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Genetic variation, Heritability and Genetic Advance For Yield Components in Indian Mustard [*Brassica juncea* (L) Czern and Coss]

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Abstract:-

Twenty three variant strains/cultivars of Indian mustard were grown in Ballia (U.P., India) to estimate the presence of genetic variability, GCV and PCV, heritability broad sense and genetic advance. The predominantly often self pollinated Indian mustard gave high significant 'F' test values (ANOVA) for yield and other 11 characters viz. days to 50% flowering, number of primary branches, plant height (cm), days to maturity, number of siliquae per plant, siliqua length (cm), number of secondary branches, seeds per siliqua, biological yield, test weight and harvest index. The highest and lowest mean, range and C.D. were accounted for number of siliquae/plant and test-weight respectively. A slight PCV over GCV was noted for all attributes due to additional values of environmental influence in the expression of corresponding character. Ten characters expressed more than 90 per cent heritability broad sense (h^2) which exhibited to assess the extent of the character transmission among coming generations. The magnitude of heritability was influenced by presence of extent of variability between the two generations of population. A high heritability coupling with high genetic advance like siliquae per plant and biological yield would be prominent attributes to enhance the yield per plant at the time of selection of parents.

Key words: *- **Brassica juncea** (L.), **Genetic variability** and **Heritability**.*

INTRODUCTION:-

Rapeseed mustard ranks third in production among seven edible oils after soybean and groundnut. It shares about 35% of available vegetable oils followed by groundnut (25%) and soybean (25%). The area (more than 25 lakh ha), production (record 100 M tones,more than double from 97-98) and productivity estimated in 2020-21 which helped GOIto launch the oilseed mission. The declaration of Yellow Revolution by GOI in 1986-87 advised by Sam Pitroda to enhance the production of

quality mustard and sesame seeds to achieve self reliance and minimize the load of import expenditure on edible oils. However, India imported 74.40 lakh MT (upto May 21, DACFW released on 25.05.2021) edible oils on cost of 10.60 billion US$. Globally India account for 19.8% and 9.8% of total acerage and production since eight years. Therefore, percent productivity per ha in India is below the world average and need to evolve new
genotypes in *brassicas* for their exploitation in developing HYV with good quality and tolerant to biotic and abiotic stresses.

India stands at third position in rapeseed and mustard production in the world after China and Canada. Main states of India producing more rapeseed mustard are Rajasthan, M.P., Gujarat and Uttar Pradesh. The whole North Indian population likes mustard oil for their cooking purposes as well as pickles and other consumption in everyday life due to its pungency. Due to its low water requirement (80-240 mm) rapeseed mustard crop production is well fit for rain-fed cropping system. Rapeseed mustard belongs to family *Brassicacea*, a group of oil seeds. In Brassicacea family, important species are cultivated for oil and cake purposes except *B. oleracea* (cabbage species). The family has more than 3500 species and 350 genus. But, this Brassica
genus has three basic species, *viz*., *B. oleracea* (2n=CC=18) *gobhi* group; and *B. compestris* (2n=AA=20), dicotoma (brown *sarson*, yellow *sarson* and *toria*). Two basic species were involved in natural hybridization and chromosome doubling *i.e*. *B. compestris* (2n=AA=20) X *B. nigra* (2n=BB=16) for its evolution. Indian mustard was originated in Middle East due to interspecific hybridization (Prakash, 1980). Hemingway (1976) believed China is secondary centre of origin of Indian mustard from where it reached into India.

As written earlier, the good cultivars in objects of HYV, better quality of oil and cake,

sag tolerant to stress can be evolved from the existing appropriate genetic variability with high heritability for yield per se and its components by their exploitation in forms of hybridization, mutation, hybrid varieties, synthetic *brassicas*, somaclonal variants and transgenic development. The potential parents would be selected on the basis of variability, characters identification and genetic parameters.

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Materials and Methods:-

Twenty three variant genotypes of Indian mustard were sown on Nidharia farm, SMM Town PG College, Ballia in *rabi* season 2018-19 with spacing of two rows. Each row consisted of 2 m length with spacing of 0.45 m between the rows and 0.30 m between the plants. Appropriate agronomic practices including manuring, use of fertilizers, interculture operations, etc were done to raise a good crop. Five randomly selected plants from each and every replication per treatment (plot) were averaged for data on seed yield per plant (g) and other 11 attributes namely days to 50% flowering, number of primary branches, plant height (cm), days to maturity, number of siliquae per plant, siliqua length (cm), number of secondary branches, number of seeds per siliqua, biological yield (g) per plant, 1000 seed weight (g) and harvest index. The days between sowing and the day of 50% blossom of each plot; and turning of pale yellow colour of plot from the day of sowing were treated as days to flowering and days to maturity, respectively. The harvest index was computed by the formula:

$$HI = \frac{\text{Grain yield/plant}}{\text{Biomass yield/plant}} \text{X } 100$$

The observed data were analyzed as per method suggested by Panse and Sukhatme, (1961) while other parameters were computed as per procedure illustrated by Singhand Chaudhary (1985).

Results and Discussions:-

The ANOVA table is given in Table No-1. All attributes (treatments) were found highly significant at 1 per cent level of significance by 'F' table comparison. However, siliqua length and biological yield per plant were also found significant at replication variance. The high significance of treatment estimates provide information that the genotypes taken in the study were really having very high variability and would may be used for estimates of first and second degrees of genetic parameters.

The average mean; range; critical difference; phenotypic coefficient of variation (PCV and GCV); heritability (broad sense) and genetic gain are depicted in Table 2. A higher average mean values were noted for number of siliquae per plant (391.52)

followed by plant height (152.42 cm) and days to maturity (113.16). But the least one was noted for test weight and siliqua length.

Similarly the range and critical difference were also observed highest for number of siliqua. The plant height, days to flowering and days to maturity had also more range. Usually all attributes had a slightly higher magnitude of PCV in comparison to its corresponding genotypic coefficient of variation (GCV), elucidating the importance of environment during gene expression. The highest PCV and GCV were noted for harvest index followed by secondary branches, primary branches, seed yield and siliqua number.

Another valuable parameter heritability (b.s.) was recorded (>90%) for nine attributes including yield per plant except seeds per siliqua (76.90) and primary branches (43.40). The genetic advance was computed for all traits and found highest for siliquae number followed by biological yield, days to flower and harvest index. Though seed yield perplant per se showed 6.68% which is not meaningful.

Mather (1943 and 1973) opined that crossing of inbreds/purelines segregation and recombination along with mutation are main sources of redistribution of genetic variability among the various levels which could exist earlier but lack of mutation, random change the total amount of genetic variability must remain unchanged like Hardy-Weinberg law. He also told the phenotypic differences between homozygotes contribute the D values of the variation detectable among the individuals of family/generation.

Mather and Jinks (1982) illustrated the estimates formulae for heritability broad sense and narrow sense and gave the difference between these two parameters in segregating population. They observed usually very higher magnitudes of heritability broad sense in comparison to heritability narrow sense in *Nicotiana rustica* as 70% and 90% respectively. Though heritability broad sense was also used for the computation of genetic advance but the accuracy and precision for it would more depend upon heritability narrow sense because it is based only on additive and additive X additive gene interaction only.

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Table-1 Analysis of Variance for 12 characters in Indian mustard

Sources of Variation	Df	Days to 50 % flowering	Number of primary branches	Plant height (cm)	Days to maturity	Number of siliquae per plant	Siliqua length (cm)	No. of secondary branches	No. of seeds per siliqua	Biological yield per plant(g)	Test weight(g)	Harvest index (%)	Seed yield per plant (g)
Replication	2	0.34	1.04	2.51	0.29	124.33	0.21**	4.76	0.42	14.19*	0.09	2.55	0.38
Treatment	22	167.40**	1.66**	885.41**	90.44**	11585.50**	1.08**	178.98**	6.92**	647.35**	1.04**	126.43**	34.19**
Error	44	0.40	0.50	6.32	0.93	162.34	0.03	2.72	0.63	3.30	0.06	1.35	0.68

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Table-2. Mean, Range, Coefficient of variation, Heritability and Genetic advance

Characters	Mean	Range	Critical difference	Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability ($h^2_{b.s.}$)	Genetic advance
Days to 50% flowering	51.23	38.52-67.20	1.05	14.62	14.56	99.30	15.31
No of primary branches	439	3.27-6.27	1.17	21.49	14.16	43.40	0.84
No of secondary branches	34.04	20.27-47.63	2.72	23.04	22.52	95.60	15.44
Plant height (cm)	152.42	98.36-173.27	4.14	11.35	11.23	97.90	34.89
No of sliquae per plant	391.52	247.53 547.47	20.97	16.09	15.76	95.90	124.49
Sliqua length (cm)	4.67	3.63-6.91	0.29	13.21	12.68	92.10	1.17
Days to maturity	113.16	103.33-124.00	1.58	4.90	4.83	97.00	11.08
Seeds per sliqua	126.72	9.22-16.29	1.31	12.99	11.39	76.90	2.62
Biological yield(g)	71.96	39.09-98.59	2.94	20.51	20.36	98.50	29.96
Test weight (g)	4.26	3.00-5.19	0.40	14.56	13.38	84.40	1.08
Harvest index (%)	24.20	2.71-42.42	1.91	27.11	26.68	96.90	13.09
Seed yield per plant (g)	16.84	10.66-23.13	1.36	20.44	19.85	94.20	6.68

References:-

Chaurasiya, J., Prasad, S., M: and Tomar, P; 2019. Genetic variability, heritability, genetic advance and character association of Indian mustard .: Jo *of oilseed Brassica* , 10 (2): 80-86 July 2019.

Hemingway, J.S. 1976 Mustard : Brassica species and synapsis also (Cruciferae), pp 55-59: In

N.W. Simonds (ed) *Evolution of crop plants*, Longman, London.

Mather, K. *Polygenic inheritance and natural selection*. Biol. Revs, 18. 32-64. Mather, K.

1973. *The genetic structure and population*, Chapman and Hall, London.

Mather, S.K. and Jinks, J.L. 1982. Estimating the components of variation. *Biometrical genetics: The study of continuous variation*. Pub. MacMillan Indian Limited Bangalore. Pp. 275-279.

Panse, V. G. and P. V. Sukhatme 1961. *Statistical methods for Agriculture Workers.* II Ed. ICAR New Delhi.

Prakash, S 1980 Cruciferous oilseeds in India. pp 151-163. In;Tsunoda, K.Hinata.C Gemez- campo (ed.). *Brassica crops and wild Allies*, Japan Scientific Societies Press, Tokyo.

Singh, R. K. and Chaudhary, B.D. *Biometrical Methods in Quantitative Genetics Analysis*. New Delhi-Ludhiana, 1985.

Singh; Dwivedi, A; Ashutosh; Meena, Omesh; and Kumar, Kamlesh.:(2018)- Geonoty pic variability, heritability and genetic advance in Indian mustard genetypes.: *Journal of pharmcognosy and phyto chemistry* 2018; 7(3): 350- 352.

Tiwari A; Singh S; , Tomar ,A; and Singh., M; 2017 Heritability genetic advance and correction coefficient analysis in Indian mustard.: *J. Pharmacog and Phytochemis* 6(1) :356-359