Original Research Article

Genetic Analysis of some Genotypes of Indian Mustard (*Brassica juncea* L.)

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ABSTRACT

Twenty-four genotypes of Indian mustard were evaluated for seed yield and yield attributing characters with randomized block design with three replications. The analysis of variance showed significant differences among all the 24 genotypes against all the characters. The phenotypic and genotypic coefficient of variation were higher for most of the traits like seed yield per plant, number of secondary branches per plant and number of siliquae per plant. High heritability coupled with high genetic advance in percent of mean was registered for number of siliquae per plant, number of primary and secondary branches per plant, plant height, 1000 seed weight, siliqua length per plant and seed yield per plant suggesting predominant role of additive gene action for expression of these traits. The correlation study revealed that seed yield per plant was positively and significantly correlated with number of primary and secondary branches per plant, number of siliquae per plant, siliqua length per plant and 1000 seed weight at both phenotypic and genotypic level. The traits namely, number of secondary branches per plant recorded as highest positive direct effect followed by number of seeds per siliqua, number of siliquae per plant and plant height.

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Keywords: Mustard, genetic variability, heritability, genetic advance, correlation, path analysis.

INTRODUCTION

Rapeseed and mustard (*Brassica species*) group of crops is the second most important oilseed crop after groundnut, contributing nearly about 25-30% of the total oilseed production in the country. Indian Mustard (*Brassica juncea* L.) belongs to the family *Cruciferae*, commonly known as rai or laha. It is pre-dominantly a self-pollinated crop, but out crossing rates of 20-30% [1]. Rapeseed-mustard is the third most important oilseed crop in the world after soybean and palm. In India this crop is the second most important edible oilseed after groundnut sharing about 28% in the Indian oilseed economy. It is grown for oil as well as vegetable, green manure, forage, medicines, pharmaceutical, industries, biodiesel and components of many other products. Mustard seed contains 30% - 46% oil content which is one of the most important and popular oil in India. Seed protein content ranges from 17.8% - 22.0%.

Though India is fourth largest contributor of oilseeds, but its average productivity is less than 50% of the world's average productivity. Being the natural repository of oilseed crop, yet Indian subcontinent is importing about 40% of the Country's edible oil. It leads as major vegetable oil importing Country, though during the November-March period of 2019-20 oil year, total edible oils imports declined to 53,91,807 tonnes from 60,05,067 tonne in the year-ago period (Data released by SEA,2020). The performance of available land races and introduced varieties are poor due to fluctuating environment and pest-disease incidence. In order to exploit and explore consumer demand, introduction of high grain yielding varieties is indispensable. Henceforth, to meet out the present oil requirements, there is an urgent need to break the yield barrier, by increasing the yield potential of *B. juncea* through genetic interventions. Yield is complex trait and the increasing seed yield is depending upon several factors including various

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yield attributing traits. The development of an intensive breeding and improvement programme needs detailed biological information and ~~an~~ understanding of nature and magnitude of variability of the yield and its components. Hence the present investigation is undertaken to estimate the genetic parameters viz. variability, heritability, genetic advance, genotypic and phenotypic coefficient of variation for different yield attributing characters among mustard genotypes and also to assess direct and indirect effects of different traits on seed yield per plant using path analysis.

MATERIALS AND METHODS

Experiment involved twenty-four genotypes (Table 1) including two checks Pusa Bold and Gujarat Local. The experiment was conducted at Agricultural Experimental Farm, Integrated Rural Development Management (IRDM), Faculty Centre, Ramakrishna Mission Vivekananda Educational and Research Institute (RKMVERI), Narendrapur, Kolkata. The experiment conducted with randomized block design (RBD) with three replications. The row length kept was two metres with standard spacing (30cm X 10cm). All the recommended cultural practices were followed throughout the crop season to raise a good crop.

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Table 1. List of Genotypes of Indian Mustard

Sr. No.	Name of Genotypes	Source	Sr. No.	Name of Genotypes	Source
1	PM-21	Mali Agritech Private Ltd. Ranaghat, West Bengal	13	Pusa Karisma	Mali Agritech Private Ltd. Ranaghat, West Bengal
2	PM-22	----------do-----------	14	Pusa Vijay	----------do------------
3	PM-24-4	----------do-----------	15	Bhagirathi	----------do------------

4	PM-25	----------do-----------	16	Seeta	----------do------------
5	PM-26	----------do-----------	17	Sarna	----------do------------
6	PM-27	----------do-----------	18	NRCHB-101	----------do------------
7	PM-28	----------do-----------	19	Bankura Black	----------do------------
8	PM-29	----------do-----------	20	Shivani	----------do------------
9	PM-30	----------do-----------	21	Bullet	Sasya Shyamala Krishi Vigyan Kendra, Arapanch, West Bengal
10	PusaTarak	----------do-----------	22	Kranti	Mali Agritech Private Ltd. Ranaghat, West Bengal
11	DRMR -150-35	----------do-----------	23	Gujarat Local (Check)	----------do------------
12	Sanjuktaasech	----------do-----------	24	Pusa Bold (Check)	----------do------------

The characters under studies were days to 50% flowering (D50%F), days to maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), number of siliquae per plant (NSPP), length of siliqua (LS) (cm), number of seeds per siliqua (NSPS), 1000-seed weight (1000 SW) (g) and seed yield per plant (SYPP) (g). The data were recorded on the basis of five randomly selected competitive

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STATISTICAL ANALYSIS

The components of variance were calculated by [2] and coefficient of variation, Correlation coefficient between different characters as per [3] and Path coefficient analysis suggested by [4]. The data recorded for various traits were statistically analysed through software 'OPSTAT' and 'Genres'.

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among all the 24 genotypes against all the characters viz., days to 50% flowering, days to maturity, plant height, primary and secondary branches per plant, number of siliquae per plant, siliqua length per plant, number of seeds per siliqua, 1000 seed weight and seed yield per plant (Table 2) indicating wide spectrum of variation among the genotypes under study and had wide scope for improvement.

Genetic parameters are presented in Table 3. Wide range of variability present among the genotypes for almost all the traits. This would offer a great scope for selection of desirable traits of genotypes. Phenotypic Variances (PV) are found higher than the corresponding Genotypic Variances (GV) against all the characters. Number of siliquae per plant was found to be highest PV and GV followed by plant height, days to maturity, days to 50% flowering and seed yield per plant. Similarly, lowest Environmental Variance was found in primary branch per plant, followed by 1000 seed weight, siliqua length, days to 50 % flowering and secondary branch per

Table 2: Analysis of variance for different characters in Indian Mustard genotypes (Mean sum of square).

Source of variation	**DF**	D50%F	DM	PH	NPBPP	NSBPP	NSPP	LS	NSPS	1000 SW	SYPP
Replication	2	5.895	42.341	42.374	0.245	1.307	117.250	0.151	14.311	0.453	19.699
Treatment	23	56.262**	114.230**	1467.616**	2.405*	27.038**	6536.132**	2.319*	14.491**	2.047*	29.380**
Error	46	1.443	8.991	23.661	0.053	2.508	21.578	0.150	4.971	0.071	3.148

** Significant at 1% level, *Significant at 5% level, degree of freedom (DF), days to 50% flowering (D50%F), days to maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), number of siliquae per plant (NSPP), length of siliqua (LS) (cm), number of seeds per siliqua (NSPS), 1000-seed weight (1000 SW) (g) and seed yield per plant (SYPP) (g)

Table 3: Variability and genetic parameters for different characters of Indian Mustard genotypes

Characters	Mean	Range	Variance			G.C.V.	P.C.V.	h^2 (%) (BS)	G.A.	G.A. as % of mean
			Phenotypic	Genotypic	Environmental					
D50%F	49.816	43.000-59.500	19.716	18.273	1.443	8.581	8.913	92.679	8.477	17.017
DM	129.379	111.500-138.500	44.068	35.085	8.983	4.578	5.131	79.599	10.885	8.414
PH	171.216	127.700-213.500	504.979	481.320	23.659	12.814	13.125	95.314	44.123	25.770
NPBPP	5.531	3.967-7.062	0.837	0.784	0.053	16.008	16.540	93.675	1.765	31.917
NSBPP	11.983	7.096-16.100	10.684	8.177	2.507	23.863	27.278	76.530	5.153	43.005
NSPP	196.651	123.900-320.500	2193.095	2171.530	21.565	23.697	23.814	99.016	95.522	48.574
LS	4.976	2.969-6.962	0.873	0.723	0.150	17.087	18.776	82.826	1.594	32.035
NSPS	14.370	10.414-18.460	8.144	3.173	4.971	12.397	19.860	38.963	2.291	15.941
1000 SW	5.236	3.802-6.893	0.730	0.659	0.071	15.501	16.319	90.227	1.588	30.332
SYPP	12.314	7.860-17.920	11.892	8.744	3.148	24.013	28.005	73.525	5.223	42.416

days to 50% flowering (D50%F), days to maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), number of siliquae per plant (NSPP), length of siliqua (LS) (cm), number of seeds per siliqua (NSPS), 1000-seed weight (1000 SW) (g) and seed yield per plant (SYPP) (g) plant. It indicates that these characters were less interaction with environment. In the present investigation, all the Phenotypic Coefficient of Variation (PCV) are higher than the Genotypic Coefficient of Variation (GCV) which indicates that effect of environment on the expression of different characters. It was found that seed yield per plant recorded highest PCV’s and GCV’S which was followed by secondary branch per plant, number of siliquae per plant, number of seeds per siliqua and siliqua length and lowest for days to maturity. Similar findings were recorded by Mahla et al. [5], Singh et al. [6], Shekhawat et al. [7], Bind et al. [8], [9], Rauf et al. [10], Tripathi et al. [11] and Ray et al. [12].

From the present investigation almost all the characters had high heritability i.e., more than 60 per cent (Table 4) except number of seeds per siliqua. The highest heritability was recorded by number of siliquae per plant and it was followed by plant height, primary branch per plant, days to 50% flowering and 1000 seed weight. Similar results were corroborated with Sikarwar et al. [13], Prasad et al. [14], Swarnakar et al. [15], [16], Yadava et al. [17] and Ray et al. [12]. Large variation was observed for Genetic Advance (GA) for all the characters among the genotypes of the investigation. The highest GA was observed in number of siliquae per plant and it was followed by plant height. Rest of the characters estimated low GA. Among them, 1000 seed weight was found lowest GA and it was followed by siliqua length per plant and primary branches per plant. This finding was also recorded by [16], [9] and Ray et al. [12].

The highest GA as a percent of mean was observed in number of siliquae per plant and it was followed by secondary branches per plant, seed yield per plant and siliqua length per plant. Similar results were obtained by Mahla et al. [5], [18], [16], [9], [19], Tripathi et al. [11] and Ray et al. [12]. Other characters like days to maturity were observed as the lowest GA as percent of mean followed by number of seeds per siliqua and days to 50% flowering. High heritability

Table 4: Phenotypic (P) and Genotypic (G) correlation among yield and other characters of Indian Mustard genotypes.

Characters		DM	PH	NPBPP	NSBPP	NSPP	LS	NSPS	1000 SW	SYPP
D50%F	**P**	0.287*	0.739**	0.17	0.198	0.350**	0.179	-0.114	0.026	0.153
	G	0.193	0.737**	0.142	0.237*	0.339**	0.134	-0.376**	-0.008	0.110
DM	**P**		0.336**	-0.223	-0.122	-0.067	0.383**	0.333**	-0.332**	-0.042
	G		0.297*	-0.330**	-0.164	-0.123	0.342**	0.263*	-0.457**	-0.185
PH	**P**			0.335**	0.173	0.389**	0.430**	-0.069	0.118	0.172
	G			0.326**	0.202	0.384**	0.460**	-0.280*	0.110	0.166
NPBPP	**P**				0.545**	0.575**	0.163	-0.076	0.501**	0.452**
	G				0.672**	0.584**	0.172	-0.208	0.506**	0.500**
NSBPP	**P**					0.556**	0.167	-0.00	0.473**	0.528**
	G					0.637**	0.177	-0.029	0.577**	0.692**
NSPP	**P**						0.106	-0.071	0.626**	0.552**
	G						0.093	-0.178	0.650**	0.623**
LS	**P**							0.328**	0.015	0.254*
	G							0.389**	0.025	0.255*

NSPS	**P**	-0.048	0.202
	G	-0.111	0.283*
1000 SW	**P**		0.424**
	G		0.495**

** Significant at 1% level, *Significant at 5% level, days to 50% flowering (D50%F), days to maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), number of siliquae per plant (NSPP), length of siliqua (LS) (cm), number of seeds per siliqua (NSPS), 1000-seed weight (1000 SW) (g) and seed yield per plant (SYPP) (g) couple with moderate GA as a percent of mean was observed in days to 50% flowering and number of seeds per siliqua. It indicated that these characters were predominantly controlled by additive and non-additive gene action. *i.e.*, it might be dominance or epistatic gene effects and the high heritability is being exhibited due to the influence of environmental rather than genotypes. This result was in agreement with Mahla et al. [5], Yadava et al. [17], [9] and Ray et al. [12]. High heritability accompanied with high genetic advance as a per cent of mean was recorded for number of siliquae per plant, primary and secondary branches per plant, plant height, 1000 seed weight, siliqua length per plant and seed yield. This indicated that these characters were governed by additive gene action. Therefore, these characters could be improved through direct selection. Similar results were obtained by Mahla et al. [5], [16], [9], Tripathi et al. [11] and Ray et al. [12]. High heritability along with low GA as a per cent of mean was found in days to maturity, suggested that the character was governed by non-additive gene action and the improvement of the character could not possible through direct selection.

The characters which showed positive and significant genotypic and phenotypic correlation with yield were number of primary and secondary branches, number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua and 1000 seed weight (Table 5). Similar results were reported by Mahla et al. [5], Gangapur et al. [20], Lodhi et al. [21], Mustafa et al. [22] and [23]. Therefore, these are the main determining characters for the improvement of yield in Indian mustard. Number of secondary branches per plant showed maximum positive direct effect on seed yield per plant as reported previously by Roy et al. [24]. and it was followed by number of seeds per siliquae, number of siliquae per plant respectively while minimum positive direct effect on seed yield was recorded by plant height. These results were in agreed with Mahla et al. [5], and Mahak et al. [25]. Similarly, maximum negative direct effect imparted from days

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Table 5: Path coefficient (Genotypic) analysis showing direct and indirect effects of different characters of Indian Mustard genotypes.

Characters	D50%F	DM	PH	NPBPP	NSBPP	NSPP	LS	NSPS	1000 SW	SYPP
D50%F	**-0.075**	-0.060	0.175**	-0.009	0.115*	0.147**	-0.004	-0.178**	0.001	0.110
DM	-0.014	**-0.313**	0.070*	0.023**	-0.079	-0.053	-0.011**	0.125*	0.067**	-0.185
PH	-0.055**	-0.092*	**0.237**	-0.022**	0.098	0.166**	-0.015**	-0.133*	-0.016	0.166
NPBPP	-0.010	0.103**	0.077**	**-0.070**	0.327**	0.253**	-0.006	-0.099	-0.075**	0.500**
NSBPP	-0.017*	0.051	0.047	-0.047**	**0.487**	0.276**	-0.006	-0.013	-0.085**	0.692**
NSPP	-0.025**	0.038	0.091**	-0.041**	0.310**	**0.433**	-0.003	-0.084	-0.096**	0.623**
LS	-0.010	-0.107**	0.109**	-0.012	0.086	0.040	**-0.033**	0.185**	-0.004	0.255*
NSPS	0.028**	-0.082*	-0.066*	0.014	-0.014	-0.077	-0.013**	**0.476**	0.016	0.283*
1000 SW	0.001	0.143**	0.026	-0.035**	0.281**	0.281**	-0.001	-0.053	**-0.149**	0.495**

** Significant at 1% level, *Significant at 5% level, days to 50% flowering (D50%F), days to maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), number of siliquae per plant (NSPP), length of siliqua (LS) (cm), number of seeds per siliqua (NSPS), 1000-seed weight (1000 SW) (g) and seed yield per plant (SYPP) (g) to maturity followed by 1000 seed weight, primary branches per plant while minimum negative direct effect was showed by siliqua length per plant. Similar result was also reported by [18]. The path coefficient studies (Table 5) indicated that number of primary and secondary branches per plant, number of siliquae per plant, length of siliqua, number of seeds per siliqua, 1000 seed weight were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

Comment [Gh9]: Discussion part is not suitable. Because just results were reported. Please add more explanations and reasons for your findings and compare them with both similar and no-similar reports

CONCLUSIONS

From the present investigation, the only genotype NRCHB-101 was surpassed their yield potential to the both check varieties. Other genotypes like Bullet, PM 22, DRMR-150-35, Seeta, PM-27 were also showed superior yield performance to nearby check varieties. In addition to this, other yield attributing characters like days to 50% flowering, primary branch per plant, number of siliquae per plant, siliqua length, number of seeds per siliqua and 1000 seed weight were also found outstanding in these superior genotypes. Therefore, they may be carried out further evaluation in multi-location trials, biotic and abiotic stress like environmental conditions to check their stability and adaptability.

Comment [Gh10]: What were the limitations of your research?

COMPETING INTERESTS DISCLAIMER:

Authors have declared that no competing interests exist. The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

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Comment [Gh11]: Please add more updated references. These are so old

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