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Genetic variability parameters studies in mustard (*Brassica juncea* Czern & Coss)

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Abstract

The present investigation consists of ten mustard genotypes and the experiment was conducted during rabi-2010 in Randomized Block Design with three replications. The data were recorded for 10 quantitative characters to study genetic variability, heritability and genetic advance. On the basis of mean performance, high grain yield per plant were exhibited by different genotypes. Analysis of variance among 10 genotypes showed significant differences for all characters studied. Highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for days to maturity followed by no. of seed per siliquae, 1000 seed weight, no. of siliquae on main fruiting branches, yield per plant, no. of primary branches, days to 50% flowering and number of secondary branches indicating that these characters could be used as selection for crop improvement. On the basis of high estimates of heritability coupled with high genetic advance was observed for plant height, days to maturity, yield per plant and days to 50% flowering indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

Keywords: Mustard, *Brassica juncea*, genetic variability, heritability and genetic advance

Introduction

Mustard is the third most important source of edible oil of the world after soybean and palm. In India it ranks second in acreage superseded by groundnut only. Mustard crop is grown both in tropical and subtropical countries. Out of seven edible oilseed crops cultivated in India, rapeseed mustard occupies second position in area and production next to groundnut sharing 27.80% in the India oilseed economy and countries 28.60 % in the total oilseeds production (Bineeta Devi 2017). Indian mustard (*Brassica juncea* L. Czern & Coss) is an important Rabi season crop extensively grown as under irrigated condition. Yield is complex character which dependent on the various yield contributing traits. Thus the study of correlation between yield and its component is of primary importance in formulating the selection criteria under crop improvement. Selection of any desirable trait is generally preformed based on the phenotypic value of the plants. Which is partly determined by genotypes? Which is heritable and partly by environment which is non-heritable. Therefore, it is necessary to know the various components of the yield and its mutual correlation with other independent traits. This is because, selection would be more efficient if it is based on some components which less sensitive to environment. It is well known that correlation mainly does not fulfill the purpose of the researcher because it does not detect the characters having indirect effects on seed yield. In such situation path coefficient analysis developed by Wright (1921) [20] put forward the real importance of such characters of partitioning the correlation coefficient in to direct as well as indirect effects. The correlation between two characters can be partitioned into a portion that is due to genetic cause and the other due to environmental factors.

Material and Methods

The present field experiment was conducted at Crop Research Center Department of Genetics & Plant Breeding, Institute of Agricultural Sciences, Bundelkhand University Jhansi (UP) in Randomized block design (RBD) with three replications. The mustard crop was recommended packages of practices were followed with ten genotypes viz. KNR-10-2, YSK-09-306, STV TORI RABI (I), STV TORI RAI, KANTI, VAIBHAV, ROHANI, BARDAN, KRISHNA and VARUNA of Indian mustard during Rabi- 2010. Observations were recorded on five randomly selected plants in each genotype and replication for different ten characters. These traits were computed on basis of mean data after computing for each character was subjected to standard method of analysis of variance following Panse and Sukhatme (1978) [14] phenotypic and genotypic coefficient of variation, heritability (Broad Sense) and genetic advance as percent of

Mean were estimated by the formula as suggested by Burton (1952) [6] and Johanson *et al.* (1955).

Results and Discussion

Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. The analysis of variance for different characters indicated the existence of highly significant differences for all the ten characters study at 1% level of significance suggesting each and every genotype are genetically divergent from each other and there is ample scope for selection of characters from these diverse sources for yield and its components (Table 1). These findings were in accordance with the findings of Sen *et al.* (2013) [15]. A wide range of variance was observed for all the ten attributes. In general the phenotypic coefficient of variance was higher than genotypic coefficient variance for all yield and its contributing characters indicate the influence of environmental factors on these characters. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) ranged between (1.57 and 2.12) to (16.09 and 16.45) for plant height and days to maturity respectively. The highest GCV and PCV was recorded for days to maturity (16.09 and 16.45) followed by number of seed per siliquae (15.52 and 14.90), 1000 seed weight (12.06 and 10.97), number of siliquae on main fruiting branches/recame (9.91 and 9.06), yield per plant (9.52 and 8.31), no. of primary branches (9.36 and 8.11), days to 50% flowering (8.92 and 8.57) and number of secondary branches (5.69 and 3.40). Similar results were also reported by Bineeta Devi (2017). Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV is presenting Table-2 among the all characters and high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of yield improvement through selection of these traits. Closely relationship between GCV and PCV was found in all the attributes and PCV values were slightly greater than GCV, observing very little influence of environment for their expression. The amount of genetic variation considered alone will not be of much use to the breeder unless supplemented

with the information on heritability estimate, which gives a measure of the heritable portion of the total variation. It has been suggested by Burton and Devane that the GCV along with heritability estimate could provide a better picture of the amount of advance to be expected by phenotypic selection. Since genetic advance is dependent on phenotypic variability and heritability in addition to selection intensity, the heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection. Heritability in broad sense includes both additive and non-additive gene effects. While, narrow sense heritability includes only additive components. In the present study, heritability in broad sense was estimated. Highest heritability in broad sense (> 60%) was recorded in the case of days to maturity (95.70) followed by days to 50% flowering (92.40), number of seed per siliquae (92.20), number of siliquae on main fruiting branch (83.60), 1000 seed weight (82.60) and yield per plant (76.20). The high heritability denotes high proportion of genetic effects in the determination of these characters and can be adopted for improving yield per plant. Studied have been reported earlier also by Singh *et al.*, Sharma *et al.*, Kumar *et al.* and Yadava *et al.* Maximum genetic advance expressed as percentage of mean was observed high (>20%) for plant (32.20), days to maturity (31.45) and yield per plant (20.19). Moderate genetic advance as percentage of mean (10-20%) was revealed for length of main fruiting branch (18.90) and number of secondary branches (10.10). High heritability (h^2) coupled with high genetic advance was observed for number of siliquae on main fruiting branch, yield per plant, number of seeds per siliquae, length of main fruiting branch, number of primary branches, plant height and number of secondary branches. High heritability coupled with high genetic advance for some of these attributes have also been observed earlier by Mahla *et al.*, Kumar *et al.*, Tiwari *et al.* and Kumar *et al.* This indicates substantial contribution of additive genetic variance in the expression of these traits and can be more useful in hybridization and selection for higher grain yield and these characters are largely controlled by additive gene action.

Table 1: Analysis of variance for different characters in Indian mustard

Source of variation	Replication (r)	Treatment (t)	Error (e)
d. f.	2	9	18
Days to 50% flowering	8.234	67.200**	1.788
Plant height	0.687	17.030**	3.662
Number of primary branches	9.092	9.336**	0.543
Number of secondary branches	0.309	3.246*	1.217
Length of main fruiting branch	11.769	7.070*	1.852
Number of siliquae on main fruiting branch	2.905	10.119**	0.621
Days to maturity	4.203	741.165**	10.816
Number of seeds per siliquae	0.259	12.355**	0.340
1000 seed weight	0.041	6.505**	0.042
Yield per plant	163.875	417.576**	39.399

*significant at 5%, ** significant at 1%

Table 2: Estimation of parameters of Coefficient of Genetic Variability, Heritability and Genetic advance for Characters in Mustard

Characters	Coefficient of Variation		Heritability % (bs)	Genetic advance	Genetic advance (% of mean)
	GCV (%)	PCV (%)			
Days to 50% flowering	8.571	8.924	92.405	9.512	9.512
Plant height	1.573	2.128	54.932	32.234	39.350
Number of primary branches	4.112	9.362	19.335	0.332	4.245
Number of secondary branches	3.405	5.697	35.754	1.017	1.086
Length of main fruiting branch	2.236	3.203	48.432	1.897	2.453
Number of siliquae on main fruiting branch	9.068	9.915	83.645	3.354	9.549

Days to maturity	16.097	16.454	95.731	31.452	39.432
Number of seeds per siliquae	14.096	15.525	92.235	3.964	1.876
1000 seed weight	10.973	12.066	82.658	0.967	2.879
Yield per plant	8.311	9.528	76.245	20.197	39.235

Conclusion

In the present investigation which included 10 genotypes of mustard was carried out in order to study the nature and amount of variability, heritability and genetic advance for 10 quantitative/polygenic traits. In this study illustrated the existence of wide ranges of variations for most of the trait among the Indian mustard genotypes and opportunities of the genetic gain through selection or hybridization. Hence, improving one or more of these traits could result in high seed yield for Indian mustard. Analysis of variance among 10 genotypes showed significant difference for all characters under studied. Highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for Days to maturity, Number of seeds per siliquae, 1000 seed weight, Number of siliquae on main fruiting branch and Yield per plant indicating that these characters could be used as selection for crop improvement. High heritability coupled with high genetic advance as percent of mean estimated for Days to maturity, Plant height and Yield per plant indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

Reference

- Al-Jibouri HA, Miller PA, Robinson HF. Genotype and environmental variances and co-variance in upland cotton cross of interspecific origin. *Agron. J.* 1958; 50:633-637.
- Ali N, Pak J Bot. 1985; 17(2):297-303.
- Anonymous. Agriculture centers for monitoring. *Indian Economy*, 2006, 163-169.
- Asheesh Kumar Tiwari, Sanjay Kumar Singh, Amit Tomar, Mahak Singh. Heritability, genetic. Advance and correlation coefficient analysis in Indian mustard (*Brassica Juncea* (L.) Czern & Coss). *Journal of Pharmacognosy and Phytochemistry*. 2017; 6(1):356-359.
- Bineeta Devi. Correlation and path analysis in Indian mustard (*Brassica juncea* L.) in agro – climatic conditions of Jhansi (U.P.). *Journal of Pharmacognosy and Phytochemistry*. 2018; 7(1):1678-1681.
- Burton GW. Quantitative Inheritance in Grasses in: *Proc. 6th Int. Grassland Congress*. 1952; 7:273-283.
- Chaudhary SK, Sharma SK. Notes on inheritance of some quantitative characters in a cross of Indian mustard. *Indian J Agric Sci.* 1982; 5(2):23-25.
- Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J* 1957; 5(1):515-518.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agron. J.* 1955; 47:314-318.
- Kumar Rajeev, Gaurav SS, Jayasudha S, Kumar Hitesh. Study of correlation and path coefficient analysis in germplasm lines of Indian mustard (*Brassica juncea* L.). *Agricultural Science Digest*. 2016; 36(2):92-96.
- Kumar S, Mishra MN. Genetic variation and association analysis in Indian mustard (*Brassica juncea* (L.) Czern and Coss] and *Brassica campestris* L. variety toria, *Crop Research*. 2006; 31(3):391-393.
- Mahla HR, Jambhulkar SJ, Yadav DK, Sharma R. Genetic variability, correlation and path analysis in Indian mustard (*Brassica juncea* (L.) Czern and Coss.]. *Indian J Genet Plant Breed.* 2003; 6(3):171-172.
- Mondal SK, Khajuria MR. Genetic analysis for yield attributes in mustard (*Brassica juncea* (L.) Environment and Ecology. 2000; 18(1):1-5.
- Panse VG, Sukhatme PV. *Statistical methods for Agricultural Workers*. ICAR, New Delhi. 1978, 235-246.
- Sen, Ramraj, Singh, Bhuri and Singh, SP. Relationship among Yield Components and Selection Criteria for Yield Improvement in Indian Colaza (*Brassica juncea* (L) Czern & Coss). *Jour Pl Sci Res*. 2013; 29(2):121-127.
- Sharma Ram, Mohan Kumar, Brijendra Kumar K, Chauhan MP. Variability Analysis for Yield and its component of Indian mustard (*Brassica juncea* (L.) Trends in Biosciences. 2014; 7(17):2539-2543.
- Shweta, Om Prakash. Correlation and path co-efficient analysis of yield and yield components of Indian mustard (*Brassica juncea* (L.) Czern and Coss International Journal of Plant Sciences. 2014; (2):428-430.
- Singh SK, Singh AK. Inter-relationship and path analysis for seed yield in Indian mustard. *Indian J Ecol.* 2010; 3(7):8-12.
- Singh VK, Singh D, Singh AK. Genetic divergence for important economic and quality traits in Indian mustard (*Brassica juncea* L. Czern &Coss), *Pantnagar Journal of Research*. 2011; 9(2):183-188.
- Wright S. Correlation and causation. *J. Agric. Res.* 1921; 1(20):557-585.
- Yadava DK, Giri SC, Vignesh M, Vasudev Sujata, Yadav KA, Dass B *et al.* Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). *Indian J Agril Sci*, 2011; 8(1):712-716.