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GENETIC VARIABILITY AND CORRELATION STUDIES FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN ADVANCE LINES OF INDIAN MUSTARD (*Brassica juncea*)

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ABSTRACT

The present research was carried out to determine the best selection criteria for yield improvement in rapeseed (*Brassica juncea* L.). Fifty-four genotypes of *Brassica juncea* were sown at AICRP on Mustard at Nagpur (M.S) during the years 2018-2019 to evaluate the components of variability (genotypic and phenotypic), heritability, correlation (genotypic and phenotypic) for yield and it related components.High to moderate values of GCV and PCV were recordedfor yield per plot,number of siliqua per plant and 1000 seed weight 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 yield per plot, number of sliquae per plant and 1000 seed weight. This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance. Naturally, selection based on phenotypic observations for these characters would be effective. At phenotypic and genotypic level, yield per plot had significant positive correlation with number of primary branches, plant height andnumber siliquae per plant.These characters are playing important role in indirectselection for yield.

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

Agricultural sector plays a significant role in India's social security and overall economic welfare. Oilseed crops are the second most important determinant of agricultural economy after cereals. In India, Mustard is the second most important edible oilseed crop after soybean sharing 27.8% in the India's oilseed economy. Out of the total cropped area in India, the share of oilseed is 14.1% and mustard itself accounts for 3% of it. Mustard is predominantly grown India for extraction of oil. In terms of area under oilseeds, India holds premier position in the world but the yield of the most of oilseeds is less than the world average. Hence, the aim of any plant breeder to achieve the above target will be to evolve strains superior to those of existing strains.

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

Experimental material comprising of Fifty-four diverse genotypes of Indian mustardwere grown in randomized block design with three replications at Research Farm ofAICRP on Mustard, College of Agriculture Nagpur, Maharashtraduring Rabi season 2019-2020. Each genotype was sown in two rows and each row having 4.0 m length. Row to row and plant to plant distance was maintained at 45 cm and 15 cm respectively. For the growth of healthy crops all agronomical practices were recommended along with plant protection measures. 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 plot whereas for plant height, primary branches per plantand 1000 seed weightfrom 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 (Panse and Sukhatme, 1954), estimation of genotypic and phenotypic coefficient of variation (1) and estimation of heritability in broad sense (2). Phenotypic and genotypiccorrelation co-efficients for seed yield were calculated foreach pair of traits as described by (3).

RESULTS AND DISCUSSION

The analysis of variance (Table-1) revealed that the treatments were highly significant for all the characters except plant height and number of primary branches plant. This suggested that the genotypes selected were genetically variable and considerable amount of variability existed among them. (4, 5) have reported similar results yield and its contributing traits in their studies.

The mean performance, range, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean for

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

Source	DF	Yield per plot	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of siliquaeper plant	1000 seed weight (gm)
Replications	1	248.67	6.26	1.81	1594.68	2.49	4.90	0.30
Treatments	53	26355.45**	23.17**	22.91**	729.85	0.37	2197.05**	0.66**
Error	53	3883.87	2.50	3.02	423.49	0.34	255.34	0.01

*,** Significant at 5% and 1% level respectively.

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

Parameters	Yield per plot	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of siliquae per plant	1000 seed weight (gm.)
Mean	496.43	37.52	105.67	145.10	3.95	166.64	4.99
Min.	307.00	30.00	97.00	71.00	3.00	106.00	4.00
Max.	764.00	53.00	120.00	199.00	6.00	241.00	6.00
Genotypic Covariance	11235.79	10.33	9.94	153.17	0.01	970.85	0.33
Phenotypic Covariance	15119.66	12.84	12.96	576.67	0.36	1226.19	0.34
GCV (%)	21.35	8.56	2.98	8.53	3.18	18.69	11.44
PCV (%)	24.77	9.55	3.41	16.55	15.09	21.01	11.62
Heritability (%)	74.31	80.49	76.69	26.56	4.45	79.18	96.88
GA	188.23	5.94	5.69	13.14	0.05	57.11	1.16
GAM	37.92	15.83	5.38	9.06	1.38	34.27	23.20

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 theinfluence of environment on the expression of the traits. Among yield attributes maximum PCV was observed for yield per plot (24.77) followed by number of siliquae per plant (21.01) whereas moderate PCV was recorded in plant height (16.55), number of primary branches per plant (15.09), 1000 seed weight (gm) (11.62). Similarly,maximum GCVwas observed for yield per plot (21.35) while number of siliquae per plant (18.69) and 1000 seed weight (gm) (11.44) showed moderate GCV. Yield per plot,number of siliqua per plant and 1000 seed weight exhibited low difference between the GCV and PCV indicates least influence of environment on these traits.High to moderate values of GCV and PCV for yield per plot,number of siliqua per plant and 1000 seed weight indicates that there is substantial variation is present but it also suggest that there is scope to enrich variation for these characters.The present results are in accordance with (4, 6, 7).

High heritability was observed for 1000 seed weight (96.88), followed by days to 50% flowering (80.49), number of siliqua per plant (79.18), days to maturity (76.69) and yield per plot (74.31). Genetic advance as per cent of mean was highest in yield per plot (37.92) followed by number of siliqua per plant (34.27%), 1000 seed weight (23.20). High heritability coupled with high genetic advance as percent mean was observed for yield per plot, number of sliquae per plant and 1000 seed weight. This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance. Naturally, selection based on phenotypic observations for these characters would be effective. (4, 6, 7) 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. Yield per plot had highly significant positive genotypic and phenotypic correlation with plant height and number of siliquae per plant whereas yield per plot showed highly significant positive correlation atgenotypic level and significant positive correlation at phenotypic level with number of primary branches per plant.Similar observations were made by (4, 8) for yield and its related traits. Among traits, plant height and days to maturityshowed highly significant strong positive correlation with days to 50% flowering at both levels suggested the high degree of association between these traits while days to 50% flowering exhibited highly significant positive correlation withnumber of primary branches at genotypic level.

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

Source		**Yield per plot**	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**No. of primary branches per plant**	**No. of siliquae per plant**	**1000 seed weight (gm.)**
Yield per plot	rg	1.000	-0.093	-0.105	0.426**	0.556**	0.919**	0.064
	rp	1.000	-0.027	-0.036	0.295**	0.253*	0.974**	0.080
Days to 50% flowering	rg		1.000	0.902**	0.840**	0.994**	-0.096	-0.080
	rp		1.000	0.966**	0.375**	0.145	-0.025	-0.076
Days to maturity	rg			1.000	0.792**	0.946**	-0.107	-0.110
	rp			1.000	0.379**	0.124	-0.033	-0.108
Plant height (cm)	rg				1.000	0.744**	0.408**	0.110
	rp				1.000	0.362**	0.285**	0.055
No. of primary branches per plant	rg					1.000	0.691**	0.193
	rp					1.000	0.225*	0.056
No. of siliquae per plant	rg						1.000	-0.029
	rp						1.000	-0.008
1000 seed weight (gm.)	rg							1.000
	rp							1.000

*,** Significant at 5% and 1% level respectively.

Similarly, plant height had highly significant positive genotypic and phenotypic correlation with number of siliquae per plant and number of primary branches per plant. Days to maturity showed highly significant positive correlation at both level with plant height and genotypic level with number of primary branches per plant. Highly significant positive genotypic and significant positive phenotypic correlation was reported between number of primary branches per plant and number of siliquae per plant.

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