

Original Research Article

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Genetic Characterization of Indian mustard (*Brassica juncea* L.) Germplasm for Quantitative Traits through Principal Component Analysis

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ABSTRACT

Information on the extent of genetic variability among agronomically important traits is a prerequisite to plan an appropriate plant breeding method. Thirty-five Indian mustard germplasm accessions from ICAR-NBPGR, RS, Jodhpur were evaluated for 11 quantitative characters for determining the pattern of variation, relationship among individuals and their characteristics. Principal component analysis was used to know the variation and to estimate the relative contribution of various traits towards total variability. Results showed that there are five axes which accounted for 74.87% cumulative variance of the total variability for eleven agro-morphological traits. PC1 exhibited 25.32% of the total variability contributed by the traits like days to 50% flowering, days to maturity, plant height and siliqua length. PC2 showed 18.71% of the total variation and the traits *viz.*, number of secondary branches, number of siliqua per plant, test weight and seed yield per plant contribute to the variation. PC3 had the contribution from the characters like number of primary branches per plant, length of main branch and number of seeds per siliqua which contributed 13.63% of the total variation. Days to 50% maturity, number of secondary branches per plant, number of siliqua per plant and test weight had contributed 8.91% of the total variation in PC4. PC5 exhibited 8.30% of the total variability. Thus, the results revealed vast genetic variability exists in the germplasm accessions which may be useful as source for variable characters in Indian mustard improvement.

Keywords

Indian mustard,
Multivariate
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Introduction

Indian mustard [*Brassica juncea* (L.) Czern&Coss] is an important oilseed crop of Brassicaceae family which accounts more than 70 % under rapeseed and mustard. The Brassicaceae, contains about 3500 species and 350 genera, is one of the 10 most

economically important plant families. Rapeseed-mustard comprising eight different species *viz.* Indian mustard, toria, yellow sarson, brown sarson, gobhisarson, karanrai, black mustard and taramira are being cultivated in 53 countries spreading all over the world. Indian mustard (*Brassica juncea* L.) is the second most important oilseed crop

of the world as well as India. In India, mustard and rape seed are being grown largely in states like Uttar Pradesh, Rajasthan, Haryana, Assam, Gujarat, Punjab, West Bengal and Madhya Pradesh. Indian mustard is a natural amphidiploid ($2n=36$) of *Brassica campestris* ($2n=20$) and *Brassica nigra* ($2n=16$). It is self-compatible and largely self-pollinated crop (85-90 %).

Mustard is a *Rabi* season crop of temperate region, which requires relatively cool temperature. This crop prefers moderate temperature during growth *i.e.* below 28°C day temperature and it is resistant to frost at all the growth stages. It is grown on a wide range of soil types from fairly heavy clay to light sandy soil. Mustard seed is largely crushed for oil, which is perhaps the cheapest source of oil in our daily diet. Mustard seeds contain about 38-42% oil, which is golden yellow, fragrant and considered among the healthiest and most nutritional cooking medium. In addition to this, it is also utilized as condiment, for medicinal uses and in preparation of soaps, hair oil, lubricants, paints, plasticizers and as a condiment in pickles.

The extent of diversity available any crop decides the success of any crop improvement programme with manifested objectives. Assemblage and assessment of divergence in the mustard germplasm is essential to know the spectrum of diversity as many such studies have been conducted across the India. In the present investigation, 35 germplasm accessions of Indian mustard were studied for the assessment of genetic diversity by multivariate analysis.

Materials and Methods

This experiment consisted of 35 national elite germplasm accessions of Indian mustard including 3 checks conserved in Medium

Term Storage, NBPGR, RS, Jodhpur. The trial was laid out in a randomized block design with three replications during *Rabi*2019 at Research field of NBPGR, Regional Station, Jodhpur, India situated at about $28^{\circ} 35'$ N, longitude of $70^{\circ}18'$ E and an altitude of 227 m above mean sea level. The observations for 11 morphological traits were recorded on five randomly selected plants of each accession as per the standard descriptors by NBPGR.

The 11 traits are as follows: days to 50 % flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, length of main branch, number of silique per plant, length of silique, number of seeds per silique, 1000 seed weight and seed yield per plant. The data were subjected to PCA was performed using the statistical package R 3.6.1 version. Principal component analyses (PCA) based on 11 quantitative traits was carried out to find the relative importance of different traits in capturing the variation in germplasm.

Results and Discussion

PCA is a powerful technique in genetic diversity studies for data reduction. PCA removes interrelationships among components and identify variables which contribute most to genetic variability to be selected for further characterizing genotypes. In present investigation data collected on the quantitative characters were analyzed for principal component analysis using R software.

The PCA produced eigenvalues and factor scores that were used respectively to measure the relative discriminative power of the axes and their associated characters. The result of the PCA showed that four of the 5 principal component axes had eigenvalues greater than

one and altogether accounted for 74.87% of the total variation among 35 accessions evaluated for eleven different agromorphological traits. The traits in first component (PC1) contributing in a positive direction are number of primary branches per plant, length of main branch, number of silique per plant, number of seeds per silique, 1000 seed weight and seeds yield per plant.

These are the major characters of plant morphological and seed yield contributing

traits contributed maximum 25.32 per cent variability to the first principal component (PC 1) (Table 1, Fig. 1) indicating that the high yielding lines were differentiated on the basis of these characters.

Similar trend using PC analysis in Indian mustard for the traits seed yield per plant, number of primary branches per plant and plant height was reported by Belete *et al.*, (2011), Ray *et al.*, (2014) and Neeru *et al.*, (2015).

Table.1 Eigen value and percent of total variation for various principal components

Components	Eigen value	Variance explained (%)	Cumulative (%)
PC1	2.794	25.32	25.32
PC2	2.308	18.71	44.03
PC3	1.592	13.63	57.66
PC4	1.093	8.91	66.57
PC5	1.012	8.30	74.87

Table.2 Factor loadings of eleven characters with respect to different PC's (Principal components)

Characters	1	2	3	4	5
Days to 50 % flowering	-0.745	0.061	0.135	0.027	0.082
Days to maturity	-0.555	0.177	-0.378	0.486	-0.119
Plant height	-0.616	0.469	-0.047	0.214	0.222
Number of primary branches per plant	0.545	-0.208	-0.601	0.076	0.223
Number of secondary branches per plant	-0.077	0.573	-0.227	-0.597	0.208
Length of main branch	0.560	0.560	-0.200	-0.114	0.449
Number of siliqua per plant	0.377	0.673	0.0455	0.414	0.235
Length of siliqua	-0.302	0.084	0.588	-0.102	0.541
Number of seeds per siliqua	0.527	-0.254	0.633	0.171	-0.067
1000 seed weight	0.122	0.682	0.094	-0.336	-0.478
Seed yield per plant	0.616	0.661	0.159	0.262	-0.092

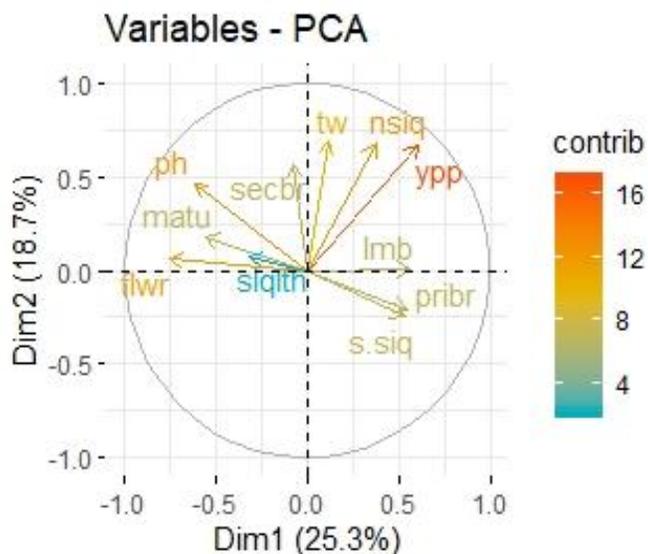


Figure.1 Plot of Principal component analysis (PCA) of different variables showing their contribution towards total variation

Occurrence of both positive and negative loading in a single component shows the presence of positive and negative correlation trends between the components and the variables. All the characters except number of secondary branches per plant and number of seeds per silique were contributed positively to the second principal component (PC2) accounting for 18.71 per cent of the variability explained.

The third component accounts for 13.63 per cent of total variability and the characters *viz.*, days to 50% flowering, length of silique, number of seeds per silique, 1000 seed weight and seed yield per plant contributed in positive way. The fourth component had positive loadings for all the characters except number of secondary branches per plant, length of main branch, length of silique and 1000 seed weight accounting for 8.91 per cent of the total variability.

The fifth component had positive and high loadings for all the characters except days to maturity, number of seeds per silique, 1000 seed weight and seed yield per plant and contributed 8.30 per cent of the total

variability. Pattern of relationships obtained through PCA are useful to evaluate potential breeding value of germplasm through traits loaded on various components. Factor loadings of eleven characters with respect to different PC's are shown in Table 2. Using PCA, it was possible to access the degree of divergence to understand the trend of their evolutionary pattern and to assess the relative contribution of different components to the total divergence.

The results are in agreement with various other studies that reported the maximum contribution of number of silique per plant, number of seeds per silique and 1000 seed weight towards genetic divergence in Indian mustard. These results were in accordance with the studies conducted by Naznin *et al.*, 2015, Pankaj *et al.*, 2017, Chandra *et al.*, 2018 and Gupta *et al.*, 2019. The prominent characters identified in a particular principal component as prime contributors to total variability have the tendency to perform together and can be used effectively for selection in crop breeding programmes. In all the five components traits like number of silique per plant, seed yield per plant and

number of seeds per silique contributed positively to the total variation. Hence these traits can be used for selection in crop breeding programmes in Indian mustard.

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