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GENE ACTION FOR CERTAIN QUANTITATIVE CHARACTERS IN GREENGRAM (*VIGNA RADIATA* (L.) WILCZEK)

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ABSTRACT

The nature of gene effects for yield and six yield traits in greengram were studied in six crosses involving four parents through generation mean analysis. The mean data of six populations (both parents, F_1, BC_1, BC_2 and F_2) were subjected to scaling test. In the presence of epistasis, six-parameter model was used to detect all type of gene effects. The analysis indicated that most of characters appeared to be complex in the expression of gene effects in different crosses. The additive gene effect was important in most crosses for majority of the traits. The dominance gene action was involved in the expression of yield, pods/plant, plant height, pod length and clusters/plant in some crosses. Among the digenic interactions additive x additive and dominance x dominance played important role in the expression of plant height, branches/plant, clusters/plant, pods/plant and grain yield/plant in some crosses.

Key words: Greengram, gene effects, generation mean.

The information on nature and magnitude of genetic components of variation for yield and its component traits is essential to adopt an effective breeding programme for its improvement. Gene action for quantitative traits in greengram has been determined earlier using diallel method [1 – 4] which demonstrated the operation of additive and dominance type of gene action. The importance of epistatic gene effects in the expression of characters has been observed earlier [5, 6]. In view of the meager information available about all type of gene effects controlling the yield and its trait in greengram, the present study aims to understand the nature and magnitude of genetic components in divergent parents.

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MATERIALS AND METHODS

Four divergent genotypes of greengram (ML-5, Coll-6, Coll-2 and PLM-20) were selected on the basis of plant height, number of pods/plant, pod length, grain size and tolerance to diseases (*Cercospora* leafspot and powdery mildew).

Among the parents, ML-5 is the standard high yielding variety, and PLM-20 a collection sample received from NBPGR, New Delhi. Coll-6 and Coll-2 are indigenous collections from the Andaman Islands. The genotype Coll-2 has very long pod (11–12 cm) with very bold seed and is tolerant to *Cercospora* leaf spot. Coll-6 produces small pods (6 cm), small seed, more pods/plant and is more tolerant to powdery mildew. PLM-20 is a genotype with more pods/plant, small seed, more branches, and is susceptible to *Cercospora* leaf spot. These genotypes were inter crossed in six possible combinations. The six basic populations of each cross namely two parents, their F_1 and F_2 and back-crosses BC_1 (F_1 x male parent) and BC_2 (F_1 x female parent) were developed and grown in compact family block design with three replications. The parents, F_1 and back-crosses were sown in one row each, F_2 in 15 rows with the row length of 3.75 m, and the spacing between rows and plants 30 and 15 cm, respectively. One row of the parent was grown in the beginning of each block as border line. The crop was grown in rainfed conditions in rice fallows with the fertilizer dose of 15, 30 and 15 kg/ha N, P and K, respectively. Observations on seven quantitative traits were recorded on 15 random plants in each parent and F_1, 20 plants in each back-cross and 75 plants in each F_2 population. The individual scaling test [7] was used to detect epistasis. In the absence of epistasis, the three-parameter model [8] was used to analyse m, (d) and (h) components. In the presence of epistasis, the additive (d) dominance (h) effects and nonallelic interaction components (i, j and l) of generation means were estimated according to Hayman [9]. Heterosis and inbreeding depression were also estimated.

RESULTS AND DISCUSSION

The individual scaling tests (A, B and C) differed significantly from zero (Table 1) for plant height, branches/plant, clusters/plant and grain yield/plant in ML-5 x Coll 6, Plant

Table 1. Scaling test and gene effects for yield and its components in greengram

Cross	Scales			Genetic components						Type of nonallelic interaction
	A	B	C	m	d	h	i	j	l	
				Plant height						
ML-5 x Coll-6	14.5	28.2^{**}	5.4	51.7^{**}	1.2	41.0^{*}	37.3^{*}	–6.8	-79.9^{**}	Duplicate
Coll-2 x Coll-6	25.8^{**}	15.5^{**}	–16.5	47.5^{**}	15.5^{**}	62.2^{**}	57.9^{**}	5.2^{**}	-99.2^{**}	Duplicate
PLM-20 x Coll-2	–2.2	-5.3^{*}	6.6	63.7^{**}	1.4	–5.3	-14.1^{*}	1.5	21.6^{**}	Duplicate
ML-5 x PLM-20	–0.17	3.8	–12.3	41.1^{**}	–0.4	37.9^{*}	—	—	—	—
Coll-6 x PLM-20	4.0	4.8	-10.0^{*}	47.2^{**}	-9.7^{**}	21.8^{**}	19.8^{**}	–0.9	-29.5^{**}	Duplicate
ML-5 x Coll-2	-16.0^{**}	-7.6^{*}	1.5	65.9^{**}	-5.7^{**}	-10.3^{*}	-24.9^{**}	-4.1^{*}	48.3^{**}	Duplicate

(Contd.)

Table 1 (contd.)

Cross	Scales			Genetic components						Type of nonallelic interaction
	A	B	C	m	d	h	i	j	l	
Number of branches/plant										
ML-5 x Coll-6	–0.3	–0.5*	–1.0	1.0**	0.5*	0.4	0.2	0.1	0.6*	Complementary
Coll-2 x Coll-6	–61.4**	–0.1	–0.1	0.9**	0.9**	1.8**	1.4**	0.7**	–2.7**	Duplicate
PLM-20 x Coll-2	–0.1	–0.5	–1.4*	0.9**	0.5**	1.3*	0.8	0.2	–0.2	—
ML-5 x PLM-20	0.7	–0.6	–0.3	0.9*	–0.1	0.6	—	—	—	—
Coll-6 x PLM-20	–0.3**	–0.2	–0.6*	1.1**	0.6**	0.5	0.1	–0.1	0.4	—
ML-5 x Coll-2	–0.3	–0.6*	–3.2**	0.7**	0.1	2.7**	2.3**	0.1	–1.4	—
Number of clusters/plant										
ML-5 x Coll-6	1.5	4.8**	–1.9	7.3**	–0.1	9.3**	8.2**	–1.7	–14.5**	Complementary
Coll-2 x Coll-6	–0.1	–0.8	–1.4	8.3*	0.4*	–2.9	—	—	—	—
PLM-20 x Coll-2	–1.8	–3.1	–4.2	8.9**	2.8**	0.7	–0.7	0.7	5.6*	Complementary
ML-5 x PLM-20	1.4	–2.2	–5.6	4.9*	–2.3**	10.9	—	—	—	—
Coll-6 x PLM-20	0.1	–3.3*	–6.9**	7.5**	–1.4	4.3*	3.7*	–1.4	–0.6	—
ML-5 x Coll-2	–0.4	–1.2	–5.3*	7.4**	1.6**	6.1*	3.7	0.4	–0.6	—
Number of pods/plant										
ML-5 x Coll-6	–7.9	–4.6	–14.4	25.7**	3.3**	–4.6	—	—	—	—
Coll-2 x Coll-6	–8.2	–15.8**	–17.0*	24.0**	3.5	1.1	–6.9*	3.8*	–1.4	—
PLM-20 x Coll-2	–6.1	–12.2**	15.0**	29.1**	11.3**	3.4	–3.4	3.0	21.7*	Complementary
ML-5 x PLM-20	1.7	–2.5	–34.6**	28.3**	–5.1**	37.6**	33.8**	2.1	–33.1**	Duplicate
Coll-6 x PLM-20	–5.4	–6.7**	–1.25	36.9**	8.3**	–6.7	–13.3*	0.7	25.4**	Duplicate
ML-5 x Coll-2	–6.8*	–9.00**	–14.9*	28.3**	6.1**	7.9	–0.9	1.1	16.7*	Complementary
Pod length										
ML-5 x Coll-6	–0.3	–0.2	–0.1	7.5**	0.3	–1.8	—	—	—	—
Coll-2 x Coll-6	1.0	–0.2	–2.3	5.6*	2.3**	8.5	—	—	—	—
PLM-20 x Coll-2	–1.4**	–0.4	–6.1**	8.4**	–2.6**	5.6**	4.3*	–0.5	–2.6	Duplicate
ML-5 x PLM-20	–0.5	–0.5	–1.6	6.6**	–0.1	–0.2	—	—	—	—
Coll-6 x PLM-20	–0.1	–1.1	–2.6	5.5**	–0.2	2.2	—	—	—	—
ML-5 x Coll-2	–0.3	0.5	–7.6**	7.9**	–2.7**	8.5**	7.7**	–0.9	–7.9**	Duplicate
Number of grains/pod										
ML-5 x Coll-6	–0.2	–0.9	–2.0	11.3**	–0.1	0.6	—	—	—	—
Coll-2 x Coll-6	–0.8	–2.0	–6.7*	12.8**	3.7**	2.9	3.9	0.6	–1.1	—
PLM-20 x Coll-2	–3.5**	–2.7	–8.2**	13.3**	–3.2**	2.6	2.0	0.4	4.2*	Complementary
ML-5 x PLM-20	–0.4	–0.5	–0.9	12.2*	–0.1	–8.9	—	—	—	—
Coll-6 x PLM-20	–2.0*	–0.7	–1.0	12.0**	–0.7	–1.9	–1.8	–0.6	4.5*	Duplicate
ML-5 x Coll-2	–2.6	–3.3	–7.8*	13.3**	–2.8*	2.0	1.9	0.4	3.9*	Complementary
Grain yield/plant										
ML-5 x Coll-6	3.8	1.6	–10.8**	7.9**	2.7*	19.5**	16.1**	1.1	–21.4*	Duplicate
Coll-2 x Coll-6	–1.7	–0.5	–4.2	8.1*	2.7**	4.7	—	—	—	—
PLM-20 x Coll-2	–5.1**	–2.5	–6.3*	11.0**	–1.9*	–0.5	–1.2	–1.3	8.8*	Duplicate
ML-5 x PLM-20	0.2	2.4**	–9.4*	9.1**	–1.7**	11.9**	11.9**	–1.1	–14.4**	Duplicate
Coll-6 x PLM-20	0.9	0.2	–4.0	4.4**	–2.2**	14.3**	—	—	—	—
ML-5 x Coll-2	–3.1	–2.7	–17.2**	9.9**	–1.3	16.9**	11.4**	–0.2	–5.7	Duplicate

*,**Significant at 5% and 1% levels, respectively.

height, branches/plant, pod/plant and grains/pod in Coll-2 x Coll-6, plant height, length of pods, branches/plant, pods/plant, grains/pod and grain yield in PLM-20 x Coll-2, pods/plant and grain yield in ML-5 x PLM-20, and plant height, branches/plant, clusters/plant, pods/plant and grains/pod in Coll-6 x PLM-20 for plant height, pod length, branches/plant, clusters/plant, pods/plant, grains/pod and grain yield/plant in ML-5 x PLM-20. The significant estimates of scales suggest the influence of epistasis in the inheritance of characters. The presence of epistasis indicated that the additive and dominance models are inadquate. The analysis of gene effects for plant height indicated that the additive and dominance gene effects were important in the crosses Coll-2 x Coll- 6, Coll-6 x PLM-20, ML-5 x Coll-6. However, the dominance effect was predominant over the additive one. Among the epistatis components, (i) and (l) were important in the crosses ML-5 x Coll-6, Coll-2 x Coll-6, PLM-20 x Coll-2, Coll-6 x PLM-20 and ML-5 x Coll-2, whereas (i) component was significant in Coll-2 x Coll-6 and ML-5 x Coll-2. All the crosses showed duplicate type nonallelic interaction. In general, the epistatic components were more important than the additive and dominance effects. The crosses ML-5 x Coll-2 and PLM-20 x Coll-2 expressed desirable heterosis (25.1 and 15.2%, respectively).

The additive gene effect was more important in the crosses ML-5 x Coll-6, PLM-20 x Coll-2 and Coll-6 x PLM-20 for branches/plant. The crosses Coll-2 x Coll-6 and ML-5 x Coll-6 also expressed significant (h) component for number of branches. The digenic components (i, j and l) played important role in the expression of this character in the cross Coll-2 x Coll-6, where as additive x additive type gene effect was significant in the cross ML-5 x Coll-2. Complementary type epistatic interaction was observed in the cross ML-5 x Coll 6. The crosses Coll-2 x Coll-6, PLM-20 x Coll-2, Coll-6 x PLM-20 and ML-5 x Coll-2 showed high heterosis (59.4, 52.7, 42.1 and 32.5%, respectively) followed by higher inbreeding depression.

For number of clusters/plants, three crosses showed epistatic gene effect. Additive type gene action was important in PLM-20 x Coll-2, ML-5 x PLM-20 and ML-5 x Coll-2. The dominance, additive x additive, and dominance x dominance gene effects were important in the cross ML-5 x Coll-6, and complementary type epistatis in ML-5 x Coll-6 and PLM-20 x Coll-2. The crosses Coll-2 x Coll-6 and ML-5 x Coll-2 expressed higher heterosis for number of branches (30.1 and 30.8%, respectively). Inbreeding depression was high in ML-5 x Coll-2, Coll-6 x PLM-20 and ML-5 x PLM-20.

Number of pods/plant was influenced by additive gene action in all the crosses except Coll-2 x Coll-6. Dominant gene effect was important only in ML-5 x PLM-20. Among the epistatic components, (i) and (l) were significant in ML-5 x PLM-20 and Coll-6 x PLM-20. Only the cross Coll-2 x Coll-6 showed additive x dominance type gene effect. Complementary type of nonallelic interaction was observed in the crosses PLM-20 x Coll-2 and ML-5 x Coll-2. Appreciable heterosis was observed in the crosses Coll-2 x Coll-6, ML-5 x Coll-2, PLM-20 x Coll-2 and Coll-6 x PLM-20 (33.2, 32.2, 23.1 and 19.7%, respectively).

For pod length, additive gene action was important in the cross Coll-2 x Coll-6, but additive, dominance and additive x additive type gene effects were mainly responsible for the expression of this character in the cross PLM-20 x Coll-2. The cross ML-5 x Coll-2 expressed all types of gene effects except additive x dominance. Duplicate nonallelic interaction was also observed in the crosses PLM-20 x Coll-2 and ML-5 x Coll-2.

The additive gene effect was mainly important in the inheritance of number of grains/pod in the crosses Coll-2 x Coll- 6, PLM-20 x Coll-2 and ML-5 x Coll-2. Among the nonadditive gene effects, only dominance x dominance was significant in PLM-20 x Coll-2, Coll-6 x PLM-20 and ML-5 x Coll-2. The crosses PLM-20 x Coll-2 and ML-5 x Coll-2 showed complementary and Coll-6 x PLM-20 duplicate type of nonallelic interactions.

In respect of yield, additive and dominance type of gene effects were important in the crosses ML-5 x Coll-6, ML-5 x PLM-20 and Coll-6 x PLM-20. Additive gene effect was responsible for the expression of yield in the crosses Coll-2 x Coll-6 and PLM-20 x Coll-2, and dominance in ML-5 x Coll-2. Among the nonallelic, interactions additive x additive and dominance x dominance were significant in ML-5 x Coll-6 and ML-5 x ML-20. The cross ML-5 x Coll-2 expressed additive x additive type gene effect also. Duplicate type of nonallelic interaction was observed in the crosses ML-5 x Coll-6, ML-5 x Coll-2, PLM-20 x Coll-2 and ML-5 x PLM-20. The crosses ML-5 x Coll-6, ML-5 x Coll-2, Coll-6 x PLM-20 and Coll-2 x Coll-6 expressed high heterosis (39.1, 40.6, 33.4, and 31.6%, respectively) for grain yield. Inbreeding depression was more pronounced in ML-5 x Coll-2, ML-5 x Coll-6 and ML-5 x PLM-20.

The relative magnitude of additive and dominance effects for the characters in some crosses differed leading to the variation in inheritance. The additive gene action was important for most of characters in the crosses Coll-2 x Coll-6, PLM-20 x Coll-2 and ML-5 x Coll-2. When compared to additive gene effect, dominant gene effect had a greater contribution in ML-5 x Coll-6, Coll-6 x PLM-20 and ML-5 x PLM-20 for some of the important economic characters. Similar results have been reported [1, 2 and 4] using entirely different genotypes in diallel cross analysis in green gram. Further, the partitioning of epistasis revealed that over all additive x additive and dominance x dominance effects were present in many cases which are in agreement with the findings of Muker et al. [6]. The duplicate type nonallelic interaction was common, except a few crosses for some characters. Similar results were also reported by Thimmappa [5].

The characters, for which additive and additive x additive type gene effects are more important, the pedigree method of selection would be more effective for the improvement of the characters. For exploitation of all type of gene effects biparental approach inter se crossing and/or reciprocal recurrent selection may be practiced for developing elite population for selection of high yielding lines in advance generation. The breeding procedure involving multiple crosses followed by selected intermating in early segregating generations, as they utilize simultaneously both additive and nonadditive type of gene effects, is suggested when a character shows different gene effects in different crosses and the same cross gives different gene effects for different traits.

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