



*40(20): 34-57, 2021; Article no.CJAST.72869 ISSN: 2457-1024 (Past name: British Journal of Applied Science & Technology, Past ISSN: 2231-0843, NLM ID: 101664541)*

# **Genetic Components and Diversity Analysis in Indian Mustard [***Brassica juncea* **(Linn.) Czern & Coss] Based on Different Morpho-physiological Traits**

**Chitralekha Shyam<sup>1</sup> , M. K. Tripathi1\*, Sushma Tiwari1 and Niraj Tripathi2**

*1 Department of Genetics & Plant Breeding, College of Agriculture, RVS Agricultural University, Gwalior, 474002 M.P., India. <sup>2</sup> Directorate of Research Services, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur 482004, India.*

#### *Authors' contributions*

*This work was carried out in collaboration among all authors. Conceptualization of research and*  designing of the experiments done by authors CS, MKT and ST. Contribution of experimental *materials done by author CS. Author CS did the execution of field experiments and data collection. Authors CS, MKT and NT did the analysis of data and interpretation. Authors NT and MKT prepared the manuscript. All authors read and approved the final manuscript.*

#### *Article Information*

DOI: 10.9734/CJAST/2021/v40i2031462 *Editor(s):* (1) Dr. Bishun Deo Prasad, Bihar Agricultural University, India. *Reviewers:* (1) Shreenivas A. Desai, University of Agricultural Sciences, India. (2) Majid Abdulhameed Ibrahim, University of Basrah, Iraq. Complete Peer review History: https://www.sdiarticle4.com/review-history/72869

*Original Research Article*

*Received 22 June 2021 Accepted 27 August 2021 Published 30 August 2021*

## **ABSTRACT**

**Aim:** Indian mustard [*Brassica juncea* (Linn.)] is the third vital oilseed crop in the world which contributes 28.6% in the production of oilseeds. Genetic diversity assessment plays a fundamental role in the preservation and improvement of the targeted plant species.

**Study Design:** In the present investigation, 196 Indian mustard genotypes including checks were grown in the field and evaluated based on different morpho-physiological traits.

**Place and Duration of the Study:** All the genotypes were grown in randomized block design with two replications in Rabi 2016-17 and 2017-18 at the experimental field of Department of Genetics & Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, M.P., India.

\_

*<sup>\*</sup>Corresponding author: E-mail: drmanojtripathi64@gmail.com;*

**Methodology:** The study was conducted to record different morphological and physiological traits that play a major role in differentiating the targeted genotypes.

**Results:** Based on the present study, the highest genotypic and phenotypic coefficients of disparity were documented for seed yield per plant tracked by harvest index and numbers of silique per plant. Maximum heritability and genetic advance were documented for seed yield per plot tracked by harvest index, biological yield per plot, days to 50% flowering, length of the main raceme, numbers of silique per plant, seed yield per plant, numbers of seeds per silique, 1000-seed weight and numbers of silique per the main raceme.

**Conclusions:** In principal component analysis, 15 principal components were evidenced while cluster analysis gave 16 clusters. The highest inter-cluster distance was evidenced between cluster 9 and cluster 16 which suggests that the hybridization scheme considering parents from these clusters is supposed to be given a higher occurrence of better-wanted combination(s) for expansion of beneficial genetic stocks.

*Keywords: Indian mustard; genetic variability; correlation; quantitative traits; principle component analysis.*

## **1. INTRODUCTION**

Indian mustard [*Brassica juncea* (Linn.)] is the most crucial oilseed crop of India and it engages significantly gigantic acreage amongst the Brassica group of oilseed crops. It is being cultivated in Rajasthan, Haryana, Punjab, Madhya Pradesh, Uttar Pradesh, West Bengal, Gujarat, Bihar, Jharkhand, Assam, Jammu Kashmir, Uttaranchal, Chhattisgarh, Orissa and Maharashtra states of India. It is mostly a selfpollinating crop, however, about 30% crosspollination does happen underneath normal field circumstances, contingent upon wind and bee actions [1]. It is used as an oil, condiment, medicine, soap, lubricant, etc [2-6]. For these reasons, it is necessitating quantitative and qualitative improvement [7,8].

The success of any crop improvement program is usually depending upon a selection which is further determined by the availability and occurrence of genetic capriciousness in the population of a fastidious crop species [9,10]. Selection depends on heritability, selection intensity, and the genetic advance of traits [2]. Heritability measures the notch of semblance between the phenotypic and breeding worth. Genetic advance is the enhancement in the mean of selection personal over the base populace. So that, it helps the researchers to pertain to suitable breeding methods in the crop improvement program. The different quantitative and qualitative characters vary in their relationship with yield [7,3,4,11]. Most of the quantitative characters are controlled by polygenes and they show a continuous variation and are influenced by the environment. Correlation delivers a better thought of the connotation of diverse traits associated with

yield. The parameters which have extremely heritable and positively correlated with yield could be employed in the indirect selection for yield. When the characters are associated indirectly, path coefficient analysis proved obliging to treasure out direct and indirect causes of association among the unlike variables. Therefore, the information of direct and indirect effects of diverse parameters on yield is significant in selection. Considering the above facts, the current study was commenced by involving some germplasm lines and varieties of Indian mustard for genetic components and Euclidean distance cluster analysis for yield and its attributing traits along with discovering the presence of considerable variability among different genotypes accompanied by the analysis of different breeding parameters for yield and its attributing parameters for further utilization in breeding programs.

#### **2. MATERIALS AND METHODS**

A total of 196 Indian mustard genotypes were employed in the present investigation. Experimental materials were obtained from the Zonal Agricultural Research Station, Morena, RVSKVV, Gwalior M.P. (AICRP on Rapeseed and Mustard) and IARI, New Delhi. These were placid from diverse portions of India and the world. All the genotypes were grown in randomized block design with two replications in Rabi 2016-17 and 2017-18 at the experimental field of Department of Genetics & Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, M.P., India. Each genotype was cultivated in a plot of one row of 2-meter length with an arrangement of 30 cm apart between rows and 15 cm plant to plant. The crop was fascinated with protective irrigations and recommended packages of practices right through the growing season. Five arbitrarily chosen plants from each treatment were marked for taking the observations for the parameters, viz. plant height (cm), numbers of primary and secondary branches per plant, days to 50 percent flowering, days to maturity, length of the main raceme (cm), numbers of silique per the main raceme, numbers of silique per plant, silique length (cm), numbers of seeds per silique, seed yield per plant (g) and per plot (g), 1000 seed weight (g), biological yield and harvest index (%) for analysis of mean performance.

Genotypic (GCV and phenotypic coefficient of variation (PCV) was calculated as per formula prearranged by Burton [12]; heritability in the broad sense (h2) as suggested by Burton and De [13] and genetic advance as per the method described by Johnson et al. [14]. The correlation coefficients were calculated to know the degree of association of a character with yield and also among the yield attributing components. Genotypic and phenotypic correlations were calculated by means of the formula furnished by Weber and Moorthy [15] and Miller [16]. The share of direct and indirect contributions of diverse traits to the total correlation coefficients with yield was assessed through path coefficient analysis as recommended by Wright [17,18] and particularized by Dewey and Lu [19]. Principal component analysis was done on PAST v3.14 software based on correlation matrix (normalized variance-covariance) because the variables are unrushed in dissimilar units; this suggests normalizing all variables employing division by their standard deviations.

#### **3. RESULTS AND DISCUSSION**

In plant breeding, assessment of genetic diversity is a fundamental task since hybrids between lines of assorted sources usually; parade greater heterosis than those between closely related parents. The preference of genetically divergent parents for hybridization is a principal chin of any crop improvement scheme for receiving desired segregates. Analysis of variance was found considerable for most of the characters that suggested the presence of a substantial sum of variability in investigated materials for further improvement of diverse characters (Table 1). Pooled variances for two years discovered that genotypes were extremely and significantly differing for all the investigated characters. Plant height ranged between 224 cm (PM-25) to 343.95 cm (MRNJ-127) with a mean

value of 296.90 cm. The number of primary branches per plant was lowest at 7.8 for MRNJ-73 to13.0 for genotype Karishma, with a mean number of 10.55. Maximum numbers of secondary branches (20.65) per plant were produced by genotype IDM-42 while minimum value (11.45) was recorded for genotype RB-50. Days to 50% flowering was found to be lowest 53.70 for MRNJ-102 while it was highest (105.53) for IDM10, with a mean performance of 72.42 days. Genotype JD-6 entailed fewer days to mature (222.75), whereas, the maximum days to maturity was evidenced for genotype MRNJ-56 (295.7days). The length of the main raceme was evidenced between 86.5cm to 185.4cm. Genotype MRNJ-138 had the highest length of the main raceme intimately followed by a group of three genotypes including MRNJ-90, MRNJ-125 and IDM-12 with at par performance while the lowest value was displayed by genotype MRNJ-138. The numbers of silique/main raceme were ranged from 58.23 (MRNJ-134) to 125.03 (MRNJ-35), with mean of 89.98. Silique per plant ranged between 215.15 (MRNJ-44) to 586.8 (MRNJ-73), with a mean value of 366.31. Length of silique was found to be highest at 12.77 for genotypes MRNJ-48 while it was lowest at 6.92 for MRNJ-135. Maximum seeds per silique (40.07) were witnessed for genotype MRNJ-15 while; the lowest value (17.75) was noted for genotype MRNJ-131. Seed yield per plant was arrayed between 11.17g to 40.54g, with a mean of 21.95g. Genotype MRNJ-118 produced maximum seed per plant, however, the lowest value was recorded for genotype MRNJ-11. The comparable outcomes were also addressed by Shekhawat et al. [20], Akabari et al. [21], Salam et al. [22], Sikarwar et al. [23] Bafra et al. [2] and Dawar et al. [24]. Genotype L-6 showed the highest 1000-seed weight (16.14g) whereas; the lowest value (7.05g) was recorded for genotype MRNJ-6. Genotype MRNJ-60 had a maximum harvest Index (65.61%), while a minimum value (16.77%) was recorded for genotype MRNJ-26. According to the findings of different studies, Brassica genotypes may possess variability due to their sowing time and genetic makeup. These factors may affect the plant height, the number of branches, silique, seed yield, seed weight and crude oil content also. The reasons behind the differences may be temperature, humidity and precipitation also [25- 27]. The findings of the present investigation suggest that each parameter selected for the analysis has proven its suitability to analyze genetic variability present among Indian mustard genotypes.



# **Table 1. Mean performance for yield and its attributes**









## *Shyam et al.; CJAST, 40(20): 34-57, 2021; Article no.CJAST.72869*



The coefficient of variation was premeditated at both genotypic and phenotypic levels (Table 2). The maximum genotypic coefficient of variation was noted for seed yield per plant trailed by harvest index and numbers of silique per plant. Current findings are in accordance with the results of preceding workers including Akbar et al. [28] for high seed yield per plant and low for plant height; Dawar et al. [24] high for seed yield per plant. The highest magnitude of the phenotypic coefficient of variation was recorded for seed yield per plant tracked by harvest index and number(s) of silique per plant. Plant height and days to maturity exhibited very low PCV values. These outcomes are in confirmation with the consequences of Gangapur et al. [29] who stated low PCV for days to maturity and plant height. Tripathi et al. [30] reported maximum PCV for seed yield per plant (g), moderate values for number(s) of primary branches, length of the main raceme, number(s) of siliqua per the main raceme, number(s) of seeds per siliqua, 1000-seed weight and low for days to maturity. Synerm et al. [31] also observed moderate PCV for the number(s) of seeds per siliqua and low for plant height and days to maturity. Moderate for days to 50% flowering and number(s) of primary branches by Amsalu et al. [32] while highest for seed yield per plant, moderate for length of main raceme and low for days to maturity by Singh et al. [33] also reported.

Heritability and genetic advance are cooperative in selecting superior individuals. Higher heritability (Table 2) has been evidenced for

seed yield per plot, harvest index, biological yield per plot, days to 50% flowering, length of the main raceme, numbers of silique per plant, seed yield per plant, plant height, numbers of seeds per silique, 1000-seed weight and numbers of silique per the main raceme. However, silique length, numbers of primary and secondary branches exhibited low estimates of heritability. Earlier, Lodhi et al. [34] have testified moderate heritability for days to maturity; Akabari et al. [21] for number (s) of siliqua per plant and seed yield per plant; Salam et al. [22] for number(s) of seeds per siliqua and seed yield per plant; Sikarwar et al. [23] for 1000- seed weight; Dawar et al. [24] for number(s) of siliqua per plant and number (s) of seeds per siliqua and Singh et al. [33] for days to 50 % flowering and number(s) of silique per the main raceme.

The estimation of genetic advance (Table 2) was found to be highest for seed yield per plant, harvest index, numbers of silique per plant, seed yield per plot, 1000-seed weight, length of the main raceme, days to 50% flowering, biological yield per plot and numbers of silique per the main raceme. It was low for plant height, silique length, days to maturity, the numbers of primary and secondary branches. Comparable pronouncements were also reported low GA for days to maturity by Bind et al. [35]; for days to maturity and plant height by Lodhi et al. [34] and for days to maturity by Akabari et al. [21]. Moderate were observed for the number(s) of seeds per siliqua by Bibi et al. [36].

S. No.	<b>Characters</b>	GCV(%)	<b>PCV</b> (%)	h <sup>2</sup>	GA	GA (%)
	Plant height (cm)	4.47	4.99	80.26	12.27	8.26
2	Numbers of primary branches	1.58	11.41	1.92	0.02	0.45
3	Numbers of secondary branches	3.59	17.49	4.21	0.11	1.52
4	Days to 50% flowering	12.72	13.12	94.05	9.20	25.42
5	Days to maturity	2.81	3.714	57.59	5.93	4.40
6	Length of main raceme (cm)	13.63	14.08	93.74	17.85	27.19
7	Numbers of silique per main raceme	14.36	18.22	62.08	10.49	23.31
8	Numbers of silique per plant	21.61	22.45	92.60	78.46	42.84
9	Silique length (cm)	7.32	15.32	22.81	0.34	7.20
10	Numbers of seeds per silique	10.89	12.89	71.38	2.51	18.96
11	Seed yield per plant (g)	26.72	28.03	90.93	5.76	52.50
12	Seed yield per plot (g)	18.95	19.04	99.07	66.68	38.87
13	1000- seed weight $(q)$	16.67	19.91	70.05	1.53	28.74
14	Biological yield per plot (g)	12.61	12.92	95.28	315.16	25.36
15	Harvest index (%)	22.52	22.84	97.20	6.47	45.75

**Table 2. Pooled estimates of GCV, PCV, heritability and genetic advance for 15 quantitative characters over 2 years**

Correlation investigations stretch a clear depiction of traits alliance which is common as a result of linkage, pleiotropy, physiological relationship in developmental pathway. The quantifiable dimension of a specific trait clarifies diverse variability characters. Days to 50% flowering exhibited a significant positive correlation with days to maturity (Table 3), plant height and 1000-seed weight. Parallel results were documented by Rathod et al. [37] for days to 50 % flowering as they reported a significant positive correlation with days to maturity and plant height, days to maturity with numbers of primary branches, plant height with a number(s) of secondary branches. Amsalu et al. [32] documented significant positive correlation for days to 50 % flowering with days to maturity. Devi et al. [38] authenticated significant positive correlation for days to 50 % flowering with days to maturity and for plant height with number (s) of secondary branches while Raliya et al. [39] for days to 50 % flowering with days to maturity and 1000- seed weight. The numbers of primary branches proved highly significantly positively correlated with numbers of silique per the main raceme, numbers of secondary branches, seed yield per plot, harvest index and silique length. The numbers of secondary branches had a significant positive correlation with numbers of silique per plant, seed yield per plant and numbers of seeds per silique. The numbers of silique per the main raceme exhibited a significant positive correlation with silique length. The numbers of silique per plant showed a significant positive correlation with seed yield per plant. The numbers of seeds per silique showed positive and negative correlations. However, all were found non-significant.

Days to 50% flowering had a significant positive correlation with days to maturity and plant height (Table 4). Plant height, had a significant positive correlation with 1000- seed weight, whereas, significant negative correlation was documented with numbers of silique per the main raceme. The numbers (s) of primary and secondary branches had a significant positive correlation with the numbers of silique per the main raceme. Number (s) of silique per main raceme had significant a positive correlation with seed yield per plot (0.167), biological yield per plot and silique length. The number(s) of silique per plant exhibited a significant positive correlation with seed yield per plant and silique length had a significant positive correlation with the numbers of seeds per silique. Seed yield per plot demonstrated significant positive correlation with harvest index. Present results are in agreement with the findings of Doddabhimappa et al. [40] where they found a significant positive correlation between plant height with 1000-seed weight. For days to 50 % flowering a significant positive correlation with days to maturity and for plant height, a significant positive correlation with 1000-seed weight was reported by Gupta et al. [41]. Whereas, Kumar et al. [42] documented a significant negative correlation for days to 50% flowering with a length of the main raceme, number(s) of seeds per siliqua and 1000-seed weight and for days to maturity with a length of the main raceme, number(s) of siliqua per plant and seed yield per plant (g) while in the study of Raliya et al. [39] number(s) of siliqua per plant showed a significant positive correlation with seed yield per plant (g).

Genotypic path coefficient analysis revealed an extreme positive direct effect of numbers of silique per plant on seed yield per plant tracked by harvest index, plant height, days to 50% flowering, number(s) of seeds per silique, biological yield per plot and number(s) of silique per main raceme (Table 5). Days to maturity showed maximum positive indirect effect via the number(s) of secondary branches followed by days to 50% flowering. Numbers of primary branches exhibited a positive indirect effect on seed yield per plant through 1000 -seed weight, harvest index, length of the main raceme and numbers of silique per the main raceme. Number (s) of secondary branches demonstrated maximum positive indirect effect via 1000-seed weight, while negative indirect effect via the number(s) of primary branches. Number(s) of silique per the main raceme showed a positive indirect effect through the number(s) of secondary branches, whereas negative indirect effect through the number(s) of primary branches. Number(s) of silique per plant exhibited a positive indirect effect via the number (s) of primary branches. Silique length showed a positive indirect effect through the number (s) of secondary branches, number(s) of seeds per silique, days to maturity, harvest index, number(s) of silique per the main raceme, length of the main raceme and biological yield per plot. Similar findings were also documented for the numbers of siliqua per plant and per the main raceme and the numbers of seeds per siliqua as they exerted a positive direct effect on seed yield per plant. Afrin et al. [43] reported that plant height and the numbers of siliqua per plant had a positive direct effect on seed yield per plant. Yadav et al. [44] found that seed yield per plant had a positive direct effect on the numbers of siliqua per plant. Dawar et al. [24] reported a positive direct effect on the numbers of siliqua per plant, plant height, numbers of seeds per siliqua on seed yield per plant and a negative direct effect on siliqua length and Gupta et al. [41] documented that harvest index, numbers of seeds per siliqua, plant height had a positive direct effect on seed yield per plant and length of the main raceme and 1000-seed weight had a negative direct effect with seed yield per plant.

Phenotypic path coefficient examination (Table 6) interpreted that the highest positive direct effect of seed yield per plant was positively and directly depended up on number(s) of silique per plant, days to 50% flowering, harvest index, plant height, biological yield per plot, number(s) of secondary branches, length of main raceme, number(s) of silique per main raceme and number(s) of seeds per silique. Similarly, Yadav et al. [44] reported that numbers of siliqua per plant directly affected seed yield per plant. In a different investigation, Dawar et al. [24] demonstrated that seed yield per plant was positively and directly affected by numbers of siliqua per plant, plant height and numbers of seeds per siliqua. Days to maturity showed maximum positive indirect effect via days to 50% flowering, harvest index, 1000-seed weight, number(s) of silique per main raceme, silique length and number(s) of seeds per silique. Numbers of secondary branches exhibited maximum positive indirect effect through numbers of silique per plant, 1000-seed weight, numbers of primary branches, biological yield per plot and numbers of seeds per silique. Number(s) of silique per plant exhibited maximum positive indirect effect through days to maturity, number(s) of secondary branches, harvest index, number(s) of primary branches, length of main raceme, seed yield per plot and silique length. In the same way, Kardam et al. [45] reported that numbers of siliqua per plant, numbers of seeds per siliqua and numbers of silqua per main raceme had positive direct effect on seed yield per plant. Gupta et al. [41] documented that seed yield per plant had positively and directly affected by harvest index, numbers of secondary branches per plant, and numbers of seeds per siliqua.

Fifteen principal components of the data over pooled years (Table 7, Fig. 1) were analyzed and found that the first principle component contributed 13.55% variation for plant height, numbers of primary branches, days to 50% flowering, days to maturity, numbers of silique

per the main raceme, silique length, 1000-seed weight, seed yield per plot and harvest index. The second principle component contributed a total of 12.56% having plant height, numbers of secondary branches, days to 50% flowering, days to maturity, numbers of silique per plant, 100-seed weight and seed yield per plant. The principal component three accounted for 12.19 % of divergence and among those values recorded for numbers of secondary branches, length of the main raceme, numbers of silique per plant, numbers of seeds per silique, seed yield per plant and per plot and harvest index. The total contribution of the 4th component was 9.48 % while the component 5th explained 7.98 % of the total variation. The sixth component estimated 7.71 % variance and the 7th principal component accounted for 6.77 % of diversity. The eighth component possessed 6.07 % variance by plant height, number(s) of primary and secondary branches, length of main raceme while the 9th principal component accounted for 5.67 % of divergence. The total contribution of the 10th principal component was 4.65 %, created by plant height, number(s) of primary branches, number (s) of silique per plant and principal component 11th showed 4.59% variance. The 12th component contributed 3.76 %, 13th principal component 3.03%, 14th contributed 1.82 % and 15th component showed 0.11 % variance.

The multivariate analysis based on Euclidean distance cluster analysis (Fig. 2) was used for divergence analysis. Based on these values, 16 clusters were formed (Table 8). Outcomes of cluster examination exposed that the cluster 5 was the major which contain 40 genotypes tracked by cluster -1 (37 genotypes), cluster-7 (34 genotypes), cluster-3 (31 genotypes), cluster-6 (18 genotypes), cluster-4 (17 genotypes), cluster-2 and cluster- 10 (each having 4 genotypes), cluster-16 (3 genotypes), cluster- 15 (2 genotypes) and cluster 8, 9, 11, 12, 13 and 14 (one genotype each). The supreme inter-cluster distance was evidenced between cluster-9 and cluster-16 (998.7) followed by cluster-9 and cluster-15 (856.4), cluster-10 and cluster-16 (795.4), cluster-4 and cluster-9 (792.7), cluster-13 and cluster-16 (720.9), cluster-1 and cluster-9 (715.5), cluster-14 and cluster-16 (669.5), cluster-2 and cluster-9 (656.9), cluster-10 and cluster-15 (653.3) and cluster-12 and cluster-16 (635.1). The minimum inter-cluster distance (82.4) was documented between clusters-1 and 4. However, the intra-cluster distance was noted as zero.



# **Table 3. Genotypic correlation coefficient for 15 quantitative traits over pooled years**

Seed yield per plant (g)	0.027 <sup>ns</sup>	$-0.161$	0.094 <sup>NS</sup>	0.686	0.497	$0.048^{\text{NS}}$	$-0.106$	0.436	$-0.152$	-0.031 $^{\sf NS}$	$0.001^{\rm NS}$	-0.028 $^{\sf NS}$	$0.038$ <sup>N'</sup>		
Harvest index (% )	$0.049^{N5}$	$0.030^{\sf{Ns}}$	$-0.020$ <sup>NS</sup>	0.404	$-0.047^{N5}$	$-0.029$ <sup>NN</sup>	0.078 <sup>ns</sup>	$0.057^{N5}$	$0.056^{Nc}$	$0.030^{\rm NS}$	0.083 <sup>nt</sup>	$-0.562$	0.787	0.057	

**Table 4. Phenotypic correlation coefficient for 15 quantitative traits over pooled years**





**Table 5. Genotypic path-coefficient direct and indirect effects of various quantitative characters on seed yield per plant over pooled years**



*Shyam et al.; CJAST, 40(20): 34-57, 2021; Article no.CJAST.72869*

Numbers of silique per plant	$-0.009$	0.022	$-0.020$	0.023	$-0.236$	$-0.005$	$-0.008$	0.719	0.012	$-0.01$	$-0.063$	$-0.005$	0.0003	0.015	$0.436^{\degree}$
Silique length (cm)	$-0.0320$	0.020	$-0.0319$	$-0.108$	0.368	0.007	0.012	$-0.034$	$-0.265$	0.024	$-0.127$	0.003	$-0.003$	0.015	$-0.152$
Numbers of seeds per silique	$-0.028$	0.002	$-0.027$	0.061	$-0.062$	$-0.01$	$-0.007$	$-0.073$	$-0.058$	0.110	0.056	$-0.001$	$-0.002$	0.008	$-0.031^{NS}$
1000- seed weight (g)	0.036	0.001	0.072	0.163	0.381	0.005	$-0.009$	0.068	$-0.050$	$-0.009$	$-0.674$	$-0.015$	0.008	0.023	$-0.001^{NS}$
<b>Biological</b> yield per plot (g)	$-0.019$	0.003	$-0.022$	0.018	$-0.003$	$-0.021$	0.006	$-0.061$	$-0.015$	$-0.002$	0.188	0.053	$-0.002$	$-0.152$	$-0.028^{NS}$
Seed yield per plot (g)	0.000	$-0.011$	$-0.023$	$-0.153$	0.005	$-0.008$	0.009	$-0.003$	$-0.011$	0.003	0.080	0.002	$-0.065$	0.213	0.038 <sup>NS</sup>
Harvest index $(\%)$	0.008	$-0.004$	$-0.004$	$-0.138$	0.021	0.007	0.004	0.041	$-0.015$	0.003	$-0.056$	$-0.030$	$-0.051$	0.270	$0.057^{NS}$

*Residual effect = 0.599*

**Table 6. Phenotypic path-coefficient direct and indirect effects of various characters on seed yield per plant over pooled years**





*Residual = 0.79*

# **Table 7. Principal components for morpho-physiological traits over pooled years**



*Shyam et al.; CJAST, 40(20): 34-57, 2021; Article no.CJAST CJAST.72869*





Principal Component 1

**Fig. 1. Scatter plot for the genetic relationship among 196 Indian mustard as revealed by first second principal components**

*Shyam et al.; CJAST, 40(20): 34-57, 2021; Article no.CJAST.72869*



**Fig. 2. Dendogram of pooled Morpho-physiological traits using XLSTAT software**

<b>Cluster</b> number	<b>Numbers</b> of	Name of genotypes
	genotypes	
$\mathbf{1}$	37	MRNJ-1, MRNJ-6, MRNJ-10, MRNJ-18, MRNJ-33, MRNJ-39, MRNJ-44, MRNJ- 49, MRNJ-53, MRNJ-54, MRNJ-72, MRNJ-76, MRNJ-77, MRNJ-79, MRNJ-85, MRNJ-90, MRNJ-92, MRNJ-98, MRNJ-101, MRNJ-105, MRNJ-120, MRNJ-123, MRNJ-125, MRNJ-129, MRNJ-135, MRNJ-138, IDM-8, IDM-25, IDM-42, Rohini, DRMRIJ-31, Kranti, PM-25, MC-25, ISC-12, PM-22 and Karishma
2	4	MRNJ-2, MRNJ-7, MRNJ-25 and MRNJ-40
3	31	MRNJ-3, MRNJ-9, MRNJ-14, MRNJ-17, MRNJ-20, MRNJ-29, MRNJ-31, MRNJ- 30, MRNJ-35, MRNJ-37, MRNJ-38, MRNJ-41, MRNJ-47, MRNJ-58, MRNJ-64, MRNJ-66, MRNJ-80, MRNJ-94, MRNJ-103, MRNJ-106, MRNJ-107, MRNJ-108, MRNJ-110, MRNJ-113, MRNJ-119, MRNJ-140, MRNJ-142, IDM-53, JM-2, ISC-3 and ISC-17
$\overline{4}$	17	MRNJ-4, MRNJ-131, MRNJ-143, MRNJ-141, IDM-12, MRNJ-144, IDM-10, IDM- 31, IDM-41, IDM-58, IDM-64, Maya, JM-1, L-4, ISC-18, PM-24 and PM-29
5	40	MRNJ-5, MRNJ-13, MRNJ-15, MRNJ-19, MRNJ-22, MRNJ-23, MRNJ-24, MRNJ- 27, MRNJ-42, MRNJ-48, MRNJ-45, MRNJ-56, MRNJ-57, MRNJ-62, MRNJ-67, MRNJ-68, MRNJ-70, MRNJ-71, MRNJ-74, MRNJ-82, MRNJ-83, MRNJ-84, MRNJ-89, MRNJ-95, MRNJ-99, MRNJ-100, MRNJ-111, MRNJ-112, MRNJ-117, MRNJ-118, MRNJ-130, MRNJ-133, MRNJ-136, MRNJ-145, IDM-69, CS-54, PM- 26, DRMR-150-35, RB-50 and RH-74.9
6	18	MRNJ-8, MRNJ-28, MRNJ-46, MRNJ-51, MRNJ-55, MRNJ-61, MRNJ-65, MRNJ- 78, MRNJ-91, MRNJ-93, MRNJ-96, MRNJ-97, MRNJ-115, MRNJ-126, MRNJ- 127, MRNJ-132, IDM-67 and PM-28
7	34	MRNJ-11, MRNJ-12, MRNJ-21, MRNJ-43, MRNJ-50, MRNJ-52, MRNJ-59, MRNJ-81, MRNJ-86, MRNJ-88, MRNJ-102, MRNJ-104, MRNJ-109, MRNJ-114, MRNJ-116, MRNJ-121, MRNJ-122, MRNJ-124, MRNJ-128, MRNJ-134, MRNJ- 137, MRNJ-139, IDM-11, IDM-15, IDM-16, IDM-66, RVM-1, RVM-2, JM-3, NRCDR-2, NRCHB-101, L-6, PM-21 and PM-30
8	1	MRNJ-16
$\overline{9}$	1	MRNJ-26
10	4	MRNJ-34, MRNJ-69, MRNJ-75 and MRNJ-87
11	1	MRNJ-36
$\overline{12}$	1	MRNJ-60
13	1	MRNJ-63
14	1	MRNJ-73
15	$\overline{c}$	IDM-2 and ISC-20
16	3	GM-2. JD-6 and ISC-23

**Table 8. Grouping of 196 Indian mustard genotypes in various clusters**

The cluster means from various characters (Table 9) disclosed that cluster-8 had the highest mean value for days to maturity (143.88), number(s) of primary branches (5.85) and number(s) of seeds per silique (17.80). Similarly; genotypes included in cluster-9 recorded the highest mean value for silique length (5.65) and biological yield per plot (1819.55). The cluster-11 revealed maximum values for the length of the main raceme (83.65), silique per the main raceme (53.51) and 1000-seed weight (7.29). The cluster-12 had high mean values for plant height (156.48), number(s) of secondary branches (8.80), seed yield per plot (449.38) and harvest index (32.81) whereas, the cluster-14 exhibited the highest mean value for days to 50 % flowering (40.37), silique per plant (293.40) and seed yield per plant (15.96).

The preference of genetically assorted parents for hybridization progrms is an imperative feature of any crop improvement program to accomplish enviable sergeants [46-51]. Since the identification of morphological data-based variation is important for effective evaluation and utilization of genotypes in a breeding program, screening is the only valid way to develop new genotypes for cultivation [46,52-54]. It is demonstrated that the mustard genotypes used in this study have high genetic variability which makes them potential genotypes to foster new cultivars through future mustard breeding. This is the first report on such a big set of Indian mustard genotypes.



# **Table 9. Mean performance of individual clusters for 15 quantitative characters**

## **4. CONCLUSION**

In conclusion, based on results of genetic components, correlation and path analysis related to different morpho-physiological traits, it is advocated that the genotypes with having higher values with desired association may be utilized to improve the seed yield per plant (g) of Indian mustard genotype (s) through hybridization and selection. From the study of cluster analysis for morpho-physiological traits diverse parents belonging to cluster 9 viz., MRNJ-26 and cluster 16 viz., GM-2, JD-6 and ISC-23 may be used in the mustard breeding programme for getting a higher response.

### **COMPETING INTERESTS**

Authors have declared that no competing interests exist.

#### **REFERENCES**

- 1. Rakow G, Woods DL. Outcrossing in rape and mustard under Saskatchewan prairies conditions. Can. J. Plant Sci. 1987;67: 147-151.
- 2. Barfa D, Tripathi MK, Kandalkar VS, Gupta J C and Kumar G. Heterosis and combining ability analysis for seed yield in Indian mustard [*Brassica Juncea* (L.) Czern & Coss.]. Ecology, Environment and Conservation. 2017;23(Suppl):75-83.
- 3. Baghel R, Sharma AK, Tiwari S, Tripathi M K, Tripathi N. Genetic diversity analysis of Indian mustard (*Brassica* spp.) germplasm lines using SSR molecular markers. Int. J. Curr. Microbiol. App. Sci. 2020;9(12):137-143 DOI:https://doi.org/10.20546/ijcmas.2020.9 12.018.
- 4. Rajpoot NS, Tripathi MK, Tiwari S, Tomar RS, Kandalkar VS. Characterization of Indian mustard germplasm on the basis of morphological traits and SSR markers. Current Journal of Applied Science & Technology. 2020;39(48):300- 311.
- 5. Shyam C, Tripathi MK, Tiwari S, Tripathi N, Solanki RS, Sapre S, Ahuja A, Tiwari S. In vitro production of somaclones with decreased erucic acid content in Indian mustard [*Brassica juncea* (Linn.) Czern & Coss. Plants. 2021a;10:1297. Available:https://doi.org/ 10.3390/plants10071297
- 6. Shyam C, Tripathi MK, Tiwari S, Ahuja A, Tripathi N, Gupta N. *In vitro* regeneration from callus and cell suspension cultures in Indian mustard [*Brassica juncea* (Linn.) Czern & Coss] International Journal of Agricultural Technology. 2021b;17(3): 1095-1112.
- 7. Shyam C, Tripathi MK. Biochemical studies in Indian mustard (*Brassica juncea* L.) Czern and Coss for fatty acid profiling. Int. J. Chem. Stud. 2019;7:338-343.
- 8. Shyam C, Tripathi M K, Tiwari S, Tripathi N, Ahuja A. Molecular characterization and identification of Brassica genotype(s) for low and high erucic acid content using SSR markers. Global J. Biosci. Biotechnol. 2020;9(2):56-66.
- 9. Yadav LN, Tripathi MK, Sikarwar RS, Mishra AK. Heterosis in sesame. Sesame & Safflower Newsl. 2005;20:6-10.
- 10. Tripathi MK, Tomar SS, Tiwari VK, Awasthi D, Gupta J C. Heterosis in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. Prog. Res. 2015;10(Special-VI):3376- 3379.
- 11. Verma K, Tripathi MK, Tiwari S, Tripathi, N. Analysis of genetic diversity among *Brassica juncea* genotypes using morphophysiological and SSR markers. Int. J. Curr. Microbiol. App. Sci. 2021;10(01): 1108-1117.

DOI:https://doi.org/10.20546/ijcmas.2021.1 001.134

- 12. Burton GW. Quantitative inheritance in grasses. Proced.  $6<sup>th</sup>$  Int. Grassland Cong., 1952;1:127-183.
- 13. Burton GW, De V. Estimating heritability in tall Fescue from replicated clonal material. Agron. J. 1953;45:475-481.
- 14. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in wheat. Agron. J. 1955;47: 314-318.
- 15. Webber CR, Moorthy BR. Heritable and non-heritable relationship and variability of oil content and agronomic characteristics in the F generation of soybean crosses. J. Agron. 1952;44:202-209.
- 16. Miller PA, Williams JE, Robinson HF, Comstock R E. Estimates of variance and co-variance in upland cotton and their implications in selection. Agron. J. 1958; 50:126-131.
- 17. Wright S. Correlation and causation. J. Agril. Res. 1921;20:557-587.
- 18. Wright S. The analysis of variance and the correlations between relatives with respect

to deviations from an optimum. J. Genet. 1935;30:243-256.

- 19. Dewey DR, Lu KHA. Correlation and path coefficient analysis of component in crested wheat grass seed production. Agron. J. 1959;51:515-518.
- 20. Shekhawat N, Jadeja GC, Singh J. Genetic variability for yield and its components in Indian mustard (*Brassica juncea* L. Czern & Coss). Elect. J. Plant Breed. 2014;5: 117-119.
- 21. Akabari VR, Niranjana M. Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). Int. J. Agril. Sci. 2015;11(1):35-39.
- 22. Salam J L, Mehta N, Tomar NS, Saxena RR, Saxena RR, Sarawagi AK. Genetic variability analysis of yield and its components in *Brassica compestris* var. toria. Elect. J. Plant Breed. 2017;8(1):320- 323.
- 23. Sikarwar R S, Satankar N, Kushwah M K and Singh A K. Genetic variability, heritability and genetic advance studies in yellow sarson (*Brassica rapa* var. yellow sarson). Int. J. Agri. Innov. Res. 2017;5: 831-833.
- 24. Dawar S, Kumar N, Mishra S P. Genetic variability, correlation and path coefficient analysis in the Indian mustard (*Brassica juncea* L. Czern and Coss) varieties grown in Chitrakoot, India. Int. J. Curr. Microbiol. Appl. Sci. 2018;7:883-890.
- 25. Christensen JV, Legge WG, Depauw RM, Hennig AMF, McKenzie JS. Effect of seeding date, nitrogen and phosphate fertilizer on growth, yield and quality of rapeseed in Northwest Alberta. Canad. J. Plant Sci. 1985;65:275-284.
- 26. Ilyasi M G, Shabbir M A, Rabbani S I, Malik N M, Cheema M. Genetic divergence in *Brassica napus* L., germplasm as determined by quantitative attributes. Pak. J. Bot. 2018;50:1039-1045.
- 27. Kayaçetin F, Önemli F, Yılmaz G, Kınay A, Hatipoğlu H. Effect of row spacing on yield, yield components and crude oil of autumn and spring sowed mustard (*Sinapis arvensis* L.) in eight locations of Turkey. J. Agril. Sci. 2018;24:471-487.
- 28. Akbar M, Mahmood T, Yaqub M, Anwar M, Ali M, Iqbal N. Variability, correlation and path coefficient studies in summer mustard (*Brassica juncea* L.). Asian J. Plant Sci. 2003;2(9):696-698.
- 29. Gangapur DR, Prakash BG, Hiremath CP. Genetic diversity analysis of Indian

mustard (*Brassica juncea* L.). Elect. J. Plant Breed. 2010;1(4):407-413.

- 30. Tripathi N, Kumar K, Verma O P. Genetic variability, heritability and genetic advance in Indian mustard (*Brassica juncea* L. Czern and Coss.) for seed yield and it's contributing attributes under normal and saline/alkaline condition. Int. J. Sci. Res. 2013;4:983-985.
- 31. Synrem G J, Rangare N R, Myrthong I, Bahadure D M. Variability studies in Intra specific crosses of Indian mustard [*Brassica juncea* (L.) Czern and Coss.] genotypes. IOSR J. Agri. Vet. Sci. 2014;7: 29-32.
- 32. Amsalu F, Alamerew S, Woyessa B. Genetic variability, heritability, genetic advance, genetic advance as percent mean and character association of Ethiopian mustard (*Brasica carinata* A. Braun) land races. Int. J. Plant Breed. Crop Sci. 2017;4(1):166-177.
- 33. Singh S, Dwivedi A K, Ashutosh K, Kumar K. Genetic Divergence Analysis in Indian mustard (*Brassica juncea* L.). Int. J. Curr. Microbiol. Appl. Sci. 2018;7:2496-2503.
- 34. Lodhi B, Thakral N K, Avtar R, Singh A. Genetic variability, association and path analysis in Indian mustard (Brassica *juncea*). J. Oilseed Brass. 2014;5:26-31.
- 35. Bind D, Singh D, Dwivedi VK. Genetic variability and character association in Indian mustard [*Brassica juncea* (L) Czerns & Coss]. Agril. Sci. Digest. 2014; 34(3):183-188.
- 36. Bibi T, Rauf S, Mahmood T, Haider Z, Din SU. Genetic variability and heritability studies in relation to seed yield and its component traits in mustard (*Brassica Juncea* L.). Acad. J. Agril. Res. 2016;4(8): 478-482.
- 37. Rathod VB, Mehta DR, Solanki HV. Correlation and path coefficient analysis in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. AGRES – An Int. E-J. 2013;2: 514-519.
- 38. Devi TR, Devi ND, Vivekananda Y, Sharma P R. Genetic diversity analysis in Indian mustard (*Brassica juncea* L. Czern and Coss) genotypes using agromorphological parameters. Elect. J. Plant Breed. 2017;8(3):749-753.
- 39. Raliya B, Kumar K, Ramesh P, Jat R, Meena H S, Mundiyara R. Genetic variability and character association In Indian mustard (*Brassica juncea* L.). Int. J. Agri. Sci. 2018;10:5993-5996.
- 40. Doddabhimappa RG, Prakash BG, Salimath PM, Ravikumar RL, Rao MSL. Correlation and path analysis in Indian mustard (*Brassica juncea* L. Czern and Coss). Karnataka J. Agril. Sci. 2009;22: 971-977.
- 41. Gupta A, Pant NC, Dwivedi U, Tiwari S, Pandey CS, Dhoundiyal R, Maurya KN, Verma OP. Studies on correlation and path coefficient analysis for yield and yield related traits in Indian mustard (*Brassica juncea* L. Czern & Coss.) under timely and late sown conditions. J. Pharmacog. Phytochem. 2018;7:2545- 2551.
- 42. Kumar A, Singh M, Yadav RK, Singh P, Lallu. Study of correlation and path coefficient among the characters of Indian mustard. The Pharma Innov. J. 2018;7: 412-416.
- 43. Afrin KS, Mahmud F, Bhuiyan MSR, Rahim M A. Assessment of genetic variation among advanced lines of *Brassica napus* L. Agron. Glasn. 2011; 4(5):201-226.
- 44. Yadav DK, Giri SC, Vignesh M, Vasudev S, Yadav AK, Dass B, Singh R, Singh N, Mohapatra T, Prabhu KV Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). Indian J. Agril. Sci. 2011;81:712-176.
- 45. Kardam DK, Singh VV. Correlation and path analysis in Indian mustard (*Brassica juncea* (L.) Czern & Coss) grown under rainfed condition. J. Spices Arom. Crops. 2005;14(1):56-60.
- 46. Jan SA, Shinwari ZK, Rabbani MA, Niaz IA, Shah SH. Assessment of quantitative agro-morphological variations among *Brassica rapa* diverse populations. Pak. J. Bot. 2017;49:561-567.
- 47. Pramanik A, Tiwari S, Tomar RS, Tripathi MK, Singh AK. Molecular characterization of groundnut (*Arachis hypogaea* L.) germplasm lines and varietal set for yield and yield attributing traits. Indian J. Genet., 2019;79(1):56-65. DOI:https://doi.org/10.31742/IJGPB.79.1.8.
- 48. Mishra N, Tripathi MK, Tiwari S, Tripathi N, Trivedi HK. Morphological and molecular screening of soybean genotypes against yellow mosaic virus disease. Legume Research an International Journal; 2020. DOI: 10.18805/LR4240.
- 49. Mishra N, Tripathi MK, Tiwari S, Tripathi N, Ahuja A, Sapre S, Tiwari S. Cell suspension culture and in vitro screening for drought tolerance in soybean using poly-ethylene glycol. Plants. 2021a;10(3): 517-536.
- 50. Upadhyay S, Singh AK, Tripathi MK, Tiwari S, Tripathi N. Validation of simple sequence repeats markers for charcoal rot and Rhizoctonia root rot resistance in soybean genotypes. I.J.A.B.R. 2020a; 10(2):137-144.
- 51. Choudhary ML, Tripathi MK, Tiwari S, Pandya RK, Gupta N, Tripathi N, Parihar P. Screening of pearl millet [*Pennisetum glaucum* (L.) R. Br.] germplam lines for drought tolerance based on morphophysiological traits and SSR markers. Current Journal of Applied Science and Technology. 2021;40(5):46-63. Available:https://doi.org/10.9734/cjast/2021 /v40i531303.
- 52. Neeru, Thakral NK, Avtar R, Singh A. Evaluation and classification of Indian mustard (*Brassica juncea* L.) genotypes using principal component analysis. J. Oilseed Brass. 2015;6:167-174.
- 53. Mishra N, Tripathi M K, Tiwari S, Tripathi N, Gupta N, Sharma A. Morphological and physiological performance of Indian soybean [*Glycine max* (L.) Merrill] genotypes in respect to drought. Legume Research an International Journal; 2021b. DOI: 10.18805/LR-4550
- 54. Upadhyay S, Singh AK, Tripathi MK, Tiwari S, Tripathi N, Patel RP. *In vitro* selection for resistance against charcoal rot disease of soybean [*Glycine max* (L.) Merrill] caused by *Macrophomina phaseolina* (Tassi) Goid. Legume Research an International Journal; 2020b. DOI: 10.18805/LR-4440.

 $\_$  , and the set of th © 2021 Shyam et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License *(http://creativecommons.org/licenses/by/4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.*

> *Peer-review history: The peer review history for this paper can be accessed here: https://www.sdiarticle4.com/review-history/72869*