Electronic Journal of Plant Breeding, 10 (3): 1240 - 1245(Sep 2019) DOI: 10.5958/0975-928X.2019.00157.1
ISSN 0975-928X

Research Article

Genetic analysis for yield and yield attributing traits in pigeonpea [*Cajanas cajan* (L.) Millsp.]

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(Received: 25 May 2018; Revised: 11 Jul 2019; Accepted: 20 Aug 2019)

Abstract
The basic information on gene action and inheritance of quantitative traits, which is necessary to develop future breeding programme, is not widely studied in pigeonpea because it is a long duration crop and widely affected by stresses (biotic & abiotic). Therefore, present study was conducted among six generations in five pigeonpea crosses to know significance of additive-dominance model, gene action involved in inheritance of quantitative traits. These six population (P_1, P_2, F_1, F_2, BC_1 and BC_2) of five cross combinations of pigeonpea were studied during *Kharif*, 2014-15 for plant height, number of primary and secondary branches, pods plant^{-1}, pod length, seeds pod^{-1}, 100-seed weight and Seed yield plant^{-1}.Significant deviation of scale(s) (A, B, C & D) from zero in all the crosses for most of the traits were evidence of presence of epistasis and hence further subjected to six parameter model to estimate the main gene effects (additive [$\hat{d}$] and dominance [$\hat{h}$]) and their digenic interactions (additive × additive [$\hat{i}$], additive × dominance [$\hat{j}$] and dominance × dominance [$\hat{l}$]). The estimates of six parameter model revealed that both additive and dominant gene effects were important in all the crosses for almost all the traits. However, the relative contribution of dominant gene effects was much higher than additive gene effects for plant height, pods plant^{-1}, seed pod^{-1} and seed yield plant^{-1}. Higher frequency of duplicate type of epistasis also confirms the prevalence of dominance gene effects for above traits except for seed yieldplant^{-1}.

Key words
Pigeonpea, Scaling test, Generation mean analysis, Additive, Dominance.

Introduction

Pigeonpea [*Cajanus cajan*(L.) Millsp.] commonly known as Arhar or red gram or tur is one of the second most important pulse crop after chickpea in India. It accounts for about 11.8% of the total pulse area and 17% of total pulse production of the country. Pigeonpea is cultivated worldwide in developing countries under tropical and sub-tropical climatic conditions with various cropping systems. Globally, it is cultivated in about 7.03 million hectares area with an annual production of 4.89 million tonnes with an average productivity around 695 kg/ha. In India, it is cultivated on 5.60 million hectares area with an annual production of 3.29 million tonnes with productivity around 587 kg/ha which is lower than global average [FAOSTAT (2017)]. It plays an important role in vegetarian diet as seeds constitutes protein, vitamins, and mineral elements such as potassium, phosphorus, zinc and magnesium and also serves as a good source of carbohydrate and food fibers. The protein content in split seeds is similar to soybean and ranges from 21–28% (Phatak *et al.,* 1993). Pigeonpea seeds provide essential amino acids like lysine, tyrosine and arginine, whereas cystine and methionine contents are low (Saxena *et al*., 2010). The seed and pod husks are quality feed for cattle's, whereas dry branches and stems serve as domestic fuel. Productivity of pigeonpea worldwide in comparison to cereals is very low and stagnant due to several biotic and abiotic stresses. This low productivity is due to its low harvest index (19%) because of limited man made selections and widely affected by biotic and abiotic stresses (Varshney *et al.*, 2010 and Ajay *et al.*, 2012).

Several studies have shown that yield of pigeonpea could reach as high as cereals which may be up to 2.0 to 3.5 tonnesha^{-1}in short and long duration varieties, respectively (IIPR, 2011) by developing suitable plant type through improved harvest index. However, the precise knowledge of gene effects including epistasis is paramount importance for adopting efficient breeding programme for achieving the targeted yield potential of this important pulse crop. The information on the nature of gene action and partitioning of variances areessential in deciding the effective breeding programme for improving a crop. Scaling tests is usually used to detectonly inter-allelic interactions

in the respective crosseswhereas, generation means analysis provides estimate ofmain gene effects and their interactions effects. Generation meansanalysis has been applied in the past by few workers mostly in medium to long duration genotypes.

Generation mean analysis, which provides the estimates of the main gene actions ([$\hat{d}$] and [$\hat{h}$]) and their digenic interactions ([$\hat{i}$],[$\hat{j}$] and [$\hat{l}$]), helps in understanding the performance of the parents used in the crosses and potential of the crosses to be used either for heterosis exploitation or pedigree selection. In the present study, six-parameter model has been utilized to study and analyse the genetical control of yield and yield controlling characters of five crosses involving six diverse cultivars of pigeonpea.

Materials and Methods

The experimental materials consisted of six elite and diverse genotypes (MAL-18, BWR-133, Bahar, BSMR-846, BWR-23 and ICP-2376) along with their parents received from AICRP on MULLaRP, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, BHU, Varanasi were sown in Compact Family Block Design during the previous three year of *Kharif*, 2014-15 to obtain F_1in first generation by cross between two diverse parents and F_1 were selfed to obtain F_2 generation, in the second year we make backcrosses F_1 crossed with both the parent like this BC_1 (F_1× P_1) and BC_2 (F_1× P_2).In the third and last year all the six populations P_1, P_2, F_1, BC_1, BC_2 and F_2 were grown in Compact Family Block Design. The experimental material consisted crossed (hybrid) seeds of five crosses (MAL 18 × BWR-133, Bahar × BSMR 846, Bahar × BWR 23, MAL-18 × BSMR 846 and ICP 2376 × BSMR 846) were grown into two sets. Each plot consisted of a single row of parents and F_{1s} each, two rows of BC_1 and BC_2 each and five rows of F_2 generation (20 plants in parents and F_1 generation, 50 plants in BC_1 and BC_2 generation and 200 plants in F_2 generation). Recommended package of practices were followed throughout the crop season. Data were recorded on ten randomly selected plants from each row excluding border plants. Each row was consisted of 4m length and row to row and plant to plant distance 75 and 25 cm, respectively. All the recommended agronomic practices were followed to raise a good crop. For each family the plot means values in each generation were averaged over replication to obtained generation means. These generations mean formed the basis of calculation of various genetic parameters.

The procedure for estimating the scaling test (A, B, C and D) was followed as suggested by Mather (1949) and Hayman and Mather (1955) for testing the adequacy of additive-dominance model and analysis of data was performed following six parameter model of Hayman (1958) and Jink& Jones (1958).

Further, analysis of data was performed following six parameter model. At least, six generations are required for estimation of six parameters[$\hat{m}$], [$\hat{d}$], [$\hat{h}$], [$\hat{i}$], [$\hat{j}$] and. [$\hat{l}$] These were provided by the mean values of parents, F_1, F_2, BC_1 and BC_2 generations. Hayman (1958) and Jink and Jones (1958) gave the following six parameter model for estimation of various genetic components.

m = $\overline{F}_2$

d = $\overline{B}_1 - \overline{B}_2$

h = $\overline{F}_1 - 4\overline{F}_2 - 1/2\,\overline{P}_1 - 1/2\,\overline{P}_2 + 2\,\overline{B}_1 + 2\,\overline{B}_2$

i = $2\,\overline{B}_1 + 2\,\overline{B}_2 - 4\,\overline{F}_2$

j = $\overline{B}_1 - 1/2\,\overline{P}_1 - \overline{B}_2 + 1/2\,\overline{P}_2$

l = $\overline{P}_1 + \overline{P}_2 + 2\,\overline{F}_1 + 4\,\overline{F}_2 - 4\,\overline{B}_1 - 4\,\overline{B}_2$

When dominance [$\hat{h}$] and dominance × dominance [$\hat{l}$] effects had the same sign the effects were complementary while different signs indicated duplicate epistasis (Kearsey and Pooni 1996).

Results and Discussion

Scaling test was found significant deviation of scale(s), (A, B, C and D) from zero for most of the traits in all the five crosses **(Table 1).** This shows that higher value interactions (inter-allelic interactions) play a vital role in the expression of a character and the adequacy of additive-dominance model alone is not sufficient (Shahid, 1996). In this situation, populations had to be advanced to next generations in order to arrive at the best suitable model of Mather and Jinks(1982).

Due to presence of epistatic interaction along with additive and dominance gene effects for these crosses as per six-parameter model,suggested thatdominance gene effect was significant for plant height, number of primarybranches, pods plant^{-1}, pod length, seed pod^{-1}, 100-seed weight and yield plant^{-1}(Table 2),the relative contribution of dominance gene effect was much higherthan additive gene effect indicating the prevalence of dominance gene effects for the inheritance of these characters(Ramya *et. al.,* 2012). Further, higher frequency of duplicate type of epistasis for each of

above traits further confirms the predominance of dominant gene effects for the expression of these traits. Similarly, the greater importance of dominance gene effects for the expression of most of the above traits was also reported previously by Hooda *et al.* (2003), Singh and Bajpai (2005), Kumar *et al.* (2009), Ajay *et al.* (2012).Moreover, Bahar × BWR-23 and MAL-18 × BWR-133 was found high additive gene effect for plant height and secondary branches respectively, while in other crosses,plant height, pod plant^{-1} and secondary branches were found high additive as well as dominance gene effects, which is equally important for the inheritance of these traits.

In general, almost all the hybrids had positive dominance effect for yield plant^{-1}, 1000-seed weight, pods plant^{-1} and seed pod^{-1} and their magnitude was also higher than that of additive effect, suggesting greater importance of dominance effects in the expression of these characters. The significance of only duplicate type of epistasis for these characters further confirms the prevalence of dominance effects. However, the sign of dominance gene effects were almost positive indicating the enhancing effect for the expression of the traits in respective crosses.

Considering the contribution of epistatic gene effects over the crosses for a character, the magnitude of[$\hat{l}$] gene effects(considering value only) was comparatively higher than [$\hat{\imath}$] and [$\hat{\jmath}$] for plant height, number of primary and secondary branches, pods plant^{-1}, pod length andthe [$\hat{\imath}$] interaction had enhancing effect in the expression of yield plant^{-1}, 100-seed weight and seed pod^{-1}, also confirmed by Singh, (1980). But for seed pod^{-1}, [$\hat{\jmath}$] interaction had slightly greater effect as compared to [$\hat{\imath}$] and [$\hat{l}$]. Comparing the magnitude of the main gene actions ([$\hat{m}$] and [$\hat{d}$]) along with their digenic epistatic interactions ([$\hat{\imath}$], [$\hat{\jmath}$] and [$\hat{l}$]), the [$\hat{l}$] interaction was usually higher or at least at par with [$\hat{\imath}$] and [$\hat{\jmath}$] for all the characters. However, the sign of [$\hat{l}$] gene interaction was mostly positive, indicating their enhancing effect in the expression of almost all the characters. The gene interaction, [$\hat{\imath}$] or any digenic complementary gene interaction is fixable and thus can be exploited effectively.

Scaling tests and Six generation model had 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, the traits that are controlled by additive[$\hat{d}$] and additive × additive [$\hat{\imath}$]gene effects (fixable) can be improved by mass selection in self-pollinated species and synthetic breeding in cross pollinated species, while heterosis breeding may be recommended for those under the control of dominance [$\hat{h}$]and dominance × dominance [$\hat{l}$](non-fixable) gene effects. But for exploiting all three types of gene effects, reciprocal recurrent selection breeding procedure seems to be the best available method, for isolating the desirable recombinants in advanced generations.

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Electronic Journal of Plant Breeding, 10 (3): 1240 - 1245(Sep 2019) DOI: 10.5958/0975-928X.2019.00157.1
ISSN 0975-928X

Table 1. Test of significance of A, B, C and D scales for ten characters in pigeonpea

CROSSES/PARAMETER	A	B	C	D
Plant Height				
1. MAL-18×BWR-133	-29.5**	-28.36**	87.73**	72.80**
2. Bahar × BSMR-846	35.13**	37.26**	2.26	-35.1**
3. ICP-2376×BSMR-846	6.00**	3.26	74.73**	32.73**
4.Bahar × BWR-23	-5.86**	-23.00**	-4.06	12.40**
5. MAL-18 ×BSMR-846	-27.0**	-15.73**	-72.6**	-14.9**
No. of primary branches				
1. MAL-18×BWR-133	-4.40**	-4.13**	-2.00**	3.26**
2. Bahar × BSMR-846	6.96**	1.56**	0.13	-4.20**
3. ICP-2376×BSMR-846	4.70**	4.66**	14.90**	2.76**
4.Bahar × BWR-23	-2.63**	-3.46**	0.30	3.20**
5. MAL-18 ×BSMR-846	1.60**	-4.73**	-6.53**	-1.70**
No. of secondary branches				
1. MAL-18×BWR-133	6.60**	-3.20**	9.00**	2.80**
2. Bahar × BSMR-846	8.53**	-3.23**	-9.90**	-7.60**
3. ICP-2376×BSMR-846	12.10**	8.46**	-12.4**	-16.5**
4.Bahar × BWR-23	-8.26**	-3.56**	-13.0**	-0.60**
5. MAL-18 ×BSMR-846	4.10**	-4.33**	-1.10**	-0.43**
Pod Per Plant				
1. MAL-18×BWR-133	11.00**	-47.80**	-127**	-45.2**
2. Bahar × BSMR-846	10.73**	24.50**	10.43**	-12.4**
3. ICP-2376×BSMR-846	-8.66**	115.50**	-5.43	-56.2**
4.Bahar × BWR-23	-15.3**	-14.63**	-1.50	14.20**
5. MAL-18 ×BSMR-846	6.33**	2.50	-69.6**	-39.2**
Pod length				
1. MAL-18×BWR-133	0.10	-0.43**	0.80**	0.56**
2. Bahar × BSMR-846	0.40**	0.03	-0.16**	-0.30**
3. ICP-2376×BSMR-846	-0.40**	0.23**	0.56**	0.36**
4.Bahar × BWR-23	1.20**	1.90**	1.56**	-0.76**
5. MAL-18 ×BSMR-846	-0.20**	-0.66**	0.53**	0.70**

***Significance at P=0.05, ** Significance at P=0.01**

CROSS/PARAMETER	A	B	C	D
Seeds Per Pod				
1. MAL-18×BWR-133	-0.50**	-0.43**	-0.66**	0.13**
2. Bahar × BSMR-846	1.06**	0.30**	-0.56**	-0.96**
3. ICP-2376× BSMR-846	-1.10**	1.30**	-2.00**	-1.10**
4.Bahar × BWR-23	0.66**	0.30**	-0.83**	-0.90**
5. MAL-18 × BSMR-846	0.30**	-0.10	-1.66**	-0.93**
Yield per plant				
1. MAL-18×BWR-133	-14.7**	-31.53**	-91.2**	-22.46**
2. Bahar × BSMR-846	6.46**	3.60**	-9.06**	-9.56**
3. ICP-2376× BSMR-846	-3.06	8.66**	-8.26**	-6..93**
4.Bahar × BWR-23	-12.6**	-9.2**	-12.9**	4.40**
5. MAL-18 × BSMR-846	-6.26**	1.63	-50.1**	-22.70**
100 SEED WEIGHT				
1. MAL-18×BWR-133	-1.96**	-2.00**	-8.96**	-2.50**
2. Bahar × BSMR-846	0.96**	1.20**	-4.03**	-3.10**
3. ICP-2376× BSMR-846	-2.30**	1.16**	-10.4**	-4.63**
4.Bahar × BWR-23	-1.23**	-0.90**	-6.86**	-2.36**
5. MAL-18 × BSMR-846	-1.26**	-1.03**	-1.36**	0.46**

Electronic Journal of Plant Breeding, 10 (3): 1240 - 1245(Sep 2019) DOI: 10.5958/0975-928X.2019.00157.1
ISSN 0975-928X

Table 2. Estimation of gene effects through generation mean analysis

CROSSES	$\hat{m}$	$\hat{d}$	$\hat{h}$	$\hat{i}$	$\hat{j}$	$\hat{l}$	Epistasis
			Plant Height				
1. MAL-18×BWR-133	174.90**	7.00**	-136.5**	145.60**	-0.56	203.46**	D
2. Bahar × BSMR-846	160.46**	-2.00	86.33**	70.13**	-1.06	-142.5**	D
3. ICP-2376×BSMR-846	166.36**	-10.0**	-52.83**	-65.46**	1.36	56.20**	D
4.Bahar × BWR-23	148.70**	15.00**	-14.23**	-24.80**	8.56**	53.66**	D
5. MAL-18 ×BSMR-846	143.53**	-4.00	44.50**	29.86**	-5.63**	12.86	_
No. of primary branches							
1. MAL-18×BWR-133	10.83**	0.13	-4.20**	-6.53**	-0.13	15.06**	D
2. Bahar × BSMR-846	9.40**	2.00**	10.06**	8.40**	2.70**	-16.93**	D
3. ICP-2376×BSMR-846	10.93**	-1.30**	-6.95**	-5.53**	0.01	-3.83**	C
4.Bahar × BWR-23	10.00**	-0.40	-3.85**	-6.40**	0.41**	12.50**	D
5. MAL-18 ×BSMR-846	9.50**	3.70**	6.13**	3.40**	3.16**	-0.26	_
No. of secondary branches							
1. MAL-18×BWR-133	14.00**	7.20**	-2.70**	-5.60**	4.90**	2.20**	D
2. Bahar × BSMR-846	8.40**	5.40**	14.65**	15.20**	5.88**	-20.50**	D
3. ICP-2376×BSMR-846	8.50**	4.90**	26.78**	33.00**	1.81**	-53.56**	D
4.Bahar × BWR-23	14.00**	-5.40**	8.28**	1.20**	-2.35**	10.63**	C
5. MAL-18 ×BSMR-846	14.23**	4.70**	5.65**	0.86	4.21**	-0.63	_
Pods per plant							
1. MAL-18×BWR-133	121.40**	42.00**	130.00**	90.40**	29.40**	-53.60**	D
2. Bahar × BSMR-846	124.13**	10.66**	31.75**	24.80**	-6.88**	-60.03**	D
3. ICP-2376×BSMR-846	127.26**	-47.3**	139.01**	112.26**	-62.1**	-219.1**	D
4.Bahar × BWR-23	137.26**	3.00	-17.68**	-28.40**	-0.31	58.30**	D
5. MAL-18 ×BSMR-846	126.73**	24.66**	120.158**	78.40**	1.91	-87.23**	D
			Pod length				
1. MAL-18×BWR-133	4.73**	0.30**	-0.60**	-1.13**	0.26**	1.46**	D
2. Bahar × BSMR-846	4.20**	0.30**	0.51**	0.60**	0.18**	-1.03**	D
3. ICP-2376×BSMR-846	4.23**	-0.30**	-0.91**	-0.73**	-0.31**	0.90**	D
4.Bahar × BWR-23	4.26**	0.10	1.38**	1.53**	-0.35**	-4.63**	D
5. MAL-18 ×BSMR-846	4.40**	0.30**	-1.33**	-1.40**	0.23**	2.26**	D
Seeds per pod							
1. MAL-18×BWR-133	3.06**	0.20**	-0.13	-0.26**	-0.03	1.20**	_
2. Bahar × BSMR-846	2.86**	0.30**	2.11**	1.93**	0.38**	-3.30**	D
3. ICP-2376×BSMR-846	2.80**	-1.10**	2.60**	2.20**	-1.20**	-2.40**	D
4.Bahar × BWR-23	2.70**	0.10	1.78**	1.80**	0.18**	-2.76**	D
5. MAL-18 ×BSMR-846	2.93**	0.40**	2.16**	1.86**	0.20**	-2.06**	D
Yield per plant							
1. MAL-18×BWR-133	32.36**	20.20**	65.81**	44.93**	8.41**	1.30	_
2. Bahar × BSMR-846	40.16**	3.43**	33.86**	19.13**	1.43	-29.2**	D
3. ICP-2376×BSMR-846	31.80**	-1.40	6.53**	13.86**	-5.86**	-19.5**	D
4.Bahar × BWR-23	35.73**	0.93	0.26**	-8.80**	-1.70	30.53**	C
5. MAL-18 ×BSMR-846	46.53**	7.76**	73.91**	45.40**	-3.95**	-40.8**	D
100- seed weight							
1. MAL-18×BWR-133	8.70**	1.10**	6.11**	5.00**	0.01	-1.03**	D
2. Bahar × BSMR-846	11.33**	-0.70**	7.18**	6.20**	-0.11	-8.36**	D
3. ICP-2376×BSMR-846	9.03**	-2.90**	10.00**	9.26**	-1.73**	-8.13**	D
4.Bahar × BWR-23	8.40**	1.36**	5.50**	4.73**	-0.16	-2.60**	D
5. MAL-18 ×BSMR-846	12.53**	-0.60**	0.91**	-0.93**	-0.11	3.23**	C

* = Significant at P = 0.05, ** = Significant at P = 0.01, D = Duplicate type of epistatic interaction, C = Complimentary type of epistatic interaction.