Genetic Variability and Character Association Studies in Indian Mustard (*Brassica juncea* L.)

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Authors' contributions

Article Information

Original Research Article

ABSTRACT

India is a nation which has got huge scope for modernization. The pace of increasing modernization in India coupled with its ever increasing human population is posing a very serious impact on environment mainly due to global warming. Abrupt rainfall conditions coupled with drought conditions prevailing during the *Kharif* season often hampers paddy transplantation in eastern parts of India. It results in late harvesting of paddy which in turn leads to late sowing of mustard crop in the fields during *Rabi* season. Hence, the need of the hour is to develop Indian mustard varieties having high yield potential as well as suitable for late sown conditions in Eastern India. An investigation was carried out to study the genetic variability, correlation and path analysis of ten quantitative traits in 33 genotypes of Indian mustard procured from diverse agro-climatic zones of the country. Analyses of variance were found to be highly significant for all the characters studied. Genotypic Coefficient of Variability as well as Phenotypic Coefficient of Variability were found high for number of primary branches, number of secondary branches, number of siliqua and seed yield per plot. High heritability coupled with higher genetic advance was found for plant height, number of siliqua per plant and seed yield per plot suggesting due importance of these traits for selection in breeding program.The phenotypic and genotypic correlation studies revealed that seed yield per plot exhibited significant positive correlation with plant height, number of

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primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, seeds per siliqua and 1000 seed-weight. Path coefficient analysis revealed that seed yield per plot, days to maturity, plant height, number of primary branch, number of secondary branch, number of siliqua per plant had positive direct effect on seed yield per plot suggesting that direct selection for these triats can be practiced for yield improvement in Indian mustard.

1. INTRODUCTION

Indian mustard is considered as the 3rd most important source of edible oil after soyabean and palm globally. It is mostly grown in tropical as well as sub-tropical countries of the world. In India; it ranks second only after groundnut in terms of acreage. Out of seven edible oilseed crops cultivated in India, Indian mustard holds the second rank in area and production next to groundnut sharing 26.85% in the India's oilseed economy and 29.35 % in the total oilseeds production [19]. It is an important *Rabi* oilseed crop grown extensively under irrigated condition. With the ever increasing human population and changing agro-climatic conditions, introduction of high grain and oil yielding varieties are needed in order to fulfill consumer demand. Under such circumstances, efforts have been made to collect and evaluate diverse germplasm for their yield potential and pest-disease resistance [4]. For improving the genetic stock by adopting a suitable breeding program, it is necessary to partition the existing variability of the germplasm lines into genetic and environmental components. The estimate of broad sense heritability solely fails to provide an idea about expected gains in the desired trait over successive generations [9]. Therefore, besides heritability; estimates of genetic advance must also be considered. The quantum of genetic variability existing in a population depends on the amount of genetic differences present among the genotypes which offers wider scope for selection among them. For accepting the potential of a genotype in breeding program, large amounts of genetic variability coupled with heritable variation in the traits plays a major role [5]. Exploitation of the germplasm lines in breeding programs demands a wide variability for economic traits. Hence, estimation of different variability parameters is a pre-requisite for making effective selection [7].

2. MATERIALS AND METHODS

Thirty-three diverse germplasm lines of Indian mustard were planted at Oilseed Research Section, Bihar Agricultural University, Sabour (Bhagalpur) in Randomized block design (RBD) with three replications. The crop was raised during the R*abi* season in 2019 following recommended package and practices needed for a healthy crop. Observations were recorded for ten quantitative traits *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, seeds per siliqua, 1000 seed-weight and seed yield per plot. Data for days to 50% flowering, days to maturity and seed yield per plot were taken on plot basis while rest data were taken from random sample of five individual plant basis. The data of observations recorded for each trait was subjected to analysis of variance following Panse and Sukhatme [13]. The phenotypic and genotypic coefficients of variation in per cent were calculated by the method given by Burton [6]. Heritability (H_{bs}) in broad sense and genetic advance was calculated as reported by Lush [11].

3. RESULTS AND DISCUSSION

ANOVA revealed highly significant differences for all the genotypes for all ten quantitative characters as presented in Table 1 indicating significant amount of genetic variability was present in the experimental genotypes. In the current investigation, days to 50% flowering ranged from 48 days (NPJ 236) to 63 days (RGN 463). Three genotypes viz. NPJ 236 (48), NPJ 235 (48.67) and DRMRCI 115 (48.67) were found to be significantly superior in earliness for days to 50% flowering. The average day to maturity was 111.79 which ranged from105.33 (TM 134) to 118.67 days (DRMR 2017-26). The average seed yield per plot was 922.65 g which ranged from 618.67 g (TM134) to 1595.0 g (DRMRCI 115). Two genotypes viz. DRMR 2017-26 (1583 g) and DRMRCI 115 (1595 g) were found significantly superior for seed yield per plot.

The perusals of data revealed that phenotypic variance was found to be higher than the corresponding values of genotypic variance for all the traits suggesting the influences of

environmental factors on these traits. Maximum GCV and PCV was recorded for number of primary branches followed by number of secondary branches and seed yield per plot as presented in Table 2 which depicts various parameters of genetic variability. These results were on similar lines with the findings of Awasthi et al. [2], Devi B. [8] and Tiwari et al. [25]. PCV and GCV were found higher for traits such as number of primary branches and grain yield per plot suggesting that yield can be improved by effective selection for these traits.

High heritability were found for traits such as test weight (87%) followed by days to 50% flowering (86.7%), number of siliqua per plant (74.9%), number of secondary branches (70.7%) and yield per plant (70.5%) revealing that these traits were least affected by environmental influences. Moderate heritability were found for siliqua length (55%) followed by number of seeds per siliqua (54%), plant height (54%) and days to maturity (46%). All the characters under study revealed moderate to high heritability except number of primary branches (29%). High estimate of heritability for most of the traits under study was also reported earlier by Tiwari et al. [20] and Rout et al. [17] they found that number of secondary branches per plant, number of siliqua per plant, length of siliqua, test weight and seed yield per plot possessed high heritability.

High genetic advance were found for yield per plot (30.15) followed by number of siliqua per plant (64.08) and plant height (24.99) whereas low genetic advance were found for number of primary branches (0.438), siliqua length (0.58), days to 50% flowering (8.16), days to maturity (2.94), number of secondary branches (2.27), seeds per siliqua (1.78) and 1000 seed-weight (0.88).

Higher value of genetic advance as per cent of mean were showed by yield per plant (32.67%) followed by number of secondary branches (32.25%), number of siliqua per plant (31.39%) and test weight (23.3%). Moderate genetic advance as percent of mean were showed by days to 50% flowering (14.48%) followed by siliqua length (13.96%), seeds per siliqua (13.26%) and plant height (12.3%). Low genetic advance as percent of mean were showed by number of primary branches (9.33%) followed by days to maturity (2.63%). High heritability coupled with high genetic advance was found for yield per plot followed by number of siliqua per plant and plant height suggesting that these traits were governed by additive genes and selection might be effective for these traits. In support to existing study, Pal et al. [12] has found high heritability coupled with high genetic advance for number of siliqua per plant. Similar findings were also revealed by Bibi et al. [4] who reported high heritability coupled with high genetic advance for number of siliqua per plant. Thus, the heritability estimates along with genetic advance are more reliable for selecting the leading genotype in breeding program.

Genotypic and phenotypic correlation coefficient found in the current experiment revealed that the traits *viz.* number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, seeds per siliqua as well as test weight showed highly significant positive correlation with the seed yield which were in accordance with the results reported by Begum et al. 2018 [3], Roy et al. 2018 [18]; Tiwari et al 2019 [20] Awasthi et al. [2]; indicating that considerable importance should be given to these traits in selection of elite genotypes for potential seed yield in Indian mustard.

Table 1. ANOVA for different characters in the present investigation

Sl. No.	Characters	Mean sum of square		
		Replication (d.f.= 02)	Treatment (d.f.=32)	Error (d.f.=64)
1.	Days to 50% flowering	0.394	57.174**	2.790
2.	Days to maturity	3.101	18.520**	5.205
3.	Plant height (cm)	8902.991	1050.437**	232.488
4.	No. of primary branches	0.566	0.845**	0.379
5.	Number of secondary branches	2.355	5.894**	0.716
6.	Number of siliqua per plant	1854.417	4306.377**	431.923
7.	Siliqua lenght	0.074	0.553**	0.117
8.	Seeds per siliqua	1.305	5.285**	1.158
9.	1000-seed wight (g)	1.021	0.656**	0.030
10.	Yield per plot (g/plot)	6567.283	103873.9**	12716.63

*, **significant at 5% and 1% level of significance respectively

Table 2. Estimates of GCV, PCV, Heritability, Genetic Advance & Genetic Advance as % of mean

Sl. No.	Character	GCV	PCV	Heritability (bs)	Genetic Advance	Genetic advance as % of mean
1.	Days to 50% flowering	7.554	8.114	0.867	8.165	14.487
2.	Days to maturity	1.884	2.778	0.46	2.944	2.633
3.	Plant height (cm)	8.185	11.141	0.54	24.99	12.387
4.	No. of primary branches	8.402	15.571	0.291	0.438	9.339
5.	Number of secondary branches	18.626	22.155	0.707	2.275	32.258
6.	Number of siliqua per plant	17.607	20.339	0.749	64.086	31.397
7.	Siliqua length	9.114	12.257	0.553	0.584	13.961
8.	Seeds per siliqua	8.738	11.859	0.543	1.78	13.264
9.	1000-seed weight (g)	12.376	13.238	0.874	0.88	23.836
10	Yield per plot (g/plot)	18.893	22.501	0.705	30.15	32.677

Table 3. Phenotypic correlation coefficients for 10 characters of Indian mustard varieties

Traits	DFF DM	PH	NPB	NSB	NSP	SL	SPS	TW	YPP
DFF	0.0089 0.298**	-0.1599	-0.0890	-0.209*	-0.450**	-0.220*	-0.602**	-0.24*
DM		-0.1159	0.1341	0.0903	0.1602	0.1823	0.1838	0.1176	0.1696
PH			-0.0548	-0.0648	0.1504	-0.220*	-0.291**	-0.1880	0.1307
NPB				0.347**	0.377**	0.212*	0.377**	0.405**	0.357**
NSB					0.596**	0.1302	0.339**	0.224*	0.453**
NSP						0.268**	0.222*	0.306**	0.5737**
SL							0.394**	0.285**	0.3253**
SPS								0.27**	0.3966**
TW									0.4724**

*, **significant at 5% and 1% level of significance respectively*

Table 4. Phenotypic path matrix of 10 traits on seed yield of 33 genotypes of Indian mustard

Character	DFF	DM	PH	NPB	NSB	NSP	SL	SPS	TW
DFF	**0.0596**	0.0005	0.0178	-0.0095	-0.0053	-0.0125	-0.0269	-0.0132	-0.0359
DM	0.0003	**0.0384**	-0.0044	0.0051	0.0035	0.0061	0.007	0.0071	0.0045
PH	0.0721	-0.028	**0.2416**	-0.0132	-0.0156	0.0364	-0.0533	-0.0703	-0.0454
NPB	0.0055	-0.0046	0.0019	**-0.0343**	-0.0119	-0.013	-0.0073	-0.0129	-0.0139
NSB	-0.0127	0.0129	-0.0092	0.0495	**0.1427**	0.0851	0.0186	0.0485	0.032
NSP	-0.059	0.0451	0.0423	0.1062	0.1677	**0.2813**	0.0755	0.0626	0.0863
SL	-0.0548	0.0222	-0.0268	0.0258	0.0158	0.0327	**0.1216**	0.048	0.0348
SPS	-0.0511	0.0425	-0.0673	0.0872	0.0786	0.0514	0.0912	**0.2312**	0.064
TW	-0.2084	0.0407	-0.0651	0.1404	0.0776	0.1062	0.0989	0.0958	**0.346**
YPP	-0.2484	0.1696	0.1307	0.3573	0.453	0.5737	0.3253	0.3966	0.4724
Partial R²	-0.0148	0.0065	0.0316	-0.0123	0.0646	0.1614	0.0396	0.0917	0.1635

Note: DFF= Days to 50% maturity, DM= Days to maturity, PH= Plant Height (cm), NPB= Number of primary branches, NSB=Number of secondary branches, NSP= Number of siliqua per plant, SL= Siliqua length (cm), SPS= Number of seeds per siliqua, TW= Test weight (gm), YPP= Yield per plot (g)

Path coefficient analysis revealed that seed yield per plot, plant height, days to maturity, number of primary branches, number of secondary branches, number of siliqua per plant exerted a positive direct effect on seed yield per plant suggesting that direct selection of these traits should be practiced for yield improvement in Indian mustard which were in agreement with the results of Ray et al. [15].; Lakra et al. [11] Pal et al. [12]. The residual effect was found to be

0.208 indicating that most of the traits contributing to genetic diversity have been included in the study.

4. CONCLUSION

Results found in the present investigation revealed that a wide range of genetic variability existed for seed yield and its attributing characters in the germplasm lines of Indian mustard. The highest genotypic coefficient of variation was observed for 1000 seed-weight and seed yield per plant. High heritability along with high genetic advance was found in seed yield per plant, silique per plant and plant height indicating less effect of environment. Hence, selection based on basis of these traits will be rewarding.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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