

Analysis of Gene Effects in Vegetable-Type Pigeon Pea under Foothill of Nagaland

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ABSTRACT: The experiment on Analysis of gene effects in vegetable-type pigeon pea under foothill of Nagaland was conducted at the farm of Department of Genetics and Plant Breeding, School of Agricultural Sciences and Rural Development, Medziphema Campus, Nagaland University. Twelve crosses were generated, using five parameter model (P1, P2, F1, F2 and F3) generation mean analysis was done to assess the gene effects and its interaction for yield component traits. Epistatic gene effects were also found important for almost all the characters in all the crosses. Two crosses namely, BRG-2 × BRG-1 and BRG-2 × BRG-3 recorded positive significant for all the components of gene effect ([m], [d], [h], [i] and [I]) for seed yield also hybrid B2-10 × values BRG-1 and BRG-2 × BRG-1 were found significant for all the components of gene effect for seed yield and all the yield traits whereas, cross, B2-10 × BRG-3, BRG-2 × BRG-3, BRG-2 × B1-169 -1 and B3-13 × BRG-1 recorded significant values for yield and seven yield attributing traits. Similarly, in crosses, B2-10 × B1-169 -1, B2-5-2-1 × BRG-1, B2-5-2-1 × B1-169 -1, B3-13 × BRG-3 and B2-5-2-1 × BRG-3 were found significance for all component of gene effects for some yield traits. Dominance (h) and dominance x dominance interaction effect followed by additive (d) and additive x additive interaction appears to play a significant role for the expression of yield per plant and its attributes. Breeding of pigeonpea is more challenging as compared to other food legumes; this may be attributed to various crop specific traits, and high sensitivity to changes in environment. Therefore, there is a need to identify the parents and the crosses that can be exploited for breeding program suitable for the agro climatic conditions of Nagaland.

Keywords: Pigeon pea, additive gene action, dominance gene action, additive x additive, dominance x dominance.

INTRODUCTION

Pigeonpea (*Cajanus cajan* (L.) Mills) is among the major grain legume crops of the world, in the tropical and subtropical regions. Primary centre of origin and diversification of pigeonpea is considered as India (Van der Maesen, 1990). The species is diploid ($2n=2x=22$). Pigeon peapods are consumed as green vegetable in many countries. Dry seeds are consumed as split dhal. Pigeonpea straws are palatable and green leaves can be used as fodder, it is also used as ration for milch cattle. Pigeonpea sticks are used for various purposes, such as thatch and basket making.

Pigeonpea plant is capable of fixing atmospheric nitrogen, being a leguminous and thereby capable of restoring lot of nitrogen in the soil. Pigeonpea is a well recognized as a valuable source of dietary proteins, in addition of its nutritional value, it also possesses unique property of biological nitrogen fixation, and soil fertility restoration, thereby improving soil physical properties because of its deep root system.

Breeding of pigeonpea is more challenging as compared to other food legumes; this may be attributed to various crop specific traits, and high sensitivity to changes in environment, in order to achieve further genetic improvement in yield, it is necessary to identify the parents and the crosses that can be exploited for systematic breeding programme. Knowledge of the different types of gene action for quantitatively inherited traits is important to decide on appropriate breeding methods that could be used in crop improvement. The genetic mechanism governing yields and their components is important, given that breeding for improved varieties takes place continuously and requires a great deal of knowledge. Therefore, there is a need for knowledge of genetic variations, levels of dominant and the significance of genetic effects to be understood as regards gene action. Hence the present investigation was conducted to study the pattern of inheritance and gene effects for different metric traits in number of pigeonpea crosses.

MATERIALS AND METHODS

The present investigation was undertaken to study the “Generation mean analysis in vegetable-type pigeonpea [(*Cajanus cajan* (L.) Millsp.)]”. In the foothills of Nagaland. The experimental study was performed on a farm under the auspices of the Department of Genetics and Plant Breeding, School of Agricultural Sciences and Rural Development, Nagaland University. Each of the P1 parent *viz.*, BRG-2, B3-13, B2-10 and B2-5-2-1 were crossed with each of parent P2 *viz.*, BRG-1, BRG-3 and B1-169-1 to generate F1 seed of 12 cross combinations. At the same time experimental materials of F2 generation already maintained and present were collected from AICRP for pigeonpea, Medziphema center, this F2 from the previous generation was raised to produce F3 population and some F2 were sun dried and stored and saved for next year.

An experimental materials composed of five populations, e.g. P1, P2, F1, F2 and F3 of 12 cross combinations *viz.*, BRG-2 × BRG-1, BRG-2 × BRG-3, BRG-2 × B1-169-1, B3-13 × BRG-1, B3-13 × BRG-3, B3-13 × B1-169-1, B2-10 × BRG-1, B2-10 × BRG-3, B2-10 × B1-169-1, B2-5-2-1 × BRG-1, B2-5-2-1 × BRG-3 and B2-5-2-1 × B1-169-1 was evaluated in a Randomized Block Design (RBD) with three replications to estimate the nature of gene action and its effects. As suggested by Mather (1949), a scaling test has been conducted. Using the C and D scaling test, proposed by Mather and Jinks (1971), it was possible to determine whether the simplest additive × dominance model is adequate. Following Hayman and Jinks (1958), estimates have been made of the genetics parameters.

RESULT AND DISCUSSION

Estimation of C and D scaling tests were significance for most of the crosses indicating the present of epistasis in twelve crosses for different characters. The D scaling test was non-significant in cross B2-10 × BRG-3 whereas both C and D scaling test were non-significant for crosses B2-5-2-1 × BRG-3 for days to 50% flowering. In plant height both C and D scales were non-significant in crosses B3-13 × BRG-3 followed by B3-13 × B1-169-1 which exhibited non-significant for D scaling test. For number of primary branches per plant B2-5-2-1 × B1-169-1 recorded non-significant for D scaling test. In case of number of secondary branches per plant D scaling tests were non-significant for the crosses B3-13 × B1-169-1. For days to pods initiation C scale was non-significant in the crosses B3-13 × BRG-3 and D scale were non-significant in the cross combination B3-13 × B1-169-1.

A. Days to 50 % flowering

Among major gene effects, additive gene effect exhibits maximum negative significant for day to 50% flowering in crosses *viz.*, BRG-2 × B1-169-1, B2-5-2-1 × BRG-3, B2-5-2-1 × B1-169-1 whereas the dominant gene effect exhibit maximum negative significant for the crosses B3-13 × BRG-1, B2-10 × BRG-3, B2-10 × B1-169-1, estimates of additive × additive gene effects indicate maximum negative significant for B3-13 × BRG1, B210-9 × BRG 1 and B210-9 × BRG 3.

The maximum negative significant dominance × dominance effects were shown for crosses of B2-5 -2-1 × BRG-1, B2-10 × BRG-1, and B1-169 × BRG1. The magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects in majority of the crosses and in case of non-allelic interaction the magnitude of dominance × dominance (l) effects were mostly positive and higher than additive × additive (i) interaction for the expression of this character. Similar result was also reported by Singh and Singh (2016).

B. Plant height at maturity

The maximum positive significant additive gene effects (d) for plant height are recorded in crosses B2-5-2-1 × B1-169-1, B3-13 × BRG-1 and B3-13 × B1-169-1, whereas cross combinations B2-5 -2-1 × BRG-1, B2-5-2-1 × BRG-3 and B3-13 × BRG-3, showed negative significant additive gene effects (d). Significant and negative dominant gene effects (h) was recorded in crosses B2-5-2-1 × BRG-1, B2-5-2-1 × BRG-3 and B2-5-2-1 × B1-169-1, dominance × dominance (l) effects was recorded in crosses B3-13 × BRG-1 and B3-13 × B1-169-1, positive and significant dominance × dominance (l) effects are recorded in crosses B2-5 -2-1 × BRG-1, B2-5-2-1 × BRG-3, B2-5-2-1 × B1-169-1, Positive and significant additive × additive (i) effects, was recorded in crosses B2-5-2-1 × BRG-1, B3-13 × BRG-1, B3-13 × B1-169-1, B2-10 × B1-169-1. The magnitude of dominance gene effect (h) was mostly negative and magnitude of dominant × dominant (l) gene effects was comparatively higher than additive × additive (i) gene effects for plant height. This is in conformity with the finding of Sarode *et al.* (2009); Singh and Singh (2016); Ashutosh *et al.* (2017).

C. Number of primary branches

Additive gene effect (d) recorded positive and significant for number of primary branches/plant in crosses B2-5 -2-1 × BRG-1, B2-5-2-1 × BRG-3, B2-5-2-1 × B1-169-1, whereas positive and significant dominant gene effects (h) are recorded in the crosses B2-5 -2-1 × BRG-1, B3-13 × BRG-1, B3-13 × BRG-3 and B2-10 × B1-169-1. estimates of additive × additive (i) gene effects were positive and significant for the crosses B2-5 -2-1 × BRG- 1, B3-13 × BRG-1 and B3-13 × BRG-3, whereas positive and significant dominance × dominance (l) effects are recorded in crosses B2-5-2-1 × BRG-3, B2-5-2-1 × B1-169-1 and B2-10 × BRG-1. Among the main effect, dominant (h) gene effects was mostly negatively significant in all the crosses and its magnitude was usually higher than that of additive (d) gene effects and in case of non-allelic interaction magnitude of dominance × dominance (l) gene effects was comparatively higher than additive × additive (i) gene effects. This is in conformity with the finding of Kadalkar (2006); Sarode *et al.* (2009); Nagarajan *et al.* (2022).

D. Number of secondary branches

In the case of the number of secondary branches, the additive gene effect (d) was found to be positive and significant for the number of secondary branches in the crosses B2-5 -2-1 × BRG-1, B2-5-2-1 × BRG-3, B2-10 × BRG-1, B2-10 × BRG-3, B2-10 × B1-169-1 and

BRG-2 x BRG-1 whereas positive and significant dominant gene effects (h) are recorded in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BI-169-1. Additive x additive (i) gene effects were positive and significant for the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas positive and significant dominance x dominance (l) effects are recorded in crosses B3-13 x BRG-1, B3-13 x B1-169-1 and BRG-2 x BRG-3. The estimates of additive (d) and dominant (h) gene effects were significant in eleven and nine crosses, respectively but the magnitude of dominant (h) gene effect was comparatively higher than additive (d) gene effect. Among the non-allelic interaction, the magnitude of dominance x dominance (l) gene effects was much higher than additive x additive (i) gene effects, but mostly negatively significant. This is in conformity with the finding of Ashutosh *et al.* (2017).

E. Days to pod initiation

Additive gene effect (d) recorded negative and significant for days to pods initiation in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x B1-169-1, BRG-2 x BRG-1, B2-10 x BRG-1 and BRG-2 x BI-169-1, whereas negative and significant dominant gene effect (h) are recorded in the crosses B2-5-2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3 and BRG-2 x BRG-3. Estimates of additive x additive (i) gene effects were negative and significant for the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-1, B2-10 x BRG-3, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas negative and significant dominance x dominance (l) effects are recorded in crosses BRG-2 x BRG-1 and BRG-2 x BI-169-1. Magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects in majority of the crosses and additive x additive (i) gene effects was observed to be highly significant in eleven crosses. This is in conformity with the finding of Singh *et al.* (2003); and the magnitude of dominance x dominance (l) gene interaction was mostly positive. Similar result was also reported by Ashutosh *et al.* (2017) and Rathore *et al.* (2019).

F. Number of pods per plant

Additive gene effect (d) recorded positive and significant for number of pods per plant in the crosses B2-5-2-1 x BRG-3, BRG-2 x BRG-1, B2-10 x B1-169-1, B3-13 x B1-169-1 and BRG-2 x BI-169-1, whereas positive and significant dominant gene effect (h) are recorded in the crosses BRG-2 x BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3, B2-10 x B1-169-1, B2-5-2-1 x BRG-1 and B2-5-2-1 x B1-169-1. Estimates of additive x additive (i) gene effects were positive and significant for the crosses B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x BRG-3, B3-13 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas positive and significant

dominance x dominance (l) effects are recorded in crosses B2-5 -2-1 x BRG-1, B2-10 x BRG-1 and BRG-2 x BRG-3. Magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects in majority of the crosses. Among epistatic interaction, additive x additive (i) gene effects were positively significant in ten crosses, and negatively significant in two crosses, and its magnitude was comparatively higher than dominance x dominance (l) gene effects. This is in conformity with the finding of Singh *et al.* (2003); Abou Sen (2020).

G. Pod length (cm)

In case of pods length additive gene effect (d) recorded positive and significant in the crosses B2-5-2-1 x B1-169-1, B3-13 x B1-169-1, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas positive significant dominant gene effect (h) are recorded in the crosses B2-5 -2-1 x BRG-1. Additive x additive (i) gene effects for pods length were positive and significant for the crosses B2-5 -2-1 x BRG-1, B2-10 x BRG-1, BRG-2 x BRG-1 and BRG-2 x BRG-3, whereas positive and significant dominance x dominance (l) effects are recorded in crosses BRG-2 x B1-169-1, BRG-2 x BRG-3, B2-10 x BRG-3, B2-10 x BRG-1, B2-10 x B1-169-1, BRG-2 x BRG-1 and B2-5-2-1 x BRG-3. Among the main gene effect, additive (d) and dominant (h) gene effects were significant in eleven crosses, respectively but the magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects and magnitude of dominance x dominance (l) effects was much higher than additive x additive (i) gene effects. Shinde *et al.* (2021) also reported the similar result.

H. 100-seed weight (g)

Additive gene effect (d) recorded positive and significant for 100-seed weight in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-1, B2-10 x BRG-3, BRG-2 x BRG-1 and B2-10 x B1-169-1, whereas positive and significant dominant gene effect (h) are recorded in the crosses B2-5 -2-1 x BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3, BRG-2 x BI-169-1 and BRG-2 x BRG-3. For 100-seed weight estimates of additive x additive (i) gene effects were positive and significant for the crosses B3-13 x BRG-1, B2-10 x BRG-3, B2-10 x BRG-1, BRG-2 x BRG-3, BRG-2 x BRG-1, B3-13 x BRG-3 and BRG-2 x BI-169-1, whereas positive and significant dominance x dominance (l) effects are recorded in crosses B2-5-2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B2-10 x BRG-1, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BI-169-1. Among the main gene effect, magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects and magnitude of dominance x dominance (l) effects was much higher than additive x additive (i) gene effects for the expression of this trait. Similar results were also reported by Nagarajan *et al.* (2022).

I. Seed yield per plant (g)

For seed yield per plant additive gene effect (d) recorded positive and significant for the crosses B2-5-2-1 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10

x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BRG-3, whereas positive dominance gene effect (h) are recorded in the crosses B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1. Estimates of additive x additive (i) gene effects were positive and significant for the crosses B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3, B2-10 x BRG-1, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BI-169-1 and BRG-2 x BRG-3, whereas positive and significant dominance x dominance (l) effects are recorded in crosses B2-5 -2-1 x BRG-1, B2-5-2-1x BRG-3, B2-5-2-1 x B1-169-1,

B3-13 x B1-169-1, B2-10 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BRG-1. Among the main gene effect, additive (d) and dominant (h) gene effects were significant in all the crosses, respectively but the magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects and Among the non-allelic interaction magnitude of dominance x dominance (l) gene effects was much higher than additive x additive (i) gene effects, indicating the prevalence of dominant component for the expression of this trait which is in conformity with Singh and Singh (2016) and Ashutosh *et al.* (2017).

Table 1: Scaling tests and estimates of gene effects over a period of days to 50% of flowering in crosses.

Sr. No.	Crosses	Scale		Gene effects					Type of epistasis
		C	D	Main effects			Interaction effects		
				(m)	(d)	(h)	(i)	(l)	
1.	B2-5 -2-1 x BRG-1	-26.67**	-11.00**	126.01**	7.21**	11.86**	18.12**	-11.34**	D
2.	B2-5-2-1 x BRG-3	0.87*	-0.77	132.43**	-10.58**	5.34	1.43	3.42	
3.	B2-5-2-1 x B1-169-1	-27.53**	-5.00**	126.65**	-2.13**	9.56**	6.23**	7.34**	C
4.	B3-13 x BRG-1	11.67**	10.00**	134.57**	-3.58**	-21.00**	-21.00**	31.45**	D
5.	B3-13 x BRG-3	-9.67**	-3.47**	126.12**	-0.76	6.43**	7.34**	-4.34	
6.	B3-13 x B1-169-1	13.81**	-3.53**	131.13**	4.67**	-2.75	-5.36**	-0.36	
7.	B2-10 x BRG-1	-45.23**	-7.53**	126.11**	2.94**	15.58**	-11.45**	-14.68**	D
8.	B2-10 X BRG-3	8.57**	4.33	124.76**	4.86**	-12.76**	-8.37**	19.12**	D
9.	B2-10 x B1-169-1	-25.33**	-8.33**	154.24**	-0.87**	-7.56**	6.17**	-11.25**	C
10.	BRG-2 x BRG-1	-25.03**	1.43*	120.25**	-1.55**	-6.43**	-2.87*	10.37**	D
11.	BRG-2 x BRG-3	26.53**	6.10**	122.24**	-0.87**	7.56**	-5.67**	-7.25**	D
12.	BRG-2 x BI-169-1	-3.63**	-19.77**	129.45**	-11.47**	-15.65**	14.43**	-12.68**	C

Table 2: Scale tests and estimates of gene effects on plant height in crosses.

Sr. No.	Crosses	Scale		Gene effects					Type of epistasis
		C	D	Main effects			Interaction effects		
				(m)	(d)	(h)	(i)	(l)	
1.	B2-5 -2-1 x BRG-1	-191.54**	-20.71**	182.76**	-16.76**	-62.09**	38.45**	83.34**	D
2.	B2-5-2-1 x BRG-3	67.39**	80.67**	214.67**	-25.31**	-31.74**	-12.76**	67.54**	D
3.	B2-5-2-1 x B1-169-1	23.22**	14.14**	215.76**	21.65**	-31.76**	-25.35**	30.64**	D
4.	B3-13 x BRG-1	-89.36**	-55.67**	191.64**	12.54**	24.86**	110.54**	-113.35**	D
5.	B3-13 x BRG-3	-2.39	1.74	205.65**	-14.03**	-19.61**	-7.32	8.06	
6.	B3-13 x B1-169-1	-32.56**	-1.98	211.71**	12.56**	38.12**	28.65**	-17.78**	D
7.	B2-10 x BRG-1	23.63**	28.65**	217.83**	-24.76**	-57.65**	-54.53**	68.65**	D
8.	B2-10 x BRG-3	49.19**	39.59**	216.45**	-22.43**	-73.54**	-79.56**	98.85**	D
9.	B2-10 x B1-169-1	31.35**	50.80**	224.76**	-24.54**	-105.67**	101.45**	256.47**	D
10.	BRG-2 x BRG-1	11.22*	29.25**	199.56**	23.45**	-57.34**	-56.63**	98.37**	D
11.	BRG-2 x BRG-3	-76.52**	-14.51**	183.65**	19.85**	-31.55*	-43.85**	131.45**	D
12.	BRG-2 x BI-169-1	85.73**	-15.71**	216.65**	22.54**	-73.32**	62.79**	158.8**	D

*Significant at 5% level of probability; **Significant at 1% level of probability; D = Duplicate type of interaction; C = Complementary type of interaction; (M) =mean; (d) = additive effect; (h) =dominance effects; (i) = additive x additive; (l) = dominance x dominance

Table 3: Scaling tests and estimates of gene effects on number of primary branches in crosses.

Sr. No.	Crosses	Scale		Gene effects					Type of epistasis
		C	D	Main effects			Interaction effects		
				(m)	(d)	(h)	(i)	(l)	
1.	B2-5 -2-1 x BRG-1	-27.34**	-8.30**	12.45**	12.49**	21.34**	14.37**	-2.79	
2.	B2-5-2-1 x BRG-3	16.28**	15.63**	19.57**	2.56**	-27.56**	-29.45**	22.56**	D
3.	B2-5-2-1 x B1-169-1	-6.57**	-0.34	19.37**	7.34**	-2.34*	0.25	5.21**	D
4.	B3-13 x BRG-1	-7.75**	-7.12	16.47**	5.47**	16.36**	12.47**	-19.74**	D
5.	B3-13 x BRG-3	-12.55**	5.66	18.34**	-6.36**	12.67**	14.81**	-16.48**	D
6.	B3-13 x B1-169-1	-6.85**	6.77**	19.25**	4.36**	-4.34**	-1.37	9.35**	D
7.	B2-10 x BRG-1	-10.67**	6.34**	20.45**	7.67**	-17.76**	16.85**	23.26**	D
8.	B2-10 x BRG-3	15.22**	6.84**	21.35**	-12.56**	-14.45**	-11.57**	13.01**	D
9.	B2-10 x B1-169-1	16.06**	-9.81**	17.64**	15.12**	21.45**	18.46**	-21.43**	D
10.	BRG-2 x BRG-1	-9.24**	-1.87**	17.98**	-10.35**	-17.45**	13.27**	19.26**	D
11.	BRG-2 x BRG-3	21.52**	8.16**	16.36**	11.36**	-18.45**	-17.43**	21.65**	D
12.	BRG-2 x BI-169-1	-13.21**	-11.28**	18.86**	5.57**	14.65*	19.68**	-12.27**	D

Table 4: Scaling tests and estimates of gene effects on number of secondary branches in crosses.

Sr. No.	Crosses	Scale		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1.	B2-5 -2-1 x BRG-1	-31.54**	-18.13**	15.45**	4.61**	21.53**	31.47**	-32.56**	D
2.	B2-5-2-1 x BRG-3	33.22**	3.67*	18.35**	3.76**	-0.65	-6.87*	-18.68**	
3.	B2-5-2-1 x B1-169-1	9.12**	-4.84**	13.37**	1.87	11.56**	9.34**	-27.68**	D
4.	B3-13 x BRG-1	-20.39**	-6.45**	14.26**	-7.45**	6.04	0.85	17.56**	
5.	B3-13 x BRG-3	-12.54**	-15.72**	16.66**	-6.65**	39.32**	31.64**	-57.84**	D
6.	B3-13 x B1-169-1	7.67**	1.22	20.23**	-6.13**	6.54	-8.54*	17.56**	
7.	B2-10 x BRG-1	-46.76**	-17.35**	20.75**	9.47**	45.68**	38.75**	-22.56**	D
8.	B2-10 x BRG-3	5.50**	6.31**	18.78**	8.62**	21.34**	13.86**	-30.57**	D
9.	B2-10 x B1-169-1	-92.84**	-7.32**	17.46**	5.36**	28.51**	14.82**	-19.48**	D
10.	BRG-2 x BRG-1	-25.87**	-11.64**	19.63**	15.86**	46.81**	36.65**	-21.45**	D
11.	BRG-2 x BRG-3	13.05**	4.45**	17.35**	-14.43**	-21.06**	17.94**	21.46**	D
12.	BRG-2 x B1-169-1	5.71**	-4.87**	15.63**	-6.52**	18.71**	10.46**	-26.86**	D

*Significant at 5% level of probability; **Significant at 1% level of probability; D = Duplicate type of interaction; C = Complementary type of interaction ; (M) =mean; (d) = additive effect; (h) =dominance effects; (i) = additive x additive ;; (l) = dominance x dominance

Table 5: Scaling tests and estimates of gene effects on days to pods initiation in crosses.

Sr. No.	Crosses	Scale		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1.	B2-5 -2-1 x BRG-1	-6.33**	4.67*	169.65**	-1.58**	-8.45	-7.34**	8.23	
2.	B2-5-2-1 x BRG-3	-3.33*	4.53*	178.24**	-2.45**	-17.45**	-6.45**	4.36	
3.	B2-5-2-1 x B1-169-1	-3.53**	-7.73**	171.34**	4.67**	-29.00**	26.47**	12.45**	D
4.	B3-13 x BRG-1	9.73**	5.45**	181.35**	5.86**	-23.50**	-17.46**	7.37**	D
5.	B3-13 x BRG-3	-1.67	-9.10**	194.34**	6.45**	14.83**	12.48**	1.34	
6.	B3-13 x B1-169-1	-11.47**	2.06	183.24**	-10.45**	-7.68**	-2.48	-0.86	
7.	B2-10 x BRG-1	-12.20**	-3.63**	167.47**	-11.67	-10.01**	-9.67**	18.34**	D
8.	B2-10 x BRG-3	-10.77**	-20.87**	184.36**	4.36**	-34.68**	-29.59**	31.37**	D
9.	B2-10 x B1-169-1	-4.30**	15.66**	196.88**	1.87**	6.45**	6.48**	-3.46	
10.	BRG-2 x BRG-1	-10.00**	6.07**	203.45**	-6.37**	9.34**	12.48**	-5.57**	D
11.	BRG-2 x BRG-3	-8.65**	-10.00**	183.47**	2.65**	-7.76**	-11.38**	12.56**	D
12.	BRG-2 x B1-169-1	-11.00**	8.08**	168.43**	-4.36**	11.34**	-6.47**	-8.57**	D

Table 6: Scaling tests and estimates of gene effects on number of pods per plant in crosses.

Sr. No.	Crosses	Scale		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1.	B2-5 -2-1 x BRG-1	-201.44**	35.47**	185.65*	-33.56**	24.67**	-65.47**	234.65**	C
2.	B2-5-2-1 x BRG-3	184.45**	33.51**	222.54**	142.46**	-50.86**	-62.86**	-133.68**	C
3.	B2-5-2-1 x B1-169-1	-273.54**	-129.75**	119.67**	-14.23	331.56**	258.57**	-245.87**	D
4.	B3-13 x BRG-1	-471.65**	-178.40**	116.46**	-23.86**	411.67**	257.74**	-238.64**	D
5.	B3-13 x BRG-3	-159.45**	-110.87**	178.87**	-24.76**	301.46**	221.85**	-285.79**	D
6.	B3-13 x B1-169-1	-34.19*	-79.76**	169.76**	75.87**	-333.76**	159.58**	-137.58**	D
7.	B2-10 x BRG-1	225.12**	-64.53**	161.84**	-141.45**	-314.82**	267.64**	286.67**	D
8.	B2-10 x BRG-3	231.77**	144.37**	207.85**	-143.75**	278.67**	285.76**	-271.47**	D
9.	B2-10 x B1-169-1	-262.85**	-118.09**	185.35**	10.58**	465.76**	234.97**	-182.69**	D
10.	BRG-2 x BRG-1	-292.07**	-89.28**	227.53**	150.76**	424.56**	556.67**	-231.81**	D
11.	BRG-2 x BRG-3	-249.98**	-112.77**	209.57**	-162.87**	-387.81**	313.65**	121.59**	D
12.	BRG-2 x B1-169-1	-84.79**	-37.24**	113.66**	45.98**	-127.84**	292.65**	-79.79**	D

*Significant at 5% level of probability; **Significant at 1% level of probability; D = Duplicate type of interaction; C = Complementary type of interaction ; (M) =mean; (d) = additive effect; (h) =dominance effects; (i) = additive x additive; (l) = dominance x dominance

Table 7: Scaling tests and estimates of gene effects on pods length (cm) in crosses.

Sr. No.	Crosses	Scale		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1.	B2-5 -2-1 x BRG-1	-1.05**	-1.54**	4.13**	-1.19**	2.69**	2.47**	-4.23**	D
2.	B2-5-2-1 x BRG-3	1.50**	1.62**	5.67**	-0.16	-2.85**	-3.08**	4.71**	D
3.	B2-5-2-1 x B1-169-1	0.02	0.44**	6.53**	0.43**	-0.56*	-0.65**	0.19	
4.	B3-13 x BRG-1	3.26**	1.39**	5.79**	-0.26**	-2.26**	-2.61**	-1.56**	D
5.	B3-13 x BRG-3	0.36	0.58**	5.06**	-0.43**	-0.89**	-0.91**	-1.68**	D
6.	B3-13 x B1-169-1	-1.26**	-0.60**	4.76**	0.46**	1.31	1.31	-0.51**	
7.	B2-10 x BRG-1	1.01**	1.75**	6.79**	-0.54**	-3.06**	3.21**	5.76**	D
8.	B2-10 x BRG-3	1.61**	1.73**	5.91**	-0.19**	-2.51**	-3.12**	4.69**	D
9.	B2-10 x B1-169-1	-0.74**	-0.56**	3.47**	0.11**	-0.57**	0.05	0.78**	D
10.	BRG-2 x BRG-1	-2.32**	-0.82**	4.52**	0.27**	-3.08**	4.54**	5.17**	D
11.	BRG-2 x BRG-3	-3.12**	-0.33*	6.47**	0.20**	-0.80**	0.58*	2.19**	D
12.	BRG-2 x B1-169-1	0.68**	0.62**	4.18**	0.31**	-1.35**	-1.31**	2.49**	D

Table 8: Scaling tests and estimates of gene effects on 100-seed weight in crosses.

Sr. No.	Crosses	Scale		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1.	B2-5 -2-1 x BRG-1	-6.76**	-4.97**	10.76**	0.76**	2.43**	-2.76**	3.89**	c
2.	B2-5-2-1 x BRG-3	7.31**	3.83**	11.36**	0.81**	-7.65**	-6.59**	7.15**	D
3.	B2-5-2-1 x B1-169-1	2.62**	1.28**	11.45**	-0.08	-2.08**	-2.18**	3.76**	D
4.	B3-13 x BRG-1	-4.69**	-1.79**	9.79**	0.86**	3.36**	3.46**	-2.51**	D
5.	B3-13 x BRG-3	1.81**	-0.89**	11.35**	-1.09**	1.29**	0.81**	-3.61**	D
6.	B3-13 X B1-169-1	1.54**	0.43**	11.51**	-0.28**	-0.88**	-1.08	0.81	
7.	B2-10 x BRG-1	-2.57**	-1.13**	11.64**	0.24**	-2.08**	2.02**	7.32**	D
8.	B2-10 x BRG-3	1.15**	1.38**	11.73**	1.27**	3.61**	2.61**	-6.18**	D
9.	B2-10 x B1-169-1	2.43**	0.55**	11.68**	0.72**	-0.57	-0.96**	1.64**	
10.	BRG-2 x BRG-1	1.85**	1.08**	11.72**	0.80**	-5.67**	3.08**	6.32**	D
11.	BRG-2 x BRG-3	3.49**	-1.31**	10.51**	-0.32**	2.14**	3.51**	-5.03**	D
12.	BRG-2 x B1-169-1	-3.69**	-0.42**	10.27**	-0.21**	0.86**	0.72**	2.25**	c

*Significant at 5% level of probability; **Significant at 1% level of probability; D = Duplicate type of interaction; C = Complementary type of interaction; (M) =mean; (d) = additive effect; (h) =dominance effects; (i) = additive x additive; (l) = dominance x dominance

Table 9: Scaling tests and estimates of gene effects on seed yield per plant in crosses.

Sr. No.	Crosses	Scale		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1.	B2-5 -2-1 x BRG-1	-75.62**	3.87*	27.81**	-3.91**	-51.43**	-5.91*	18.51**	D
2.	B2-5-2-1 x BRG-3	56.71**	15.85*	42.61**	39.46**	-33.12**	-29.08**	12.31**	D
3.	B2-5-2-1 x B1-169-1	-47.65**	-52.77**	29.76**	-17.87**	-44.52**	-25.17**	15.09**	D
4.	B3-13 x BRG-1	108.97**	-57.64**	18.46**	-20.12**	66.71**	34.61**	-20.65**	D
5.	B3-13 x BRG-3	-45.58**	-22.65**	34.85**	-6.43**	71.17**	32.71**	-40.78**	D
6.	B3-13 x B1-169-1	-88.83**	-8.98**	31.67**	-9.83**	-41.07**	-18.12**	24.41**	D
7.	B2-10 x BRG-1	-37.74**	-16.78**	32.91**	20.76**	69.83**	29.61**	33.87**	C
8.	B2-10 x BRG-3	66.83**	-19.63**	46.74**	17.34**	38.76**	38.67**	-46.62**	D
9.	B2-10 x B1-169-1	-65.64**	-7.72**	42.81**	1.08*	75.81**	15.06**	-34.67**	D
10.	BRG-2 x BRG-1	-69.91**	-15.91**	16.58**	9.79**	-29.73**	31.03**	81.56**	D
11.	BRG-2 x BRG-3	-49.39**	-5.00**	22.61**	4.20**	25.34**	10.63**	29.31**	C
12.	BRG-2 x B1-169-1	-30.63**	-12.09**	21.83**	-11.21**	34.81**	24.61**	-17.82**	D

*Significant at 5% level of probability; **Significant at 1% level of probability; D = Duplicate type of interaction; C = Complementary type of interaction (M) =mean; (d) = additive effect; (h) =dominance effects; (i) = additive x additive; (l) = dominance x dominance

CONCLUSIONS

The relative contribution and magnitude of dominant gene effect (h) and dominance x dominance (l) effect was much higher than additive gene effect (d) and additive x additive gene effect (i), indicating the prevalence of dominant gene effects (h) and dominance x dominance gene effect (l) in case of epistasis for the inheritance of yield and attributing characters.

In addition, the predominance of dominant gene effects, taking into account the main gene effects and their interactions, dominance gene effects and dominance x dominance gene effects appear to play a significant role in the expression of yield per plant and its characteristics, with a higher frequency of duplicate type of epistasis for most of the traits, including seed yield per plant. It's clear that the dominant gene effect is being controlled more closely by complex characters such as the yield of the seed and its attributing genes. Based on above findings, it may be suggested that in those crosses where additive and additive x additive gene effects were predominant, one should follow the pedigree or modified pedigree method of selection, whereas in those crosses where dominance and dominance x dominance gene effect were significant heterosis breeding would be effective. To exploit all types of gene effects, reciprocal recurrent selection could be the most effective breeding method

The overall results revealed that parent BRG-1, BRG-2 and BRG-3 was proved to be good combiner for seed yield per plant and its contributing traits. Based on all the components of gene effect for seed yield per plant and its component traits the hybrid BRG-2 x BRG-1 and BRG-2 x BRG-3 was found most promising. Therefore, it needs to be exploited in future breeding programme of pigeon pea in Nagaland.

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Conflict of Interest. None.

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