

Studies on Heterosis and Inbreeding Depression for Yield and its Component Traits in Green gram [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

A ten parent line x tester analysis was carried out to study the extent of heterosis and inbreeding depression for yield and its component traits in green gram at Brahmanand Mahavidyalaya Rath (Hamirpur), Uttar Pradesh. Heterosis over mid parent and better parent was significant to highly significant for seed yield/plant along with other attributing traits. The crosses exhibiting high heterosis also expressed high inbreeding depression both in the positive and negative direction for days to 50% flowering, pods/plant, pods/cluster, harvest index and seed yield/ plant. Heterosis coupled with inbreeding depression revealed the predominance of both non-additive and additive gene action for most of the characters studied. Owing to its autogamous genetic architecture and biological constraints of the crop, the heterosis could be exploited only by isolating the desirable segregants for yield and its attributes adopting selection in early segregating generations followed by single plant selection in subsequent generations.

Key words: Heterosis, Inbreeding depression, *Vigna radiata*, Gene action, Yield

Green gram [*Vigna radiata* (L.) Wilczek] is the third most important pulse crop after chickpea and black gram with more nutritive, palatable and digestible values. The productivity of green gram is very low and is often related to its poor genetic architecture. The exploitation of heterosis is a quick and convenient way of combining desirable genes present in different parents into a single genotype has important implications for obtaining desirable transgressive segregants for many quantitative characters in advanced generations [1]. Green gram being an autogamous crop, commercial hybrid seed production is not readily feasible. However, the presence of desirable heterosis and inbreeding depression particularly in negative direction can be utilized in pulse crops for the development of high yielding pure line varieties [2]. Heterosis or inbreeding depression plays an important role in the choice of breeding methodologies as well as selection of parents so as to obtain desirable segregants. Therefore, the present investigation was carried out to estimate the magnitude of the heterosis and inbreeding depression for traits of economic importance at F₁ and F₂ generations of twenty-four crosses of green gram.

MATERIALS AND METHODS

Twenty-four crosses including both F₁s and F₂s of green gram along with ten parents were evaluated in randomized block design with three replications at the Brahmanand Mahavidyalaya Rath (Hamirpur), Uttar Pradesh during Zaid, 2018. The row to row and plant to plant distance was 30 cm and 10 cm, respectively. All the recommended package of practices were followed in raising a good crop. Data were recorded on 5 randomly selected competitive plants in non-segregating and segregating generations, respectively for thirteen characters viz. days to 50% flowering, days to maturity, branches/ plant, plant height, clusters/plant, pods/cluster, pods/plant, seeds/pod, seed weight per pod, 100 seed weight, biological yield (dry weight/plant), harvest index, and seed yield/plant. Heterosis over mid parent (relative heterosis), better parent (heterobeltiosis) and inbreeding depression from F₁ to F₂ in each cross was estimated for 13 characters using standard formulae.

RESULTS AND DISCUSSION

Relative heterosis, heterobeltiosis and standard heterosis as well as inbreeding depression in five crosses of green gram for 13 quantitative traits are presented in (Table 1). The magnitude of relative heterosis for seed yield/plant ranged from 21.26 (PKVAKM 4 × PDM 1) to 98.79 per cent (JM 10 × AKM 8802) while heterobeltiosis ranged from 6.93 (PKVAKM 4 × PDM 1) to 78.96 per cent (JM 10 × AKM 8802) and inbreeding depression ranged from -7.51 (JM 10 × PDM 1) to 15.15 (PKVAKM 4 × AKM 8802). Significant and positive heterotic effects with negative to moderate inbreeding depression recorded in crosses for seed yield/plant suggests the operation of both additive and non-additive gene effects in the

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inheritance of seed yield/plant in green gram. The crosses viz. JM 10 × AKM 8802 and BM4 × PDM1 recorded maximum significant relative heterosis and heterobeltiosis with low to moderate inbreeding depression (11.54 and 9.06) indicating the preponderance of non-additive genes with significant presence of additive gene effects for seed yield. However, the crosses

viz. PKVAKM 4 × AKM 8802 and ML131 × HUM 1 recorded significant heterosis effects coupled with considerable inbreeding depression (15.15 & 14.72) indicating the presence of epistatic gene effects which may likely to give desirable segregants in the subsequent generations [3]. [4], [5], [6] also reported high heterobeltiosis for seed yield in green gram.

Table 1 Relative heterosis (MP), heterobeltiosis (BP) and inbreeding depression (ID) in 24 crosses of green gram

Cross combination	Days to 50% flowering			Days to maturity			Prim. branches plant ⁻¹			Plant height (cm)		
	MP	BP	ID	MP	BP	ID	MP	BP	ID	MP	BP	ID
JM 721 × AKM 8802	0.00ns	-2.03*	-6.90	-5.65**	-7.66**	-5.99	17.81**	14.67**	17.44	3.52**	0.06ns	4.39
JM721 × TJM 3	-15.48**	-28.87**	-3.96	-8.07**	-16.44**	-3.19	32.95**	11.43**	12.82	7.77**	1.16ns	3.71
JM721 × PDM 1	-3.79**	-10.56**	-5.51	-0.23ns	-2.22**	-3.18	37.25**	28.05**	13.33	11.73**	11.47**	5.48
JM721 × HUM 1	-5.38**	-13.38**	-6.50	-3.21**	-6.22**	-4.74	51.45**	28.43**	18.32	-2.66*	-6.61**	7.01
BM 4 × AKM 8802	-4.93**	-8.78**	11.85	-7.08**	-10.64**	4.76	25.32**	19.28**	15.15	-3.45**	-11.90**	4.56
BM 4 × TJM 3	-8.15**	-21.32**	0.00	-6.73**	-13.82**	-4.28	39.36**	24.76**	14.50	21.59**	21.13**	10.25
BM 4 × PDM 1	-13.18**	-17.65**	0.00	-7.62**	-7.83**	0.00	30.91**	30.12**	13.89	18.73**	11.60**	4.01
BM 4 × HUM 1	-9.45**	-15.44**	0.00	-4.21**	-5.53**	0.00	24.32**	12.75**	12.17	14.63**	12.46**	6.73
PKVAKM 4 × AKM 8802	-6.62**	-9.46**	-11.19	-3.45**	-4.68**	-5.36	34.50**	19.79**	13.91	8.53**	7.25**	5.40
PKVAKM 4 × TJM 3	-6.78**	-20.86**	-2.73	-7.51**	-16.59**	-4.19	13.43**	8.57**	15.79	6.52**	-2.08ns	3.19
PKVAKM 4 × PDM 1	-2.68**	-8.63**	0.00	-4.27**	-6.99**	0.00	19.10**	10.42**	16.98	9.41**	7.23**	3.04
PKVAKM 4 × HUM 1	5.84**	-2.16*	0.00	-0.45ns	-4.37**	0.00	12.12**	8.82**	13.51	9.89**	3.19*	4.05
TARM 2 × AKM 8802	-0.37ns	-9.46**	-6.72	-8.03**	-9.79**	-7.55	7.79*	5.06ns	16.87	5.70**	3.75**	3.43
TARM 2 × TJM 3	14.68**	3.31**	-2.40	-2.44**	-11.50**	-3.00	9.78**	-3.81ns	14.85	-0.32 ns	-7.79**	1.50
TARM 2 × PDM 1	5.35**	4.92**	-1.56	-8.14**	-10.18**	-5.91	14.29**	12.20**	10.87	0.60 ns	-0.73ns	3.93
TARM 2 × HUM 1	7.11**	5.79**	-1.56	-8.47**	-11.50**	-1.50	12.71**	-0.00ns	15.69	5.66**	-0.13ns	5.89
ML131 × AKM 8802	-8.09**	-15.54**	-1.60	-13.59**	-17.45**	-3.09	32.57**	16.00**	25.00	11.48**	6.23**	4.01
ML131 × TJM 3	-0.45ns	-11.29**	-2.73	-5.53**	-12.15**	-3.19	14.15**	11.43**	11.97	17.37**	11.73**	4.90
ML131 × PDM 1	1.63ns	0.81ns	-1.60	-6.98**	-7.41**	-4.50	24.18**	13.00**	14.16	10.90**	9.02**	4.04
ML131 × HUM 1	6.61**	4.03**	-0.78	-4.47**	-5.14**	-5.91	8.91**	7.84**	14.55	6.06**	3.23*	4.42
JM 10 × AKM 8802	0.72ns	-5.41**	0.71	-7.52**	-11.06**	0.00	20.00**	10.00**	14.14	5.99 *	2.99*	4.08
JM 10 × TJM 3	-0.44ns	-13.08**	-0.88	-6.23**	-13.36**	-4.79	9.74**	1.90ns	14.95	14.22**	6.68**	7.33
JM 10 × PDM 1	8.73**	5.38**	1.46	-2.54**	-2.76**	-3.32	17.44**	12.22**	13.86	8.69**	8.36**	4.42
JM 10 × HUM 1	12.10**	6.92**	1.44	0.47ns	-0.92ns	-4.65	13.54**	6.86*	9.17	10.28**	5.26**	6.53
SE	0.356	0.411		0.335	0.387		0.078	0.090		0.555	0.641	

.....Table 1 Continued.....

Cross combination	Pods/ cluster			Clusters per plant			Pods per plant			Biological yield per plant		
	MP	BP	ID	MP	BP	ID	MP	BP	ID	MP	BP	ID
JM 721 × AKM 8802	34.55**	14.20**	4.86	42.04**	33.85**	8.05	79.03**	52.05**	10.81	87.42**	63.93**	7.57
JM721 × TJM 3	23.66**	0.00ns	-1.85	16.00**	11.54*	4.14	39.34**	16.44**	8.24	40.00**	19.67**	-6.65
JM721 × PDM 1	16.46**	-14.81**	-17.39	20.62**	19.23**	4.52	42.11**	10.96ns	-6.17	74.79**	47.78**	9.35
JM721 × HUM 1	-10.86**	-26.54**	-11.76	38.21**	30.77**	0.00	22.83**	6.85ns	-8.97	27.73**	6.79**	13.60
BM 4 × AKM 8802	35.11**	18.79**	-8.47	61.26**	55.65**	6.70	116.67**	105.26**	17.09	46.10**	33.77**	12.82
BM 4 × TJM 3	38.96**	16.11**	5.78	39.21**	31.67**	12.03	83.02**	70.18**	16.49	67.15**	49.35**	10.43
BM 4 × PDM 1	39.29**	4.70ns	-12.82	46.15**	34.65**	7.60	83.67**	57.89**	-2.22	94.71**	71.95**	9.06
BM 4 × HUM 1	11.02**	-5.37ns	-14.89	85.65**	78.45**	5.31	72.97**	68.42**	-9.38	51.49**	32.21**	11.98
PKVAKM 4 × AKM 8802	29.96**	15.97**	-9.58	45.70**	20.45**	18.87	74.47**	36.67**	21.14	49.01**	22.97**	10.41
PKVAKM 4 × TJM 3	18.85**	0.69 ns	6.21	31.76**	10.80**	16.92	39.57**	7.78ns	13.40	28.30**	3.66**	11.18
PKVAKM 4 × PDM 1	-0.46ns	-24.31**	-19.27	11.55**	-3.98ns	12.43	9.92ns	-20.00**	5.56	7.50**	-14.02**	12.29
PKVAKM 4 × HUM 1	26.91**	9.72**	-3.16	32.88**	10.23**	6.19	45.83**	16.67**	12.38	28.37**	1.63ns	8.80
TARM 2 × AKM 8802	7.14 ns	6.19 ns	-15.83	24.14 **	23.08**	3.47	30.77**	28.30**	10.29	45.51**	44.17**	13.40
TARM 2 × TJM 3	5.21 ns	-0.00 ns	-8.11	1.27 ns	-0.00ns	-5.00	-3.92ns	-7.55ns	8.16	41.18**	36.20**	11.26
TARM 2 × PDM 1	1.08 ns	-15.32**	-12.77	27.87 **	22.83**	10.26	-0.00ns	-11.32ns	-2.13	33.66**	27.30**	9.40
TARM 2 × HUM 1	4.63 ns	1.80 ns	-15.04	31.33 **	30.77**	14.38	15.89 *	14.81ns	4.84	22.68**	15.34**	-7.71
ML131 × AKM 8802	13.24 **	9.73 *	-12.10	41.55 **	34.78**	10.97	47.92 **	39.22**	21.13	33.65**	30.94**	13.13
ML131 × TJM 3	22.33**	18.87**	-7.94	26.79**	18.33**	-7.04	48.94**	42.86**	2.86	44.92**	43.97**	7.92
ML131 × PDM 1	18.23**	0.94ns	2.80	14.29**	3.94ns	-7.58	25.58**	20.00*	9.26	35.22**	32.57**	-7.86
ML131 × HUM 1	7.11ns	6.60ns	-20.35	24.55**	18.10**	16.06	19.19*	9.26ns	15.25	34.01**	29.64**	-2.51
JM 10 × AKM 8802	17.14**	8.85ns	-12.20	52.08**	26.96**	-11.64	54.84**	41.18**	4.17	71.95**	60.94**	9.32
JM 10 × TJM 3	13.71**	12.00*	-20.54	36.04**	11.67*	-25.37	42.86**	32.65**	-21.54	58.42**	52.15**	4.77
JM 10 × PDM 1	16.28**	3.09ns	-36.00	23.53**	-0.79ns	-8.73	25.30**	23.81*	-36.54	51.92**	47.80**	6.19
JM 10 × HUM 1	20.79**	16.19**	-14.75	33.68**	11.21*	-25.58	35.42**	20.37*	-15.38	77.74**	75.26**	4.17
SE	0.151	0.175		0.171	0.198		1.250	1.443		0.197	0.227	

.....Table 1 Continued.....

Seeds per pod			Seed weight / pod (g)			100-seed weight (g)			Harvest Index (%)			Seed yield per plant (g)		
MP	BP	ID	MP	BP	ID	MP	BP	ID	MP	BP	ID	MP	BP	ID
0.00ns	5.35*	6.27	24.58**	15.75**	-3.40	-5.80**	-12.43**	6.99	5.33*	5.13*	3.75	97.3**	72.31**	10.17
0.21ns	2.20ns	6.46	12.40**	7.09**	-2.21	2.03ns	1.92ns	8.39	4.36ns	3.82ns	16.74	46.36**	25.58**	11.16
-0.49*	-5.66*	3.33	13.56**	5.51**	0.00	11.84**	-3.06*	0.74	3.50ns	2.43ns	-3.08	80.55**	51.29**	6.56
0.28ns	5.66*	5.95	12.71**	4.72**	3.76	-8.97**	-14.2**	2.21	17.80**	17.6**	-2.85	50.45**	25.58**	11.16
-0.37ns	3.27ns	0.00	9.49**	-9.09**	6.00	-23.8**	-30.65**	2.17	23.90**	16.7**	0.15	82.03**	76.47**	12.92
0.50*	17.69**	9.51	2.14ns	-13.33**	-0.70	-19.7**	-31.66**	2.21	17.04**	9.54**	0.11	97.22**	77.50**	10.59
0.33ns	20.53**	8.20	0.73ns	-16.36**	0.72	-4.60**	-27.64**	6.25	20.70**	14.66**	0.02	98.79**	69.12**	9.06
-0.46*	0.00ns	-0.65	-2.92*	-19.39**	-9.02	-22.24**	-30.15**	0.00	27.45**	20.05**	0.50	84.73**	72.41**	12.30
0.44*	9.48**	6.27	7.27**	6.31**	-5.93	-7.29**	-13.59**	3.61	38.76**	22.90**	5.60	72.75**	59.04**	15.15
-0.26ns	5.67*	3.69	2.65ns	0.87ns	-6.03	0.39ns	-0.00ns	2.91	18.17**	4.02ns	-8.01	56.88**	41.91**	4.19
-0.13ns	5.67*	10.40	4.55**	3.60ns	-8.70	14.92**	-0.64ns	4.42	9.31**	-2.45ns	-18.22	21.26**	6.93**	-3.70
-0.05ns	2.29ns	7.03	7.27**	6.31**	1.69	-0.53ns	-5.99**	2.01	10.81**	-1.88ns	-8.67	47.31**	29.37**	3.06
-0.41*	-1.96ns	3.33	1.83ns	1.83ns	-2.70	-13.44**	-23.70**	3.69	3.10ns	2.29ns	-2.26	50.06**	49.77**	11.46
-0.13ns	0.69ns	3.77	1.79ns	-0.87ns	4.39	-6.20**	-11.36**	2.50	7.89**	6.29*	-5.44	52.31**	48.99**	6.28
0.37ns	4.48ns	3.63	-1.83ns	-1.83ns	0.00	1.10ns	-7.70**	5.22	0.64ns	0.59ns	-9.65	34.48**	27.93**	0.61
0.17ns	1.31ns	5.16	6.42**	6.42**	1.72	-18.76**	-27.44**	8.70	8.73**	7.82**	1.45	33.44**	26.37**	-6.17
0.15ns	0.31ns	0.63	-0.89ns	-3.48ns	-4.50	-22.66**	-29.58**	15.65	1.80ns	1.39ns	-9.73	36.09**	33.91**	4.68
0.16ns	-4.72*	3.96	0.87ns	0.87ns	7.76	12.37**	10.00**	1.95	7.00**	6.67**	-6.91	55.16**	54.53**	1.57
-0.07ns	-8.18**	-7.53	0.00ns	-2.61ns	-41.07	15.61**	2.16ns	3.65	16.80**	15.34**	3.85	57.96**	52.91**	-3.70
-0.24ns	-5.66*	4.33	2.68ns	0.00ns	-5.22	5.26**	-2.84*	1.30	23.43**	22.98**	16.80	65.41**	59.39**	14.72
0.19ns	6.54**	3.07	11.02**	3.15ns	4.58	4.83**	-3.61**	-1.02	39.12**	39.07**	2.52	89.13**	78.96**	11.54
-0.48*	-4.92*	-6.21	0.83ns	-3.94*	1.64	3.25**	2.14ns	5.59	1.90ns	1.21ns	-10.56	61.47**	54.16**	-5.29
-0.01ns	-1.64ns	-3.33	-2.54ns	-9.45**	2.61	3.38*	-9.49**	5.65	0.18ns	-0.71ns	-14.61	52.29**	49.52**	-7.51
0.30ns	5.23*	1.86	0.85ns	-6.30**	-3.36	6.26**	-0.95ns	3.18	3.47ns	3.47ns	-5.26	83.99**	81.50**	-0.96
0.201	0.232		0.006	0.007		0.055	0.063		0.888	1.025		0.106	0.122	

*Significant at 5% level, **Significant at 1% level

Among the component traits, relative heterosis and heterobeltiosis for days to 50% flowering ranged from -15.48 (IM721 × TJM3) to 12.10 (JM 10 × HUM 1) and -28.87 (JM721 × TJM 3) to 6.92 (JM 10 × HUM 1) respectively. Thirteen crosses out of twenty-four manifested significant and negative heterotic effects with low negative inbreeding depression for days to 50 per cent flowering and days to maturity suggesting the preponderance of non-additive gene effects in the expression of these characters. However, out of 24 crosses, 6 crosses exhibited positive heterotic effects with low inbreeding depression indicating the operation of additive and additive × additive type of inter-allelic interactions in the inheritance of earliness. Heterosis for earliness was also reported by [7], [8].

In the present investigation all the crosses showed positive and significant relative heterosis. However, four crosses could not excel the better parent. The cross JM721 × HUM 1 exhibited highest heterosis both relative and over better parent (51.45 and 28.43 respectively) followed by the crosses BM 4 × TJM 3 and JM721 × HUM1 with low to moderate inbreeding depression indicating the role of non-additive and additive × additive type of gene interaction in the inheritance of primary branches/plant. Similar results of higher magnitude of relative heterosis and heterobeltiosis for branches/plant were reported by [3], [8], [9].

For plant height most of the crosses had significant but low to moderate heterotic effects, the maximum heterosis was found with cross BM4 × TJM3 (21.50 MP and 21.13 BP) followed by BM4 × PDM1(18.73MP and 11.60BP) and BM4 × HUM1(14.63MP and 12.46BP), with lower inbreeding depression indicating the operation of additive and/or additive × additive type of variance. However, three crosses out of twenty-four showed significant and negative heterobeltiosis while three other showed non-significant negative values [8], [10], [8].

Out of 24 crosses 18 crosses showed positive and significant relative heterosis for pods per cluster. BM4 × PDM1 exhibited maximum (39.29) followed by BM4 × TJM3 (38.96) and BM4 × AKM8802 (35.11). Relative heterosis ranged from -10.86 (JM721 × HUM1) to 39.29 (BM4 × PDM1) while heterobeltiosis ranged from -26.54 (JM721 × HUM1) to 18.87 (ML131 × TJM3). Inbreeding depression was mostly significant and negative ranging from -36.00 (JM10 × PDM1) to 6.21 (PKVAKM4 × TJM3) indicating preponderance additive gene action and additive × additive interaction. Relative heterosis for cluster per plant was significant for all the crosses except one (TARM2 × TJM3) and it ranged from 1.27 (TARM2 × TJM3) to 85.65 (BM4 × HUM1). Heterobeltiosis was significant for all the crosses except four crosses. Significant and positive heterotic effects were seen for most of the crosses for clusters/plant with low to moderate inbreeding depression and negative for seven crosses suggesting the predominance of non-additive gene action along with additive × additive epistasis [8], [9]. A significant extent of heterosis over better parent was also reported by [3], [8] for pods/cluster.

All the crosses except a few (three in relative heterosis and 5 in heterobeltiosis) exhibited significant and positive heterotic effects for pods/plant with low to moderate inbreeding depression indicating the operation of non-additive gene action. Therefore, selecting superior lines and intermating them followed by recurrent selection may improve the character. Out of 24 crosses, eight expressed the negative inbreeding depression indicating the role of additive or additive × additive type of gene action for pods/pant. Similar results of positive heterosis over mid-parent and better parent were also reported by [8], [9].

All the crosses showed positive and significant heterosis over mid parent and better parent except two crosses over better parent for biological yield (dry weight) per plant with

low to moderate inbreeding depression. This indicates the predominance of non-additive gene action with additive \times additive gene action. It provides a lot of scopes to get transgressive segregants in desirable direction at later generations in the crosses having lower or negative inbreeding depression.

The number of seeds per pod is an important component of seed yield and it will help break the yield ceiling in green gram. Nine crosses out of twenty-four exhibited significant and positive relative heterosis while it was mostly non-significant over better parent except two crosses viz. BM4 \times TJM3 and PKVAKM4 \times AKM8802 (0.50 and 0.44 percent respectively) with lower magnitude of inbreeding depression. It indicates the operation of additive gene action and additive \times additive gene interaction [11], [8], [6].

Seed weight per pod is one of the most important components of seed yield per plant. Out of 24, ten crosses exhibited significant and positive heterosis and seven heterobeltiosis. Maximum heterosis was recorded for cross JM721 \times AKM8802 (24.58 and 15.75 percent relative heterosis and heterobeltiosis respectively). Most of the crosses exhibited low and negative inbreeding depression which indicates preponderance of additive and additive \times additive interaction of genes.

Out of twenty four crosses, one cross viz. ML131 \times TJM 3 exhibited significant positive relative heterosis and heterobeltiosis (12.37 and 10.00 respectively) for 100 seed weight with low inbreeding depression (1.95) while other seven crosses viz. JM721 \times PDM1, ML131 \times PDM 1, ML131 \times HUM1, PKVAKM4 \times PDM1, JM10 \times AKM8802, JM10 \times TJM3 and JM10 \times HUM1 expressed the significant positive related heterosis with low inbreeding depression (2.92, -0.37 and 2.26) suggesting the role of additive and/or additive \times

additive variance. The rest of the crosses showed significant negative or non-significant positive heterosis. Similar results of significant negative or positive heterosis over mid parent and better parent were also reported by [12], [7], [10], [13].

Two cross combinations PKVAKM4 \times AKM8802 and ML131 \times HUM1 exhibited significant heterotic effects over mid and better parents for harvest index with low to moderate inbreeding depression (5.60 and 16.80) indicating the presence of additive gene action. Nine crosses exhibited non-significant heterobeltiosis and/or relative heterosis with considerable negative inbreeding depression. The other crosses expressed significant positive relative heterosis and heterobeltiosis with mostly negative low to moderate inbreeding depression. This suggests the role of non-additive and additive \times additive gene actions in the expression of the character. The significant positive heterosis for harvest index was reported by [3], [14].

CONCLUSIONS

Use of heterosis breeding may be promising for yield improvement in green gram as the heterosis for yield was the result of cumulative occurrence of heterosis for branches per plant, pods/cluster, clusters per plant, pods/plant, biological yield, seeds/pod and harvest index. The nature and magnitude of heterosis and inbreeding depression varied among crosses as well as characters. A close relationship between heterotic response and inbreeding depression for characters suggests the predominance of non-additive genetic variance as well as additive \times additive inter allelic gene action. Therefore, a few cycles of recurrent selection following the pedigree method would be effective and useful in utilizing all types of gene effects by maintaining considerable heterozygosity through the mating of selected plants in early segregating generations.

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