Morphological characterization and correlation analysis of $F_{2:3}$ cross of Indian mustard × East-European mustard for yield traits in *Brassica juncea*

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Abstract

The Indian mustard (*Brassica juncea* L.) is one of most important oilseed crops in the country. Three hundred and fifty-nine F_2 plants were morphologically characterized for different traits, which served as the foundation for the development of F_3 population as a result of crossing of Pusa Mahak (Indian mustard) with Primus (East-European mustard) genotypes. The characters studied were days to 50% flowering, plant height, main shoot length, number of primary and secondary branches, number of siliquae per plant, siliqua length, seed yield per plant etc. Results revealed that plant height was significantly correlated with number of secondary branches (r =0.94), number of siliquae on main shoot (r =0.89), seed yield per plant (r =0.51) and main shoot length (r =0.48) in F_3 population. Similarly, the number of siliquae on the main shoot detected a high correlation with number of secondary branches (r =0.83), main shoot length (r =0.47) and seed yield per plant (r =0.46). A wide range of trait values were obtained for the entire population of F_2 and F_3 plants, as indicated by the data analysis.

Keywords: Morphological characters, genotypic correlation coefficient, Indian mustard, phenotypic correlation coefficient, yield contributing traits

Introduction

Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] is a member of the Brassicaceae plant family, commonly known as the mustard family which encompasses about 3500 species and 350 genera. It is considered one of the ten most economically important plant families (Warwick *et al.*, 2000). However, despite its significance, the productivity of rapeseed-mustard in India has been relatively low compared to other major rapeseed-mustard growing countries. Mustard production has jumped by 40% from 91.24 to 128.18 lakh tonnes in last 3 years. The productivity saw 11% increase from 1331 to 1447 kg/ha. The area under rapeseed-mustard enhanced by 29% from 68.56 lakh ha in 2019-20 to 88.58 lakh ha in 2022-23 (Anonymous, 2023).

The genetic composition of crop varieties plays a pivotal role in achieving higher productivity. Improved varieties are essential for initiating and accelerating crop production programs, with high-yielding varieties (HYVs) contributing not only to optimal yields but also to the highest percentage of oil. Effective breeding programs hinge on the presence or creation of genetic variability for various economically important traits within the gene pool. The two pillars of plant breeding are variability and selection. Variability helps to assess the diverse genotypes to select for the desired character

and selection for it is done either by directly selecting for the related to yield or by indirectly selecting for it. This selection can be done by assessing the variability and studying the dependence of yield on various characters *via* correlation studies and it serves as a pre-requisite for any breeding programme aimed at improving the yield and other characters. In Indian mustard, this variability and selection is done similarly. This variability is crucial for successful selection, as effective selection relies on high levels of genetic variability. Studies by various researchers underscore the importance of genetic variability in *B. juncea*. Abideen *et al.* (2013) observed significant differences among genotypes for various traits, highlighting the importance of genetic variability in achieving desired outcomes. Bibi *et al.* (2016) reported significant differences for multiple traits in *B. juncea*, emphasizing the need for diverse genetic material to address specific characteristics. Gupta *et al.* (2019) demonstrated substantial variability among oilseed *Brassica* genotypes for yield-related characters, reinforcing the importance of genetic diversity in breeding programs. Kumari and Kumari (2018) noted significant differences among genotypes, with phenotypic coefficient of variation being higher than genotypic coefficient of variation, further highlighting the existence of genetic diversity. Mahla *et al.* (2003) delved into the genetic variation in 55 Indian mustard genotypes, revealing significant variation among them

for various traits. Mahmood *et al*. (2003) emphasized the heritability of specific traits, pointing to the potential for these traits to be passed on to future generations. Maurya *et al*. (2018) revealed significant differences for all studied agronomic characters, reinforcing the notion that genetic variability is a fundamental aspect of successful breeding programs. Priyamedha *et al*. (2018) observed significant differences among Indian mustard genotypes, indicating sufficient variability. Rout *et al*. (2019) highlighted substantial variability among genotypes for agronomical traits, underscoring the importance of genetic diversity in addressing various agricultural challenges.

Understanding the magnitude of genetic variability is crucial for selecting appropriate breeding methods and ensuring the success of crop improvement programs. Assessing associations between characters helps identify the relative importance of independent characters contributing to dependent ones. Furthermore, character associations between yield components serve as a guide for successful yield improvement through indirect selection. Thorough knowledge of genetic variability, mode of inheritance, and heritability is essential for successful crop improvement programs. An investigation was conducted using correlation analysis and morphological characterization to develop the wide genetic diversity between Indian and European mustard gene pools.

Materials and Methods

The research was conducted at the experimental farm of the Division of Genetics and Plant Breeding, Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Chatha, Jammu during the *Rabi* seasons of 2019-20 and 2020-21. The experimental material consisted of F_2 individuals resulting from the cross between Pusa Mehak (Indian genotype with early flowering) and Primus (European genotype having late flowering) and selfing of obtained F_1s to obtain F_2 population. The F_2 population, totalling 359 plants in 2019-20, served as the foundation for the development of the F_3 population. Plots measuring 2.7 m^2 (3 m × 0.9 m) were established with four rows. The row-to-row distance was maintained at 30 cm, while the

plant-to-plant distance was set at 10 cm. Recommended fertilizer doses and plant protection measures were implemented to ensure optimal crop growth. Morphological data for the F_2 and F_3 populations were systematically recorded, encompassing the traits: plant height, length of the main shoot, number of primary branches, number of secondary branches, number of siliquae on the main shoot and average length of siliqua on the main shoot. Additionally, F_3 population data included days to flowering and seed yield per plant. All data were subjected to statistical analysis using the statistical package for the social sciences (SPSS) software. The average value of a character was worked out using the formula:

$$\overline{X} = \frac{\sum x}{n}$$

Where, denotes the average (arithmetic mean), $\sum x$ denotes sum of all observations and n denotes number of observations.

The simple correlation coefficients between different characters were worked out using the formula:

$$r = \frac{Cov.XY}{\sqrt{Var.X \times Var.Y}}$$

Where, r denotes the simple correlation coefficient, Cov. XY denotes co-variances between the characters X and Y; Var. X and Var. Y denotes variance for characters X and Y.

The significance of different correlation coefficients was tested against (g-2) degrees of freedom at 5% and 1% where g is the number of genotypes on which the observation was recorded.

Results and Discussion

Morphological characterization of segregating population

The data analysis indicated that there was a wide distribution of trait values obtained for the entire population of F_2 and F_3 plants. The values for various traits recorded for parents, F_2 population and F_3 population are summarized in Table 1, Table 2 and Table 3.

Table 1: A summary of trait data for two parental genotypes (Pusa Mehak and Primus)

Trait	Pusa Mehak	Primus
Days to 50% flowering	58	137
Plant height (cm)	164	226
Main shoot length (cm)	55	31
Number of primary branches	9	12
Number of secondary branches	16	23
Number of siliquae per plant	40	46
Average siliqua length (cm)	3.84	2.5

Table 2: A summary of trait data for F_2 segregating population

Trait	Minimum value	Maximum value	Average
Plant height (cm)	135	290	220
Main shoot length (cm)	22	108	59
Number of primary branches	3	14	8
Number of secondary branches	3	37	19
Number of siliquae per plant	21	76	46
Average siliquae length (cm)	1.22	4.94	2.85

Table 3: A summary of trait data for F_3 segregating population

Trait	Minimum value	Maximum value	Average
Days to 50% flowering	67	90	80
Plant height (cm)	127	278	202
Main shoot length (cm)	32	100	59
Number of primary branches	3	16	8
Number of secondary branches	3	37	17
Number of siliquae per plant	17	89	44
Average siliquae length (cm)	1.94	5.46	3.64
Yield per plant (gm)	8.77	31.95	20.15

The days to flowering was scored in F_3 population only. It took between 67 to 90 days to reach 50% flowering with an average of 80 days for the F_3 population. The data when plotted indicated a near normal distribution with unimodal distribution (Fig. 1). For yield per plant, the values ranged between 8.8 g to 32.0 g with an average
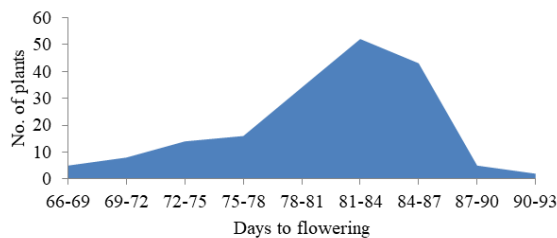
value of 20.2 g in F_3 population. The yield per plant gave a normal distribution with a unimodal distribution (Fig. 2). In accordance to our results, Poonam and Singh (2004) also reported the highest genetic advance in 1000 seed weight followed by seed yield per plant, days to 50% flowering and siliquae per plant.
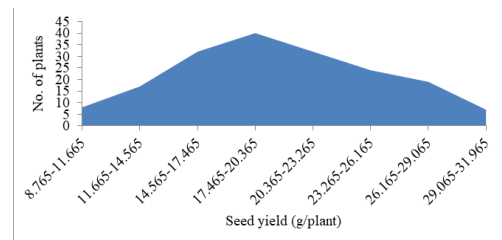

Fig. 1: Frequency distribution of days to flowering in F_3 population comprising of 175 individuals

Fig. 2: Frequency distribution of seed yield per plant (g) in F_3 population comprising of 175 individuals

Correlation between morphological traits for F_2 and F_3 populations

The effectiveness of plant selection was compared through correlation coefficients with their corresponding F_2 and F_3 generation. The correlation values between traits for F_2 and F_3 population was calculated to understand the relationship between different traits (Table 4 and Table 5). These results indicate that selection was effective in both F_2 and F_3 stages and that the selection at F_3 stage was relatively was more effective than at F_2 stage. For F_2 population, plant height was positively correlated with number of secondary branches (r=0.88**), number of primary branches (r =0.43**) and average siliqua length (r =0.40**). Similarly, high

correlation was also detected between main shoot length and number of siliquae on main shoot r =0.57**).

The correlation values between traits were of higher order in F_3 population than F_2 population. In F_3 population, the plant height was significantly correlated with number of secondary branches (r =0.94**), number of siliquae on main shoot (r =0.89**), yield per plant (r =0.51**) and main shoot length (r =0.48**). Similarly, number of siliquae on main shoot detected high correlation with number of secondary branches (r =0.83**), main shoot length (r =0.47**) and yield per plant (r =0.46**). High correlation was also detected between main shoot length and number of secondary branches (r =0.45**). A detailed analysis of correlation

between all possible combinations of traits has been presented in Table 5. In F$_3$ population, the days to flowering trait was found to be negatively correlated with plant height (r = -0.63**), number of siliquae on main shoot (r= -0.63**), yield per plant (r = -0.61**) and number of secondary branches (r = -0.57**). Similar findings were reported by Tahira *et al.* (2014), Kumar *et al.* (2016) and Kumar *et al.* (2018).

Table 4: Correlation coefficients between different characters of F$_2$ segregating population of Indian × East European cross of *B. juncea*

Character	Plant height	Main shoot length	Primary branches	Secondary branches	Siliqua length	Siliquae on main shoot
Plant height	1.00	0.39**	0.43**	0.88**	0.40**	0.37**
Main shoot length		1.00	0.26**	0.36**	0.28**	0.57**
Primary branches			1.00	0.39**	0.30**	0.29**
Secondary branches				1.00	0.36**	0.35**
Siliqua length					1.00	0.26**
Siliquae on main shoot						1.00

*Where; ** Significant at 1% level of significance*

Table 5: Correlation coefficients between different characters of F$_3$ segregating population of Indian × East European cross of *B. juncea*

Character	Plant height	Main Shoot lenght	Primary branches	Secondary branches	Siliqua length	Siliquae on main shoot	Days to flowering	Seed yield/ plant
Plant height	1.00	0.48**	0.22**	0.94**	- 0.090	.89**	- 0.63**	0.51**
Main shoot length		1.00	0.17*	0.45**	- 0.04	0.47**	- 0.34**	0.24**
Primary branches			1.00	0.24**	0.10	0.15*	- 0.09	0.11
Secondary branches				1.00	-0.10	0.83**	- 0.57**	0.45**
Siliqua length					1.00	-0.16*	- 0.01	0.07
Siliquae on main shoot						1.00	- 0.63**	0.46**
Days to flowering							1.00	-0.61**
Seed yield/ plant								1.00

*Where; *: significant at 5% level of significance, **: Significant at 1% level of significance*

The utilization of genetic diversity within a species offers a pathway for enhancing economically significant traits in essential crops, facilitated by the intervention of plant breeders, ultimately benefiting farmers and consumers (Salgotra *et al*., 2015). Among the paramount economic traits, yield stands out, representing the intricate product of multiplicative interactions among contributing characters (Kant and Gulati, 2001). Addressing these intricate interactions necessitates a multifaceted strategy that amalgamates both agronomic and breeding approaches (Saroj *et al*., 2021). Consequently, the primary objective of the mustard improvement program is to cultivate varieties showcasing high-yield potential by incorporating various yield component traits from lines characterized by elevated trait values. The identification of F$_{2:3}$s with superior trait values through the exploration of germplasm is, therefore, of paramount significance.

Conclusion

The morphological data analysis indicated that there was a wide distribution of trait values obtained for the entire population of F$_2$ and F$_3$ plants. The correlation among traits came out to be positively correlated for all characters studied in F$_2$ population. Similarly for F$_3$ population, correlation between all traits was positive except for the traits days to flowering and average siliqua length which showed a negative correlation with all the other traits under this study. The results of this study can be utilized to select for high yield by selecting traits which are positively correlated with yield of plant.

References

Abideen SN, Nadeem F and Abideen SA. 2013. Genetic variability and correlation studies in *B. napus* (L) genotypes. *Intl J Innov Appl Stu* **2**: 574-581.

Bibi T, Rauf S, Mahmood T, Haider Z and Salah-ud-Din. 2016. Genetic variability and heritability studies in relation to seed yield and its component traits in

mustard (*B. juncea*). *Acad J Agril Res* **4**: 478-482.

Gupta MC, Roy HS and Bhadauria SS. 2019. Genetic variability analysis in F_2/F_3 population derived through interspecific hybridization in oilseed *brassica. Elect J Plant Breed* **10**: 1275–1282.

Kant L and Gulati SC. 2001. Genetic analysis for yield and its components and oil content in Indian mustard (*B. juncea*). *Ind J Genet* **61**: 37–40.

Kumar PP, Ramana Rao SV, Choudhary VK, Koshta AK, Khan MA, Lakshera ML and Teja IK. 2022. Performance of rapeseed-mustard in India- a temporal analysis. *J Oilseed Brassica* **13**: 45-52.

Kumar R, Gaurav SS, Jayasudha S and Kumar H. 2016. Study of correlation and path coefficient analysis in germplasm lines of Indian mustard (*B. juncea*). *Agric Sci Dig* **36**: 92-96.

Kumar R, Kaur R, Singh I, Kaur S and Singh H. 2018. Trait association and diversity in exotic lines of Indian mustard. *J Oilseeds Brassica* **9**: 53-58.

Kumari A and Kumari V. 2018. Genetic variability and divergence studies for seed yield and component characters in Indian mustard (*B. juncea* L). *Intl J Curr Microbl App Sci* **7**: 3376-3388.

Mahla HR, Jambhulkar SJ, Yadav DK and Sharma R. 2203. Genetic variability, correlation and path analysis in Indian mustard (*B. juncea*). *Ind J Genet* **63**: 171-172.

Mahmood T, Ali M, Iqbal S and Anwar M. 2003. Genetic variability and heritability estimates in summer mustard (*B. juncea*). *Asian J Plant Sci* **2**: 77-79.

Maurya SK, Maurya KN, Lal K, Singh Y, Singh S, Dixit B and Singh S. 2018. Assessment of genetic variability, heritability and genetic advance in Indian mustard (*B. juncea*). *Int J Curr Microbiol App Sci* **7**: 13-18.

Poonam S and Singh DN. 2004. Path coefficient analysis in Indian mustard (*B. juncea*). *J Res Bisra Agric Univ Ranchi* **16**: 293-295.

Priyamedha, Haider ZA, Kumar A, Ram B, Kumar B, Singh VV and Rai PK. 2018. Analysis of genetic parameters and correlation for yield and quality traits in Indian mustard (*B. juncea*). *J Oilseed Brassica* **9**: 146-150.

Rout S, Gupta A and Kerkhi SA. 2019. Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard (*B. juncea*). *J Pharmacog Phytochem* **8**: 4119-4123.

Salgotra RK, Gupta BB, Bhat JA and Sharma S. 2015. Genetic diversity and population structure of basmati rice (*O. sativa*) germplasm collected from northwestern Himalayas using trait linked SSR markers. *PLoS One* **10**: e0131858.

Saroj R, Soumya SL, Singh S, Sankar MS, Chaudhary R, Yashpal, Saini N, Vasudev S and Yadava DK. 2021. Unraveling the relationship between seed yield and yield-related traits in a diversity panel of *Brassica juncea* using multi-traits mixed model. *Front Plant Sci* **12**: 651936.

Tahira Rashid A, Khan MA and Amjad M. 2014. Seed yield improvement mustard (*B. juncea*) via genetic parameters, heritability, genetic advance, correlation and path coefficient analysis. *Intl J Agric Innov Res* **3**: 727- 731.

Warwick SI, Francis A and La FJ. 2000. Guide to wild germplasm of *Brassica* and allied crops (tribe Brassicaceae). http:// res2.agr. ca/ ecorc/ staff/ warwick/ warw-s1.htm.