



GENETIC VARIABILITY STUDIES OF SOME QUANTITATIVE TRAITS IN ADVANCED BIPARENTAL PROGENY LINES OF MUSTARD

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Abstract

Information about the genetic variability and the extent and type of relationship of some quantitative characters in Indian mustard is important for an efficient breeding program. Eighty eight advanced biparental progenies along with six checks (RH-819, Geeta, Pusa bold, Varuna, Ashirwad, ACN-9) were evaluated in two 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* 2013. Data were recorded on days to maturity, plant height, number of branches plant⁻¹, number of siliqua plant⁻¹, 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 six 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^2_f and σ^2_w were suggested to be considered for selection. Genetic parameters estimated revealed that number of siliqua plant⁻¹ and seed yield plant⁻¹ were the only two characters which were found to be influenced by additive gene action and selection would be effective in improving these traits.

Key words: Advanced biparental progenies, genetic variability, quantitative traits.

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, 2013). 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, 2013) 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 Vidarbha it is grown as mixed cropping rather than sole cropping. Considering the low productivity in Vidarbha 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* is mostly grown under arid and semi arid environment therefore, could serve as model crop. Adverse environmental factors, of which water scarcity represent

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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 progenies.

Materials and method

During *rabi* 2013, 88 advanced biparental progenies obtained through biparental mating (BIP) in two crosses (Ashirwad×RH 819 and ACN 9×Geeta) of mustard along with six check varieties (ACN-9, Ashirwad, Geeta, RH-819, Varuna, and Pusa bold) were raised in randomized block design with 2 replications for evaluation, with a spacing of 45×15 cm² and with 2 row plots⁻¹ at the experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur. The parents RH-819 and Geeta involved as one of the parent in the evolution of the progenies were drought tolerant (Singh and Chaudhary, 2003). In addition to the regular components to be evaluated, an attempt to find out the ability of the progenies to tolerate stress was also done in this study. Hence, the experimental material were raised in shallow field to drain any kind 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. Total 20 plants were chosen randomly from BIP progenies and 5 randomly selected plant in each check varieties for recording observations. in BIP F_2 generations on days to maturity, plant height (cm), number of primary branches

plant⁻¹, chlorophyll content index (SPAD), leaf relative water content (%), number of siliqua plant⁻¹, 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 (G A) as per the standard formulas given by Hanson *et al.*(1956); Robinson *et al.* (1949) and Burton (1953).

Results and discussion

The results on analysis of variance (table 1) showed highly significant mean squares due to between families for six traits *i.e.* plant height, number of branches plant⁻¹, number of siliqua plant⁻¹, seed yield plant⁻¹, chlorophyll content index, and leaf relative water content. For days to maturity mean square value due to between family was found to be non significant. These results revealed the presence of significant genetic variability between the families where present for all the six characters except days to maturity. This allowed the further estimation of genetic parameters. In accordance to this results significant genetic variability between the families were also reported by Cheema and Sadaqat (2005 b), Khan *et al.* (2008), Sadat *et al.* (2010) and Afrin *et al.* (2011) in mustard. Inter class correlation (t) which is the ratio of two variances *i.e.* between family variance (σ^2_f) and total phenotypic variance (σ^2_p) were estimated in this study. This value was observed to be highest (0.291 = 29%) for seed yield plant⁻¹ followed by number of siliqua plant⁻¹ (0.254 = 25%) and number of branches plant⁻¹ (0.237 = 23%). This indicated that 29%, 25% and 23% of variation of seed yield plant⁻¹, number of siliqua plant⁻¹ and number of branches plant⁻¹ respectively in advanced biparental families were due to differences between the families and 71%, 75% and 77% were due to within families. This means that difference between individual within family is large but each family is distinctly differentiated from the other at lower level. Therefore, equal weightage should be assigned to σ^2_f and σ^2_w . This indicates between family selection followed by within family selection will be more rewarding.

Creation of variability is a prerequisite either for development of variety or inbred lines, generally amount of variability generated is more in early segregating generation as compared to later generation. If we attempt intermating in early segregating generation of different

Table 1: Analysis of variance of different traits in advanced biparental progenies.

Source of Varieties	df	Mean sum of square						
		Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of siliqua plant ⁻¹	Seed yield plant ⁻¹ (g)	Chlorophyll content index (SPAD)	Leaf relative water content (%)
Between families	93	20.61	1280.96**	8.08**	9256.82**	32.62**	41.08**	486.56**
Within families	1786	18.02	871.41	1.12	1184.83	3.61	24.27	75.68
Inter class correlation (t)		0.007	0.023	0.237	0.254	0.291	0.033	0.213

** Significant at 1% level

individuals additional variability will be released since biparental mating among the segregant in the F₂ of a cross may provide opportunity for the recombination. Variability parameters like mean, range, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance were estimated for seven characters in advanced biparental progenies and are presented in table 2 and the *per se* performance of 88 families along with checks are presented in table 3.

Days to maturity: The difference between 88 families studied were found to be non significant for days to maturity which indicates that there is no variation between families. This is also observed from the low coefficient of variation of (5.23%) and narrow range (78 - 83.6 days). Therefore, the other genetic parameter for this trait were not estimated. However BAR/08 matured early at 78 days followed by BAG/13 (78.8 days) and BAR/79 (79 days), BAG/10 matured late at 83.60 days followed by BAG/26 (83.40 days) and BAR/16 (83.20 days). Similar to this result Sadat *et al.* (2010) also reported non significant differences for days to maturity. Hence this trait could not be considered for selection.

Plant height (cm) : The final plant height reflex the growth behavior of a crop besides genetic characteristic, environmental factor also plays vital role in determining the height of the plant. The data recorded on the plant height varied significantly among the families. The overall mean value of the plant height was recorded to be 112.44 cm. The coefficient of variation was observed to be high for plant height (26.25%) which indicates the best genetic potential and more influence of environmental fluctuation. Data for plant height was in the range of (100 - 142.79 cm). The maximum plant height was found in BAG/83 (142.79 cm) followed by BAG/25 (137.63cm) and BAR/63 (135.84 cm) and the minimum value was 100 cm in BAG/05. The phenotypic variance (891.89%) appeared to be very high than the genotypic variance (20.48%) suggesting considerable influence of environment on the expression of the genes controlling this traits. Similarly phenotypic coefficient of variation (26.56%) also appeared to be higher than genotypic coefficient of variation (4.02%). Low heritability (2.29%) along with low genetic advance in percentage of mean (1.07%) were estimated for this trait. This indicate that this trait is highly

Table 2: Genetic parameter estimates of different traits in advanced biparental progenies.

Parameter	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of siliqua plant ⁻¹	Seed yield plant ⁻¹ (g)	Chlorophyll content Index (SPAD)	Leaf relative water content (%)
CV	5.23	26.25	27.84	31.45	45.20	12.35	10.50
Mean	81.08	112.44	3.80	109.42	4.19	39.88	82.82
Range	78.00- 83.60 (5.6)	100.00- 142.79 (42.79)	2.70- 5.85 (3.15)	44.90- 167.80 (122.9)	2.02- 7.75 (5.73)	36.63- 43.60 (6.97)	62.65- 98.06 (35.41)
Genotypic variance	-	20.48	0.34	403.59	1.48	0.84	20.54
Phenotypic variance	-	891.89	1.470	1588.43	5.09	25.10	96.22
GCV (%)	-	4.02	15.49	18.36	29.05	2.29	5.47
PCV (%)	-	26.56	31.86	36.42	53.83	12.56	11.84
Heritability (%)	-	2.29	23.65	25.40	29.13	3.34	21.34
GA	-	1.20	0.504	17.82	1.15	0.29	3.68
GA (X of mean)	-	1.07	13.26	16.28	27.60	0.74	4.45

- Not estimated as the mean square was non significant

Table 3: *Per se* performance of 88 advanced biparental progenies and check for different traits.

Sr. no	Progeny	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of siliqua plant ⁻¹	Seed yield plant ⁻¹ (g)	Chlorophyll content index (SPAD)	Leaf relative water content (%)
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
1	BAR/30	79.45	107.89	4.55	108.30	4.60	37.91	74.85
2	BAR/40	80.90	122.16	3.45	128.25	3.50	39.31	72.20
3	BAR/80	82.60	121.05	4.40	113.30	4.12	41.41	79.58
4	BAR/43	79.90	124.74	4.35	124.20	4.41	40.52	85.95
5	BAR/29	80.60	116.00	4.00	111.10	4.90	38.95	79.59
6	BAR/66	81.00	115.37	3.95	113.85	4.35	39.64	76.24
7	BAR/79	79.45	111.21	4.05	95.90	2.10	40.72	81.03
8	BAR/93	79.95	115.53	4.85	97.70	2.62	38.46	81.05
9	BAR/90	81.20	117.24	3.30	89.25	2.41	37.23	73.50
10	BAR/48	81.95	106.95	2.85	74.90	2.88	39.25	74.40
11	BAR/98	82.10	115.84	4.10	132.10	5.19	39.99	62.65
12	BAR/69	81.50	118.74	3.80	111.45	3.33	40.56	75.51
13	BAR/45	80.60	118.79	4.00	115.60	3.10	41.61	75.85
14	BAR/83	82.05	119.68	3.65	121.70	5.49	40.05	85.68
15	BAR/16	83.20	120.79	3.60	118.00	3.44	39.56	81.45
16	BAR/05	81.25	122.11	3.55	114.45	3.97	39.98	82.62
17	BAR/33	80.15	111.63	4.90	101.40	6.47	40.92	79.45
18	BAR/19	79.75	110.84	3.90	114.75	5.46	40.13	80.20
19	BAR/56	79.75	113.89	4.00	114.30	5.00	38.24	76.21
20	BAR/95	82.20	117.11	4.00	132.50	5.28	39.28	79.15
21	BAR/39	81.20	118.58	3.90	113.90	3.90	38.75	78.10
22	BAR/97	82.35	117.74	3.50	102.00	3.57	38.94	81.70
23	BAR/06	82.85	123.53	3.90	124.30	4.21	41.30	76.80
24	BAR/63	81.40	135.84	3.85	133.00	5.58	43.60	77.05
25	BAR/41	80.15	118.95	3.70	104.45	4.24	42.72	79.85
26	BAR/27	81.65	113.68	3.35	105.25	2.49	38.89	77.49
27	BAR/36	79.95	119.47	3.10	106.25	4.83	38.94	79.45
28	BAR/55	80.95	115.11	4.20	99.35	2.03	40.60	80.85
29	BAR/13	80.85	133.21	3.55	142.70	5.36	41.64	87.70
30	BAR/72	79.80	113.42	4.80	99.20	4.29	40.47	80.35
31	BAR/77	80.60	118.68	3.75	167.80	7.75	39.90	98.06
32	BAR/22	80.90	110.79	3.15	98.50	4.13	41.64	80.80
33	BAR/91	80.30	115.79	3.40	74.40	3.18	40.24	83.75
34	BAR/84	80.20	105.00	3.35	53.00	2.42	39.90	85.05
35	BAR/54	79.50	125.74	3.30	109.10	4.46	41.39	87.10
36	BAR/08	78.00	113.47	3.05	111.00	2.71	39.27	84.85
37	BAR/52	81.70	110.79	3.45	52.25	3.42	40.28	80.75
38	BAR/58	81.40	114.53	3.20	111.05	3.61	41.64	81.00
39	BAR/86	82.20	118.37	3.90	79.25	2.35	41.41	80.05
40	BAR/64	81.30	120.42	3.35	116.60	5.66	39.19	82.10
41	BAR/10	80.60	126.05	4.10	116.65	2.78	38.17	80.25
42	BAR/67	80.30	120.26	2.95	128.75	3.37	39.53	82.30
43	BAR/87	82.50	119.47	3.40	83.80	2.02	40.96	83.05
44	BAR/89	81.40	119.47	3.05	104.65	3.16	40.37	88.30
45	BAR/94	81.45	102.79	2.95	91.55	2.78	39.22	84.95
46	BAG/45	80.85	105.89	3.70	104.70	2.73	39.26	85.30
47	BAG/16	81.00	122.89	3.30	86.80	3.81	38.97	82.15

Continue table 3

Continue table 3

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
48	BAG/47	80.55	118.89	4.25	136.75	5.15	39.65	86.05
49	BAG/26	83.40	130.00	3.60	136.80	5.46	37.57	85.60
50	BAG/51	81.30	124.47	2.90	101.65	4.20	40.63	84.45
51	BAG/75	81.45	110.00	2.90	101.40	3.02	38.04	88.75
52	BAG/05	80.45	100.00	3.25	54.00	2.93	40.05	82.00
53	BAG/66	79.95	114.74	3.75	101.95	3.64	41.09	80.90
54	BAG/76	81.30	113.47	3.35	101.20	3.61	40.40	83.60
55	BAG/74	81.35	119.21	3.05	107.15	3.19	38.47	84.60
56	BAG/97	82.85	107.26	3.25	76.25	2.97	38.70	85.04
57	BAG/10	83.60	109.74	3.50	94.45	2.83	41.50	84.95
58	BAG/28	80.65	106.05	3.25	99.90	3.51	37.68	84.30
59	BAG/58	80.30	123.42	3.20	118.55	4.34	38.07	83.90
60	BAG/46	81.15	102.37	2.90	98.30	3.79	39.97	83.52
61	BAG/98	81.65	106.95	3.75	74.50	2.68	40.64	91.14
62	BAG/77	81.05	121.32	4.35	129.90	5.46	40.71	85.42
63	BAG/89	79.70	115.53	4.90	126.20	6.11	42.18	92.42
64	BAG/67	79.80	114.21	4.55	100.50	3.41	41.19	84.89
65	BAG/23	81.75	103.58	3.95	108.70	4.70	39.46	84.19
66	BAG/34	81.05	123.16	3.60	107.35	4.96	40.37	86.48
67	BAG/07	81.85	125.74	4.55	122.20	5.91	39.99	86.64
68	BAG/61	81.30	120.26	3.95	127.35	4.83	41.40	85.54
69	BAG/01	81.65	134.26	5.25	127.20	3.73	40.54	84.59
70	BAG/13	78.80	134.26	4.30	133.05	5.74	39.36	87.77
71	BAG/36	80.15	126.37	4.30	139.45	5.42	40.19	85.00
72	BAG/83	80.95	142.79	5.85	134.20	5.14	39.16	84.46
73	BAG/92	80.45	122.42	5.25	111.65	4.57	41.34	88.38
74	BAG/48	80.50	102.37	4.45	106.15	4.27	42.03	83.22
75	BAG/21	80.60	116.26	4.80	150.05	5.77	41.69	90.25
76	BAG/25	80.05	137.63	4.95	133.15	4.45	40.89	82.06
77	BAG/84	79.90	124.42	4.75	122.70	4.79	39.55	83.23
78	BAG/19	81.00	132.37	4.55	126.85	5.59	38.53	81.20
79	BAG/86	81.15	131.84	3.55	96.80	5.16	38.86	82.17
80	BAG/31	81.40	121.00	3.55	104.15	4.02	40.34	83.32
81	BAG/78	80.90	125.00	4.45	107.95	4.67	42.35	81.44
82	BAG/54	79.85	118.21	3.35	85.10	2.73	40.72	83.87
83	BAG/43	81.95	120.00	3.20	81.20	3.73	40.99	80.47
84	BAG/90	80.65	119.21	3.15	99.55	4.05	40.50	80.22
85	BAG/82	82.20	130.53	3.95	141.20	7.25	38.27	92.60
86	BAG/06	81.60	129.42	3.90	132.00	4.82	38.64	82.77
87	BAG/12	82.70	119.47	2.70	101.90	2.69	40.96	84.09
88	BAG/74	81.50	109.74	3.90	86.80	2.99	43.37	80.49
89	RH-819	81.00	108.47	4.60	103.10	5.90	36.63	80.23
90	Geeta	80.70	127.05	3.00	134.10	5.45	37.09	80.69
91	Pusa bold	80.50	124.79	3.85	130.55	5.82	39.19	90.43
92	ACN-9	81.60	115.00	3.35	134.25	6.50	38.24	92.49
93	Varuna	79.60	119.21	4.20	117.40	5.94	38.06	82.56
94	Ashirwad	82.55	114.89	3.65	96.50	5.20	38.51	88.15
GM		81.04	112.44	3.80	109.42	4.19	39.88	82.82
S.E±		0.09	0.68	0.024	0.79	0.04	0.11	0.20
C.D(5%)		0.27	1.94	0.06	2.26	0.12	0.32	0.57

influenced by the environmental effect and selection would be ineffective. Similar to this result Akbar *et al.* (2003) also reported low genotypic coefficient of variation of 5.94% for plant height in mustard and Singh *et al.* (2011a) reported low genetic advance as percentage of mean (6.2) in mustard suggested in efficiency of selection in this trait.

Number of branches plant⁻¹ Highly significant differences were observed among the families for the number of branches plant⁻¹. The mean number of branches over all the families was observed to be 3.80 with a range of (2.70 - 5.85). This trait recorded high coefficient of variation value of 27.84% which shows more influence of environmental fluctuation. The highest number of branches plant⁻¹ was observed in BAG/83 (5.85) followed by BAG/01, BAG/92 (5.25) and lowest in BAG/12 (2.70). The highest number of branches plant⁻¹ was observed in BAG/83 (5.85) followed by BAG/01, BAG/92 (5.25) and lowest in BAG/12 (2.70). The phenotypic variance (1.47%) and phenotypic coefficient of variation (31.86%) were higher than the corresponding genotypic variance (0.34%) and genotypic coefficient of variation (15.49%) respectively. The estimate of heritability (23.65%) was low with moderate genetic advance as percentage of mean (13.26%) indicating selection based on this trait could not be judicious. Similar to this result Akbar *et al.* (2003) reported moderate genetic advance as percentage of mean in mustard crop for number of branches plant⁻¹.

Number of siliqua plant⁻¹: The variance due to number of siliqua plant⁻¹ showed significant differences among the families. The number of siliqua plant⁻¹ ranged from 44.90% to 167.80% with a mean value of (109.42) and high coefficient of variation of 31.45%. Maximum number of siliqua plant⁻¹ was borne in the progeny BAR/77 (167.80) followed by BAG/21 (150.05) and BAR/13 (142.70). The phenotypic variance and phenotypic coefficient of variation (1588.43%, 36.42% respectively) were much higher than genotypic variance and genotypic coefficient of variation (403.59 and 18.36% respectively) indicating that phenotypic expression of this character is highly governed by environment. The low heritability estimate (25.40%) with moderate genetic advance as percentage of mean (16.28%) observed for this trait suggested that this trait can give good opportunity for selecting high valuable family for breeding programme, as this character is influenced by additive genetic component. In accordance to this result Akbar *et al.* (2003), (Cheema and Sadaqat (2005a and b), Afrin *et al.* (2011) and Ahmed *et al.* (2013) also observed the influence of additive gene action in the expression of number of siliqua plant⁻¹ in mustard and reported the

efficiency of considering this trait for selection.

Seed yield plant⁻¹ (g) : Seed yield plant⁻¹ showed highly significant differences between the families that suggested considerable range of variation for this trait. The mean seed yield plant⁻¹ over 88 families was observed to be 4.19 g with a range of (2.02 g-7.75 g) and high coefficient of variation (45.20%). The phenotypic variance (5.09%) and phenotypic coefficient of variation (53.83%) were greater than their corresponding genotypic variance (1.48%) and genotypic coefficient of variation (29.05%), indicating high environmental influence in this traits. Both genotypic coefficient of variation and phenotypic coefficient of variation for seed yield plant⁻¹ was observed to be high which revealed that this trait was governed by additional gene action. The estimated heritability was low (29.13%) with high genetic advance in percentage of mean (27.60%) indicating that phenotypic selection for seed yield plant⁻¹ would be effective. In accordance to this result Akbar *et al.* (2003), Cheema and Sadaqat (2005a and b) Afrin *et al.* (2011), Singh *et al.* (2011a) and Ahmed *et al.* (2013) also observed the influence of additive gene action in the expression of seed yield plant⁻¹ in mustard and reported the efficiency of considering this trait for selection.

Chlorophyll content index and Leaf relative water content (%) : The 88 families used in this study involves RH-819 or Geeta (drought tolerance genotypes) as one of the parents. An attempt to provide exposure to stress during the experiment was given by raising the experiment in shallow field to drain water and irrigated only once for germination. In order to find out the influence of drought tolerant gene in the progenies and their ability to tolerate moisture stress condition, observations on chlorophyll content index and leaf relative water content were recorded. Significant differences among the various families were observed for both chlorophyll content index and leaf relative water content. The highest chlorophyll content index was observed in RH-819 (43.60) and Geeta (43.37%). This was followed by the progeny BAR/41 (42.72%), BAG/78 (42.35%) and BAG/89 (42.18), and the lowest chlorophyll content index in BAR/74 (36.63%), but the mean value was 39.88%. Moderate coefficient of variation of 12.35% was recorded for this trait with a range of 36.63 to 43.60. The phenotypic variance (25.10%) and the phenotypic coefficient of variation (12.56%) were much higher than the corresponding genotypic variance (0.84%) and genotypic coefficient of variation (2.29%) respectively. This suggested the considerable influence of environment on the expression of genes controlling this traits. Low heritability estimate (3.34%) along with low genetic advance as percentage

of mean (0.74%) was observed for this traits. This result revealed that this trait is highly influenced by environmental fluctuation and selection will be ineffective. However in contrary to this result Sadaqat and Cheema (2005b) reported chlorophyll content to exhibit high coefficient of variability, high heritability and high genetic advance as percentage of mean and hence chlorophyll content can be considered as good selection criteria for drought tolerance. The families varied significantly for leaf relative water content with a mean value of (82.82%) and ranged from 62.65% (BAR/98) to 98.06% (BAR/77). The coefficient of variation recorded by this trait was found to be moderate (10.50%). The phenotypic variance (96.22%) and phenotypic coefficient of variation (11.84%) were observed to be higher than genotypic variance (20.54%) and genotypic coefficient of variation (5.47%) revealing high influence of environmental fluctuation. The trend similar to chlorophyll content index was observed for heritability and genetic advance for leaf relative water content also *i.e.* low estimates of heritability (21.34%) accompanied with low genetic advance as % of mean (4.45%) indicating in efficiency of selection based on this result. Cheema and Sadaqat (2005) reported a range of (69.76%) to (83.58%) in Brassica for this trait and high genetic advance as percentage of mean (21.13%) and suggested leaf relative water content index as criteria for selecting genotype for drought tolerance.

When all the six characters were considered, number of siliqua plant⁻¹ showed highest range of variation (122.9) that means a wide range of variation was present for this character. This character also showed the highest mean value (109.42). However, the phenotypic variance and phenotypic coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under study. Higher influence of environment for the expression of all the characters studied were observed. Seed yield plant⁻¹ (29.13%) exhibited maximum value of heritability followed by number of siliqua plant⁻¹ (25.40%), number of branches plant⁻¹ (23.65%), leaf relative water content (21.34%), chlorophyll content index (3.34%) and plant height (2.29%) but all the characters showed low heritability. Genetic advance as expressed in percentage of mean was high for seed yield plant⁻¹ (27.60%), moderate for number of siliqua plant⁻¹ (16.28%) and number of branches plant⁻¹ (13.26%) and low for leaf relative water content index (4.45%), plant height (1.07) and chlorophyll content index (0.74). Thus, it can be suggested here that the traits seed yield plant⁻¹ and number of siliqua plant⁻¹ were influenced by additive gene action, as they exhibited low heritability with high (or) moderate

genetic advance as percentage of mean, high phenotypic coefficient of variation and high or moderate genotypic coefficient of variation. In accordance to these result Sadat *et al.* (2010), Singh *et al.* (2011), Afrin *et al.* (2011) and Priyamedha *et al.* (2013) also reported the importance of number of siliqua plant⁻¹ and seed yield plant⁻¹ in Brassica as the selection criteria for identifying superior progenies.

From this study it was found that seed yield plant⁻¹ and number of siliqua plant⁻¹ were the only two characters which exhibited high or moderate genotypic coefficient of variation, high phenotypic coefficient of variation, low heritability along with high or moderate genetic advance as percentage of mean. This revealed that these two characters were influenced by additive gene action and selection would be effective in improving these traits. Simultaneously chlorophyll content index and leaf relative water content though exhibited low variability, heritability and genetic advance were should also be considered in order to observe the potential of promising lines towards drought tolerance. Between family variance, within family variance and inter class correlation (t) when considered, it was observed that difference between individuals within a family is large and each family is different from the other but at lower level. Hence, it is suggested to give equal weightage to σ^2_f and σ^2_w during selection in BIP F₂ generation Therefore, it is concluded from this study that selection of individual plants exhibiting significant superiority over the check for seed yield plant⁻¹ and number of siliqua plant⁻¹ from different progeny should be done for forwarding to the next generation.

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