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Analysis of gene effects governing yield and yield contributing traits in pigeonpea [*Cajanus cajan* (L.) Millspaugh]

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Abstract

Generation mean analysis study in pigeopea was undertaken to estimate the gene action operating in the inheritance of yield and its components. Six basic generations *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 of three crosses, namely ASHA x NPMK 15-05 (Cross-I), BDN 711 x BSMR-853 (Cross-II) and PKV TARA x ICPL 87 (Cross-III) were studied. Scaling test was applied to test the adequacy of additive-dominance model for the traits under investigation. All additive, dominance and epistatic interactions were found operating in the inheritance of almost all characters. Dominance (Dominance and dominance x dominance) gene action was found predominant in control of grain yield and its components. All the characters under study showed duplicate type of gene action for one, two or three crosses. Both, additive and non-additive gene action contributes significantly in the inheritance of various quantitative characters in pigeonpea.

Keywords: Gene effects governing yield, yield, contributing traits, pigeonpea, *Cajanus cajan* (L.)

Introduction

Pigeonpea (*Cajanus cajan* L.) is the sixth most important pulse crop after in the world with almost all production confining to developing countries. Being its most commercial value, India is the largest producer and consumer but due to low productivity, availability of pigeonpea seed yield is not enough. Yield is the product of cumulative effect of all genes having small action and traits governing such type of genes cannot be selected. The information on the nature of gene action and partitioning of variances are essential in deciding the effectiveness of breeding method for improving a crop. Scaling tests is usually used to detect only inter-allelic interactions in the respective crosses whereas, generation means analysis provides estimate of main gene effects and interactions effects. Thus, in the present investigation, genetic parameters namely, additive, dominance and epistatic gene effects were estimated through generation mean study for eleven quantitative traits in 3 crosses of pigeonpea.

Materials and Methods

The present study was carried out during kharif 2019-20, at field of Pulses Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. Experimental material comprised of 6 generations i.e., P_1, P_2, F_1, F_2, BC_1 (F_1xP_1) and BC_2 (F_1xP_2) of three crosses namely ASHA x NPMK 15-05 (Cross-I), BDN 711 x BSMR-853 (Cross-II) and PKV TARA x ICPL 87 (Cross-III). The six generations of each cross were grown separately in ramdomized block design with three replications at field of Pulses Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during *Kharif* 2019-2020. Parents and $F_{1's}$ were represented by single row and F_2 by 8 rows and BC_1 and BC_2 by 3 rows of 4.0 mt. length spaced at 90 cm apart with 30 cm distance between plants in a row. All cultural practices were followed to have a satisfactory crop growth. Observations were recorded on 10 randomly selected plants from each of parents and $F_{1's}$; 30 plants from each of $BC_{1's}$ and $BC_{2's}$ and 50 plants from each of $F_{2's}$ per replication excluding border plants on days to 50% flowering, days to maturity, plant height (cm.), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, pod length (cm.), number of seeds pod^{-1}, 100-seed weight (g.), harvest Index (per cent of the proportion of economic yield over the biological yield) and seed yield plant^{-1} (g.). The analysis of variance for randomized block design (RBD) was carried out separately for each character as per the Panse and Sukhatme (1985) [10]. The procedure for estimating the scaling test (A, B, C and D) was followed as suggested by Mather (1949) [8]; For testing the adequacy of additive-dominance model an analysis of data was performed following six parameter model of Hayman (1958) [5] and Jink & Jones (1958) [6].

Results and Discussion

Assessment of relative magnitude of various gene effects including epistasis is of great importance in formulating the appropriate breeding procedure for further improvement. Considering the significant deviation of scale (s), (A, B, C and D) from zero indicated the evidence of epistasis in all three crosses for all the traits (Table 1) and hence, six parameter model was extended for their practical implication.

The estimates of six parameters model revealed the significant contribution of both additive and dominance gene effects in most of the traits studied (Table 2). In general, the relative contribution of dominance gene effect was even higher than those of additive gene effect. Further, higher frequency of duplicate type of epistasis for all traits except for no. of pods plant and harvest index, confirms the predominance of dominant gene effects for the expression of traits studied which was in conformity with earlier reports in this crop by Dahiya and Satija (1978) [2], Singh (1989) [3], Oommen, *et al.* (1999) [9], and Hooda *et al.* (2000) [4], Singh *et al.* (2005) [11], Kumar *et al.* (2009) [7] and Ajay *et al.* (2012) [1]. On the other hand, additive gene effect is found important for the inheritance of the trait 100-seed weight. The epistatic gene effects were found to play an important role for the inheritance of almost all the characters in variable number of crosses. Considering the importance of epistatic gene interaction, dominance × dominance effect appeared to contribute maximum followed by additive × additive and additive × dominance effects. It may be concluded that the complex character like yield per plant followed by pods per plant were under the controlled of relatively higher proportion of dominance gene effect whereas an important yield component viz., 100 seed weight exhibited relatively higher proportion of additive gene effect which was in conformity with earlier reports given Oommen *et al.* (1999) [9] and Hooda *et al.* (2000) [4].

It indicated that as the inheritance of quantitative characters becomes more complex, the contribution of dominance gene effect for their inheritance becomes greater. However, the additive gene effects are greater in the traits which are assumed to have less complex inheritance.

Table 1: Estimates of individual and joint scaling tests for grain yield and its components in all three crosses, cross-I (ASHA X NPMK 15-05), cross-II (BDN 711 X BSMR 853) and cross-III (PKV TARA X ICPL 87) in pigeonpea

S. No.	Character	Crosses	Scaling tests				Goodness of fit
			A	B	C	D	X^2
1	Days to 50% Flowering	C-I	5.33	-8.00	-30.67*	-14.00*	13.23**
		C-II	-6.33	19.67*	-5.33	-9.33	8.90**
		C-III	33.00**	12.33	46.67**	0.67	25.53**
2	Days to maturity	C-I	13.00	-6.33	-50.00**	-28.33**	20.08**
		C-II	3.33	6.33	-40.33*	-25.00**	9.99**
		C-III	20.00*	17.00*	45.67**	4.33	17.13**
3	Plant height (cm)	C-I	24.79	61.45	2.95	-41.65	4.54*
		C-II	49.93	22.00	41.26	-15.33	3.71*
		C-III	-30.00	37.76	59.89	26.06	6.36**
4	No. of primary branches plant^{-1}	C-I	-0.37	-0.42	-1.23**	-0.22*	11.61**
		C-II	-2.38**	-1.98**	-0.32	2.02**	
		C-III	0.60*	-0.20	0.32	-0.04	11.25**
5	No. of secondary branches plant^{-1}	C-I	13.58**	4.67	3.81	-7.22*	14.40**
		C-II	-9.69**	-12.13**	10.09*	15.96**	74.44**
		C-III	28.24**	7.79**	15.25**	-10.39**	93.25**
6	No. of pods plant^{-1}	C-I	110.35	-90.31	-171.13	-95.58*	11.70**
		C-II	-32.93	-63.11	-46.26	24.89	2.11
		C-III	-70.93*	152.87**	17.33	-32.30**	115.15**
7	No. of seeds pod^{-1}	C-I	-0.62**	0.25	-1.80**	-0.71**	155.49**
		C-II	-0.05	-0.02	-0.60*	-0.27**	23.27**
		C-III	-0.20	0.04	-0.48**	-0.16**	20.49**
8	Pod length (cm)	C-I	-0.29	0.34	-1.48**	-0.76**	44.85**
		C-II	-0.05	-0.94**	0.04	0.52**	100.92**
		C-III	0.27	-0.20	-0.95	-0.51	4.18*
9	100 grain wt. (gm)	C-I	0.09	-0.03	-0.84	-0.45	1.26
		C-II	0.13	-0.08	-0.02	-0.04	1.98
		C-III	0.12	-0.03	0.73	0.32	4.01*
10	Harvest index (%)	C-I	-0.51	-2.94	-8.58	-2.56	4.08*
		C-II	-3.61	-1.52	-7.53	-1.20	4.24*
		C-III	-2.86*	0.96	-1.01	0.44	9.83**
11	Seed yield plant^{-1} (gm)	C-I	10.00	-20.13	-151.44*	-70.66	6.22**
		C-II	-29.63	-34.08	-88.37	-12.33	2.17
		C-III	-53.89	37.32*	-39.23	-11.33	18.80**

Table 2: Estimates of gene effects for grain yield and its components of all three crosses, cross-I (ASHA X NPMK- 15-05), cross-II (BDN 711 X BSMR 853) and cross-III (PKV TARA X ICPL 87) in pigeonpea

S. No.	Character	Crosses	X^2	Genetic components						Type of epistasis
				m	d	h	i	j	l	
1	Days to 50 % flowering	C-I	13.23**	135.00**	8.00*	30.00*	28.00*	6.67	-25.33	Duplicate
		C-II	8.90**	133.33**	-24.67**	23.33	18.67	-13.00*	-32.00	Duplicate
		C-III	25.53**	130.00**	25.33**	1.33	-1.33	10.33	-44.00	Duplicate
2	Days to Maturity	C-I	20.08**	193.00**	12.33*	56.33*	56.67**	9.67	-63.33*	Duplicate
		C-II	9.99**	186.00**	-20.33**	59.83**	50.00**	-1.50	-59.67*	Duplicate
		C-III	17.13**	184.33**	25.67**	-1.83	-8.67	1.50	-28.33	Complementary
3	Plant height (cm)	C-I	4.54*	243.51**	-20.00	106.17	83.29	-18.33	-169.53	Duplicate
		C-II	3.71*	232.00**	-12.00	93.96	30.67	13.96	-102.59	Duplicate
		C-III	6.36**	243.72**	29.29	14.38	-52.12	-33.88	44.35	Complementary
4	No of primary branches plant^{-1}	C-I	11.61**	4.66**	0.96**	1.30**	0.43*	0.02	0.36	Complementary
		C-II		5.65**	-0.80**	-1.77**	-4.04**	-0.20*	8.40**	Duplicate
		C-III	11.25**	4.48**	0.93**	1.55**	0.08	0.40**	-0.48	Duplicate
5	No. of secondary branches plant^{-1}	C-I	14.40**	35.55**	12.39**	18.17**	14.44*	4.46	-32.69**	Duplicate
		C-II	74.44**	43.74**	-2.01	-17.42**	-31.91**	1.22	53.73**	Duplicate
		C-III	93.25**	33.46**	11.73**	30.56**	20.79**	10.22**	-56.82**	Duplicate
6	No. of pods plant^{-1}	C-I	11.70**	410.72**	180.84**	537.37**	191.17*	100.33**	-211.20	Duplicate
		C-II	2.11	420.43**	-109.43**	246.77*	-49.78	15.09	145.82	Complementary
		C-III	115.15**	472.02**	55.52**	370.37**	64.61**	-111.90**	-146.55**	Complementary
7	No. of Seeds pod^{-1}	C-I	155.49**	4.38**	-1.43**	1.63**	1.43**	-0.43**	-1.05*	Duplicate
		C-II	23.27**	3.80**	-0.31**	0.77**	0.53**	-0.01	-0.47	Duplicate
		C-III	20.49**	3.48**	-0.25**	0.72**	0.32**	-0.12	-0.16	Duplicate
8	Pod length (cm)	C-I	44.85**	5.86**	-1.56**	1.47**	1.53**	-0.31	-1.57*	Duplicate
		C-II	100.92**	5.12**	0.50**	-0.87**	-1.04**	0.45**	2.04**	Duplicate
		C-III	4.18*	4.94**	-0.16	1.31*	1.02	0.23	-1.09	Duplicate
9	100 grain wt. (gm)	C-I	1.26	10.12**	0.52	0.05	0.89	0.06	-0.95	Duplicate
		C-II	1.98	11.10**	-0.07	0.30	0.07	0.11	-0.12	Duplicate
		C-III	4.01*	10.08**	0.20	0.01	-0.65	0.07	0.56	Complementary
10	Harvest Index (%)	C-I	4.08*	24.06**	3.32*	11.27*	5.13	1.22	-1.67	Duplicate
		C-II	4.24*	22.17**	-0.58	8.84	2.39	-1.05	2.74	Complementary
		C-III	9.83**	22.10**	1.62	4.08	-0.89	-1.91*	2.79	Complementary
11	Seed yield plant^{-1} (gm)	C-I	6.22**	182.73**	32.04	313.45**	141.31	15.07	-131.19	Duplicate
		C-II	2.17	172.33	-61.61	164.55	24.67	2.22	39.04	Complementary
		C-III	18.80**	155.55	6.59	160.57	22.66	-45.60	-6.09	Duplicate

Conclusion

Scaling tests and Six generation model have revealed that both intra (dominance gene action) and inter-allelic (epistasis) interaction play an important role in the inheritance of all the traits studied. Under such a situation, improvement in such characters may be expected through standard selection procedure which may first exploit additive gene effects. In this situation recombination breeding could be followed by postponing selection to later generations. Simultaneously, care should be taken that dominant gene effects are not dissipated, rather they should be concentrated. Under such circumstances, the reciprocal recurrent selection breeding procedure seems to be the best available method, as it will utilize simultaneously all three types of gene effects resulting for the isolation of desirable recombinants in advanced generations.

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