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VR Akabari
Department of Genetics and Plant Breeding, Anand Agricultural University, Anand, Gujarat, India

N Sasidharan
Department of Genetics and Plant Breeding, Anand Agricultural University, Anand, Gujarat, India

VN Kapadia
Department of Genetics and Plant Breeding, Anand Agricultural University, Anand, Gujarat, India

Correspondence
VR Akabari
Department of Genetics and Plant Breeding, Anand Agricultural University, Anand, Gujarat, India

Inbreeding depression heritability and genetic advance for yield and yield components in Indian mustard

VR Akabari, N Sasidharan and VN Kapadia

Abstract

Seed yield per plant had significant and negative estimates of inbreeding depression in the crosses GM-3 x B-351, GM-2 x RH-8813 and GM-3 x RH-8813, which showed possibilities of desirable segregants in F_2 population. The additive effects and gene interaction viz., dominance x dominance (l) or other type of digenic complementary gene interactions can be exploited effectively by selection. The high estimates of narrow sense heritability and expected genetic advance in most of families for most of characters. Use of reciprocal recurrent selection or bi-parental mating could be suggested for improving those characters when additive and non- additive gene effects are involved. In addition to additivity and dominance, epistatic interactions of various kinds were also observed; one or two cycles of intermating of selected segregants may be adopted to accumulate favorable genes through recurrent selection which will result in the improvement of seed yield.

Keywords: Inbreeding depression heritability and genetic advance

Introduction

Indian mustard is an important *rabi* season oilseed crop and occupies a prime position among the oilseed crops. It is popularly say as rai, raya or laha in India. The India contributes about 7% oilseed production at the global level. India, with an area of 7.20 million hectares, 7.88 million metric tonnes production and 1094 kg/ha productivity, ranks second in area and third in production in rapeseed-mustard scenario of the world in 2014-2015 [2]. To fulfill requirement of ever-increasing population of India, there is a dire need of improving genotypes for better seed yield potential per unit area basis. This could be achieved by exploring the maximum genetic potential from the available germplasm of Indian mustard.

Breeders should concentrate on development of productive mustard varieties by crossing good heritability and genetic advance of lines for seed yield and selecting transgressive segregants from the resulting hybrids. The success of any breeding programme largely depends upon the choice of parents and the breeding procedure adopted.

Materials and methods

The experimental material comprised of three females, 20 male parents (Table 1) and their 6 F_1S developed by crossing two females with three males in a Line x tester mating system. The seeds of 6 F_1 hybrids produced by hand emasculation-hand pollination and selfing, respectively during *rabi* 2013-14. These 6 F_1 hybrids were evaluated in randomized block design with three replications during *rabi* 2014-15 at Anand Agricultural University, Anand. This site located at 220 35' North Latitude and 720 55' East longitude at an elevation of 45.1 m above mean sea level. Inter and intra row spacing was kept 40 and 15 cm, respectively. All the recommended package of practices was adopted to raise a good crop.

For recording observations, five competitive plants were randomly selected and tagged from each treatment in each replication and the mean value per plant was computed for various yield and its attributing traits viz., plant height (cm), number of primary branches, number of secondary branches, effective length of main branch (cm), number of siliquae on main spike, number of siliquae per plant, siliqua length (cm), number of seeds per siliqua, seed yield per plant (g), thousand seed weight (g), oil content (%) and protein content (%). The phenological characters viz., days to flowering and days to maturity were recorded on plot basis.

The quantitative traits are largely influenced by environments; therefore, those are not highly heritable. High, moderate and low heritability are not rigidly defined as it varies with character to character, but the following values are widely accepted. Were as Low heritability: < 20%, Moderate heritability: 20 to 50% and High heritability: > 50%

The value of expected genetic advance as percentage of mean for various characters is demarcated into three categories *viz.*, low, moderate and high, as follows [3] e.g. Low genetic advance as percentage of mean: < 10%, Moderate genetic advance as percentage of mean: 10 to 20% and High genetic advance as percentage of mean: > 20%.

Result:

Days to 50% flowering: The estimates for inbreeding depression ranged from 2.88 (GM-3 x B-351) to 8.37 (GM-2 x NUDH-45-1) per cent. The magnitude of inbreeding depression was found positive and significant in all the crosses; hence these crosses would likely to yield beneficial transgressive segregants. The estimates of narrow sense heritability were high for family I (116.40%), family II (101.96%), family III (102.73%), and family VI (67.40%); however, extremely high heritability estimates for families I, II and III would be because of sampling error due to small population size of generation involved, thereby heritability estimates would be less reliable. Whereas negative estimate for family IV and V indicates preponderance of non-allelic interaction. High narrow sense heritability coupled with low genetic advance as percentage of mean for family VI (8.56%) showed preponderance of non-additive gene effect for the inheritance of character, and it would be difficult to improve through direct selection. The estimates of genetic advance were moderate for families I (17.05%), II (13.75%) and III (14.02%). High estimates of narrow sense heritability and moderate estimates of expected genetic advance revealed possibility of existence of both additive and non-additive gene effects; therefore population improvement is suggested for improvement of the character [4, 5, 7, 10, 12, 13, 17, 19].

Days to maturity: The estimates for inbreeding depression ranged from 1.26 (GM-3 x B-351) to 3.25 (GM-2 x RH-8813) per cent. The magnitude of inbreeding depression was found positive and significant in all the crosses, hence these crosses would likely to yield transgressive segregants for early maturity. The cross GM-2 x RH-8813 (3.25%) exhibited the highest positive and significant inbreeding depression followed by GM-2 x NUDH-45-(3.05%) and GM-3 x RH-8813 (3.03%). The estimates of narrow sense heritability were high for family I (116.39%), family II (100.97%), family III (103.72%), and family VI (65.40%); however, extremely high heritability estimates for families I, II and III would be because of sampling error due to small population size of generation involved, there by heritability estimates would be less reliable. Whereas negative estimate for family IV and V indicates preponderance of non-allelic interaction. High narrow sense heritability coupled with low genetic advance as percentage of mean for all the families revealed preponderance of non-additive gene effect for the inheritance of character, and it would be difficult to improve through direct selection [5, 7, 10, 13].

Plant Height: All the mustard hybrids showed significant and positive inbreeding depression indicating possibilities for the desirable segregants. The magnitude for inbreeding depression ranged from 7.36 (GM-3 x NUDH-45-1) to 17.93 (GM-3 x B-351) per cent. For plant height narrow sense heritability estimate was low with family V (0.49%), whereas it was the highest with family I (125.63%) followed by family VI (69.04%) and family III (53.39%), thus it was varying with different crosses. Low narrow sense heritability coupled with low genetic advance (0.07%) were observed for family V; while, with family III narrow sense heritability estimates were high with low genetic advance (8.11%), it would be difficult to improve the character through selection as there would be possibility of preponderance of non-additive gene action. High heritability with moderate genetic advance for families I (11.63%) and VI (20.94%) were observed. The bi-parental mating could be followed in families I, and VI, as both additive and non-additive gene effects would be at work. Negative estimate for family II and IV indicates preponderance of non-allelic interaction [1, 5, 7, 8, 9, 14, 18].

Number of primary branches per plant: The crosses GM-3 x NUDH-45-1 (20.83%), GM-3 x B-351 (10.40%) and GM-2 x B-351 (8.81%) exhibited significant and positive inbreeding depression; hence these crosses would not likely to yield beneficial transgressive segregants. he narrow sense heritability estimates were high with family III (51.23%), family IV (62.43%), family V (79.47%), and family IV (74.05%), and moderate with family I (24.25%) and II (42.96%). Moderate heritability with low genetic advance in family I (9.50%) and in family II (16.78%) revealed the possibility of existence of both additive and non-additive gene effects; therefore population improvement is suggested for enhancement of this character. Whereas, high heritability coupled with high genetic advance *i.e.* 21.19, 25.72, 31.95 and 29.12 per cent respectively for families III, IV, V and VI suggested preponderance of additive gene action and direct selection for improvement of the character in segregating generation of these families would be effective [5, 7, 10, 11, 13, 14].

Number of secondary branches per plant: Crosses GM-2 x NUDH-45-1 (-35.32%), GM-2 x RH-8813 (-9.77%) and GM-3 x RH-8813 (-9.03%) had significant and negative inbreeding depression which is desired for transgressive segregants. In contrast to this, cross GM-3 x NUDH-45-1 (15.96%) exhibited significant and positive inbreeding depression. Narrow sense heritability estimates were high with families IV (50.29%) and V (105.43%). Whereas, family II (33.29%) and family VI (23.09%) had moderate estimates. Low estimates of expected genetic advance as percent of mean for families I (0.40), II (10.90), III (5.60) and VI (9.36) suggested prime role of non-additive gene effect, indicating that it would be difficult to improve through direct selection [5, 14, 19].

Length of main branch: The crosses GM-3 x NUDH-45-1 (-5.48%) and GM-3 x B-35 (-11.78%) exerted significant and negative inbreeding depression, which is desired for beneficial transgressive segregants. The cross GM-2 x NUDH-45-1 (14.23%) followed by GM-2 x RH-8813 (7.37%) depicted significant and positive inbreeding depression. For narrow sense heritability, families III (92.72%), IV (64.63%), V (76.15%) and VI (94.52%) had high estimates, and for family I (48.76%) and II (27.02%) it was moderate. The high narrow sense heritability estimates and moderate expected genetic advance for families IV (19.61%) and V (18.07%), while high expected genetic advance for families III (23.10%) and VI (26.87%) revealed that direct selection would be effective for improvement of the character; as additive gene effect is preponded [13,17,19].

Number of siliquae on main branch: For inbreeding depression only two crosses *i.e.,* GM-2 X B-351 (-10.10%) and GM-2 x RH-8813 (-5.39%) exerted significant and negative inbreeding depression, which is desired for beneficial transgressive segregants. Narrow sense heritability estimates were high with families III (76.35%), IV (63.14%), V (74.35%) and VI (85.17%). Whereas, family I (47.36%)

had moderate estimates. Negative estimate for family II indicated preponderance of non-allelic interaction. Moderate narrow sense heritability coupled with moderate genetic advance as percentage of mean for family I (14.15%) showed importance of both additive and non-additive gene effect for the inheritance of character, and it would be difficult to improve through direct selection. The high narrow sense heritability estimates and high expected genetic advance for families III (22.02%), IV (22.11%) and VI (26.81%) revealed that direct selection would be effective for improvement of the character; as additive gene effect preponded [4, 5].

Number of siliquae per plant: For inbreeding depression only one cross *i.e.,* GM-3 x RH-8813 (-16.97%) exerted significant and negative inbreeding depression, which indicated possibilities for the desirable segregants. The cross, GM-3 x NUDH-45-1 (16.26%) followed by GM-2 x B-351 (11.64%), GM-2 x RH-8813 (10.56%) and GM-3 x B-351 (8.27%) depicted significant and positive inbreeding depression which yielded undesirable transgressive segregants. The narrow sense heritability estimates were high with family I (73.85%), family V (106.11%) and family VI (62.40%). However, extremely high heritability estimates were observed in family V (106.11%) because of sampling error due to small population size of generation involved. Negative estimate for family II and family IV indicated preponderance of non-allelic interaction. Low heritability (2.74%) with low genetic advance (1.05%) in family III revealed preponderance of non-additive gene action. The high heritability with high genetic advance in families I (25.94%), V (49.07%) and VI (25.51%) revealed preponderance of additive gene action, there by direct selection would be effective for improving this trait in subsequent generations [5,11-14].

Siliquae length (cm): The cross GM-3 x B-351 (-6.94%) exerted significant and negative inbreeding depression, which is desired for beneficial transgressive segregants. The cross GM-2 x NUDH-45-1 (10.61%) followed by GM-2 x B-351 (5.48%) and GM-3 x RH-8813 (4.57%) depicted significant and positive inbreeding depression. For narrow sense heritability, estimates were moderate for family IV (25.82%), V (35.12%) and VI (22.94%), while it was extremely high with family II (123.60%) and III (140.88%) which might be due to sampling error because of small population size. The high narrow sense heritability estimates and high expected genetic advance for families II (29.79%) and III (38.04%) revealed that direct selection would be effective for improvement of character; with preponderance to additive gene effect. The bi-parental mating could be followed in families IV, V and VI, as prime role of non-additive gene effect [4, 5, 13, 19].

Number of seeds per siliquae: The estimate of inbreeding depression was significant and negative for cross GM-2 x RH-8813 (-15.92%) followed by GM-3 x B-351 (-9.59%), GM-3 x RH-8813 (-9.23%) and GM-3 x NUDH-45-1 (-8.46%) which is desirable for transgressive segregants. The cross GM-2 x NUDH-45-1 (9.85%) andGM-2 x B-351 (6.25%) depicted significant and positive inbreeding depression. For the character number of seeds per siliquae, narrow sense heritability estimates were high for families II (56.43%), V (66.72%) and VI (81.98%). Whereas estimate of narrow sense heritability were moderate with family III (21.37%) and family IV (41.59%). Low values of narrow sense heritability (8.44%) and low estimates of expected genetic advance (2.00%) in family I, suggested the preponderance of non-additive gene effect, and it would be difficult to improve the character through direct selection. Moderate to high values of narrow sense heritability and moderate estimates of expected genetic advance in families II (14.58%), IV (11.10%), V (15.54%) and VI (19.07%) revealed importance of both additive and non-additive gene effect [4, 5, 7, 10, 12, 13].

Seed yield per plant: The estimates for inbreeding depression ranged from -17.80 (GM-3 x RH-8813) to 0.44 (GM-3 x NUDH-45-1) per cent. The cross GM-3 x RH-8813 (-17.80%) followed by GM-3 x B-351 (-14.62%) and GM-2 x RH-8813 (-12.30%) expressed significant negative inbreeding depression desired for transgressive segregants. The crosses GM-2 x NUDH-45-1 (21.05%) and GM-2 x B-351 (20.99%) expressed significant positive inbreeding depression, suggesting considerable reduction in seed yield per plant in F_2 generation. For narrow sense heritability, estimates were high for families family II (57.59%), V (95.65%) and VI (50.68%). Negative estimate for family III and VI indicated preponderance of non-allelic interaction. The high narrow sense heritability estimates and high expected genetic advance for families II (28.94%), IV (56.63%) and VI (25.34%) revealed that direct selection for improvement of seed yield per plant in segregating generation of these families would be effective [1, 4, 5, 7, 11, 13, 16].

1000 seed weight: The inbreeding depression was highly significant and negative in crosses GM-3 x B-351 (-14.31), GM-2 x RH-8813 (-9.11%) and GM-3 x NUDH-45-1 (-8.24%), indicating desirability of these crosses for isolation of transgressive segregants. For narrow sense heritability, the estimates were high for families I (110.71%), II (115.30%), III (53.01%), IV (102.67%) and VI (93.53%). Moderate estimates were found for family V (19.84%). However, extremely high heritability estimates for families I, II and IV would be because of sampling error due to small population size of generation involved, there by heritability estimates would be less reliable. Moderate narrow sense heritability coupled with low genetic advance as percentage of mean for family V (5.65%) showed preponderance of non-additive gene effect for the inheritance of character, and it would be difficult to improve through direct selection. high narrow sense heritability and genetic advance for families I (26.96%), II (36.45%), IV (24.99%) and VI (31.71%) revealed the importance of additive gene effect so, direct selection would be effective for improvement of 1000 seed weight. The bi-parental mating could be followed in families III as both additive and non-additive gene effects are involved [7, 11-14].

Oil content: Inbreeding depression estimates were positive with crosses GM-2 x B-351 (4.94%) and GM-3 x RH-8813 (3.22%). Whereas, crosses GM-2 x NUDH-45-1 (-8.88%) and GM-3 x B-351 (-3.99%) exhibited significant and negative effect desired for beneficial transgressive segregants. The estimates of narrow sense heritability were high for family I (58.10%), family II (80.48%), family III (90.26%), and family IV (64.60%); however, extremely high heritability estimates for families VI (107.72%) would be because of sampling error due to small population size of generation involved. Whereas negative estimate for family V indicated preponderance of non-allelic interaction. High narrow sense heritability coupled with low genetic advance as percentage of mean for families I

(6.86%) and IV (8.12%) showed preponderance of non-additive gene effect for the inheritance of character, and it would be difficult to improve through direct selection. The estimates of genetic advance were moderate for families II (10.85%) and VI (15.62%). High estimates of narrow sense heritability and moderate estimates of expected genetic advance revealed possibility of existence of both additive and non-additive gene effects; therefore population improvement is suggested for improvement of the character [4, 5, 7, 10, 12, 13, 17].

Protein content: In respect to inbreeding depression, crosses GM-2 x NUDH-45-1 (-5.27%) followed by GM-3 x B-351 (-5.14%), GM-2 x RH-8813 (-3.36%) and GM-3 x NUDH-45-1 (-2.80%) exhibited significant and negative estimates, which is desirable as transgressive segregants would be superior to F_1 for protein content. The cross GM-2 x B-351 (2.71%) expressed significant positive inbreeding depression. The narrow sense heritability estimates were high for family I (58.09%), family II (80.58%), family IV (84.98%), and moderate in family V (27.35%); however, extremely high heritability estimates for families VI (109.95%) would be because of sampling error due to small population size of generation involved. Whereas negative estimate for family III indicated preponderance of non-allelic interaction. High narrow sense heritability coupled with low to moderate genetic advance as percentage of mean for families I (9.22%), II (14.26%), IV (14.75%), V (3.49%) and VI (20.21%) showed importance of both additive and non-additive gene effect with preponderance of non-additive gene effect for the inheritance of character, and it would be difficult to improve through direct selection. Therefore population improvement like recurrent selection and bi-parental mating is suggested for improvement of the character [5, 6, 12, 13, 15].

Discussion:

The inbreeding depression is an important criterion for crop breeding programme. The character and cross-wise results of inbreeding depression are presented in Table 2, in which positive and significant inbreeding depression was observed in the all the families for days to 50% flowering, days to maturity and plant height indicating possibilities to get the desirable segregants in the segregating generations.

Seed yield per plant had significant and negative estimates of inbreeding depression in the crosses GM-3 x B-351, GM-2 x RH-8813 and GM-3 x RH-8813, which showed possibilities of desirable segregants in F_2 population. These crosses also exhibited significant and negative values of inbreeding depression for yield attributing characters *viz.,* number of secondary branches per plant, number of seeds per siliquae and 1000 seed weight. However, crosses GM-3 x B-351 and GM-3 x RH-8813 showed significant and positive estimates of inbreeding depression for seed yield per plant, average siliquae length, number of seeds per siliquae and 1000 seed weight; hence these crosses would not likely to yield beneficial transgressive segregants.

The magnitude of mean performance of F_2 populations for seed yield per plant and its related traits showed significant inbreeding depression for various characters in majority of crosses studied. The results revealed that the crosses which depicted significant inbreeding depression for seed yield per plant also exhibited positive inbreeding depression for its related traits also.

Overall, high estimates of narrow sense heritability and expected genetic advance in most of families for number of primary branches per plant, number of siliquae on main branch, number of siliquae per plant, seed yield per plant and 1000 seed weight, revealed that direct selection would be effective for improvement of character; and an additive gene effect was preponded. While high narrow sense heritability coupled with low to moderate expected genetic advance as per cent of mean for characters *i.e.* days to 50% flowering, days to maturity, plant height, length of main branch, oil content and protein content, revealed importance of both additive and non-additive gene effect with preponderance of non-additive gene effect for the inheritance of character, and it would be difficult to improve through direct selection. Therefore population improvement like recurrent selection and bi-parental mating is suggested for improvement of the character. However estimates of heritability were moderate to high with low to moderate expected genetic advance as per cent of mean for number of secondary branches per plant, average siliquae length and number of seeds per siliquae, which suggested the preponderance of non-additive gene effect, and it would be difficult to improve the character through direct selection.

Table: 1: List of Parental genotypes of proposed study

Sr. no.	Parents	Origin/Source of seed
Female Parents		
1.	GM-2	Main Castor and Mustard Research Station, S.D.A.U., Sardar Krishi Nagar-385-505 (Gujarat).
2.	GM-3	
Male Parents		
3	NUDH-45-1	Narendra deva University of Agriculture & Technology, Faizabad (U. P.).
4.	B-351	Birsa Agricultural University, Bihar.
5.	RH-8813	CCS Haryana Agriculture University, HISSAR-125 004.

Table 2: Estimates of inbreeding depression (ID), narrow sense heritability (h^2ns) and expected genetic advance as percent of mean (GA %) for various characters in six crosses in Indian mustard.

	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	Length of main branch (cm)	No. of siliquae on main branch
I. GM-2 x NUDH-45-1							
ID	8.37** (0.70)	3.05** (0.70)	9.80** (3.18)	1.12 (0.25)	-35.32** (0.66)	14.23** (1.67)	11.72** (1.24)
h2ns	116.4	116.39	125.63	24.45	1.01	48.76	47.36
GA	17.05	7.62	20.94	9.5	0.4	12.07	14.15
II. GM-3 x NUDH-45-1							
ID	4.45** (0.62)	1.98** (0.62)	7.36** (4.03)	20.83** (0.31)	15.96** (0.79)	-9.2064	1.52 (1.53)
h2ns	101.96	100.97	-	42.96	33.29	27.02	-
GA	13.75	6.13	-	16.78	10.9	6.78	-
III. GM 2 x B-351							
ID	4.77** (0.69)	2.09** (0.67)	13.10** (3.86)	8.81* (0.29)	5.00 (0.86)	1.40 (1.52)	-10.10** (1.33)
h2ns	102.73	103.72	53.39	51.23	15.47	92.72	76.35
GA	14.02	6	8.11	21.19	5.6	23.1	22.02
IV. GM-3 x B-351							
ID	2.88* (0.60)	1.26* (0.60)	17.93** (4.14)	10.40** (0.26)	6.63 (0.79)	-11.78** (1.92)	-2.70 (1.56)
h2ns	-	-	-	62.43	50.29	64.63	63.14
GA	-	-	-	25.72	19.2	19.61	22.11
V. GM-2 x RH-8813							
ID	3.59** (0.67)	3.25** (0.67)	17.56** (3.70)	-1.41 (0.32)	-8.0114	7.37** (1.88)	-5.39** (1.19)
h2ns	-	-	0.49	79.47	103.42	76.15	74.35
G A	-	-	0.07	31.95	44.68	18.07	17.94
VI. GM-3 x RH-8813							
ID	4.91** (0.67)	3.03** (0.67)	15.88** (3.74)	-6.18 (0.26)	-6.2307	3.59 (1.97)	2.52 (1.40)
h^2ns	67.4	65.4	69.04	74.05	23.09	94.52	85.17
GA	8.56	3.86	11.63	29.12	9.36	26.87	26.81
*,** significant at 5% and 1% level of significance, respectively, Values in parentheses represent S Em values, "-" Indicates abnormal negative values, Bold values indicate abnormal heritability							

Table 3: Estimates of inbreeding depression (ID), narrow sense heritability (h2ns) and expected genetic advance as percent of mean (GA %) for various characters in six crosses in Indian mustard.

	No. of siliquae per plant	Siliquae Length (cm)	No. of seeds per siliquae	Seed yield per plant	1000 seed weight	Oil content	Protein content
I. GM-2 x NUDH-45-1							
ID	5.63 (12.67)	10.61** (0.11)	9.85*(0.46)	21.05** (1.10)	7.06**(0.09)	-8.88** (0.38)	-5.27** (0.38)
h2ns	73.85	83.56	8.44	5.37	110.71	58.1	58.09
GA	25.94	17.98	2	2.04	26.96	6.86	9.22
II. GM-3 x NUDH-45-1							
ID	16.26** (15.88)	-0.37 (0.11)	-3.5532	0.44 (1.14)	-8.24** (0.09)	-0.01 (0.31)	-2.80** (0.31)
h2ns	-	123.6	56.43	57.59	115.3	80.48	80.48
GA	-	29.79	14.58	28.94	36.45	10.85	14.26
III. GM 2 x B-351							
ID	11.64** (14.18)	5.48* (0.13)	6.25* (0.43)	20.99** (1.21)	5.28* (0.09)	4.94** (0.43)	2.71* (0.27)
h2ns	2.74	140.88	21.37	-	53.01	90.26	-
GA	1.05	38.04	5.39	-	13.33	33.07	-
IV. GM-3 x B-351							
ID	8.27* (14.52)	-1.1798	-5.5622	-21.4914	-14.31** (0.11)	-3.99** (0.36)	-5.14** (0.34)
h2ns	-	25.82	41.59	-	102.67	64.6	84.98
GA	-	5.67	11.1	-	24.99	8.12	14.75
V. GM-2 x RH-8813							
ID	10.56** (17.42)	-1.69 (0.14)	-15.92** (0.38)	-17.097	-9.11** (0.096)	1.87 (0.35)	-3.36** (0.30)
h2ns	106.11	35.12	66.72	95.65	19.84	-	27.35
GA	49.07	7.55	15.54	56.63	5.65	-	3.49
VI. GM-3 x RH-8813							
ID	-16.97** (14.23)	4.57** (0.09)	-9.23** (0.36)	-17.80** (1.07)	7.68** (0.12)	3.22** (0.36)	-1.89 (0.33)
h2ns	62.4	22.94	81.98	50.68	93.53	107.72	109.95
GA	25.51	4.87	19.07	25.34	31.71	15.62	20.21
*,** significant at 5% and 1% level of significance, respectively, Values in parentheses represent SEm values, "-" Indicates abnormal negative values, Bold values indicate abnormal heritability							

Conclusion

Most of the crosses showed high heritability for different traits. The higher estimates of heritability indicated that these traits were comparatively less affected by environment and their phenotype is a good reflection of genotype. Therefore in order to select a superior genotype on the basis of its phenotypic performance, these matric traits could be efficiently utilized. However, in case of lower heritability, pedigree, sib or progeny test can be employed to improve it.

The different types of gene effects are useful for analyzing the genetic architecture of a crop so as to further improve desirable traits. The estimates obtained from each cross may be unique to that cross and may not be applicable to the parental population. The additive effects and gene interaction *viz.,* dominance x dominance (l) or other type of digenic complementary gene interactions can be exploited effectively by selection**.** Use of reciprocal recurrent selection or bi-parental mating could be suggested for improving those characters when additive and non- additive gene effects are involved. In addition to additivity and dominance, epistatic interactions of various kinds were also observed; one or two cycles of intermating of selected segregants may be adopted to accumulate favorable genes through recurrent selection which will result in the improvement of seed yield. It was also noted that even though generation mean analysis utilized compact family block design for layout of the experiment, sampling errors do occur resulting in abnormal statistical estimates. Increasing the number of replications may be the only way to overcome this limitation which becomes all the more difficult due to the non-availability of viable seeds of different generations involved in the study. By making sufficient number of crosses and increasing the base population, this drawback can be overcome to a considerable extent.

Inbreeding depression refers to decrease in fitness and vigour due to continuous selfing. It decreases heterozygosity and cause fixation of unfavourable/lethal recessive alleles in F_2, while in case of heterosis, undesirable recessive genes of one parent are masked by favourable dominant alleles of other parent.

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