Website : www.asthafoundation.in
Progressive Research : An International Journal
Vol 18 (2) : 132-135 (July-2023), Print ISSN : 0973-6417, Online ISSN : 2454-6003
Society for Scientific Development in Agriculture and Technology, Meerut (U.P.) India

Studies on Genetic Variability, Heritability and Genetic Advance for Yield and Yield AtTributes in Indian mustard [*Brassica juncea* (L.) Czern and Coss.]

Manoj M.S.[1], B.R. Patil[1] and S.P. Singh[2]
[1]Deptt. of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad, Karnataka, India
[2]CSAUAT–Agriculture Research Station, Kalai, Aligarh, U.P.
**Corresponding Author Email : manojms005@gmail.com*

Abstract

Indian mustard is one of the prominent edible oil yielding crops cultivated in India, with oil content ranging from 37 to 48 percent. An experiment was conducted to evaluate the variability in eight promising genotypes of Indian mustard along with two checks, Dodda Sasive and NRCHB-101, laid in RCBD with three replications at five different locations across Karnataka. The observations were recorded for 12 biometric traits of mustard, including seed yield and oil content and analysed using a combined ANOVA. The components of genetic variability like heritability and genetic advance are essential biometric tools for assessing dissimilarity in populations to make a selection. The genotypic coefficient of variance was high for the number of secondary branches and racemes per plant. The traits, days to 50% flowering, days to maturity, number of secondary branches per plant, racemes per plant, siliqua per raceme, seeds per siliqua, siliqua length and oil content, registered high heritability, indicating less influence of the environment. Among all the traits, only seed yield exhibited a high genetic advance coupled with moderate heritability, which signifies that seed yield is governed by additive gene effects. Genetic advance as a percent mean was high for the number of secondary branches per plant and racemes per plant, indicating the possibility of rapid improvement. The genotypes TM-210, TM-136 and KMR(E) 16-11 were the top seed yielders across all the locations.

Key words : *Indian mustard, genetic advance, heritability, variability, oil content.*

Introduction

Indian mustard [*Brassica juncea* (L.) Czern and Coss.] is an important oil yielding crop that belongs to the family Brassicaceae. Mustard, having chromosome number 2n=36, is a natural amphidiploid derived from an interspecific cross between *B. nigra* and *B. campestris* (1). Autogamy is the mode of pollination in mustard, but a certain amount (2 to 15%) of cross-pollination occurs due to insects, wind and other factors. The Middle East has been considered the primary centre of origin (2), whereas South western China and North western Himalayan regions have been the centres of maximum diversity (3). The oil content of mustard ranges from 37 to 48 percent, similarly, protein content ranges from 24 to 30 percent and 35 to 40 percent based on whole seed and meal, respectively. These properties made it suitable for culinary and flavouring purposes. The leaves of immature plants are used as green vegetables, oil cakes are used as fodder and organic manure. Mustard oil finds its usage in the preparation of medicines, detergents, biodegradable plastics and is blended with mineral oils for lubrication, leather softening in the tanning industry and manufacturing of greases (4).

The existence of genetic variability is a pre-requisite for crop improvement, which is largely dependent on the scale of genetic variability and the degree to which desired traits are inherited (5). The components of genetic variability like heritability and genetic advance (GA) are essential biometric tools for assessing dissimilarity in populations and making selections (6). Seed yield is considered to be the most complex character, which depends on various morphological traits in addition to extraneous environmental factors. Partitioning phenotypic variability into genotypic (heritable) and environmental (non-heritable) components is essential to practising selection. Estimates of heritability and genetic advance enhance the efficiency of predicting genetic gain under selection (7). With this background, a set of 10 Indian mustard genotypes was used for estimating phenotypic and genotypic coefficients of variance, heritability in a broad sense and genetic advance as a percent mean.

Materials and Methods

The experimental material containing ten promising genotypes of *Brassica juncea* (Table 1) was evaluated during *rabi* 2017 over five different locations in northern Karnataka, *viz*., Main Agriculture Research Station, University of Agricultural Sciences, Dharwad; Agriculture Research Station, Bailhongal; Agriculture Research Station, Bheemarayanagudi; Agriculture Research Station, Mundgod and Agriculture Research Station, Sankeshwar. The Randomised Complete Block Design (RCBD) was laid out with three replications of 10 genotypes of *Brassica juncea* in a plot size of 2.25 m × 5 m

Received : June-2023; Revised : June-2023; Accepted : July-2023

across all the locations. In order to maintain optimum crop stand, a recommended package of practises was adopted.

Five plants were randomly selected in each genotype and labelled. Observations on various plant morphological characters, *viz*., days to 50 percent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of racemes per plant, number of siliqua per raceme, number of seeds per siliqua, siliqua length, 1000 seed weight, oil content and seed yield, were recorded on these plants at different stages of crop growth. Data collected on selected individual plants of each genotype at each location were used to calculate genetic parameters like phenotypic and genotypic variance, phenotypic coefficients of variability (PCV), genotypic coefficients of variability (GCV), heritability, genetic advance (GA) and genetic advance as percent mean (GAM). The obtained data was undertaken to assess and enumerate the genetic variability, heritability and genetic advance among the genotypes for the quantitative characters under consideration, as suggested by (8,9,10).

Results and Discussion

The present study comprised eight Indian mustard genotypes along with two checks (NRCHB-101 and Dodda Sasive) which were evaluated in RCBD across five locations for yield and yield attributes. The results of the analysis of variance for all the characters investigated revealed the existence of significant variation among the 10 mustard genotypes used in this experiment. The mean squares due to genotype were highly significant for all the characters, which indicated that the genotypes under study were genetically diverse. The mean sum of squares due to replication showed non-significant differences for all the traits under consideration, indicating good homogeneity among replications. The recorded data pertaining to twelve characters from ten varieties of Indian mustard was pooled and analysed to realise their performance across five locations. The results pertaining to mean, range and genetic parameters, *viz*., PCV, GCV, heritability, GA and GAM for yield and yield attributes, are presented in Table-2. The statistical figures for traits that have a count are rounded off in the text in order to ease comparison.

Maximum variability was realised for the characters, *viz*., plant height, number of secondary branches per plant, number of racemes per plant, number of siliqua per raceme and seed yield, showing that the choice of these traits will have a significant bearing on crop improvement. The effectiveness of selection for any component of yield depends not only on the amount of variability but also on how much of it is readily amenable to improvement. The genotypic coefficient of variation along with the heritability estimates would provide the best information of the amount of advance to be expected from selection (8). The magnitude of the phenotypic coefficient of variation was frequently greater than the genotypic coefficient of variation for all characteristics evaluated, demonstrating the environment had an impact on how the traits under investigation were expressed. PCV and GCV values were classified as low (0-10%), moderate (10-20%) and high (>20%) by (11). Higher values of PCV and GCV were obtained for the characters, *viz.,* number of secondary branches per plant and number of racemes per plant. This indicated that substantial variability exists for these characters in the material studied and specifies greater scope for selection to increase the expression of these characters. Hence, there is scope for augmenting the genotypes for wider variability, which will form a source to improve the seed yield and its component characters. Similar findings were reported by (12,13,14).

The characters plant height, number of primary branches per plant, number of secondary branches per plant, number of racemes per plant, 1000 seed weight and seed yield exhibited larger differences between GCV and PCV, reflecting a substantial influence of the environment. These characters were more sensitive to environmental changes. Selection based on phenotypic observations may not be very effective for the above traits. The characters days to 50 percent flowering, days to maturity, number of siliqua per raceme, number of seeds per siliqua, siliqua length and oil content exhibited lower differences between GCV and PCV, but their values were low to moderate; therefore, selection is difficult to practise for these characters as variation among the genotypes is less. Parallel conclusions were drawn by (14,15). The use of genotypic coefficient of variation would be limited as it is prone to change with fluctuations in the environment. So the estimates of heritability have a role to play in determining the effectiveness of selection of character, provided they are considered in conjunction with the predicted genetic advance, as suggested by (10,16).

The heritability expressed in percentage was classified as low (0-30%), moderate (30-60%) and high (>60%), as given by (17). The estimate of heritability can be used for the prediction of genetic gain, which indicates the genetic improvement that would result from the selection of the best individual. High estimates of broad sense heritability were observed for oil content (82.05), number of racemes per plant (80), number of secondary branches per plant (79.54), days to 50% flowering (77.32), siliqua length (68.42), days to maturity (67.30), number of siliqua per raceme (64.20) and number of

Table-1 : List of mustard genotypes evaluated across five locations.

Sl. No.	Genotypes	Source of collection
1.	KMR(E) 16-1	Directorate of Rapeseed and Mustard Research, Bharatpur, Rajasthan
2.	DRMR 4005	
3.	PRE-2013-19	
4.	NRCHB-101	
5.	TM-210	Bhabha Atomic Research Centre, Trombay, Mumbai, Maharashtra
6.	TM-136	
7.	TM-138-1	
8.	TM 2776	
9.	TM-267-1	
10.	Dodda Sasive	Local collection from Haveri, Karnataka

Table-2 : Pooled analysis of mean, range and genetic parameter values for yield and yield attributes in mustard across five locations.

Characters	Mean	Range		Coefficient of variation		Heritability (%)	Genetic Advance	Genetic advance as percent of mean
		Minimum	Maximum	Genotypic	Phenotypic			
Days to 50% flowering	36.58	34.27	37.87	2.94	3.35	77.32	1.95	5.33
Days to maturity	85.44	80.93	89.07	2.02	2.70	67.30	3.16	3.70
Plant height (cm)	142.60	130.42	152.57	3.84	6.90	30.93	6.27	4.39
Number of primary branches per plant	4.30	3.62	5.01	9.12	12.19	56.02	0.61	14.07
Number of secondary branches per plant	6.25	3.68	9.86	27.92	33.56	79.54	3.43	54.98
Number of racemes per plant	12.36	8.16	16.00	19.73	22.06	80.00	4.51	36.35
Number of siliqua per raceme	25.05	22.43	28.91	6.93	8.67	64.20	2.87	11.49
Number of seeds per siliqua	12.03	10.81	13.40	5.98	7.57	62.35	1.17	9.73
Siliqua length (cm)	5.10	4.32	5.98	9.97	12.06	68.42	0.86	17.00
1000 seed weight (g)	4.20	3.56	4.60	6.86	10.21	45.14	0.40	9.49
Oil content (%)	38.92	38.01	39.75	1.45	1.60	82.05	1.05	2.71
Seed yield (kg ha^{-1})	493.08	410.12	579.26	10.30	18.46	31.15	58.40	11.84

seeds per siliqua (62.35), indicating that a plant breeder can concentrate on these traits to exploit effective selection for genetic improvement.

Genetic advance is the improvement in the mean genotypic value of a selected individual over the parental population. Genetic advance as percent mean was categorised as low (0-10%), moderate (10-20%) and high (>20%) by (10). Among all the traits, only seed yield exhibited high genetic advance (58.40) coupled with moderate heritability (31.15) which signifies that seed yield is governed by additive gene effects. The low heritability is due to high environmental effects and practising selection may be effective in such cases, as reported by (14). In the present investigation, high heritability and low genetic advance were exhibited by characters *such as* days to 50% flowering, days to maturity, number of secondary branches per plant, number of racemes per plant, number of siliqua per raceme, number of seeds per siliqua, siliqua length and oil content, which indicate the predominance of non-additive gene action. The high heritability is due to the favourable influence of environment rather than genotype and selection for such characters may not be rewarding. Similar results were obtained by (18,19). Likewise, the characters, *viz.,* plant height, number of primary branches per plant and 1000 seed weight, revealed moderate heritability and low genetic advance. These outcomes are in accordance with (20).

The genotypes TM-210, TM-136 and KMR(E) 16-11 were the top seed yielders across all the locations. These lines could be recommended for multi-location trials for their stability. Selection based on phenotypic observation alone may not be very effective. Hence to achieve the defined high variability for the selection programme, systematic efforts need to be made to combine hybridization and recombination in mustard to generate desirable variability. So, approaches like hybridization of superior, diverse genotypes followed by selection are suggested to generate the desired variability to develop transgressive segregants for economically important traits.

References

1. Nagaharu U., (1935). Genome analysis in Brassica with special reference to the experimental formation of *B. napus* and peculiar mode of fertilization. *Japanese J. Bot.* 7: 389-452.
2. Prakash S. and Hinata K. (1980). Taxonomy, cytogenetics and origin of Brassica, a review. *Per. Bot*. 55: 1-57.
3. Vaughan J.G., Hemingway J.S. and Schofield H.J. (1963). Contribution to a study of variations in *Brassica juncea* Czern & Coss. *Bot. J. Linn. Soc*. 58: 435-447.
4. Manoj M.S. (2019). Studies on Stability for Yield and Yield Attributes, Resistant Gene Homologue Polymorphism and Diversity in Indian Mustard [*Brassica juncea* (L.) Czern and Coss.]. *M.Sc. (Agri.) Thesis, University of Agricultural Sciences,* Dharwad, Karnataka.
5. Kumar S., Prasad L.C. and Kumar S. (2002). Variability and correlation studies in barley *Research on Crop,* 3(2): 432-436.
6. Akhter M., Apon F.N., Bhuiyan M.M.R., Siddique A.B., Husna A. and Zeba N. (2021). Genetic variability, correlation coefficient, path coefficient and principal component analysis in tomato (*Solanum lycopersicum* L.) genotypes. *Plant Cell Biotech. Mol. Biol.* 22: 46–59.
7. Prasad G. and Patil B.R. (2018). Genetic variability and heritability studies for yield and attributes in Indian mustard. *Journal of Pharmacognosy and Phytochemistry*, 7(5): 519-522.
8. Burton G.W. and Devane E.M. (1953). Estimating heritability in tall fescue (*Festuca circunclinaceae*) from replicated clonal material. *Agron. J*. 45: 478-480.
9. Hanson C.H., Robinson H.F. and Comstock R.K. (1956). Biometrical studies on yield in segregating population of Korean Lasphadezia. *Agron. J.* 48: 314-318.
10. Johnson H.W., Robinson H.F. and Comstock R.E. (1955). Genotypic and phenotypic correlations on soybean and their implications in selection. *Agron. J*. 47: 477-483.
11. Sivasubramanian S. and Menon M. (1973). Heterosis and inbreeding depression in Rice. *Madras Agric. J.* 60: 1139.
12. Swamy G. (1993). Variability and Genetic Divergence in Mustard (*Brassica juncea* L. Czern and Coss) and Rapeseed (*Brassica compestris* L.). *Ph.D. Thesis*, *University of Agricultural Sciences,* Bangalore, Karnataka.
13. Ghosh S.K. and Gulati S.C. (2001). Genetic variability and association of yield components in Indian mustard (*Brassica juncea* L.). *Crop Res. Hisar*, 21(3): 345-349.
14. Gangapur D.R. (2008). Studies on Genetic Variability in the Indian Mustard (*Brassica juncea* L. czern and coss) Germplasm and its Suitability to northern Karnataka. *M.Sc. (Agri.) Thesis, University of Agricultural Sciences,* Dharwad, Karnataka.
15. Tahira A.R., Muhammad A.K. and Muhammad A. (2014). Seed yield improvement in [*Brassica juncea* (L.) Czern & Coss.] genetic advance, correlation and path coefficient analysis. *Int. J. Agric. Innov. Res.* 3(3): 2319-2324.
16. Panse V.G. and Sukhatme P.V. (1967). Statistical Methods for Agricultural workers. Indian Council of Agricultural Research, New Delhi.
17. Robinson H.F., Comstock R.E. and Harey P.H. (1949). Estimates of heritability and degrees of dominance in corn. *Agron. J*. 43: 353-359.
18. Ram K.J. (2014). Stability Analysis in Mustard [*Brassica juncea* (L.) Czern and Coss.]. *M.Sc. (Agri.) Thesis*, *Sri Karan Narendra Agricultural University*, Jobner, Rajasthan.
19. Synrem G.J., Rangare N.R., Myrthong and Bahadure D.M. (2014). Variability studies in intra specific crosses of Indian mustard [*Brassica juncea* (L.) Czern and Coss.] genotypes. *J. Agric. Vet. Sci.* 7(9): 29-32.
20. Zebarjadi A., Kakaei M. and Mostafaie A. (2011). Genetic variability of some traits in rapeseed (*Brassica napus* L.) under drought stress and non-stress condition. *Biharean Biologist,* 5(2): 127-131.