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Studies of genetic variability in Indian mustard (*Brassica juncea* L. Czern and Coss)

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Abstract

The present research was carried out at Research cum Instructional form of S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur (C.G.) at during the year 2020-21. Studies undertaken to estimate the genetic variability for 20 characters among 20 different genotype of Indian mustard. The analysis of variance show large variability present among the genotype studied. High to moderate GCV and PCV estimates for the traits number of siliqua per plant, harvest index (%), seed yield per plant and number of secondary branches per plant. High heritability coupled with high genetic advanced as percentage of mean were observed for the character like number of siliqua per plant, harvest index (%), seed yield per plant (g) and number of secondary branches per plant.

Keywords: Genetic, variability, mustard, *Brassica juncea* L.

Introduction

Indian mustard (*Brassica juncea* L.) belong to family brassicaceae or cruciferae with chromosome number $2n=36$. Indian mustard is one of the most important edible oil with lowest amount of saturated fats of the country and it occupies considerably large acreage among the brassica group oil seed, leafy vegetable rich in minerals, antioxidant and tasteful condiment crop. (Akabri *et al.* 2015)^[1]. Brassica constitute different crop comprising two distinct form from their breeding point of view, one is self compatible and self pollinated forms comprising yellow sarson, toriya type brown sarson (*Brassica campestris*), Indian mustard (*Brassica juncea* L. Czern and Coss) and gobhi sarson (*Brassica napus* L.) while, other group consists of self incompatible and highly cross- pollinated crop *viz.*, lotni type brown sarson (*Brassica campestris* L.) and taramira (*Eruca sativa* L.). It has 38 to 42% of oil and 24% protein. Since oilseed account for nearly 14% of gross national product and 7% of the value of all agriculture products, therefore Indian mustard assumes as an important crop. (Bhanu, 2019)^[3].

Material and Method

The present study was carried out at Research cum instructional farm S.G. College of Agriculture and Reaserch Station kumhrawand, Jagdalpur (C.G.) at during *rabi* season in 2020-21. Geographically, Chhattisgarh is situated at longitude (E) $19^{\circ} 5' 39''$ and latitude (N) $81^{\circ} 59' 33''$. Twentee different genotype of Indian mustard including two check variety (C.G. Saraso and Pusa mustard 25) were taken for study obtained from DRMR Bharatpur, (Rajasthan). This genotype was grown under late sowing and early maturity condition in a Randomized Complete Block Design using three replication each. Each plot consisted of single row of 5 meter length and 1.8 meter width. The distance between plant to plant 10 cm and row to row 30 cm is maintained. All the recommended culture and plant protection practice were adopted for raising a good crop. Data were recorded on five Randomly selected plants from each plot for twenties character *viz.* days to 50% of flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of silqua per plant, siliqua length (cm), number of seed per siliqua, test weight of 1000 seed (g), harvest index (%), oil seed content (%) and seed yield per plant.

Genotypic and phenotypic coefficient of variation was estimate by using the formula suggested by Burton and De Vane (1953):

$$GCV (\%) = \frac{\sigma_g^2}{mean} \times 100$$

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$$PCV (\%) = \frac{\sigma_p^2}{mean} \times 100$$

Where, σ_g^2 = Genotypic variance, σ_p^2 = phenotypic variance. Heritability in broad sense for each character was analysed by using the method suggested by Hanson *et al.* (1956) [6].

$$Heritability (h^2) (bs) \% = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where, h^2 (bs) % = heritability in broad sense, σ_g^2 = genotypic variance, σ_p^2 = phenotypic variance

Genetic advanced as percentage of the mean (GAM) estimated by using the formula suggested by Johnson *et al.* (1955) [8].

$$Genetic\ advanced\ as\ percentage\ of\ the\ mean = \frac{GA}{GM} \times 100$$

Where, GA = Genetic advanced, GM = General mean

Result and Discussion

The result on analysis of any breeding program lies upon the thorough knowledge of genetic variability, heritability and type of gene action involved in the inheritance of importance of improvement of desirable characters thus, and success of genetic enhancement is attributed to the magnitude and nature of variability present for a specific character.

Genotypic and phenotypic coefficient of variation was high in case of number of siliqua per plant (18.95, 19.34), harvest index (18.68, 19.10), seed yield per plant (15.84, 16.42) and number of secondary branches per plant (13.66, 14.27) which indicates the presence of high amount of variation among the genotype. Lowest genotype and phenotype coefficient of variation estimate was found in traits seed oil content (2.44, 4.39), days to maturity (3.77, 4.32), plant height (4.83, 5.63) and days to 50% flowering (5.89, 7.32). the other character which recorded moderate GCV and PCV have in number of primary branches per plant (11.15, 11.84), leaf length (8.50, 9.37), 1000 seed weight (8.10, 8.95), number of seed per siliqua (7.76, 8.65), leaf width (7.31, 8.50) and siliqua length

(7.05, 8.05). Respectively, these approximations of the current study were authorized with the outcome by Verma *et al.* (2021), Kumar *et al.* (2019) [9], bind *et al.* (2015) [4], Amsalu *et al.* (2020) [2], Singh *et al.* (2018) [17], Raut *et al.* (2019) [15], Lyngdoh *et al.* (2017) [10].

Heritability estimate ranged from 30.95 (seed oil content) to 96.01 (number of siliqua per plant). High heritability coupled with high genetic advance as percentage of mean indicated presence of additive gene action in these traits *viz.*, number of siliqua per plant (96.01, 49.03), harvest index (95.63, 48.22), seed yield per plant (93.02, 40.32), number of secondary branches per plant (91.61, 34.52), number of primary branches per plant (88.72, 27.72). High heritability with low genetic advance as percentage of mean it is indicated non-additive gene action in these traits *viz.*, leaf length (82.22, 20.34), 1000 seed weight (81.89, 19.35), number of seed per siliqua (80.61, 18.40), siliqua length (76.84, 16.32). Respectively, the high heritability is being exhibited due to favourable influence of environment rather than genotype and selection for such traits may not be rewarding. Moderate heritability and low genetic advance as percentage of mean was recorded for the characters plant height (73.77, 10.96), and days to 50% flowering (64.83, 12.52). The finding of present study was in agreement with the finding by Jat *et al.* (2019) [7], Pal *et al.* (2019) [13], Rout *et al.* (2019) [15], Yadav *et al.* (2011), Shekhawat *et al.* (2018) [16], Lyngdoh *et al.* (2017) [10], Verma *et al.* (2016) [18], and Malik *et al.* (2018) [12].

The value of phenotypic coefficient of variation (PCV) is higher than genotypic coefficient of variation (GCV) recorded for the traits number of siliqua per plant followed by harvest index, seed yield per plant, number of secondary branches per plant, number of primary branches per plant, leaf length, 1000 seed weight, number of seed per siliqua, leaf width, siliqua length, days to 50% flowering, plant height, days to maturity and seed oil content suggested that, the apparent variation is not only due to genotype but also due to the influence of environment. Selection for such traits sometimes may be misleading.

Table 1: Analysis of variances for seed yield and its attributing traits in Indian mustard

Source of variation	Degree of freedom	DF	DM	PH(cm)	LL(cm)	LW (cm)	NPBPP	NSBPP	NSPP	SL (cm)	NSPP	TW (g)	HI	OC (%)	SYPP
Replication	2	6.38	4.94	0.52	0.04	0.93	0.001	0.23	602.93	0.031	0.030	0.022	0.293	2.50	0.04
Treatment	19	29.27**	55.59**	242.67**	15.56**	2.74**	1.65**	11.41**	9526.64**	0.365**	3.67**	0.379**	69.03**	5.0**	10.18**
Error	38	4.48	5.24	25.71	1.05	0.29	0.07	0.34	130.09	0.033	0.27	0.026	1.04	2.13	0.25
SE(d)		1.73	1.87	4.14	0.84	0.44	0.21	0.48	9.31	0.15	0.43	0.13	0.83	1.19	0.41
C.D.at 5%		3.51	3.80	8.41	1.70	0.89	0.43	0.96	18.93	0.30	0.87	0.27	1.69	2.42	0.83
C.V.(%)		4.34	2.11	2.88	3.95	4.33	3.98	4.13	3.86	3.87	3.81	3.81	3.99	3.65	4.34

*, ** significant 5% and 1% level respectively,

DF = days to 50% flowering, DM = days to maturity, PH = plant height, LL = leaf length, LW = leaf width, NPBPP = number of primary branches per plant, NSBPP = number of secondary branches per plant, NSPP = number of siliqua per plant, SL = siliqua length, NSPP = number of siliqua per plant, TW = 1000 seed weight, HI = harvest index, OC = oil content, SYPP = seed yield per plant

Table 2: Genetic parameters of variation for seed yield and its component traits in Indian mustard

S. No.	Character	Mean	Min	Max	GCV (%)	PCV (%)	Heritability	GA% mean
1	DF	48.80	43.33	53.67	5.89	7.32	64.83	9.77
2	DM	108.63	102.67	118.00	3.77	4.32	76.21	6.78
3	PH	175.91	159.04	195.07	4.83	5.63	73.77	8.55
4	LL	25.89	21.35	29.15	8.50	9.37	82.22	15.87
5	LW	12.36	10.57	14.44	7.31	8.50	74.05	12.97
6	NPBP	6.52	5.23	8.20	11.15	11.84	88.71	21.63
7	NSBPP	14.06	11.47	19.20	13.66	14.27	91.61	26.93
8	NSPP	295.30	174.27	383.20	18.95	19.34	96.01	38.26

9	SL	4.71	4.21	5.37	7.05	8.05	76.84	12.74
10	NSPS	13.71	12.27	16.13	7.76	8.65	80.61	14.36
11	TW	4.24	3.69	5.25	8.10	8.95	81.89	15.10
12	HI	25.49	18.26	33.32	18.68	19.10	95.63	37.63
13	OC	40.03	36.97	42.17	2.44	4.39	30.95	2.80
14	SYPP	11.49	6.58	14.48	15.84	16.42	93.02	31.46

DFF = days to 50% flowering, DM = days to maturity, PH = plant height, LL = leaf length, LW = leaf width, NPBPP = number of primary branches per plant, NSBPP = number of secondary branch per plant, NSPP = number of siliqua per plant, TW = 1000 seed weight, HI = harvest index, OC = oil content, SYPP = seed yield per plant

Conclusion

High heritability coupled with high genetic advance as percentage of mean indicated presence of additive gene action in these traits viz., number of siliqua per plant, harvest index, seed yield per plant, number of secondary branches per plant and number of primary branches per plant, additive gene action is pronounced in the expression of these character early generation selection would be effective in breeding programme. High heritability is found with low genetic advance as percentage of mean for traits leaf width, 1000 seed weight, number of seed per siliqua, siliqua length, days to maturity, leaf width which is indicative of aforesaid characters are governed under non additive gene action.

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