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Estimation of heterosis for yield and yield contributing characters in pigeonpea [*Cajanus cajan* (L.) millsp.]

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Abstract

Six generations (P₁, P₂, F₁, F₂, BC₁ and BC₂) 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 crosses BDN 708 X BSMR 571 and BDN 711 X SKNP 0632 were found superior for various traits. Magnitude of heterosis was calculated over better parent and standard check BDN 716 which revealed that crosses BDN 708 X BSMR 571, BDN 708 X BDN 2010-1 and BDN 711 X SKNP 0632 showed significant heterosis over better parent and standard check for various traits which were undertaken for study.

Keywords: Heterosis, inbreeding depression, seed yield, number of pods, 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., P₁, P₂, F₁, F₂, B₁ and B₂ 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, F₁s, BC₁ and BC₂ each and four rows of F₂ 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

The heterosis over better parent was in the range of -3.81 per cent (BDN 708 X BSMR 571) to 5.63 per cent (BDN 711 X SKNP 0632) and over standard check viz., BDN 716 it was in the range of 2.27 per cent (BDN 711 X SKNP 0632) to 3.81 per cent (BDN 708 X BSMR 571). The negative heterosis was considered as desirable for days to 50 per cent flowering.

The heterosis over better parent was significant and negative in only one cross BDN 708 X BSMR 571. These results are in agreement with earlier results reported by Reddy *et al.* (1979). The least inbreeding depression was recorded in the cross BDN 708 X BSMR 571 (0.00%). These results are in agreement with earlier results reported by Aher *et al.* (2006) [2].

The heterosis over better parent was in the range of -5.62 per cent (BDN 711 X SKNP 0632) to 0.30 per cent (BDN 708 X BDN 2010-1) and over standard check viz., BDN 716 it was in the range of 1.27 per cent (BDN 711 X SKNP 0632) to 3.49 per cent (BDN 708 X BDN 2010-1) for Days to Maturity. The heterosis over better parent 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 Reddy *et al.* (1979). The least inbreeding depression was recorded in the cross BDN 708 X BSMR 571 (0.00%). These results are in agreement with earlier results reported by Aher *et al.* (2006) [2].

The heterosis over better parent for Plant height was in the range of 3.51 per cent (BDN 708 X BDN 2010-1) to 9.99 per cent (BDN 708 X BSMR 571) and over standard check viz., BDN 716 it was in the range of 6.16 per cent (BDN 708 X BDN 2010-1) to 7.55 per cent (BDN 708 X BSMR 571). The heterosis over better parent was significant and positive in all the crosses. However the heterosis over the standard check BDN 716 was significant and positive in all the crosses. These results are in agreement with earlier results reported by Veeraswamy *et al.* (1973), Aher *et al.* (2006) [2], Gite *et al.* (2014) and Patil *et al.* (2014) for plant height. The least inbreeding depression was recorded in the cross BDN 711 X SKNP 0632 (5.31%). These results are in agreement with earlier results reported by Anantha and Muthian *et al.* (2008), Kumar and Krishna *et al.* (2008) and Ajay (2015) [3].

The heterosis over better parent for number of primary branches per plant was in the range of -38.09 per cent (BDN 711 X SKNP 0632) to 9.91 per cent (BDN 708 X BDN 2010-1) and over standard check viz., BDN 716 it was in the range of 0.03 per cent (BDN 708 X BSMR 571) to 25.59 per cent (BDN 708 X BDN 2010-1). The heterosis over better parent was significant and positive in the cross BDN 708 X BDN 2010-1 (9.91%).

Table 1: Heterosis and components of heterosis for different in crosses of pigeonpea (*Cajanus cajan* (L.) Millsp.).

Characters and cross	Per cent heterosis over		Inbreeding depression	Components of heterosis			
	BP	SC		(h)	(i)	(d)	(l)
1) Days to 50% flowering							
BDN 708 X BSMR 571	-3.81*	3.81*	0.00	8.00**	10.00**	2.00	-16.00**
BDN 708 X BDN 2010-1	-0.43	3.63*	0.88	-6.00*	-6.00**	1.00*	16.00*
BDN 711 X SKNP 0632	5.63**	2.27	1.33	18.5**	19.00**	3.50	-31.00**
2) Days to maturity							
BDN 708 X BSMR 571	-3.27*	3.17*	0.00	7.75**	9.00**	0.50	-15.50**
BDN 708 X BDN 2010-1	0.30	3.49*	0.92	-19.50**	-25.00**	-0.50	45.00**
BDN 711 X SKNP 0632	-5.621**	1.27	0.94	23.50**	29.00**	1.50	-41.00**
3) Plant height (cm)							
BDN 708 X BSMR 571	9.99**	7.55**	11.68**	47.80**	29.40**	-3.10	27.20
BDN 708 X BDN 2010-1	3.51*	6.16**	7.27**	43.10	-----	3.40	-----
BDN 711 X SKNP 0632	3.92*	6.74**	5.31**	-22.80	-30.10	3.50	76.50*
4) No. primary branches							
BDN 708 X BSMR 571	-15.84**	0.03	-8.53**	-0.40	4.30	0.70	-9.70*
BDN 708 X BDN 2010-1	9.91**	25.59**	12.39**	7.40**	5.10*	2.20*	-9.30*
BDN 711 X SKNP 0632	-38.09**	4.59**	1.10	3.95	6.20*	-0.30	-7.50*
5) No. secondary branches							
BDN 708 X BSMR 571	-12.88**	-14.45**	-9.68**	9.20	10.70*	-2.50	-23.90*
BDN 708 X BDN 2010-1	2.77*	11.45**	6.89**	27.90	-----	2.40**	-----

BDN 711 X SKNP 0632	-15.28**	0.60	2.55	8.20	-----	-1.20	-----
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Table 1: Contd...

Characters and cross	Per cent heterosis over		Inbreeding depression	Components of heterosis			
	BP	SC		(h)	(i)	(d)	(l)
6)Number of pods/plant							
BDN 708 X BSMR 571	-16.33**	-33.35**	-9.46**	288.45	-----	20.05	-----
BDN 708 X BDN 2010-1	8.55**	-18.53**	6.13**	373.00	-----	20.50	-----
BDN 711 X SKNP 0632	-32.99**	-39.33**	-47.94**	-304.60*	-246.70**	27.20	281.30
7)Number of seeds/pod							
BDN 708 X BSMR 571	0.00	4.761**	5.11**	1.95	-----	-0.05	-----
BDN 708 X BDN 2010-1	2.38	2.38	1.16	0.25	-----	-0.05	-----
BDN 711 X SKNP 0632	-6.66**	0.00	-2.98*	1.10	-----	0.20	-----
8)Pod length							
BDN 708 X BSMR 571	-1.28	3.07*	4.47**	0.83	0.86	-0.39	-0.71
BDN 708 X BDN 2010-1	-2.74*	1.92	1.55	-0.07	-----	-0.15	-----
BDN 711 X SKNP 0632	-0.35	8.83**	2.95*	1.32	-----	-0.05	-----
9)100-seed weight							
BDN 708 X BSMR 571	1.45	-12.54**	1.84	-1.16	-1.80*	-0.42	-3.94*
BDN 708 X BDN 2010-1	-11.37**	-18.89**	-5.10**	-0.54	-----	-0.12	-----
BDN 711 X SKNP 0632	-4.54**	-7.97**	7.07**	3.90**	3.93**	0.26	-4.19*
10)Seed yield/plant							
BDN 708 X BSMR 571	-19.62**	-42.59**	-19.29**	7.51	-----	8.51	-----
BDN 708 X BDN 2010-1	-1.93	-34.48**	-6.09**	39.38	-----	2.52	-----
BDN 711 X SKNP 0632	-36.04**	-42.64**	-36.06**	-121.76	-----	-13.56	-----

* -Significant at 5% level of significance

SC = Standard check BDN-716

** -Significant at 1% level of significance

However the heterosis over standard check BDN 716 was significant and positive in the crosses BDN 708 X BDN 2010-1 (25.59%) and BDN 711 X SKNP 0632 (4.59%). These results are in agreement with earlier results reported by Pandey and Singh *et al.* (2002), Pandey *et al.* (2004) and Aher *et al.* (2006) [2]. The least inbreeding depression was recorded in the cross BDN 708 X BSMR 571 (-8.53%). These results are in agreement with earlier results reported by Aher *et al.* (2006) [2], Anantha and Muthian *et al.* (2008), Kumar and Krishna (2008) and Ajay (2015) [3].

The heterosis over better parent for secondary branches per plant was in the range of -15.28 per cent (BDN 711 X SKNP 0632) to 2.77 per cent (BDN 708 X BDN 2010-1) and over standard check *viz.*, BDN 716 it was in the range of -14.45 per cent (BDN 708 X BSMR 571) to 11.45 per cent (BDN 708 X BDN 2010-1). The heterosis over better parent was significant and positive in the crosses BDN 708 X BDN 2010-1 (2.77%). These results are in agreement with earlier results reported by Pandey and Singh (2002), Aher *et al.* (2006) [2], Gite *et al.* (2014) and Patil *et al.* (2014). The least inbreeding depression was recorded in the cross BDN 708 X BSMR 571 (-9.68%). These results are in agreement with earlier results reported by Anantha and Muthian *et al.* (2008), Kumar and Krishna (2008) and Ajay (2015) [3].

The heterosis over better parent for number of pods per plant was in the range of -32.99 per cent (BDN 711 X SKNP 0632) to 8.55 per cent (BDN 708 X BDN 2010-1) and over standard check *viz.*, BDN 716 it was in the range of -39.33 per cent (BDN 711 X SKNP 0632) to -18.53 per cent (BDN 708 X BDN 2010-1). The heterosis over better parent was significant and positive in the cross BDN 708 X BDN 2010-1 (8.55%), while it was significant and negative in the crosses BDN 708 X BSMR 571 (-16.33%) and BDN 711 X SKNP 0632 (-32.99%). These results are in agreement with earlier results reported by Hooda *et al.* (1999) [8], Aher *et al.* (2006) [2], Acharya *et al.* (2009) [1], Sarode *et al.* (2009) [10], Gite *et al.* (2014) and Patil *et al.* (2014).

The heterosis over better parent for number of seeds per pod was in the range of -6.66 per cent (BDN 711 X SKNP 0632)

to 2.38 per cent (BDN 708 X BDN 2010-1) and over standard check *viz.*, BDN 716 it was in the range of 0.00 per cent (BDN 711 X SKNP 0632) to 4.76 per cent (BDN 708 X BSMR 571). The heterosis over better parent was significant and negative in only one cross BDN 711 X SKNP 0632 (-6.66%). The heterosis over standard check BDN 716 was significant and positive in only one cross BDN 708 X BSMR 571 (4.76%). These results are in agreement with earlier results reported by Aher *et al.* (2006) [2] and Patil *et al.* (2014). The least inbreeding depression was recorded in the cross BDN 708 X BDN 2010-1 (1.16%). These results are in agreement with earlier results reported by Anantha and Muthian (2008), Kumar and Krishna (2008) and Valarmathi *et al.* (1998).

The heterosis over better parent for pod length was in the range of -2.74 per cent (BDN 708 X BDN 2010-1) to -0.35 per cent (BDN 711 X SKNP 0632) and over standard check *viz.*, BDN 716 it was in the range of 1.92 per cent (BDN 708 X BDN 2010-1) to 8.83 per cent (BDN 711 X SKNP 0632). The heterosis over better parent was significant and negative in only one cross BDN 708 X BDN 2010-1 (-2.74%). The heterosis over standard check BDN 716 was significant and positive in the crosses BDN 708 X BSMR 571 (3.07%) and BDN 711 X SKNP 0632 (8.83%). These results are in agreement with earlier results reported by Patel *et al.* (2013) and Patil *et al.* (2014). The least inbreeding depression was recorded in the cross BDN 708 X BDN 2010-1 (1.55%). These results are in agreement with earlier results reported by Gumber and Singh (1996) [7] and Kumar *et al.* (2002).

The heterosis over better parent for 100-seed weight was in the range of -11.37 per cent (BDN 708 X BDN 2010-1) to 1.45 per cent (BDN 708 X BSMR 571) and over standard check *viz.*, BDN 716 it was in the range of -18.89 per cent (BDN 708 X BDN 2010-1) to -7.97 per cent (BDN 711 X SKNP 0632). The heterosis over better parent was significant and negative in the crosses BDN 708 X BDN 2010-1 (-11.37%) and BDN 711 X SKNP 0632 (-4.54%). These results are in agreement with earlier results reported by Acharya *et al.* (2009) [1], Gite *et al.* (2014), Patel *et al.* (2013) and Patil *et al.*

al. (2014). The least inbreeding depression was recorded in the cross BDN 708 X BDN 2010-1 (-5.10%). These results are in agreement with earlier results reported by Anantha and Muthian *et al.* (2008), Kumar and Krishna *et al.* (2008) and Valarmathi *et al.* (1996).

The heterosis over better parent for seed yield per plant was in the range of -36.04 per cent (BDN 711 X SKNP 0632) to -1.93 per cent (BDN 708 X BDN 2010-1) and over standard check *viz.*, BDN 716 it was in the range of -42.64 per cent (BDN 711 X SKNP 0632) to -34.48 per cent (BDN 708 X BDN 2010-1). The heterosis over better parent was significant and negative in the crosses BDN 708 X BSMR 571 (-19.62%) and BDN 711 X SKNP 0632 (-36.04%). These results are in agreement with earlier results reported by Hooda *et al.* (1999)^[8], Pandey and Singh (2002), Pandey (2004), Aher *et al.* (2006)^[2], Acharya *et al.* (2009)^[1], Sarode *et al.* (2009)^[10], Gedam *et al.* (2013) and Patil *et al.* (2014). The least inbreeding depression was recorded in the cross BDN 711 X SKNP 0632 (-36.06%). These results are in agreement with earlier results reported by Gumber and Singh (1996)^[7] and Kumar *et al.* (2002).

Conclusion

The cross BDN 708 X BDN 2010-1 had recorded the highest desirable better parent, standard heterosis over check *viz.*, BDN 716 for major yield contributing characters *viz.*, number of primary branches, number of secondary branches, number of pods per plant and number of seeds per pod. The cross BDN 708 X BDN 2010-1 also showed the dominance (h) and dominance x dominance (l) type of gene action for most of the characters, hence heterosis breeding may be suggested for the genetic improvement of pigeonpea crop. The cross *viz.*, BDN 708 X BSMR 571 had recorded least inbreeding for days to 50 per cent flowering, days to maturity, number of primary branches and number of secondary branches and while the cross *viz.*, BDN 708 X BDN 2010-1 for pod length and 100-seed weight. The cross *viz.*, BDN 711 X SKNP 0632 had recorded least inbreeding depression for plant height, number of pods per plant, number of seeds per pod and seed yield per plant.

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