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Genetic Analysis of Seed Yield and Quantitative Traits in Pigeonpea

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ABSTRACT

Success of breeding programme depends upon the nature of gene action involved in controlling the traits. Hence, the present study was conducted using six generations (P1, P2, F1, F2, B1 and B2) of the crosses T 15-15 × BSMR 853, AVPP 1 × LRG 41, AGT 2 × ICP 8863 and GT 101 × ICPL 84060 of pigeonpea to know significance of additive-dominance model, nature of gene action, heterosis and inbreeding depression. The individual scaling test and χ2 value of joint scaling test was significant with all the crosses for most of the quantitative traits. Non-additive gene action was important for seed yield per plant while additive and non-additive effects were found to be more pronounced for yield contributing traits. Dominace x dominance inter-allelic interaction (l) was more important than additive x additive (i) for the traits days to 50 per cent flowering, days to maturity, plant height, primary branches per plant, pods per cluster and harvest index in most of the crosses. Therefore, reciprocal recurrent selection or heterosis breeding was suggested to improve the seed yield in pigeonpea. Complementary gene action was present in most of the traits with few exhibiting duplicate gene action.The cross GT 101 x ICPL 84060 depicted significant and beneficial heterotic effects for seed yield. The estimates of inbreeding depression were noticed significant and in desired direction for the traits plant height, pods per plant, pod length, 100 seed weight and harvest index.

KEYWORDS : Additive (d), dominant (h), additive x additive(i), additive x dominance (j) and dominance x dominance (l), Gene action, heterosis, six parameter model, duplicate epistatis, complementary epistasis

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is a cross pollinated (20-70%), short lived perennial shrub cultivated as an annual crop in developing countries. Pigeonpea is one of the most important grain legumes in the world and second most important pulse crop after chickpea in India, which is grown in the Indian subcontinent accounting for the 90% of the world's crop with 40 lakh hectare area, an annual production of around 26.54 lakh tons and productivity of 760 kg/ha (Anon, 2013). In Gujarat, total area under pigeonpea cultivation was 2.65 lakh hectares with an annual production of 2.94 lakh tons and productivity of 1109 kg/ha (Anon, 2011).

Plant breeders identify superior genotypes and develop new cultivars by selecting plants possessing desirable phenotypes derived from genetic recombination. While dealing with characters of major agronomic importance, successful identification of genotypes based on their phenotypes requires an understanding of how do genes act and interact to control complex characters, what kind of gene action do breeding systems exploit and what conditions optimize heritability.

The knowledge of nature of gene action governing the expression of various traits could be helpful for making an effective and sound breeding programme; whereas, the knowledge of heritability of any character is necessary to determine the extent to which it can be transmitted from parent to off-springs, and can be improved through selection. Further, the response of selection is determined by the types of generation involved in expression of a trait. The partitioning of means into different components is a simple procedure and it yields excellent degree of statistical precision. Hayman and Mather (1955) introduced individual scaling tests A, B, C and D for different generations to detect epistasis. Hayman (1958) and Jinks and Jones (1958) proposed six parameter model for the estimation of additive, dominance and epistatic genetic effects. However, Cavalli (1952) suggested a procedure called joint scaling test which helps to test the adequacy of additive-dominance model from analysis of different generations. Highly reliable genetic information can be obtained from generation mean analysis, though it is rather difficult and time consuming.

Keeping above in view, the present study has been planned to estimate the nature and magnitude of gene actions, heritability and expected genetic advance for yield and its component traits involved in the inheritance of various characters under study.

Materials and methods

The six generations *viz*., P_1, P_2, F_1, F_2, B_1 and B_2 of four crosses *viz*., T 15-15 x BSMR 853, AVPP1 x LRG 41, AGT 2 x ICP 8863 and GT 101 x ICPL 84060 were developed at the Hill Millet Research Station, AAU, Dahod by hand crossing using standard technique during *kharif* 2011-12 and the same hybrids were selfed to obtain F_2 and backcrossed to obtain B_1 [F_1 x P_1] and B_2 [F_1 x P_2] generations. The six generations of each crosses were grown in the compact family block design with four replications. The experimental plot consisted of one row each of parents and F_1, two rows each of the B_1 and B_2 generations and four rows for F_2 generation. Each row consisted of 10 plants with row to row and plant to plant distance of 60 and 30 cm, respectively. Data for seed yield and its related thirteen component traits like days to 50 per cent flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, 100 seed weight and harvest index were recorded from five randomly tagged plants from P_1, P_2 and F_1; ten randomly tagged plants from each of B_1 and B_2 and twenty randomly tagged plants from F_2 generation and subjected for statistical analysis.

For all the characters under study, means of all six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of all four crosses were first subjected for simple scaling test A, B, C and D (Hayman and Mather, 1955). The results of simple scaling test were further confirmed byJoint Scaling Test (Cavalli, 1952), which effectively combines the whole set of simple scaling tests, and thus offers a more general convenient, adaptable and informative approach for estimating gene effects, and also for testing adequacy of additive-dominance model as well as three parameters model (Jinks and Jones, 1958). In those cases, where three parameter model did not fit to the data, then gene effects were calculated on the basis of six parameter model (Hayman, 1958). The significance of any one of these scales is taken to indicate the presence of non-allelic interaction. Generation mean analysis provides information about the types of epistasis, the cross which have opposite sign of components (h) and (l) reveals duplicate epistasis and similar sign of both the components reveals complementary epistasis (Singh and Narayanam, 2009).

RESULTS AND DISCUSSION

The analysis of variance between crosses revealed significant differences among different crosses for all the characters except primary

branches per plant, secondary branches per plant, pod length, seeds per pod and harvest index (Table 1). The analysis of variance among generations within family comparison of all the crosses exhibited significant differences for the traits days to 50 per cent flowering, plant height and seeds per pod. The generations differed significantly for the traits days to maturity in T 15-15 x BSMR 853, AVPP 1 x LRG 41 and GT 101 x ICPL 84060; primary branches per plant in AGT 2 x ICP 8863; clusters per plant in T 15-15 x BSMR 853, AVPP 1 x LRG 41 and AGT 2 x ICP 8863; pods per cluster in AVPP 1 x LRG 41 and AGT 2 x ICP 8863; pods per plant in T 15-15 x BSMR 853 and AVPP 1 x LRG 41; pod length in T 15-15 x BSMR 853 and GT 101 x ICPL 84060; 100 seed weight in T 15-15 x BSMR 853 and AVPP 1 x LRG 41; seed yield per plant in GT 101 x ICPL 84060; and harvest index in AVPP 1 x LRG 41 and AGT 2 x ICP 8863. Thus, the data for different characters showing significant variation among the generations in respective crosses were subjected to genetic analysis of generation mean and analysis of heterosis and inbreeding depression.

SCALING TESTS AND ESTIMATION OF GENE EFFECTS

Results of individual scaling test (A, B, C, and D) and χ^2 value of joint scaling test were significant in all the crosses for all the characters except days to 50 per cent flowering (T 15-15 x BSMR 853), clusters per plant (AVPP 1 x LRG 41 and AGT 2 x ICP 8863) and 100 seed weight (AVPP 1 x LRG 41) and seed yield per plant (GT 101 x ICPL 84060) indicating inadequacy of additive dominance model and possibility for presence of non-allelic interaction for these traits (Table 2). Similar result was reported by Ajay (2012). In such cases, populations have to be forwarded to next generations in order to arrive at the best fit model (Mather and Jinks, 1982).

Nature of gene action for different traits among four crosses is presented in Table 2. For inheritance of days to 50 per cent flowering in T 15-15 × BSMR 853,the gene effects (d) and (h), in AVPP 1 x LRG 41 and AGT 2 x ICP 8863,gene effects(d) and (l), and in the cross GT 101 x ICPL 84060,gene effect(l) were predominant. Duplicate epistasis was reported only in the cross AVPP 1 x LRG 41 for inheritance of this trait. For inheritance of days to maturity in T 15-15 x BSMR 853 gene effects (d), (h), (j) and (l); in AVPP 1 x LRG 41 gene effects (d) and (l); in GT 101 x ICPL 84060,gene effects (h) and (l) were predominant. Complimentary epistasis was evidenced in above three crosses for inheritance of this trait. Plant height was governed by gene effects (d) and (h) and digenic interaction (i) in T 15-15 x BSMR 853; (i), (j) and (l) epistatis in the cross AVPP 1 x LRG 41; (h), (i), (j) and (l) in the cross AGT 2 x ICP 8863 and (j) epistasis in the cross GT 101 x ICPL 84060. Duplicate epistasis was present in all four crosses for this trait except in GT 101 x ICPL 84060.

The inheritance of primary branches per plant in AGT 2 x ICP 8863was governed bygene effect (l). For inheritance of pods per cluster gene effects (i) and (j) in AVPP 1 x LRG 41;gene effect (l) in AGT 2 x ICP 8863 were important. In AVPP 1 x LRG 41duplicate types of epistasis was evidenced for pods per cluster. For Pods per plant in T 15-15 x BSMR 853 predominant role of gene effects (d),(h), (i), (j) and (l); in AVPP 1 x LRG 41 gene effects (h), (i) and (l) were important. Duplicate epistasis was present in above both crosses for this trait. For inheritance of Pod length, the gene effects (h), (i), (j) and (l) were predominant in T 15-15 x BSMR 853;gene effects (d) and (h) as well as all digenic interactions (i), (j) and (l) found significant in GT 101 x ICPL 84060. Duplicate epistasis was present for inheritance of this character in both the crosses. Inheritance of seeds per pod was governed by non-allelic interaction (j) in the cross T 15-15 x BSMR 853;(h) in AVPP 1 x LRG 41;(h), (i) and (l) in AGT 2 x ICP 8863; and gene effects (d), (h), and (i) were important in the cross GT 101 x ICP 84060.Duplicate type of epistasis was evidenced in the cross AGT 2 x ICP 8863.

For 100 seed weight in the cross T 15-15 x BSMR 853, scaling test B and C were significant but none of the estimates were observed significant in six parameter model. The complementary epistasis was present. In AVPP 1 x LRG 41 non significant value of individual scaling test indicated adequacy of additive-dominance model and presence of both (d) and (h) gene effects evidenced for inheritance of this character.

Data for seed yield per plant fitted well to three-parameter model because of non-significant values of individual scaling tests andχ^2 value of joint scaling test in the cross GT 101 x ICPL 84060 and the (h) gene effect was predominant for inheritance of this trait. Inheritance of harvest index was governed by the gene effect (j) in the cross AVPP 1 x LRG 41;(h), (i), (j) and (l) in the cross AGT 2 x ICP 8863. The complementary epistasis was evidenced in both the crosses for this trait.

All the traits lacked significant (d) effect alone in all the crosses. Mathews *et al*., 2008 suggested that such traits are under the control of complex gene pathway and these crosses involed several minor genes of small effect with different expression. The both gene effects (d) and (h) both pronounced for the characters like days to 50 per cent flowering, plant height, clusters per plant, pods per plant, pod length, seeds per pod, and 100 seed weight in the crosses like T 15-15 x BSMR 853, GT 101 x ICPL 84060, AVPP 1 x LRG 41. Sreelakshmi and Shivani (2013) observed significance of both (d) and (h) for traits like days to 50 per cent flowering, plant height, pods per plant and seed weight. The dominant gene effect (h) was more prominent for clusters per plant, seeds per pod and seed yield per plant. Patel *et al*. (1992); Baskaran and Muthiah (2007) and Vaghela *et al*. (2009) observed significant dominant (h) gene effect for seeds per pod and seed yield per plant. The presence of dominant (h) gene effect indicates that selection should be delayed until heterozygosity is reduced in population.

Non-allelic interactions (epistasis) (i), (j) and (l) were more important for the traits like plant height, clusters per plant, pods per plant, pod length and harvest index. Baskaran and Muthiah (2007) reported significance of non-allelic interactions for most of the yield contributing traits under study. In some of the crosses for most of the traits (j) and (l) were more prominent. In the cross T 15-15 x BSMR 853, the scaling test was significant but any of the non allelic interaction was not significant for 100 seed weight. This indicated that such traits were governed by higher order interactions or under the control of complex genetic control (Milus and Lie, 1986). It has been observed that higher order epistasis among more than two genes may play crucial role in genetic interactions. Such higher order interactions have also been reported in pigeonpea (Ajay, 2012).

The variability in segregating generations may be reduced due to presence of duplicate epistasis which hinders the selection process. Hence, it is difficult to utilize such traits in the breeding programme (Sameer *et al*. 2009). Presence of complementary gene action for most of the traits indicated that parents selected for crossing were diverse. Ajay (2012) suggested that if parents selected for crossing are complementary for traits, then it is possible to realise enhanced genetic gain in breeding programme.

HETEROSIS AND INBREEDING DEPRESSION

For seed yield, cross GT 101 x ICPL 84060 depicted significant and positive estimates for heterobeltiosis and relative heterosis. It had also significant and negative estimates of relative heterosis as well as heterobeltiosis for days to 50 per cent flowering and days to maturity, which is desirable. The heterobeltiosis for plant height and relative heterosis for seeds per pod were in desired direction in the cross GT 101 x ICPL 84060. Estimates of heterobeltiosis and relative heterosis were in desired direction for most of the yield contributing traits like; primary branches per plant (AGT 2 x ICP 8863), clusters per plant (in all the crosses except GT 101 x ICPL 84060), pods per cluster (AGT 2 x ICP 8863). For pods per plant in AVPP 1 x LRG 41, heterobeltiosis was in desired direction. For seeds per pod all the crosses depicted desired relative heterosis and AVPP 1 x LRG 41 depicted desired heterobeltiosis for seeds per pod. The cross T 15-15 x BSMR 853 depicted desired relative heterosis for 100 seed weight.

Positive and significant inbreeding depression was observed in all the four crosses for plant height indicating possibilities to get dwarf plants in the segregating generations. The inbreeding depression was in desired direction for the trait pods per plant (T 15-15 x BSMR 853), pod length (T15-15 x BSMR 853 and GT 101 x ICPL 84060),100 seed weight (T15-15 x BSMR 853 and AVPP 1 x LRG 41) and harvest index (AVPP 1 x LRG 41 and AGT 2 x ICP 8863). Therefore, there would be possibility to get desired segregants for these characters in repetitive crosses.

CONCLUSION

The gene effects obtained in the present study in all the crosses were

inconsistent from cross to cross. Both additive and dominance effects and epistasis interactions were found to play important role in inheritance of various economic characters. In this situation recombination breeding could be followed by postponing selection to later generations. As the duplicate type of epistasis was observed in some of the traits, selection intensity should be mild in the earlier and intense in the later generations.The cross GT 101 x ICPL 84060 depicted significant and beneficial heterotic effects for seed yield. This cross had also significant and desired estimates of heterosis for days to 50 per cent flowering, days to maturity, plant height and seeds per pod. The estimates of inbreeding depression were significant and in desired direction in some of the crosses for plant height, pods per plant, pod length, 100 seed weight and harvest index indicating possibilities to get the desired segregants to improve such traits.

Table 1. ANOVA of four families and their six generations for different characters in pigeonpea

Source	df	Mean sum of squares												
		DF	DM	PH	PBP	SBP	CP	PC	PP	PL	SP	SW	SY	HI
Between family comparison														
Replications	3	25.88	55.99*	66.31	3.04*	7.34	7099.23	0.13	763.57	0.88	0.04	0.09	2301.73	73.03
Families	3	158.78**	131.08**	4280.95**	2.52	219.86	19628.21*	3.77**	98425.77**	0.89	0.01	5.47**	6584.16*	18.68
Error	9	8.28	13.40	272.22	0.74	70.17	2919.57	0.23	11601.28	0.61	0.02	0.69	1022.00	21.39
Between progenies within family comparison														
Cross I (T15-15 x BSMR 853)														
Replications	3	0.80	4.73	227.88	0.31	52.52	1838.32	0.25*	6129.67	0.64*	0.01	0.91	1990.46	36.44*
Generations	5	22.31*	847.45*	913.35*	0.13	32.10	5621.37*	0.05	26245.22*	1.11*	0.19*	1.74*	2293.97	11.02
Error	15	3.80	20.59	204.85	0.11	20.41	1193.03	0.07	8957.66	0.15	0.01	0.59	878.68	10.33
Cross II (AVPP 1 x LRG 41)														
Replications	3	26.54	33.19	184.13	2.01*	20.23	3905.27*	0.28	10928.48	1.24*	0.01	0.37	1156.21	64.69*
Generations	5	158.30*	385.13*	3246.40*	0.10	12.83	4993.19*	2.07*	36444.34*	0.26	0.05*	2.06*	1259.77	106.48*
Error	15	21.152	23.45	91.60	0.17	21.06	555.08	0.16	7512.27	0.11	0.01	0.24	447.07	2.49
Cross III (AGT 2 x ICP 8863)														
Replications	3	13.68	39.41	390.87*	2.45*	128.60	9208.06*	0.03	13369.01	0.60*	0.07	0.84*	1960.25	25.66
Generations	5	19.03*	31.59	1029.31*	0.62*	22.98	5714.09*	0.26*	17801.77	0.45	0.13*	0.32	544.66	102.15*
Error	15	5.46	15.49	76.99	0.15	40.00	730.33	0.07	7620.16	0.17	0.03	0.22	608.44	10.43
Cross IV (GT 101 x ICP 84060)														
Replications	3	9.71	18.86	80.09	0.47*	16.49	906.29	0.26*	5140.27	0.23	0.01	0.04	260.80	10.43
Generations	5	17.19*	59.71*	603.35*	0.09	40.31	1863.16	0.10	18020.45	1.09*	0.19*	1.44	729.86*	14.38
Error	15	3.312	11.65	154.90	0.043	18.08	686.62	0.06	6347.44	0.25	0.01	0.86	242.52	14.43

*, ** Significant at 5 and 1 % levels, respectively.

DF= Days to 50 per cent flowering, DM= Days to maturity,PH= Plant height, PBP= Primary branches per plant, SBP= Secondary branches per plant, CP= Clusters per plant, PC= Pods per cluster, PP= Pods per plant, PL= Pod length, SP= Seeds per pod, SW= 100 seed weight, SY= Seed yield per plant, HI= Harvest index, SSI= Seed size index

Table 2. Estimates of Simple Scaling Test and gene effects for days to 50 per cent flowering, days to maturity, plant height, primary branches per plant, cluster per plant and pods per plant.

Crosses	Gene effect														Epistasis
	Scaling Test				Six parameter model						Three parameter model			χ^2 at 3 d.f.	
	A	B	C	D	m	d	h	i	j	l	m	d	h		
Days to 50 % flowering															
T 15 15 x BSMR 853	-1.05	1.30	-1.30	-0.76	-	-	-	-	-	-	117.15**	-2.94**	-2.87**	2.91	
AVPP 1 x LRG 41	12.95**	9.15**	16.15**	-2.98	118.08**	-6.38 **	2.085	5.95	1.90	-28.05 **	-	-	-	23.39**	D
AGT 2 x ICP 8863	5.00**	3.90**	7.30*	-0.80	112.06**	-1.82 **	-1.67	1.60	0.55	-10.50 **	-	-	-	14.96**	C
GT 101 x ICPL 84060	8.05 **	6.15**	14.20**	0.001	114.02**	0.20	-3.15	0.001	0.95	-14.20**	-	-	-	44.84**	C
Days to maturity															
T 15 15 x BSMR 853	24.20**	11.80**	46.20**	5.10	221.01**	-14.03**	-13.12 *	-10.20	6.20 **	-25.80 **	-	-	-	113.63**	C
AVPP 1 x LRG 41	19.00**	16.50 **	35.40**	-0.05	223.33**	-11.15**	-4.05	0.10	1.25	-35.60 **	-	-	-	50.40**	C
GT 101 x ICPL 84060	9.95 **	6.15	18.10**	1.00	221.53**	-40.00	-10.90 *	-2.00	1.90	-14.10 **	-	-	-	17.55**	C

Plant height															
T 15 15 x BSMR 853	-7.15	-10.50	-55.00**	-18.68 **	225.44 **	21.40 **	39.38 **	37.35 **	1.68	-19.70	-	-	-	34.13**	D
AVPP 1 x LRG 41	24.10 *	-44.20 **	44.80 **	32.45 **	218.98 **	0.20	-17.85	-64.90**	34.15 **	85.00 **	-	-	-	47.59**	D
AGT 2 x ICP 8863	1.70	37.45 **	9.85	-14.65 *	217.74 **	1.63	50.85 **	29.30 *	-17.88 **	-68.45 **	-	-	-	22.23**	D
GT 101 x ICPL 84060	-18.30 *	2.70	-0.10	7.75	228.96 **	6.03	0.93	-15.50	-10.50 *	31.10	-	-	-	5.96	C
Primary branches per plant															
AGT 2 x ICP 8863	-1.10 *	-1.05 *	-1.95 **	0.10	1.90**	0.0001	0.725	-0.199	-0.025	2.349 *	-	-	-	10.95*	C
Clusters per plant															
T 15 15 x BSMR 853	3.30	153.70**	12.45	-72.28 *	193.59 **	-61.75 *	196.70 **	144.55 *	-75.20 *	-301.55 *	-	-	-	12.22**	D
AVPP 1 x LRG 41	22.30	65.60	54.30	-16.80	102.019 **	-0.424	103.665**	-	-	-	-	-	-	2.591	
AGT 2 x ICP 8863	15.70	23.35	61.25	11.10	104.316 **	10.307	103.569 **	-	-	-	-	-	-	1.044	
Pods per cluster															
AVPP 1 x LRG 41	-1.11 **	0.27	-2.30 **	-0.73 *	3.50 **	0.29	0.85	1.46 *	-0.69 **	-0.62	-	-	-	18.05**	D
AGT 2 x ICP 8863	-0.98 **	-0.88**	-1.79 **	0.032	3.18 **	0.05	0.21	-0.07	-0.05	1.92**	-	-	-	3.11	C

Table 3. Estimates of Simple Scaling Test and gene effects for pods per plant, pod length, seeds per plant, 100 seed weight, seed yield per plant and harvest index.

Crosses	Gene effect													χ^2 at 3 d.f.	Epistasis
	Scaling Test				Six parameter model						Three parameter model				
	A	B	C	D	m	d	h	i	j	l	m	d	h		
Pods per plant															
T 15 15 x BSMR 853	38.80	427.20 **	106.45	-179.78 *	487.72 **	-133.55 *	357.45*	359.55 *	-194.20 **	-825.54 **	-	-	-	14.21**	D
AVPP 1 x LRG 41	173.65	234.40 **	106.05	-151.0 *	377.51 **	13.57	460.30 **	302.00 *	-30.38	-710.05 **	-	-	-	9.03*	D
Pod length															
T 15 15 x BSMR 853	0.33	1.73**	0.42	-0.82 **	4.67**	-0.03	1.00 **	1.63**	-0.70 **	-3.68 **	-	-	-	79.76**	D
GT 101 x ICPL 84060	0.41	1.33 **	0.18	-0.78 **	4.93 **	0.27 **	1.30 **	1.56**	-0.46 **	-3.29**	-	-	-	55.61**	D
Seeds per pod															
T 15 15 x BSMR 853	-0.37 *	0.35*	-0.11	-0.11	4.12**	-0.02	1.70	0.09	-0.36 **	-0.07	-	-	-	18.20**	D
AVPP 1 x LRG 41	-0.25	-0.02	-0.49*	-0.11	4.10 **	-0.09	0.52 *	0.22	-0.12	0.05	-	-	-	7.02	C
AGT 2 x ICP 8863	0.19	0.45 **	0.03	-0.31 **	4.12 **	0.12	0.63 **	0.61**	-0.13	-1.25**	-	-	-	12.08**	D
GT 101 x ICPL 84060	-0.20	-0.02	-0.74 **	-0.26*	4.06**	2.23 **	0.59 **	0.53*	-0.09	-0.31	-	-	-	15.85**	D
100 seed weight															
T 15 15 x BSMR 853	0.95	1.05 *	3.00 **	0.50	11.78	0.75	-0.85	-1.00	-0.05	-1.00	_	-	-	15.96**	C
AVPP 1 x LRG 41	0.40	0.55	-0.05	-0.50	11.25**	0.94**	-0.63 **	-	-	-	-	-	-	1.88	C
Seed yield per plant															
GT 101 x ICPL 84060	9.00	19.05	13.70	-7.18	80.13**	-5.43	34.92**	-	-	-	-	-	-	0.72	C
Harvest index															
AVPP 1 x LRG 41	2.07	-6.88*	-6.79	-0.99	19.35**	-0.36	-8.39	1.98	4.48 **	2.83	-	-	-	8.44*	D
AGT 2 x ICP 8863	8.10 **	-10.27**	11.13*	6.65**	23.29**	2.88	-20.67 **	-13.30 **	9.18**	15.47 *	-	-	-	39.39**	D

Table 4 Magnitude of heterobeltiosis (%), relative heterosis (%), and inbreeding depression (%) for different characters in four crosses of pigeonpea

	DF	DM	PH	PBP	CP	PC	PP	PL	SP	SW	YP	HI
Cross 1: T 15 15 x BSMR 853												
HB	-0.22	9.07**	-6.86**	-	21.76	-	-12.00	-23.56**	-5.84*	-5.53	-	-
RH	-2.52*	-1.39*	0.85	-	31.72**	-	-0.45	-13.09**	2.07	1.37	-	-
ID	-1.01	-6.26**	6.15**	-	10.60	-	-6.01	-9.88**	1.67	-6.04*	-	-
Cross 2: AVPP 1 x LRG 41												
HB	4.08*	4.04**	6.00**	-	76.00**	-29.66**	36.21	-	6.59**	-12.76**	-	-48.95**
RH	-3.34	-1.92*	25.54**	-	78.67**	-13.92**	58.23**	-	7.24**	-5.15**	-	-39.55**

ID	-5.33**	-5.14**	5.33*	-	14.46	7.16	12.24	-	6.18**	-2.64	-	-22.01*
Cross 3: AGT 2 x ICP 8863												
HB	-0.82	-	0.92	46.15**	71.96**	5.01	-	-	-5.07*	-	-	-44.83**
RH	-2.93**	-	10.59**	48.05**	89.12**	8.02	-	-	0.61	-	-	-30.47**
ID	-3.19**	-	3.68**	33.33**	15.66	15.65**	-	-	0.00	-	-	-38.47**
Cross 4: GT 101 x ICPL 84060												
HB	-2.16*	-3.01**	-0.04	-	-	-	-	-17.07**	-5.53**	-	31.18*	-
RH	-2.81**	-4.02**	7.44**	-	-	-	-	-4.99	1.43	-	38.99**	-
ID	-4.71**	-4.22**	3.47**	-	-	-	-	-3.57	5.15**	-	10.91	-

HB = Heterobeltiosis RH = Relative Heterosis ID = Inbreeding Depression

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