Plant Archives Vol. 18 No. 2, 2018 pp. 1689-1694 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

ASSESSMENT OF GENETIC VARIATION AND PARAMETERS AMONG ADVANCED BIPARENTAL PROGENY LINES (BIP F_3) *BRASSICA JUNCEA*

Vaishali Sapkal[1], Shanti Patil[1]*, Deepak Sapkal[2], Renu Yadav[2], Naleeni Ramawat[2].

[1]College of Agriculture, Nagpur
[2]Amity Institute of Organic Agriculture, Amity University, Sector-125, Noida (U.P.)

Abstract

Forty advanced biparental progeny lines in BIPF$_3$ generation along with six checks (RH-819, Geeta, Pusa bold, Varuna, Ashirwad, ACN-9) were evaluated in three replications with the objectives to estimate between family and within family variances, to estimate genetic parameters and to identify superior progenies at experimental farm of Agricultural Botany section, College of Agriculture, Nagpur during *rabi* 2014. Observations were recorded on days to first flower, days to maturity, plant height, number of branches plant^{-1}, number of siliqua plant^{-1}, 1000 seed weight and seed yield plant^{-1}, chlorophyll content index and leaf relative water content. Analysis of variance indicated that the mean squares due to between families were highly significant for all traits, which revealed the presence of significant genetic variability between the families. Inter class correlation (t) lead to the conclusion that differences between individuals within family is large and each family differentiated distinctly from the other one at lower level in both the generations and hence, equal weightage to σ^2f and σ^2w were suggested to be considered for selection in BIP F_3 generation. Genetic parameters estimated revealed that number of siliqua plant^{-1} and seed yield plant^{-1} were the only two characters in BIP F_3 generations to be influenced by additive gene action and selection would be effective in improving these traits. Hence, considering these two characters for selection, 51 individual plants from 31 progenies out 40 studied which recorded significant superiority were identified for evaluating them in progeny rows for one more generation before forwarding to yield trails.

Key words: BIP F_3 generation, within family variance, between family variance, genetic parameters.

Introduction

In world, area under mustard cultivation is 34.19 million hectares producing about 63.09 million tones of seeds with average productivity of 1850 Kg ha^{-1} (Anonymous, 2013a). Area under mustard cultivation in India was 6.3 mha with production of 7.4 mt and average productivity of 1176 Kg ha^{-1} (Anonymous, 2013b) and in Vidarbha region having production of 330 tones and productivity of 380 Kg ha^{-1} (Anonymous, 2011). The districts in which mustard is grown *viz.*, Chandrapur, Gondia, Bhandara, Gadchiroli, Nagpur and Wardha.

Mustard is important oilseeds crop. It contributes more than 13 per cent to the global production of edible oil. Mustard seed contains significant amount of protein *i.e.* 27% with desired amino acid profiles. In recent years, substantial efforts are being made to improve both the quality and quantity of seed yield and other yield related parameters and transfer its useful traits to related Brassica oil crop (Gupta *et al.,* 2011). The earliness and higher seed yield with higher oil per cent are the major components to increase the cash value of this crop, so there is an urgent need to develop high yielding, early maturing varieties, adopted to local semi dry agro-climatic condition (Singh and Dixit, 2007). In India the average productivity of Indian mustard is low in comparison to the developed countries, especially in Vidharbha it is grown as mixed cropping rather than sole cropping. Considering the low productivity in Vidharbha region, there is need of developing high yielding varieties with early maturity and high oil content. Identification of superior parents, promising cross combinations and suitable breeding methodology are the important pre-requisites for development of high yielding genotypes. In India, *Brassica*

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*Author for correspondence : E-mail : vaishalisapkal15@gmail.com

is mostly grown under arid and semi arid environment therefore, could serve as model crop. Adverse environmental factors, of which water scarcity represent the most severe constraint to agriculture, account for about 70% of potential yield loss worldwide. Further rapeseed mustard grown on conserved moisture received from moisture rains. Drought conditions occur ubiquitously during the growing season and have a profound negative effect on rapeseed mustard productivity. This also necessitates screening and development of drought tolerance genotypes. A series of experiment were performed to synthesize the drought tolerance breeding material (Singh *et al*., 2011). Now, it is the time to develop varieties, which can tolerate water stress to increase yield and area under oilseed crops. To evolve a variety having high yield in combination with good yield contributing traits requires the information on the nature and magnitude of variation in the available materials. This information is most important, meaningful and has practical utility in a segregating population, where selection is actually practiced. In advanced segregating generation like F_4/ F_5 of self pollinated crop, homozygosity is expected to be achieved. But if biparental mating is done in F_2 generation and then carried over to the further generations, it becomes necessary to find the extent of variability in each of the generation and also to test whether homozygosity attained or not. Keeping these ideas in mind, this study was, planned and executed to find the extent of variability and its heritable component for yield and yield components in advanced biparental progeny lines (BIP F_3).

Materials and method

During *rabi* 2014 40 advanced biparental progeny lines in BIP F_3 generation (Obtained through biparental mating in two crosses Ashirwad × RH-819 and ACN-9 × Geeta) were raised along with check varieties (ACN 9, Geeta, RH-819, Varuna, Pusa bold, Ashirwad) in randomized block design with three replications for evaluation at the experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur. As RH-819 and Geeta drought tolerant were one of the parents in development of progenies under studies, this experimental material was raised in shallow field to allow easy drainage of water. Irrigation was given only once for germination and later the field was exposed to complete moisture stress. The recommended cultural practices were followed to raise the healthy crop. Five randomly selected plants were chosen randomly from BIP progenies and each check varieties for recording observations on days to first flower, days to maturity, plant height (cm), number of primary branches plant^{-1}, chlorophyll content index (SPAD), leaf relative water content (%), 1000 seed weight, number of siliqua plant^{-1}and seed yield plant^{-1}(g). The data recorded were subjected to the following statistical and biometrical analysis *viz.,* analysis of variance to estimate between families and within families variances and Intra class correlation (t) as per the method given by (Sharma,2006), and genetic parameters like genotypic variance, phenotypic variance, genotypic coefficient of variation (%), phenotypic coefficient of variation (%), heritability (broad sense), and genetic advance (GA) as per the standard formula, given by Hanson *et al.*(1956); Robinson *et al.* (1949) and Burton (1953).

Results and discussion

Forty advanced biparental progeny lines were evaluated in BIP F_3 generation for nine characters and results are presented and discussed below. The data on the analysis of variance (table 1) resulted in highly significant mean squares due to between family for all nine traits studied *i.e.* days to flowering, days to maturity, number of branches plant^{-1}, plant height, number of siliqua plant-1, 1000 seed weight, seed yield plant^{-1}, chlorophyll content index and leaf relative water content. This indicates the presence of significant genetic variability between the families for all the nine characters which allowed the estimation of genetic parameters. In accordance to this result significant variability between the family were also reported by Cheema and Sadaquat (2005b), Khan *et al*. (2008), Sadat *et al*. (2010) and Afrin *et al*. (2011) in mustard.

The inter class correlation (t) estimated in BIP F_3 ranged from 0.036 = 3% for days to maturity to 0.699 = 69% for plant height. Highest inter class correlation value was observed for plant height 0.699 = 69% followed by 1000-seed weight 0.528 = 52.6%, number of siliqua plant^{-1} 0.286 = 28.6%, seed yield plant^{-1} 0.284 = 28.4% and chlorophyll content index 0.282 = 28.2%. This revealed that 69%, 52.8%, 28.6%, 28.4% and 28.2% of variation for plant height,1000-seed weight, number of siliqua plant^{-1}, seed yield plant^{-1} and chlorophyll content index respectively in BIP F_3 family was due to difference between the families and 31%, 47.2%, 71.4%, 71.6%, 71.8% within families. This indicates that difference between individuals within a family is large for all the characters but each family distinctly differentiated from other at lower level except for plant height in which opposite trend was observed. Therefore, equal weightage was suggested to be assigned to σ^2f and σ^2w. This results indicates that between family selection followed by within family selection will be more rewarding in BIP F_3 generation also Mean, range, genotypic coefficient of

Table 1: Analysis of variance for different traits in BIP F_3 generation.

		Mean sum of square								
Source of Varieties	**df**	**Days to 1st flower**	**Days to maturity**	**Plant height (cm)**	**No. of branches plant^{-1}**	**No. of siliqua plant^{-1}**	**Seed yield plant^{-1}**	**1000 seed weight**	**Chlorophyll content index**	**Leaf relative water content (%)**
Between families	45	42.93**	23.70**	1289.88**	1.23**	7777.48**	47.79**	2.24**	102.95**	313.54**
Within families	644	6.86	15.17	225.37	0.54	2393.70	9.74	0.18	14.94	162.26
Inter class correlation (t)		0.260	0.036	0.699	0.079	0.286	0.284	0.528	0.282	0.059

** Significant at 1% level

variation, phenotypic coefficient of variation, heritability, and genetic advance were calculated for nine characters in BIP F_3 progenies and are presented in table 2.

Coefficient of variation (CV): Significant differences were observed between the progenies for all the nine characters studied. The coefficient of variation (CV) ranged from 4.80 to 45.51% for various characters. The lowest co-efficient of variation (= 20) was observed for the character days to maturity (4.80%), days to flowering (5.82%), 1000 seed weight (9.01%), plant height (10.63%) and chlorophyll content index (10.87%), which shows the best genetic potential and its genetic influence. The high coefficient of variation was observed for seed yield plant^{-1} (45.51%), number of siliqua plant^{-1} (41.51%), number of branches plant^{-1} (24.97%) and leaf relative water content (21.49%) which indicates more influence of environmental fluctuation. Similar to this results Khan *et al.* (2008) reported low coefficient of variation for days to flowering and plant height (cm) in *Brassica napus* and Afrin *et al.* (2011) reported moderate to high coefficient of variation for number of branches plant^{-1}, number of siliqua plant-1, 1000 seed weight and seed yield plant^{-1}.

Mean and Range: The grand mean recorded over 40 families along with six checks were found to be 44.94 days for days to first flower, 81.01 days for days to maturity, 140.69 cm for plant height, 2.93 for number of branches plant^{-1}, 35.53% for chlorophyll content index, 59.25% for leaf relative water content, 117.96% for number of siliqua plant^{-1} and 6.88 g for seed yield plant^{-1}. Wide range of 99.87 was exhibited for number of siliqua plant^{-1} followed by plant height (51), leaf relative water content 25.13, days to first flower (14.13) and chlorophyll content index (13.91) which indicates wide range of variation functioning for these characters. Seed yield plant^{-1} (8.81g), days to maturity (8.33), 1000 seed weight (1.61) and number of branches plant^{-1} (1.26) exhibited low range of variation. Even though a range of only 8.81g was observed for seed yield plant^{-1} it was considerable as the maximum level of yield shown by check variety was only 11.57 g. In accordance to these results wide range of variation for yield and yield components were also reported by Cheema and Sadaqat (2005 a and b), and Ahmed *et al.* (2013) in mustard.

Genotypic variance, phenotypic variance and their respective coefficient of variation: The

Table 2: Genetic parameters estimates for different traits in BIP F_3 generation.

Parameter	**Days to 1st flower**	**Days to maturity**	**Plant height (cm)**	**No. of branches plant^{-1}**	**No. of siliqua plant^{-1}**	**1000 seed weight**	**Seed yield plant^{-1}**	**Chlorophyll content Index**	**Leaf relative water content**
CV	5.82	4.80	10.63	24.97	9.01	41.51	10.87	45.51	21.49
Mean	44.94	81.08	140.69	2.93	117.96	4.02	6.88	35.53	59.25
Range	39.47-53.60 (14.13)	83.93-75.6 (8.33)	124.53-175.53 (51)	2.27-3.53 (1.26)	63.80-163.67 (99.87)	5.05-3.44 (1.61)	3.53-11.57 (8.84)	30.34-44.25 (13.91)	46.93-72.06 (25.13)
Genotypic variance	2.40	0.56	520.64	0.046	558.91	0.146	3.87	5.86	10.08
Phenotypic variance	9.26	15.74	744.47	0.583	1952.6	0.278	13.61	20.80	172.34
GCV (%)	3.45	0.93	16.21	7.327	20.04	9.53	28.55	6.81	5.36
PCV (%)	6.77	4.89	19.34	26.02	37.46	13.12	53.62	12.83	22.15
Heritability (%)	25.96	3.61	69.34	7.92	28.62	52.82	28.43	28.20	5.85
GA	1.39	0.25	33.58	0.10	21.76	0.49	1.81	2.26	1.35
GA (X of mean)	3.09	0.31	23.87	3.63	18.46	12.20	26.30	6.37	2.28

Table 3: Performance of the plants selected from BIP F_3 progenies.

Sr. no	Progeny	Plant no. selected	Seed yield plant^{-1} (g)	No. of siliqua plant^{-1}	Chlorophyll content index	Leaf relative water content (%)
(1)	(2)	(3)	(4)	(5)	(6)	(7)
1	BAR/30-2	1	16.5	205	46.7	65
2		2	18.0	288	48.0	68
3		5	14.5	280	49.3	72
4	BAR/29-2	5	13.0	230	45.0	76
5	BAR/98-17	9	12.5	235	46.0	63
6	BAR/98-18	7	13.2	245	42.4	76
7	BAR/83-6	10	12.5	205	45.9	75
8	BAR/39-6	9	13.5	203	46.1	76
9	BAR/63-2	8	14.9	236	48.1	78
10		12	12.3	206	47.5	71
11		15	12.9	240	45.9	64
12	BAR/36-11	15	12.5	230	46.7	68
13	BAR/72-2	1	18.5	244	48.5	69
14		11	12.4	220	48.2	65
15		14	14.0	250	46.2	73
16		15	18.5	280	46.3	79
17	BAR/77-2	11	16.0	235	47.1	83
18		12	18.0	245	47.3	84
19		15	12.5	225	48.7	87
20	BAR/77-3	1	12.0	250	45.2	89
21		2	13.5	240	45.0	84
22	BAR/77-4	3	12.4	190	48.4	78
23	BAG/64-20	13	13.4	187	43.4	78
24	BAG/26-9	9	12.4	201	46.0	93
25	BAG/51-2	7	12.0	210	47.2	83
26		13	13.0	270	45.0	82
27	BAG/77-16	6	19.5	245	49.4	84
28		7	17.0	235	47.4	75
29	BAG/89-2	3	12.4	180	48.9	78
30		7	15.5	255	45.3	75
31		9	14.5	198	45.6	73
32	BAG/89-15	3	14.0	210	47.1	79
33	BAG/89-18	11	12.5	204	45.4	81
34		14	12.4	215	46.8	84
35	BAG/23-15	11	18.0	305	46.0	85
36	BAG/13-2	1	14.0	255	46.2	83
37		3	13.0	205	45.1	87
38	BAG/83-2	1	13.5	240	45.2	84
39		3	12.9	201	48.9	79
40	BAG/48-3	1	16.0	240	48.3	86
41		2	13.0	204	48.9	89
42	BAG/48-17	12	12.0	250	47.3	86
43	BAG/21-5	6	12.5	246	43.3	83

Continue table 3 ....

phenotypic variance and phenotypic coefficient variation was observed to be far higher than the genotypic variance and genotypic coefficient variance for nine characters studied. This indicates the higher influence of environment in the phenotypic expression of these characters. Similar to this result higher influence of environment on days to maturity, plant height, number of branches plant^{-1}, number of siliqua plant^{-1} and seed yield plant^{-1} were also reported by Afrin *et al.* (2011) in (*Brassica napus*). Genotypic coefficient of variation exhibited the values from low to high category. High genotypic coefficient of variation was exhibited for seed yield plant^{-1} (28.55%), moderate genotypic coefficient of variation for plant height (16.21%) and number of siliqua plant^{-1} (20.04%) and low genotypic coefficient of variation for 1000-seed weight (9.53%), number of branches plant^{-1} (7.32), chlorophyll content index (6.81%), days to first flower (3.45%), and days to maturity (0.93%).

Similarly phenotypic coefficient of variation was also observed to be low to high for different characters. High phenotypic coefficient of variation was observed for seed yield plant^{-1} (53.62%), number of siliqua plant^{-1} (37.46%), number of branches plant^{-1} (26.02%) and leaf relative water content (22.15%). Moderate phenotypic coefficient of variation was observed for plant height (19.34%), 1000 seed weight (13.12%), chlorophyll content index (12.83%) and low for days to first flower (6.77%) and days to maturity (4.89%). In accordance to these results high genotypic coefficient of variation and phenotypic co-efficient of variation for seed yield plant^{-1} and number of siliqua plant^{-1} were also reported by Akbar *et al.* (2003) and Sadat *et al.* (2010) in mustard.

Heritability and Genetic advance: The heritability estimates

Continue table 3 ....

(1)	(2)	(3)	(4)	(5)	(6)	(7)
44	BAG/25-17	11	19.5	305	45.2	74
45	BAG/84-2	1	16.0	255	46.1	79
46		2	20.0	350	42.2	69
47		3	17.0	285	43.2	78
48	BAG/19-3	8	12.5	184	42.7	76
49	BAG/82-20	1	15.0	229	46.2	85
50	BAG/06-4	3	14.0	208	45.2	81
51	BAG/06-11	6	15.3	285	46.3	78
52	RH819		6.59	108.07	34.8	57.8
53	Geeta		9.27	115.93	34.7	57.8
54	Pusa B		9.55	126.80	37.7	55.7
55	ACN-9		8.11	106.20	42.0	59.4
56	Varuna		11.57	135.20	46.2	52.2
57	Ashirwad		10.74	155.53	44.2	49.7

provides information on transmission of traits from parents to offspring. Such estimates facilitates the evaluation of genetic and environmental effect aiding in selection. Estimation of heritability is often used to predict genetic advance under selection so that the plant breeder can anticipate improvement of different type and intensity of selection. Heritability per cent ranged from 69.34% (plant height) to 3.61% for (days to maturity). Except, plant height (69.34%) and 1000 seed weight (52.82%) heritability was observed to be low for all the traits studied *i.e.* number of siliqua plant^{-1} (28.62%), chlorophyll content index (28.20%), days to first flower (25.96%), seed yield plant^{-1} (28.43%), number of branches (7.92%), leaf relative water content (5.85%) and days to maturity (3.61%). The low estimate of heritability for the above traits suggested the major role of environmental factors in the expression for these traits. In accordance to these result Khan *et al.* (2008), Singh *et al.* (2011a) and Ahmed *et al.* (2013) also reported major role of environmental factors in the expression of different traits in Brassica genotypes based on heritability.

Genetic advance as percentage of mean were high for seed yield plant^{-1} (26.30%) and plant height (23.87%), moderate for number of siliqua plant^{-1} (10.19%) and low for chlorophyll content index (6.37%), number of branches (3.63%), days to first flower (3.09%), leaf relative water content (2.28%),1000 seed weight (0.49%) and days to maturity (0.31%). Similar to these results high genetic advance as percentage of mean was also reported by Sadat *et al.* (2010) for number of siliqua plant^{-1} and seed yield plant^{-1} in rapeseed.

When all the genetic parameters for nine characters were considered, it was found that seed yield plant^{-1} exhibited high genotypic coefficient of variation, low heritability along with high genetic advance as percentage of mean. Similarly number of siliqua plant^{-1} exhibited moderate genotypic coefficient of variation, low heritability with moderate genetic advance as percentage of mean. Another character plant height also exhibited high heritability and high genetic advance as percentage of mean. This indicates that in all these three characters seed yield plant^{-1}, number of siliqua plant^{-1} and plant height additive gene action was found operating in the expression of these traits in BIP F_3 generation and hence helps as criteria for making selection. Other characters which exhibited low or moderate genotypic coefficient variation, low heritability along with low genetic advance as percentage of mean could not be used as criteria for selection.

It was observed from this study that seed yield plant^{-1} and number of siliqua plant^{-1} were the characters which exhibited high or moderate genotypic co-efficient of variation, low heritability and high or moderate genetic advance as expressed as percentage of mean suggesting the influence of additive gene action and selection would be effective in improving these traits. Hence, seed yield plant^{-1} and siliqua plant^{-1} were considered as criteria for selection. As these progenies under studies were derived using drought tolerant parents (RH-819 and Geeta), chlorophyll content index and leaf relative water content were also considered during selection even though they exhibited low heritability and the low genetic advance. The main objective of this experiment was to identify superior progenies for forwarding to yield trails expecting that homozygosity will be attained in this generation *i.e.* F_4 (BIP F_3) according to conventional method of handling segregating generation. In contrary to this expectation, between family variance, within family variance and intra class correlation (t) revealed that differences between individuals within a family is large and each family is also different from the other but at low level. This was also observed from the low mean performance of progenies when compared with check for seed yield plant^{-1} and number of siliqua plant^{-1}. This might be due to the reason that, biparental mating done in F_2 generation would have resulted in new type of recombinants which may be in the heterozygous condition. This may require more number of generations to reach homozygosity. Hence, in this BIP F_3 generation equal weightage to σ^2f (between family variance) and σ^2w (within family variance) was suggested to be given during selection. Therefore, instead of selecting superior progeny for forwarding to yield trails individual plants exhibiting significant superiority over check for seed yield plant^{-1} and number of siliqua plant^{-1} from different progenies which also recorded numerical superiority for chlorophyll content index and leaf relative water content were considered as the criteria for selection. Based on this criteria 51 individual plant from 31 progenies out of 40 progenies studied fulfilling the above criteria were identified for evaluation for one more generation. The performance of selected individual plant are presented in table 3. It was observed from the Table that seed yield plant^{-1} of selected individuals ranged from 12 to 20 g and number of siliqua plant^{-1} from 180 to 350. The yield level of the selected plants were observed to be very high as compared to check. The chlorophyll content index (SPAD) and leaf relative water content (%) were also either high or at par with check in the selected line. In this study as additive gene effect were predominant for seed yield and number of siliqua plant^{-1}, it was suggested that the selected 51 individual plants from BIP F_3 generation should be raised in progeny rows for one more generation so that homozygosity will be attained and superior progenies can be then selected for forwarding to yield trails in the next generation.

References

Afrin,K.S., F. Mahmud, S.R. Bhuiyan and A. Rahim (2011). Assessment of genetic variation among advanced lines of *Brassica napus* (L.), *Agronomski Glasnik*, 201 - 222.

Ahmad, B., S. Muhammad, J. Ali and I. Ali (2013). Genetic variability studies of some quantitative traits in advance mutant lines of winter Rapseed (*Brassica napus* L.). *Life Sci. J.,* **10(12)**:103-108.

Akbar, M., T. Mahammad, M. Yaqub, M. Anwar, M. Ali and N. Iqbal (2003). Variability, Correlation and Path Coefficient Studies in Summer Mustard (*Brassica juncea* L.). *Asian J. Pl. Sci.,* **2(9)**: 696-698.

Anonymous (2013a). Agricultural Statistics at glance.

Anonymous (2013b). Dept. of Economics and Statistics, GOI, New Delhi.

Anonymous (2011). Joint Directorate of Agriculture, Nagpur division.

Burton, G.W. and E. M. Devane (1953). Estimating heritability in tall Fescue (*Festuca circunclinaceae*) from replicated clonal-material. *Agron. J.,* **45**: 478-481.

Cheema, K.L and H. A. Sadaqat (2005 a).Variability studies of some morphological traits in canola under irrigated and drought condition. *J. Agric. Res.,* **43(4)**: 273-287.

Cheema, K.L. and H.A. Sadaqat (2005 b). Potential and genetics basis of drought tolerance in canola (*Brassica napus)* variability studies of some morphological traits in canola under irrigated and drought condition. *J. Agric. Res.,* **43(4)**: 299-315.

Gupta, P., Chaudhary and S.K. Lal (2011). Heterosis and combining ability analysis for yield and its components in Indian mustard (*Brassica juncea* L.) Czern and coss. *Acad. J. Pl. Sci.,* **4(2)**: 45-52.

Hanson, G.H., H.F. Robinson and R.E Comstock (1956). Biometrical studies on yield in segregating populations. *Agron. J.,* 268 - 272.

Khan, S., Farhatullah, I.H. Khalil, I. Munir, M.Y. Khan and N. Ali (2008). Genetic variability for morphological traits in $F_{3:4}$ Brassica populations. *Sarhad J. Agric.,* **24(2)** : 217 - 222.

Robinson, H.F., R.E. Comstock and V.H. Harvey (1949). Estimates of heritability and degree of dominance in corn. *Agron. J.,* **41**: 353 - 359.

Sadat, H.A., G.A. Nematzadeh, N.B. Jelodar and O.G. Chapi (2010). Genetic evaluation of yield and yield components at advanced generations in rapeseed (*Brassica napus* L.). *Afr. J. Agric. Res.,* **5(15)**: 1958-1964.

Sharma, J.R. (2006). Measure of variance. In Statistical and Biometrical Techniques in Plant Breeding.Ist Ed.Published by New Age International (P) Ltd. Pp.40-42.

Singh, M., A. Tomar, C.N. Mishra and S.B.L. Srivastava (2011). Genetic parameters and character association studies in Indian mustard, *J. Oilseed Brassica,* **2(1)**: 35-38.

Singh, R.K. and P. Dixit (2007). Heterosis and combining ability studies for seed yield, its attributes and oil content in Indian mustard (*B. Juncea*). *Crop Improv.,* **34**: 192-196.