Genetic analysis of pod yield and its attributes in vegetable cowpea

SNEHAL P. PATEL, K.K. DHEDHI, P.S. BHARODIA AND A.K. JOSHI

SUMMARY

The nature of gene action was studied for pod yield and eight other component traits in vegetable cowpea using 7 x 7 diallel fashion, excluding reciprocals. The preponderance of non-additive gene action was observed in the inheritance of days to 50 per cent flowering, days to first picking and seeds per pod. Whereas, the importance of both additive and non-additive gene action were noticed for pod yield per plant, leaf area, branches per plant, plant height, pods per plant and protein content. However, the magnitude of dominant gene action (H_1) was greater than their corresponding additive gene effects (D) for all the traits. This suggested that the dominant genes played a significant role in the control of all the characters. The average degree of dominance $(H_1/D)^{0.5}$ was found to be in the range of over dominance for all the characters. The distribution of genes with positive and negative effects was either close to symmetrical or not too distant. Excess of dominant genes against one recessive gene was not very high as their ratio ranged between one or two only. One or two gene groups governed characters. Narrow sense heritability estimates were moderate for branches per plant and plant height, whereas they were low for rest of characters. JCPL 2000-10 x GC 4, JCPL 2000-10 x JCPL 2000-2 and GC 3 x GC 4 were the most promising on the basis of *per se* performance, SCA effects and heterosis, which are expected to throw transgressive segregates.

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important quick growing legume crop capable of withstanding moderate drought conditions. Being a multipurpose crop, it is grown during rainy and summer seasons as a vegetable crop in most part of India and also for grain and fodder purposes. Green tender marketable pods of cowpea have excellent nutritive values for human diet. The success of any breeding programme depends upon the selection of parents together with the information of nature and magnitude of gene actions controlling various traits of importance. Diallel mating system extensively used for the estimation of gene action and combining ability is of immense value in identifying parents and crosses which are likely to yield maximum improvement for the characters under consideration. Besides high yield, correlated morphological traits are also important for harnessing the yield potential fully. In the past, improvement in autogamus crops in general and cowpea is particular, was achieved through conventional breeding procedures like selection from the naturally occurring variability or induced variability through hybridization following the traditional pedigree method of breeding. Therefore, the present study was undertaken to elucidate the nature and magnitude of gene action involved in inheritance of pod yield and its components through diallel analysis in vegetable cowpea.

MATERIALS AND METHODS

The experimental material comprised of genetically diverse seven genotypes of cowpea, namely, JCPL 2000-7, JCPL 2000-10, GC-2, JCPL 2000-2, GC-3, GC-4 and Pusakomal and their 21 F_1 hybrids obtained through mating in a diallel fashion, excluding reciprocals. Both parents and hybrids were grown during *Kharif* 2001 in a Randomized Block Design with three replications. The parents and hybrids were planted in single row of 3.0 m length spaced at 60 x 30 cm. All the recommended agronomic practices were followed to raise good crop. Data were recorded on five random, competitive plants for each genotype, in each replication for various characters (Table 1). Observations on days to 50 per cent flowering and days to first picking were noted on plot basis. Observations for number of seeds per pod, number of primary branches per plant, plant height (cm) and leaf area (cm^2) were recorded at last picking. Data on number of pods per plant and green tender pod yield per plant (g) was obtained for each picking and was summed over picking. The average values were computed. For protein content (%), the nitrogen was estimated in per cent on oven dry basis by using modified '*Kjeldhal* method' (Jackson,1973). The mean values were used for the analysis to determine genetic components of variation following Hayman (1954).

Correspondence to:
K.K. DHEDHI, Pearl Millet Research Station, Junagadh Agricultural University, JAMNAGAR (GUJATA) INDIA
Authors' affiliations:
SNEHAL P. PATEL AND P.S. BHARODIA, College of Agriculture, Junagadh Agricultural University, JUNAGADH (GUJARAT) INDIA
A.K. JOSHI, Pearl Millet Research Station, Junagadh Agricultural University, JAMNAGAR (GUJATA) INDIA

RESULTS AND DISCUSSION

The estimates of genetic parameters, their ratio and narrow sense heritability for pod yield and its components are presented in Table 1. The results revealed that the non- significant values of 't^2' for all the characters assured the fulfillment of assumptions underlying diallel analysis. The estimates of additive genetic component (D) and non-additive genetic component (H_1) were significant for pod yield per plant, leaf area, number of branches per plant, plant height, number of pods per plant and protein content, indicating the importance of both additive and dominance components in the inheritance of these traits. However, the magnitude of dominance gene effect (H_1) was higher than their respective additive gene effect (D) for all the characters, which revealed preponderance of non-additive gene effect in their expression. Similar results have also been reported by Singh and Dabas (1992) and Sawant (1994). In the present study, only dominance components (H_1 and H_2) of genetic variance were significant for days to 50 per cent flowering, days to first picking and number of seeds per pod. This advocated that these traits were primarily under control of non-additive gene action. The present findings are in agreement with the findings of Savithramma and Nagaraja (1995) for all the traits except number of branches per plant.

The estimates of average degree of dominance [H_1/D]$^{0.5}$ were found more than unity for all the characters, indicating presence of over dominance. Similar findings were reported for days to 50 per cent flowering (Zaveri et al., 1980); pods per plant (Singh and Dabas, 1992) and for branches per plant, plant height, pods per plant, seeds per pod and yield per plant (Sawant, 1994 and Savithramma and Nagaraja, 1995). The estimates of F were positive for all the traits except protein content implying that dominant genes played a significant role in the control of these traits. The equal distribution of positive and negative alleles in the parents helps the breeder in selecting a particular desirable trait without losing any other desirable trait. In the present study, asymmetrical distribution of positive and negative alleles among the parents was observed for all the traits, as estimated values of $H_2/4H_1$ were less than 0.25. Sawant (1994) and Savithramma and Nagaraja (1995) have also reported the similar results.

The proportion of $(4DH_1)^{0.5} + F / (4DH_1)^{0.5} - F$ revealed the relative value of dominant and recessive alleles among the parents, determining the extent of genetic gain that can be made in a particular direction. If the alleles present in the population are predominantly of recessive nature, the extent of genetic gain/ advance will

Table 1 : Estimates of genetic components of variation and heritability for pod yield and its component traits in vegetable cowpea

Sources	Pod yield per plant (g)	Days to 50 % flowering	Days to first Picking	Number of seeds per pod	Leaf area (cm^2)	Number of branches per plant	Plant height (cm)	Number of pods per plant	Protein content (%)
D	1366.63*	59.68	39.12	1.17	1859.66*	3.29*	2886.42**	121.15*	0.31**
	±514.14	± 28.93	±24.33	±1.11	±695.06	±0.94	±559.85	±42.41	±0.06
H_1	6252.16**	186.98*	156.59*	7.34*	6398.09*	9.04*	5833.90**	552.56**	0.73**
	±1237.77	±69.64	±58.58	±2.67	±1673.34	±2.27	±1347.83	±102.11	±0.15
H_2	4720.57**	152.13*	128.34	5.90	5710.35*	5.18*	4495.14*	413.39**	0.66**
	±1090.65	±61.36	±51.61	±2.35	±1474.45	±2.00	±1187.63	±89.97	±0.13
h^2	1218.29	3.02	13.36	-0.10	622.74	1.61	273.65	10.06	0.86**
	±732.53	±41.21	±34.67	±1.58	±990.31	±1.34	±797.66	±60.43	±0.09
F	1551.19	23.20	15.73	0.43	773.24	4.89	2627.57	69.58	-0.17
	±1233.40	±69.39	±58.37	±2.66	±1667.44	±2.26	±1343.07	±101.75	±0.15
E	71.39	2.57	3.21	0.23	37.04	0.16	62.44	4.81	0.03
	±181.77	±10.23	±8.60	±0.39	±245.74	±0.33	±197.94	±15.00	±0.02
$[H_1/D]^{0.5}$	2.14	1.77	2.00	2.50	1.85	1.66	1.42	2.14	1.53
$H_2 / 4H_1$	0.19	0.21	0.20	0.20	0.22	0.14	0.19	0.19	0.23
$\dfrac{[4DH_1]^{0.5} + F}{[4DH_1]^{0.5} - F}$	1.72	1.25	1.22	1.16	1.25	2.63	1.94	1.31	0.70
h^2 / H_2	0.26	0.02	0.10	-0.02	0.11	0.31	0.06	0.02	1.29
Heritability (ns) %	21.51	25.53	20.29	12.99	24.36	40.68	45.51	19.43	23.66
t^2	0.10	0.22	0.17	4.30	0.2	1.27	0.59	0.10	3.84

* and ** indicate significant of values at P=0.05 and 0.01, respectively

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be limited. On the other hand, it is desirable that there should be dominant genes, if any, worthwhile selection gain can be had. This ratio of dominance and recessive genes was more than unity for all the traits except for protein content, showing that the dominance genes were more frequent than recessive ones. Protein content was controlled by excess of recessive genes as the said ratio was less than unity. The estimates of two proportions of genetic components, namely, $H_2/4H_1$ and $(4DH_1)^{0.5} + F / (4DH_1)^{0.5} - F$ thus gave contradictory results regarding symmetrical distribution of alleles with positive and negative effects and were not always followed by the equal distribution of dominant and recessive alleles, respectively. In other words, dominant alleles may or may not be associated with positive effect. Likewise, a recessive allele may or may not be correlated with a negative effect. More the dominant genes more is the gain expected. The results showed that the numerical values ranged between 0.70 for protein content to 2.63 for number of branches per plant which indicated that the recessive and dominant genes were not in high disproportion and most of allelic pairs would be exist in heterozygous forms. Similar results were earlier reported by Zaveri *et al*. (1980), Singh and Dabas (1992), Sawant (1994) and Savithramma and Nagaraja (1995). Knowledge of number of genes responsible for a particular trait is important for the genetic progress through selection. The ratio of h^2/H_2 of gene groups was found less than unity for all the traits except protein content. It indicated one major group governing the inheritance of these traits, whereas protein content suggested the presence of two major gene groups. Zaveri *et al.* (1980),

Singh and Dabas (1992) and Sawant (1994) reported similar results.

Estimated narrow sense heritability ranged between 12.99 per cent (seeds per pod) to 45.51 per cent (plant height). Narrow sense heritability was found to be moderate for number of branches per plant and plant height, whereas, it was low for remaining characters. This suggested the preponderance of non-additive gene action for these traits. Bhaskaraiah (1978) reported very low heritability for days to 50 per cent flowering and number of pods per plant. Thiyagarajan (1989) observed low heritability for number of branches per plant and pods per plant; while it was high for plant height and number of seeds per pod. Narrow sense heritability was low for branches per plant and pods per plant as recorded by Savithramma and Nagaraja (1995).

Yield is a character of economic importance for which considerable magnitude of heterosis was registered in number of crosses. In all, 14 and 10 hybrids manifested significant positive relative heterosis and heterobeltiosis, respectively. The magnitude of heterosis was ranged from -43.33 (GC-2 x JCPL 2000-2) to 67.12 % (JCPL 2000-10 x GC-3) over mid parent, while, it was varied between -45.45 (GC-2 x JCPL 2000-2) to 30.84 % (JCPL 2000-10 x JCPL 2000-2) over better parent. Ten top high yielding hybrids for pod yield per plant are listed in Table 2. The cross JCPL 2000-10 x GC-4 having highest *per se* performance, high heterosis and good SCA effect for pod yield per plant. This cross also registered significant and useful heterobeltiosis for seeds per pod, pod length and branches per plant. JCPL 2000-10 x JCPL 2000-2 had highest heterobeltiosis, ranked second in *per se*

Table 2 : Ten top high pod yielding hybrids with heterosis over mid (MP) and better parents (BP), alongwith their SCA effects and component traits showing significant desirable heterobeltiosis in vegetable cowpea

Sr. No.	Promising hybrids	Pod yield per plant (g)			Heterosis (%) over		SCA effects	Significant desirable heterobeltiosis for component traits
		Hybrids	P_1	P_2	MP	BP		
1.	JCPL 2000-10 x GC-4	246.00	169.67	196.33	34.43**	25.30**	42.27**	SP, PL, BP
2.	JCPL 2000-10 x JCPL 2000-2	222.00	169.67	135.67	45.41**	30.84**	43.45**	SP, LA, PH, PP
3.	GC-3 x GC-4	211.67	77.67	196.33	54.90**	7.81**	53.79**	SP
4.	JCPL 2000-10 x Pusakomal	210.67	169.67	126.33	42.34**	24.17**	22.49**	SP, LA, PP
5.	JCPL 2000-10 x GC-2	207.00	169.67	146.67	30.87**	22.00**	20.12**	PP
6.	JCPL 2000-10 x GC-3	206.67	169.67	77.67	67.12**	21.81**	25.86**	LA, BP, PP
7.	GC-2 x GC-3	185.67	146.67	77.67	65.53**	26.59**	44.64**	BP, PP
8.	JCPL 2000-7 x Pusakomal	176.67	165.33	126.33	21.14**	6.85**	23.60**	SP, PL, PH, PP
9.	JCPL 2000-2 x Pusakomal	167.33	135.67	126.33	27.74**	23.24**	27.27**	SP, PH
10.	GC-2 x Pusakomal	163.33	146.67	126.33	19.66**	11.36**	14.94	PH
	S.E. $\pm$	11.95			10.38	12.07	7.58	

Where, SP = Seeds per pod, PL = Pod length, LA = Leaf area, BP = Branches per plant,
 PH = Plant height, PP = Pods per plant
 * and ** indicate significant of values at P=0.05 and 0.01, respectively

performance and high SCA effects. This hybrid also showed significant and desirable heterotic effects for seeds per pod, leaf area, plant height and pods per plant. Similarly, the cross combination GC 3 x GC 4 ranked third in *per se* performance, high heterosis and first ranked in SCA effect for pod yield per plant. Thus, these all three hybrids were most outstanding promising for pod yield on the basis of *per se* performance, SCA effects and high heterosis. These crosses are likely to produce superior segregants in subsequent generations.

An overall examination of results revealed that both types of gene actions were noticed in most of the characters. However, pod yield and its components had preponderance of non-additive gene effects besides additive effects. Thus, improvement in cowpea for the characters under study may be expected through standard selection procedures, which may first, exploit the additive gene effect. Simultaneously, care should be taken that non-additive effects were concentrated rather than dissipated. It is therefore, suggested that reciprocal recurrent selection breeding procedure should be followed which meets the requirement of utilizing both the gene actions.

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