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Genetic variation for yield characters of F_1 hybrids in Indian mustard (*Brassica juncea* L.)

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Abstract

Twenty F_1 hybrids generated in 5×5 diallel and evaluated during 2017-18 to study the genetic variability for seed yield and other important quantitative traits. Analysis of variance revealed significant differences for hybrids for all characters studied indicating sufficient genetic variability for all the characters. The variance due to parents were highly significant for all the characters except days to first flowering, primary branches/ plant, number of secondary branches/ plant, days to maturity, plant height and the variance due to crosses were highly significant for all the characters except plant height. Variances due F_1's were significant for all characters except plant height, and seeds/ siliquae. Phenotypic correlation coefficient revealed that seed yield/ plant had significant positive correlation with number of siliquae/ plant followed by number of primary branches/ plant and biological yield/ plant. Path coefficient analysis revealed that biological yield/ plant had highest positive direct effect with seed yield/ plant followed by days to 50% flowering, number of primary branches/ plant and harvest index.

Keywords: *Characters, correlation, genetic variability, mustard, seed yield, variance*

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is the most important oilseed crop of the India occupying considerably larger acreage among the Brassica crops (Lodhi *et al*., 2013). The Brassicaceae family consists of more than 3,000 species and 370 genera, various of which are already under cultivation (Singh *et al*., 2019). Indian mustard *(B. juncea*) is a natural amphidiploid (2n=36) *B. rapa* (2n=20) and *B. nigra* (2n=16). It is predominantly a self- pollinated crop but out-crossing does occur up to 30% under natural conditions, depending upon wind and bee activities (Rakow and Woods, 1987). Indian mustard is the premier oilseed *Brassica* which covers over 80% of the total area under rapeseed-mustard crops (Rao *et al.*, 2017 and Meena *et al*., 2017a). 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, Kumar *et al*., 2017). Oilseeds are the backbone of agricultural economy of India. Indian vegetable oil economy is the fourth largest in the world next to U.S.A, China and Brazil. An estimate of genetic advance along with heritability is helpful in assessing the reliability of character for selection (Kumar *et al*., 2018). Keeping these facts in view the present study was conducted to test the genetic variability among various hybrids (F_1's) to select best crosses for development of better genotypes.

Materials and Methods

The material for present investigation consisted five Indigenous lines (IC- 599679, IC- 571649, IC- 571663, IC-317528 and IC- 338586) of *Brassica juncea L.* which were provided by National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India and 20 F_1 hybrids generated in 5×5 diallel using these lines. The present research work was conducted at Research Farm, Department of Agriculture, Mata Gujri College, Fatehgarh Sahib, Punjab, during winter 2016-17 and 2017-18 using Randomized Block Design (RBD) with three replications. Experimental place is situated between 30-27' and 30-46' latitudes and 76-04' and 76-38'E longitude and a mean height of 247 m above mean sea level. Row to plant spacing of 70×25 cm was maintained and proper plant population maintained by thinning. The recommended agricultural package of practices was followed. Observation was recorded for various characters on five randomly selected plants in each genotype from each replication. Diallel mating using was proposed by Haymen (1958). Data were analyzed by Windostat Version 9.3 from Indostat Services, Hyderabad.

Result and Discussion

Heritability and genetic advance

Analysis of variance revealed significant differences for all the thirteen traits studied. Variance due to genotype was highly significant for all the thirteen traits indicating

Table 1: Estimates of different genetic parameters of variation for 13 traits among parents and crosses.

Characters	GCV	PCV	h^2 (Broad Sense %)	Genetic Advance -ment 5%	Genetic Advance -ment 1%	Gen.Adv as % of Mean 5%	Gen. Adv as % of Mean 1%	General Mean
Days to First Flowering	6.27	10.03	39	3.41	4.37	8.07	10.34	42.23
Days to 50% Flowering	5.30	8.84	36	3.73	4.79	6.54	8.38	57.12
Primary Branches/ Plant	22.36	27.91	64	3.03	3.88	36.89	47.28	8.21
Secondary Branches/ Plant	15.50	19.97	60	3.88	4.97	24.78	31.75	15.67
Plant Height (cm)	3.39	7.32	21	5.88	7.53	3.23	4.14	181.87
Siliquae/ Plant	21.27	23.15	84	139.85	179.22	40.25	51.59	347.41
Siliqua Length(cm)	4.68	8.66	29	0.22	0.29	5.21	6.68	4.27
Seeds/ Siliqua	6.68	9.68	48	1.19	1.52	9.50	12.18	12.50
Days to Maturity	1.10	1.93	33	1.92	2.46	1.30	1.66	148.00
Biological Yield/ Plant (g)	21.86	24.61	79	82.09	105.20	40.01	51.27	205.19
Seed Yield/ Plant (g)	21.35	24.06	79	13.97	17.90	39.03	50.02	35.79
Harvest Index (%)	26.44	30.07	77	8.73	11.19	47.88	61.36	18.24
Test Weight (g)	9.43	15.97	35	0.37	0.47	11.49	14.72	3.19

the presence of sufficient variability in the genotypes selected for this study. The estimates of genetic variability parameters for all the traits were worked out and are presented in Table 1. 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 harvest index followed by number of primary branches/ plant and biological yield/ plant and minimum by days to maturity. The high values of PCV and GCV indicating that selection may be effective on these traits. Wide difference between PCV and GCV was observed for number of seeds / siliqua, number of primary branches/ plant, number of secondary branches / plant and days to first flowering which may indicate the high contribution of environmental variance to the phenotypic variance.

The highest heritability was recorded on number of siliquae/ plant with genetic advance and expected genetic advance over percentage of mean followed by seed yield, biological yield/ plant, harvest index, primary branches / plant, secondary branches/ plant, seeds/ siliqua, days to first flowering, days to 50% flowering, test weight, days to maturity, siliqua length and plant height, respectively. The high estimate for heritability indicates that most of the variation is caused by the genotype and very small due to environment, therefore simple selection procedure would be helpful in improvement of these traits (Tiwari *et al.*, 2017).

The genetic gain that can be expected by selection for a character is given by the estimates of genetic advance. The genetic advance at 1% level of significance ranged from 0.29 (siliqua length) to 179.2 (siliquae/plant). The genetic advance as per cent of mean at 1% level of significance was found maximum for seed yield/ plant followed by harvest index, biological yield/ plant, number of primary branches/ plant, number of secondary branches/ plant, number of seeds/ siliqua. All these characters also showed high heritability estimates. Such a high heritability coupled with high genetic advance has been reported for number of siliqua/ plant (Choudhary *et al.*, 2003 and Acharya and Pati, 2008), for seed yield / plant (Yadava *et al*., 2011) and for test weight (Upadhyay and Kumar, (2009), Tahira *et al.* (2011), Kumar *el al*., (2018). High genetic advance (GA %) coupled with high heritability for seed yield, 1000-seed weight, siliqua length, plant height and number of primary branches/ plant were also reported by Meena *et al.* (2017b). Such high heritability coupled with high genetic advance for the characters mentioned above indicates the effectiveness of selection for these traits and predominance of additive gene action on these traits.

Hence, limited improvement is expected through selection in later generations. Other characters including siliqua length, test weight which had low values for heritability and genetic advance may not respond favorably to selection. From the foregoing, it is evident that number of siliquae/ plant, biological yield/ plant and harvest index recorded high GCV value, heritability estimate and genetic advance. Hence the improvement in these traits could be achieved through direct selection.

Table 2: Phenotypic correlation analysis showing effects of thirteen characters on seed component.

Characters	Days to 50% Flowering	Primary Branches/ Plant	Secondary Branches/ Plant	Plant Height (cm)	Siliquae / Plant	Siliqua Length (cm)	Seeds / Siliqua	Days to Maturity	Biological Yield/ Plant (g)	Seed Yield/ Plant (g)	Harvest Index (%)
Days to First Flowering	0.754**	-0.293**	-0.075	0.180	-0.018	0.157	0.065	-0.106	0.268*	-0.183	-0.322**
Days to 50% Flowering	1.0000	-0.235*	-0.047	0.181	0.107	0.168	0.167	-0.067	0.167	-0.045	-0.120
Primary Branches/ Plant		1.000	0.529**	-0.121	0.283*	-0.134	-0.037	-0.089	-0.229*	0.301**	0.384**
Secondary Branches/ Plant			1.000	0.032	0.441**	0.052	0.040	-0.139	-0.333**	0.101	0.342**
Plant Height (cm)				1.000	-0.138	-0.001	0.009	0.213	-0.034	-0.181	-0.090
Siliqua/ Plant					1.000	-0.041	0.085	-0.327**	0.028	0.351**	0.225*
Siliqua Length(cm)						1.000	0.042	-0.091	0.034	-0.033	-0.032
Seeds/ Siliqua							1.000	0.228*	0.094	0.229*	0.111
Days to Maturity								1.000	0.044	0.009	-0.003
Biological Yield/Plant (g)									1.000	0.245*	-0.597**
Seed Yield/ Plant (g)										1.0000	0.571**

Table 3: Path coefficient analysis showing direct and indirect effect of twelve characters on seed yield at phenotypic level.

Characters	Days to First Flowering	Days to 50% Flowering	Primary Branches / Plant	Secondary Branches / Plant	Plant Height (cm)	Siliqua / Plant	Siliqua Length (cm)	Seeds / Siliqua	Days to Maturity	Biological Yield/ Plant (g)	Harvest Index (%)	Test Weight (g)
Days to First Flowering	-0.0291	-0.0219	0.0085	0.0022	-0.0052	0.0005	-0.0046	-0.0019	0.0031	-0.0078	0.0094	-0.0087
Days to 50% Flowering	-0.0218	-0.0289	0.0068	0.0014	-0.0052	-0.0031	-0.0048	-0.0048	0.0019	-0.0048	0.0035	-0.0102
Primary Branches/ Plant	-0.0231	-0.0186	0.0788	0.0417	-0.0095	0.0224	-0.0106	-0.0029	-0.0070	-0.0181	0.0303	-0.0068
Secondary Branches/ Plant	0.0032	0.0020	-0.0223	-0.0422	-0.0013	-0.0186	-0.0022	-0.0017	0.0059	0.0141	-0.0144	-0.0068
Plant Height (cm)	-0.0041	-0.0042	0.0028	-0.0007	-0.0230	0.0032	0.0000	-0.0002	-0.0049	0.0008	0.0021	0.0008
Siliqua/ Plant	-0.0015	0.0093	0.0245	0.0381	-0.0119	0.0864	-0.0036	0.0074	-0.0283	0.0024	0.0195	0.0158
Siliqua Length(cm)	-0.0005	-0.0006	0.0005	-0.0002	0.0000	0.0001	-0.0034	-0.0001	0.0003	-0.0001	0.0001	-0.0003
Seeds/ Siliqua	0.0026	0.0066	-0.0014	0.0016	0.0003	0.0033	0.0017	0.0391	0.0089	0.0037	0.0043	0.0015
Days to Maturity	0.0010	0.0007	0.0009	0.0013	-0.0021	0.0032	0.0009	-0.0022	-0.0097	-0.0004	0.0000	0.0014
Biological Yield/ Plant (g)	0.2361	0.1473	-0.2014	-0.2932	-0.0303	0.0248	0.0296	0.0826	0.0385	0.8797	-0.5249	0.0815
Harvest Index (%)	-0.3360	-0.1251	0.4001	0.3566	-0.0939	0.2348	-0.0337	0.1153	-0.0037	-0.6217	1.0418	0.0269
Test Weight (g)	-0.0095	-0.0113	0.0028	-0.0051	0.0012	-0.0059	-0.0026	-0.0013	0.0046	-0.0030	-0.0008	-0.0320
Seed Yield/ Plant (g)	-0.1829	-0.0449	0.3005	0.1014	-0.1810	0.3511	-0.0333	0.2292	0.0098	0.2448	0.5708	0.0633

Correlation and Path analysis

Phenotypic correlation coefficients for all possible combination of characters are presented in Table 2. In general, the genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients. Days to first flowering showed highly significant positive correlation with days to 50% flowering (0.754), biological yield/ plant (0.268). Number of primary branches showed highly significant positive correlation with number of secondary branches (0.529), harvest index (%) (0.384), seed yield (0.301) and siliquae/ plant (0.283). Number of secondary branches showed highly significant positive correlation with siliquae/ plant (0.441). Seeds/ siliqua showed highly significant positive correlation with seed yield/ plant (0.229) and days to maturity (0.228). Biological yield/ plant showed highly significant positive correlation with seed yield/ plant (0.245). Seed yield/ plant showed highly significant positive correlation with harvest index (0.571). Thus, it can be inferred that by improving these traits through selection either alone or in combination, will result in improvement of yield in mustard. The estimates of phenotypic correlation coefficients revealed that seed yield/ plant were positively correlated with primary branches/ plant, siliquae/ plant, harvest index and biological yield / plant. Positive and significant associations of seed yield with these characters were reported by Singh and Singh (2010) and Sekhar *et al.* (2012).

Direct and indirect effects of twelve characters on seed yield at phenotypic level using path coefficient analysis are presented in Table 3. At phenotypic level harvest index displayed maximum order of direct positive effect on seed yield/ plant followed by biological yield/ plant, number of siliquae/ plant and number of primary branches/ plant. Similar results were also reported by Bind *et al*. (2014) and Devi, 2018. Harvest index with positive direct effect showed indirect positive effect *via* primary branches/ plant. Similar results were also reported by Tahira *et al.* (2011) and Roy *et al*., 2018. Direct effect of any character on seed yield gives an idea about effective selection *i.e.* choosing the plant trait that can be made to bring improvement in breeding programme. The indirect effect indicates the inter-relationship of component characters towards contributes to yield.

Conclusion

The ANOVA revealed significant differences in F_1s and indicating sufficient genetic variability for all the characters. The variance due to parents was highly significant for most of the yield traits and the variance due to crosses were highly significant for all the characters except plant height. Phenotypic correlation coefficient revealed that the seed yield/ plant had significant positive correlation with siliquae/ plant followed by primary branches/ plant and biological yield/ plant. Path coefficient analysis of different characters contributing towards seed yield/ plant revealed that biological yield/ plant had the highest positive direct effect followed by days to 50% flowering, number of primary branches/ plant and harvest index. Based on this study, these parents and F_1's can be used to develop high yielding cultivars by obtaining useful transgressive segregants from further generations.

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