



Research Article

GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN INDIAN MUSTARD (*Brassica juncea* L.)

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Abstract: ANOVA revealed that mean sum of squares due to genotypes (treatments) were significant for all the traits under studied. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters under study. Most of the characters including yield/ha depicted high GCV, PCV and narrow sense heritability. Genetic advance as per cent of mean was also higher for 1000-seed weight, silique length, plant height and number of primary branches. Seed yield per hectare was found to be positively correlated with 1000-seed weight, silique length, plant height, main shoot length and days to maturity at genotypic level. In general, the magnitude of genotypic correlation coefficients was higher than their corresponding phenotypic coefficients which indicated a strong inherent association between different traits studied and the phenotypic expression of these traits was less under the influence of environment. With regards to mean performance, the cross NRCHB 101 x NPJ 112 showed the highest seed yield (3293.01 kg/ha) followed by RH 406 x F1 (3077.37 kg/ha) and NPJ 112 x RRN 727 (2975.31 kg/ha) among all test genotypes where the mean seed yield was 2090.25 kg/ha. Mean oil content was 41.13 % and it was ranged from 38.6% (RRN 727) to 42.33% (DRMR 2019 x RRN 727) amongst the treatments.

Keywords: *B. juncea*, Genetic variability, Correlation, Heritability

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Introduction

Indian mustard (*B. juncea* L.) is a major *rabi* oilseed crop of the Indian subcontinent occupies more than 80% of the total rapeseed-mustard cultivated area. The enhancement in production and productivity of the crop assumes significance, not only for farmer's viewpoint but also to the edible oil industry and other vertical and horizontally linked enterprises and stakeholders. Indian vegetable oil economy is the fourth largest in the world after USA, China and Brazil. It accounts for 7.4% of world's oilseed output; 6.1 % of oil meal production; 3.9% oil meal export; 5.8% vegetable oil production; 11.2% oil import and 9.3% of the world's edible oil consumption [1]. In India, oilseeds contribute nearly 3.0% to gross national products and 10% to the value of all agricultural products respectively. About 14.0 million farmers are involved in oilseed cultivation and 1.0 million in processing. Despite being the fifth largest oilseed producing country in the world, India is also one of the biggest importers of vegetable oils. There is a spurt in the vegetable oil consumption in recent years, both for edible purposes as well as for industrial uses. The per capita consumption of oil which was only 2.5 kg in early 50's has reached to about 14.0 kg in recent years [2]. This will like in future with the growing population and changing consumption patterns. Knowledge about genetic factors responsible for the inheritance of yield contributing characters, for which there is a great genetic variability in the germplasm collections, is essential for any applied breeding programme. The knowledge of genetic correlation, which occurs between characters, can help the breeder to improve the efficiency of selection by using favorable combinations of traits and to minimize the retarding effect of negative correlations. The present investigation was under taken to study the inter-relationship and extent of genetic variability for seed yield and contributing traits.

Materials and Methods

The year- wise technical programme for the present investigation is detailed follows. Two genetically diverse genotypes (NPJ 112 and RRN 727) of *B. juncea* having various desirable traits were selected and a F1 cross viz., NPJ 112 x RRN 727 was generated during 2013-14. The two parents, F1 and 9 promising genotypes selected as lines were planted in crossing block during *rabi* 2014-15 and 27 crosses including 18 single and 9 three-way crosses [Table-1] were generated in triple test cross fashion. All these materials have been already generated under regular rapeseed-mustard breeding programme of ICAR-DRMR, Bharatpur. The crosses along with testers and lines were planted in randomized complete block design with three replications during *rabi* 2015-2016. All 39 treatments (lines, testers and crosses) were raised in rows of 4.5 m length with a distance of 30 cm between rows and 15 cm between plants, where each treatment was represented by two rows. Standard agronomic practices were followed to raise the good crop. Observations were recorded on randomly selected five competitive plants for twelve quantitative traits. Observations on days to flowering and maturity were recorded on per plot basis, seed yield was expressed in kg per hectare and the observations on remaining traits were recorded on randomly selected five competitive plants in each replication.

Differences between treatments for different characters were tested for significance using analysis of variance technique [3]. The coefficient of variation for different characters was estimated by formula as suggested by Burton [4]. The expected genetic advance was calculated by the formula given by Johnson, *et al.* [5]. Phenotypic and genotypic correlation coefficients were calculated by using the formulae suggested by Al-Jibouri, *et al.* [6].

Results and Discussion

Treatment analysis of variance revealed that the [Table-2] genotypes were significant for all the traits under studied. Therefore, a general conclusion can be that there is considerable amount of genetic variability for various traits among different parental genotypes and crosses. Similarly, the genetic variability for various traits in Indian mustard has been reported by many workers [7-13].

Table-1 List of genotypes, their pedigree, origin and source

SN	Genotype	Pedigree	Origin	Source
1	NPJ-112	SEJ-8 x Pusa Jagannath	IARI, New Delhi	IARI
2	RRN 727	RW-01-02 x Patan 67	ARS, Navgoan	Navgaon
3	RH-749	RH-781 x RH-9617	CCSHAU, Hisar	Hisar
4	RH-406	RH-6908 x RH-8812	CCSHAU, Hisar	Bharatpur
5	Rohini	Pure line selection from varuna	CSAU&T, Kanpur	Kanpur
6	NRCDR-2	MDOC-43 x NBPGR-36	DRMR, Bharatpur	Bharatpur
7	NRCHB101	BL-4 x Pusa Bold	DRMR, Bharatpur	Bharatpur
8	SEJ-2	<i>B. Campestris</i> x <i>B. Nigra</i>	IARI, New Delhi	IARI
9	DRMRIJ-31	HB-9908 x HB-9916	DRMR, Bharatpur	Bharatpur
10	DRMR2019	EC-399288 x BEC-107	DRMR, Bharatpur	Bharatpur
11	DRMR2035	PHR-1 x BEC-107	DRMR, Bharatpur	Bharatpur

Table-2 Mean sum of squares for various sources of variation in RBD analysis for 12 traits

S N	Characters	Mean sum of squares		
		Replication n(d.f.=2)	Treatment (d.f.=38)	Error (d.f.=76)
1	Day to flowering	13.41	158.09**	17.07
2	Day to maturity	105.24	295.86**	40.96
3	Plant height (cm)	158.96	2817.91**	113.01
4	Number of primary branches/plant	0.11	5.22**	0.71
5	Number of secondary branch/plant	2.37	43.12**	9.84
6	Number of siliquae on main shoot	29.27	188.64**	40.25
7	Main shoot length (cm)	63.96	283.69**	45.06
8	Siliqua length (cm)	0.19	1.58**	0.07
9	Number of seeds/siliqua	0.32	7.32**	1.53
10	1000-Seed weight (g)	0.03	3.17**	0.12
11	Oil content (%)	1.75	2.07**	0.93
12	Seed yield/ha (kg)	13513.95	1064598.26**	13654.73

* and ** indicate significant at 5% (p=0.05) and 1% (p=0.01) levels, respectively

Table-3 Estimates of different genetic parameters of variation for 12 traits among parents and crosses

S.No.	Character	Mean	Range	PCV (%)	GCV (%)	H ² (%)	GA	GA% Mean
1	Day to flowering	45.61	31.33- 63.33	17.55	15.03	73.36	12.1	26.52
2	Day to maturity	125.98	105.33- 142.33	8.91	7.32	67.47	15.6	12.38
3	Plant height (cm)	182.65	99.13- 235.67	17.44	16.44	88.86	58.31	31.92
4	Number of primary branches/plant	7.05	4.93- 10.07	21.11	17.39	67.87	2.08	29.51
5	Number of secondary branches/plant	21.16	14.13- 28.8	21.62	15.74	52.99	4.99	23.6
6	Number of siliquae on main shoot	56.91	44.0- 76.13	16.64	12.36	55.14	10.76	18.9
7	Main shoot length (cm)	82.19	55.07- 102.33	13.58	10.85	63.84	14.68	17.86
8	Siliqua length (cm)	4.17	2.7- 6.08	18.18	17.03	87.79	1.37	32.87
9	Number of seeds/siliqua	16.1	12.93- 19.73	11.54	8.63	55.88	2.14	13.29
10	1000-Seed weight (g)	3.82	1.42- 6.07	27.96	26.43	89.35	1.96	51.46
11	Oil content (%)	41.13	38.6- 42.33	2.79	1.5	29.05	0.69	1.66
12	Seed yield/ha (kg)	2090.25	829.63- 3293.01	28.86	28.32	96.25	1196.17	57.23

PCV: Phenotypic coefficients of variation; GCV: Genotypic coefficients of variation; H₂: Heritability; GA: Genetic advance

Table-4 Genotypic (above diagonal) and phenotypic (below diagonal) correlations of 12 characters in 39 genotypes in Indian mustard

Character	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
X1	1.000	0.854**	0.833**	0.699**	0.325*	0.443**	0.172	0.504**	-0.19	0.568**	-0.431**	0.298
X2	0.532**	1.000	0.642**	0.512**	0.222	0.078	0.135	0.573**	-0.049	0.548**	-0.115	0.351*
X3	0.663**	0.534**	1.000	0.698**	0.421**	0.381*	0.415*	0.642**	-0.11	0.828**	-0.201	0.632**
X4	0.521**	0.372**	0.566**	1.000	0.589**	0.259	-0.19	0.337*	-0.382*	0.499**	-0.501**	0.292
X5	0.206	0.135	0.322	0.537**	1.000	0.216	-0.156	0.033	-0.201	0.064	-0.203	0.318
X6	0.266	0.082	0.293	0.178	0.227	1.000	0.470**	0.098	-0.098	0.178	-0.05	0.006
X7	0.069	0.101	0.366*	-0.168	-0.048	0.524**	1.000	0.474**	0.464**	0.415*	0.317	0.374*
X8	0.359**	0.454**	0.592**	0.267	0.038	0.038	0.354*	1.000	0.350*	0.803**	0.119	0.603**
X9	-0.185	-0.007	-0.052	-0.237	-0.011	-0.101	0.256	0.328*	1.000	0.034	0.387*	0.324
X10	0.521**	0.406*	0.732**	0.387*	0.055	0.122	0.317	0.686**	0.021	1.000	-0.106	0.741**
X11	-0.227	0.051	-0.099	-0.324	-0.166	-0.099	0.129	0.094	0.169	0.022	1.000	0.119
X12	0.252	0.273	0.590**	0.276	0.24	0.009	0.305	0.557**	0.236	0.693**	0.014	1.000

X1: Day of flowering, X2: Day of maturity, X3: Plant height, X4: Number of primary branches, X5: Number of secondary branches, X6: Number of siliquae on main shoot, X7: Main shoot length, X8: Siliqua length, X9: Number of seeds/siliqua, X10: 1000-Seed weight, X11: Oil content, X12: Seed yield/hectare, *, **: Significant at 5% and 1% levels.

Table-5 Mean performance of parents and crosses related parameters for 12 traits in Indian mustard

S.No.	Genotype/Cross	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
A. Crosses													
1	1. RH-749 × NPJ-112	52.33	133.67	235.67	9.80	25.27	60.53	81.33	4.69	14.67	4.60	40.29	2716.87
2	2. RH-749 × F1	49.67	131.33	174.20	8.20	26.00	65.93	67.00	4.33	16.13	3.75	41.61	1763.79
3	3. RH-749 × RRN 727	44.33	124.00	152.33	6.33	22.20	46.13	63.20	3.16	15.40	2.52	41.24	1497.94
4	4. RH-406 × NPJ-112	49.67	132.67	208.00	10.07	24.20	59.87	75.00	4.27	14.93	4.31	41.55	2534.16
5	5. RH-406 × F1	42.33	130.00	196.33	6.67	26.07	62.87	91.40	3.71	17.33	4.02	40.92	3077.37
6	6. RH-406 × RRN 727	49.33	134.33	229.67	9.20	21.93	55.33	82.67	5.00	13.80	6.07	40.41	2609.05
7	7. ROHINI × NPJ-112	48.33	124.33	216.20	7.47	21.40	66.93	88.00	4.47	15.13	4.67	40.63	2588.48
8	8. ROHINI × F1	44.67	127.67	180.00	4.93	20.07	59.80	94.00	3.84	15.60	3.27	40.88	1576.13
9	9. ROHINI × RRN 727	41.33	121.67	161.20	5.60	19.47	44.00	70.67	3.55	17.40	2.71	42.12	1809.05
10	10. NRCDR-02 × NPJ-112	51.33	131.33	224.33	8.20	24.53	60.80	89.00	4.20	16.07	4.23	40.67	2455.14
11	11. NRCDR-02 × F1	43.67	126.00	193.00	6.73	22.33	54.27	85.67	4.19	16.67	3.53	42.23	2946.50
12	12. NRCDR-02 × RRN 727	44.67	126.67	186.67	7.60	25.33	64.80	80.47	3.87	17.00	2.77	42.03	1707.00
13	13. NRCHB-101 × NPJ-112	44.00	137.00	190.00	6.27	19.13	49.13	85.20	5.16	19.73	4.61	41.47	3293.01
14	14. NRCHB-101 × F1	36.33	105.33	181.67	5.87	18.27	50.67	86.13	4.22	16.87	3.93	41.05	2156.38
15	15. NRCHB-101 × RRN 727	31.33	119.33	136.67	6.53	21.53	51.33	78.67	3.25	13.60	2.68	42.04	1896.30
16	16. SEJ-2 × NPJ-112	47.33	107.33	202.67	7.73	24.27	63.53	92.00	4.50	17.27	4.65	41.02	2197.53
17	17. SEJ-2 × F1	44.00	107.33	160.33	6.40	16.47	76.13	96.00	3.89	16.53	3.05	41.17	1701.23
18	18 SEJ-2 × RRN 727	36.67	118.67	143.33	6.20	22.33	61.33	83.00	3.21	15.27	2.22	40.99	1023.87
19	19. IJ-31 × NPJ-112	44.00	128.33	170.00	7.27	17.53	49.60	78.33	5.02	16.93	4.62	42.01	1997.53
20	20. IJ-31 × F1	38.00	121.67	171.67	5.20	21.60	62.60	102.33	3.85	18.13	3.69	41.85	2258.44
21	21. IJ-31 × RRN 727	41.67	121.67	134.33	5.53	19.07	60.73	77.33	3.82	17.53	2.51	41.42	1506.17
22	22. WR-2019 × NPJ-112	42.67	128.00	184.67	7.47	16.33	44.13	87.33	4.87	18.67	4.27	41.32	2215.64
23	23. WR-2019 × F1	42.33	127.67	172.00	5.47	16.87	52.47	85.33	4.73	16.53	3.13	42.05	1804.12
24	24. WR-2019 × RRN 727	38.33	122.67	140.67	5.53	14.13	51.87	82.67	3.61	16.60	2.41	42.33	1069.14
25	25. WR-2035 × NPJ-112	53.67	132.00	204.67	8.20	25.27	65.47	94.67	4.25	18.87	3.35	39.85	1818.11
26	26. WR-2035 × F1	48.33	130.33	177.33	7.40	21.73	51.13	78.00	3.61	14.07	3.31	40.50	1665.84
27	27. WR-2035 × RRN 727	47.33	126.67	156.00	5.93	19.53	53.33	70.67	3.34	14.67	2.24	40.79	1013.99
	Mean of hybrids	44.36	125.10	180.87	6.96	21.22	57.21	83.19	4.10	16.35	3.60	41.28	2033.29
B. Lines													
28	1. RH-749	62.67	142.33	231.00	8.73	22.93	69.07	85.67	5.13	14.80	4.85	39.66	2360.49
29	2. RH-406	59.33	140.67	218.00	8.67	18.67	55.40	77.33	4.35	15.53	5.16	40.26	2026.34
30	3. ROHINI	54.33	135.67	230.67	9.20	28.80	55.20	72.33	4.09	13.33	4.51	41.43	1970.37
31	4. NRCDR-02	51.67	135.67	206.67	7.80	28.13	63.73	94.80	5.82	16.13	4.47	41.66	2434.57
32	5. NRCHB-101	47.67	132.67	196.33	6.67	19.27	46.07	82.67	6.08	18.13	5.24	41.15	2886.09
33	6. SEJ-2	44.00	108.33	177.67	5.87	15.00	62.73	78.87	3.21	12.93	3.80	40.92	1687.24
34	7. IJ-31	45.67	133.00	183.67	6.67	16.40	69.47	88.33	4.40	16.53	5.25	41.96	2212.35
35	8. WR-2019	45.67	133.67	179.00	5.47	14.87	53.60	95.00	4.52	15.73	4.78	42.30	2159.67
36	9. WR-2035	63.33	138.67	197.33	7.87	21.33	56.27	80.20	3.92	15.20	4.36	40.09	2724.28
	Mean of lines	52.70	133.41	202.26	7.44	20.60	59.06	83.91	4.61	15.37	4.71	41.05	2273.49
C. Testers													
37	1. P1- NPJ-112	39.33	119.67	169.33	6.13	19.00	49.80	78.20	4.35	16.60	4.37	40.02	2354.73
38	2. P2- RRN 727	32.67	109.67	99.13	7.67	20.80	46.60	55.07	2.70	14.73	1.42	38.60	829.63
39	3. F ₁ -NPJ-112× RRN 727	35.00	105.67	151.00	6.47	27.27	46.73	71.00	3.49	17.00	3.54	41.43	2975.31
	Mean of testers	35.67	111.67	139.82	6.76	22.36	47.71	68.09	3.51	16.11	3.11	40.02	2053.22
	Mean of parents (B+C)	44.19	122.54	171.04	7.10	21.48	53.39	76.00	4.06	15.74	3.91	40.53	2163.36
	G. Mean	45.61	125.98	182.65	7.05	21.16	56.91	82.19	4.17	16.10	3.82	41.13	2090.25
	S.E.	2.38	3.69	6.14	0.49	1.81	3.66	3.87	0.15	0.71	0.20	0.56	67.46
	C.D. 5%	6.72	10.41	17.29	1.37	5.10	10.32	10.91	0.43	2.01	0.57	1.57	190.03

X1: Day to flowering, X2: Day to maturity, X3: Plant height(cm), X4: Number of primary branches, X5: Number of secondary branches, X6: Number of siliques on main shoot, X7: Main shoot length (cm), X8: Silique length (cm), X9: Number of seeds/silique, X10: 1000-Seed weight (g), X11: Oil content (%), X12: Seed yield/hectare (kg)

The mean values, range, PCV, GCV, H₂ and GA of treatments for 12 characters are presented in [Table-3]. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters under study. The high PCV and GCV were observed for seed yield/ha, 1000-seed weight, number of primary & secondary branches / plant, silique length, plant height, days to flowering and number of silique on main shoot. The high GCV and PCV have been reported earlier by Kardam and Singh and Yadava, et al., for different yield contributing traits in Indian mustard [12, 13]. Similar findings pertaining to occurrence of high genetic variability has also been reported by Singh for different traits including seed yield [14]. The results indicated the presence of high amount of genetic variability in the evaluated treatment for the major yield contributing traits along with seed yield which showed that further improvement for these traits is possible. Days to flowering, days to maturity, number of primary & secondary branches, number of silique on main shoot, main shoot length, number of seeds / silique, seed yield / hectare, 1000-seed weight, silique length and plant height exhibited high heritability. High heritability for various traits has also been reported earlier [10, 12, 14, 15]. Genetic advance as per cent of mean was higher for 1000-

seed weight, silique length, plant height and number of primary branches indicating that selection for these traits would be effective for the improvement. Similar findings related to high genetic advance as per cent of mean have been reported by earlier workers for various traits [10, 12, 14, 15]. High heritability with high genetic advance for seed yield/plant has also been reported, which supports the results of the present investigation [10, 12, 14].

Knowledge of inter-relationships between different traits is of great significance to plant breeders. Firstly, they are highly useful in selecting characters which are neither easily observed nor genotypic values of which are modified by the environmental effects. Thus, any morphological character, which is associated with seed yield or makes a significant contribution to yielding ability, would be useful in the improvement of seed yield. Secondly, inter-relationships between characters help the breeder to assess the nature, extent and direction of selection pressure on characters. Seed yield per hectare was found to be positively correlated with 1000-seed weight, silique length, plant height, main shoot length and days to maturity. Similar results were also reported earlier [8, 12, 16-21].

Hence, selection for these traits would also help in improving the seed yield in this crop. Days to flowering showed significant positive correlations with days to maturity, plant height, number of primary & secondary branches, siliqua on main shoot, siliqua length and 1000-seed weight and negative with oil content. Days to maturity was positively correlated with plant height, primary branches, siliqua length, 1000-seed weight and seed yield; plant height with primary & secondary branches, siliquae on main shoot, main shoot length, siliqua length, 1000-seed weight and seed yield. Number of primary branches were positively correlated with secondary branches, siliqua length and 1000-seed weight and negatively with number of seeds per siliqua and oil content. Number of siliqua on main shoot was positively correlated with main shoot length; main shoot length with siliqua length, seeds / siliqua, 1000-seed weight and seed yield; siliqua length with number of seeds / siliqua, 1000-seed weight and seed yield; while number of seeds / siliqua was correlated with oil content. Similar results for different traits [Table-4] were reported earlier in rapeseed-mustard [8, 12, 14, 16-26]. Mean performance of the cross NRCHB 101 x NPJ 112 showed the highest seed yield (3293.01 kg/ha) followed by RH 406 x F1 (3077.37 kg/ha) and NPJ 112 x RRN 727 (2975.31 kg/ha) among all test genotypes where the mean seed yield was 2090.25 kg/ha. Genotype RRN 727 revealed lowest seed yield (829.63 kg/ha). Hence, the parental genotype RRN 727 was not included for seed yield but it has many desirable traits like short height, early maturity and more branches. It has reduced plant height and duration of maturity in all the crosses where it was one of the parent and resulted into many heterotic crosses viz., RH 406 x RRN 727 and NPJ 112 x RRN 727, RH 406 x F1 (NPJ 112 x RRN 727), NRCRD 2 x F1 directly and indirectly [Table-5]. Mean oil content was 41.13 % and ranged from 38.6% (RRN 727) to 42.33% (DRMR 2019 x RRN 727) amongst the treatments. Heterotic crosses with desirable traits has been earlier reported [13, 27-33].

Conclusion

The present study revealed that considerable amount of genetic variability for the major yield contributing traits along with seed yield which indicated that further improvement for these traits is possible. Genotypic correlation coefficients were higher than their corresponding phenotypic coefficients except siliqua on main shoot which indicated that the phenotypic expression of these traits was less under the influence of environment.

Application of research: This research will help in future for developing high yielding hybrid by selecting diverse genotypes and that will ultimately help to edible oil self-sufficiency in our country.

Research Category: Plant breeding and Genetics

Abbreviations:

GCV: Genotypic coefficients variation

PCV: Phenotypic coefficients variation

H²: Heritability

GA: Genetic advance

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