.607	0.876
SE for gca Tester	0.578	1.553	2.191	0.436	0.147	12.674	2.164	0.126	0.048	0.381	0.089	2.237	0.543
SE for (gi-gj) lines	1.318	3.542	4.995	0.994	0.335	28.902	4.935	0.286	0.108	0.870	0.202	5.101	1.239
SE for (gi-gj) tester	0.602	1.617	2.280	0.454	0.153	13.192	2.253	0.131	0.050	0.397	0.092	2.328	0.565

Table 3. Three best heterotic cross combination (specific combiner) for different characters

Character	Hybrid	sca effect
Days to 50 % flowering	ICPA 2078 X JKM189	13.708**
	ICPA 2050 X Asha	7.55**
	ICPA 2048 X TJT 501	6.50**
Days to maturity	ICPA 2086 X JKM189	9.42**
	ICPA 2048 X JKE 114	7.92**
	GT 33 X GT 101	7.84**
Plant height	ICPA 2098 X TJT 501	18.457**
	ICPA 2050 X JKE 114	15.287**
	GT 33 X JKM 189	12.096**
Primary branches	ICPA 2089 X JKM 189	4.16**
	ICPA 2078 X TJT 501	2.64**
	ICPA 2052 X GT 101	2.68**
Stem girth	ICPA 2047 X GT 101	1.76**
	ICPA 2043 X JKE 114	1.916
	ICPA 2043 X JKM 189	1.50**
Pods/plant	GT 33 X TJT 501	128.86**
	ICPA 2042 X JKM 189	90.426**
	ICPA 2079 X TJT 501	66.36**
Cluster/plant	ICPA 2047 X GT 101	37.42**
	ICPA 2050 X GT 101	20.59**
	GT 33 X JKM 189	20.29**
Pod/cluster	GT 33 X TJT 501	1.556**
	ICPA 2052 X JKE 114	0.922**
	ICPA 2042 X TJT 501	0.786**
Pod length	ICPA 2043 X GT 101	1.00**
	ICPA 2050 X GT 101	0.810**
	ICPA 2052 X Asha	0.565**
Fruiting branch length	GT 33 X TJT 501	4.27**
	ICPA 2047 X JKM 189	3.637**
	ICPA 2048 X JKM 189	3.083**
100 Seed weight	ICPA 2048 X TJT 501	1.665**
	ICPA 2079 X JKE 114	1.273**
	ICPA 2086 X JKE 114	1.116**
Grain yield / plant	ICPA 2086 X Asha	64.242**
	ICPA 2089 X JKE 114	40.735**
	GT 33 X JKM 189	33.059**
Harvest index	ICPA 2048 X Asha	5.78**
	ICPA 2098 X Asha	4.769**
	ICPA 2078 X JKE 114	4.328**

as the best male sterile (A) line and source of favourable gene for enhancing seed yield in hybrid programme. In addition, ICPA 2086 and ICPA 2089 were good general combiner for seed yield/plant and important yield attributes.

Among testers, GT 101 revealed good general combining ability for days to 50% flowering, days to maturity, plant height (cm), primary branches, stem girth (cm), pods/plant, clusters/ plant, pods/cluster, pod length (cm), fruiting branch length and 100-seed weight. The genotype Asha showed good general combining ability for plant height, primary branches, number of pods/plant, clusters/plant, seed yield/plant and harvest index. JKE 114 was also good general combiner for 100-seed weight. Therefore, these fertility restorer lines can be used in breeding program for enhancement of yield and yield attributes.

For specific combining ability (Table 3), three cross combinations *viz.*, ICPA 2086 x Asha, ICPA 2089 x JKE 114 and GT 33 X JKM 189 were identified for seed yield/plant. Two crosses *viz.*, ICPA 2079x Asha and ICPA 2086 x JKE 114 were found best for yield contributing characters like pods/plant and 100-seed weight. Since these crosses involved at least one good general combiner parent, therefore, better performance of these crosses might be due to interaction of dominant gene contributed by one such parent.

It may be concluded that parents with good general combining ability should be used for development for high yielding hybrids. Beside, best cross combinations showing high sca effects may also be exploited for development of high yielding hybrids.

REFERENCES

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