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Assessment of genetic variability, correlation and path analysis in Indian mustard (*Brassica juncea* L)

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Abstract

A study assessed the genetic variability, inter-relationship among yield components and their direct and indirect effect on seed yield in Indian mustard. Thirty-six genotypes of Indian mustard were evaluated in a randomized complete block design with three replications for 14 traits. A significant level of genetic variation, with minimal environmental impact, indicated consistent performance across genotypes. The analysis of variance showed that there were significant differences among all the traits across the treatments. The genotypic coefficient of variation, phenotypic coefficient of variation and heritability, and genetic advance were found to be higher for the harvest index, biological yield per plant, seed yield per plant, siliquae per plant and primary branches per plant. Genotypic correlation indicated that the siliquae per plant, protein content, primary branches per plant, biological yield per plant, secondary branches per plant, harvest index and oil content positively correlated with seed yield per plant. Path coefficient analysis revealed that harvest index, siliquae per plant, biological yield per plant, siliqua length and plant height positively affected seed yield. The genetic variability found in this set of breeding materials provides a basis for selection and offers valuable insights into selecting diverse parents for use in a hybridization program.

Keywords: *Genetic variability, GCV, heritability, PCV*

Introduction

Rapeseed-mustard is one of the most significant edible oilseed crops grown in the *Rabi* season. *Brassica* belongs to the Brassicaceae (Cruciferae) family and includes six cultivated species. The *Brassicaceae* family currently consists of 3709 species and 338 genera, and it is one of the ten most economically important plant families. An evolutionary relationship exists among the six cultivated *Brassica* species. Among them, *B. nigra* (n=8), *B. oleracea* (n=9) and *B. rapa* (n=10) are diploids. The rest of the three *B.* spp. Namely, *B. carinata* (n=17), *B. napus* (n=19), and *B. juncea* (n=18) are amphidiploids (Nagaharu, 1935). Indian mustard (*B.a juncea*) is a natural amphidiploid (2n=36) of *B. rapa* (2n=20) and *B. nigra* (2n=16). China is the centre of the diversity of *Brassica*, having originated in Asia (Vaughan, 1977). It originated in China and was brought to India, from where it spread to Afghanistan and other nations. 85–90 % of the crop is self-pollinated. However, the degree of cross-pollination varies from 4.0 to 16.6 % because of insects, particularly honeybees. Oilseed crops are mainly recognized as a major source of protein and fats in the human diet. Six edible (groundnut, rapeseed-mustard, soybean, sesame, sunflower and Niger) and non-edible (linseed and castor) oils comprise more than 85 % of the nation's vegetable oil supply. After oil palm and soybeans, rapeseed mustard is the third-largest oilseed crop in the world. The main nations that produce rapeseed-mustard are France, Germany, China and Canada. Oilseeds have a crucial role in the Indian economy, as proven by the impact of the yellow revolution. India accounts for 21.1 % of the world's rapeseed-mustard planted area but only 12.6 % of the world's total production (Choudhary *et al.,* 2023). India, with an area of 8.06 million hectares, 11.75 million tonnes of production and 1458 kg/ha productivity, ranks second in area and third in production in the rapeseed-mustard scenario of the world. (Anonymous, 2022-23). Rajasthan is the largest producer of rapeseed mustard, followed by Uttar Pradesh, Haryana, Madhya Pradesh, West Bengal, Gujarat and Assam. Rajasthan state ranks first in area and production, *i.e.*, 3.37 million hectares and 5.48 million tonnes, respectively, with an average productivity of 1627 kg/ha (Anonymous, 2022-23).

The success of a breeding program, particularly in improving a specific trait through selection, depends on the genetic variability level within a given crop's available germplasm. This is because the effectiveness of selection and, consequently, the rate of genetic improvement depends on the trait's heritability, the selection intensity and the expected genetic gain. Estimations of heritability and genetic advance for specific traits provide breeders with crucial information, allowing them to choose the most suitable breeding strategies to achieve their crop improvement goals. Different morphological traits have varying relationships with yield regarding the nature and magnitude of their influence. Despite showing continuous variation, these traits are also subject to environmental factors. Components with high heritability and a positive correlation with yield can be utilized for indirect selection, providing an alternative approach for yield improvement. However, when indirect associations among traits become complex, path coefficient analysis becomes the most effective method for identifying these relationships direct and indirect causes. This analysis helps distinguish between actual correlations and those that might be inflated due to hidden variables or complex interactions. Therefore, understanding various components direct and indirect effects on yield is crucial for selecting high-yielding genotypes. Considering these points, the current study was conducted using a selection of widely cultivated and newly developed varieties of Indian mustard.

Materials and Methods

The experiment was carried out during *Rabi*, 2022-23 at Agronomy Farm, SKN College of Agriculture, Jobner, Jaipur, Rajasthan. Thirty-six Indian mustard advanced lines/ genotypes were grown in randomized complete block design with three replications. Row-to-row and plant-to-plant distances were 30 and 10 cm, respectively. The data was recorded on fourteen characters, *viz.,* days to 50 % flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, siliquae per plant, siliqua length, seeds per siliqua, 1000-seed weight, seed yield per plant, biological yield per plant, harvest index, oil content, protein content. Data on days to 50 % flowering, days to maturity, protein content, oil content and 1000-seed weight were recorded on a whole plot basis. Data on the remaining morphological traits were collected from ten randomly selected, competitive plants from each plot across all three replications. The recommended agricultural practices were followed to ensure healthy crop growth.

The analysis of variance (ANOVA) was performed using standard statistical procedures. The phenotypic and genotypic coefficients of variation were calculated following Burton's (1954) method, while the genotypic and phenotypic correlation coefficients were computed according to the approach described by Johnson *et al.* (1955). Path coefficient analysis was conducted using correlation coefficients, as suggested by Dewey and Lu (1959). In this study, path coefficient analysis was performed with seed yield per plant as the dependent variable and the other observed traits as independent variables.

Results and Discussion

Variability within a crop population is crucial for advancing crop breeding programs (Hasan *et al*., 2006). The analysis of variance for 14 yield and yield-attributing traits across 36 mustard germplasm genotypes, as shown in Table 1 indicated that the mean sum of squares for genotypes was highly significant for all traits studied. This shows a substantial degree of genetic variation among the genotypes for all the traits under study providing an opportunity for further examination and analysis of variability parameters of Indian mustard. The estimates of the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and genetic

Table1: Analysis of variance for seed yield and yield attributing traits in mustard genotypes

Traits	Replication (2)	Genotypes (35)	Error (70)
Days to 50% flowering	3.3	25.1**	1.2
Days to maturity	0.3	19.0**	9.3
Plant height (cm)	3.6	212.7**	89.2
Primary branches per plant	0.7	1.6**	0.2
Secondary branches per plant	0.5	15.3**	3.6
Siliquae per plant	117.9	5373.9**	228.3
Siliqua length (cm)	0.4	0.5**	0.1
Seeds per siliqua	1.5	2.4**	0.9
1000-seed weight (g)	0.01	0.1**	0.01
Biological yield per plant (g)	0.7	685.7**	5.1
Harvest index (%)	0.01	54.6**	2.9
Oil content (%)	0.1	3.3**	0.1
Protein content (%)	0.01	7.5**	0.1
Seed yield per plant (g)	0.1	18.7**	1.2

*, ** = Significant at 5 % and 1 % levels, respectively.

Table 2: Estimates of genetic parameters in mustard genotypes

Traits	Mean	Range		PCV (%)	GCV (%)	H^2(bs) (%)	Genetic Advance	GA 5%
		Minimum	Maximum					
Days to 50% flowering	50.2	44.0	55.0	5.6	6.0	85.9	4.5	10.7
Days to maturity	135.2	131.3	141.3	1.3	2.6	25.5	5.3	1.3
Plant height (cm)	187.5	173.0	207.5	3.4	6.0	31.5	1.8	3.9
Primary branches per plant	6.0	4.8	8.3	11.2	14.2	62.3	17.4	18.3
Secondary branches per plant	20.8	16.2	24.3	9.4	13.1	51.9	1.1	14.0
Siliquae per plant	303.8	236.4	389.6	13.6	14.5	88.2	22.9	26.3
Siliqua length (cm)	5.5	4.3	6.5	6.7	9.7	47.7	80.1	9.5
Seeds per siliqua	12.6	11.2	14.5	5.5	9.5	33.5	0.5	6.5
1000-seed weight (g)	5.0	4.7	5.7	4.2	5.5	60.2	0.8	6.8
Biological yield per plant (g)	73.7	49.0	111.4	20.4	20.6	97.7	0.3	41.6
Harvest index (%)	19.6	12.7	28.3	21.1	22.9	85.4	30.6	40.3
Oil content (%)	39.6	37.1	41.5	2.6	2.8	84.5	7.9	4.9
Protein content (%)	21.2	17.6	23.4	7.4	7.5	96.4	1.9	15.0
Seed yield per plant (g)	14.0	10.4	20.1	17.2	18.9	82.7	3.2	32.2

Table 3: Genotypic correlation coefficient between different traits in mustard genotypes

Traits	DM	PH	NPBPP	SBPP	SPP	SL	SPS	TW	BY	HI	OC	PC	SYPP
DF	-0.16	-0.18	-0.59	0.27**	0.20*	0.24**	0.40**	-0.13	0.22*	0.11	0.30**	0.06	-0.17
DM	1.00	0.39**	-0.37**	-0.17	-0.29**	-0.39**	0.35**	0.31**	-0.17	-0.75	-0.28**	-0.20*	-0.25**
PH		1.00	0.05	-0.18	-0.18	-0.29**	0.36**	-0.28**	-0.19*	0.06	-0.14	-0.12	-0.78
NPBPP			1.00	0.41**	0.48**	-0.17	-0.16	-0.29**	0.20*	0.22*	0.12	0.39**	0.53**
SBPP				1.00	0.59**	-0.19*	0.36**	0.26	0.29**	0.09	0.21*	0.32**	0.38**
SPP					1.00	0.04	0.02	-0.05	0.40**	0.16	0.14	0.46**	0.68**
SL						1.00	-0.04	0.54**	0.43**	-0.16	0.03	0.15	-0.04
SPS							1.00	-0.20*	-0.44**	-0.23*	-0.38**	-0.20*	-0.44**
TW								1.00	0.14	-0.27**	0.19	-0.12	-0.10
BY									1.00	-0.66**	0.12	0.09	0.44**
HI										1.00	0.13	0.50**	0.38**
OC											1.00	0.23*	0.29**
PC												1.00	0.65**

*, ** = Significant at 5 % and 1 % levels, respectively. G = Genotypic level, DF: Days to 50 % flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Primary branches per plant, SBPP: Secondary branches per plant, SPP: Siliquae per plant, SL: Siliqua length (cm), SPS: Seeds per siliqua, TW: 1000-seed weight (g), BY: Biological yield per plant (g), HI: Harvest index (%), OC: Oil content (%), PC: Protein content (%), SYPP: Seed yield per plant (g).

Table 4: Direct (diagonal) and indirect effects of yield components on seed yield per plant at genotypic level in mustard genotypes

Traits	DF	DM	PH	NPBPP	SBPP	SPP	SL	SPS	TW	BY	HI	OC	PC	SYPP
DF	-0.034	-0.004	-0.002	-0.012	-0.016	-0.005	0.03	0.005	-0.012	-0.269	0.143	0.005	-0.007	-0.178
DM	0.006	0.02	0.044	-0.029	-0.01	-0.006	-0.049	0.004	0.03	-0.199	-0.096	0.005	0.024	-0.251**
PH	0.001	0.01	0.11	0.00	-0.011	-0.004	-0.036	0.004	-0.027	-0.23	0.086	0.002	0.015	-0.078
NPBPP	0.005	-0.009	0.001	0.07	0.024	0.011	-0.02	-0.002	-0.028	0.239	0.279	-0.002	-0.047	0.526**
SBPP	0.009	-0.004	-0.021	0.031	0.05	0.013	-0.024	0.004	0.002	0.346	0.012	-0.004	-0.039	0.384**
SPP	0.007	-0.007	-0.021	0.037	0.034	0.22	0.001	0.00	-0.005	0.476	0.199	-0.002	-0.056	0.685**
SL	-0.008	-0.01	-0.033	-0.013	-0.011	0.00	0.12	-0.003	0.00	0.646	-0.543	0.00	0.00	0.147
SPS	-0.014	0.009	0.041	-0.013	0.021	0.00	-0.036	0.01	0.018	-0.196	-0.258	0.008	0.028	-0.381**
TW	0.004	0.008	-0.032	-0.023	0.001	-0.001	0.00	0.002	0.09	0.171	-0.341	-0.003	0.015	-0.104
BY	0.008	-0.004	-0.022	0.015	0.017	0.009	0.067	-0.002	0.014	0.18	-0.838	-0.002	-0.012	0.437**
HI	-0.004	-0.002	0.008	0.017	0.001	0.004	-0.053	-0.002	-0.025	-0.78	0.37	-0.002	-0.06	0.376**
OC	0.01	-0.007	-0.016	0.009	0.012	0.003	-0.002	-0.005	0.018	0.146	0.169	-0.018	-0.028	0.293**
PC	-0.002	-0.005	-0.014	0.030	0.019	0.01	0.00	-0.003	-0.012	0.114	0.634	-0.004	-0.121	0.648**

*, ** = Significant at 5 % and 1 % levels, respectively. G = Genotypic level, DF: Days to 50 % flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Primary branches per plant, SBPP: Secondary branches per plant, SPP: Siliquae per plant, SL: Siliqua length (cm), SPS: Seeds per siliqua, TW: 1000-seed weight (g), BY: Biological yield per plant (g), HI: Harvest index (%), OC: Oil content (%), PC: Protein content (%), SYPP: Seed yield per plant (g).

advance (GA) as a percentage of the mean are presented in Table 2. The GCV, PCV, heritability and GA were found to be higher for the harvest index, siliqua length, siliquae per plant and primary branches per plant. Similar findings were reported by Singh *et al.* (2011), Gupta *et al.* (2019), Patel *et al.* (2019), Rout *et al.* (2019) and Awasthi (2020). High heritability combined with a high genetic advance as a percentage of the mean was observed for traits such harvest index, biological yield per plant, seed yield per plant, siliquae per plant and primary branches as per plant, indicating the influence of additive gene action in the inheritance of these traits, suggesting that they can be enhanced through straight forward selection methods. Similar observations were discussed by Shekhawat *et al*. (2014), Devi (2018), Rout *et al*. (2019) and Pradhan *et al*. (2021).

The genotypic correlation analysis of 14 quantitative traits of Indian mustard is presented in Table-4, illustrating the relationships between pairs of traits and between seed yield and other parameters at both 1 % and 5 % significance levels. Traits like siliquae per plant (0.68), protein content (0.65), primary branches per plant (0.53), biological yield per plant (0.44), secondary branches per plant (0.38), harvest index (0.38) and oil content (0.29) all exhibited significant and positive correlations with seed yield per plant. Similar results were obtained by Singh *et al.* (2011), Begum *et al.* (2018), Kumar *et al.* (2019) and Laghari *et al.* (2020). Siliquae per plant showed a strong positive significant correlation with days to 50 % flowering, primary branches per plant, secondary branches per plant, biological yield per plant, protein content and seed yield per plant; siliqua length showed a strong positive significant correlation with days to 50 % flowering, 1000-seed weight and biological yield per plant; seeds per siliqua showed a strong positive significant correlation with days to 50 % flowering, days to maturity, plant height and secondary branches per plant; 1000-seed weight showed a strong positive significant correlation with days to maturity and siliqua length; biological yield per plant showed a strong positive significant correlation with days to 50 % flowering, primary branches per plant, secondary branches per plant, siliquae per plant, siliqua length and seed yield per plant; oil content showed a strong positive significant correlation with days to 50 % flowering, secondary branches per plant, protein content and seed yield per plant and protein content showed a strong positive significant correlation with primary branches per plant, secondary branches per plant, siliquae per plant, harvest index, oil content and seed yield per plant. These results suggest that selecting plants based on these traits is advantageous for crop improvement. Similar conclusions were also drawn by Tiwari (2019) and Chakraborty *et al.* (2021). The impact of genotypic association on seed yield per plant was analyzed in terms of direct and indirect effects (Table 4), indicating that the harvest index (0.35) showed the highest positive direct effect on seed yield per plant followed by siliquae per plant (0.22), biological yield per plant (0.18), siliqua length (0.12) and plant height (0.11). Thus, selecting for these traits can lead to an increase in seed yield. Similar findings were reported by Lodhi *et al*. (2014) and Roy (2018). A positive association between desirable characteristics is advantageous, enabling all traits to develop concurrently. On the other hand, a negative correlation would hinder the simultaneous expression of multiple high-value traits requiring some form of trade-off or compromise in such scenarios.

Conclusion

Based on these findings, which consider the genotypic coefficient of variation, phenotypic coefficient of variation, heritability alongside genetic advance and direct effects on seed yield per plant, were recorded higher for the harvest index, biological yield per plant, seed yield per plant, siliquae per plant and primary branches per plant. It suggests that greater emphasis should be placed on these traits when selecting for crop improvement. At the genotypic level, siliquae per plant, protein content, primary branches per plant, biological yield per plant, secondary branches per plant, harvest index and oil content had significant and positive correlations with seed yield per plant, suggesting that straightforward selection could be advantageous for these traits. Path coefficient analysis revealed that harvest index, siliquae per plant, biological yield per plant, siliqua length and plant height positively affected seed yield per plant. Thus, based on this study, selection indices for crop development programs can be established by incorporating the identified traits.

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