The Pharma Innovation

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Character association, divergence and genotype X environments interaction analysis in Indian mustard (*Brassica juncea* (L.) Czern & Coss) genotypes under microenvironments

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Abstract
An attempt has been made in the present investigation entitled "Character association, divergence and genotype X environments interaction analysis in Indian mustard (*Brassica juncea* (L.) Czern & Coss) genotypes under microenvironments" 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 pant, 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 EII 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. Percent contribution of individual traits towards the total divergence was found maximum for number of secondary branches per plant, days to 50% flowering showed contribution toward the divergence in all the environments. Genotypes were grouped into IV clusters in EI, XI clusters in EII IV clusters in and EIII. In EI, EII and EIII cluster I exhibited largest among all the clusters comprising of 17, 7 and 17 genotypes respectively. Intra cluster distance was recorded maximum for cluster I whereas three clusters *viz*., cluster II, III and cluster IV showed zero value in EI. The dendrogram constructed based on UPGMA (Unweighted Pair Group Method with Arithmetic Mean) between genotypes showed that 20 genotypes formed two clusters (cluster I and II). Cluster I encompassed only 1 genotype and Cluster II included remaining 19 genotypes. Analysis of variance carried out as per the model given by Ebrehart and Russell (1966) indicated that variance due to Env. + (G (varieties) x E) was significant for all the characters. The significant G (varieties) x E (linear) for the days to 50 per cent flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, number of siliquas on main receme, biological yield per plant and seed yield per plant indicate divergent linear response to environmental changes.

Keywords: Mustard, correlation, heritability, stability, path coefficient analysis

Introduction
Rapeseed-mustard is a group of crops comprising rapeseed (toria, brown sarson and yellow sarson), cultivar of Brassica campestris; Indian mustard (*Brassica juncea*); black mustard (*Brassica nigra*) and taramira (*Eruca sativa*). Some exotic species of Brassica like gobhisarson (B. napus), Ethiopian mustard or karanrai (B. carinata) and white mustard (Sinapi's alba) have been brought into cultivation in India. The genus Brassica is one of 51 genera of Brassiceae family. *Brassica juncea* (n = 18) is an amphidiploid species derived from interspecific crosses between B. nigra (n = 9) and *B. rapa* (n = 10). Rapeseed-Mustard is the second most important oilseed crop of India (third most important in the World) and plays a significant role in Indian economy by contributing about 27.8% of the total edible oilseed production (Singh *et al*., 2010) [11]. Globally, India account for 19.3% and 11.1% of the world average and production.

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These crops are cultivated on an area 5.76 million ha. With a total net production of 6.79 million tones and with an average yield of 1184 kg/ha. (Agril. Stats. At a glance, 2016). The major growing states in India are Rajasthan (48%), Haryana (12%), MP (10%), UP (9%) and West Bengal (7%) contributes >80% of area and >85% of production of mustard oil. It contains about 38 to 43 per cent oil which is golden-yellow in color, fragrant and is considered to be the healthiest and nutritious cooking medium. Oil possess one of the best fatty acids profiles (low saturated fatty acids (8%), high monounsaturated fatty acids (70%) and alpha linolenic acid (10%), among the various vegetable oils, which reduces the risk of coronary heart diseases by almost 70%. Removal of glycosylates increases the nutritional quality of deviled cake and makes it less pungent for consumption as fodder. During the past years, a major gain in its productivity has been achieved, but still there is a great scope for further enhancement in its productivity. The estimated demand for vegetable oils is likely to be around 34 million tons by 2020 A.D., of which nearly 14 million tones is to be met out by the Rapeseed-mustard crops. The production can be enhanced through the development of high yielding varieties. Therefore, emphasis should be given to develop high yielding varieties with through hybridization followed by selection.

Estimation of degree of divergence between biological population and computation of relevant contribution of different components to the total divergence is done completely. Genetic variability in respect to genetic diversity is the prerequisite for the crop improvement through selection of high yielding genotypes. Genetic diversity arises either due to geographical separation or due to genetic barriers to cross ability. The quantification of genetic diversity by biometrical approaches can help choose diverse parents for a successful hybridization programmed. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains (Singh, 1986) which permits to select the genetically divergent parents to obtain the desirable recombination in the segregating generations (Uddin and Chowdhury, 1994) [15]. Selection of parents based on genetic divergence has become successful in several crops (Ashana and Pandey, 1980; Ananda and Rawat, 1984) [2, 1]. Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991) [15]. Therefore, the present investigation was carried out to determine the divergence among the different genotypes of Indian mustard.

Materials and Methods
The experiment was laid out on Bhagalpur district is located in the eastern part of Rajasthan. It stretches between 26º 41' 58.67" to 27º 49' 41.74" north latitude and 76º 52' 06.42'' to 77º 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 33.7ºC, whereas minimum temperature goes below 14.1ºC 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 replications. 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 "Character association, divergence and genotype X environments interaction analysis in Indian mustard (*Brassica juncea* (L.) Czern & Coss) genotypes under microenvironments" 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 programmed. 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.

The ANOVA indicated that the mean sums of squares due to genotypes were significant for all the traits under study *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). The mean performance of 20 genotypes of Indian mustard for 8 attributes exhibited a broad range of variation. Days to 50% flowering ranged from 49.00 (PM-27) to 57.00 (Pusa mahak) days with a mean of 51.85 days. Out of 20 genotypes JMM-927 (49 days), JM-2 (49 days), JM-1 (50 days), RVM-2 (49 days) and JM-3 (50 days) showed early in the days to 50% flowering. This trait exhibited an average value of 129.25 days and varied from 121.33 (PM-25) to 140.00 (RVM-2) days. Out of 20 genotypes JM-3 (125 days) and Pusa Jaikisan (134 days) showed early in the maturity. The plant height was recorded from 133.40 (PM-27) to 154.40 (JMM-991) cm with an average performance of 144.80 cm. Number of primary branches per plant ranged from 9.55 to 12.48 with a mean of 10.78. The genotype PM-27 (9.55) has minimum value and the genotype JM-2 (12.48) showed maximum value. Number of secondary branches per plant exhibited mean value of 16.09 and ranges from 13.37 to 19.71. The genotype PM-28 has minimum value and the genotype RVM-2 showed maximum value. This trait had an average of 57.45 with a range of a minimum 52.98 (Pusa vijay) and maximum being 61.18 (Varuna). Biological yield had a mean value of

66.7071.50g and varied from 67.63g (JM-3) to 74.90 g (RVM-1). Seed yield per plant ranged from 23.01(PM-27) to 34.86 (Varuna) g with a mean value of 29.66.

Table 1: Estimation of mean, range and different genetic parameters for different characters in 20 genotypes of Indian mustard

S. No.	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability (%) (Broad sense)	Genetic advance as % of mean 5%
			Min	Max				
1	Days to 50% flowering	51.85	49.00	57.00	4.86	4.83	98.60	9.88
2	Days to maturity	129.25	121.33	140.00	3.64	3.62	94.10	7.43
3	Plant height (cm)	144.8	133.4	154.40	8.51	8.51	93.70	17.52
4	Number of primary branches per plant	10.78	9.55	12.48	11.63	11.40	96.10	23.03
5	Number of secondary branches per plant	16.09	13.37	19.71	18.31	18.16	98.40	37.09
6	Number of siliquae on main raceme	57.45	52.98	61.18	4.73	4.73	94.80	9.72
7	Biological yield	71.5	67.63	74.90	3.54	3.50	97.60	7.11
8	Seed yield per plant (g)	29.66	23.01	34.86	15.70	15.69	95.90	32.31

Genotypic and Phenotypic Coefficient of Variation was classified as high (>20%), moderate (10-20%) and low (<10%). In the Table 4.2 (EI) summarized the genotypic and phenotypic coefficients of variation for yield and its contributing characteristics.

The high genotypic coefficient of variation (>20%) not recorded for any trait. Genotypic coefficient of variation estimated moderate for number of secondary branches per plant (18.31%) followed by seed yield per plant (15.69%) and number of primary branches per plant (11.63%), while it was low for plant height (cm) (8.51%), days to 50% flowering (4.83%), number of siliquae on main raceme (4.73%), days to maturity (3.62%) and biological yield (3.54%).

Broad sense heritability was categorized as high (>70 percent), moderate (50-70 percent) and low (<50 percent). The estimations of heritability in broad sense for yield and its component features reported in table 4.2 (EI). High heritability estimated for all the traits included in the study. Highest heritability recorded for Days to 50% flowering (98.6%) followed by number of secondary branches per plant (98.4%), Biological yield (97.6%), number of primary branches per plant (96.1%), Seed yield (g) (95.9%), number of siliquae on main raceme (94.8%), Days to maturity (94.1%) and Plant height (cm) (93.7%).

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^2, correlated means of characters were converted into standard uncorrelated means using Torcher'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.

Table 2: 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	-0.0882	0.0065	-0.0512	-0.0004	-0.0083	0.0025	0.0233	-0.0736
Days to maturity	-0.0002	0.0025	-0.0008	-0.0006	0.0002	0.0000	0.0010	-0.0551
Plant height (cm)	0.0332	-0.0193	0.0571	0.0186	0.0005	-0.0014	-0.0210	0.0284
Number of primary branches per plant	0.0005	-0.0305	0.0423	0.1301	0.0417	0.0295	-0.0044	0.3674
Number of secondary branches per plant	0.0049	0.0051	0.0005	0.0168	0.0523	0.0137	-0.0109	0.3223
Number of siliquae on main raceme	-0.0254	-0.0172	-0.0214	0.2027	0.2347	0.8937	0.0768	0.9376
Biological yield	0.0014	-0.0022	0.0020	0.0002	0.0011	-0.0005	-0.0055	0.0593

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, a greater 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 programmed. 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 per cent flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, number of siliquae on main raceme, biological yield per plant and seed yield per plant indicate divergent linear response to environmental changes. The S²d was not estimate significant for any variety, therefore the any variety did not find unstable there was all varieties were desirable and stable.

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