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ASSESSMENT OF GENE COMBINATION EFFECTS FOR YIELD RELATED TRAITS IN LONG DURATION PIGEONPEA (*CAJANUS CAJAN*L.MILL SP.)

Ashutosh[1], Anurag Tripathi[2*], Km Pratiksha[3], Monu Kumar[4], Sudhir Kumar Jha[5] and M.N. Singh[1]

[1]Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, BHU, Varanasi, U.P., India.
[2]Department of Genetics and Plant Breeding, J.V.College, BarautBaghpat. U.P., India.
[3]Department of Horticulture, School of Agricultural Sciences & Technology, BBAU, Lucknow, U.P., India.
[4]ICAR-Indian Agricultural Research Institute, Jharkhand, India.
[5]ICAR-Division of Plant Biotechnology, IIPR Kanpur, U.P., India.
***Corresponding author E-mail: anuragtripathi855@gmail.com**

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ABSTRACT

In this study, we examined the gene combination effects for eleven pigeonpea traits across four different crosses, focusing on six generations: P_1, P_2, F_1, F_2, B_1 and B_2. Using six parameter models, we observed epistasis interactions in all crosses and attributes, as determined by the significance of the scaling test(s). Our discoveries underscored the significance of both additive and dominant gene effects. Notably, dominant gene effects played a significantly larger role in traits such as plant height, pods plant^{-1} and seed yield plant^{-1}. Duplicate type epistasis was more frequent, indicating the prevalence of dominance gene effects in these traits, except for seed yield pod^{-1}. Interestingly, di-genic gene interaction was found to have a stronger influence on most traits compared to dominance. Based on our results, we recommend employing reciprocal recurrent selection strategies to create elite pigeonpea populations, enabling more effective selection processes.

Key words: Pigeonpea, additive, dominance, generation mean analysis (GMA) and scaling test.

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) holds significant agricultural importance in India, ranking second only to chickpea among pulse crops. India leads production at 77%, followed by Malawi (11%), Myanmar (8%), Kenya, and Tanzania (2% each). In India, it occupies 4.5 million hectares of land, with a productivity rate of 832 kg/ha and an annual yield of 3.68 million tons. According to the FAO's report (2023), India leads in pigeonpea cultivation, with an extensive area of 5.58 million hectares and a production of 4.29 million tons, accounting for nearly 80 percent of the total production and cultivation area of pigeonpea worldwide. Despite its versatility — the seeds provide 19–25% protein and can be consumed in various forms, and different parts of the plant are used for different purposes, such as premium feed and home fuel — pigeonpea's productivity has remained consistently low over the years. This stagnation is primarily due to several biological and environmental challenges, limiting its global productivity in comparison to cereals.

The limited progress in pigeonpea yield improvement can be attributed to a lack of adequate artificial selections. While the fallen plant leaves enrich the soil with essential nutrients, and the plant itself enhances soil quality through nitrogen fixation, pigeonpea yields have remained relatively stable, ranging from 2.0 to 3.5 tonnes per hectare annually for short and long-duration cultivars, respectively, as reported in various studies. Achieving higher yields requires strategic planning, including the development of appropriate plant types and improved harvest indices. To enhance pigeonpea production, it is essential to implement effective breeding programs that capitalize on the crop's genetic potential.

A comprehensive understanding of gene effects, including epistasis, is crucial for selection successful

Table 1: The lineage, geographical roots, and primary attributes of the different varieties/genotypes.

S. No.	Genotypes	Pedigree	Source	Characteristic features
1.	Bahar	Selection from Motihari district, Bihar, India	Dr RPCAU, TCA, Dholi, Bihar, India	Medium height, compact, yellow flower, purple pod containing medium brown seed, highly susceptible to wilt and resistant to all the variants of SMD
2.	IPA-204	Bahar × Ac-314- 314	IIPR, Kanpur	Semi-compact, yellow flower with red strips, indeterminate growth habit, Plants are tall (1.75–2.0m), Pods green with black stripes, Seeds medium bold (12 g/100 seeds) and light-brown in colour, resistant to wilt.
3.	BSMR-846	–	ARS, Badnapur, Maharastra	Semi-compact, yellow flower with red streaks, pod green with streaks, highlyresistance toWilt and S MV
4.	MAL-13 (Malaviya Chamatkar)	(MA-2 × MA-166) × Bahar	BHU, Varanasi, Uttar Pradesh	Spreading, light yellow flower, pod large green with purplish black streaks with constricted loculescontaining large brown seed (13g/100 seeds) and moderately resistant to Sterility Mosaic Virus, wilt and phytophthora blight.
5.	MA-6 (Malaviya Vikas)	MA-2 × Bahar	BHU, Varanasi, Uttar Pradesh	Semi-spreading, yellow flower, purple pod, highly resistant to Sterility Mosaic Virus, moderate resistant to wilt
6.	BDN-2029	–	ARS, Badnapur, Maharastra	Semi-compact, dark red flower, pod green with purplish streaks, highly resistant to wilt

breeding programs. Evaluating the performance of parents involved in crosses and potential of the crosses to be used either for heterosis exploitation or pedigree selection. Generation means analysis, estimating the primary gene actions, including additive (d) and dominance (h), as well as their interactions such as additive-additive (i), additive-dominance (j), and dominance-dominance (l), is a key focus, facilitates this evaluation process. In our current study, a six-parameter model was employed to investigate the genetic factors influencing yield and yield-related traits in four crosses, six distinct pigeonpea cultivars.

Materials and Methods

Plant materials

An extensive study was carried out at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, during the *Kharif*, 2015–2016 and 2016–17. Geographically, it is situated at 25.18^{0}N latitude and 83.03^{0}E longitudes in the North Gangetic plain in the eastern part of Uttar Pradesh. In the breeding program, four particular crossings were used: Bahar × IPA-204, Bahar × BSMR-846, MAL-13 × BSMR-846, and MA6 × BDN-2029 along with their parents received from AICRP on MULLaRP, were sown in crossing block during *Kharif*, 2015-16 to obtain B1 (F1× P1) and B2 (F1× P2). The F_1 were selfed to procure seed for F2 generation besides obtaining fresh crossed seed of each of four crosses. Half of the seed of each of six basic population of four crosses were grown into three sets during *Kharif*, 2016-17. The genotypes and varieties subjected to this study are outlined in Table 1, along with detailed information about their lineage, origin, and key characteristics.

For every one of the six unique and productive genotypes, these crosses produced six basic populations (P_1, P_2, F_1, F_2, B_1 and B_2). Many agricultural variables, including as days to 50% flowering, days to maturity, plant height, number of primary and secondary branches, pod length, number of seeds pod^{-1}, weight of 100 seeds, number of seeds plant^{-1}, and harvest index, were used to evaluate these populations.

The breeding process involved the use of "Compact Family Design" with two subsets labeled B_1 and B_2, each having three replicates. The design incorporated the parental lines (P_1 and P_2), their first-generation hybrids (F_1), second-generation hybrids (F_2), and backcross generations (B_1 and B_2). Parents and F1 have one row each, B1 and B2 of two rows and each F2 of five rows. Each plot spanned a length of 4 meters, with a spacing of 75 centimeters between rows and 25 centimeters within each row.

To ensure optimal crop quality, rigorous agronomic practices were adhered to throughout the experiment. Ten plants from each row (excluding border) randomly tagged and data were recorded for following 11 quantitative traits (Appendix- I).

Statistical analysis

For testing the suitability of the additive-dominance model (Deb and Khaleque 2009), the method for estimating the scaling test (A, B, C, and D) was carried out as suggested by Mather (1949) and Hayman and

APPENDIX I: Mean performances of various generations (progenies)

S. N.	Populations	Days to flowering	Days to Maturity	Plant height (cm)	No. of primary branches	No. of Secondary branches	Pod per plant	Pod length (cm)	Seed per pod	100-seed weight	Yield per plant (gm)	Harvest index (%)
Parent												
1	Bahar	138.4	243.17	140.2	12.93	6.23	111.67	4.67	3.59	12.73	28.42	20.47
2	IPA-204	147.8	249.27	204.2	13.93	4.2	133.33	4.55	3.24	12.94	34.89	19.21
3	BSMR-846	112.80	190.80	175.33	13.60	4.73	63.33	4.81	3.44	16.21	30.27	18.35
4	MAL-13	139.60	245.53	154.53	13.47	6.13	154.67	4.87	3.69	13.34	44.93	20.77
5	MA-6	146.77	255.60	165.87	15.07	4.07	147.00	4.35	3.40	12.30	34.53	16.03
6	BDN-2029	108.80	185.47	157.20	15.00	8.07	142.33	4.99	3.47	15.10	41.57	19.13
F_1												
1	Bahar× IPA-204	142.13	244.27	200.87	14.27	5.07	130.67	4.93	3.69	13.17	33.81	19.31
2	Bahar× BSMR-846	123.27	217.40	176.47	15.27	6.13	130.67	4.87	3.87	14.11	39.13	20.72
3	MAL-13 × BSMR-846	120.80	213.07	170.73	13.60	5.27	146.00	4.79	3.87	14.55	48.48	21.03
4	MA-6 × BDN-2029	128.00	227.93	159.93	14.07	4.60	121.33	4.79	3.60	13.47	43.67	19.53
F_2												
1	Bahar× IPA-204	133.93	226.00	192.07	15.07	5.73	144.00	4.28	3.15	12.28	39.70	14.50
2	Bahar× BSMR-846	119.40	232.67	170.13	13.67	5.13	102.33	4.57	3.16	11.95	45.16	19.03
3	MAL-13 × BSMR-846	124.47	230.07	182.7	13.00	4.93	106.67	4.49	3.08	13.42	38.13	17.81
4	MA-6 × BDN-2029	123.00	234.47	172.2	13.33	4.53	138.00	4.69	2.95	13.37	36.93	18.10
B_1												
1	(Bahar× IPA-204) ×Bahar	146.67	246.03	164.3	12.33	4.33	124.00	4.25	3.59	13.91	41.02	20.20
2	(Bahar× BSMR-846) ×Bahar	143.27	242.00	159.3	11.80	5.93	105.67	4.77	3.63	12.29	37.92	18.67
3	(MAL13×BSMR-846) ×MAL-13	138.20	256.20	161.0	11.73	5.07	132.00	4.82	3.18	14.39	41.37	18.42
4	(MA-6 × BDN-2029) × MA-6	139.00	248.93	161.0	12.80	3.47	117.67	4.05	3.16	13.47	31.47	19.97
B_2												
1	(Bahar× IPA-204) × IPA-204	142.93	255.80	204.7	14.13	6.13	140.00	4.27	3.03	13.59	43.78	17.97
2	(Bahar× BSMR-846) × BSMR-846	117.13	194.40	172.7	12.87	5.07	62.33	4.60	3.21	11.26	27.04	18.53
3	(MAL-13 × BSMR-846) ×BSMR - 846	103.60	192.60	171.7	13.07	6.60	80.00	4.52	3.00	14.73	33.63	17.60
4	(MA-6 × BDN-2029) × BDN-2029	117.60	205.93	155.0	13.80	3.87	122.00	4.22	3.27	14.47	33.93	18.07

Mather (1955), and data analysis was done using the six-parameter model of Hayman (1958) and Jink & Jones (1958).

Scaling Test

Analyzing predicted relationships between generation means, a process known as scaling, involves ensuring that gene effects are sufficient and that heritable components are independent of non-heritable ones. The first condition tests for the presence of gene interactions. Estimating additive and dominant components of variance usually assumes no gene-gene interaction, making the scale adequacy test crucial.

Scaling test which is suggested by Mather (1949) used to test dominance model's suitability. The procedure uses certain formulas for generation means (P_1, P_2, F_1, F_2, B_1, and B_2) and scales (A, B, C, D) for characters then Variance is calculated for sample means.

Various tests (A, B, C, D) detect particular interaction configurations that deviate from zero. The significance value of C+D indicated presence of both additive-additive (i) and dominance-dominance (l) types of gene interactions. The value of D test indicates presence of

Table 2: Test of significance of A, B, C and D scales for ten characters in pigeonpea.

Crosses / Parameter	A	B	C	D
DAYS TO 50% FLOWERING				
Bahar × IPA-204	12.80**	-4.07**	-34.73**	-21.73**
Bahar × BSMR-846	24.87**	-1.80**	-20.13**	-21.60**
MAL-13 × BSMR-846	16.00**	-23.07**	7.20**	7.13**
MA-6 × BDN-2029	3.23	-1.60	-19.57**	-10.60**
DAYS TO MATURITY				
Bahar × IPA-204	4.63**	18.07**	-76.97**	-49.83**
Bahar × BSMR-846	23.43**	-19.40**	61.90**	28.93**
MAL-13 × BSMR-846	53.80**	-12.13**	64.33**	11.33**
MA-6 × BDN-2029	14.33**	-1.53*	40.93**	14.07**
PLANT HEIGHT				
Bahar × IPA-204	-11.60**	3.87**	22.13**	14.93**
Bahar × BSMR-846	3.20*	-6.47**	12.07**	7.67**
MAL-13 × BSMR-846	-3.27*	1.60*	64.87**	33.27**
MA-6 × BDN-2029	-2.20**	-6.73**	45.87**	27.40**
PRIMARY BRANCH				
Bahar × IPA-204	-2.53**	0.07	4.87**	3.67**
Bahar × BSMR-846	-4.60**	-3.13**	-2.40**	2.67**
MAL-13 × BSMR-846	-3.60**	0.20	-1.00	1.20*
MA-6 × BDN-2029	-3.53**	-1.47**	-4.87**	0.07
SECONDARY BRANCH				
Bahar × IPA-204	-2.63**	3.00**	2.37*	1.00
Bahar × BSMR-846	-0.50	-0.73	-2.70**	-0.73**
MAL-13 × BSMR-846	-1.27*	3.27**	-1.60*	-1.80**
MA-6 × BDN-2029	-1.73**	-4.93**	-3.20**	1.73**
POD PER PLANT				
Bahar × IPA-204	5.67	16.00**	69.67**	24.00**
Bahar × BSMR-846	-31.00**	-69.33**	-27.00**	36.67**
MAL-13 × BSMR-846	-36.67**	-64.67**	-98.67**	1.33
MA-6 × BDN-2029	-33.00**	-19.67**	20.00**	36.33**
POD LENGTH				
Bahar × IPA-204	-1.10**	-0.94**	-1.95**	0.05
Bahar × BSMR-846	0.02	-0.48**	-0.95**	-0.24**
MAL-13 × BSMR-846	-0.02	0.15**	-0.58**	-0.35**
MA-6 × BDN-2029	-1.03**	-1.33**	-0.17*	1.10**
SEED PER POD				
Bahar × IPA-204	-0.10	-0.88**	-1.63**	-0.33**
Bahar × BSMR-846	-0.21	-0.88**	-2.13**	-0.52**
MAL-13 × BSMR-846	-1.20**	-0.69**	-1.93**	-0.02
MA-6 × BDN-2029	-0.68**	-0.53**	-2.28**	-0.53**
100 SEED WEIGHT				
Bahar × IPA-204	1.91**	1.07**	-2.89**	-2.93**
Bahar × BSMR-846	-2.25**	-7.80**	-9.37**	0.34**
MAL-13 × BSMR-846	0.90**	-1.00**	-4.70**	2.30**
MA-6 × BDN-2029	1.17**	0.37**	-0.87**	-1.20**
YIELD PER PLANT				
Bahar × IPA-204	11.80**	18.87**	19.87**	-5.40**
Bahar × BSMR-846	0.30	-15.27**	35.70**	25.33**
MAL-13 × BSMR-846	-10.98**	-12.08**	-20.52**	1.27
MA-6 × BDN-2029	-15.27**	-17.37**	-15.70**	8.47**
HARVEST INDEX				
Bahar × IPA-204	0.62**	-2.59**	-20.31**	-9.17**
Bahar × BSMR-846	-3.87**	-2.03**	-4.17**	0.87**
MAL-13 × BSMR-846	-4.95**	-13.05**	-18.82**	-0.41**
MA-6 × BDN-2029	4.37**	-2.53**	-1.83**	-1.83**

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

additive-additive types of gene interaction, whereas C value reveals that dominance-dominance types of gene interaction.

The six-parameter model (Hayman, 1958; Jink and Jones, 1958) was also used in the data analysis. This model requires at least six generations to estimate parameters [i], [j], and [l] based on the mean values of parents, F_1, F_2, B_1, and B_2 generations. The following equations are used in the model, which was presented by Hayman (1958) and Jink and Jones (1958), to estimate separate genetic components: When dominance and dominance × dominance effects have the same sign, they are complementary; different signs indicate duplicate epistasis (Kearsey and Pooni 1996).

Results and Discussion

The optimal breeding strategy must take into account the relative amount of each gene effect, including epistasis, when analyzing the cross combinations separately. Although linkage also influences the epistatic term in generation means, epistasis is predicted to favor dominance and additive gene effects (Hayman, 1958). Six parameter models give good estimates of the main gene effects and epistatic interactions for crossovers where scaling tests reveal epistasis. An attempt has been made to ascertain whether or not epistatic gene effects are present in the research data and, if so, what role they play in the transmission of these traits.

Four important crossings, taking scales (s), (A, B, C, and D), which indicated the presence of epistasis, demonstrated the insufficiency of the additive-dominance model for all attributes (Table 2). Estimates of dominance gene effects, additive effects, and epistatic interaction were derived using a six-parameter model suggested that additive gene effect was significantly positive for yield plant^{-1} in the cross MAL-13 × BSMR-846, for pod plant^{-1} in Bahar × BSMR-846 and MAL-13 × BSMR-846, respectively, for days to 50% flowering in MAL-13 × BSMR-846 and for days to maturity in MAL-13 × BSMR-846 and MA-6 × BDN-2029, respectively (Table 3). This clearly indicated that additive gene effects play significant contribution in the inheritance of these characters in the above respective crosses.

However, dominance gene effects were more prominent in influencing the inheritance of these traits, as evidenced by their greater impact on the days to 50% flowering, days to maturity, plant height, number of primary and secondary branches, pods plant^{-1}, pod length, seed pod^{-1}, 100-seed weight, yield plant^{-1} and harvest index (Ramya *et al.*, 2012). For the majority of these qualities, earlier research by Hooda *et al.*, (2003), Singh and Bajpai (2005), Kumar *et al.*, (2009), Ajay *et al.*, (2012) and Rathor *et al.*, (2019) also confirmed the importance of dominance gene effects for the expression of most of the above traits studied. On the other hand, notably it is found that both additive and dominant gene effects contributed nearly equally to the inheritance of days to 50% flowering, days to maturity, plant height, and pod plant^{-1}.

Dominant gene effects were stronger and more common in almost all of the hybrids compared to additive gene effects, indicating a higher significance of dominance effects in the expression of these traits. The significance of only duplicate type of epistasis for most of the characters further confirms the prevalence of dominance effects. The contribution of additive effect for these characters was not unidirectional and in most crosses, it had reducing (-) effect, whereas, in other increasing (+).

For the following epistatic gene effects: days to 50% flowering, days to maturity, plant height, number of primary and secondary branches, pods plant^{-1}, pod length,

Table 3: Estimation of gene effects through generation mean analysis.

CROSSES/PARAMETER	$\hat{m}$	$\hat{d}$	$\hat{h}$	$\hat{i}$	$\hat{j}$	$\hat{l}$	Epistasis
DAYS TO 50% FLOWERING							
Bahar× IPA-204	133.93**	3.73**	42.50**	43.47**	8.43**	-52.20**	D
Bahar× BSMR-846	119.40**	26.13**	40.87**	43.20**	13.33**	-66.27**	D
MAL-13 × BSMR-846	124.47**	34.60**	-18.00**	-14.27**	19.53**	21.33**	D
MA-6 × BDN-2029	123.00**	21.40**	21.42**	21.20**	2.42*	-22.83**	D
DAYS TO MATURITY							
Bahar× IPA-204	226.00**	-9.77**	97.72**	99.67**	-6.72**	-122.37**	D
Bahar× BSMR-846	232.67**	47.60**	-57.45**	-57.87**	21.42**	53.83**	D
MAL-13 × BSMR-846	230.07**	63.60**	-24.50**	-22.67**	32.97**	-19.00**	C
MA-6 × BDN-2029	234.47**	43.00**	-20.73**	-28.13**	7.93**	15.33**	D
PLANT HEIGHT							
Bahar× IPA-204	192.07**	-39.73**	-1.20	-29.87**	-7.73**	37.60**	_
Bahar× BSMR-846	170.13**	-12.73**	3.37	-15.33**	4.83**	18.60**	_
MAL-13 × BSMR-846	182.67**	-10.07**	-57.97**	-66.53**	-2.43*	68.20**	D
MA-6 × BDN-2029	172.20**	6.60**	-56.40**	-54.80**	2.27*	63.73**	D
PRIMARY BRANCHES							
Bahar× IPA-204	15.07**	-1.80**	-6.50**	-7.33**	-1.30	9.80**	D
Bahar× BSMR-846	13.67**	-1.07**	-3.33**	-5.33**	-0.73	13.07**	D
MAL-13 × BSMR-846	13.00**	-1.33**	-1.70	-2.40*	-1.90	5.80**	_
MA-6 × BDN-2029	13.33**	-1.00**	-1.10*	-0.13	-1.03	5.13**	D
SECONDARY BRANCHES							
Bahar× IPA-204	5.73**	-1.80**	-2.15*	-2.00	-2.82**	1.63	_
Bahar× BSMR-846	5.13**	0.87**	2.12**	1.47**	0.12	-0.23	_
MAL-13 × BSMR-846	4.93**	-1.53**	3.47**	3.60**	-2.27*	-5.60**	D
MA-6 × BDN-2029	4.53**	-0.40*	-4.93**	-3.47**	1.60	10.13**	D
POD PER PLANT							
Bahar× IPA-204	144.00**	-16.00**	-39.83**	-48.00**	-5.17**	26.33**	D
Bahar× BSMR-846	102.33**	43.33**	-30.17**	-73.33**	19.17**	173.67**	D
MAL-13 × BSMR-846	106.67**	52.00**	26.67**	-2.67	14.00**	104.00**	C
MA-6 × BDN-2029	138.00**	-4.33**	-96.00**	-72.67**	-6.67**	125.33**	D
POD LENGTH							
Bahar× IPA-204	4.28**	-0.02	0.23	-0.093	-0.08	2.13**	_
Bahar× BSMR-846	4.57**	0.17**	0.61**	0.48**	0.25	-0.01	_
MAL-13 × BSMR-846	4.49**	0.30**	1.00**	0.71**	-0.08	-0.83**	D
MA-6 × BDN-2029	4.69**	-0.17**	-2.08**	-2.20**	0.15	4.57**	D

Continue ...

SEED PER POD							
Bahar× IPA-204	3.15**	0.57**	0.93**	0.65**	0.39	0.33	_
Bahar× BSMR-846	3.16**	0.41**	1.39**	1.04**	0.34	0.05	_
MAL-13 × BSMR-846	3.08**	0.18**	0.65**	0.04	-0.26	1.85**	C
MA-6 × BDN-2029	2.95**	-0.11**	1.23**	1.07**	-0.07	0.15	_
100 SEED WEIGHT							
Bahar× IPA-204	12.28**	0.32**	6.20**	5.87**	0.42	-8.85**	D
Bahar× BSMR-846	11.95**	1.03**	-1.05**	-0.68**	2.77**	10.73**	D
MAL-13 × BSMR-846	13.40**	-0.30**	4.58**	4.60**	0.95	-4.50**	D
MA-6 × BDN-2029	13.37**	-1.00**	2.17**	2.40**	0.40	-3.93**	D
YIELD PER PLANT							
Bahar× IPA-204	39.70**	-2.76**	8.95**	10.80**	-3.53**	-41.47**	D
Bahar× BSMR-846	45.17**	10.87**	-44.88**	-50.67**	7.78**	65.63**	D
MAL-13 × BSMR-846	38.13**	7.73**	7.90**	-2.53	0.55	25.59**	C
MA-6 × BDN-2029	36.93**	-2.47**	-11.32**	-16.93**	1.05	49.57**	D
HARVEST INDEX							
Bahar× IPA-204	14.5**	2.23**	17.80**	18.33**	1.60	-16.35**	D
Bahar× BSMR-846	19.03**	0.13*	-0.42**	-1.73**	-0.92	7.64**	D
MAL-13 × BSMR-846	17.81**	0.82**	-2.16	0.81**	4.05**	17.19**	_
MA-6 × BDN-2029	18.10**	1.9**	5.62**	3.67**	3.45**	-5.50**	D

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

100-seed weight, yield plant^{-1}, and harvest index, the magnitude of dominance × dominance gene effects (ignoring the sign) were stronger than those of (i) and (j). However, for plant height, number of primary branches, pods plant^{-1}, and yield plant^{-1}, the sign of dominant × dominant gene effects were almost positive and indicating the enhancing effect for the expression of the traits in respective crosses. The dominance gene effect has a stronger effect on the transmission of quantitative traits like seed yield plant^{-1} followed by pods plant^{-1} were under greater control of dominance gene effect, which indicates that as the inheritance of quantitative characters becomes more complex, the contribution of dominance gene effect for their inheritance becomes greater (Parmar and Kathiria, 2016; Singh and Singh, 2016).

When comparing the strength of the digenic epistatic interactions ([i], [j], and [l]) with the major gene actions ([m] and [d]), it was found that for all characters, the (l) interaction was frequently higher or at least on par with (i) and (j). However, the majority of (l) gene interactions were positive, suggesting that they were becoming more and more important in influencing the expression of almost all the traits. However, gene interaction, (i) or any digenic complementary gene interaction is fixable and thus can be exploited effectively. This crop has also demonstrated evidence of dominant × dominant (Singh *et al.*, 2003), as well as additive × additive (Chandrashekhar *et al.*, 1998), and additive gene effect (Hooda *et al.*, 2000 and 2001) type interactions for the expression of most of the studied traits, in contrast to the previously mentioned finding. Duplicate epistasis is common for nearly all traits, indicating that this kind of epistasis has little effect on selection.

From the perusal of Table 4, it is interesting to note that three crosses (Bahar × IPA-204, Bahar × BSMR-846 and MA-6 × BDN-2029) scored significant values for all the components of gene effect ($[\hat{m}]$, $[\hat{d}]$, $[\hat{h}]$, $[\hat{i}]$, $[\hat{j}]$, and $[\hat{l}]$) for seed yield plant^{-1}, pods plant^{-1}, days to 50% flowering and days to maturity, besides 100-seed weight in cross, Bahar × BSMR-846 and plant height and harvest index in cross, MA-6 × BDN-2029. However, MAL-13 × BSMR-846 could be able to manage significant values to all the component of gene effects for days to 50% flowering, days to maturity, plant height, and

Table 4: Name of those crosses in pigeon pea showing significant values for all the six components of gene effects for yield and/or yield contributing traits.

S.	Crosses	Yield and/or yield components
1.	Bahar × IPA-204	Day to 50% plants flowering, days to plants maturity, pods per plantand **seed yields plant^{-1}**
2.	Bahar × BSMR-846	Days to 50% flowering, days to maturity, pods plant^{-1}, 100-seed weight and **seed yield plant^{-1}**
3.	MA-6 × BDN-2029	Days to 50% flowering, days to maturity, plant height, pods plant^{-1}, **seed yield plant^{-1}** and harvest index
4.	MAL-13 × BSMR-846	Days to 50% flowering, days to maturity, plant height, and secondary branches

secondary branches.

Furthermore, all forms of gene impacts for expressions of these qualities were shown for the days to 50% flowering and maturity, which had four crossings each; plant height, which had two crosses; number of secondary branches, which had one cross; pods, which had one cross; seed yield, which had three crosses; and harvest index, which had two crosses each. Given that both intra-allelic (dominance gene action) and inter-allelic (epistasis) interaction are involved in the inheritance of all the traits under investigation. In this instance, the traits that are controlled by additive and additive × additive gene effects (fixable) can be improved by pedigree method of selection, while heterosis breeding may be recommended for those under the control of dominance or dominance × dominance (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.

Conclusion

The inheritance of the considered traits involves both intra-allelic interactions (epistasis) and inter-allelic interactions (dominance gene action) as indicated by scaling tests and the six-generation model. In such cases, a selection method that initially benefits from additive gene effects is likely to yield gains in these traits. Recombination breeding can be employed in this scenario, with selection delayed until later generations. It is crucial to ensure that the effects of dominant genes are amplified rather than diminished. The reciprocal recurrent selection breeding procedure, which utilizes all three types of gene effects simultaneously, appears to be the best choice. This approach leads to the isolation of desirable recombinants in subsequent generations. Disparities between homozygote occur where the parental distribution of positive and negative alleles prevails, especially when additive variance is predominant. Breeding programs primarily focus on yield but depend on various other quantitative characteristics. Traits such as pods plant^{-1}, branches per plant, and plant height can be utilized in ongoing breeding efforts.

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