GENETIC ANALYSIS OF SOME QUANTITATIVE CHARACTERS IN PIGEONPEA

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Abstract: Out of the eleven quantitative characters studied in pigeonpea, days to flowering alone was influenced by non-additive genes and all the remaining characters by additive genes. The proportion of dominant and recessive genes was equal for plant height and number of clusters per plant, whereas more than one recessive gene was present for every dominant gene in the expression of days to maturity. The remaining eight characters showed the presence of one to two dominant genes for every recessive gene.

Key words: Additive gene effect, diallel analysis, nonadditive gene effect, pigeonpea.

INTRODUCTION

Pigeonpea (*Cajanus cajan* [L] Millsp) is one of the important legumes in India. But its improvement by breeding has received attention only in the recent past. Information on the nature and mode of gene action is important to direct the breeding programmes in any crop. The present study was undertaken to determine the genetics of some important characters in pigeonpea.

MATERIALS AND METHODS

Five diverse cultivars of pigeonpea namely UPAS-120, PLA-550, PLA-600, PLA-345-1 and IC 15708 were crossed in all possible combinations excluding reciprocals in 1988. The resulting F_1s and five parents were grown in a randomised block design, replicated thrice at the farm attached to the College of Horticulture, Vellanikkara during 1989. Each entry was grown on ridges of 3 m long and 1 m apart with a plant spacing of 60 cm. Observations were recorded from all the individual plants in respect of 11 quantitative characters viz., height of plant at harvest, number of primary branches, number of secondary branches, days to first flowering, days to maturity, number of clusters per plant, number of pods per plant, length of pod bearing branches, number of seeds per pod, hundred seed weight and seed yield. The genetic analysis was done following Hayman (1954).

RESULTS AND DISCUSSION

Diallel analysis by Hayman's method provides an overall genetic evaluation which would be helpful in selecting the parents and their potential crosses in early segregating generations. Hayman (1954) emphasised the fulfilment of certain assumptions. To examine this, t^2 was estimated for all characters. The t^2 value was not significant for 10 characters. This revealed the satisfaction of all the assumptions of the diallel for these characters in the present material. The significance of t^2 for days to first flowering indicated that some of the assumptions were not satisfied for this character. The genetic parameters for this character might have biased estimates to some extent.

The estimates of D, H_1, H_2, h^2 and F obtained from diallel analysis (Hayman, 1954) for all the 11 quantitative traits are presented in Table la. The genetic parameter D, which is an index of the variance due to additive gene effects was highly significant for all characters. The dominance component H_1 was also significant for all characters except plant height. The higher magnitude of additive genetic effect for characters other than days to flowering indicated the preponderance of additive gene action. This was supported by the high estimates of their narrow sense heritability.

H_1 and H_2 were of equal magnitude for days to flowering, days to maturity and 100 seed

Table 1a.   Estimates of genetic components of variance for quantitative characters by Hayman's approach

Characters	Components				
	D	H₁	H₂	h²	F
1 Plant height	9561**	303	216	-7.68	-24.69
2 Number of primary branches	145**	35.12 *	25.18	-0.42	30.38*
3 Number of secondary branches	754**	572**	436*	3.50	414*
4 Days to first flowering	82.66**	1864**	1852**	5864**	58.47
5 Days to maturity	4625**	12.52**	11.31**	5.06	-65.11*
6 Number of clusters per plant	14033**	2394**	1712**	306	-141
7 Number of pods per plant	60419**	6962**	3477	183	11307
8 Length of pod bearing branches	674**	50.50**	38.08	9.16	39.52*
9 Number of seeds per pod	4.26**	0.11**	0.08*	0.02	0.35**
10 Hundred seed weight	20.50**	1.02**	0.91**	0.17	0.70*
11 Seed yield per plant	1809**	472*	374*	113	485**

D-Additive variance; H₁=Dominance variance; H₂=1-{1-(u-v)²} where 'u' is the proportion of positive and 'v' is the proportion of negative genes in the parent; h² = Dominance effect; F=Covariance of additive and dominance effects.

Table 1b.   Estimates of genetic components of variance for quantitative characters by Hayman's approach

Characters	Components									
	E		(H₁/D)¹ᐟ²		H₂/4H₁	i	KD/KR		h²/H₂	i......t²
1 Plant height	17.77		0.18		0.18	i	0.99		-0.04	i	0.23
2 Number of primary branches	0.86	i	0.49		0.18		1.54	i	-0.02		0.07
3 Number of secondary branch	4.29		0.87		0.19	!	1.92	!	-0.01	i	2.53
4 Days to first flowering	1.25		4.75		0.25		1.16		3.16		20.38
5 Days to maturity	1.37*		0.05		0.23		0.76	!	0.45	i	0.05
6 Number of clusters per plant	237*		0.41		0.18		0.98		0.18		0.21
7 Number of pods per plant	1583**		0.34		0.13		1.76		-0.05	i	0.84
8 Length of pod bearing branches	5.99		0.27		0.19		1.24	i	0.24	i	0.24
9 Number of seeds per pod	i 0.02**		0.16		0.18		1.68	!	0.20	i	2.84
10 Hundred seed weight	i 0.04		0.22		0.22	i	1.16		0.19	i	2.20
11 Seed yield per plant	; 14.47		0.51		0.20	i	1.71		0.30	i	0.19

E=Environmental variance; (H₁/D)¹ᐟ² =Mean degree of dominance; H₂/4H₁=Proportion of genes with positive and negative effects in parents; KD/KR=Proportion of dominant and recessive genes in parents; h²/H₂=Number of groups of genes controlling the character and exhibiting dominance.

weight, which indicated equal proportion of genes with positive and negative effects in the loci governing these characters. For the other eight characters H₁ was greater in magnitude than H₂ suggesting that genes with positive and negative effects were not in equal proportions in the parents in the loci governing these characters. The ratio of H₂/4H₁ (Table 1b) which also gives the proportion of genes with positive and negative effects in the parents, approached the expected ratio of 0.25 for the same three characters viz., days to flowering, days to maturity and 100 seed weight, confirming the equal distribution of

positive and negative alleles in the parents for these three characters. The remaining eight characters indicated asymmetry of loci. Asymmetric distribution of positive and negative alleles in the parents was observed in pigeonpea by Dahiya and Brar (1977) for flowering time, pod number, seed size and seed yield; and by Sidhu el al. (1981) for seed yield, days to 50% flowering, seed size, plant height and number of pods per plant. Yadava and Rao (1986) also reported asymmetric distribution of genes with positive and negative effects in green gram for all characters except pods per cluster.

The insignificant value of F for plant height, days to flowering, number of clusters per plant and number of pods per plant showed an equal distribution of dominant and recessive genes in the parents, for these characters. For the other seven traits, an unequal distribution of dominant and recessive genes was seen due to the significance of F value. The degree of dominance (Table 1b) was in the range of over-dominance for days to flowering; and partial dominance for all the other characters. The value of h^2, which gives the dominance effect, was significant only for days to flowering. Based on the above facts, it is concluded that non-additive gene effect played an important role in the inheritance of clays to flowering; and additive gene effects for all the remaining 10 characters. Additivity was reported by Dahiya and Brar (1977) in the case of 100 seed weight in red gram. But the inheritance of seed yield, number of pods per plant and plant height was reported to be affected by non-additive gene effects by Reddy et al. (1979) and Sidhu et al. (1981). There are varying reports regarding the nature of gene action for different characters. This variation may be due to different materials and genotype-environment interaction.

In the Wr-Vr graph, the slope of the regression line for the traits did not deviate significantly from unity, which indicated the absence of epistasis. The positive interception of Wr axis with the regression line suggested partial dominance for number of primary branches, number of clusters per plant, number of pods per plant and seed yield. Even though the interception of Wr axis and the regression line was positive, the presence of the parabola limit, very near to the regression line for plant height, days to maturity, length of pod bearing branches, number of seeds per pod and 100 seed weight showed no dominance. For number of secondary branches, the interception of the regression line near the origin indicated complete dominance of this trait. Days to flowering exhibited over-dominance by the negative interception of the regression line with the Wr axis. In contrast to this, Singh and Bains (1982) indicated predominance of

over-dominance for secondary branches and grain yield per plant, and partial dominance for all the other traits in chickpea.

The estimates of the number of dominant genes or gene groups controlling the characters (Table 1b) were more than one for days to flowering alone; whereas it was less than one for all other characters. The proportion of dominant and recessive genes (Table 1b) was almost one for plant height and number of clusters per plant, which revealed the 1:1 occurrence of dominant and recessive genes or gene groups for these characters. However, days to maturity obtained a ratio of less than one indicating the presence of more than one recessive gene per dominant gene. The remaining eight characters showed the presence of one to two dominant genes for every recessive gene.

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