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# Evaluation of Genetic Diversity in Indian and Exotic Brassica Juncea Genotypes through Phenotypic

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**ANALYSIS**

**ABSTRACT**

**Background:** Rapeseed-mustard stands as one of India's key oilseed crops, yet its genetic diversity remains largely unexplored. A comprehensive understanding of this aspect is crucial for effectively harnessing genotypes in crop enhancement endeavors.

**Methods:** This study aimed to assess the genetic diversity among 95 diverse genotypes of Brassica juncea (L.) grown in paired rows of 4 m length with a spacing of 30 x 10-15 cm (row × plant). Data were collected on 11 distinct agro-morphological traits.

**Results:** The 95 genotypes were categorized into five distinct clusters based on Manhattan dissimilarity coefficients. Clusters V and IV contained the highest number of genotypes (35 and 23 genotypes, respectively), while cluster II had the fewest (three genotypes). Manhattan dissimilarity coefficients ranged from 0.741 to 8.299. The largest dissimilarity (8.299) was observed between genotypes DRMRIJ-15-133 and M 62. Cluster III exhibited medium plant height with medium early maturity, while cluster I displayed the highest mean values for most agro-morphological traits. This study underscores the significant genetic diversity among genotypes, offering potential utility in future breeding programs aimed at developing mustard cultivars and managing germplasm effectively.

**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 *Brassiceae* within the family *Cruciferae (Brassicaceae)*. *Brassica juncea* (L.) Czern and Coss., 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 poolis prerequisite to assists plant breeding programme. Evaluation of genetic divergence to understand breeding materials has significant implications for the improvementof 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; Alie *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* inorder to identify the utmost divergent parents, which maybe 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 different centers of India *viz.,* Directorate of Rapeseed- Mustard Research (DRMR), Bharatpur; CCS Haryana Agricultural University (CCS HAU), Hisar; Indian AgriculturalResearch Institute (IARI), New Delhi and Punjab AgriculturalUniversity (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 of4 m length with a spacing of 30 × 10-15 cm (row × plant) at Research Area of Oilseeds Section, Department of Geneticsand 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 seedswere 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 PrincipalCoordinate 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 Alie *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 quantitativecharacters (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 consideredas the most important fruiting zone in mustard. Hence, its length and number of siliquae 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 whichthree 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, Gohol 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,

**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 | DRMRIJ-14-139 | ICAR-DRMR | 25 | RC-12 | HAU | 49 | EC-27-2 | ICAR-IARI | 73 | M 28 | PAU |
| 2 | DRMRIJ-15-109 | ICAR-DRMR | 26 | RC-273 | HAU | 50 | EJ-17 | ICAR-IARI | 74 | M 62 | PAU |
| 3 | DRMRIJ-14-272 | ICAR-DRMR | 27 | RC-112 | HAU | 51 | NPJ-112 | ICAR-IARI | 75 | M 78 | PAU |
| 4 | DRMRIJ-15-108 | ICAR-DRMR | 28 | RC-142 | HAU | 52 | Pusa Vijay | ICAR-IARI | 76 | M 22 | PAU |
| 5 | DRMRIJ-14-137 | ICAR-DRMR | 29 | RC-18 | HAU | 53 | EC 62-1 | ICAR-IARI | 77 | M 27 | PAU |
| 6 | DRMRIJ-14-278 | ICAR-DRMR | 30 | RC-20 | HAU | 54 | Pusa Kishan | ICAR-IARI | 78 | M 74 | PAU |
| 7 | DRMRIJ-14-66 | ICAR-DRMR | 31 | RC-25 | HAU | 55 | EC 28 | ICAR-IARI | 79 | M 81 | PAU |
| 8 | DRMRIJ-15-143 | ICAR-DRMR | 32 | RC-46 | HAU | 56 | Pusa Barani | ICAR-IARI | 80 | M-23-B line | PAU |
| 9 | DRMRIJ-15-85 | ICAR-DRMR | 33 | RC-106 | HAU | 57 | EC 27-4 | ICAR-IARI | 81 | M 13 | PAU |
| 10 | DRMRIJ-15-133 | ICAR-DRMR | 34 | RC-275 | HAU | 58 | LES-39 | ICAR-IARI | 82 | M 34 | PAU |
| 11 | DRMRIJ-14-23 | ICAR-DRMR | 35 | RC-53 | HAU | 59 | MST II 14-2 | ICAR-IARI | 83 | M 47 B line | PAU |
| 12 | DRMRIJ-14-65 | ICAR-DRMR | 36 | RC-111 | HAU | 60 | Pusa | ICAR-IARI | 84 | M 61 | PAU |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | Agrani | | | | |
| 13 | DRMRIJ-15-123 | ICAR-DRMR | 37 | RC-8 | HAU | 61 | SEJ-8 | ICAR-IARI | 85 | M 16 | PAU |
| 14 | DRMRIJ-15-150 | ICAR-DRMR | 38 | RC-81 | HAU | 62 | TN-3 | ICAR-IARI | 86 | M 5 | PAU |
| 15 | DRMRIJ-14-261 | ICAR-DRMR | 39 | RC-110 | HAU | 63 | LET-17 | ICAR-IARI | 87 | M 20 | PAU |
| 16 | DRMRIJ-14-99 | ICAR-DRMR | 40 | RC-162 | HAU | 64 | NPJ-139 | ICAR-IARI | 88 | M 37 | PAU |
| 17 | DRMRIJ-15-148 | ICAR-DRMR | 41 | RC-175 | HAU | 65 | Pusa Jagannath | ICAR-IARI | 89 | M 82 | PAU |
| 18 | DRMRIJ-15-104 | ICAR-DRMR | 42 | RC-107 | HAU | 66 | YS-7 | ICAR-IARI | 90 | M 75 | PAU |
| 19 | DRMRIJ-15-03 | ICAR-DRMR | 43 | RC-15 | HAU | 67 | Pusa Tarak | ICAR-IARI | 91 | M-80 | PAU |
| 20 | DRMRIJ-15-52 | ICAR-DRMR | 44 | RC-38 | HAU | 68 | LES-1-27 | ICAR-IARI | 92 | M 49 | PAU |
| 21 | DRMRIJ-15-95 | ICAR-DRMR | 45 | RC-116 | HAU | 69 | EC-29-2 | ICAR-IARI | 93 | M 67 | PAU |
| 22 | DRMRIJ-14-30 | ICAR-DRMR | 46 | RC-51 | HAU | 70 | LES-43 | ICAR-IARI | 94 | M 65 | PAU |
| 23 | DRMRIJ-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).

**Fig 1:** Dendrogram based on Manhattan dissimilarity coefficients representing relationship among 95 genotypes of *B. juncea*.

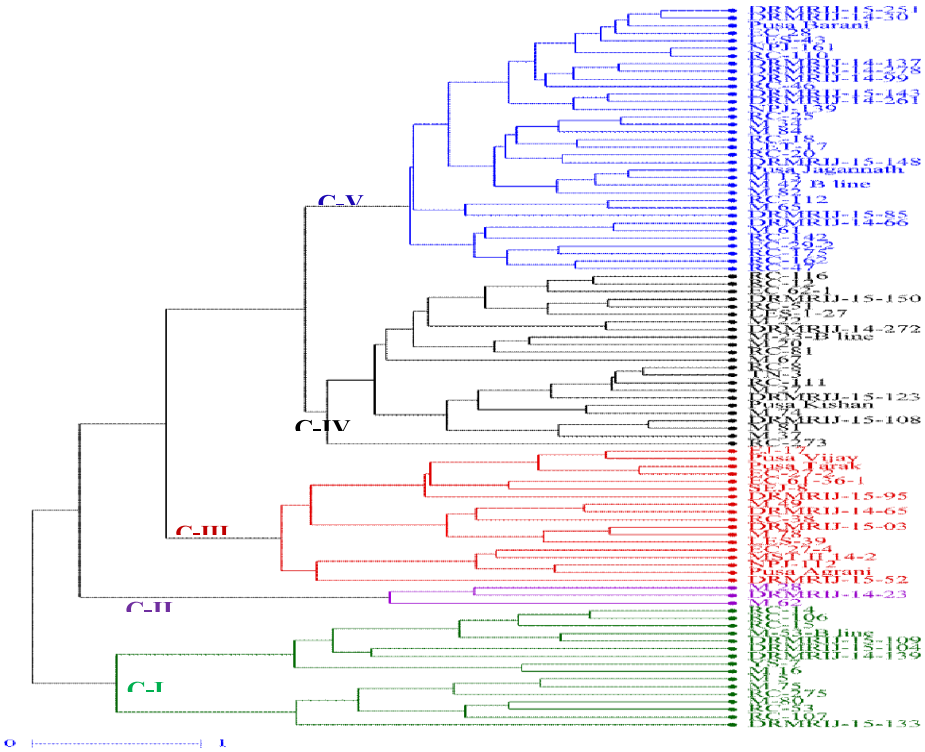


**Table 2:** Mean performance of different clusters based upon eleven agro- morphological traits.

| 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 (%).

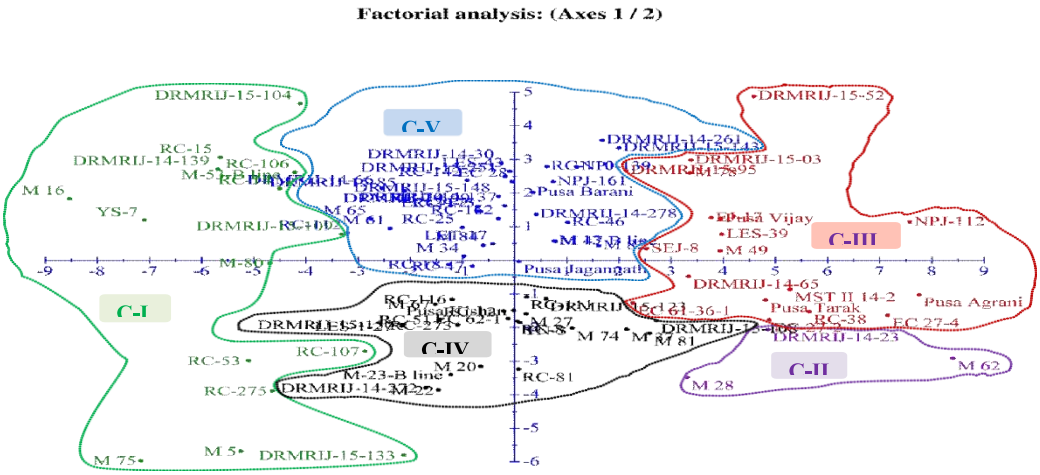


**Fig 2:** Scatter diagram of 95 genotypes of *B. juncea* based on principal coordinates analysis superimposed with clustering.

**Table 3:** List of identified diverse genotypes of *B. juncea* 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 siliqua, Seed yield, Oil content. | HAU, Hisar |
| YS-7 | I | Early maturity, No. of primary branches, No. of siliqua on main shoot, Main shoot length, Siliqua length, Seeds per siliqua, Seed yield, 1000-seed weight, Oil content. | IARI, Delhi |
| M 16 | I | Early maturity, No. of primary branches, No. of secondary branches, No. of siliqua 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 siliqua, Seed yield, 1000-seed weight. | IARI, Delhi |
| M 5 | I | Early maturity, No. of primary branches, No. of secondary branches, 1000-seed weight, Oil content. | PAU, Ludhiana |
| DRMRIJ-14-139 | I | No. of primary branches, No. of secondary branches, No. of siliqua on main shoot, Main shoot length, 1000-seed weight. | DRMR, Bharatpur |
| DRMRIJ-15-148 | V | Main shoot length, Siliqua length, Seeds per siliqua, 1000-seed weight. | DRMR, Bharatpur |
| DRMRIJ-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 siliqua on main shoot, Seed yield, Oil content. | HAU, Hisar |
| RC-275 | I | No. of secondary branches, Seed yield, Oil content. | HAU, Hisar |

between DRMRIJ-14-30 and Pusa Barani; DRMRIJ-15-251 and Pusa Barani. The genotype, DRMRIJ-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 canbe 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 goodtool to determine the phenotypic differences among the genotypes, which agrees with the results of Crossa and Cornelius (1997); Marijanovic-Jeromela *et al.* (2009). Similarresults 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). Thereis 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, numberof 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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