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Research Note

Inheritance study of qualitative and quantitative characters in cowpea varieties (*Vigna unguiculata* (L.) Walp)

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Abstract

Two parents namely Konkan Safed and Konkan Sadabahar were used to study inheritance of four qualitative characters (i.e., growth habit, flower colour, seed coat colour and seed coat colour pattern) and four quantitative characters i.e. pod length (centimeters), number of pods/plant, number of seeds/pod and 100 seed weight (gm). The qualitative characters were studied using chi-square test. The results showed monogenic inheritance for all four qualitative traits. Joint segregation was studied and linkage was revealed. The quantitative characters were studied by comparison of range, mean, standard deviation and coefficient of variation in parents, F_1 and F_2 generation. The amount of variability generated in F_2 for pod length was more than both the parents and F_1. This result can be used for further selection of plant progenies for crop improvement programme.

Keywords

Cowpea, quantitative traits, joint segregation, χ^2 test, qualitative traits

Pulses occupy a unique position in the world agriculture by virtue of their high protein content. Pulses are the backbone of Indian agriculture. In many of the developing countries, pulses are the major source of dietary protein. Pulses occupy 68.32 million hectare area and contribute 57.51 million tones to the world food basket. India is a major pulse growing country in the world with an area of 23.47 million ha producing 18.34 million tonnes annually with an average productivity of 781 kg/ha. It grows well in poor soils with more than 85% sand and with less than 0.2% organic matter and low levels of Phosphorus (Singh *et al*., 2003) and covers the ground so well that it checks the soil erosion. Cowpea is a short season crop with relatively high drought tolerant ability (Muchero *et al*., 2009). As a leguminous crop, it fixes about 70 – 240 kg nitrogen per ha per year. Cowpea seed is reported to contain 24% crude protein, 53% carbohydrates and 2% fat.

Great research work on inheritance of various qualitative and quantitative characters is being done since long time as India is the largest producer and consumer of pulses in the world. India produces a quarter of the world’s pulses. The genetics of these characters is not well understood and there is controversy with regard to the nature of inheritance i.e. number of genes controlling the same character, type of gene action and segregation pattern (whether independent assortment, interactions or linkages). For example a single character “growth habit” has been reported to be controlled by single, double and triple genes. Brittingham (1950) stated its inheritance as simple Mendelian monogenic segregation and trailing being dominant. Kolhe (1970) stated that growth habit is digenically controlled and having the duplicate gene action.

Yields can be improved by eliminating undesirable genes/ traits linked with desirable genes / traits by breaking the linkages. There is lot of scope for improvement in yield by gene manipulation. This is possible only when the genetic construction of plant is known. As such it is emphasized that the knowledge of inheritance of various characters in cowpea is a prerequisite as it is in other crop plants.

The present investigation was carried out with following objectives such as to study the inheritance of qualitative characters *viz.,* growth habit, Flower colour, seed coat colour and seed coat colour pattern and quantitative characters *viz.,* Pod length (cm), Number of pods per plant, Number of seeds per pod and 100 seed weight (g) and to identify the promising segregants for further use in future breeding programmes and combining the desirable characters present in both the parents.

A field experiment was conducted at Research Farm, Department of Agricultural Botany, College of Agriculture, Dr. B. S. K. K. V., Dapoli to study the inheritance of qualitative and quantitative characters in cowpea (*Vigna unguiculata* (L.) Walp) from October 2012 - March 2014.Two parents *viz.,* Konkan Safed and Konkan Sadabahar were obtained from germplasm maintained by Department of Agricultural Botany, College of Agriculture, Dapoli. The characters of the two parents used in breeding programme are given in Table 1. Crossing was carried out during *rabi* 2012. Emasculation was done from 4 p.m. to 6 p.m. at the time when there was no dehiscence. The emasculated flowers were pollinated during 8 a.m. to 9 a.m. on next day morning. In the month of November 2013 the F_2 seeds were obtained. The F_1 and F_2 seeds along with parents were grown simultaneously in January 2014 to observe the inheritance of characters under study. All recommended package of practices were followed during growth period of the crop. The spacing between and within rows was maintained at 30 × 30 cm. Seed coat colour observations was recorded at 12 % grain moisture percentage and not at the time of harvesting. All the qualitative characters were visually recorded on parents, F_1 and F_2 from each plant. The data obtained for the various generations were tested for their goodness to the proposed genetic ratios using the chi-square test (Pearson, 1900). The measurement of quantitative characters for parents, F_1 and F_2 were recorded in each individual plant. Collected data for quantitative characters was analyzed for calculating mean, range, Standard deviation and coefficient of variation.

Behavior of Parents, F_1 and segregating generation F_2 are presented in Table 1. In cross Konkan Safed × Konkan Sadabahar, erect growth habit was dominant over semi erect type. Light violet standard colour was dominant over white standard colour and violet wing colour was dominant over white wing colour. Brown seed coat colour was dominant over White. Watson seed coat colour pattern was dominant over small eye type. Segregation pattern of the progeny of a cross Konkan Safed × Konkan Sadabahar in F_2 generation is presented in Table-2. Growth habit was controlled by single gene (3:1) .This result is in accordance with the result of Premsekar and Raman (1972) that the character is controlled by single gene having ratio 3:1 in F_2 generation. Flower colour in cowpea is controlled monogenically. Capinpin (1935), Kolhe (1970) and Premsekar and Raman (1972) effected crosses between coloured × white flower and reported a monogenic segregation in 3:1 ratio. Ukarande (1985) crossed V-50× CM-11 and C0-1 × V-50 reported monogenic segregation in 3:1 ratio. Pethe (1990) crossed wali-1 × VCM-8 reported monogenic ratio for flower colour. Seed coat colour was also controlled by a single gene. Saunders (1959) and Kolhe (1970) effected crosses between coloured × coloured and coloured × white seed coat and reported a simple monogenic ratio of 3:1,Ukarande (1985) crossed C0-1 × V-50 reported monogenic ratio and Pethe (1990) crossed Wali-1× VCM-8 obtained 3:1 ratio, Sangwam and Lodhi (1998) showed that the seed coat colour follow a monogenic Mendelian inheritance. This result are in agreement with Mustapha (2009) and Egbadzor *et al.*, (2014) for coat colour in cowpea. Monogenic ratio was obtained for seed coat colour pattern with Watson seed coat colour pattern being dominant as reported by Saunders (1960) and Pethe (1990). When joint segregation of growth habit was considered with other characters like standard colour, wing colour, seed coat colour and seed coat colour pattern it indicated that single gene governing the growth habit was independent to the single gene controlling the other characters. It was revealed that all the genes involved assort independently.

The genetic constitution of parents and their F_1 is presented in Table 3. Linkage was observed when joint segregation of standard colour (ll) was considered with wing colour which (VV) was governed by single gene. The total χ^2value on the basis of ratio 9:3:3:1 was higher than table value (177.08> 7.82). Since P value was below 0.001 and the expected and observed ratio are not comparable. There was possibility of linkage, hence linkage value was worked out. The cross over value obtained was 3%, which was not different from the earlier results reported by Pethe (1990) except the difference in cross over value (17.66%). Also linkage was observed when standard colour (ll) was considered with seed coat colour (BB) and its pattern (WW) which was governed by single gene. The total χ^2 value on the basis of ratio 9:3:3:1 was higher than table value (22.13> 7.82 and 37.17 > 7.82 respectively). Since P value was below 0.001. The cross over value obtained was 36% and 45.85% respectively. This indicated that there was linkage between gene controlling standard colour and genes controlling seed coat colour and its pattern. In regards to this Capinpin (1935) observed association between flower colour and seed coat colour and assumed close linkage. On this assumption of linkage Kolhe (1970) worked out interrelationship of gene and he found that there was linkage between these two characters with cross over value 20.28%. Also the results are in agreement with Ukarande (1985) who reported 24.87% cross over value. This has been further confirmed by Pethe (1990) who reported that there was linkage between standard colour with seed coat colour in cross Gujrat-1 × VCM-8 and Wali-1 × VCN-8 with cross over value of 21.71% and 39.31 % respectively. Standard colour (ll)was linked with seed coat colour pattern (WW) with cross over value 45.85% which was not different from the earlier results reported by Pethe (1990) except the difference in cross over value (26.71%). Linkage was observed when joint segregation of wing colour (VV) was considered with seed coat colour (BB) which was governed by single gene. The total χ^2 value on the basis of ratio 9:3:3:1 was higher than table value (22.13 > 7.82). Since P value was below 0.001 and there was possibility of linkage, hence linkage value was worked out. The cross over value 36% was obtained. This indicated that genes governing wing colour and genes governing seed coat colour were linked. When joint segregation of wing colour (VV) was considered with seed coat colour pattern (WW) linkage was observed. The total χ^2 value on the basis of ratio 9:3:3:1 was higher than table value (37.17 > 7.82). Since P value was below 0.001 and there was possibility of linkage, hence linkage value was worked out. The cross over value 45.85% was obtained. This indicates linkage between two characters.Results of present study are similar to results of Pethe (1990). When joint segregation of seed coat colour (BB) was considered with seed coat colour pattern (WW)(which was governed by a single gene) linkage was obtained. The total χ^2 value on the basis of ratio 9:3:3:1 was higher than table value (25.80 > 7.82). Since P value was below 0.001 and there was possibility of linkage, hence linkage value was worked out. The cross over value 95.6% was obtained. This indicated that the gene governing seed coat colour was linked with single gene controlling character seed coat colour pattern. Results of present study are similar to results of Pethe (1990).

Segregation of quantitative characters in cross Konkan Safed × Konkan Sadabahar is presented in Table-4.Mean pod length of F_1 (11.82cm) was intermediate and F_2 (17.47cm) was found to be superior over both the parents and F_1. This indicated presence of over dominance and these transgressive segregants could be used for plant improvement programme. Mean number of pods/plant of F_1 was 19.45 which was superior over Konkan Safed and Konkan Sadabahar and mean number of pods/plant in F_2 (14.91) was found to be lower than both the parents. Mean number of grains/pod of F_1 and F_2 (10.18 and 10.37 respectively) was intermediate between both the parents. 100 seed weight of F_1 was 12.54 grams which was superior to Konkan Sadabahar. While F_2 (11.72g) was lower than Konkan Safed (P_1) and Konkan Sadabahar (P_2) (Table 4). These results were recorded first time in cowpea.

There was evidence of the linkage between seed coat colour and seed coat colour pattern in the cowpea used in the experiment. Knowledge on seed coat genetics can be very useful in cowpea breeding as it is important in farmer and customer preference. Furthermore, linkage between the traits studied can be expanded to other important ones such as maturity period, post-harvest storability and palatability. The finding could be very useful to gene banks in their conservation activities to prevent genetic loss in cowpea germplasm. The knowledge should be used to identify within accession variability in cowpea germplasm to protect each type from being loss. Seed size is reduced and biomass is increased so these progenies can be used for further selection of plants in crop improvement programme for fodder purpose.

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Table 1. The details of morphological characters of the parents and their hybrid in cross Konkan Safed × Konkan Sadabahar

Sr. No.	Characters	Parents		Hybrid
		Konkan Safed	Konkan Sadabahar	
1.	Growth habit	Semi erect (ee)	Erect (EE)	Erect (Ee)
2.	Flower colour:			
	i) Standard colour	White (ll)	Light violet (LL)	Light violet (Ll)
	ii) Wing colour	White (vv)	Violet (VV)	Violet (Vv)
3.	Seed coat colour	White (bb)	Brown (BB)	Brown (Bb)
4.	Seed coat colour pattern	Small eye (ww)	Watson (WW)	Watson (Ww)

Table 2. Segregation pattern of the progeny of a cross Konkan Safed × Konkan Sadabahar in F_2 generation

Sr. No.	Characters	Ratio tested	Number of plants in F_2 generation			χ^2	P
1.	Growth habit	3:1	O	113	36	0.056	0.70-0.50
			E	111.75	37.25		
2.	Flower colour:						
	i) Standard colour	3:1	O	107	42	0.807	0.50-0.30
			E	111.75	37.25		
	ii) Wing colour	3:1	O	107	42	0.807	0.50-0.30
			E	111.75	37.25		
3.	Seed coat colour	3:1	O	105	44	1.63	0.30-020
			E	111.75	37.25		
4.	Seed coat colour pattern	3:1	O	103	46	2.75	0.10-0.05
			E	111.77	37.25		

*** O – Observed value, E – Expected value**

Table 3. The genetic constitution of parents and their F_1

Konkan Safed	Konkan Sadabahar	F_1	F_2 (Ratio)
ee	EE	Ee	3:1
ll	LL	Ll	3:1
vv	VV	Vv	3:1
bb	BB	Bb	3:1
ww	WW	Ww	3:1

Table 4. Segregation of quantitative characters in cross of Konkan Safed × Konkan Sadabahar

Character	Generation	Range	Mean	S.D.	C.V.
Pod length (cm)	Konkan Safed (P_1)	13-14.5	13.47	0.61	4.56
	Konkan Sadabahar (P_2)	9-11.8	10.23	0.83	8.20
	F_1	10.7-12.9	11.82	0.63	5.38
	F_2	9-14	17.47	73.78	422.19
No. of pods/plant	Konkan Safed (P_1)	14-21	18.15	2.29	12.62
	Konkan Sadabahar (P_2)	10-21	16.41	3.13	19.11
	F_1	14-29	19.45	4.78	24.58
	F_2	8-22	14.91	2.85	19.12
No. of grains/pod	Konkan Safed (P_1)	10-13	12.10	0.99	8.21
	Konkan Sadabahar (P_2)	7-11	8.90	1.01	11.36
	F_1	8-11	10.18	0.87	8.58
	F_2	9-13	10.37	0.99	9.62
100 seed weight (g)	Konkan Safed (P_1)	12-19	15.47	1.71	11.06
	Konkan Sadabahar (P_2)	9-16	12.03	1.90	15.83
	F_1	9-15	12.54	2.06	16.47
	F_2	8-22	11.72	2.46	20.99