



ISSN (E): 2277-7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2022; 11(12): 6138-6142  
© 2022 TPI  
[www.thepharmajournal.com](http://www.thepharmajournal.com)  
Received: 03-10-2022  
Accepted: 12-11-2022

**Veer Vikram Singh Bhandari**  
Ph.D., Research Scholar,  
Faculty of Agriculture Science  
and Technology, MGU,  
Bilkisganj, Madhya Pradesh,  
India

**Dr. AN Tikle**  
GPB, Rajmata Vijayaraje  
Scindia Krishi Vishwa  
Vidyalaya, Gwalior,  
Madhya Pradesh, India

**Ratnakar Pandey**  
SMS, KVK, ANDUAT,  
Kumarganj, Uttar Pradesh,  
India

## Genotype X environments interaction analysis in Indian mustard (*Brassica juncea* (L.) Czern & Coss) genotypes under micro environments

**Veer Vikram Singh Bhandari, Dr. AN Tikle and Ratnakar Pandey**

### Abstract

An attempt has been made in the present investigation entitled “Genotype X environments interaction analysis in Indian mustard (*Brassica juncea* (L.) Czern & Coss) genotypes under micro environments” to know genetic diversity and stability parameters of diverse genotypes during Rabi 2021-22 with three environments at the village Naugaya, Bharatpur, Rajasthan. Experimental material consisted of 20 Indian mustard genotypes under Randomized Complete Block Design and observation recorded for eight quantitative traits viz., Days to 50% flowering, Days to maturity, Plant height, Number of primary branches per plant, Number of secondary branches per plant, Number of siliquae on main raceme, Biological yield per plant, Seed yield per plant. Analysis of variance showed genotypes were highly significant for all the traits in EI, EII and EIII. Magnitude of PCV % and GCV % for different traits revealed that the maximum amount of variability was found for number of secondary branches per plant in EII and EIII of Indian mustard. High heritability was observed for all traits viz., Days to 50% flowering, Days to maturity, Plant height (cm), Number of primary branches per plant, Number of secondary branches per plant, Number of siliquae on main raceme, Biological yield and Seed yield per plant (g) in EI, EII and EIII of Indian mustard. Significant and positive correlation was observed for seed yield per plant with number of primary branches per plant, number of secondary branches per plant, number of siliqua on main raceme and biological yield in all the environments. Path coefficient analysis revealed that number of siliquae on main raceme, number of primary branches per plant, number of secondary branches per plant, days to maturity and plant height had the highest positive direct effect on seed yield per plant. Two different dates of sowing creating eight artificial environments. Variance due to G x E interaction was significant for all the characters except for days to 50% flowering, while G x E (linear) was found to be significant for number of secondary branches per plant, number of siliquae per plant, siliqua length, seed yield per plot and 1000 seed weight. Genotypes, GM-2, JD-6 and Pusa Bold could be recommended for general cultivation and their utilization in future breeding programme. Under favourable environments, genotypes Kranti, NDRE-7, NDRE-22 and Sej- 2 are suitable for general cultivation. On the contrary, Urvashi could be recommended for poor/unfavourable environmental conditions.

**Keywords:** Correlation, heritability, stability, D<sup>2</sup> statistics and genetic divergence

### Introduction

Oilseed Brassicas are important source of edible oil in India. These crops mainly belonging to four species viz *Brassica juncea*, *B. napus*, *B. campestris* syn *rapa* and *B. carinata* of tribe Brassicaceae within the family Cruciferae (Brassicaceae), are grown worldwide. The genus *Brassica* is comprises of several economically important species which yield edible roots, stems, leaves, buds, flowers and seed as condiment. Most of the species are used as oilseed crop and some as for age. Indian mustard (*B. juncea* L. Czern and Coss) popularly known as sarson, rai, or laha is one of the most important oil seed crops of the country and it occupies considerably large acreage among the *Brassica* group of oil seed crops. The crop is grown both in tropical and subtropical countries. The oil obtained from the different types show slight variation in percentage of oil content. The oil content of the seeds of different forms ranges from 30- 49%. The oil obtained is the main cooking medium in northern India and cannot be easily replaced by any other edible oil. The seed and oil of mustard have a peculiar pungency due to presence of glucosinolate and its hydrolysis products such as allyl-isothio-cyanate. Indian mustard is predominantly cultivated in Rajasthan, Madhya Pradesh, Haryana, Uttar Pradesh and Gujarat. It is also grown under some nontraditional area of South Indian including Karnataka, Tamil Nadu and Andhra Pradesh. Globally, India continues to be at rank 4<sup>th</sup> after Canada, China and Europe an Union in acreage (17.19%) and after European Union, Canada

**Corresponding Author:**  
**Veer Vikram Singh Bhandari**  
Ph.D., Research Scholar,  
Faculty of Agriculture Science  
and Technology, MGU,  
Bilkisganj, Madhya Pradesh,  
India

and China in production (8.54%). The global demand of edible oils and its products is increasing continuously. Therefore, for the increasing population, it is essential that the enhance yield and oil content in mustard. The area under mustard cultivation has remained meager and presently is not enough as per demand.

Total area, production and yield of rapeseed-mustard in world during 2018-19 was 36.59 million hectares (mha), 72.37 million tonnes (mt) and 1980kg/ha, respectively. The total oilseeds production has been hovering around 30-31 million tonnes during last few years. In India, the rapeseed-mustard acreage increased from 5.98 mha (2017-18) to 6.12 m ha (2018-19), production got increased from 8.43 mt (2017-18) to 9.26 mt (2018-19) and productivity got increased from 1410 kg/ha (2017-18) to 1511 kg/ha (2018-19) (PC Report, DRMR, 2020). In Madhya Pradesh, the total area, production and productivity are 0.78 million hectare, 1.11million tones and 1422 Kg per hectare, respectively (Agriculture Statistics at a glance, 2019).

The knowledge about the factors responsible for high yield is a difficult problem as yield is a very complex character and an interactive effect per multiplication of different traits. Therefore, for attainment of high yield level, the breeder is required to simplify this complex situation through handling of yield components which have negative correlation with each other. For this rational approach it is essential to get information on the nature and magnitude of association between different yield components and to resolve and quality/ quantity and their mode of contribution to yield.

D<sup>2</sup>-statistic as multivariate analysis is a powerful tool in the estimating genetic divergence in crop plants. Being a numerical estimate this method has an added advantage over other as it permits precise comparisons among all possible traits of population in a group and its commutation offers the automatic removal of the effects of correlations among the genetic variables involved to its efficiencies and usages. The utility of Mahalanobis's generalized distance (D<sup>2</sup>) is not only limiting factor for determining the degree of divergence in different populations but also for selecting genetically diverse parents for an efficient breeding programme.

Stability in performance of genotype for economic characters is one of the desirable properties for selection or recommendation of new genotypes in plant breeding program. For this purpose, growing of breeding lines over time and space has become an integral part of any crop improvement programme. The knowledge of G x E interaction is of great importance to the plant breeders in developing improved varieties/hybrids. When genotypes are tested over a series of environments/locations, the relative ranking of these genotypes for any given attribute is rarely the same at each environment/location. Such changes in order, ranking and relative values among the genotypes over several environments are due to the phenomenon of G x E interaction.

### Materials and Methods

The experiment was laid out on Bharatpur district is located in the eastern part of Rajasthan. It stretches between 26° 41' 58.67" to 27° 49' 41.74" north latitude and 76° 52' 06.42" to 77° 47' 05.51" east longitude covering area of 5079.4 sq km. The maximum temperature during the month of May and June reaches up to 33.7 °C, whereas minimum temperature goes below 14.1°C in the month of December or January. The average rainfall in this region is 698.21 mm which is mostly

received during monsoon season between mid - June to end of September with little occasional showers in other seasons. Experimental material consisted of 20 Indian mustard genotypes. The experiment was conducted in Randomized Complete Block Design, using recommended agronomic practices for normal growth of crop. Experimental area was uniform in respect of topography and fertility.

The experiment was laid out design RCBD with 20 genotypes and three replication. The material used in the experiment was fertilizer dose NPK (80:40:40 kg/ha). The crop mustard 20 different genotypes, spacing of 30cm X 10 cm. Observations were recorded on single plant basis. For recording single plant observations five competitive plants from each plot were randomly selected. Experimental area occupied was quite uniform in respect of topography and fertility. All of the growth characters viz. plant height, number of branches, number of capsule and days of maturity etc.

### Result and Discussion

The results obtained in the present investigation entitled "Genotype X environments interaction analysis in Indian mustard (*Brassica juncea* (L.) Czern & Coss) genotypes under micro environments" was carried out with 20 genotypes of Indian mustard laid out in Randomized Complete Block Design at the village Naugaya, Bharatpur, Rajasthan, during rabi 2021-22. To assess variability in the germplasm, studied genetic parameters of variability. Correlation analysis was performed to find out the degree of relationship between the characters. Path analysis was conducted to know the direct and indirect effect of various independent characters on dependent one. Divergence analysis was performed to know the grouping of genotypes into various clusters and to select diverse line for hybridization programme. Stability analysis carried out to generate information on the adaptive potential and stability parameters of 20 diverse genotypes of Indian mustard. Stability assessed for their performance to characterize the nature of genotype x environment interaction for various yield and yield related traits at different environments. The data for various quantitative and qualitative traits were analyzed for standard statistical procedures.

It is a statistical tool that offers information on the degree and direction of relationships between variables at the phenotypic and genotypic levels. It describes the kind, amount, and direction of the selection pressure to be applied for practical purposes. Seed yield per plant was used as a dependent variable to analyze genotypic and phenotypic correlations for various yield attributing characteristics. Phenotypic correlation is the relationship of two variables that may be observed directly and is evaluated using phenotypic variance and covariance. It indicates the degree and direction of the association between variables at the phenotypic level, whereas genotypic correlation demonstrates the heritable linkage between characteristics.

The path coefficient is a standardized partial regression coefficient used to divide the correlation coefficient. Path coefficient analysis quantifies the direct and indirect impact of numerous independent characters on the dependent character. It indicates whether the relationship of these independent characters with seed yield is due to a direct influence on yield or an indirect effect through other component characters.

To calculate D<sup>2</sup>, correlated means of characters were converted into standard uncorrelated means using Tocher's

technique. The statistical distance (Mahalanobis  $D^2$ ) between two genotypes were calculated as the sum of the squares of the difference between any two genotypes evaluated at the same time.

The percent contribution of individual traits towards the total divergence was found highest for plant height (cm) (54.74%) followed by seed yield per plant (g) (34.74%), number of siliquae on main raceme (4.74%) Days to maturity (3.68%), Number of secondary branches per plant (1.05%), Days to 50% flowering (0.54%) and Biological yield (0.53%) and

number of primary branches per plant (0.00%) showed negligible contribution toward the divergence.

Phenotypic path coefficient analysis revealed that number of siliquae on main raceme (0.8937) had the highest positive direct effect on seed yield per plant followed by number of primary branches per plant (0.1301), plant height (0.0571), number of secondary branches per plant (0.0523) and days to maturity (0.0025). However, maximum negative direct effect on seed yield per plant was found through days to 50% flowering (-0.0882) followed by biological yield (-0.0055).

**Table 1:** Phenotypic path coefficient analysis for yield and its component characters in Indian mustard

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of siliquae on main raceme	Biological yield	Seed yield per plant (g)
Days to 50% flowering	-0.0871	0.0064	-0.0510	-0.0008	-0.0084	0.0025	0.0235	-0.0732
Days to maturity	-0.0002	0.0027	-0.0009	-0.0006	0.0003	-0.0001	0.0011	-0.0563
Plant height (cm)	0.0322	-0.0187	0.0550	0.0182	0.0005	-0.0013	-0.0205	0.0282
Number of primary branches per plant	0.0011	-0.0317	0.0439	0.1323	0.0440	0.0308	-0.0052	0.3741
Number of secondary branches per plant	0.0048	0.0050	0.0005	0.0166	0.0498	0.0132	-0.0107	0.3244
Number of siliquae on main raceme	-0.0258	-0.0174	-0.0215	0.2082	0.2369	0.8946	0.0774	0.9391
Biological yield	0.0017	-0.0026	0.0023	0.0002	0.0013	-0.0005	-0.0062	0.0593

The intra and inter cluster  $D^2$  mean values are presented in Table 4.8 (EI). On the basis of  $D^2$  values, 20 genotypes were grouped into IV clusters. Intra cluster distance ranged from 0.00 to 39.66. Cluster I showed highest intra cluster value (39.66) whereas cluster II III and IV had displayed zero value for Intra cluster distance.

The highest inter cluster divergence was observed between genotypes of cluster II and cluster III (130.52), followed by cluster II and cluster IV (118.85), cluster I and cluster IV (89.40), cluster I and cluster III (83.93), cluster III and cluster IV (66.21) and cluster I and cluster II (61.12).

**Table 2:** % Contribution of different traits towards clustering in Indian mustard

S. No.	Source	Times Ranked 1 <sup>st</sup>	Contribution %
1	Days to 50% flowering	1	0.54
2	Days to maturity	7	3.68
3	Plant height (cm)	104	54.74
4	Number of primary branches per plant	0	0.00
5	Number of secondary branches per plant	2	1.05
6	Number of siliquae on main raceme	9	4.74
7	Biological yield	1	0.53
8	Seed yield per plant (g)	66	34.74
	Total		100%

**Table 3:** Inter and intra cluster  $D^2$  values for different clusters in 20 Indian mustard genotypes

Cluster No.	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	39.66	61.12	83.93	89.40
Cluster II		0.00	130.52	118.85
Cluster III			0.00	66.21
Cluster IV				0.00

The cluster mean for different characters are presented in Table 4.9 (EI). In case of Days to 50% flowering, cluster II (48.90 days) showed maximum days, while cluster IV (43.86 days) had minimum mean value. Cluster III showed

maximum (141.33 days) and cluster IV had minimum (131.33 days) cluster mean value for Days to maturity respectively. Plant height (cm) showed maximum mean value in cluster II (224.53) and minimum in cluster IV (156.72) respectively. Number of primary branches per plant exhibited maximum in cluster I (6.06) and minimum in cluster IV (4.75). The mean values for the Number of secondary branches per plant were recorded maximum in cluster III (14.91) and minimum in cluster IV (9.35). Number of siliquae on main raceme had highest mean in cluster III (55.42) and minimum in cluster IV (48.19). Biological yield had maximum mean in cluster IV (68.60) and minimum in cluster II (63.10), for seed yield per plant (g) cluster III showed maximum (27.17) and cluster IV showed minimum (16.01) mean values.

## Conclusions

High heritability coupled with high genetic advance as percentage of mean and estimates of genotypic coefficient of variation were higher for number of secondary branches per plant in all the environments of Indian mustard have consequent chances of improving these traits through simple selection, indicating additive gene action may be responsible for expression of these traits. The correlation and path analysis studies showed that for developing new plant type in Indian mustard should be multiple primary and secondary branches, more number of siliquae on main raceme, plant height, high biological yield and seed yield which improve the productivity of plant, while in addition to these traits large seed size should provide more emphasis for developing plant types in Indian mustard under different environments. A subsequent genetic diversity among the genotypes was observed. The maximum contribution towards the total divergence was found through days to 50% flowering, seed yield per plant number of secondary branches per plant and biological yield in Indian mustard. These traits were responsible for expressing maximum diversity between the clusters. Six advanced breeding lines viz., Pusa Mahak PM-30, JM-3, Pusa Vijay, PM-25, Pusa jaikisan, JMM-991, and

RVM- 1 Varuna, were found most divergent are selected and be used for further hybridization/ breeding programme. On the basis of dendrogram constructed based on UPGMA two clusters formed among 20 genotypes these results indicate that despite extensive breeding efforts, the varieties under current cultivation are closely related among themselves. In the stability analysis the significant G (varieties) x E (linear) for the days to 50 percent flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, number of siliqua on main receme, biological yield per plant and seed yield per plant indicate divergent linear response to environmental changes. The S<sup>2</sup>d was not estimate significant for any variety, therefore the any variety did not found unstable there was all varieties were desirable and stable.

## Reference

1. Das K, Barua PK, Hazarika GN. Genetic variability and correlation in Indian mustard. J Agric. Sci. 1998;11(2):262-264.
2. Dastidar KKG, Patra MM. Character association for seed yield components in Indian mustard (*Brassica juncea* L. Czern and Coss). Jr. Inter academica. 2004;8(2):155-160.
3. Devi TR, Devi ND, Vivekananda Y, Sharma PR. Genetic diversity analysis in Indian mustard (*Brassica juncea* L. Czern and Coss) genotypes using agro-morphological parameters. Electronic Journal of Plant Breeding. 2017;8(3):749-753.
4. Devi B. Correlation and path analysis in Indian mustard (*Brassica juncea* L.) in agro-climatic conditions of Jhansi (U.P.). Journal of Pharmacognosy and Phytochemistry. 2018;7(1):1678-1681.
5. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agron. J. 1959;51:515-518.
6. Dipti N, Khan M, Ali S. Assessment of genetic variability and traits association in Indian mustard (*Brassica juncea* L.). Progressive Research: An International Journal. 2016;10(1):455-458.
7. Fisher RA, Yates F. Statistical tables for biological, agriculture and medical research. 5 Aufl. Oliver and Boyd. Edinburgh. 1938.
8. Gangapur DR, Prakash BG, Salimath PM, Ravikumar RL, Rao MSL. Correlation and path analysis in Indian mustard (*Brassica juncea* L. Czern and Coss). Karnataka J Agri. Sci. 2009;22(5):971-977.
9. Ghosh SK, Gulati SC. Genetic variability and association of yield components in Indian mustard (*Brassica juncea* L.). Crop Res. 2001;21(3):345-349.
10. Gupta Anuj, Chandra Pant Naveen, Dwivedi Upendra, Tiwari Shailendra, Pandey CS, Dhoundiyal Rakesh, et al. 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. Journal of Pharmacognosy and Phytochemistry. 2018;7(2):2545-2551.
11. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean Lespedeza. Agronomy Journal. 1956;48:268-272.
12. Hussain S, Hazarika GN, Barua PK. Genetic variability, heritability and genetic advance in Indian rapeseed (*Brassica campestris* L.) and mustard (*B. juncea* Czern and Coss). Progressive Research: An International Journal. 1998;11(2):260-261.
13. Jahan N, Khan M, Ghosh S, Bhuiyan S, Hossain S. Variability and heritability analysis in F4 genotypes of *Brassica rapa* L. Bangladesh Journal of Agricultural Research. 2014;39(2):227-241.
14. Jajoria RN. Genetic divergence for seed yield and its components in taramira (*Eruca sativa* Mill). M.Sc. (Ag.) Thesis, Submitted to Rajasthan Agricultural University, Bikaner, Campus-Jobner. 2001.
15. Jankowski K, Budzynski W. The role of yield components in the management of yielding of some spring oilseed crops. Rosliny Oleiste. 2003;24(2):443-454.
16. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Jr. Agron. 1955;47:314-318.
17. Kardam DK, Singh VV. Correlation and path analysis in Indian mustard (*Brassica juncea* (L.) Czern & Coss) grown under rainfed condition. Jr. Spices and Aromatic Crops. 2005;14(1):56-60.
18. Karkoo SK, Jindla LN, Satija DR. Genetic determination of seed yield through its components in Indian mustard (*Brassica juncea* (L.) Coss.). Crop Improv. 2000;27(2):247-249.
19. Kaushik SK. Association analysis of morphological characters in taramira (*Eruca sativa* Mill.) M.Sc. (Ag.) Thesis submitted to Rajasthan Agricultural University, Bikaner, Campus- Jobner. 1998.
20. Kumar B, Panday A. Association analysis of yield and its components in Indian mustard (*Brassica juncea* (L.)). Environment and Ecology. 2014;32(4B):1778- 552.
21. Kumar M, Sinha TS, Kumar M, Kumar V. Genetic variability, heritability, genetic advance and character association in Indian mustard (*Brassic juncea* L. Czern and Coss) grown in semi-reclaimed alkali soils. Jr. of Farming Syst. Res. and Develop. 2007;13(2):284-287.
22. Kumar P, Lamba A, Yadav RK, Singh L, Singh M. Analysis of yield and its components based on heterosis and combining ability in Indian mustard (*Brassica juncea* L. Czern & Coss), The Bioscan. 2013;8(4):1497-1502.
23. Kumar S, Sangwan RS. Genetic variability, heritability and genetic advance in Brassica species under dryland conditions. Agric. Sci. Digest. 1994;14(3-4):172-176.
24. Kumar A, Nath S, Yadav AK. Variability and heritability analysis in F4 genotypes of *Brassica juncea* L. Bangladesh Journal of Agricultural Research. 2018;39(2):227-241.
25. Kumar R, Waldia RS, Kumar R. Generation mean analysis and genetic parameters for yield and contributing traits in Indian Mustard (*Brassica juncea* L.). Indian Journal of Agricultural Science. 2016;82(6):528-31.
26. Khan RSA, Khan FA. Evaluation of genetic potential of some Brassica germplasm collections. International Journal of Agriculture of Biology. 2003;5(4):630-631.
27. Khulbe RK, Pant DP. Correlation and path coefficient analysis of yield and its components in Indian mustard. Crop Res. 1999;17(3):371-375.
28. Labana KS, Chaurasia BD, Singh B. Genetic variability and intra character associations in the mutants of Indian mustard. Indian Jr. Agric. Sci. 1980;501(11):803-806.
29. Larik AS, Rajput LS. Estimation of selection indices in *Brassica juncea* L. and *Brassica napus* L. Pak. Jr.

- Botany. 2000;32(2):323-330.
30. Lekh Raj, Singh H, Singh VP. Variability studies in rapeseed and mustard. Ann. Agric. Res. 1998;19(1):87-88.
  31. Lodhi B, Thakral NK, Ram Avtar, Singh A. Genetic variability, association and path analysis in Indian mustard (*Brassica juncea*). Journal of Oilseed Brassica. 2014;5(1):26-31.
  32. Mahalanobis PC. A statistical study at Chinese head measurement. Journal of the Asiatic Society of Bengal. 1928;25:301-377.
  33. Maurya JS, Mohammadi K, Talebi R. Interrelationships and genetic analysis of seed yield and morphological traits in mini core collection of Iranian landrace, breeding lines and improved Indian mustard (*Brassica juncea*) cultivars. Genetika. 2013;47(2):383-393.
  34. Mahla HR, Jambhulkar SJ, Yadav DK, Sharma R. Genetic variability, correlation and path analysis in Indian mustard [*Brassica juncea* (L.) Czern and Coss.]. Indian J Gen. and Pl. Breed. 2003;63(2):171-172.
  35. Meena BK. Genetic divergence in the germplasm of taramira (*Eruca sativa* Mill.) M.Sc. (Ag.) Thesis submitted to Rajasthan Agricultural University, Bikaner, campus- Jobner; c1996.
  36. Miller PA, Willans JC, Robinson HF, Comstock RE. Estimates of genotypic and environmental variance and covariance in upland cotton and their implication in selection. Agron. Jr. 1958;50:126-131.