Assessment of Genetic Diversity among Indian and Exotic Genotypes of *Brassica juncea* using Phenotypic Evaluation

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**ABSTRACT**

**Background:** Rapeseed-mustard is one of the most important oilseed crops in India, however, its genetic diversity is barely known. A better understanding on this topic is essential for the proper utilization of genotypes in crop improvement.

**Methods:** Present study was carried out to determine the genetic diversity among 95 diverse genotypes of *Brassica juncea* (L.) in paired rows of 4 m length with a spacing of 30 x 10-15 cm (row x plant). Data were recorded on 11 different agro-morphological characters.

**Result:** All the 95 genotypes were grouped into five distinct clusters based on Manhattan dissimilarity coefficients. Amongst the five clusters, cluster V and IV had the maximum number of genotypes (35 and 23 genotypes respectively) and cluster II with least number of genotypes (three). The Manhattan dissimilarity coefficients ranged from 0.741 to 8.299. Based on the genetic dissimilarity matrix, the maximum dissimilarity (8.299) was observed between the genotypes, DRMRIJ-15-133 and M 62. Cluster III recorded for medium plant height with medium early maturity and cluster I, had maximum mean values for most of the agro-morphological traits. The present work indicated the presence of high genetic diversity among genotypes, which can be used in future breeding programmes for developing mustard cultivars and germplasm management purposes.

**Key words:** *Brassica juncea*, Genetic diversity, PCoA.

**INTRODUCTION**

Oilseeds *Brassica* also referred to as rapeseed-mustard, are the third most important oilseed crops of the world after soybean and palm. Globally these crops belong to four species viz., *Brassica napus*, *Brassica juncea*, *Brassica rapa* and *Brassica carinata* of tribe *Brassicaceae* within the family *Cruciferae* (*Brassicaceae*). *Brassica juncea* (L.) Czern and Cos., commonly known as ‘Indian mustard’; is a natural amphidiploid (2n = 36). It is naturally autogamous species, yet in this crop frequent out-crossing occurs which varies from 5 to 30% depending upon the environmental conditions and random variation of pollinating insects (Rakow and Woods, 1987). *B. juncea* is one of the important sources of edible oil in India and it contributes a major share in mustard production globally. India is the second largest rapeseed-mustard growing country after China, occupying 20.23% area and contributing 11.70% share to the global production (Avtar et al. 2016). Vinu et al. (2013) reported that *B. juncea* is an important element in the oilseed sector contributing more than 80% to the total rapeseed-mustard production in the country.

In India *per capita* oil consumption has been increased enormously due to the increasing population and improving life standards (Avtar et al., 2016). Hence to cope with the increased oil demand, there is an urgent need to enhance the seed yield as well as oil yield potential of rapeseed and mustard. Assessment of genetic diversity in any gene pool is prerequisite to assists plant breeding programme. Evaluation of genetic divergence to understand breeding materials has significant implications for the improvement of crop plants. Information on genetic diversity in *B. juncea* could help breeders and geneticists to understand the structure of germplasm, predict which combinations would produce the best progenies (Vaishnava et al., 2006; Hu et al., 2007; Ali et al., 2009; Singh et al., 2010) and facilitate to broaden the genetic basis of breeding material for selection (Qi et al., 2008).

The objective of present study was to assess the genetic diversity among Indian and exotic genotypes of *B. juncea* in order to identify the utmost divergent parents, which may be used for hybridization programme and are likely to produce more divergent segregates in segregating generations. The divergent parents are also expected to show more heterosis and may be used as parents for hybrid development.

**MATERIALS AND METHODS**

**Plant materials**

The plant material comprised of 95 diverse genotypes of *B. juncea*, including varieties/purelines developed by four
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different centers of India viz., Directorate of Rapeseed-Mustard Research (DRMR), Bharatpur; CCS Haryana Agricultural University (CCS HAU), Hisar; Indian Agricultural Research Institute (IARI), New Delhi and Punjab Agricultural University (PAU), Ludhiana and 6 genotypes of exotic origin (maintained at ICAR - Indian Institute of Agricultural Research, New Delhi) (Table 1).

**Field Evaluation and data collection**

All 95 genotypes of *B. juncea* were grown in paired rows of 4 m length with a spacing of 30 x 10-15 cm (row x plant) at Research Area of Oilseeds Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar during *rabi*, 2017-18. All the recommended package and practices were followed to raise the healthy crop. Observations were recorded on five random and competitive plants for eleven agronomic traits viz; days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliqua on main shoot, main shoot length (cm), siliqua length (cm), number of seeds per siliqua, seed yield per plant (g), 1000-seed weight (g) and oil content (%). Data on days to maturity was recorded on plot basis. Number of seeds per siliqua was estimated on 10-15 siliquae plucked from main shoot of each of five plants. One thousand seeds were counted from random bulk of each genotype and weighed. Dendrogram based on dissimilarity coefficients was generated on the basis of Manhattan dissimilarity coefficients with the help of DARwin 6.0 programme (Perrier and Jacquemoud-Collet, 2006). To depict the similarity or dissimilarity among groups or individual genotypes Principal Coordinate Analysis (PCoA; Gower, 1966) was done using DARwin 6.0 programme.

**RESULTS AND DISCUSSION**

Genetic distance provides a measure of the degree of relatedness between individuals in a population (Garcia et al., 2004) and it also plays a key role in genetic improvement through breeding methods (Liu et al., 2019). Results indicating genetic diversity showed sufficient dissimilarity characteristics and reflected significant genetic diversity among Indian mustard genotypes. Such significant genetic variation has also been reported by Alle et al. (2009); Singh et al. (2010) on metric traits in *B. juncea*. On the basis of Manhattan dissimilarity coefficients, 95 genotypes of Indian mustard were demarcated into five diverse clusters and discriminated these genotypes on the basis of 11 quantitative characters (Fig 1). Vinu et al. (2013) and Sheikh et al. (2011) also estimated genetic diversity among 44 genotypes of Indian mustard into four clusters using Manhattan methods. Mahmud et al. (2008) and Nath et al. (2003) reported four and five clusters in *Brassica* species, respectively. Mean value of diverse clusters for eleven agronomic traits is presented in Table 2.

The first cluster comprised of 16 genotypes developed/maintained mainly by three centre viz., ICAR-DRMR, Bharatpur (Rajasthan), PAU, Ludhiana (Punjab) and HAU, Hisar (Haryana). The genotypes of this cluster were characterized by tall plants (236.6 cm) higher seed yield per plant (19.87 g), high oil content (39.90%), long main shoots (87.40 cm), more number of siliqua on main shoot (64.6), more number of primary branches per plant (6.27), more number of secondary branches per plant (15.10) and maturity period of 139 days. Main shoot length is considered as the most important fruiting zone in mustard. Hence, its length and number of siliqua on main shoot are desirable traits for increasing seed yield. The genotypes of cluster-I may be used as donor parents for these traits. The second cluster had only 3- genotypes developed/maintained at ICAR-DRMR, Bharatpur and PAU, Ludhiana. These genotypes were poor performer for most of the characters possessing low seed yield, lower test weight and medium plant stature etc. Eighteen genotypes were grouped in cluster III of which three were having exotic origin. Genotypes of this cluster belong mainly to three centers viz., DRMR, Bharatpur, IARI, New Delhi and PAU, Ludhiana (except one from HAU, Hisar). In this cluster genotypes were characterized by medium early maturity (137 days), medium tall plant stature (177.6 cm), medium siliqua length (3.78 cm) along with medium number of seeds per siliqua (13.9), medium to high test weight and medium main shoot length. Low plant height is considered as desirable trait due to ease in carrying out agronomic practices; hence genotypes of cluster-III may be used as donor for this trait. Such results are in concurrence with the results of Singh et al. (2013). The fourth cluster comprised of 23 genotypes from three centers (except two from IARI, New Delhi). The genotypes of this cluster were characterized with oil content (38.90%), moderate to high plant height and seed yield per plant. These genotypes were average performer for most of the characters. Thirty five genotypes were grouped in cluster V which randomly belonged to all four centers. The genotypes of this cluster had high test weight, taller plant stature, high main shoot length and moderate estimates for remaining characters. In earlier study, Gohel and Mehta (2014); Anushree and Pandey (2017); Chandra et al. (2018) reported similar trend of genetic diversity in some oilseed genotypes. None of the cluster/genotypes was found to be most promising collectively for all the quantitative traits. However, some genotypes can be identified as promising for different traits (Table 3). In breeding programmes, these genotypes can play a significant role in achieving specific goals and also be helpful in broadening the genetic base of mustard germplasm.

The Manhattan dissimilarity coefficients ranged from 0.741 to 8.299 indicating the diverse nature of genotypes under study. Based on the genetic dissimilarity matrix, the maximum dissimilarity (8.299) was observed between the genotypes, DRMRIJ-15-133 and M 62. On the other hand, a minimum dissimilarity value of 0.741 was found between genotypes, RC-110 and NPJ-161 which was followed by 1.236, between M 13 and Pusa Jagannath and 1.240, between DRMRIJ-14-30 and Pusa Barani; DRMRIJ-15-251...
Table 1: List of 95 germplasm accessions of *B. juncea* used in present study.

| Sr. No. | Germplasm   | Source Centre* | Sr. No. | Germplasm   | Source Centre | Sr. No. | Germplasm   | Source Centre | Sr. No. | Germplasm   | Source Centre |
|---------|-------------|----------------|---------|-------------|---------------|---------|-------------|---------------|---------|-------------|---------------|
| 1       | DRMRU-14-139 | ICAR-DRMR      | 25      | RC-12       | HAU           | 49      | EC-27-2     | ICAR-IARI     | 73      | M 28        | PAU           |
| 2       | DRMRU-15-109 | ICAR-DRMR      | 26      | RC-273      | HAU           | 50      | EJ-17       | ICAR-IARI     | 74      | M 62        | PAU           |
| 3       | DRMRU-14-272 | ICAR-DRMR      | 27      | RC-112      | HAU           | 51      | NPJ-112     | ICAR-IARI     | 75      | M 78        | PAU           |
| 4       | DRMRU-15-108 | ICAR-DRMR      | 28      | RC-142      | HAU           | 52      | Pusa Vijay  | ICAR-IARI     | 76      | M 22        | PAU           |
| 5       | DRMRU-14-137 | ICAR-DRMR      | 29      | RC-18       | HAU           | 53      | EC 62-1     | ICAR-IARI     | 77      | M 27        | PAU           |
| 6       | DRMRU-14-278 | ICAR-DRMR      | 30      | RC-20       | HAU           | 54      | Pusa Kishan | ICAR-IARI     | 78      | M 74        | PAU           |
| 7       | DRMRU-14-66  | ICAR-DRMR      | 31      | RC-25       | HAU           | 55      | EC 28       | ICAR-IARI     | 79      | M 81        | PAU           |
| 8       | DRMRU-15-143 | ICAR-DRMR      | 32      | RC-46       | HAU           | 56      | Pusa Barani | ICAR-IARI     | 80      | M-23-B line | PAU           |
| 9       | DRMRU-15-85  | ICAR-DRMR      | 33      | RC-106      | HAU           | 57      | EC 27-4     | ICAR-IARI     | 81      | M 13        | PAU           |
| 10      | DRMRU-15-133 | ICAR-DRMR      | 34      | RC-275      | HAU           | 58      | LES-39      | ICAR-IARI     | 82      | M 34        | PAU           |
| 11      | DRMRU-14-23  | ICAR-DRMR      | 35      | RC-53       | HAU           | 59      | MST II 14-2 | ICAR-IARI     | 83      | M 47 B line | PAU           |
| 12      | DRMRU-14-65  | ICAR-DRMR      | 36      | RC-111      | HAU           | 60      | Pusa Agrani | ICAR-IARI     | 84      | M 61        | PAU           |
| 13      | DRMRU-15-123 | ICAR-DRMR      | 37      | RC-8        | HAU           | 61      | SEJ-8       | ICAR-IARI     | 85      | M 16        | PAU           |
| 14      | DRMRU-15-150 | ICAR-DRMR      | 38      | RC-81       | HAU           | 62      | TN-3        | ICAR-IARI     | 86      | M 5         | PAU           |
| 15      | DRMRU-14-261 | ICAR-DRMR      | 39      | RC-110      | HAU           | 63      | LET-17      | ICAR-IARI     | 87      | M 20        | PAU           |
| 16      | DRMRU-14-99  | ICAR-DRMR      | 40      | RC-162      | HAU           | 64      | NPJ-139     | ICAR-IARI     | 88      | M 37        | PAU           |
| 17      | DRMRU-15-148 | ICAR-DRMR      | 41      | RC-175      | HAU           | 65      | Pusa Jagan Nath | ICAR-IARI | 89 | M 82        | PAU           |
| 18      | DRMRU-15-104 | ICAR-DRMR      | 42      | RC-107      | HAU           | 66      | YS-7        | ICAR-IARI     | 90      | M 75        | PAU           |
| 19      | DRMRU-15-03  | ICAR-DRMR      | 43      | RC-15       | HAU           | 67      | Pusa Tarak  | ICAR-IARI     | 91      | M-80        | PAU           |
| 20      | DRMRU-15-52  | ICAR-DRMR      | 44      | RC-38       | HAU           | 68      | LES-1-27    | ICAR-IARI     | 92      | M 49        | PAU           |
| 21      | DRMRU-15-95  | ICAR-DRMR      | 45      | RC-116      | HAU           | 69      | EC 29-2     | ICAR-IARI     | 93      | M 67        | PAU           |
| 22      | DRMRU-14-30  | ICAR-DRMR      | 46      | RC-51       | HAU           | 70      | LES-43      | ICAR-IARI     | 94      | M 65        | PAU           |
| 23      | DRMRU-15-251 | ICAR-DRMR      | 47      | RC-47       | HAU           | 71      | NPJ-161     | ICAR-IARI     | 95      | M 84        | PAU           |
| 24      | RC-14        | HAU            | 48      | EC 61-36-1  | ICAR-IARI     | 72      | M-53 B line | PAU           |

*ICAR-DRMR (Indian Council of Agricultural Research - Directorate of Rapeseed-Mustard Research); HAU (CCS Haryana Agricultural University); ICAR-IARI (Indian Council of Agricultural Research - Indian Agricultural Research Institute); PAU (Punjab Agricultural University).
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Table 2: Mean performance of different clusters based upon eleven agro- morphological traits.

| Clusters | DM  | PH  | PBr | SBr | SqMS | MSL  | SqL  | S/Sq | SY  | TW  | OC  |
|----------|-----|-----|-----|-----|------|------|------|------|-----|-----|-----|
| C-I      | 139 | 236.6 | 6.27 | 15.1 | 64.6 | 87.4 | 3.33 | 12.7 | 19.87 | 3.38 | 39.9 |
| C-II     | 139 | 192.4 | 5.4  | 11.6 | 29.6 | 49.6 | 3.67 | 13   | 10.31 | 3.33 | 38.5 |
| C-III    | 137 | 177.6 | 5.27 | 13.1 | 42   | 77.8 | 3.78 | 13.9 | 14.89 | 4.05 | 38.8 |
| C-IV     | 138 | 216.9 | 6.07 | 14.2 | 46.7 | 69.3 | 3.53 | 12.7 | 17.78 | 3.59 | 38.9 |
| C-V      | 138 | 208.5 | 5.07 | 11.1 | 53.4 | 86.7 | 3.7  | 12.9 | 15.26 | 4.28 | 38.8 |

Note: DM = Days to maturity, PH = Plant height (cm), PBr = Primary branches per plant, SBr = Secondary branches per plant, SqMS = Siliqua on main shoot, MSL = Main shoot length (cm), SqL = Siliqua length (cm), S/Sq = Seeds per siliqua, SY = Seed yield (g), TW = 1000-seed weight (g) and OC = Oil content (%).

Fig 1: Dendrogram based on Manhattan dissimilarity coefficients representing relationship among 95 genotypes of *B. juncea*. 
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Factorial analysis: (Axes 1 / 2)

![Principal Coordinate Analysis (PCoA)](image)

**Table 3:** List of identified diverse genotypes of *B. juncea* based on the basis of various agro-morphological traits.

| Genotype     | Cluster | Traits                                                                 | Centre          |
|--------------|---------|------------------------------------------------------------------------|-----------------|
| RC-273       | IV      | Early maturity, No. of primary branches, No. of secondary branches, Seeds per silique, Seed yield, Oil content. | HAU,Hisar       |
| YS-7         | I       | Early maturity, No. of primary branches, No. of silique on main shoot, Main shoot length, Silique length, Seeds per silique, Seed yield, 1000-seed weight, Oil content. | IARI,Delhi      |
| M 16         | I       | Early maturity, No. of primary branches, No. of secondary branches, No. of silique on main shoot, Main shoot length, Siliqua length, Seed yield, 1000-seed weight, Oil content. | PAU,Ludhiana    |
| Pusa Vijay   | III     | Early maturity, Medium plant height, Main shoot length, Siliqua length, Seeds per silique, Seed yield, 1000-seed weight, Oil content. | IARI,Delhi      |
| M 5          | I       | Early maturity, No. of primary branches, No. of secondary branches, 1000-seed weight, Oil content. | PAU,Ludhiana    |
| DRMRU-14-139 | I       | No. of primary branches, No. of secondary branches, No. of silique on main shoot, Main shoot length, 1000-seed weight, | DRMR,Bharatpur  |
| DRMRU-15-148 | V       | Main shoot length, Siliqua length, Seeds per silique, 1000-seed weight, | DRMR,Bharatpur  |
| DRMRU-15-85  | V       | Early maturity, Main shoots length, Seed yield, 1000-seed weight, Oil content. | DRMR,Bharatpur  |
| RC-53        | I       | No. of primary branches, No. of secondary branches, No. of silique on main shoot, Seed yield, Oil content. | HAU,Hisar       |
| RC-275       | I       | No. of secondary branches, Seed yield, Oil content. | HAU,Hisar       |

and Pusa Barani. The genotype, DRMRU-15-133 was found to be the most diverse as it showed the highest dissimilarity coefficient values (8.299) with all of the genotypes viz. M 62; DRMRIJ-14-23 and M 28 etc. These diverse genotypes can be used effectively in the mustard breeding programme to select some desirable recombinants. Thus the obtained results confirmed that the use of diversity analysis is a good tool to determine the phenotypic differences among the genotypes, which agrees with the results of Crossa and Cornelius (1997); Marijanovic-Jeromela *et al.* (2009). Similar results concerning the genetic diversity for yield and its component traits have also been reported by Singh *et al.* (2013); Vinu *et al.* (2013); Chandra *et al.* (2018).

**Principal Coordinate Analysis (PCoA)**

A two dimensional scattered plot of the genotypes was constructed based on two principal axes to visualize the resemblance or divergence between individual genotypes.
The genotypes were distantly located from each other. The scatter plot revealed that majority of samples placed at the center of a two-dimensional coordinate plane formed five apparent clusters C-I, C-II, C-III, C-IV and C-V (Fig 2). There is a strong tendency for the PCoA to show the same trends with clustering of lines as in the dendrogram. Vinu et al. (2013) also used PCoA to delineate and visualize 44 Indian mustard genotypes into four clusters.

CONCLUSION

The B. juncea genotypes studied, exhibited wide genetic variations from cluster analyses at morphological level. The genotypes of cluster-I may be used as donor parents for main shoots length, number of siliqua on main shoot, number of primary branches per plant, seed yield per plant and oil content. DRMRIJ-15-133 was found to be the most diverse genotype as it showed the highest dissimilarity coefficient values with all of the genotypes. This outcome will form a major criterion for selection of genetic materials with great diversity for breeding programmes, particularly to increase the germplasm base of the mustard improvement programme.

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