Association of genetic parameters among its components in Indian mustard (*Brassica juncea* L.)

ABSTRACT

Present study was conducted with 12mustard genotypes, raised in randomized block design with three replications during the *Rabi* season 2023-2024 at Organic Farm, Karguanji, Institute of Agricultural Sciences, Bundelkhand University, Jhansi (U.P.). Analysis of variance in the present investigation revealed existence of significant differences among the genotypes of mustard for all the characters studied and wide range of variability in the genotypes was observed.The highest mean performance for grain yield/ plant was observed for genotype TM-28 followed by radhika and ANG-73 indicating that these genotypes can be used in hybridization programme to achieve higher yield. The very high heritability and very high GAM was observed in number of siliqua per plan, number of secondary branches per plant, number of total branches and number of primary branches per plant indicating the presence of additive gene action for governing of these traits and selection based on these traits will be effective.This shows that improvement of these traits during selection will simultaneously improve the yield per plant.

Keywords :mustard, genetic advance, heritability, genotypes,additive gene action, yield

INTRODUCTION

Mustard made from rapeseeds (Brassica juncea L.) is a self-pollinated (2n=2x=36) annual oil seed crop of family Brassicaceae. B. juncea (L.) Czern and coss. is the scientific biological name of the Indian mustard plant, In the regional Indian languages of India, i.e., in hindi it is called as Rai, Banarasi rai Kalee sarson, in sanskrit it is called as Asuri, Bimbata, Indian mustard (B. juncea L.) is a major rabi oilseed crop of the Indian subcontinent occupies more than 80% of the total cultivated area under rapeseed-mustard in the country. It is an amphidiploid species that originated through the inter-specific hybridization of Brassica rapa (2n=20) and Brassica nigra (2n=18) (Nagaharu Us, 1935). Indian mustard is the second most important oil seed crops of the world as well as India after groundnut (Syed et al, 1994).The availability of genetic variation is advantageous for crop improvements. Such types of variability brought about by a group of genes which have a small individual effect, can be studied through quantitative measurement. The genetic facts are inferred from observation on phenotypes. Because phenotype is determined by the interaction of genotype and environment, non-genetic factors have a significant impact on genetic variation. As a result, multiple genetic indices such as heritability, genetic progress, and others must be used to assess exploitable variability. A study like this appears to be critical for planning genetic improvements in Indian mustard.

The study of genetic advance is equally important as it measures the genetic gain based on selection in a particular character. Therefore, for any crop improvement programme through selection, the study of genetic variability and heritability together with genetic advance is necessary. A number of variables are studied in correlation, which give an idea about indirect selection as well. Indirect selection is equally important in influencing the final product, grain yield in any crop species. For this, path coefficient analysis has emerged as a very strong tool as it determines the direct and indirect causes of association giving the idea of specific forces which act to produce strong correlation and measures relative importance of each causal factor.

MATERIALS AND METHODS

The experimental material used in the present study comprised of the 12 genotypes. The experiment was laid-out in randomized block design with three replications of the plant geometry was maintained at 30 cm x 20 cm. Observations on plot basis were recorded for days to 50 per cent flowering, days to maturity, which observations based on single plant were recorded for plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of

total branches per plant, number of siliqua per plant, number of seed per siliqua, biological yield per plant (g), harvest index, seed yield per plant. For recording single plant observations five competitive plants were randomly selected from each plot. Average of these five plants with respect to plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of total branches per plant, number of siliqua per plant, number of seed per siliqua, biological yield per plant (g), harvest index and seed yield per plant was used for statistical analysis.The data collected for each character on individual plant basis (except days to 50 per cent flowering and days to maturity) for five randomly selected plants were analyzed first by randomized block design (Panse and Sukhatme, 1985) to test the significance of differences among the genotypes and the variability parameters were measured by the formula suggested by Johnson et al. (1955).

RESULTS AND DISCUSSION

The data were subjected to analysis of variance adopting standard statistical methods. The analysis of variance including source of variations, their degree of freedom and expectations of mean squares are given below:

Table 1. Analysis of variance (ANOVA) for yield and its component traits in mustard genotypes

Source of variation	Degree of freedom (df)	Mean sum of squares										
		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	Number of total branches	Number of seeds per siliqua	Number of siliqua per plant	Harvest index	Seed yield per plant	Biological yield
Replications	2	4.33	3.44	101.81	0.027	1.63	1.34	0.96	382.2	0.86	4.22	167.17
Genotypes	11	28.49**	30.77**	100.27*	1.18**	25.56**	33.83**	7.74**	18519.8**	11.90*	12.74**	376.00*
Error	22	1.93	2.92	42.63	0.083	0.53	0.57	1.18	583.1	4.53	3.25	150.29

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

Genetic parameters of variation for seed yield and its components in mustard are presented in Table 2. The overall mean and range for yield and its components revealed that there is substantial amount of genetic variability present for most of the characters under study in mustard. Genetic parameters of variation are discussed character wise here as under.

Table 2. Mean values of 12 genotypes for 11 characters in mustard

Chraracter	DF 50	DM	PH	NPB	NSB	NTB	NSS	NSP	HI	BY	SYP
DRMR-150-35	49.33	120	175.17	4.40	12.07	16.47	13.07	290.47	19.89	71.71	14.23
PM-25	45.67	121.33	171.00	5.13	12.33	17.47	13.73	290.60	19.92	56.02	11.10
TM-28	45.33	118.33	158.65	6.13	18.20	24.33	17.53	467.87	19.62	88.33	17.30
RH-0119	46.33	123	172.78	4.33	10.83	15.17	13.80	356.20	18.27	73.20	13.14
NRCSR-02	48.33	122	170.88	5.47	14.10	19.57	13.27	282.53	20.23	68.55	13.74
Radhika	44.33	121	176.43	4.82	12.40	17.22	16.87	469.53	19.82	86.89	17.20
Pitambrit	44.67	116.66	161.08	5.87	18.67	24.53	12.20	373.00	14.92	72.16	10.77
PBR-210	52.00	127	172.93	4.33	8.87	13.20	14.60	241.67	15.04	96.36	14.51
NRCHB-101	45.67	120	164.82	4.53	15.80	20.33	13.40	283.53	17.81	70.95	12.13
ANG-73	48.67	124.6	173.61	5.40	11.87	17.27	12.67	422.07	17.56	85.78	15.06
DRM-31	46.33	122	175.41	4.53	15.33	19.87	14.87	265.27	15.70	83.07	12.89
RNG-226	54.33	127.33	172.51	5.47	13.00	18.47	13.93	347.80	19.44	69.94	13.57
GM	47.58	121.94	170.44	5.04	13.62	18.66	14.16	340.88	18.18	76.91	13.80
SE	0.8040	0.9881	3.77	0.1672	0.4229	0.4379	0.6281	13.9412	1.229	7.0779	1.0416
CD 5%	2.3581	2.8981	11.0571	0.4903	1.2404	1.2843	1.8422	40.8882	3.6046	20.7587	3.0548
CV	2.93	1.40	3.83	5.75	5.38	4.07	7.68	7.08	11.71	15.94	13.07

Table 3: Genetic variability parameters for yield and its attributing traits in mustard genotypes

Character	DF50	DM	PH	NPB	NSB	NTB	NSS	NSP	HI	BY	SYP
Maximum	56.0000	129.0000	187.31	6.4000	20.0000	26.2000	18.2000	485.6000	22.4542	100.11	18.4000
Minimum	42.0000	115.0000	156.3	4.0000	8.6000	12.8000	11.4000	224.4000	14.5557	40.22	8.4800
Grand Mean	47.5833	121.9444	170.4392	5.0350	13.6222	18.6572	14.1611	340.8778	18.1849	76.9158	13.8028
SEm	0.8040	0.9881	3.77	0.1672	0.4229	0.4379	0.6281	13.9412	1.229	7.0779	1.0416

CD 5%	2.3581	2.8981	11.0571	0.4903	1.2404	1.2843	1.8422	40.8882	3.6046	20.7587	3.0548
CD 1%	3.2051	3.9391	15.0285	0.6664	1.6860	1.7456	2.5038	55.5742	4.8993 NS	28.2147	4.1520
ECV	2.9267	1.4035	3.8312	5.7503	5.3777	4.0653	7.6823	7.0837	11.7061	15.9385	13.0701
GCV	6.2523	2.4985	2.5717	12.0417	21.2035	17.8465	10.4447	22.6836	8.6197	11.2771	12.8827
PCV	6.9034	2.8657	4.6143	13.3439	21.8748	18.3037	12.9657	23.7640	14.5372	19.5246	18.3518
H (Bs)	0.8203	0.7601	0.3106	0.8144	0.9396	0.9507	0.6489	0.9111	0.3516	0.3336	0.4928
GA	5.5506	5.4721	5.0323	1.1271	5.7675	6.6878	2.4545	152.0450	1.9146	10.3204	2.5714
GA % mean	11.6650	4.4874	2.9525	22.3853	42.3389	35.8456	17.3327	44.6040	10.5285	13.4178	18.6296

All of the traits under study showed a wide range of variation. The variation was highest for number of siliqua per plant ranged from 241.67 pods to 467.87 pods with highest pod TM-28 genotype, plant height ranged from 158.65 cm to 176.43 cm with lowest height TM-28, days to maturity ranged from 116.66 days to 127.33 days with earlier mature RNG-226, biological yield per plant ranged from 56.02 gm to 96.36 gm with highest PM-25, days to 50% flowering ranged from 44.33 days to 54.33 with early flowering genotype Radhika, harvest index ranged from 14.92 to 20.23 with highest harvest index NRCSR-02 genotype, number of total branches ranged from 13.20 to 24.53 with highest branches Pitambrit, number of secondary branches per plant ranged from 8.87 to 18.67 with highest branches Pitambrit, seed yield per plant ranged from 10.77 gm to 17.30 gm with highest yield TM-28, number of seeds per siliqua ranged from 12.20 to 17.53 with highest seeds TM-28 and number of primary branches per plant ranged from 4.33 to 6.13 with highest branches TM-28. The similar outcomes were also reported by Rai et al. (2005), Singh et al (2007), Aytac and Kınaci (2009), Sohan and Nutan (2010), Tripathi et al. (2013), Zada et al. (2013), Shekhawat et al. (2014), Synrem et al. (2014), Akabari and Niranjana (2015), Iqbal et al. (2015), Singh et al. (2016), Chauhan et al. (2017), Meena et al. (2017) and Malik et al. (2018).

In the present investigation, high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (above 20%) were observed for number of siliqua per plant (PCV =23.7, GCV =22.68) and number of secondary branches per plant (PCV =21.87, GCV =21.20). This high value of PCV and GCV indicates the existence of high genetic variability of these traits among the genotypes and hence, better scope for the improvement of the character through selection. Similar findings were reported by Aytac and Kınaci (2009), Sohan and Nutan (2010), Sharma et al. (2014), Synrem et al. (2014), Akabari and Niranjana (2015), Iqbal et al. (2015), Chauhan et al. (2017), Meena et al. (2017) and Singh et al. (2018). In present study none of the characters shown low heritability. Similar results were reported earlier by Aytac and Kınaci (2009), Tripathi et al. (2013), Zada et al. (2013), Synrem et al. (2014), Akabari and Niranjana (2015), Iqbal et al. (2015), Chauhan et al. (2017), Meena et al. (2017), Singh et al. (2018) and Tiwari (2019). High genetic advance as per cent of mean (above

20%) exhibited by number of siliqua per plant(44.60%), number of secondary branches per plant (42.33%), number of total branches (35.84%) and number of primary branches per plant (22.38%). Similar results have also been reported by Rai et al. (2005), Aytac and Kınaci (2009), Sohan and Nutan (2010), Zada et al. (2013), Synrem et al. (2014), Akabari and Niranjana (2015), Iqbal et al. (2015), Meena et al. (2017) and Raliya et al. (2018).

CONCLUSION

The present study has revealed valuable information on different yield traits in mustard improvement. Genotypes TM-28, radhika and ANG-73 were found to be the promising genotypes for yield and yield contributing traits. Hence these genotypes can be utilized as potential donor for future hybridization programme to develop high yielding varieties.

REFERENCES

Akabari, V.R. and Niranjana, M. (2015). Genetic variability and trait association studies in Indian mustard (Brassica juncea L.). Int. J. Agril. Sci., 11(1):35-39.

Aytac, Z. and Kınacı G. 2009. Genetic variability and association studies of some quantitative characters in winter rapeseed (Brassica napus L.) Afri. J. Biotech. Vol. 8 (15): 3547-3554.

Chauhan, JS., Singh, KH., Singh, Manju., Bhadauria, V.P.S. and Kumar, A. (2017). Studies on genetic variability and path analysis for quality characters in Rapeseedmustard (Brassica species). J. Plant Genet. Resour., 21(2):113-117.

Iqbal, A. M., Shikari, A. B., Ashaq, H., & Dar, Z. A., (2015). Genetic variability Brassica rapa var. Brown sarson for maturity, yield and yield attributing traits. Environmental and Ecology, 33(1 A), 267-270.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimate of genetic and environmental variability in soybeans. Agron. J., 47(7): 314-318.

Malik, V. K., Singh1, S. K., Kumar, V., Singh, N. P., Malik2, A. and Dwivedi, V. K. (2018). Association among genetic parameters in Indian mustard (Brassica juncea L. Czern&Coss.). Int J. Agril. Invention., 3(1):11-15.

Meena, H.S., Kumar, A., Singh, VV., Meena, PD., Ram B. and Kulshrestha, S. (2017). Genetic variability and inter-relation of seed yield with contributing traits in Indian mustard (Brassica juncea L.) J. Oilseed Brassica, 8(2):131-137.

Panse, V.G. and Sukhatme, P.V. (1978). Statistical Methods for Agricultural Workers. ICAR Publications, New Delhi.

Shekhawat, N., Jadeja, G.C. and Singh, J. (2014). Genetic variability for yield and its components in Indian mustard (Brassica juncea L. Czern&Coss.). Electronic J. Plant Breeding, 5(1):117-119.

Rai, S.K., Verma, A. and Pandey, D.D. (2005). Genetic variability and character association analysis in Indian mustard [Brassica juncea (L.) Czern and Coss.]. Ann. Agri.Bio. Res., 10(1):29-34.

Raliya, B., Kumar, K., Ramesh, Pukhraj, Meena, H.S. and Mundiyara, R. (2018). Genetic variability and character association in Indian mustard (Brassica juncea L.). Int. J. Agri. Sci., 10(9):5993-5996.

Singh, M., Tomar, A., Kumar, R.,(2016). Genetic analysis for estimates components of genetic variance in Indian mustard (Brassica juncea (L.) Czern&Coss), Journals of Pharmacognosy and Phytochemistry, 216; 6(1): 352-355.

Singh, S.K., Singh, A.K. and Kumar, K. (2007). Genetic variability for yield and its components in Indian mustard (Brassica juncea L. Csern and Coss.). New Botanist, 34(1/4):147-150.

Sohan,R., &verma,N.,(2010). Genetic Variability and yield components in Indian mustard, Journal of Oilseeds Research 27 (2):170-171.

Syed, S.A., Ali, A. and Rehman, K. (1994). Improvement of rapeseed for agronomic and quality characters through induced mutation and hybridization. IAEA -TECDOC - 781, Viena,25-35.

Synrem, G.J., Rangare, N.R., I. Myrthong, I. and Bahadure, D.M. (2014) Variability studies in Intra specific crosses of Indian mustard [Brassica juncea (L.) Czern and Coss.] genotypes. J. agri. and Veterinary Science, 8(3):29-32.

Tripathi, N., Kumar, K., Verma O.P. 2013. Genetic Variability, Heritability and Genetic Advance in Indian Mustard (Brassica juncea L. Czern and Coss.) for Seed Yield and it's Contributing Attributes Under Normal and Saline/Alkaline Int. J. of sci. And Res. Condition Index Copernicus. 6.14.

Zada, M., Zakir, N., Rabbani, M.A. and Shinwari, Z.K. (2013). Assessment of genetic variation in Ethiopian mustard (Brassica Carinata A. Braun) germplasm using multivariate techniques. Pak. J. Bot., 45(S1): 583-593.