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Genotypic variability, heritability and genetic advance in Indian mustard [*Brassica juncea* (L.) Czern & Coss.] Genotypes

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Abstract
Sixty germplasm of Indian mustard were undertaken to determine relationships among yield and some yield components using direct selection parameters like variability, heritability, and genetic advance for eleven yield and its contributing characters. Analysis of variance for the design of the experiment indicated highly significant differences for all the characters. High phenotypic coefficient of variation (PCV) was recorded for seed yield plant^{-1}, secondary branches plant^{-1}, 1000-seed weight, primary branches plant^{-1} and length of main raceme and genotypic coefficient of variation (GCV) was highest for seed yield plant^{-1} followed by secondary branches plant^{-1}, 1000-seed weight, length of main raceme and plant height. The magnitudes of PCV and GCV were high for seed yield plant^{-1}, 1000-seed weight, secondary branches plant^{-1} and length of main raceme. High heritability estimates were observed for days to 50% flowering, days to maturity, plant height, oil content, 1000-seed weight and yield plant^{-1}. The expected genetic advance as percent of mean was high for seed yield per plant, 1000-seed weight, secondary branches plant^{-1}, plant height and length of main raceme. The high heritability coupled with high genetic advance for 1000-seed weight, plant height, seed yield plant^{-1} and length of main raceme would be helpful for indirect selection in improvement of seed yield.

Keywords: variability, heritability, genetic advance, Indian mustard

Introduction
Indian mustard [*B. juncea* (L.) Czern & Coss.] is one of the most important oil seed crops of the country and it occupies considerably large acreage among the Brassica group of oil seed crops. At global level, rapeseed-mustard crops are grown in 53 countries spreading over the 6 continents, covering an area of 22.33 million hectare with on average production of 33.17 million tonnes and an average yield of 1468 kg/hectare ranging from 333 kg/hectare (Tazikistan) to 6667 kg/hectare (Algeria). The contribution of rapeseed-mustard to the total oilseed acreage and production in India was 23.7% and 26% respectively during the year 2012-13. India stands first both in acreage and production of rapeseed and mustard in Asia. Rapeseed and mustard is cultivated in an area of 5.79 million hectares with a production of 6.31 million tonnes and with an average yield of 1089 kg/ha (Anonymous, 2015)[1]. In India, mustard and rape seed are being grown largely in states like, Uttar Pradesh, Rajasthan, Haryana, Assam, Gujarat, Punjab, West Bengal and Madhya Pradesh.

The average production of Indian Mustard is low in the country; this may be attributed to the lack of high yielding varieties, resistant to diseases and pests, high response to high inputs and other management practices. Keeping in view these problems, it is of prime importance to evaluate the limiting factors contributing to growth and yield of Indian Mustard. Creation of genetic variability and selection for important traits is a crucial activity that any plant breeder should apply to achieve better yield and other desirable agronomic traits. However, to carry out effective selection, the information on available genetic variation among Indian Mustard genotypes, the nature of component traits on which selection would be effective and the influence of environmental factors on each trait need to be known. Information on the nature and magnitude of variability and heritability in a population is one of the prerequisite for successful breeding programme in selecting genotypes with desirable characters. It is therefore, of great importance for breeder to know the heritability of the agronomical characters to improve the yield of the crop effectively.

Material and Methods
A field experiment was conducted in Augmented Block Design at Research Farm of Department of Genetics & Plant Breeding, NDUAT, Faizabad during *Rabi*, 2011-12.

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The experimental material comprised of Sixty diverse genotypes of Indian Mustard including elite lines and land races with four popular checks viz., Vardan, Ashirwad, Kranti, and Maya. These genotypes were obtained from the germplasm maintained at Oilseed section of Genetics and Plant Breeding Department. These lines were grown in single row plot of 5 meter length. Each block consisted of 10 entries plus 4 checks. The spacing between row to row and plant to plant was 30 cm and 15 cm maintained by thinning. On the basis of five randomly selected plants, data were recorded on days to maturity, plant height, primary and secondary branches plant[-1], length of main raceme, number of siliquae on main raceme, number of seeds siliqua[-1], seed yield plant[-1], 1000-seed weight, oil content (%) except days to 50% flowering which was recorded on plot basis.

Analysis of variance (ANOVA) for Augmented Block Design for all attributes (major and minor) was done using statistical software, Windostat ver.80. Analysis of variance and the genetic parameters were computed by following standard statistical procedure. The mean data were subjected to analysis of variance as per standard procedure outlined by Panse and Sukhatme (1967) [2]. The Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV) and heritability in broad sense were calculated using the formula suggested by Burton and de Vane (1953) [3]. Genetic advance was calculated by the method suggested by Johnson et al. (1955) [4].

Results and Discussion

The analysis of variance exhibited highly significant difference among genotypes for all the characters indicating the presence of adequate amount of genetic variability among the genotypes. The mean squares due to blocks, checks and error for all the characters are presented in (Table-1). The existence of genetic variability in the population provides sample opportunities for selection being effective. For any sound breeding programme, it is essential to have a large variation in the material at the hand of breeder. The characters of economic important are generally quantitative in nature and exhibited a considerable degree of interaction with the environment. The phenotypic coefficients of variation (PCV) were invariably slightly higher than their corresponding genotypic coefficients of variation (GCV) due to environmental influence (Table-2). The higher estimates of phenotypic and genotypic coefficient of variation were observed for seed yield plant[-1], secondary branches plant[-1], 1000-seed weight. Length of main raceme, primary branches plant[-1], plant height and secondary branches plant[-1] showed moderate value of coefficient of variation. In general the phenotypic coefficient of variation was higher than genotypic

coefficient of variation which indicated that environment played a considerable role in expression of these traits. Relatively smaller values of environmental coefficients of variation (ECV) for these traits suggested that their phenotypic expression is less influenced by environments. Highest genetic variability was observed in Indian mustard for secondary branches per plant, seed yield per plant as reported by Kumar and Mishra (2007) [5], Ram and Verma (2011) [6] and Yadava et al. (2011) [7].

Knowledge of heritability of a character is important as it indicates the possibility and extant to which improvement is possible through selection (Robinson et al. (1949) [8]. The efficiency of selection depends upon the magnitude of heritability of traits, because it measures the transmissibility of characters from parents to off-spring. Through the estimates of heritability in biometrical studies are influenced by method of estimation, generation of study, sample size and environment even through it helps the breeders during selection. The present study revealed that estimates of broad sense heritability (Table-3) were high (>50%) for all the traits studied except number of primary and secondary branches plant[-1] and seeds siliqua[-1]. High heritability for different traits under study viz., days to 50% flowering, days to maturity, plant height, oil content and seed yield plant[-1].

High genetic advance in per cent of mean (>20%) was recorded for seed yield plant[-1] (39.02), 1000-seed weight (29.64), number of secondary branches plant[-1] (25.24), plant height (23.59) and length of main raceme (21.13) indicating that direct selection for these traits would be effective for the improvement. Moderate estimates of genetic advance in per cent of mean (10-20%) were recorded for number of primary branches (16.32), silique on main raceme (15.69) and days to 50% flowering (15.36), and its low estimate (<10%) was recorded for seeds siliqua-1 (9.01), days to maturity (5.51) and oil content (4.69). The character having high heritability with high genetic advance generally indicates that heritability is more due to the additive gene effect and advocated the use of high estimates of heritability along with high magnitude of genetic advance for genetic improvement in any trait through selection. Higher heritability does not always ensure an increased genetic advance. Heritability estimates together with genetic advance are generally regarded to be more useful in predicting the grain through selection (Johnson et al. 1955). High heritability coupled with high genetic advance in per cent of mean were observed for days to 50% flowering, das to maturity, plant height, 1000-seed weight and oil content. The estimates of genetic variability and genetic advance in per cent of mean for most of the characters under study are in accordance with earlier reports Upadhyay and Kumar (2008) [9], Ram and Verma (2011) [6, 10], Yadava et al. (2011) [7, 11].

Table 1: Analysis of variance of Augmented Block Design for 11 characters in mustard

	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Length of main raceme (cm)	Siliquae on main raceme	Seeds/ siliqua	1000-seed weight (g)	Oil content (%)	Seed yield/ plant(g)
Block (ignoring Treatments)	5	22.50**	20.36**	3672.30**	0.76	14.54*	698.54**	146.40**	2.11	1.18**	1.96**	38.32**
Treatment (eliminating Blocks)	63	31.67**	21.76**	338.25**	1.09*	11.30*	76.86*	35.42*	2.42	0.54**	1.71**	7.62*
Checks	3	78.49**	39.82**	235.82**	0.80	12.74	152.71**	96.95**	0.70	1.10**	10.52**	0.35
Checks+Var vs. Var.	60	29.33**	20.86**	343.37**	1.10*	11.23*	73.07	32.34	2.51	0.51**	1.27**	7.98*
ERROR	15	0.49	1.15	41.65	0.41	4.37	31.27*	15.19	1.50	0.09	0.12	3.22
Block (eliminating Check+Var.)	5	2.04*	3.77*	879.66**	0.82	14.96*	109.39	5.77	0.57	0.08	0.30	5.27
Entries (ignoring Blocks)	63	33.29**	23.08**	559.89**	1.08*	11.27*	123.62**	46.58**	2.54	0.62**	1.85**	10.24**
Checks	3	78.49**	39.82**	235.82**	0.80	12.74	152.71**	96.95**	0.70	1.10**	10.52**	0.35
Varieties	59	30.37**	17.55**	555.41**	0.92*	9.56*	120.90**	44.76*	2.67	0.61**	1.44**	10.76**
Checks vs. Varieties	1	70.30**	298.81**	1796.62**	11.57**	107.51**	196.58*	2.77	0.41	0.13	0.06	9.40
ERROR	15	0.49	1.15	41.65	0.41	4.37	31.27	15.19	1.50	0.09	0.12	3.22

* Significant at 5 per cent probability level,   ** Significant at 1 per cent probability level

Table 2: Estimates of range, mean, coefficients of variation (PCV and GCV), heritability and genetic advance for 11 quantitative characters in Indian mustard.

Parameter	Range	Mean	GCV (%)	PCV (%)	Heritability (h^2b)	Genetic Advance	Genetic Advance (% of mean)
Days to 50% flowering	47.29-76.79	62.94	7.53	7.61	97.89	9.69	15.36
Days to maturity	110.12-133.12	125.53	2.80	2.92	91.05	6.94	5.51
Plant height (cm)	98.96-208.95	162.94	12.05	12.68	90.32	38.59	23.59
Primary branches/ plant	3.27-7.32	5.50	11.38	16.35	48.47	0.89	16.32
Secondary branches/plant	4.12-20.27	11.27	17.81	25.90	47.31	2.80	25.24
Length of main raceme (cm)	49.38-90.06	66.17	12.40	14.99	68.44	14.03	21.13
Siliquae on main raceme	28.70-61.30	47.93	9.87	12.79	59.56	7.52	15.69
Seeds/ siliqua	9.05-16.65	13.09	7.18	11.78	37.14	1.18	9.01
1000-seed weight (g)	2.80-6.40	3.93	15.92	17.62	81.63	1.17	29.64
Oil content (%)	37.33-43.80	41.29	2.41	2.55	89.03	1.93	4.69
Seed yield/ plant(g)	3.62-18.78	10.11	23.70	29.66	63.89	3.93	39.03

* Significant at 5 per cent probability level, ** Significant at 1 per cent probability level

Conclusions

Thus it may be concluded that there is sufficient genetic variability for most of the economic traits studied in the above genetic material and a combination of various traits contributes to seed yield. In this study it is find that Seed yield plant^{-1}, 1000-seed weight, length of main raceme, number of primary and secondary branches plant^{-1} showed maximum potential for effectiveness of selection, because these traits show high PCV, GCV, heritability and genetic advance. This would help us in designing the selection methodology which can further be utilized in the breeding programme for improvement of seed yield in Indian Mustard.

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