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INHERITANCE AND LINKAGE STUDIES IN COWPEA (*VIGNA UNGUICULATA* (L.) WALP.)

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ABSTRACT

Inheritance and linkage relationships of growth habit, seed size, stipule colour, and stem pigmentation were studied in a cross involving cv. Selection-2 and K. 11 of cowpea. A trigenic ratio of 39:25 was observed for growth habit of which one is the basic gene, and the other two are inhibitory and antiinhibitory genes. Large seed size and red stipule colour were monogenically dominant over small seed and green stipule, respectively, with a good fit of 3:1 ratio in F_2. A complementary digenic ratio of 9:7 was observed for stem pigmentation. The following gene symbols are proposed: growth habit (V_i-1, V_i-2, V_i-3), big seed (Bg), stipule colour (Sti), and stem pigmentation (P_{p-1}, P_{p-2}). Joint phenotypic segregation studies revealed that the basic gene for growth habit is linked with the dominant gene for seed size with a crossover value of 46%, whereas 17.4% crossing over was observed between one of the complementary genes for stem pigmentation and the gene for stipule colour.

Key words: Inheritance, linkage, digenic and trigenic inheritance, cowpea.

Cowpea (*Vigna unguiculata* (L.) Walp.) is among the important pulse crops of India and is one of the major grain legumes in Tropical Africa, and provides a significant portion of dietary protein for the people. Knowledge on inheritance and relationships among various qualitative and quantitative characters is essential in any plant breeding programme. Such studies are very few in cowpea. The present paper communicates the findings of genetic analysis of four morphological characters in cowpea.

MATERIALS AND METHODS

Genetic studies on growth habit, seed size, stipule colour, and stem pigmentation was undertaken in a cross involving true breeding varieties, viz., Selection-2 and K. 11. The parents and F_1 were grown during kharif 1982 and the segregating generation (F_2 and F_3) were grown during 1983 summer and kharif seasons, respectively, at the College of

Agriculture, Dharwad. Observations were recorded on all the characters at appropriate time of their expression. The χ^2 test was used to test the F_2 ratios and confirm the breeding behaviour of F_2 segregates in F_3 generation. Joint phenotypic segregation was worked out to determine the gene relationships. After getting the clue for the probable existence of linkage, recombination values were estimated by the product ratio method of Fisher and Balmukund [1]. The formulae for quadratic expression of P^2 were obtained by the direct method suggested by Kolhe [2]. The gene nomenclature followed in Cucurbitaceae was adopted in *Vigna* [3].

RESULTS AND DISCUSSION

The details of qualitative morphological characters of parents and their F_1 and F_2 are presented in Table 1. It is clear from the data that cross between parent genotypes having tendrillar x nontendrillar growth habit, big x small seed size, red x green stipule colour, and absent x present stem pigmentation resulted in tendrillar growth, large seed, red stipule, and stem pigmentation in F_1 generation, followed by F_2 dominant : recessive segregation ratios of 39:25 (tendrillar : nontendrillar), 3:1 (big : small seed), 3:1 (red : green stipule), and 9:7 (presence : absence of stem pigmentation), respectively, indicating dominant nature of the former characters. The F_2 analysis confirmed that all the four characters had good fit to the expected ratios with high probability. These ratios were further confirmed by the analysis of F_3 breeding behaviour (Table 3).

Table 1. Inheritance of four quantitative morphological characters in the cowpea cross Selection-2 x K. 11

Character	Selection-2	K. 11	F_1	F_2 segregation		F_2 ratio	χ^2	P
				dominant	recessive			
Growth habit	Tendrillar	Non-tendrillar	Tendrillar	354	226	39:25	0.0017	0.95–0.98
Seed size	Big	Small	Big	439	141	3:1	0.417	0.70–0.80
Stipule colour	Red	Green	Red	434	146	3:1	0.009	0.90–0.95
Stem pigmentation	Absent	Present	Pigmented	324	256	9:7	0.035	0.80–0.90

Growth habit is trigenically controlled with the F_2 segregation ratio of 39:25. It involves one basic gene, and the other two are inhibitory and antiinhibitory genes. Earlier reports [4–6] concluded that the climbing characteristic (tendrillar) is governed by one dominant gene, designated as T. Norton [7] and Kolhe [8] showed that indeterminate or vining characteristics is conditioned by two duplicate genes, designated (as per Fery's proposal [3]) as Vi-1 and Vi-2. We propose three genes to be designated as Vi-1, Vi-2 and Vi-3. This is in line with the findings of Singh and Jindla [9]. The basic and inhibitory genes in the present

Table 2. Joint phenotypic segregation for four qualitative characters in the cowpea cross Selection-2 x K. 11

Character (ratio)	Joint ratio	Remarks	O/E	AB	Ab	aB	ab	χ^2	P
Growth habit (39:25) with seed size (3:1)	117:39: 75:25		O	302.0	52.0	137.0	89.0		
		On independent basis	E	265.1	88.4	169.9	56.6	45.1	> 0.001
		On linkage basis Cov 46% (basic gene linked) or 0.46±0.0207	E	299.3	52.6	134.1	92.4	0.2	0.95–0.952
Stem pigmentation (9:7)	27:9: 21:7		O	219.0	105.0	215.0	41.0		
		On independent basis	E	244.7	81.6	190.3	63.4	20.6	> 0.001
		On linkage basis Cov 17.4 % or 0.174±0.0157	E	220.8	105.5	214.2	39.5	0.075	> 0.99

AB—Both the genes dominant, Ab—first gene dominant and other gene recessive, aB—first gene recessive and second dominant, and ab—both the genes recessive.

Table 3. Breeding behaviour of four characters in F_3 generation of the cowpea cross Selection-2 x K. 11

Character (F_2 ratio)	B.T. for dominant	F_3 segregation into 3:1	1:3	9:7	13:3	3:13	39:35	B.T. for recessive	P
Plant habit (39:25):									
Expected ratio	7	16	4	4	4	4	8	17	
No. of families: obs.	11	22	4	4	3	6	12	18	
exp.	8.75	20.00	5.00	5.00	5.00	5.00	10.00	21.25	0.7–0.8
Seed size (3:1):									
Expected ratio	1	2						1	
No. of families: obs.	23	33						24	
exp.	20	40						20	0.2–0.3
Stipule colour (3:1):									
Expected ratio	1	2						1	
No. of families: obs.	17	37						26	
exp.	20	40						20	0.2–0.3
Stem pigmentation (9:7):									
Expected ratio	1	4			4			7	
No. of families: obs	3	22			22			31	
exp.	5	20			20			35	0.5–0.7

B.T. Breeding true.

study are assumed to be the duplicate genes discovered earlier for vining.The differences in the gene action for the same character may be attributed to gene mutations in the course of evolution of genotypes. The earlier reports regarding the seed size reveal that seed size is governed by partial dominance and F_1 was intermediate between the parents [10–12]. The present study shows complete dominance of big seed over small. We designate the big seed gene as Bg. Stipule colour in cowpea is either green or red. There is no report on the inheritance of this character. It is monogenically controlled with red colour being dominant over green. We designate the gene for stipule colour as Sti. There is much variation with reference to intensity and distribution of pigmentation on different parts. The present study has revealed that pigmentation along the stem was determined by two complementary genes with the digenic segregation ratio of 9:7 in F_2, while the earlier reports [13] indicate that pigmentation is controlled by two duplicate genes, Pp-1 and Pp-2. The same gene symbols hold good for complementary genes in the present study.

The joint phenotypic segregations for four qualitative morphological characters are given in Table 2. The analysis clearly shows that the basic gene for growth habit is linked with the gene for seed size with crossover value of 46%, and the gene for stem pigmentation is linked with the dominant gene for stipule pigmentation having 17.4% crossing over. There is a reduction of χ^2 value from significant to nonsignificant level for the expected ratios in both cases (from 45.1 to 0.2 and 20.6 to 0.075).

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