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# Revealing genetic diversity of Indian mustard (*Brassica juncea*) for yield improvement

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## ABSTRACT

The study was carried out during *rabi* 2015–17 to understand the nature and magnitude of genetic variability and character association of 45 accessions of Indian mustard. These accessions were evaluated for 16 quantitative traits under standard package of practices. The results indicated high PCV and GCV for 1000 seed weight, stover nitrogen uptake (STNU) and seed nitrogen uptake (SNU) while it was low for NUE. High heritability coupled with high genetic advance as percent of mean was observed for 1000 seed weight, STNU and oil content which indicates the involvement of additive gene action, thus feasibility of improvement through simple selection. Seed yield had a positive and significant correlation with seed uptake efficiency, nitrogen harvest index and NUE. First five principal components gave eigenvalues >1.0 and cumulatively expressed 80.67% of the total variation (Table 2). PCA exhibited that plant height, NBP, number of siliquae in the main branch, nitrogen (%) in seed, total nitrogen (%), SNU and seed yield (Kg/ha) were among the most important traits accounting for more than 50% phenotypic variation. Therefore, these quantitative traits should be considered to enhance yield potential as they will be beneficial to develop promising varieties. Accessions such as IC67693, IC277700, IC268336 and RH-30 were identified to be distantly plotted on the dendrogram, thus more diverse in nature. Donors for various traits were also determined based on their pooled performance e.g. IC267693, IC338494, IC571625, IC339605 and IC571654 for seed yield.

**Key words:** Genetic variability, Mustard, Quantitative traits, Yield

Indian mustard [*Brassica juncea* (L.) Czern & Coss] belongs to Cruciferae (Brassicaceae) family grown extensively in *rabi*, is an amphidiploid (2n=36; AABB). In India, *B. juncea* contributes approximately 80% of total mustard-rapeseed production. Globally, 36.68 mha area is under mustard cultivation with a production of 72.42 mt and productivity of 1974 Kg/ha, whereas, India produces 7.92 mt on an area of 6.07 mha with a productivity of 1304 Kg/ha (Anonymous 2017–18). Uttar Pradesh leads by producing 0.84 mt on 0.66 mha with a productivity of 1080 Kg/ha (Anonymous 2016–17).

Mustard is rich in oil (28–32%) and protein (28–36%) content (Sharif *et al.* 2017). Among rapeseed and mustard, Indian mustard is more popular among farmers owing to higher yield and relative tolerance to various biotic and abiotic stresses. Having genetically diverse donors is a pre-requisite for any breeding program as it serves as a base for providing valuable genetic material. Yield is a multifaceted trait; therefore, evaluation of yield and its contributing traits is significant for crop improvement, which is analyzed based on their phenotypic value and partially determined by the performance of accessions (Khan *et. al.* 2015). The productivity traits are primarily quantitative and are affected by several genes of either large or small effect, or a combination of both. Seed yield being a quantitative trait is largely influenced by environmental factors, thus traits having strong positive correlations need to identify for more genetic gains (Rashmi *et al.* 2018). Additionally, some morphological characteristics are difficult to evaluate quantitatively but may be useful as markers in a breeding program (Karimi *et al.* 2009, Mansyah *et al.* 2010). Therefore, the objectives of the present study were to understand nature and magnitude of genetic variability and to identify the potential of the genotype towards yield and its association with other agro-morphological traits.

## MATERIALS AND METHODS

The study was carried out at experimental Farm, ICAR – National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi during *rabi* 2015–2016 and 2016–2017. The farm is situated at the latitude of 28°38'56.0"N and longitude

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77°09'07.7"E and an altitude of 228.61 meters above mean sea level. The annual rainfall at the area is 500-750 mm from of which most part is received during monsoon (July–September) season. Forty germplasm accessions having diverse variability were evaluated along with five released varieties, viz. Rajat, RH-30, Pusa Jai Kisan, Varuna & Laxmi in Randomized Complete Block Design (RCBD) with three replications. All the 45 accessions and checks were grown in three rows of three-meter length with a spacing of 60 cm × 10 cm. The recommended agronomic practices were adopted for raising a healthy crop.

The accessions have been evaluated on the basis of their variations between 16 agronomic traits such as plant height [*p*H (cm)], NBP [NBP], number of siliqua in main branch [SMB], 1000 seed weight [TSW (g)], oil content [OC (%)], stover yield [STY (q/ha)], nitrogen % in plant [NP (%)], nitrogen% in seed [NS (%)], total nitrogen% [TN (%)], Seed Nitrogen Uptake (Kg N/ha), Stover Nitrogen Uptake [STNU (Kg N/ha)], total nitrogen uptake [TNU (Kg N/ha)], seed uptake efficiency [SUE], nitrogen harvest index [NHI], nitrogen use efficiency [NUE] and seed yield [SY (Kg/ha)] and data were recorded as per minimal descriptors for *Brassica* spp.

*Statistical analysis*: The two years mean data of each accession were subjected to ANOVA (Panse and Sukhatne 1954), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) analysis (Allard 1960) and genetic advance and heritability as per Burton (1952). Genotypic correlation coefficients and principal component analysis were calculated using XL-STAT and INDO-STAT. Cluster analysis was performed on SPAR 4.03.

## RESULTS AND DISCUSSION

*Variability Parameters*: The analysis of variance carried out for 16 traits showed positive and significant differences amongst all the accessions and traits. Highly significant differences were found for all the traits especially for stover yield, seed yield and plant height. The presence of highly significant differences showed the existence of high variability among accessions studied. Therefore, there is a great opportunity for selection of promising donors for yield and its related components in Indian mustard.

The analysis of data revealed that PCV was higher than the respective GCV for all the traits indicating the influence of environmental factors (Table 1). The highest PCV and GCV was for recorded for 1000 seed weight (24.30, 22.90), STNU (23.55, 21.84) and SNU (19.02, 17.09), whereas it was lowest for NUE (2.64, 1.35), nitrogen % in seed (3.62, 3.29) and oil content (4.04, 3.81). The heritability was ranging from as low as 0.11 in the number of siliquae for

Table 1 Variability parameters of different agro-morphological traits in Indian mustard

| Trait | Minimum | Maximum | Mean | GCV | PCV | $H^2$ | GA as percent of Mean | Promising accessions |
|---|---|---|---|---|---|---|---|---|
| Plant Height (cm) | 131.28 | 195.53 | 179.79 | 4.54 | 8.46 | 0.29 | 5.01 | PL, IC538665 |
| Number of branches | 7.38 | 11.3 | 8.74 | 3.46 | 10.20 | 0.11 | 2.41 | PL , IC265385 , IC296741, |
| Number of Siliqua in Main Branch | 51.71 | 68.76 | 63.34 | 0.6 | 30.34 | 0.96 | 59.89 | PL, IC571669, IC228571 |
| 1000 Seed Weight (g) | 2.26 | 5.57 | 3.71 | 22.9 | 24.3 | 0.89 | 44.46 | IC424415, IC571629, IC571625 |
| Oil Content (%) | 31.4 | 37.78 | 35.36 | 3.81 | 4.04 | 0.89 | 7.39 | IC335852, IC335855, IC571649 |
| Stover Yield (Kg/ha) | 35.48 | 67.38 | 57.28 | 13.09 | 14.95 | 0.77 | 23.61 | PL, IC339605, IC560690 , IC228571 |
| Nitrogen % in Plant | 0.58 | 1.48 | 1.21 | 12.99 | 18.78 | 0.48 | 18.5 | PL, IC491028 , IC401571 |
| Nitrogen % in Seed | 3.95 | 4.55 | 4.21 | 3.29 | 3.62 | 0.83 | 6.17 | IC571636, IC571661, IC311819 |
| Total Nitrogen % | 4.93 | 5.91 | 5.42 | 3.7 | 4.96 | 0.56 | 5.69 | PL, IC311819, IC491028 |
| Seed Nitrogen Uptake (Kg N/ha) | 70.58 | 150.14 | 112.08 | 17.09 | 19.02 | 0.81 | 31.63 | IC338494, IC339605, IC571654, IC571625 |
| STNU (Kg N/ha) | 23.87 | 95.02 | 68.08 | 21.84 | 23.55 | 0.86 | 41.74 | IC228571, IC538719, IC311819 |
| Total Nitrogen Uptake (Kg N/ha) | 131.86 | 237.82 | 180.16 | 13.21 | 14.41 | 0.84 | 24.94 | IC339605, IC338494, IC571625, IC228571, IC491028 |
| Seed Uptake Efficiency | 11.05 | 19.22 | 14.72 | 11.78 | 13.15 | 0.8 | 21.74 | IC424415 |
| Nitrogen Harvest Index | 48.39 | 83.71 | 62.2 | 11.56 | 12.83 | 0.81 | 21.47 | IC424415, IC571661 |
| Nitrogen Use Efficiency | 50.84 | 57.86 | 53.6 | 1.35 | 2.64 | 0.26 | 1.42 | PL, IC424415 |
| Seed Yield (Kg/ha) | 19.51 | 35.18 | 26.44 | 11.62 | 13.58 | 0.73 | 20.48 | IC267693, IC338494, IC571625, |

Table 2 Vector loading, Eigen value and percentage of variation explained by first five principal components and correlations between PC scores and agro-morphological traits

| Character | PCA1 | PCA2 | PCA3 | PCA4 | PCA5 | Latent Roots (Eigenvalues) |
|---|---|---|---|---|---|---|
| Plant Height (cm) | 0.01 | 0.32 | -0.76 | 0.32 | -0.22 | 5.11 |
| Number of primary branches | -0.20 | -0.22 | -0.15 | 0.30 | 0.48 | 3.27 |
| Number of Siliqua in Main Branch | 0.10 | 0.23 | -0.67 | 0.45 | -0.21 | 1.77 |
| 1000 Seed Weight (g) | 0.04 | 0.33 | -0.31 | -0.19 | 0.55 | 1.42 |
| Oil Content (%) | 0.15 | 0.09 | 0.13 | 0.33 | -0.63 | 1.34 |
| Stover Yield (Kg/ha) | -0.49 | 0.44 | -0.41 | -0.20 | 0.18 | 0.99 |
| Nitrogen % in Plant | -0.73 | 0.23 | 0.26 | -0.08 | -0.29 | 0.79 |
| Nitrogen % in Seed | -0.25 | -0.01 | 0.27 | 0.74 | 0.42 | 0.68 |
| Total Nitrogen % | -0.75 | 0.18 | 0.39 | 0.44 | 0.05 | 0.31 |
| Seed Nitrogen Uptake (KgN/ha) | 0.44 | 0.86 | 0.22 | 0.08 | 0.08 | 0.27 |
| Stover Nitrogen Uptake (KgN/ha) | -0.87 | 0.43 | -0.05 | -0.20 | -0.03 | 0.04 |
| Total Nitrogen Uptake (KgN/ha) | -0.19 | 0.96 | 0.14 | -0.06 | 0.04 | 0.01 |
| Seed Uptake Efficiency | 0.97 | 0.19 | 0.10 | 0.00 | -0.03 | 0.00 |
| Nitrogen Harvest Index | 0.94 | 0.18 | 0.17 | 0.20 | 0.08 | 0.00 |
| Nitrogen Use Efficiency | 0.80 | -0.18 | -0.06 | -0.08 | 0.15 | 0.00 |
| Seed Yield (Kg/ha) | 0.47 | 0.85 | 0.16 | -0.06 | 0.00 | 0.00 |
| Percent of Total Variance Explained | 31.91 | 20.44 | 11.07 | 8.85 | 8.40 | |

the main branch to the 0.89 for 1000 seed weight (g) and oil content (%). High heritability coupled with high genetic advance was observed for 1000 seed weight, STNU and oil content while it was low for branches per plant, siliqua in the main branch and NUE (Table 1).

Several studies conducted earlier have reported similar results for various parameters of variability, heritability and genetic advance (Thakral *et al.* 2014, Synrem *et al.* 2015, Akabari and Niranjana 2015 and Rashmi *et al.* 2018). The association between heritability and genetic advance of a trait helps breeder to predict the performance of those traits in next generations and response to selection (Arifullah 2013, Rashmi *et al.* 2017). Narrow difference between PCV and GCV in most traits showed that they were comparatively stable to environment pressure. Estimates of high heritability coupled with high genetic advance are usually more helpful in predicting increase under selection than heritability alone (Johnson *et. al.* 1995). Therefore, traits such as seed yield, oil content, stover yield and 1000 seed weight suggest the possibility of yield improvement through selection.

*Genotypic Correlation Coefficient*: The genotypic correlation coefficient was estimated between seed yield and other traits. The data revealed that the number of siliquae in the main branch showed highly significant and positive correlation with plant height (0.65*). Total nitrogen (%) showed significant and positive correlation with nitrogen (%) in the plant (0.74*). STNU showed a highly significant positive correlation with nitrogen (%) in the plant (0.75*), stover yield (0.69*) and total nitrogen (%) (0.61*). Total nitrogen uptake showed significant positive correlation with SNU (0.78*), STNU (0.59*), stover yield (0.49*) and nitrogen (%) in the plant (0.39*). Seed uptake efficiency showed significant positive correlation with SNU (0.60*) whereas significant negative correlation with SNU (-0.77*), total nitrogen (%)(-0.64*), nitrogen (%) in the plant (-0.59*) and stover yield (-0.48*). Nitrogen harvest index showed a significant positive correlation with seed uptake efficiency (0.96*) and SNU (0.62*) whereas significant and negative correlation with SNU (-0.80*), nitrogen % in the plant (-0.64*), total nitrogen % (-0.50*) and stover yield (-0.49*). NUE showed significant and positive correlation with seed uptake efficiency (0.69*) and nitrogen harvest index (0.65*) whereas significant negative correlation with SNU (-0.69*), total nitrogen (%)(-0.61*), nitrogen (%) in the plant (-0.56*) and stover yield (-0.43*). Seed yield showed significant and positive correlation with seed uptake efficiency (0.52*), nitrogen harvest index (0.47*) and NUE (0.44*).

The significant positive correlations among traits gave positive results while making selection in the breeding programme. It also helps in understanding the basis of genetic linkage that is determined within and between the traits and crop improvement program can be designed to pyramid desirable genes and removing undesirable. Similar estimates were also recorded by Kumar *et al.* (2018) and Devi (2018). The selection depending on the genetic variability studies alone sometimes doesn't account for expected genetic gain due to the presence of G × E interactions. The unfavourable association among the yield and yield contributing traits under selection may result in genetic slippage and limit the genetic advance (Lozada *et al.* 2020). Hence, knowledge of the correlations among such traits is basic while aiming for a rational improvement

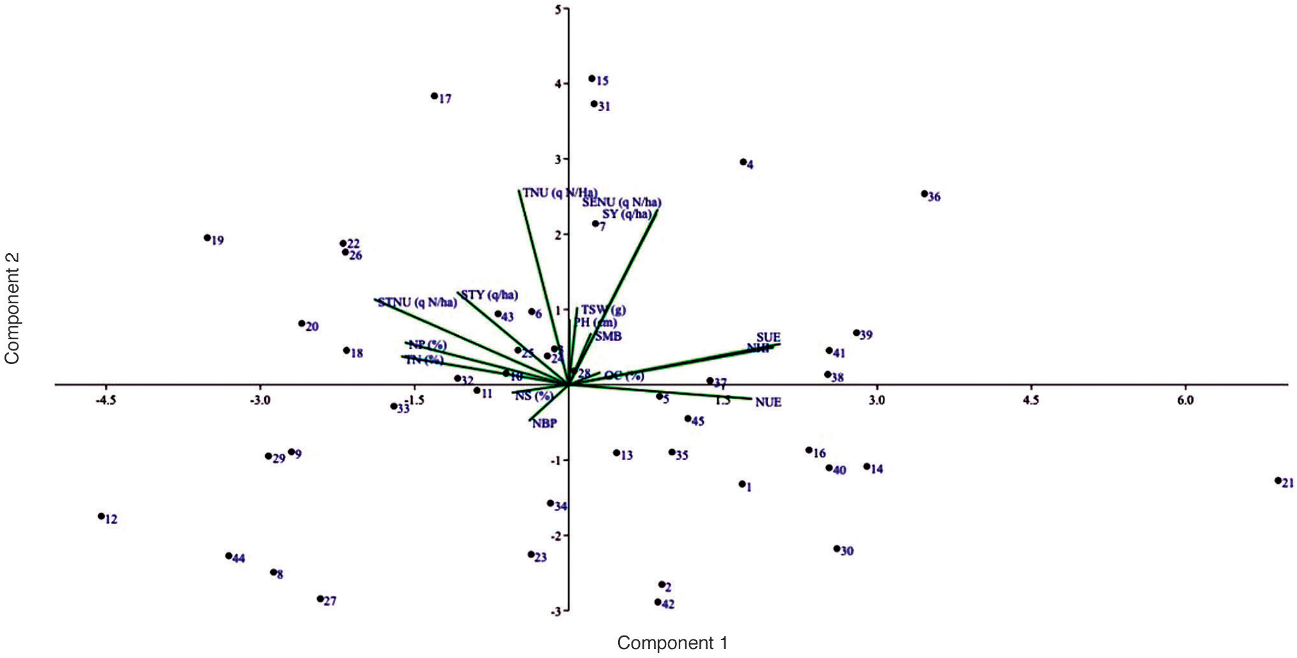

Fig 1 Bi plot between principal component 1 and 2.

in yield through selection (Rashmi *et al.* 2018, Neyhart *et al.* 2019).

*Principal Component Analysis (PCA)*: The results of PCA revealed that the first five Principal components (PCI to PCV) gave eigenvalues >1.0 and cumulatively accounted for 80.67% of the total variation. There are no guidelines to determine the significance or importance of a coefficient, that is, eigenvectors, however higher coefficients for a certain trait indicate the relatedness of that trait to respective PC axes (Duzyaman 2005). The variation in PC I explained 31.91% of the total variance and was mainly associated with seed uptake efficiency, nitrogen harvest index, NUE and seed yield. PC II explained 20.44% of the total variance and correlated mainly to the traits like plant height, the number of siliquae in the main branch, SNU, STNU, total nitrogen uptake, stover yield and seed yield. PC III explained 11.07% of the total variation and was mainly contributed by the traits, viz. nitrogen (%) in plant, total nitrogen (%) and SNU while plant height, NBP, number of siliqua in the main branch, 1000 seed weight, stover yield, STNU. PC IV explained 8.85% of the total variance and found to be associated with traits viz. plant height, NBP, number of siliquae in the main branch, nitrogen (%) in seed and total nitrogen (%). PC V explained 8.40% of the total variance and correlated mainly to the traits, viz. NBP and nitrogen (%) in seed while a negative association with plant height, number of siliqua in the main branch and oil content, nitrogen (%) in plant, STNU and seed uptake efficiency. The traits like plant height, NBP, number of siliqua in the main branch, nitrogen (%) in seed, total nitrogen (%), SNU and seed yield were among the most important traits which contributed for >50% phenotypic variation in the germplasm accessions based on coefficient values in PC I to V. Thus, it is suggested that the use of these traits will save a considerable amount of time for identification and characterization of *B. juncea* germplasm. Rashmi *et al.* (2015) while evaluating 148 accessions of *Brassica juncea* reported that first five PC cumulatively accounted for 59.8% of the total variance. Similar results had been reported by Rashmi *et al.* 2017 while studying the different germplasm accessions.

A biplot was also drawn using the values of PCA I and PCA II (Fig 1). However, no obvious grouping of accessions was observed, and some overlapping occurred among groups demonstrating the relatedness of the accessions across the collection.

*Cluster Analysis*: Genetic divergence analysis divided 45 accessions into two major clusters based on yield and yield contributing traits (Fig 2). Cluster I and cluster II comprised of 21 and 24 genotypes, respectively. Therefore, hybridization between the accessions that are distantly located in clusters is more likely to give good progenies. The maximum inter-cluster distance was observed between IC267693 and RH-30, whereas, the maximum intra-cluster distance was observed between IC67693 and IC277700 in cluster I and IC268336 and RH-30 in cluster II. Similar observations were also recorded by Pandey *et al.* (2013).

*Promising Lines*: The current investigation was also performed to identify the promising accessions for various significant traits (Table 1), which may be used as donors for developing better varieties. A few accessions demonstrated unrivalled performance for more than one characters, viz. IC424415 for 1000 seed weight, seed uptake efficiency and nitrogen harvest index, IC 571625 for 1000 seed weight, SNU, total nitrogen uptake and seed yield, IC311819 for nitrogen (%) in seed and STNU, IC338494, IC339605 and IC571625 for SNU, total nitrogen uptake and seed yield, IC571654 for SNU and seed yield, IC228571 for

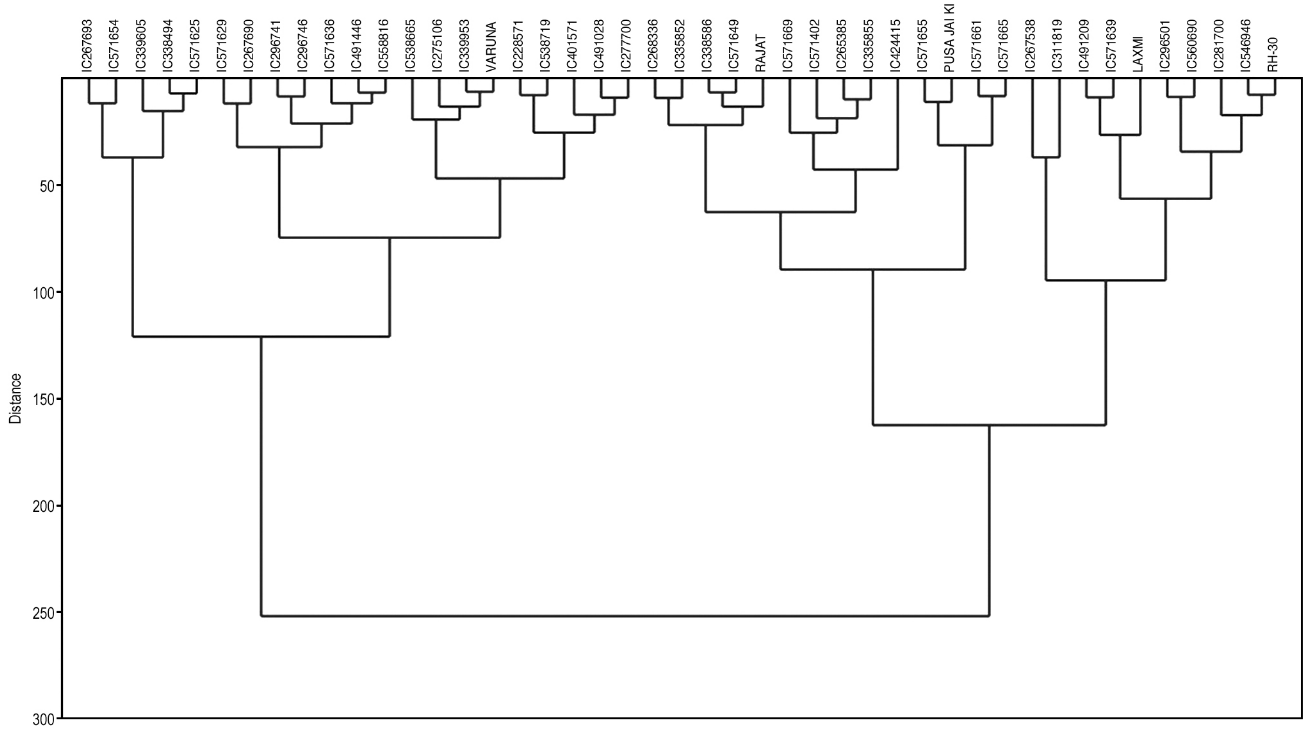

Fig 2 Dendrogram of 45accessions of Indian Mustard.

STNU and total nitrogen uptake, IC424415 for seed uptake efficiency and nitrogen harvest index. We found these as best performing accessions and can be utilized for the genetic improvement of Indian mustard.

We conclude that 45 accessions of *Brassica juncea* which were evaluated showed high variations for all the traits especially for seed yield, stover yield, nitrogen (%) in seed, total nitrogen (%), nitrogen harvest index, NUE, 1000 seed weight and the NBP. Further, correlation and PCA analysis showed that traits like plant height, NBP, number of siliqua in the main branch, nitrogen (%) in seed, total nitrogen (%), SNU and seed yield were among the most important traits which contributed for >50% phenotypic variation in the germplasm accessions. Accessions which are diverse from each other were also enlisted using cluster analysis. The promising accessions were also identified based on the cumulative performance for yield and their related trait for use in breeding India mustard.

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