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Gene effects for yield contributing characters in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Abstract
Six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) derived from three crosses (BDN 708 X BSMR 571, BDN 708 X BDN 2010-1 and BDN 711 X SKNP 0632) between different parents (BDN 708, BSMR 571, BDN 2010-1, BDN 711 and SKNP 0632) along with check BDN 716. The material was evaluated during *Kharif* 2018 in randomized block design with randomization of generation replicated twice at Agricultural research station, Badnapur. The estimates of six parameters model revealed the significant contribution of both additive and dominance gene effects in most of the traits studied. Generally in the crosses, additive x additive (i) and dominance x dominance (l) type of gene action played an important role in the inheritance of the plant days to 50% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, number of pods per plant and 100-seed weight. However, dominance (h) type of gene action had major contribution in the inheritance of characters *viz.*, days to 50% flowering and days to maturity. All the characters under study except number of seeds per pod and seed yield per plant showed duplicate type of gene action for two or three crosses.

Keywords: Additive, dominance, generation means, pigeonpea.

Introduction
Pigeonpea (*Cajanus cajan* (L.) Millsp.) is the sixth most important grain legumes of tropics and subtropics. Pigeonpea [*Cajanus cajan* (L.) Millsp.] is an often cross pollinated crop (20 – 70%) with diploid (2n = 2x) chromosome number of 22. It is commonly known as tur, red gram or arhar. It belongs to family leguminosae, sub family papilionaceae. It is a short-lived perennial shrub in which plants may grow for about five years and turn into small trees. It is a hardy, widely adapted and drought tolerant crop with a large temporal variation (90–300 days) for maturity. These traits allow its cultivation in a range of environments and cropping systems. It is the most versatile food legume with diversified uses as food, feed, fodder and fuel. It is one of the important pulse crop of India and ranks second to chickpea in area and production. Invariably, the traditional pigeonpea cultivars and landraces are of long duration and grown as intercrop with other earlier maturing cereals and legumes. It is an important pulse mostly grown in Asia, Africa, Latin America and the Caribbean islands. Considering the vast natural genetic variability in local germplasm and presence of various wild relatives, India is considered as the primary centre of origin of pigeonpea. Pulses are also important for sustainable agriculture, enriching the soil through biological nitrogen fixation. They enrich the soil with nitrogen up to 20-40 kg N/ha and organic matter through leaf fall and profuse underground root growth. Its roots help in releasing soil-bound phosphorus to make it available for plant growth with so many benefits at low cost, pigeonpea has become an ideal crop for sustainable agriculture systems in rain-dependent areas. In India pigeonpea is grown on an area of 4.45 M. ha with average total production of 4.18 M. tones and productivity about 937 kg/ha during 2018-19. In Maharashtra during 2018-19 pigeonpea cover the area about 12.20 lakh ha with production about 10.56 lakh tones and productivity about 866 kg/ha (Anonymous, 2019). Major pigeonpea producing states are Maharashtra (27.56%, 25.33%), Karnataka (19.85%, 17.44%), Madhya Pradesh (14.51%, 20.07%), Andhra Pradesh (6.23%, 2.82%), Uttar Pradesh (6.32%, 7.25%) and Gujarat (6.08%, 7.68%) with area and production respectively. In pigeonpea Maharashtra is first in area (27.56%) and production (25.33%).
The choice of an appropriate selection/breeding method and its success for improvement of quantitative traits largely depends on the extent of genetic variability present in segregating material and gene action. Knowledge on genetic architecture of yield and related traits plays an important role in deciding breeding strategies and methodologies for crop improvement.

In comparison to other economically important crops, relatively less effort has been made to understand the genetics of important quantitative traits in pigeonpea. Pleiotropic effects of gene, physiological changes and highly sensitive nature of pigeonpea towards the environmental changes make it difficult to interpret the inheritance of yield and associated traits. There are different analysis methods to estimate genetic basis of quantitative variability of the selected plant characters. One of the best methods for the estimation of genetic parameters is the generation mean analysis, in which epistatic effects could also be estimated. Information about nature and magnitude of gene action can be useful for breeding program. Yield and its component characters that are quantitative in nature exhibit all the three types of gene action.

Materials and Methods

Six basic generations *viz.*, P_1, P_2, F_1, F_2, B_1 and B_2 derived from two crosses *viz.*, BDN 708 × BSMR 571, BDN 708 × BDN 2010-1 and BDN 711 × SKNP 0632 were produced and evaluated in a Compact Family Block Design with two replications during *Kharif* 2018 season at Agricultural Research Station, Badnapur. Each plot consisted of a two rows of parents, F_{1s}, BC_1 and BC_2 each and four rows of F_2 generation. Recommended package of practices were followed throughout the crop season. Data were recorded on five randomly selected plants from each generations excluding border plants. Each row was consisted of 3m length and row to row and plant to plant distance being 90 and 20 cm, respectively. All the 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 means, variance, variances of mean and standard errors of each of the six generations were estimated. Analysis of data was performed following six parameter model.

Result and Discussion

Scaling tests and joint scaling test were used to the test adequacy dominance model. Generation mean in crosses were calculated. The results of scaling tests in the three crosses for 10 characters are given in table 1.

Chi-square value for 10 characters are in all the crosses were calculated as per the method of joint scaling test. It was observed that chi-square values were significant for most of the characters in all the three crosses except for number of pods per plant, number of seeds per plant and seed yield per plant in the cross BDN 708 X BSMR 571, for plant height, number of secondary branches, number of pods per plant, seeds per pod, pod length, 100-seed weight and seed yield per plant in the cross BDN 708 X BDN 2010-1 and for number of secondary branches, seeds per pod, pod length and seed yield per plant in the cross BDN 711 X SKNP 0632.

The three crosses showed the A and D scaling tests were significant for days to 50% flowering, except B scaling test in the crosses BDN 708 X BSMR 571 and BDN 711 X SKNP 0632 and scaling test C in the crosses BDN 708 X BSMR 571 and BDN 708 X BDN 2010-1. Among the epistatic, additive x additive (i) and dominance (h) components were significant and positive in the crosses BDN 708 X BSMR 571 and BDN 711 X SKNP 0632, while it was significant and negative in the cross BDN 708 X BDN 2010-1. Additive x dominance (j) component was significant and positive in all the crosses while the component dominance x dominance (l) it was significant and positive in the cross BDN 708 X BDN 2010-1, while it was significant and negative in the crosses BDN 708 X BSMR 571 and BDN 711 X SKNP 0632. These results are in agreement with earlier results reported by Pandey and Singh (2002), Sarode *et al.* (2009a), Jahagirdar (2003), Shivani *et al.*(2013) and Ashutosh *et al.*(2017) [11].

All the crosses showed significant deviations from zero in A and D scaling tests for days to maturity.Among the epistatic, dominance (h) additive x additive (i) and additive x dominance (j) component was significant and positive in the crosses BDN 708 X BSMR 571 and BDN 711 X SKNP 0632, while it was significant and negative in the cross BDN 708 X BDN 2010-1. Dominance x Dominance (l) component were significant and positive in the cross BDN 708 X BDN 2010-1 while it was significant and negative in the crosses BDN 708 X BSMR 571 and BDN 711 X SKNP 0632. These results are in agreement with earlier results reported by Singh *et al.* (1983), Sarode *et al.* (2009a), Shivani *et al.* (2013) Pandey and Singh (2002) and Ashutosh *et al.* (2017) [11].

Scaling test B was significant in the cross BDN 711 X SKNP 0632 and scaling test C and D was significant in cross BDN 708 X BSMR 571 for plant height. Among the epistatic, additive x additive (i) and dominance (h) components were positive and significant in the cross BDN 708 X BSMR 571. dominance x dominance (l) component was significant and positive in the cross BDN 711 X SKNP 0632. These results are in agreement with earlier results in the crosses BDN 708 X BSMR 571 and BDN 711 X SKNP 0632 reported by Laxman and Pandey (1974), Mehetre *et al.* (1989), Sarode *et al.* (2009a), Shivani *et al.* (2013) and Pandey and Singh (2002).

Cross BDN 708 X BSMR 571 showed B scaling test significant, cross BDN 708 X BDN 2010-1 showed D scaling test significant and the cross BDN 711 X SKNP 0632 showed C and D scaling test as significant for number of primary branches per plant. Among the epistatic, component additive x additive (i) was significant and positive in the crosses BDN 708 x BDN 2010-1and BDN 711 X SKNP 0632, component dominance x dominance (l) was significant and negative in the crosses BDN 708 X BSMR 571 and BDN 708 x BDN 2010-1, while additive (d) and dominance (h) component were significant and positive in the cross BDN 708 x BDN 2010-1 and component additive x dominance (j) was significant and positive in the cross BDN 711 X SKNP 0632. These results are in agreement with earlier results reported by Sarode *et al.* (2009a), Shivani *et al.* (2013) and Vanniarajan *et al.* (1999).

The cross BDN 708 X BSMR 571 showed B and D scaling tests were significant for number of secondary branches per plant, indicating the presence of non-allelic interaction. The estimates of epistatic gene effects were also similar to the results observed in six parameter. These results are in agreement with earlier results in the cross BDN 708 X BSMR 571 reported by Sarode *et al.* (2009a), Pandey and Singh (2002), Shivani *et al.* (2013), Vanniarajan *et al.* (1999) and Ashutosh *et al.* (2017) [11].

The cross BDN 711 X SKNP 0632 showed that C and D scaling test was significant for number of pods per plant, indicating the presence of non-allelic interaction . Among the epistatic, dominance (h) and additive x additive (i) component were significant and negative in the cross BDN 711 X SKNP 0632. The components of three parameter model were not found significant in the crosses BDN 708 X BSMR 571 and BDN 708 X BDN 2010-1. These results are in agreement with earlier results in the cross BDN 711 X SKNP 0632 reported

by Patel *et al.* (1990) and Sarode *et al.* (2009a) and in the cross BDN-707 X BSMR 571 and BDN 708 X BDN 2010-1 reported by Samad *et al.* (2016) in chickpea.

The crosses did not show any significance in the four scaling tests and for chi square value (x^2) for number of seeds per pod. The component mean (m) of three parameter model was significant and positive in all the crosses. These results are in agreement with earlier results reported by Samad *et al.* (2016) in chickpea.

The cross BDN 708 X BSMR 571 showed A, C and D scaling test were significant for pod length. The crosses BDN 708 X BDN 2010-1 and BDN 711 X SKNP 0632 did not show significance to all the four scaling test and for the chi square value (x^2) as a result three parameter model was used to explain the genetic variability of this trait. These results are in agreement with earlier results in the cross BDN 708 X BSMR 571 reported by Patel *et al.*(1990), Vanniarajan *et al.* (1999), Sarode *et al.* (2009a) and Ashutosh *et al.* (2017) [11].

Scaling test A, C and D were significant in the cross BDN 711 X SKNP 0632 and scaling test A and D was significant in cross the BDN 708 X BSMR 571 for 100-seed weight. Among the epistatic, component additive x additive (i) was significant and negative in the cross BDN 708 X BSMR 571 and it was significant and positive in the cross BDN 711 X SKNP 0632, while the component dominance x dominance (l) was significant and positive in the cross BDN 708 X BSMR 571 was significant and negative in the cross BDN 711 X SKNP 0632 and component dominance (h) was found significant and positive in cross BDN 711 X SKNP 0632. These results are in agreement with earlier results in the crosses BDN 708 X BSMR 571 and BDN 708 X BSMR 571 reported by Singh *et al.* (1983), Patel *et al.* (1990), Vanniarajan *et al.* (1999), Shivani *et al.* (2013) and Ashutosh *et al.* (2017) [11].

The crosses did not show and any significance in the four scaling tests and for chi square value (x^2) for seed yield per plant. The component mean (m) of three parameter model was significant and positive in the crosses BDN 708 X BSMR 571 and BDN 711 X SKNP 0632. These results are in agreement with earlier results reported by Samad *et al.* (2016) in chickpea.

Conclusion

In most of the crosses, additive x additive (i) and dominance x dominance (l) type of gene action played an important role in the inheritance of the plant days to 50% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, number of pods per plant and 100-seed weight. However, dominance (h) type of gene action had major contribution in the inheritance of characters *viz.*, days to 50% flowering and days to maturity.

Table 1: Scaling tests for different characters in three crosses in pigeonpea (*Cajanus cajan* (L.) Millsp.).

Characters and cross	Scaling tests			
	A	B	C	D
1) Days to 50% flowering				
BDN 708 X BSMR 571	7.50±1.50**	-1.50±2.40	-4.00±2.53	-5.00±1.06**
BDN 708 X BDN 2010-1	-3.50±1.30*	-6.50±1.30**	-4.00±2.86	3.00±1.07**
BDN 711 X SKNP 0632	16.00±1.61**	-4.00±4.19	-7.00±2.75*	-9.50±2.15**
2) Days to maturity				
BDN 708 X BSMR 571	8.00±1.17**	-1.50±1.97	-2.50±1.89	-4.50±0.91**
BDN 708 X BDN 2010-1	-15.5±2.03**	-4.50±1.42**	5.00±4.21	12.50±1.94**
BDN 711 X SKNP 0632	11.50±2.45**	0.50±1.86	-17.00±1.90**	-14.50±1.34**
3)Plant height				
BDN 708 X BSMR 571	-9.30±7.34	7.10±6.97	-31.60±9.88**	-14.70±5.05**
BDN 708 X BDN 2010-1	-6.90±9.28	1.50±7.80	-25.50±13.4	-10.05±5.79
BDN 711 X SKNP 0632	-21.50±12.60	-24.90±9.48*	-16.30±14.83	15.05±7.80
4)No. primary branches				
BDN 708 X BSMR 571	1.60±1.66	3.80±1.36**	1.10±2.07	-2.15±1.11
BDN 708 X BDN 2010-1	3.00±1.48	1.20±0.39	-0.90±2.06	-2.55±1.05*
BDN 711 X SKNP 0632	3.70±2.01	-2.40±1.91	-4.90±2.13*	-3.10±1.41*
5) No. secondary branches				
BDN 708 X BSMR 571	4.70±2.99	8.50±3.00**	2.50±5.14	-5.35±2.64*
BDN 708 X BDN 2010-1	2.50±4.19	6.30±3.78	0.70±4.81	-4.05±3.05
BDN 711 X SKNP 0632	3.00±3.50	-3.20±3.22	-5.30±4.05	-2.55±2.43

* -Significant at 5% level of significance

**-Significant at 1% level of significance.

Table 1: Contd…

Characters and cross	Scaling tests			
	A	B	C	D
6)Number of pods/plant				
BDN 708 X BSMR 571	51.50±72.36	75.40±38.21	37.80±77.15	-44.55±41.80
BDN 708 X BDN 2010-1	33.30±52.52	92.10±86.95	20.90±64.92	-52.52±53.56
BDN 711 X SKNP 0632	36.20±69.33	-70.80±58.42	212.1±81.29*	123.3±52.26*
7)Number of seeds/pod				
BDN 708 X BSMR 571	-0.30±0.34	0.40±0.40	-0.80±0.46	-0.45±0.24
BDN 708 X BDN 2010-1	0.40±0.37	-0.30±0.28	0.10±0.46	----------
BDN 711 X SKNP 0632	0.10±0.39	0.50±0.36	0.30±0.44	-0.15±0.27
8)Pod length				
BDN 708 X BSMR 571	-0.51±0.21*	0.36±0.23	-1.01±0.30**	-0.43±0.17*
BDN 708 X BDN 2010-1	-0.08±0.24	-0.41±0.25	-0.40±0.38	0.04±0.18
BDN 711 X SKNP 0632	-0.05±0.30	0.08±0.30	-0.60±0.43	-0.31±0.21
9)100-seed weight				

BDN 708 X BSMR 571	-1.44±0.36**	-0.69±0.67	-0.32±0.52	0.90±0.39*
BDN 708 X BDN 2010-1	-0.22±0.45	0.23±0.39	-0.23±0.69	-0.12±0.32
BDN 711 X SKNP 0632	1.20±0.38**	-0.22±0.48	-2.95±0.53**	-1.96±0.32**
10)Seed yield/plant				
BDN 708 X BSMR 571	4.16±21.00	21.45±13.11	32.32±20.74	3.35±12.15
BDN 708 X BDN 2010-1	3.45±12.95	21.00±26.94	17.64±18.00	-3.45±15.58
BDN 711 X SKNP 0632	19.50±22.36	-25.05±21.87	44.13±25.46	24.84±15.53

* -Significant at 5% level of significance
**-Significant at 1% level of significance.

Table 2: Estimated of gene effects in 3 crosses in pigeonpea (*Cajanus cajan* (L.) Millsp.) for 10 characters.

Characters and cross	Parameters						Types of epistasis	X^2 value
	(m)	(d)	(h)	(i)	(j)	(l)		
1) Days to 50% flowering								
BDN 708 X BSMR 571	113.50±0.08**	2.00±1.05	8.00±2.47**	10.00±2.13**	4.50±1.15**	-16.00±4.92**	Duplicate	S
BDN 708 X BDN 2010-1	113.00±0.48**	1.00±0.47*	-6.00±2.38*	-6.00±2.14**	1.50±0.58*	16.00±3.42**	Duplicate	S
BDN 711 X SKNP 0632	111.00±0.32**	3.50±2.06	18.50±4.48**	19.00±4.31**	10.0±2.09**	-31.00±8.69**	Duplicate	S
2) Days to maturity								
BDN 708 X BSMR 571	162.50±0.08**	0.50±0.89	7.75±2.04**	9.00±1.82**	4.75±0.99**	-15.50±4.05**	Duplicate	S
BDN 708 X BDN 2010-1	161.50±0.88**	-0.50±0.83	-19.50±4.06**	-25.00±3.89**	-5.50±1.02**	45.00±5.37**	Duplicate	S
BDN 711 X SKNP 0632	158.00±0.16**	1.50±1.30	23.50±2.82**	29.00±2.68**	5.50±1.50**	-41.00±5.54**	Duplicate	S
3)Plant height								
BDN 708 X BSMR 571	129.30±1.53**	-3.10±4.01	47.80±10.82**	29.40±10.11**	-8.20±4.49	-27.20±18.84	Duplicate	S
BDN 708 X BDN 2010-1	116.3±11.85**	3.40±2.44	43.10±31.44	----------	----------	----------	----------	NS
BDN 711 X SKNP 0632	137.77±2.18**	3.50±6.46	-22.80±16.72	-30.10±15.61	1.70±6.83	76.50±29.82*	Duplicate	S
4)No. primary branches								
BDN 708 X BSMR 571	9.22±0.35**	-0.40±0.86	3.40±2.36	4.30±2.23	-1.1±0.99	-9.70±4.03*	Duplicate	S
BDN 708 X BDN 2010-1	9.72±0.32**	2.20±0.82*	7.40±2.25**	5.10±2.10*	0.90±0.87	-9.30±3.90*	Duplicate	S
BDN 711 X SKNP 0632	9.00±0.35**	-0.30±1.22	3.95±2.94	6.20±2.83*	3.05±1.32*	-7.50±5.33	Duplicate	S
5) No. secondary branches								
BDN 708 X BSMR 571	15.57±1.07**	-2.50±1.64	9.20±5.50	10.70±5.29*	-1.90±1.99	-23.90±8.36**	Duplicate	S
BDN 708 X BDN 2010-1	7.50±6.15	2.40±0.78**	27.90±16.81	----------	----------	----------	----------	NS
BDN 711 X SKNP 0632	13.40±4.95**	-1.20±0.94	8.20±13.62	----------	----------	----------	----------	NS

* -Significant at 5% level of significance
**-Significant at 1% level of significance.

Table 2: Contd…

Characters and cross	Parameters						Types of epistasis	X^2 value
	(m)	(d)	(h)	(i)	(j)	(l)		
6)Number of pods/plant								
BDN 708 X BSMR 571	115.55±85.52	20.05±17.96	288.45±230.84	----------	----------	----------	----------	NS
BDN 708 X BDN 2010-1	86.70±107.82	20.50±12.09	373.0±304.85	----------	----------	----------	----------	NS
BDN 711 X SKNP 0632	252.97±17.01**	27.20±39.67	- 304.60±106.87*	- 246.70±104.53*	53.50±45.19	281.30±178.30	Duplicate	S
7)Number of seeds/pod								
BDN 708 X BSMR 571	3.45±0.50**	-0.05±0.11	1.95±1.40	----------	----------	----------	----------	NS
BDN 708 X BDN 2010-1	4.15±0.50**	-0.05±0.08	0.25±1.34	----------	----------	----------	----------	NS
BDN 711 X SKNP 0632	4.00±0.55**	0.20±0.09	1.10±1.54	----------	----------	----------	----------	NS
8)Pod length								
BDN 708 X BSMR 571	5.13±0.05**	-0.39±0.13	0.83±0.35	0.86±0.34	-0.43±0.15	-0.71±0.61	Duplicate	S
BDN 708 X BDN 2010-1	5.43±0.37**	-0.15±0.05	-0.70±0.98	----------	----------	----------	----------	NS
BDN 711 X SKNP 0632	5.00±0.43**	-0.05±0.09	1.32±1.17	----------	----------	----------	----------	NS
9)100-seed weight								
BDN 708 X BSMR 571	9.52±0.08**	-0.42±0.35	-1.61±0.81	-1.08±0.79*	-0.37±0.36	3.94±1.51*	Duplicate	S
BDN 708 X BDN 2010-1	9.79±0.66**	-0.12±0.09	-0.54±1.70	----------	----------	----------	----------	NS
BDN 711 X SKNP 0632	9.49±0.09**	0.26±0.26	3.90±0.66**	3.93±0.63**	0.71±0.29*	-4.19±1.17**	Duplicate	S
10)Seed yield/plant								
BDN 708 X BSMR 571	65.40±24.89*	8.51±5.40	7.51±69.12	----------	----------	----------	----------	NS
BDN 708 X BDN 2010-1	53.53±31.42	2.52±3.94	39.38±89.47	----------	----------	----------	----------	NS
BDN 711 X SKNP 0632	120.50±32.18**	-13.56±8.39	-121.76±88.50	----------	----------	----------	----------	NS

* -Significant at 5% level of significance
**-Significant at 1% level of significance.

All the characters under study except number of seeds per pod and seed yield per plant showed duplicate type of gene action for two or three crosses as such, transgressive sergeants can be obtained in these characters. The cross BDN 711 X SKNP 0632 showed superior mean performance for seed yield per plant. However the cross BDN 711 X SKNP 0632 depicted

superior performance for maximum number of characters studied.

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