

Studies on Components of Genetic Variability in Indian Mustard (*Brassica juncea* (L.) Czern and Coss.) Genotypes Across Five Locations in Northern Karnataka

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ABSTRACT

Indian mustard is one of the prominent edible oil yielding crops cultivated in India, with oil content ranging from 37 to 48%. 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 analyzed using a combined ANOVA. Biometric tools like heritability and genetic advance

are crucial components of genetic variability that serve to assess variation in the available germplasm and assist in the selection of a desirable genotype. The traits, number of secondary branches and racemes per plant have registered a high genotypic coefficient of variance as well as a high genetic advance as a percent of the mean indicating the possibility of rapid improvement. A minimal influence of the environment was noticed in the expression of 8 traits out of 12 that exhibited high heritability in a broad sense. 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. The genotypes that exhibited superior performance with respect to yield across all the locations were TM-210, TM-136 and KMR (E) 16-11.

Keywords Genetic advance, Indian mustard, Heritability, Oil content, Variability.

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INTRODUCTION

Indian mustard (*Brassica juncea* (L.) Czern and Coss.) belongs to the family Brassicaceae with an oil content ranging from 37 to 48%, it is considered to be one of the prominent edible oil yielding crops cultivated in India. Mustard, having chromosome number $2n=36$, is a natural amphidiploid derived

from an interspecific cross between *B. nigra* and *B. campestris* (Nagaharu 1935). 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 center of origin (Prakash and Hinata 1980), whereas South western China and North western Himalayan regions have been the centers of maximum diversity (Vaughan *et al.* 1963). Apart from oil richness, the protein content of mustard ranges from 24 to 30% and 35 to 40% based on whole seed and meal, respectively. These properties made it suitable for culinary and flavoring 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 (Manoj 2019).

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. Biometric tools like heritability in a broad sense (h^2_{bs}) and genetic advance (GA) are crucial components of genetic variability that serve to assess variation in the available germplasm and assist in the selection of a desirable genotype (Akhter 2021). Seed yield is considered to be the most dynamic and complex character, which depends on various morphological traits in addition to extraneous environmental factors. Distinguishing phenotypic variability into heritable (genotypic variability) and non-heritable (environmental variability) portions is fundamental to practising selection. Estimates of h^2_{bs} and GA enhance the efficiency of predicting genetic gain under selection (Prasad and Patil 2018). With this background, an experiment involving 10 elite genotypes of Indian mustard was designed to evaluate various components of genetic variability in addition to h^2_{bs} and GA.

MATERIALS AND METHODS

The experimental material containing ten promising genotypes of *Brassica juncea* (Table 1) was conducted during *rabi* 2017 over five different locations

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

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

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 Randomized Complete Block Design (RCBD) was laid out with three replications of 10 genotypes in a plot size of 2.25 m × 5 m across all the locations. In order to maintain an optimum crop stand, a recommended package of practises was adopted.

Observations on various plant morphological traits, viz., days to 50% flowering, days to maturity, plant height, number of racemes, primary and secondary branches per plant, number of siliqua per raceme, siliqua length, number of seeds per siliqua, 1000 seed weight, oil content and seed yield, were recorded on five randomly selected and labelled plants in each genotype at appropriate stages of crop growth. The data collected on various traits in 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), h^2_{bs} , GA and GA as percent mean (GAM) as suggested by Burton and Devane (1953), Hanson *et al.* (1956) and Johnson *et al.* (1955) respectively.

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

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

Characters	Range			Coefficient of variation		Heritability (%)	Genetic advance as percent of mean	Genetic advance as percent of mean
	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

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. Genotypic mean sum of squares was highly significant for all the traits under study, which pointed out that the genotypes under study were genetically diverse. Homogeneity among three replications was depicted through non-significant differences in the mean sum of squares due to replication. The observations documented on twelve characters from ten varieties of Indian mustard across five locations were pooled and analyzed to realise their performance. 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 noticed for the traits, viz., plant height, number of secondary branches and racemes per plant, number of siliqua per raceme and seed yield, signifying that the choice of these characters will have a significant demeanour on crop improvement. The efficiency of selection for any yield attributing component depends on both the degree of variability and how much of it is accessible to improvement. The most accurate information regarding the amount of advancement to be expected from selection could be gathered from the estimates of GCV and heritability. The magnitude of the PCV was frequently greater than the GCV for all character-

istics evaluated, demonstrating the environment had an impact on how the traits under investigation were expressed. GCV and PCV values were classified as low (0-10%), moderate (10-20%) and high (>20%) by (Sivasubramanian and Menon 1973). Higher values of GCV and PCV were obtained for the characters, viz., number of secondary branches per plant and number of racemes per plant which indicated the existence of substantial variability for these characters in the material studied and specified greater scope for selection to increase the expression of these characters. As a result, there is opportunity for augmenting the genotypes for more variability, which will help to improve the yield and its attributing traits.

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 showed more distinct differences between GCV and PCV, displaying the profound effect of the environment and the same were more vulnerable to changes in the environment. Practising selection based on phenotypic observations for these traits might not be very effective. The characters days to 50% 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

Tahira *et al.* (2014). The use of genotypic coefficient of variation would be limited as they are prone to change with fluctuations in the environment. So the estimates of h^2_{bs} have a role to play in determining the effectiveness of selection of character, provided they are considered in conjunction with the predicted GA, as suggested by Johnson *et al.* (1955) and Panse and Sukhatme (1967).

The h^2_{bs} expressed in percentage was classified as low (0-30%), moderate (30-60%) and high (>60%), as given by (Robinson *et al.* 1949). The estimate of h^2_{bs} 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 h^2_{bs} 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 seeds per siliqua (62.35), indicating that plant breeders can emphasise these characteristics in order to practice selection for genetic improvement in a much more effective manner.

GA signifies the improvement achieved in the mean genotypic value of a selected individual with reference to the parental population. GAM was categorised as low (0-10%), moderate (10-20%) and high (>20%) by (10). Among all the traits, only seed yield exhibited high GA (58.40) coupled with moderate h^2_{bs} (31.15) which signifies the governance of the trait by additive gene effects. Moderate h^2_{bs} is the result of substantial environmental effects and attempting selection may be effective in such cases. High h^2_{bs} as well as low GA were displayed by traits viz., days to 50% flowering and maturity, number of secondary branches and racemes per plant, number of siliqua per raceme, siliqua length, number of seeds per siliqua and oil content, which highlight the prevalence of non-additive gene action. The high h^2_{bs} is a result of the influence of favorable environmental conditions rather than the genetic constitution of a variety and practicing selection for such characters may not serve the purpose. Similar results were obtained by Ram (2014) and Synrem *et al.* (2014). On the other hand, moderate h^2_{bs} and low GA were revealed by the traits, viz., plant height, number of primary branches per

plant and 1000 seed weight.

The genotypes TM-210, TM-136 and KMR(E) 16-11 were the top seed yielders with appreciable oil content across all the locations, which could be recommended for extensive trials across various agroclimatic zones of Karnataka for their yield stability. Phenotypic observation alone may not be sufficient for selection to be successful. Therefore, systematic efforts must be undertaken to combine hybridization and recombination in mustard to generate the desired diversity in order to attain the stipulated high variability for the selection program. Hence, hybridization of superior, diverse genotypes followed by selection is recommended to generate the desired variability to develop transgressive segregants for economically important traits.

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