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Trait association and diversity in exotic lines of Indian mustard

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Abstract

Total 41 exotic lines of Indian mustard (*Brassica juncea* L.) were evaluated during winter 2016-17 under irrigated environments. The genetic variability, heritability and genetic advance as percentage of mean for nine quantitative characters *viz.* plant height, number of primary branches number of primary branches, number of siliquae per plant, siliqua length *(*cm), number seeds per siliqua, number of seeds per plant, total seed yield (g) and test weight (g). Analysis of variance showed significant differences among the accession for all characters under study. Path coefficient analysis was carried out using correlation coefficients to know the yield contributing traits having true associations with seed yield. Improvement in seed yield can be achieved by selection using the correlation and path analysis data generated in this study. Total seed yield/ plant was positively correlated with siliqua length. Number of seeds/ plant and test weight had higher phenotypic direct effects on total seed yield/ plant, revealing that indirect selection for these traits would be effective in improving seed yield. The high heritability coupled with high genetic advance for test weight would also be of great use for indirect selection for improvement in seed yield. The material used in the study is of diverse nature and can be used in the breeding programme for development of improved genotypes in mustard.

Keywords: *Indian mustard, correlation, path analysis, heritability, seed yield*

Introduction

Brassica juncea L. commonly known as Indian mustard is globally used as oilseed, vegetable and condiments (Saleem *et al.*, 2017). Mustard is the premier oilseed *Brassica* which covers about 85-90% of the total area under cultivation of all these crops (Rao *et al.*, 2017). It is second most important edible oilseed crop of the India after groundnut. Mustard seed contains about 38 to 43 percent oil which is yellow fragrant and is considered to be the healthiest and nutritious cooking medium (Patel *et al.*, 2012). Rapeseed-mustard oil is considered the best quality oil for human consumption as compared to other edible oils because of the lowest amount of harmful saturated fatty acids and adequate amount of two essential fatty acids i.e. linoleic and linolenic acid (Porter and Crompton, 2008). It is cultivated in *Rabi* season mainly in Northwest India and contributes nearly 27 per cent to edible oil pool of the country (Singh *et al*., 2010).

Coefficient of variation is helpful in exposing and understanding the clear picture of existing variability within the population. Heritability coupled with genetic advance would be more useful tool in predicting the resultant effect in selection of the best genotypes for seed yield and its attributing traits (Synrem *et al.*, 2014). Genetic diversity plays an important role in plant breeding because hybrid between lines of diverse origin generally display a great heterosis than those between closely related strains (Singh, 1983) which permits to select the genetically divergent plants to obtain the desirable recombination of the segregating generation. The assessment of parameters including phenotypic and genotypic coefficients of variation, heritability in broad sense, and genetic advance as % of mean is a pre-requisite for making effective selection (Manjunath *et al.*, 2017). An estimate of genetic advance along with heritability is helpful in assessing the reliability of character for selection (Meena *et al.*, 2017). The character showing high heritability along with low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding (Synrem *et al.*, 2014). The proper evaluation of important crop species helps in the identification and utilization of improved genotypes (Jan *et al.*, 2016). The present investigation was planned to access heritability, association between traits and defines suitable selection criteria for mustard yield improvement.

Materials and Methods

The material comprises 41 Indigenous line of *Brassica juncea* L. for estimation of agro-morphological variation. The germplasm were provided by NBPGR New Delhi, India. The present research work was conducted in the

Experimental Farm Department of Agriculture, Mata Gujri College, Sri Fatehgarh Sahib, Punjab, during winter 2016-17 using randomized block design (RBD) with three replications. This is place situated between 30°-27' and 30° -46' latitudes and 76° -04' and 76° -38 E latitudes and at mean height of 247 meters above mean see level. Row to plant spacing of 45x15 cm was maintained and proper plant population maintained by thinning. The recommended agricultural package of practices was followed for nutrient supply. Five randomly selected plants were selected to record the data. Data were recorded for nine quantitative traits such as plant height, number of primary branches number of primary branches, number of siliquae per plant, siliqua length (cm), number seeds per siliqua, number of seeds per plant, total seed yield (g) and test weight (g). Test of significance for each character were analyzed as per methodology advocated by Panse and Sukhatme (1967). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the formula given by Burton (1952), heritability in broad sense (h^2) by Burton and De Vane (1953) and genetic advance i.e. the expected genetic gain were calculated by using the procedure proposed by Johnson *et al.* (1955).

Results and Discussion

The mean performance of genotypes is presented in table 1. Analysis of variance revealed significant differences for all the nine traits studied. Variance due to genotype was highly significant for all the nine traits indicating the presence of sufficient variability in the genotypes selected for this study. High magnitude of variability has been reported in Indian mustard germplasm and varieties for various characters by many workers for plant height, total siliquae/plant and seed yield (Kumar and Misra, 2007 and Rathod *et al*., 2017). The reason for high magnitude of variability in the present study may be due the fact that the genotypes selected were developed in different breeding programmes representing different agro-climatic conditions of the country.

The estimates of genetic variability parameters for all the traits were worked out and are presented in Table 2. It was evident from the result that the phenotypic variance is greater than genotypic variance indicating the influence of environment on the expression of the trait. Among the yield attributes maximum PCV and GCV was depicted by total seed yield (41.7 and 22.5) followed by number of secondary branches per plant (25.4 and 17.8), test weight (24.7 and 24.5), number of seeds (23.9 and 11.0), number of siliquae per plant (25.4 and 12.0) number of primary branches per plant (20.2 and 12.7), number of seeds per siliqua (7.2 and 5.4), siliqua length (9.0 and 6.5) and plant height (8.0 and 4.4), respectively. The high values of PCV and GCV indicating that selection may be effective on these traits. The lowest value for PCV and GCV was indicating less scope of selection as they are under less influence of environment. Wide difference between PCV and GCV was observed for number of siliquae per plant, number of seeds, total seed yield, number of primary branches per plant which may indicate the high contribution of environmental variance to the phenotypic variance. These characters have been reported as main yield contributing traits (Kardam and Singh 2005). Similar findings pertaining to presence of high genetic variability were reported for different traits including seed yield/ plant (Singh, 2004; Rathod *et al*., 2017; Meena *et al.*, 2017). Results revealed presence of high amount of genetic variability in the evaluated genotypes for the major yield contributing characters along with seed yield which indicated that further improvement for these traits is possible.

The highest heritability was recorded on test weight (98%) with genetic advance and expected genetic advance over percentage of mean of (1.9 and 50.0%), followed by siliqua length (52%) with genetic advance and an expected genetic advance over percentage of mean of (0.47 and 9.6) followed by number of secondary branches per plant (49) with genetic and an expected genetic advance over percentage of mean of (4.8 and 25.8%). Number of primary branches per plant (40%) with genetic advance and an expected genetic advance over percentage of mean of (1.2 and 16.6%), Number of seed per siliqua (35%) with genetic advance and an expected genetic advance over percentage of mean of (1.2 and 6.6%), plant height (31%) with genetic advance and an expected genetic advance over percentage of mean of (10.7 and 5.0%), number of siliquae per plant and total seed yield (29) with genetic advance and an expected genetic advance over percentage of mean of (56.1 and 13.3%) and (4.1 and 25.0), respectively. Total number of seeds per plant (21%) with genetic advance and an expected genetic advance over percentage of mean of 590.5 and 10.5%. The present result endured Ejaz-ul-Hasan *et al.*, 2014 and Akabari and Niranjana, 2015.

The genotypic and phenotypic correlation coefficients estimated between yield and inter-correlation among the different yield components are furnished in and only significant correlations are discussed here. In general, the magnitude of genotypic correlation coefficient was higher than the corresponding phenotypic coefficient indicating thereby a strong inherent association between various traits under study (Table 3).

Table 1: Mean performance of 41 IC lines of Indian Mustard

Characters Genotypes	Plant Height (cm.)	Number of primary branches /plant	Number of secondary branches /plant	Number of Siliquae /plant	Siliqua Length (cm)	Number of seeds /siliqua	Number of Seeds /plant	Total Seed yield /plant (g)	Test Weight (g)
IC 589662	167.1	7.0	22.3	443.3	3.9	14.3	4097.7	6.4	2.22
IC 589669	164.4	6.0	21.3	392.0	3.8	14.3	3895.7	8.4	2.78
IC 589670	158.9	5.3	15.0	294.3	3.4	12.7	3723.7	6.6	2.49
IC 589680	154.3	5.0	11.3	280.7	3.5	13.0	3339.7	6.2	2.53
IC 589681	163.3	5.7	15.0	313.3	3.7	12.7	3784.0	9.4	2.65
IC 589686	166.1	5.3	19.3	363.0	4.2	14.7	4057.3	13.6	3.84
IC 589699	173.3	6.0	12.7	337.3	3.8	13.3	4001.0	8.4	1.71
IC 597879	183.5	6.3	18.7	366.7	3.7	13.7	5316.0	13.3	2.82
IC 597919	169.2	7.3	18.0	385.3	3.5	13.3	5637.7	11.1	1.90
IC 598692	160.5	5.0	14.0	331.3	3.4	14.7	4361.3	10.2	2.63
IC 599679	174.1	6.3	12.0	292.7	3.6	13.7	4542.7	11.0	2.74
IC 571635	179.9	7.0	16.0	357.0	3.6	14.3	5219.7	17.1	3.22
IC 571648	161.3	5.7	15.3	297.3	4.2	13.3	3934.0	13.9	2.33
IC 571649	169.2	5.7	17.0	350.0	4.2	15.0	5412.7	19.7	3.69
IC 571655	171.7	6.0	16.7	393.3	3.7	14.3	5506.7	13.8	2.60
IC 571661	167.0	5.0	13.3	296.7	4.2	13.7	4055.3	12.5	4.66
IC 571663	167.9	5.0	12.3	273.7	4.4	14.3	4056.3	13.1	4.24
IC 571678	171.7	6.7	14.0	314.0	3.7	13.7	4413.3	10.1	2.36
IC 571683	182.9	5.7	13.0	332.3	3.7	13.7	4711.0	11.0	2.26
IC 571697	179.3	6.3	13.7	322.7	4.0	13.3	4161.0	12.6	2.96
IC 571699	173.6	6.3	11.0	340.0	3.6	13.7	4585.3	13.1	2.83
IC 405235	140.4	4.3	13.7	305.3	3.7	13.0	4233.0	12.9	3.06
IC 424414	149.2	5.0	14.0	358.7	3.7	13.0	4858.7	16.7	3.36
IC 447111	174.3	4.0	12.3	303.0	3.4	12.3	3922.7	8.4	2.04
IC 538699	173.7	4.7	13.3	282.3	3.7	10.7	3272.7	11.7	3.46
IC 538719	174.0	5.3	12.7	298.0	4.1	13.0	3917.3	11.0	2.83
IC 538737	166.0	6.0	12.3	328.3	3.8	13.3	4743.3	16.1	3.37
IC 558816	167.0	4.7	9.0	225.7	4.0	15.0	3753.7	13.9	3.67
IC 571625	160.1	6.0	12.0	245.7	3.8	14.7	3662.0	16.3	4.54
IC 571627	150.7	4.7	11.3	273.0	3.8	13.3	3740.0	9.6	2.75
IC 571630	154.7	6.7	12.3	314.3	3.3	14.0	4782.3	12.8	2.76
IC 311734	149.7	7.0	13.3	288.7	3.6	13.3	3859.7	10.2	2.83
IC 317528	175.0	8.3	20.3	462.3	3.5	12.0	5479.7	15.5	2.92
IC 335852	166.1	5.3	13.7	292.3	3.4	12.7	4104.3	10.3	2.54
IC 335858	176.6	5.7	11.3	238.3	3.4	12.7	3294.0	12.5	3.74
IC 338586	168.5	6.7	18.7	439.3	3.9	13.0	5826.0	12.4	2.11
IC 342777	158.9	5.7	16.3	402.3	3.7	14.7	6028.0	26.4	4.43
IC 339953	152.4	6.0	18.3	359.0	3.5	14.3	5250.3	12.5	2.42
IC 335856	156.7	5.3	16.0	322.0	4.2	14.0	4564.3	16.2	3.62
IC 393232	163.7	5.0	14.0	302.7	3.9	11.7	3647.7	14.9	4.06
IC 401560	165.0	4.7	14.0	343.0	4.3	12.7	4646.7	18.0	3.85
Mean	165.9	5.8	14.7	328.3	3.8	13.5	4400.0	12.7	3.02
C.V.	6.7	15.6	18.1	18.8	6.2	7.4	21.2	35.1	3.3
S.E.	6.40	0.52	1.53	35.72	0.13	0.57	538.49	2.57	0.06
C.D. 5%	18.01	1.46	4.31	100.52	0.38	1.62	1515.51	7.23	0.16
C.D. 1%	23.88	1.94	5.71	133.29	0.50	2.14	2009.46	9.59	0.21

Table 2: Estimates of genetic parameters for various traits of 41 indigenous line of Indian mustard

Parameters Characters	Mean ± S.E.	Range Min	Max	δ^2_p	δ^2_g	PCV (%)	GCV (%)	h^2_{bs} (%)	GA	GA as % of Mean
Plant Height (cm.)	165.90± 6.32	149	183	176.88	53.99	8.02	4.43	0.31	10.72	5.04
Number of Primary Branches/ Plant	5.75±0.51	4.00	8.33	1.34	0.54	20.16	12.73	0.40	1.22	16.56
Number of Secondary Branches/ Plant	14.66±1.51	9.00	22.33	13.84	6.82	25.38	17.81	0.49	4.84	25.75
Number of Siliquae/ plant	328.33±35.27	225	422	5386.78	1559.42	22.35	12.03	0.29	56.09	13.33
Siliqua Length (cm)	3.77±0.13	3.33	4.37	0.11	0.06	8.97	6.48	0.52	0.47	9.64
Number of Seeds/ Siliqua	13.49±0.56	10.67	14.67	1.53	0.54	9.16	5.43	0.35	1.15	6.64
Number of Seeds/ plant	4399.96±531	3272.67	6028.00	1104982.25	235078.56		23.89	11.02	0.21	590.39
10.47										
Total Seed yield (g)	12.67±2.53	6.21	26.44	27.91	8.10	41.70	22.47	0.29	4.05	24.95
Test Weight(g)	3.02±0.06	1.71	4.66	0.56	0.55	24.71	24.50	0.98	1.94	50.02

δ^2_p – phenotypic variance; δ^2_g – genotypic variance; PCV – Phenotypic coefficient of variance; GCV – Genotypic coefficient of variance; h^2_{bs} – heritability in broad sense; GA – Genetic advance (at 5% selection intensity i.e. K = 2.06), 2*Values in parenthesis are transformed values.

Table 3: Phenotypic and genotypic contribution to phenotypic correlation for yield traits

Characters		Plant Height (cm.)	No. of primary branches /plant	No. of secondary branches /plant	No. of Siliquae /plant	Siliqua Length (cm)	Number of seeds /siliqua	Total number of Seeds /plant	Test Weight (g)	Total Seed yield/ plant (g)
Plant Height (cm)	G	1.000	0.312	0.200	0.147	0.067	-0.138	0.172	-0.1555	-0.054
	P	1.000	0.297	-0.015	0.169	0.011	-0.032	0.128	-0.079	-0.002
Number of Primary	G		1.000	0.715	0.529	-0.363	0.074	0.471	-0.377	-0.281
Branches/ Plant	P		1.000	0.281	0.592	-0.137	0.197	0.512	-0.233	0.238
Number of Secondary	G			1.000	0.245	0.147	0.264	0.798	-0.224	0.023
Branches/ Plant	P			1.000	0.541	0.052	0.077	0.293	-0.145	0.085
Number of	G				1.000	-0.087	-0.014	0.759	-0.389	-0.141
Siliquae /plant	P				1.000	0.044	0.203	0.717	-0.196	0.375
Siliqua Length (cm)	G					1.000	0.093	-0.251	0.537	0.259
	P					1.000	0.327	0.054	0.388	0.357
Number of	G						1.000	0.083	0.211	-0.043
Seeds/ Siliqua	P						1.000	0.449	0.126	0.439
Total Number of	G							1.000	-0.162	0.333
Seeds/ plant	P							1.000	-0.064	0.654
Test Weight (g)	G								1.000	0.862
	P								1000	0.486

In the present investigation plant height exhibited positive and significant correlation with number of primary branches per plant (0.31 and 0.30), at genotypic and phenotypic level, respectively. Primary branches per plant exhibited positive and significant correlation with plant height (0.31 and 0.30), number of secondary branches per plant (0.72 and 0.28), number of siliqua per plant (0.53 and 0.60), number of seed per siliqua (0.74 and 0.197), total number of seed (0.51 and 0.80), total seed yield per plant (0.24 and 0.02) and negatively significant with test weight (0.38 and 0.23) at genotypic and phenotypic level, respectively. Number of secondary branches per plant was found to be positive and significant correlation with number of primary branches per plant (0.72 and 0.28), number of siliqua per plant (0.25 and 0.54), and total number of seed per plant (0.798 and 0.29) at genotypic and phenotypic level, respectively. Number of siliquae per plant was found to be positive and significant correlation with number of primary branches per plant and (0.53 and 0.59), number of secondary branches per

Table 4: Direct and indirect effect (phenotypic) of nine component characters on grain yield per plant in mustard

Characters	Plant Height (cm.)	No. of primary branches	No. of secondary branches /plant	No. of Siliquae /plant	Siliqua Length (cm) /plant	Number of seeds	Total number of Seeds /siliqua	Test Weight (g) /plant
Plant Height (cm.)	-0.0697	-0.0207	0.0011	-0.0118	-0.0008	0.0022	-0.0089	0.0056
Number of Primary Branches/ Plant	0.0209	0.0703	0.0198	0.0416	-0.0096	0.0139	0.0360	-0.0164
Number of Secondary Branches/ Plant	0.0010	-0.0173	-0.0614	-0.0332	-0.0032	-0.0047	-0.0180	0.0089
Number of Siliquae/ plant	-0.0044	-0.0156	-0.0143	-0.0264	-0.0012	-0.0054	-0.0189	0.0052
Siliqua Length (cm)	0.0016	-0.0201	0.0077	0.0064	0.1467	0.0480	0.0079	0.0570
Number of Seeds/ Siliqua	-0.0008	0.0048	0.0019	0.0050	0.0080	0.0245	0.0110	0.0031
Number of Seeds/plant	0.0862	0.3453	0.1978	0.4838	0.0364	0.3028	0.6751	-0.0431
Test Weight(g)	-0.0372	-0.1084	-0.0674	-0.0910	0.1811	0.0586	-0.0297	0.4656
Total Seed yield/ plant (g)	-0.0024	0.2384	0.0851	0.3745	0.3574	0.4399	0.6544	0.4858
Partial R^2	0.0002	0.0168	-0.0052	-0.0099	0.0524	0.0108	0.4418	0.2262

Residual effect = 0.5167

plant (0.25 and 0.54) and total seed yield per plant (0.14 and 0.38) at genotypic and phenotypic level, respectively.

Siliqua length exhibited positive and significant correlation with number of seed per siliqua (0.93 and 0.327) and test weight (0.537 and 0.388) at genotypic and phenotypic level, respectively. Number of seeds per siliqua exhibited positive and significant correlation with number of primary branches per plant (0.529 and 0.592), siliqua length (0.93 and 0.33), total number of seeds per plant (0.08 and 0.45) and total seed yield per plant (0.04 and 0.44). Total number of seed per plant positively significant correlated with number of primary branches per plant (0.47 and 0.51), number of secondary branches per plant (0.80 and 0.29) and total seed yield per plant (0.33 and 0.65) at genotypic and phenotypic level respectively. Test weight was found to be positive and significantly correlated with siliqua length (0.54 and 0.39) at genotypic and phenotypic level, respectively and significant negative association with number of primary branches per plant (0.38 and 0.23) at genotypic and phenotypic level, respectively. Total seed yield per plant exhibited positive and significant correlation with number of primary branches per plant (0.28 and 0.24), number of siliqua per plant per plant (0.14 and 0.38), number of seeds per siliqua (0.04 and 0.44), and total number of seed per plant (0.33 and 0.65) at genotypic and phenotypic level respectively.

Path coefficient analysis provides the cause and effects of chain relationships of different yield contributing characters with yield. Estimates of direct and indirect effects of different yield contributing traits on grain yield per plant using phenotypic correlation are presented in Table 4.

Analysis revealed that magnitude of direct effect on yield per plant was found to be highest for number of seeds per plant (0.68) followed by test weight (0.47), siliqua length (0.15), number of primary branches per plant (0.07) and number of seeds per siliqua (0.02) indicating true relationship between these traits as good contributors to seed yield and suggesting the importance of direct selection for these traits. On the other hand, the highest negative direct effect of plant height (-0.07) followed by number of secondary branches per plant (-0.06) and number of siliquae per plant (-0.03) was found on seed yield per plant.

Conclusion

From the present studies it is concluded that seed yield is the reliable parameter for the selection of high yielding mustard lines/varieties and number of seeds per plant, number of seeds per siliqua, number of primary branches and number of siliquae per plant are the contributory traits of seed yield. It is suggested that emphasis should be given to above characters in selecting traits for higher yield and further study should be made with more characters to find out other traits that contributed to the rest of the percentage of yield.

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