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Study on genetic variability and principal component analysis in Indian mustard [*Brassica juncea* (L.) Czern and Coss]

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Abstract
An experiment involving 18 genotypes of Indian Mustard (*Brassica juncea* L.) was conducted in randomised block design with three replications, during *Rabi* 2020. Data were recorded and analysed for fourteen characters. The analysis of variance revealed significant differences among all the characters. In general, Phenotypic coefficients of variation were more than the corresponding genotypic coefficients of variation for all the characters. The dimensionality of the data was reduced with the help of Principal Component analysis and it led to the identification of 4 principal components (PCs) which explained about 86% variability. The first principal component (PC1) explained 36.19% of the total variation. The remaining PC's explained progressively lesser and lesser of the total variation. The maximum eigen root value was observed in PC1 (5.06) which contributed 36.19% towards total variation. The other components with their eigen root values were PC2 (4.69), PC3 (1.37) and PC4 (0.97); contributing about 33.56, 9.79 and 6.90% towards total variation.

Keywords: Genetic divergence, principal component analysis, factor loading, genetic variability and Indian mustard

Introduction
Indian mustard [*Brassica juncea* (L.) Czern and Coss] is the second most important oilseed crop of the world as well as India after groundnut. It is a natural amphidiploid (2n=36) which is a cross of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16) having self-compatible and mainly self-pollinated nature (85-90%). Indian mustard is popularly known as rai, raya or laha and it occupies major acreage about 75-80% of the total area under rapeseed-mustard in the country.

Genetic variability is the most important condition for starting any genetic improvement effort. Genetic parameters aid in the recognition of gene action which helps the breeder in selecting a suitable breeding approach which can suit to the experimental material. The genotypic and phenotypic variances generally influence the heritability and environmental factors (*Bisne et al.*, 2009) [1]. As a result, any genetic improvement effort needs to know about the nature of variability present in the base germplasm collection.

Genetic diversity is a necessity for hybridization in crop development programmes. The use of a variety of parents aids in the isolation of superior recombinants. It is preferable to use breeding approaches to investigate the structure of yield. It is critical to assess the interdependence of numerous plant characteristics and identify the component traits on which a selection strategy for direct and indirect genetic yield improvement could be based. Several yield contributing traits influence seed yield and these traits have a positive or negative relationship with one another, as well as with yield. However, breeders may get measures for a number of observed factors and aim to develop a smaller number of artificial variables (principal components) to explain for the majority of the variance in the observed variables.

Principal component analysis is a multivariate analysis method that aims to explain the correlation between a large set of variables in terms of a small number of underlying independent factors. Hamman (1972) [4] suggested that the use of multivariate techniques could reduce several phenotypic measurements in large populations into fewer, more interpretable, and easily visualized dimensions. The cluster analysis is also an appropriate method for determining family relationships but the main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only (Mohammadi, 2002).

Thus, this study was conducted with the main objective to assess the genetic diversity and genetic divergence with the help of Principal component analysis in different accessions of Indian mustard.

Material and Methods

The field experiment was carried out at oil seed research farm of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur during *Rabi* season 2020-21. The experimental site was located at 26.28° N latitude, 80.20° E longitude and about 126 meters above the sea level lying in the lower Ganges-Yamuna Doab at the bank of Ganges river. This place falls in the Central Plain zone of Agro-Ecological sub region (ICAR) and Upper Gangetic Plain Zone of Agro-Climatic zone (Planning Commission). The soil type of this site is deep, loamy with proper irrigation and drainage facility which is favourable for raising good crop.

The experimental germplasm material was sown on 18th of November 2020. The experiment was carried out in a randomized block design with 3 replications. The plot for each treatment has six rows of 5-meter length. The spacing between rows and plants was maintained 45 and 20 cm respectively. Also, the recommended dose of fertilizer 80:60:20:20 N:P:K:S kg/ha was applied for good plant growth. Recommended agronomic package and practices were followed to raise healthy and competitive plants population.

The material utilized in this experiment consist of 18 genotypes of *Brassica juncea* (L.) Czern and Coss which are KMRL-20-501, KMRL-20-502, KMRL-20-503, KMRL-20-504, KMRL-20-505, KMRL-20-506, KMRL-20-507, KMRL-20-508, KMRL-20-509, KMRL-20-510, KMRL-20-511, KMRL-20-512, KMRL-20-513, KMRL-20-514, KMRL-20-515, KMRL-20-516, VARDAAN and ASHIRVAAD. This material was obtained from the breeder of section of oilseed of the department of Genetics and Plant breeding, Chandra Shekhar Azad University of agriculture and technology, Kanpur.

Five competitive plants from each plot were randomly taken for recording observations for all the quantitative characters except days to flowering and days to maturity which were recorded on the plot basis. Oil content, methionine content, tryptophan content and protein content were estimated by using pre-calibrated near infrared reflectance spectroscopy (NIR, Dickey John Instalab 600). The collected data were subjected to analysis of variance (ANOVA)**.** Genotypic and phenotypic coefficients of variation were estimated by using the formula given by Burton (1952) [2]. The principal component analysis method explained by Harman (1976) [5] was followed in the extraction of the components. The percentage variability explained by each component were determined (Harman, 1976; Sharma, 1996; Tadesse and Bekele, 2001) [5, 13, 15].

Characters under observation

The data was collected from 5 competitive plants from each plot and data was recorded for the following characters

- Days to 50% flowering
- Days to maturity
- Plant height (cm)
- Number of primary branches/plant
- Number of secondary branches/plant
- Number of siliquae/plant
- Number of grains/siliqua
- Economic yield/plant (gm)
- Biological yield/plant (gm)
- Oil content (%)
- 1000 seed weight (gm)
- Protein content (%)
- Methionine content (%)
- Tryptophan content (%)

Result and Discussion

Analysis of variance

The analysis of variance (Table-1) revealed that all the characters *viz*., days to 50% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, number of siliquae/plant, number of grains/siliqua, biological yield/plant, economical yield/plant, 1000-seed weight, oil content, protein content, methionine content, tryptophan content were highly significant for the treatments. Lodhi *et al.* (2016) [6] also made analysis of variance and found highly significant differences among all the genotypes for all fifteen characters under study. The result from ANOVA indicated that the considerable amount variability was due to genotype.

Coefficients of variation

The phenotypic coefficient of variation and genotypic coefficient of variation were carried out and results are shown in table 2. The magnitude of PCV was found higher than GCV indicating more contribution of genotypic variance to the total variance for all the traits and effect of environment is low. The high values of phenotypic coefficient of variation were observed in the characters economic yield/plant, number of secondary branches, methionine content, 1000-seed weight, biological yield and number of siliquae/plant while, number of primary branches/plant exhibited moderate value of PCV. Characters like days to maturity, protein content and oil content showed low values of phenotypic coefficient of variation. Yadava *et al.* (2011) [16] and Pant and Singh (2001) [10] also reported high PCV for most of the traits.

It was observed that economic yield, number of secondary branches/plant, methionine content, 1000 seed weight, biological yield and number of siliquae/plant exhibited high genotypic coefficient of variation. Similarly, moderate values were shown by primary branches/plant. The low genotypic coefficient of variation was observed in number of grains/siliqua, plant height, tryptophan content, days to maturity, protein content and oil content. Pal (2019) also observed high PCV and GCV for secondary branches per plant, seeds per siliqua, siliqua per plant, seed yield per plant, siliqua length and biological yield per plant. These higher magnitudes of GCV and PCV indicated more scope of phenotypic selection through these characters for further improvement.

Principal Component Analysis

The principal components were extracted from the original data and PC1, PC2 and PC3 were having eigen root value of more than 1 while, PC4 has value near to 1. All these 4 principal components contributed 86.44% towards total variation. Neeru *et al.* (2016) [7] also identified 11 principal components (PCs) which explained about 75% variability while, Pankaj *et al.* (2017) [9] identified nine principal components (PCs) which explained about 77% variability

with the help of principal component analysis.

According to Chahal and Gosal (2002) [3], characters with largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero. The eigen values and variability of different principal components are shown in table-3. The maximum eigen root value was observed in PC1 (5.06) which contributed 36.19% towards total variation. The other components with their eigen root values were PC2 (4.69), PC3 (1.37) and PC4 (0.97); contributing about 33.56, 9.79 and 6.90% towards total variation. The correlation coefficients of traits with respect to principal components (PCs) are shown in table-4. The PC1 ascribed for variables like biological yield/plant, number of siliquae/plant, number of primary branches and protein content which can be described as yield factor. Ray *et al.* (2014) [11] also showed similar findings in his studies. PC2 has high loadings of two variables *viz.*, number of grains/siliqua and methionine content. It also had high negative loadings for 1000-seed weight and economic yield/plant. The PC3 can be designated as maturity factor since variable like days to maturity was high for this component, tryptophan content and primary branches were also had high values for this component. PC4 showed high loadings for days to 50% flowering and plant height. The variables like economic yield/plant, number of grains/siliqua showed high negative loadings on PC4. Similar findings were also reported by Singh *et al.* (2014) [14] and Saleem *et al.* (2017) [12].

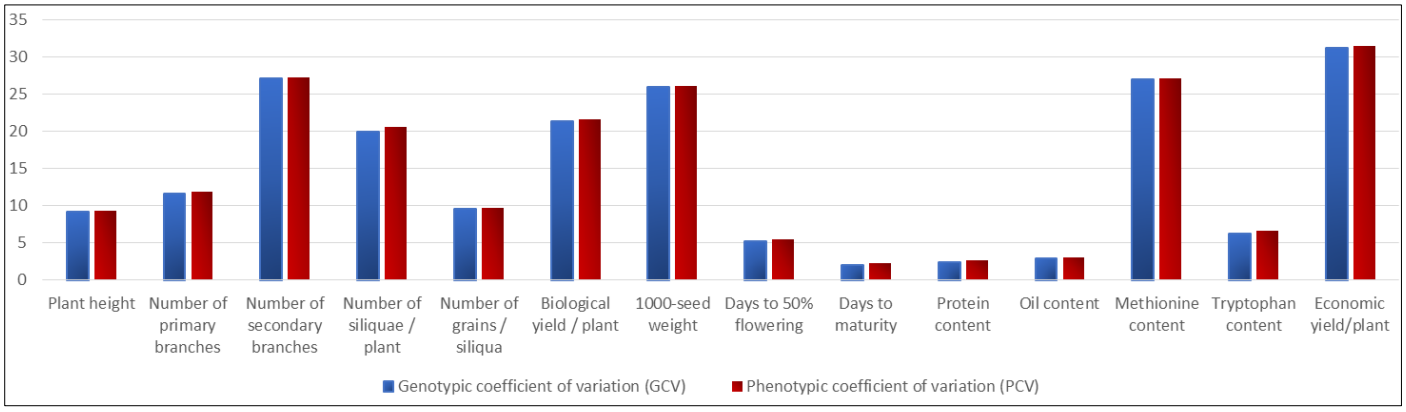
Table 1: Mean sum of squares for different characters in Indian Mustard

S. No.	Source of variation	degree of freedom	Plant height	Number of primary branches	Number of secondary branches	Number of siliquae/ plant	Number of grains/ siliqua	Biological yield/plant	1000 seed weight	Days to 50% flowering	Days to maturity	Protein content	Oil content	Methionine content	Tryptophan content	Economic yield/plant
1	Replication	2	266.08	2.27	2.66	314.49	1.28	135.65	0.000002	2.29	2.35	0.097	0.62	0.001	0.0023	21.74
2	Treatment	17	744.17*	2.45**	49.55**	12138.47*	5.69**	700.56**	0.02**	31.87**	19.98**	1.28**	3.51**	1.03**	0.045**	101.55**
3	Error	34	3.62	0.03	0.05	240.91	0.03	3.72	0.000027	1.31	1.54	0.054	0.18	0.0012	0.0016	0.62

* &** Significant at 5% & 1% respectively

Table 2: Genotypic coefficients of variation and phenotypic coefficients of variation for different characters in Indian Mustard.

Parameters	Plant height	Number of primary branches	Number of secondary branches	Number of siliquae / plant	Number of grains / siliqua	Biological yield / plant	1000-seed weight	Days to 50% flowering	Days to maturity	Protein content	Oil content	Methionine content	Tryptophan content	Economic yield/plant
Genotypic coefficient of variation (GCV)	9.26	11.61	27.20	20.02	9.59	21.43	26.06	5.20	2.00	2.45	2.86	27.06	6.25	31.27
Phenotypic coefficient of variation (PCV)	9.32	11.88	27.24	20.62	9.67	21.60	26.11	5.53	2.24	2.61	3.09	27.11	6.60	31.56
General mean	169.66	7.72	14.93	314.47	14.32	71.10	0.31	61.29	123.59	26.06	36.75	2.17	1.92	18.54



Graph 1: Graphical Comparison of GCV and PCV for different Characters

Table 3: Eigen values and variability explained by each principal component.

Canonical Roots Analysis (P. C. A.)	PC I	PC II	PC III	PC IV
Eigen Value (Root)	5.067	4.698	1.371	0.967
% Var. Exp.	36.195	33.563	9.794	6.907
Cum. Var. Exp.	36.195	69.758	79.552	86.460

Table 4: Correlation coefficients of traits with respect to principal components (PCs)

VARIABLES	PC1	PC2	PC3	PC4
Plant Height (Cm)	0.136	0.273	0.195	0.308
Number Of Primary Branches	0.346	0.143	0.315	0.102
Number Of Secondary Branches	0.277	0.219	-0.319	-0.275
Number Of Siliquae/Plant	0.375	0.123	-0.119	-0.098
Number Of Grains/Siliqua	0.079	0.381	0.136	-0.415
Biological Yield /Plant	0.415	-0.087	0.054	0.081
1000 Seed Weight(Gm)	0.181	-0.372	-0.205	0.020
Days To 50% Flowering	-0.365	-0.036	-0.255	0.368
Days To Maturity	-0.318	0.111	0.470	-0.138
Protein Content (%)	0.321	0.242	0.048	0.266
Oil Content (%)	0.256	-0.342	-0.169	0.240
Methionine Content (%)	-0.050	0.375	-0.239	0.269
Tryptophan Content (%)	0.119	-0.272	0.547	0.275
Economic Yield/Plant	0.099	-0.379	0.080	-0.442

Conclusion

From the study it can be concluded that genetic variability existence was confirmed by significant differences for different characters through ANOVA as well as genotypic coefficient of variation. All the Indian mustard genotypes were classified based on various qualitative and quantitative characters and all the variables have been reduced to four principal factors. This statistical method utilized in this study has enabled us in identifying superior genotypes for both seed yield and oil content, and genotypes promising for various combinations of characters. These results will be useful in understanding the genetic diversity within a group of genotypes which may be put to a far better use for evolving well defined approach for evaluation and characterization of genetic variation during this crop.

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