

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 F₂ plants were morphologically characterized for different traits, which served as the foundation for the development of F₃ 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 F₃ 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 F₂ and F₃ 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 F₂ individuals resulting from the cross between Pusa Mehak (Indian genotype with early flowering) and Primus (European genotype having late flowering) and selfing of obtained F₁s to obtain F₂ population. The F₂ population, totalling 359 plants in 2019-20, served as the foundation for the development of the F₃ population. Plots measuring 2.7 m² (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 F₂ and F₃ 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, F₃ 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:

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

Where, \bar{X} 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 F₂ and F₃ plants. The values for various traits recorded for parents, F₂ population and F₃ 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 F₂ 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 F₃ 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 F₃ population only. It took between 67 to 90 days to reach 50% flowering with an average of 80 days for the F₃ 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

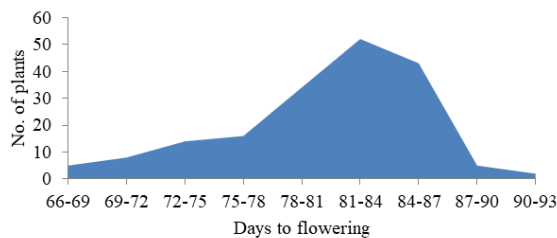


Fig. 1: Frequency distribution of days to flowering in F₃ population comprising of 175 individuals

Correlation between morphological traits for F₂ and F₃ populations

The effectiveness of plant selection was compared through correlation coefficients with their corresponding F₂ and F₃ generation. The correlation values between traits for F₂ and F₃ population was calculated to understand the relationship between different traits (Table 4 and Table 5). These results indicate that selection was effective in both F₂ and F₃ stages and that the selection at F₃ stage was relatively more effective than at F₂ stage. For F₂ 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

value of 20.2 g in F₃ 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.

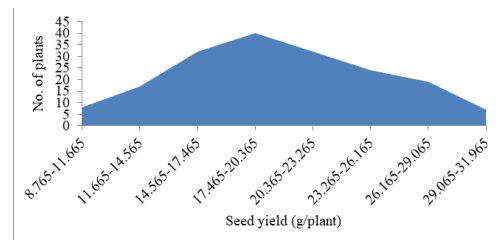


Fig. 2: Frequency distribution of seed yield per plant (g) in F₃ population comprising of 175 individuals

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 F₃ population than F₂ population. In F₃ 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 F₃ 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 F₂ 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 F₃ 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	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 F₂ and F₃ plants. The correlation among traits came out to be positively correlated for all characters studied in F₂ population. Similarly for F₃ 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.

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