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Genetic Variability, Heritability and Correlation Studies in Indian Mustard (*Brassica juncea*)

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Abstract

The present research was carried out with an aim to study the genetic variability and correlation between traits and to determine the best selection criteria for yield improvement in rapeseed (*Brassica juncea* L.). Fifty genotypes of *Brassica juncea* were sown at AICRP on Mustard at Nagpur (M.S) during the years 2020- 2021 to evaluate the components of variability (genotypic and phenotypic), heritability, correlation (genotypic and phenotypic) for yield and various yield components. High to moderate values of GCV and PCV were recorded for yield ha^{-1}, days to 50% flowering, plant height and number of siliquae $plant^{-1}$ indicates that there is substantial variation is present but it also suggest that there is scope to enrich variation for these characters. High heritability coupled with high genetic advance as percent mean was observed for number of siliquae $plant^{-1}$, plant height and days to 50% flowering. This indicates the lesser influence of environment in expression of this characters and prevalence of additive gene action in their inheritance. Naturally, selection based on phenotypic observations for these characters would be effective. Similarly, highly significant positive genotypic and phenotypic correlation was observed between number of siliquae $plant^{-1}$ and seed yield ha^{-1}. Therefore, number of siliquae $plant^{-1}$ is playing important role in indirect selection for yield.

Key words : *Brassica juncea, phenotypic, genotypic correlation, heritability, genetic variability.*

Introduction

Agricultural sector plays a significant role in India's social security and overall economic welfare. Rapeseed-mustard is the third most important crop in the world after soybean and palm oil. Among the seven edible oilseed cultivated in India, rapseed-mustard (*Brassica* spp.) contributes 28.6% in the total production of oilseeds. In India, it is the second most important edible oilseed after groundnut sharing 27.8% in the India's oilseed economy. Indian mustard is one of the most important oilseed crops of India which occupies considerably large area among the Brassica group of oilseed crops. It is self-pollinated crop but around 2-15% of cross pollination occurs due to entomophilly. For efficient selection, estimation of parameters phenotypic and genotypic coefficients of variation, heritability and genetic advance in pre-requisite.

The breeding strategy to derive high yielding cultivar depends upon the nature and magnitude of variation for different yield components. Availability of genetic variability is the prerequisite for any breeding programme. Therefore, assessment of genetic parameters like genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV) and heritability (h^2) are pre-requisite for making effective selection. Hence, the important objective in mustard improvement is oriented to develop varieties which have high yielding potential.

Materials and Methods

Fifty Indian mustard genotypes were sown in randomized block design with two replications at Research Farm of AICRP on Mustard, College of Agriculture Nagpur, Maharashtra during Rabi season 2020-2021. Recommended agronomical practices and plant protection measures were adopted to raise a healthy crop. Observations were recorded in each genotype along with each replication for seven characters. Data was recorded on whole plot basis for days to 50% flowering, days to maturity and seed yield per hectare whereas for plant height, primary branches $plant^{-1}$, number of siliquae $plant^{-1}$ and 1000 seed weight from individual randomly selected plants. The mean values of each genotype were computed for statistical analysis.

The data recorded were subjected to various statistical and biometrical analysis viz., Analysis of variance (1), estimation of genotypic and phenotypic coefficient of variation (2) and estimation of heritability in broad sense (3). Phenotypic and genotypic correlation co-efficients for seed yield were calculated for each pair of traits as described by (4).

Results and Discussion

The analysis of variance (Table-1) for the design of the experiment indicated highly significant differences for all the characters except for days to maturity. This suggested

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Table-1 : Analysis of variance for yield and its contributing characters in Indian mustard (*Brassica juncea*).

Source	DF	Days to 50% flowering	Days to maturity	Plant height. (cm)	No. of branches plant^{-1}	No. of siliquae plant^{-1}	1000 seed weight. (gm.)	Yield ha^{-1} (kg)
Replications	1	32.49	77.44	52.13	0.06	1346.89	0.06	45287.66
Treatments	49	58.75**	19.75	944.40**	0.23**	8113.60**	0.60**	127476.13**
Error	49	8.82	14.50	151.87	0.07	633.66	0.17	33269.25

**Significant -@ 15 and *Significant -@ 5%

Table-2 : Genetic parameters estimates for yield and its contributing characters in Indian mustard (*Brassica juncea*).

Parameters	Days to 50% flowering	Days to maturity	Plant height. (cm)	No. of branches plant$_{-1}$	No. of siliquae plant^{-1}	1000 seed weight. (gm.)	Yield ha^{-1} (kg)
Mean	43	124	149	3	200	5	1826
Min.	31	110	114	3	118	3	1275
Max.	60	130	204	5	392	6	2684
Genotypic Covariance	24.91	2.63	396.27	0.08	3739.97	0.21	47103.44
Phenotypic Covariance	33.83	17.13	548.13	0.15	4373.63	0.39	80372.69
GCV (%)	11.56	1.31	13.33	8.22	30.51	9.66	11.88
PCV (%)	13.47	3.34	15.68	11.26	32.1	13.03	15.52
Heritability (%)	73.64	15.33	72.29	53.3	85.51	54.9	58.61
GA	8.91	1.32	35.21	0.43	117.63	0.71	345.59
GAM	20.72	1.06	23.63	14.37	58.81	14.22	18.93

**Significant -@ 15 and *Significant -@ 5%

Table-3 : Genotypic (r_g) and phenotypic (r_p) correlation coefficients for different yield related traits.

Source		Days to 50% flowering	Days to maturity	Plant ht. (cm)	No. of branches plant^{-1}	No. of Siliquae plant^{-1}	1000 seed wt. (gm.)	Yield/ha (kg)
Days to 50% flowering	r_g	1	0.996**	0.474**	0.334**	0.036	-0.136	0.023
	r_p	1	0.364**	0.348**	0.273**	0.009	0.010	0.017
Days to maturity	r_g		1	0.920**	0.702**	0.446**	0.487**	0.564**
	r_p		1	0.221	0.160	0.009	0.032	-0.002
Plant ht. (cm)	r_g			1	0.661**	0.106	0.107	0.110
	r_p			1	0.554**	0.111	0.083	0.110
No. of primary branches plant^{-1}	r_g				1	0.160	0.013	0.145
	r_p				1	0.089	0.036	0.122
No. of Siliquae plant^{-1}	r_g					1	-0.077	1.047**
	r_p					1	0.020	0.951**
1000 seed wt. (gm.)	r_g						1	-0.133
	r_p						1	0.080
Yield/ha (kg)	r_g							1
	r_p							1

* at 5% level of significance.

that the genotypes selected were genetically variable and considerable amount of variability existed among them. (5, 6) have reported similar results yield and its contributing traits in their studies.

The estimates for mean performance, range, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean for yield and it's contributing characters are presented in the table-2. It was evident from the result that, the PCV was higher than GCV for all the characters indicating the influence of environment on the expression of the trait. Among all the characters studied maximum PCV was observed for number of siliquae plant^{-1} (32.1). Whereas, moderate PCV was recorded plant height (15.68) followed by yield ha^{-1} (15.52), days to 50% flowering (13.47), 1000 seed weight (gm) (13.03) and number of primary branches plant^{-1} (11.26). Similarly, maximum GCV was observed for number of siliquae plant-^{1} (30.51) while plant height (13.33), yield ha^{-1} (11.88) and days to 50% flowering (11.56) showed moderate GCV. Days to 50% flowering, days to maturity and number of siliquae plant^{-1} exhibited low difference between the GCV and PCV which indicates least influence of environment on these traits. High to moderate values of GCV and PCV for yield ha^{-1}, days to 50% flowering, plant height and number of siliquae plant^{-1} indicates that there is substantial variation is present but it also suggests that there is scope to enrich variation for these characters. The present results are in accordance with (7, 8, 9).

High heritability estimates were observed for number of siliquae plant^{-1} (85.51), followed by days to 50% flowering (73.64) and plant height (72.29). Number of siliquae plant^{-1} (58.81 %), plant height (23.63%) and days to 50% flowering (20.72%) recorded high genetic advance as per cent of mean. High heritability coupled with high genetic advance as percent mean was observed for number of siliquae plant^{-1}, plant height and days to 50% flowering. This indicates the lesser influence of environment in expression of this characters and prevalence of additive gene action in their inheritance. Naturally, selection based on phenotypic observations for these characters would be effective. (8, 10) reported high heritability coupled with high genetic advance percent of mean for various yield attributes which indicated that the heritability is due to additive gene effects and selection was effective.

Genotypic and phenotypic correlation coefficients among seven characters are presented in Table-3. Correlation coefficient analysis measure natural relation between various plant characters and determine the component characters on which selection can be used for genetic improvement in yield. Days to 50% flowering had highly significant positive genotypic and phenotypic correlation with days to maturity, plant height and number of branches plant^{-1} whereas plant height showed highly significant positive correlation at genotypic and phenotypic level with number of branches plant^{-1}. Days to maturity exhibited highly significant positive correlation at genotypic level with plant height, number of branches, number of siliquae plant^{-1}, 1000 seed weight and yield ha^{-1}. Similarly, highly significant positive genotypic and phenotypic correlation was reported between number of siliquae plant^{-1} and yield ha^{-1}. Similar observations were made by (6, 11).

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