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Genetic parameters and correlation studies in Indian mustard (*Brassica juncea* L.)

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Abstract

Present study carried out with total 154 genotypes including 150 test genotypes and four checks (RH-1566, RH-1499-30, RH-749 and RH-8812) of Indian mustard. These genotypes were evaluated for seed yield and its yield components for eleven characters during *rabi* season of 2020-21 at CCS Haryana Agricultural University, Hisar. Analysis of variance showed highly significant genotypic difference for all the studied traits. The maximum variability (21.2%) was recorded for test weight and minimum for oil content (0.8%). The two characters namely, secondary branches/plant (91.7%) and test weight (89.6%) had very high broad sense heritability while, genetic advance was relatively high for test weight (41.4%), number of secondary branches/plant (37.2%) and seed yield/plant (31.6%). The results revealed that plant height, number of primary branches/plant, number of secondary branches/plant, main shoot length, number of siliqua on main shoot, siliquae length, number of seeds per siliqua and test weight have significant positive association with seed yield/plant, while path analysis revealed that number of primary branches/plant, number of secondary branches/ plant and siliqua length had the highest positive direct effects on seed yield/plant. All the traits have showed high heritability. The characters identified above as indirect yield components in formulating effective selection strategy for developing high yielding mustard genotypes.

Keywords: *Correlation, genetic advance, heritability, path analysis*

Introduction

Brassica juncea (L.) Czern & Coss. (AABB, 2n = 36) commonly known as ‘Indian mustard’ is an important oilseed crop. It is a naturally occurring amphidiploid species that resulted from the mating of *B. rapa* (AA, 2n = 20) and *B. nigra* (BB, 2n = 16). Rapeseed-mustard is commonly cultivated in India, Canada, China, Germany, France, Poland and Japan. It most commonly comes under rapeseed-mustard along with other closely related cultivated *Brassica* species viz; gobhi sarson, brown mustard, yellow mustard, taramira, toria, Ethiopian mustard or karan rai and black mustard. Indian mustard alone is grown under more than 80% of the total rapeseed and mustard area. It covers an area of 6.70 million ha with a production of 10.21 million tonnes and the average productivity of 1524 kg/ha in India during 2020-21 (Anonymous, 2021). Breeding techniques to produce high yielding cultivars depend on the type and degree of variation for various yield components. The assessment of genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense - h^2bs), and genetic advance (GA %) is a prerequisite for making effective selection. Yield is a complex trait, polygenic in inheritance, more prone to environmental fluctuations than yield contributing traits such as branches per plant, seeds per siliquae, main shoot length, number of seeds per siliquae and 1000-seed weight. Thus, comprehensive selection based on seed yield vis-à-vis component traits is more effective. Although, this crop contains some information relating to these factors, it is well known that genetic variability and correlation coefficients differ from one material to another. In order to produce high yielding recombinants for the creation of high yielding cultivar(s) of Indian mustard that are suited to this region for the benefit of farmers, the current investigation is carried out to assess the nature and magnitude of genetic variability, their inter-relationships, and contribution towards seed yield.

Materials and Methods

Experimental material comprised of 154 Indian mustard genotypes (150 test genotypes and four check) selected from released cultivars, advanced breeding lines and germplasm lines available in different brassica breeding institutions. All the 154 genotypes were grown in augmented complete block design (with ten blocks) where checks (four checks viz; RH-1566, RH-1499-30, RH-749 and RH-8812) were replicated 10 times after every 15 genotypes. All the experiment were conducted with two rows of 4.0 m length at 45 cm row to row and 15 cm plant to plant spacing during *rabi* 2020-21 at Oilseeds Research Farm, CCS Haryana Agricultural University, Hisar. All the recommended cultural package of practices was followed from sown to harvesting the crop. The data were collected on the following 12 traits *viz.* days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of secondary branches/plant, main shoot length, number of siliquae on main shoot, siliqua length, number of seeds/siliqua, test weight, oil content and seed yield/plant. Oil content was determined through soxhlet method of oil extraction. These traits were computed using mean data and after computing, each character was subjected to estimate genotypic correlation coefficients (Al-Jibouri *et al*., 1958) and genetic parameters were estimated as per Singh and Chaudhary (1985). ANOVA as per augmented design (Federer, 1956) to obtain adjusted trait values for four checks as well as for 150 test genotypes were analysed using OPSTAT software. All other the statistical analysis was performed using R statistical software package.

Results and Discussion

The analyses of variances were carried out using data recorded for morphological traits with four check varieties and 150 genotypes sown in augmented block design during *rabi* 2020-21 (Table 1). Analysis of variance showed highly significant (P = 0.01) genotypic difference for all the studied traits. This indicated the presence of sufficient level of genetic variability among the evaluated genotypes for seed yield and its component traits, which could be exploited in mustard improvement programs in India. Pandey *et al.* (2020) and Choudhary *et al.* (2021) reported similar findings of significant genetic variability for various yield and its component traits in the 40 and 65 Indian mustard genotypes, respectively.

The estimates of variance components, broad-sense heritability and genetic advance for seed yield and its component traits are presented in Table 2. The analysis of genetic variance revealed significant differences among the genotypes for most of the characters except oil content, indicating presence of sufficient variability. Estimates of phenotypic coefficient of variation varied from oil content (0.9%) to test weight (22.4%) and GCV estimates also showed similar trend for the these traits. The result showed a close correspondence between the phenotypic and genotypic variance for all the characters indicating stable expression of attributes and absence of high environmental influence. Hence, these characters are more suitable for direct selection procedure. Similar results were reported by Dilip *et al*. (2016), Pandey *et al.* (2020) and Choudhary *et al.* (2021). Singh (2001) classified heritability estimates (H^2bs) as low (<40%), moderate (40-

Table 1: Analysis of variance for 12 morphological traits in Indian mustard

Source of Variation	df	DF	DM	PH	NPB	NSB	MSL	NSMS	SL	NSS	OC	TSW	SYP
Block (ignoring treatments	9	43.7**	45.0**	133.2**	3.9**	18.7**	218.5**	41.6**	3.1**	0.6**	0.1**	10.9**	145.9**
Genotypes (eliminating blocks)	153	9.4**	12.0**	95.2**	0.4**	4.3**	44.5**	23.7**	0.3**	0.6**	0.1**	0.8**	12.2**
Checks	3	29.9**	0.1	325.7**	0.2*	6.1**	36.4	18.8*	1.4**	2.6**	0.0	2.0**	123.0**
Genotypes + Checks vs Varieties	150	9.0**	12.3**	90.6**	0.4**	4.3**	44.7**	23.8**	0.3**	0.5**	0.1**	0.8**	10.0**
Error	27	1.9	2.4	19.2	0.1	0.4	16.6	6.4	0.1	0.1	0.0	0.1	3.3

*Significant at P = 0.05, **Significant at P = 0.01; DF-Days to 50% flowering; DM-Days to maturity; PH-Plant height (cm); NPB-No. of primary branches/plant; NSB-No. of secondary branches/plant; MSL-Main shoot length (cm); NSMS-No. of siliquae on main shoot; SL-Siliqua length (cm); NSS-No. of seeds/siliqua; OC-Oil content; TSW-1000-seed weight (g); SYP-Seed yield/plant (g).

59%), moderately high (40-59%) and very high (>80%). In present study, moderately high heritability was observed for plant height, main shoot length, number of siliquae on main shoot and oil content while, high heritability was observed for days to 50% flowering, days to maturity, number of primary branches/plant, number of secondary branches/plant, siliqua length, number of seeds/siliqua, test weight and seed yield/plant. GCV along with heritability estimate gave the precise picture of genetic gain to be exploited through selection as suggested by Burton (1952). High values of GCV coupled with heritability were observed for test weight, seed yield per plant, siliquae length, number of primary branches per plant and number of secondary branches per plant, indicating that additive gene action might play significant role in the expression of these characters and selection would be rewarding in further improvement of these characters. In rest of the characters, there is low GCV with high heritability and improvement is not possible through selection might be due to non-additive gene action which matched with the findings of Singh *et al.* (2011), Pandey *et al.* (2020) and Choudhary *et al.* (2021). This implies that the expected gain from selection would be high if these traits will use as selection criteria for improving seed yield. The high heritability estimates also suggest that these traits are more resilient to environmental influences. Similar to the current study, several earlier investigations in Indian mustard revealed moderate to high heritability for yield and its component traits. (Tiwari *et al.*, 2019; Ray *et al.*, 2019; Patel *et al.*, 2021).

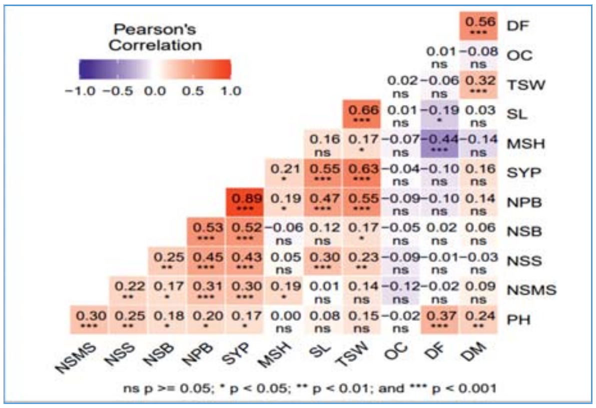
Table 2**:** Estimate of mean, range, phenotypic and genotypic coefficient of variation, heritability and genetic advance for twelve characters in Indian mustard

Trait	Mean	Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability (h^2bs)	Genetic advance in % of mean
DF	51.0	6.6	6.0	82.8	11.3
DM	138.5	2.6	2.3	81.4	4.4
PH	204.8	4.6	4.0	78.4	7.4
NPB	5.4	14.8	14.0	89.4	27.3
NSB	11.8	19.7	18.8	91.7	37.2
MSL	82.0	9.1	7.6	70.2	13.2
NSMS	52.2	9.7	8.4	75.4	15.2
SL	4.9	14.5	13.4	85.5	25.6
NSS	14.1	5.4	5.0	85.8	9.5
OC	38.8	0.9	0.8	78.3	1.5
TSW	5.2	22.4	21.2	89.6	41.4
SYP	22.7	18.8	17.0	81.5	31.6

Where, DF-Days to 50% flowering; DM-Days to maturity; PH-Plant height (cm); NPB-No. of primary branches/plant; NSB-No. of secondary branches/plant; MSL-Main shoot length (cm); NSMS-No. of siliquae on main shoot; SL-Siliqua length (cm); NSS-No. of seeds/siliqua; OC-Oil content; TSW-1000-seed weight (g); SYP-Seed yield/plant (g).

Genetic gain under selection for yield and its component traits are depends on the extent of genetic advance as percent of 5% mean for particular trait. Johnson *et al.* (1955) classified genetic advance as percentage of mean (GAM) values as low (0-10%), moderate (10-20%) and high (>20%). Genetic advance in % of mean ranged from 1.5 % (oil content) to 41.4% (test weight). Genetic advance was relatively high for number of primary branches/plant, number of secondary branches/plant, siliquae length, test weight and seed yield/plant. Three characters viz; days to 50% flowering, main shoot length (cm) and number of siliqua on main shoot showed moderate genetic advance while, days to maturity, plant height, number of seeds/siliquae and oil content showed low genetic advance.

The results of genotypic correlation coefficients between yield and its component traits have been presented in Fig. 1. Seed yield in mustard is the result of many component traits which are interdependent on each other. The present study found positive and significant correlation between seed yield/plant and plant height (0.16*), number of primary branches/plant (0.89**), number of secondary branches/plant (0.52**), main shoot length (0.20*), number of siliqua on main shoot (0.30**), siliquae length (0.54**), number of seeds per siliquae (0.43**) and test weight (0.63**). This indicates that indirect selection through these component traits will result in yield improvement of Indian mustard. Similarly, many previous studies (Kumar *et al.* 2016; Priyamedha *et al.,* 2018; Monika *et al.,* 2019; Pandey *et al.,* 2020;



	NSMS	NSS	NSB	NPB	SYP	MSH	SL	TSW	OC	DF	DM
DF											0.56 ***
OC										0.01 ns	−0.08 ns
TSW									0.02 ns	−0.06 ns	0.32 ***
SL								0.66 ***	0.01 ns	−0.19 *	0.03 ns
MSH							0.16 ns	0.17 *	−0.07 ns	−0.44 ***	−0.14 ns
SYP						0.21 *	0.55 ***	0.63 ***	−0.04 ns	−0.10 ns	0.16 ns
NPB					0.89 ***	0.19 *	0.47 ***	0.55 ***	−0.09 ns	−0.10 ns	0.14 ns
NSB				0.53 ***	0.52 ***	−0.06 ns	0.12 ns	0.17 *	−0.05 ns	0.02 ns	0.06 ns
NSS			0.25 **	0.45 ***	0.43 ***	0.05 ns	0.30 ***	0.23 **	−0.09 ns	−0.01 ns	−0.03 ns
NSMS		0.22 **	0.17 *	0.31 ***	0.30 ***	0.19 *	0.01 ns	0.14 ns	−0.12 ns	−0.02 ns	0.09 ns
PH	0.30 ***	0.25 **	0.18 *	0.20 *	0.17 *	0.00 ns	0.08 ns	0.15 ns	−0.02 ns	0.37 ***	0.24 **

ns $p >= 0.05$; * $p < 0.05$; ** $p < 0.01$; and *** $p < 0.001$

Fig. 1: Correlation coefficient for twelve characters in Indian mustard

Where, DF-Days to 50% flowering; DM-Days to maturity; PH-Plant height (cm); NPB-No. of primary branches/plant; NSB-No. of secondary branches/plant; MSL-Main shoot length (cm); NSMS-No. of siliquae on main shoot; SL-Siliqua length (cm); NSS-No. of seeds/siliqua; OC-Oil content; TSW-1000-seed weight (g); SYP-Seed yield/plant (g).

Choudhary *et al.*, 2022) showed the positive significant association of various component traits with seed yield in Indian mustard. Besides this, days to 50% flowering (-0.10^{NS}), days to maturity (0.15^{NS}) and percent oil content (-0.03^{NS}) exhibits negative correlation with seed yield. The negative association with days to 50% flowering and days to maturity is desirable because early flowering provide shorter vegetative phase and longer reproductive phase with more grain filling time while, the development of high yielding and short duration varieties is the prime objective of breeders in Indian mustard. Besides this, test weight was found positively and significantly associated with days to maturity (0.32**), number of primary branches/plant (0.55**), number of secondary branches/plant (0.17*), main shoot length (0.17*), siliquae length (0.65**) and number of seeds per siliquae (0.23**). Bold seeded trait is desirable and preferable acceptable by the farmers.

The estimates of direct and indirect effects of different character on grain yield per plant are presented in Table 3. Sometime correlations due to pleiotropic effects, gene linkages and environmental influences. As a result, from a practical and decision- making standpoint, it was preferable to determine the direct phenotypic effects using the most appropriate selection criteria. Path analysis partitioning the total correlation coefficient into indirect and direct effects, and measures the importance of the casual factor individually, which is useful in identifying target traits for yield improvement (Mengistu *et al.*, 2020). In the present study, number of primary branches/plant (0.67), number of secondary branches/ plant (0.13) and siliqua length (0.10) had the high positive direct effects on seed yield/plant. This indicates the major importance of these traits for direct selection for improvement of seed yield/plant. The remaining traits also showed the positive direct effects except plant height. The high direct effects of number of primary branches/plant was due to indirect effects of plant height (0.13), number of secondary branches/plant (0.35), main shoot length (0.12), number of siliquae on main shoot (0.20), siliqua length (0.31), number of seeds/siliqua (0.30) and 1000-seed weight (0.37). These traits are useful in indirect selection for

Table 3: Direct (diagonal) and indirect effects (above and below diagonal) of component traits on seed yield/plant in Indian mustard genotypes

Trait	DF	DM	PH	NPB	NSB	MSL	NSMS	SL	NSS	OC	TSW
DF	0.04	0.00	-0.02	-0.07	0.00	-0.02	0.00	-0.02	0.00	0.00	-0.01
DM	0.02	0.00	-0.01	0.09	0.01	-0.01	0.00	0.00	0.00	0.00	0.05
PH	0.01	0.00	-0.06	0.13	0.02	0.00	0.02	0.01	0.01	0.00	0.02
NPB	0.00	0.00	-0.01	0.67	0.07	0.01	0.02	0.05	0.02	0.00	0.09
NSB	0.00	0.00	-0.01	0.35	0.13	0.00	0.01	0.01	0.01	0.00	0.03
MSL	-0.02	0.00	0.00	0.12	-0.01	0.05	0.01	0.02	0.00	0.00	0.03
NSMS	0.00	0.00	-0.02	0.20	0.02	0.01	0.06	0.00	0.01	0.00	0.02
SL	-0.01	0.00	0.00	0.31	0.01	0.01	0.00	0.10	0.01	0.00	0.11
NSS	0.00	0.00	-0.01	0.30	0.03	0.00	0.01	0.03	0.04	0.00	0.04
OC	0.00	0.00	0.00	-0.06	-0.01	0.00	-0.01	0.00	0.00	0.03	0.00
TSW	0.00	0.00	-0.01	0.37	0.02	0.01	0.01	0.07	0.01	0.00	0.16

Residual – 0.15

Where, DF-Days to 50% flowering; DM-Days to maturity; PH-Plant height (cm); NPB-No. of primary branches/plant; NSB-No. of secondary branches/plant; MSL-Main shoot length (cm); NSMS-No. of siliquae on main shoot; SL-Siliqua length (cm); NSS-No. of seeds/siliqua; OC-Oil content; TSW-1000-seed weight (g); SYP-Seed yield/plant (g).

improvement of seed yield in Indian mustard. Previously, Kumar *et al.* (2019) and Choudhary *et al.* (2022) also reported the similar finding in Indian mustard.

Conclusion

The examined genotypes showed sufficient variability for all the traits with maximum was recorded for test weight and minimum for oil content. The heritability was high for all the traits while, genetic advance was relatively high for test weight, number of secondary branches/plant and seed yield/plant. High heritability accompanied with high genetic advance indicates that heritability likely due to additive gene effects and selection may be effective. Seed yield/plant was positively and significantly associated with plant height, number of primary branches/plant, number of secondary branches/plant, main shoot length, number of siliqua on main shoot, Siliquae length, number of seeds per siliquae and test weight. The number of primary branches/plant had maximum direct effect on seed yield/plant indicating that direct selection based on number of primary branches/plant and other indirectly associated traits will be beneficial in the selection of high seed yield genotypes. Thus, selection of genotypes based on the associated character will be useful in development of desirable breeding lines.

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