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RESEARCH ARTICLE

Combining ability and gene action in Cowpea (*Vigna unguiculata*)

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Abstract

The present investigation was undertaken to study combining ability and nature of gene action for yield and yield contributing traits in cross involving eight parents of cowpea genotypes viz., Wali 4, Konkan Safed, C-152, VCM-8, DFC-1, GC-3, Pusa Falguni, Pusa-do-Phasli and their F's (excluding reciprocal) obtained through diallel cross were evaluated during 2006 at Pulses Improvement project, M.P.K.V., Rahuri, Maharashtra. Six quantitative traits were studied during the investigation on five randomly selected plants from each genotype. The data were subjected to combining ability analysis as per method 2, model I of Griffing (1956) and Haymann (1954) diallel analysis for estimation of the genetic components, GCA and SCA. Analysis of variance revealed that significant level of diversity among the traits for both parents and their F1s. The GCA effects varied significantly for different characters and genotypes. The parent Wali-4, Pusa-do-Phasli, Konkan Safed and VCM-8 would be considered as good parents for isolating new strains through hybridization. The cross combination wali4 x DFC-1 was appeared to be the most promising for yield and its principal component.

Key words: Half diallel, cowpea, yield, combining ability

Cowpea is a tropical grain legume which plays an important nutritional role in developing countries of the tropics and subtropics, especially in Sub-Soharan Africa, Asia and Central and South America. Because of its high protein content (20-25%), cowpea has been referred to as 'poor man's meat'. Cowpea young leaves, pods and peas contain vitamins and minerals for which it is used for human consumption and animal feeding. India is a leading producer of cowpea. It is grown in central and peninsular regions. In order to replace the old out dated genetically eroded varieties, there is urgent need to develop new varieties with high yielding ability which may be achieved by systemic research programme. Precise information on the type of gene action helps the plant breeder in formulating successful genetic improvement programme for yield and yield contributing characters. Yield being a complex character, is influenced by a number of yield contributing characters controlled by polygene's and also influenced by environment. Combining ability analysis helps in identification of appropriate genotypes for further hybridization programmers.

Material and methods

Eight parents were sown in rows of 5 m length at 45x15 cm spacing and crosses were made following half diallel in all possible combination resulting in 28 F1's. Progenies were planted following the same spacing as parents and observations were recorded on 5 randomly selected plants from each progeny for 6 quantitative traits viz., days to 50 % flowering, pod length, number of seeds per pod, 100-seed weight, number of pods per plant and seed yield per plant. The experimental data of 8 x 8 half diallel was analyzed statistically for combining ability following model-I and method-2 of Griffing (1956) and diallel analysis of Hayman (1954) for genetic component analysis.

Result and discussion

Analysis of variance (Table2) revealed the significant difference for all the characters under study. The mean sum of square due to treatments, parents and crosses were significant for all the characters. The parents *vs* hybrids mean squares were also significant for all the characters studied except for pod length. The analysis of variance for combining ability (Table3) indicated significant differences for GCA and SCA for all the characters under study. However, the relative importance of GCA and SCA when compared revealed prepondence of additive gene effects for all the characters. High GCA coupled with high per se performance is the indication of an outstanding best parent with reservoir of superior genes. The parent Wali 4 was good general combiner for pod length, number of seed per pod, 100-seed weight and seed yield per plant. The parent Pusa-do-phasli was good general combiner for days to 50 % flowering, number of seeds per pod, number of pods per plant and seed yield per plant. Pusa Falguni showed good GCA effects for days to 50 % flowering and number of pods per plant. GC-3 exhibited good general combiner for days to 50 % flowering, 100-seed weight number of pods per plant, seed yield per plant. DFC-1 was good general combiner for number of seed per pod, 100-seed weight. VCM-8 was good general combiner for days to 50% flowering C-152 showed good GCA effects for 100 seed weight, number of pods per plant and seed yield per plant. Konkan safed was good general combiner for days to 50 % flowering, pod lengh, 100 seed weight, number of pods per plant, and seed yield per plant (Table 4).

Among the 28 crosses, the cross DFC-1xC-152 evinced high significant negative SCA effect for days to 50% flowering. The cross Wali 4xPusa-do-Phasli showed best specific combiner for pod length. Similar desirable high SCA effects were observed in Wali 4 x Konkan safed for number of seed per pod, GC-3 xVCM-8 for 100 seed weight, Wali 4xC-152 for number of pods per plant, wali 4 x DFC-1 for seed yield per plant (Table 5).

The component analysis revealed that dominant and non-additive gene action played an important role in the inheritance of seed yield except days to 50% flowering. Additive gene action D was significant for all the characters therefore these characters may give good response for selection. Dominent effect H1 and H2 of genes were significant for all the characters, indicating the involvement of dominant genes in the expression of these characters and hence they may yield desirable combination in heterozygous condition only. Therefore care should be taken while effecting selection from segregating population. The distribution of dominant and recessive alleles (H2 / 4H1) was asymmetrical for all the characters except number of pods/plant. The estimate of (H1 / D) ½ revealed over dominance for all the character except days to 50% flowering. The ratio of total number of dominant to recessive alleles in all the parents (KD/Kr) revealed that, dominant genes were in excess than recessive except for pod length and number of seeds/pod. The estimates of h2/H2 were less than unity for all the characters except days to 50% flowering, 100-seed weight, number of pods per plant and seed yield per plant indicated at least two groups of dominant genes was responsible for expression of the character. Low to high estimate of heritability was observed which ranges between 2 to 84%. The character days to 50% flowering had high heritability (Table 6). Diallel analysis estimated that both additive and non-additive genetic variances played a significant role for most of the characters studied. The GCA variance was higher than SCA variance for most of the characters indicating predominance of additive gene action in the in heritance of these traits. None of the parents showed desirable GCA effects simultaneously for all the characters. The parent Konkan Safed, wali 4, Pusa-do-Phasli and GC-3 were proved to be good general combiners with good per se performance for most of the yield traits studied. The hybrid wali 4 x Pusa Falguni, Wali 4 x DFC-1 and Pusa-do-Phasli x Pusa Falguni was identified as the best cross combination for seed yield.

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Table 1: Mean performance of parents and cowpea hybrids for different paprameters

Sr. No.	Parents/ hybrids	Days to 50% flowering	Pod Length (cm)	No. of seeds/ pod	100 -seed weight (g)	No. of pods/ plant	Seed yield/ plant (g)
	Parents						
1	Wali- 4	115.00	19.03	16.40	18.95	6.55	10.98
2	Pusa-do-phasali	57.00	15.02	15.46	12.25	12.08	14.82
3	Pusa falguni	53.66	14.76	14.40	9.03	9.93	7.55
4	GC-3	71.33	15.96	13.93	12.76	9.79	14.18
5	DFC-1	83.66	15.00	15.73	15.86	6.00	9.12
6	VCM-8	48.00	12.85	12.73	10.35	10.17	11.04
7	C-152	83.66	16.04	14.86	12.88	10.51	14.09
8	Konkan safed	53.00	17.89	13.66	15.02	9.99	17.26
	Crosses						
1	Wali x Pusa-do-phasali	79.00	22.21	17.00	18.88	9.88	18.03
2	Wali x Pusa falguni	80.00	18.05	14.80	18.52	10.37	21.96
3	Wali x GC-3	80.67	21.11	16.93	18.81	9.38	21.59
4	Wali x DFC-1	85.00	20.68	17.27	17.91	9.39	23.26
5	Wali x VCM-8	76.53	14.65	15.13	18.95	9.11	15.66
6	Wali x C-152	82.00	13.95	12.80	15.76	13.87	19.79
7	Wali x Konkan safed	87.00	20.15	17.33	18.06	11.93	24.45
8	Pusa-do-phasali x Pusa falguni	52.33	14.17	14.20	12.54	14.55	20.27
9	Pusa-do-phasali x GC-3	54.67	14.56	13.40	15.56	13.89	18.64
10	Pusa-do-phasali x DFC-1	58.67	15.55	14.60	18.16	10.64	15.83
11	Pusa-do-phasali x VCM-8	47.33	12.89	12.67	14.83	12.98	16.48
12	Pusa-do-phasali x C-152	58.67	14.69	14.13	14.08	13.43	15.45
13	Pusa-do-phasali x Konkan safed	51.33	15.76	11.87	15.24	12.64	17.10
14	Pusa falguni x GC-3	56.00	12.60	10.47	12.75	11.08	10.91
15	Pusa falguni x DFC-1	59.00	12.99	11.87	11.96	11.84	8.81
16	Pusa falguni x VCM-8	53.67	13.43	13.33	10.39	12.85	16.17
17	Pusa falguni x C-152	59.00	16.02	11.47	16.14	10.78	12.16
18	Pusa falguni x Konkan safed	54.00	14.92	12.47	12.11	12.10	17.31
19	GC-3 x DFC-1	56.67	15.73	15.40	16.68	12.43	17.87
20	GC-3 x VCM-8	56.00	14.87	12.87	17.93	10.89	16.69
21	GC-3 x C-152	64.33	16.04	13.67	16.24	13.01	18.13
22	GC-3 x Konkan safed	55.00	14.40	12.87	14.67	13.54	19.83
23	DFC-1 x VCM-8	56.33	14.19	14.07	13.89	9.61	16.36
24	DFC-1 x C-152	56.67	16.04	16.20	17.72	10.46	18.92
25	DFC-1 x Konkan safed	53.67	15.04	13.33	15.82	9.36	14.60
26	VCM-8 x C-152	56.67	14.75	14.07	15.47	11.11	19.10
27	VCM-8 x Konkan safed	57.00	14.05	11.47	13.44	13.68	18.39
28	C-152 x Konkan safed	76.00	14.85	14.13	19.01	11.99	23.21
	S.E.±	1.28	0.30	0.25	0.13	0.36	0.22
	CD at 5%	3.69	0.88	0.71	0.38	1.03	0.63

* Significant at 5% level ** significant at 1% level

Table 2: Analysis of variance for yield contributing characters in cowpea

Sr. No.	Sources	D.F.	Mean sum of squares					
			Days to 50% flowering	Pod length (cm)	No. of seeds/ pod	100 seed weight (g)	No. of pods/ plant	Seed yield/ plant (g)
1	Replications	2	3.95	1.02*	3.74**	0.01	0.87	0.98**
2	Treatments	35	673.17**	16.89**	9.04**	23.00**	11.44**	51.30**
3	Parents	7	1545.23**	11.10**	4.35**	29.96**	12.67**	31.55**
4	Hybrids	27	430.99**	18.99**	10.14**	18.13**	7.95**	38.42**
5	Parent vs hybrid	1	1107.43**	0.52	11.94**	105.51**	97.33**	537.33**
6	Errors	70	4.98	0.29	0.19	0.05	0.39	0.14

* Significant at 5% level ** significant at 1% level

Table 3: Analysis of variance for combining ability in cowpea

Sr. No.	Sources	D.F.	Mean sum of squares					
			Days to 50% flowering	Pod length (cm)	No. of seeds/ pod	100-seed weight (g)	No. of pods/ plant	Seed yield/ plant (g)
1	GCA	7	943.39**	16.54**	7.42**	22.49**	8.64**	25.20**
2	SCA	28	44.63**	2.90**	1.90**	3.95**	2.60**	15.07**
3	Error	70	1.66	0.09	0.06	0.01	0.13	0.04

* Significant at 5% level ** significant at 1% level

Table 4: GCA effects for yield contributing characters in cowpea

Sr. No.	Parents/ hybrids	Days to 50% flowering	Pod length (cm)	No. of seed/ pod	100-seed weight (g)	No. of pods/ plant	Seed yield/ plant (g)
1	Wali 4	21.79**	2.76**	1.58**	2.76**	-1.34**	1.77**
2	Pusa- Do-phasali	-6.60**	-0.13	0.25**	-0.33**	1.17**	0.24**
3	Pusa Phalguni	-6.07**	-0.95**	-0.88**	-2.47**	0.30**	-2.62**
4	GC-3	-1.60**	0.001	-0.27	0.10**	0.33**	0.30*
5	DFC-1	1.12**	-0.09	0.79**	0.67**	-1.47**	-1.51**
6	VCM-8	-8.27**	-1.67**	-0.91**	-1.15**	0.01	-0.80**
7	C-152	3.85**	-0.27**	-0.005	0.30**	0.52**	0.59**
8	Konkan Safed	-4.20**	0.37**	-0.54**	0.12**	0.47**	2.04**
	SE±	0.38	0.09	0.07	0.04	0.10	0.06
	CD at 5%	0.76	0.18	0.14	0.08	0.21	0.13
	CD at 1%	1.00	0.24	0.19	0.10	0.28	0.17

* Significant at 5% level ** significant at 1% level

Table 5: SCA effects of different yield contributing characters in cowpea

Sr. No.	Hybrids	Days to 50% flowering	Pod length (cm)	No. of seed/ pod	100-seed weight (g)	No. of pods/ plant	Seed yield/ plant
1	Wali 4 x Pusa-Do-phasali	-0.85	3.88**	1.13**	1.21**	-1.11**	-0.53**
2	Wali 4 x Pusa falguni	-0.39	0.54	0.07	2.98**	0.24	6.26**
3	Wali 4 x GC-3	-4.19**	2.65**	1.60**	0.70**	-0.77*	2.95**
4	Wali 4 x DFC-1	-2.59*	2.32**	0.86**	-0.76**	1.04**	6.44**
5	Wali 4 x VCM-8	-1.85	-2.13**	-1.55**	2.10**	-0.72*	-1.85**
6	Wali 4 x C-152	-8.32**	-4.22**	-2.80**	-2.54**	3.53**	0.86**
7	Wali 4 x Konkan safed	4.74**	1.32	2.26**	-0.06	1.63**	4.08**
8	Pusa-Do-phasalixPusa Phalguni	0.34	-0.43	0.80**	0.10	1.90**	6.09**
9	Pusa-Do-phasali x GC-3	-1.79	-0.99**	-0.60**	0.55**	1.21**	1.54**
10	Pusa-Do-phasali x DFC-1	-0.52	0.09	-0.47*	2.58**	-0.21	0.53*
11	Pusa-Do-phasali xVCM-8	-2.45*	-1.00**	-0.69**	1.07**	0.63	0.48*
12	Pusa-Do-phasali x C-152	-3.25**	-0.58	-0.14	-1.12**	0.58	-1.94**
13	Pusa-Do-phasali x Konkan Safed	-2.52*	-0.17	-1.87**	0.21	-0.17	-1.74**
14	Pusa falguni x GC-3	-0.99	-2.14**	-2.39**	-0.12	-0.72*	-3.31**
15	Pusa falguni x DFC-1	-0.72	-1.64**	-2.07**	-1.48**	1.84**	-3.60**
16	Pusa falguni x VCM-8	3.34**	0.35	1.10	-1.23**	1.36**	3.05**
17	Pusa falguni x C-152	-3.45**	1.56**	-1.67	3.06**	-1.21**	-2.35**
18	Pusa falguni xKonkan Safed	-0.39	-0.18	-0.13	-0.78**	0.15	1.34**
19	GC -3 X DFC-1	-7.52**	0.13	0.85**	0.67**	2.41**	2.52**
20	GC -3 X VCM-8	1.20	0.85	0.03	3.77**	-0.61	0.64**
21	GC 3 X C-152	-2.59*	0.62	-0.07	0.59**	0.99**	0.67**
22	GC -3 X Konkan Safed	-3.85**	-1.66**	-0.33	-0.79**	1.56**	0.92**
23	DFC-1 X VCM-8	-1.19	0.26	0.16	-0.86**	-0.08	2.12**
24	DFC-1 X C-152	-12.99**	0.72*	1.38**	1.50**	0.24**	3.28**
25	DFC-1 X Konkan safed	-7.92**	-0.92**	-0.94**	-0.21	-0.80*	-2.48**
26	VCM-8 X C-152	-3.59**	1.01**	0.96**	1.08**	-0.58	2.75**
27	VCM-8 X Konkan Safed	4.80**	-0.34	-1.09**	-0.77	2.03**	0.59**
28	C-152 x Konkan Safed	11.67**	-0.94**	0.65**	3.34**	-0.16	4.01**
	SE±	1.16	0.28	0.22	0.12	0.32	0.20
	CD at 5%	2.33	0.56	0.45	0.24	0.65	0.40
	CD at 1%	3.09	0.74	0.60	0.32	0.87	0.53

* Significant at 5% level ** significant at 1% level

Table 6: Genetic components of variation and related statistics for yield and yield contributing characters

Genetic parameters	Days to 50% flowering		Pod length (cm)		No. of seeds/ pod		100-seed weight (g)		No. of pods/ plant		Seed yield/ plant (g)	
	Effects	**S.E.±**	**Effects**	**S.E.±**	**Effects**	**S.E.±**	**Effects**	**S.E.±**	**Effects**	**S.E.±**	**Effects**	**S.E.±**
E	1.65	7.32	0.10	0.60	0.09	0.19	0.01	0.28	0.13	0.17	0.05	1.63
D	513.42*	21.96	3.59*	1.81	1.35*	0.27	9.96*	0.84	4.08*	0.52	10.45*	4.89
F	224.28*	51.90	-2.14	4.28	-1.19	1.35	2.32	1.99	0.95	1.23	5.97	11.55
H_1	191.90*	50.49	12.55*	4.16	7.76*	1.32	14.42*	1.94	8.18*	1.20	53.08	11.24
H_2	124.87*	43.93	10.56*	3.62	6.77*	1.14	13.04*	1.68	8.03*	1.04	46.23*	9.78
h^2	180.96*	29.46	0.04	2.43	1.91*	0.77	17.30*	1.13	15.90*	0.70	88.13*	6.55
$(H_1/D)^{1/2}$	0.61		1.86		2.39		1.20		1.41		2.25	
$(H_2/4H_1)$	0.16		0.21		0.21		0.22		0.24		0.21	
K_D/K_r	2.11		0.72		0.68		1.21		1.18		1.29	
h^2/H_2	1.44		0.004		0.28		1.32		1.97		1.90	
Heritability (ns) %	84		58		49		57		43		32	

* Significant at 5% level ** significant at 1% level