Short Communication

Genetic characterization studies of F_2 population of Indian mustard × East-European mustard through principal component analysis

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Abstract

The study was conducted during the *Rabi* season of 2019-20, focused on the principal component analysis (PCA) of F_2 generation resulting from a cross between Indian mustard and East European mustard. The F_2 population, comprising 359 plants, was systematically evaluated for agromorphological traits, and PCA revealed three principal component axes, collectively explaining 71.45% of the total variation. Notably, the first component (PC1) primarily featured plant morphological and seed yield-contributing traits, contributing maximum variability (42.70%) while PC2 contributed for 14.43% of total variability and PC3 14.32% of total variability. Additionally, subsequent principal components highlighted specific trait contributions, demonstrating the potential for effective selection in crop breeding programs. The study underscores the importance of employing PCA to evaluate genetic diversity and discerns the prime contributors to variability in Indian mustard, providing valuable insights for crop breeding programs.

Keywords: *Agromorphological traits, East European mustard, Indian mustard, principal component analysis*

Introduction

Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] is a pivotal oilseed crop, contributing significantly to the rapeseed and mustard group, representing over 80% of this category. Mustard production in India has seen a substantial increase, rising from 91.24 to 128.18 lakh tonnes in the last three years, with a productivity boost from 1331 to 1447 kg/ha. The rapeseed-mustard cultivation area has expanded by 29% from 68.56 lakh ha in 2019-20 to 88.58 lakh ha in 2022-23 (PIB, 2023). Indian mustard is a natural amphidiploid (2n=36) resulting from the fusion of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16). This self-compatible, largely self-pollinated *Rabi* season crop is grown in states like Uttar Pradesh, Rajasthan, Haryana, Assam, Gujarat, Punjab, West Bengal, and Madhya Pradesh. The mustard seed, constituting about 38-42% oil, serves as an economical and nutritious cooking medium, condiment, and has various industrial applications. Crop varieties are pivotal in enhancing productivity through their improved genetic makeup. High seed yield and oil percentage are primary breeding objectives in rapeseed-mustard programs. The crop faces genetic diversity challenges, with two distinct gene pools in *Brassica juncea*, the East European gene pool which has low erucic acid, and the Indian gene pool, though high in erucic acid, exhibits better yield under Indian subcontinent conditions. Information on the extent of genetic variability among agronomically important traits is a prerequisite in understanding composition and variability existing in any population. This study focuses on the principal component analysis of the F_2 generation resulting from a cross between Indian mustard and East European mustard. The endeavour is to contribute to the understanding of genetic intricacies in Indian mustard, aiding the development of superior varieties through hybridization efforts.

Materials and Methods

The study 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* season of 2019-20. F_2 individuals were derived from the cross between Pusa Mehak (Indian genotype) and Primus (European genotype), followed by selfing of obtained F_1s to generate the F_2 population, totaling 359 plants. Plots of 2.7 m² (3 m × 0.9 m) with four rows, a row-to-row distance of 30 cm, and a plant-to-plant distance of 10 cm were established. Recommended fertilizer doses and plant protection measures were applied. Morphological data for the F_2 population, encompassing plant height, length of the main shoot, number of primary branches, number of secondary branches, number of siliquae on the main

shoot, average length of siliqua on the main shoot, and yield per plant, were systematically recorded. The data underwent principal component analysis (PCA) using R 3.6.1 software to determine the relative importance of different traits based on seven quantitative characteristics.

Results and Discussion

Principal component analysis (PCA) stands as a potent method in genetic diversity studies, facilitating data reduction. By eliminating interrelationships among components, PCA identifies variables contributing most significantly to genetic variability, serving as a basis for further genotype characterization. In the current study, data on quantitative characters underwent PCA analysis using R software. The PCA yielded eigenvalues and factor scores, gauging the discriminative power of axes and associated characters.

The outcomes revealed that three out of the seven principal component axes exhibited eigenvalues surpassing one, collectively elucidating 71.45% of the total variation among 359 plants in the F_2 population (Table 1), evaluated for seven distinct agro - morphological traits.

Table 1: Eigen value and percent of total variation for seven principal components

Component	Eigen value	Variance explained (%)	Cumulative variance (%)
PC1	2.98	42.70	42.70
PC2	1.00	14.43	57.12
PC3	1.00	14.32	71.44
PC4	0.74	10.69	82.13
PC5	0.69	9.98	92.11
PC6	0.42	6.04	98.15
PC7	0.12	1.85	100.00

Factor loadings of seven characters concerning different PCs are presented in Table 2.

PC1: The first component (PC1) manifested positive contributions from yield per plant (0.60), number of pods on main shoot (0.49), number of secondary branches (0.47), main shoot length (0.38), plant height (0.38), number of primary branches (0.35) and average pod length (0.34). These primary characters, associated with plant morphology and seed yield, accounted for a maximum 42.70% variability in the first principal component (PC1) (Table 1), suggesting differentiation among F_2 plants based on these traits. Similar trends using PC analysis in Indian mustard, particularly for seed yield per plant and number of primary branches per plant have been reported by Belete *et al*. (2011), Ray *et al*. (2014) and Neeru *et al*. (2015).

PC2: In the second principal component (PC2), all characters, except the number of secondary branches per plant (-0.05) and plant height (-0.01), exhibited positive contributions, collectively explaining 14.43% of the variability. The coexistence of positive and negative loadings within a single component indicates the presence of both positive and negative correlation trends between components and variables.

PC3: The third component, elucidating 14.32% of total variability, featured positive contributions from main shoot length (0.58), number of pods on the main shoot (0.34) and yield per plant (0.07).

PC4: The fourth component displayed positive loadings for all characters except plant height (-0.05), number of secondary branches (-0.39), main shoot length (-0.08), number of pods on the main shoot (-0.30), and yield per plant (-0.10), accounting for 10.69% of the total variability.

PC5: The fifth component, contributing 9.98% of the total variability, demonstrated positive loadings for all characters except plant height and the number of primary branches (-0.33).

PC6: The sixth component (PC6) contributed to 6.04% of total variability and featured positive loadings, except for the number of primary branches (-0.07) and main shoot length (-0.40).

PC7: The seventh component, contributing 1.85 to total variation, exhibited positive loadings for all characters except plant height (-0.01). The patterns revealed through PCA offer valuable insights into evaluating the potential breeding value of germplasm based on traits loaded on various components.

The findings align with numerous studies highlighting the significant contribution of the number of siliquae per plant to genetic divergence in Indian mustard. Consistency with studies by Naznin *et al*. (2015), Pankaj *et al*. (2017), Chandra *et al*. (2018), and Gupta *et al*. (2019) was observed.

Conclusion

Table 2: Factor loadings of seven characters with respect to different Principal Components

Character	Number of principal components						
	1	2	3	4	5	6	7
Pods on main shoot	0.49	0.09	0.34	-0.30	0.09	0.02	0.72
Primary branches	0.35	0.13	-0.16	0.35	-0.33	-0.07	0.04
Secondary branches	0.47	-0.05	-0.36	-0.39	0.12	0.00	0.68
Main shoot length	0.38	0.06	0.58	-0.08	0.08	-0.40	0.00
Plant height	0.38	-0.01	-0.59	-0.05	-0.04	0.70	-0.01
Pod length	0.34	0.01	-0.14	0.77	0.50	0.03	0.04
Yield per plant	0.60	0.98	0.07	-0.10	0.12	0.64	0.43

Employing PCA allowed for the assessment of divergence and determination of the relative contribution of different components to total divergence. Characters identified as prominent contributors in a specific principal component, influencing total variability, tend to act cohesively and can serve as effective selection criteria in crop breeding programs. Consequently, these traits hold potential for selection in Indian mustard crop breeding programs.

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