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Exploitation of genetic variability and trait association analysis for quantitative traits in Indian mustard (*Brassica juncea* L.)

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Abstract
The present investigation entitled "Exploitation of Genetic Variability and Trait Association Analysis for Quantitative Traits in Indian mustard (*Brassica juncea* L.)" was carried out during *Rabi* 2021-22 with three environments**.** 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. Field experiment conducted at the village Naugaya, Bharatpur, Rajasthan during Rabi season 2017-18 and 2018-19. Analysis of variance showed genotypes were highly significant for all the traits in EI, EII and EIII analysis of Indian mustard, suggesting presence of substantial amount of variability among the genotypes for all the traits under study. 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. Number of primary branches per plant and Seed yield per plant exhibited moderate PCV% and GCV % in EI, EII and EII of Indian mustard but number of secondary branches per plant exhibit moderate magnitude of PCV% and GCV% in EI 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. Genetic advance as percentage of mean was noted high for number of secondary branches per plant in E, EII and EIII. 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 siliquae on main raceme and biological yield in all the environments. In the present study the 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. Contribution of individual traits towards the total divergence was found maximum for plant height (cm), seed yield per plant (g), Number of secondary branches per plant, biological yield, Days to 50% flowering, Number of primary branches per plant, Number of siliquae on main raceme and Days to maturity in all the environments. Clustering pattern of genotypes confirmed the quantum of diversity present in the material under study. In EI, EII and EIII cluster I exhibited largest among all the clusters comprising of 18, 17 and 17 genotypes respectively in Indian mustard genotypes. Intra cluster distance was recorded maximum for cluster I whereas two clusters *viz*., cluster II and cluster III showed zero value in EI, Cluster I showed maximum intra cluster D2 value whereas three clusters *viz*., II, III and IV showed zero value in EII; Cluster I was most divergent, whereas three clusters *viz*., II, III and IV showed zero value for Intra cluster distance in EIII.

Keywords: ANOVA, GCV, PCV, correlation, path, divergence

Introduction
Indian mustard (*Brassica juncea*) is a naturally autogenous species. However, in this crop frequent out crossing varies from 5 to 30 percent depending upon the environmental conditions and variations of pollinating insect. Cytologically, Indian mustard is an amphidiploid (2n=36), derived from interspecific cross of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16) followed by natural chromosome doubling. The seeds are used as medicine, spices and as components in the preparation of salad, curries and pickles. The mustard is mainly grown for oil, the cake obtained after oil extractions widely used for cattle feeding. The unrefined oil is used for edible purpose in India. There is increasing interest in preparation of detoxified high functional mustard cake which is a good source of protein and minerals. The seeds of mustard contain 39 to 44% oil and 28 to 32% protein (Tomar *et.al*. 2015) [22].
Total area, production and yield of rapeseed-mustard in world during 2018-19 was36.59 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) (Project Coordinator Report, DRMR, 2020). In Madhya Pradesh, the total area, production and productivity are 0.78 million hectare, 1.11 million tonnes and 1422 Kg per hectare, respectively (Agriculture Statistics at a glance, 2019). In spite of the availability of appropriate technologies to increase per unit area production of mustard, the total cultivated areas under these remain static. The oil crops occupy an important place in the economy of Indian agriculture. In the oil seed scenario of India groundnut ranks first and rapeseed-mustard second. In India, Madhya Pradesh is the second largest rapeseed-mustard growing state after Rajasthan. The production from this meagre area increased manifold through the development of high yielding and oil content varieties and also free the challenge of loss in production due to biotic and abiotic factors like diseases, pests and moisture stress.

Method and Material

The experiment was laid out on Bharatpur 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 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. 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 "Exploitation of Genetic Variability and Trait Association Analysis for Quantitative Traits in Indian mustard (*Brassica juncea* L.)" 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.

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 twenty genotypes of Indian mustard for 8 attributes exhibited a broad range of variation, this trait showed a mean value of 42.13 days and varied from 38.79 (PM-27) to 47.38 (Pusa Mahak) days. Out of 20 genotypes PM-27 (38 days), JMM-927 (39 days) and RVM-2 (39 days) showed early in the days to 50% flowering. This trait varied from 116.00 (PM-25) to 136.33 (RVM-2) days with an average value of 126.87 days. Out of 20 genotypes PM-25 (116 days), JM-3 (120 days) and Pusa Jaikisan (121 days) showed early in the maturity. The degree of distribution for the plant height ranged from 153.46 (PM-27) to 222.02 (JMM-991) cm with an average performance of 197.84 cm.

Table1: Estimation of mean, range and different genetic parameters for different characters in 20 genotypes of Indian mustard

S. No.	Characters	Mean	Range		GCV (%)	PCV (%)	Heritability (%) (Broad sense)	Genetic advance as % of mean 5%
			Min	Max				
1	Days to 50% flowering	42.13	38.79	47.38	5.55	5.57	99.31	11.39
2	Days to maturity	126.87	116.00	136.33	3.82	3.82	99.31	7.82
3	Plant height (cm)	197.84	153.46	222.02	8.68	8.68	98.91	17.87
4	Number of primary branches per plant	2.17	1.46	3.45	22.94	27.34	70.40	39.63
5	Number of secondary branches per plant	7.27	4.68	11.39	28.13	29.29	92.30	55.67
6	Number of siliquae on main raceme	46.92	42.19	50.53	5.32	5.33	99.60	10.94
7	Biological yield	61.78	57.91	65.18	3.77	3.82	97.60	7.68
8	Seed yield per plant (g)	16.29	9.63	21.48	21.84	21.85	99.90	44.96

Genotype PM-27 (153.46) showed shortest in the height and genotype JMM-991 (222.02) showed tallest among the 20 genotypes. This trait ranged from 1.46 to 3.45 with a mean of 2.17. The genotype PM-27 (1.46) has minimum value and the genotype JM-2 (3.45) showed maximum value. This trait dispersed from 4.68 to 11.39 with a mean of 7.27. The genotype PM-28 (4.68) has minimum value and the genotype RVM-2 (11.39) showed maximum value. This trait had an average of 46.92 with a range of a minimum 42.19 (PM-27) and maximum being 50.53 (Varuna). This trait varied from 57.91g (JM-3) to 65.18g (RVM-1) with mean value 61.78g. This trait had mean value of 16.29g with a vary 9.63g (PM-27) to 21.48g (Varuna).

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	-0.1425	0.0082	-0.0830	-0.0071	-0.0197	0.0015	0.0383	-0.0708
Days to maturity	0.0011	-0.0189	0.0061	0.0035	-0.0012	0.0006	-0.0080	-0.0522
Plant height (cm)	0.0712	-0.0396	0.1223	0.0173	0.0020	0.0009	-0.0440	0.0397
Number of primary branches per plant	-0.0023	0.0086	-0.0066	-0.0468	-0.0136	-0.0166	0.0003	0.3231
Number of secondary branches per plant	0.0175	0.0081	0.0021	0.0367	0.1265	0.0427	-0.0290	0.3931
Number of siliquae on main raceme	-0.0098	-0.0281	0.0069	0.3198	0.3043	0.9005	0.0793	0.9316
Biological yield	-0.0060	0.0094	-0.0081	-0.0001	-0.0051	0.0020	0.0224	0.0593
Seed yield per plant (g)	-0.1425	0.0082	-0.0830	-0.0071	-0.0197	0.0015	0.0383	-0.0708

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 analyse 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 variances and covariances. 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. The estimates of genotypic and phenotypic path coefficients are furnished in table 4.5 (EI).

To calculate D^2, 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.

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