Int.J.Curr.Microbiol.App.Sci (2020) *9*(1): 2556-2563

EXCELLENT PUBLISHERS

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 9 Number 1 (2020)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2020.901.290

Genetic variability and Trait association studies in Indian mustard (*Brassica juncea* L. Czern & Coss)

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Keywords

Heritability, genotypic correlation, phenotypic correlation and path analysis

Article Info

Accepted:
22 December 2019
Available Online:
20 January 2020

A B S T R A C T

The basic requirement for crop improvement program is existence of genetic variability for selection of superior genotypes. For efficient indirect selection of complex characters it is important to know the association between traits. With the aim to study the genetic variability and correlation between traits among thirty Indian mustard genotypes, these genotypes were evaluated in Randomized Block Design during *Rabi* 2016-2017. Study revealed that number of secondary branches, seed yield per plant and seed yield per plot exhibited high to moderate GCV accompanied with high to moderate PCV indicating that selection may be effective based on these traits. High to moderate heritability with high to moderate genetic advance was found for number of secondary branches and number of siliqua per plant. Correlation studies indicated seed yield per plot showed positive and significant correlation with days to 50% flowering, days to maturity, number of siliqua per plant, length of siliqua and number of seeds per siliqua. The path coefficient analysis revealed that seed yield per plot, days to 50% flowering and plant height has positive direct effect on seed yield per plant which suggests that direct selection for these traits can be done for improvement of yield.

Introduction

Indian mustard is one of the most important oilseed crops of India which occupies considerably large area among the Brassica group of oilseed crops. It is self-pollinated crop but around 2-15 per cent of cross pollination occurs due to entomophily. For efficient selection, estimation of parameters like phenotypic and genotypic coefficients of variation, heritability and genetic advance is pre-requisite. Heritability estimates coupled with genetic advance is helpful in judging the reliability of character for selection. Character with high heritability accompanied by low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding.

The present investigation was designed to access heritability, association between traits and identify the suitable selection criteria for mustard improvement. Since availability of sufficient genetic variability is important in crop improvement program it is essential for a breeder to measure the total genetic variability available in germplasm on the basis of parameters like phenotypic coefficient of variation and genotypic coefficient of variation. Heritability and genetic advance help in deciding the worth of the trait during selection.

Different yield attributing traits very often exhibit variable direct and/or indirect associations with seed yield as well as association among themselves that create a complex situation making the selection process for breeder strenuous. Path coefficient analysis offers a more realistic picture of the interrelationship, as it partitions, the correlation coefficient in direct and indirect effects of the variables. Thus character association and path analysis provides the information of yield contributing characters and breeder can practice selection using this information for the isolation of superior genotypes which can be used in further improvement programs.

Material and Methods

The experiment was conducted during *Rabi* 2016-17 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. Thirty Indian mustard genotypes were sown under Randomized Block Design in three replications. The observations were recorded on ten randomly selected plants for ten traits *viz.* days to flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, average siliqua length (cm), seeds per siliqua, number of siliqua per plant, seed yield per plant (g) and seed yield per plot (Kg). Each character was tested for significance as per methodology advocated by Panse and Sukhatme (1967). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the formula given by Al-Jibouri *et al.* (1958) while heritability in broad sense (h^2) was estimated by formula given by Burton and De Vane (1953) and genetic advance i.e. the expected genetic gain were calculated by using the procedure proposed by Johnson *et al*. (1955). The path analysis was carried out to know direct and indirect effects of the components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1957).

Results and Discussion

Analysis of variance revealed that mean sum of square due to replication showed significant variation for days to maturity, number of secondary branches, number of siliqua per plant, siliqua length, seeds per siliqua, seed yield per plant and seed yield per plot suggesting sufficient variation between blocks for these traits due to variation in soil composition etc. (Table 1). Mean sum of square due to genotype showed significant variation for all the traits studied suggesting sufficient variation among genotypes. High magnitude of variability in Indian mustard germplasm and varieties has been reported earlier for various characters like days to 50% flowering, days to maturity, plant height, total siliqua/plant and seed yield/plant (Kumar and Misra 2007). The reason for high magnitude of variability in the present study may be due the fact that the genotypes selected were developed in different breeding programmes representing different agro-climatic conditions of the country.

The mean for days to flowering ranged from 40.66 to 61.33 days with an average of 53.09 days while for days to maturity mean ranged from 118.00 to 129.00 days with an average of 122.30 days (Table 2). The minimum value of mean for plant height was 194.33 cm while maximum value was 250.86 cm with an average value of 222.37 cm. For number of primary branches minimum value was 4.66 and maximum value was 6.86 with an average value of 5.76 while for number of secondary branches minimum value was 7.20 and maximum value was 17.73 with an average of 11.95. The mean for siliqua per plant ranged from 223.53 to 482.60 with an average of 315.03 while the mean for siliqua length ranged from 3.81cm to 5.12 cm with an average of 4.50 cm. The seeds per siliqua had mean values ranging from 10.13 to 15.10 with an average value of 12.53. The minimum value for seed yield per plant was 633.33 g while maximum value was 1060.00 g, with an average value of 885.35 g. The mean value for seed yield per plot ranged from 14.07q/ha to 23.55 q/ha with an average of 19.67 q/ha.

The estimates of GCV, PCV, heritability (broad sense) and genetic advance as per cent of mean are presented in Table 3. The phenotypic coefficient of variation was found to be higher than genotypic coefficient of variation for all the traits. GCV ranged from 2.05 for days to maturity to 16.85 for number of secondary branches. GCV for number of secondary branches, number of siliqua per plant, yield per plant and yield per plot were found to be in the moderate range while all the other were in low range of GCV. PCV for the traits ranged from 2.49 for days to maturity to 20.47 for siliqua per plant. PCV for siliqua per plant (20.47) was found to be in the high range while for traits like number of primary branches, number of secondary branches, seeds per siliqua, seed yield per plant and seed yield per plot were in the moderate range, whereas all the others were in the low range of PCV. Traits like, number of secondary branches, seed yield per plant and yield per plot exhibited high or moderate GCV accompanied with high or moderate PCV indicating that selection may be effective based on these characters. Yadava *et al.* (2011) also observed high PCV and GCV for seed yield per plant and number of secondary branches per plant. These characters have been reported as main yield contributing traits by Kardam and Singh 2005. Similar findings pertaining to presence of high genetic variability were reported for different traits including seed yield per plant (Singh 2004). Results revealed presence of high amount of genetic variability in the evaluated genotypes for the major yield contributing characters along with seed yield which indicated that further improvement for these traits is possible. Heritability in broad sense ranged from 41% for siliqua length to 77% for number of secondary branches. Heritability for days to 50% flowering (62%), number of siliqua per plant (65%), days to maturity (68%) and number of secondary branches (77%) were found in the high range while all the others were in moderate range. High heritability for traits like days to flowering and number of siliqua per plant has been reported earlier by Singh in 2004 and Kumar and Misra in 2007. Genetic advance as percent of mean had minimum value of 3.47 for days to maturity and maximum value of 30.44 for number of secondary branches. The genetic advance as percent of mean for number of secondary branches (30.44) and number of siliqua per plant (27.32) were in high range, while for days to 50% flowering (15.36), number of primary branches (11.36), number of seeds per siliqua (12.82), seed yield per plant (18.09) and seed yield per plot (18.09) were in moderate range whereas all others traits were in low range of genetic advance. High to moderate heritability with high to moderate genetic advance was found for number of secondary branches and number of siliqua per plant which suggests that heritability is due to additive gene action and simple selection may be effective.

Table.1 Analysis of variance for 10 yield characters in Indian mustard (*Brassica juncea* L.)

S. No.	Characters	Mean Sum of Square			F Value
		Replication (d.f.=2)	Genotype (d.f.=29)	Error (d.f.=58)	
1.	Days to flowering	46.94	91.21**	15.45	5.9
2.	Days to maturity	18.53**	21.89**	3.01	7.2
3.	Plant height(cm)	187.99	684.29**	176.85	3.8
4.	Number of primary branches	0.68	0.87**	0.23	3.6
5.	Number of Secondary branches	7.97**	13.38**	1.21	10.9
6.	Number of Siliqua per plant	8240.09**	9548.23**	1464.75	6.5
7.	Siliqua length (cm)	0.44**	0.34**	0.08	3.9
8.	Seeds per siliqua	3.07*	4.25**	0.92	4.6
9.	Seed yield per plot	34.73**	21.85**	4.97	4.3
10.	Seed yield per plant	70317.08**	44254.82**	10075.38	4.3

** Significant at 1% level and *Significance at 5% level

Table.2 Mean, range, estimate of genotypic, phenotypic and environmental variances for ten traits in Indian mustard (*Brassica juncea* L.)

Sl. No.	Characters	Mean	Maximum	Minimum	Genotypic variance	Phenotypic Variance	Environmental variance
1.	Days to flowering	53.09	61.33	40.66	25.26	40.70	15.45
2.	Days to maturity	122.30	129.00	118.00	6.29	9.30	3.01
3.	Plant height(cm)	222.37	250.86	194.33	169.15	346.00	176.00
4.	Number of primary branches	5.76	6.86	4.66	0.21	0.45	0.23
5.	Number of Secondary branches	11.95	17.73	7.20	4.05	5.27	1.21
6.	Number of Siliqua per plant	315.03	482.60	223.53	2694.49	4159.24	1464.75
7.	Siliqua length (cm)	4.50	5.12	3.81	0.08	0.17	0.08
8.	Seeds per siliqua	12.53	15.10	10.13	1.11	2.03	0.92
9.	Seed yield/ plant (gm)	885.35	1060.00	633.33	11393.15	21468.53	10075.39
10.	Seed yield per plot	19.67	23.55	14.07	5.62	10.60	4.97

Table.3 Estimate of genetic parameter for 10 quantitative characters studied among 30 genotypes of Indian mustard

Genetic parameter	Days to flowering	Days to maturity	Plant height(cm)	Number of primary branches	Number of Secondary branches	Number of Siliqua per plant	Siliqua length (cm)	Seeds per siliqua	Seed yield/ plant (gm)	Seed yield per plot (Kg)
GCV	9.46	2.05	5.84	8.01	16.85	16.48	6.57	8.41	12.06	12.06
PCV	12.02	2.49	8.36	11.65	19.21	20.47	9.30	11.37	16.55	16.55
Broad sense Heritability (h^2)	62.00	68.00	49.00	47.00	77.00	65.00	41.00	55.00	53.00	53.00
Genetic advancement	8.15	4.25	18.73	0.65	3.64	86.07	0.43	1.60	160.18	3.56
Genetic Advance as % of Mean	15.36	3.47	8.42	11.36	30.44	27.32	9.55	12.82	18.09	18.09

Table.4 Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficient among different characters in Indian mustard (*Brassica juncea* L)

Characters	Days to Flowering	Days to Maturity	Plant Height (cm)	Number of primary branches	Number of Secondary branches	Number of Siliqua per plant	Siliqua Length (cm)	Seeds per Siliqua	Seed yield per plot (Kg)
Days to Flowering	**1.00**	0.56**	0.86**	-0.03	0.07	0.15	0.32*	0.22*	0.36*
Days to Maturity	0.48**	**1.00**	0.36*	0.22*	0.19	0.21*	0.12	0.28*	0.30*
Plant Height (cm)	0.43**	0.17	**1.00**	0.01	0.20*	-0.01	0.01	0.07	0.12
Number of primary branches	0.01	0.11	-0.02	**1.00**	0.17	0.76**	0.48**	0.55**	0.58**
Number of Secondary branches	0.03	0.13	0.19	0.21*	**1.00**	0.08	0.24*	-0.22*	-0.18
Number of Siliqua per plant	0.07	0.14	0.02	0.63**	0.11	**1.00**	0.46**	0.77**	0.92**
Siliqua Length (cm)	0.15	0.07	0.03	0.24*	0.12	0.25*	**1.00**	0.14	0.53**
Seeds per Siliqua	0.12	0.19	0.06	0.50**	-0.09	0.58**	0.16	**1.00**	0.66**
Seed yield per plot (Kg)	0.16	0.15	0.10	0.52**	0.07	0.69**	0.26*	0.59**	**1.00**

** Significant at 1% level and *Significance at 5% level

Table.5 Genotypic direct and indirect effect of nine component characters of yield on seed yield per plant in Indian mustard (*Brassica juncea* L.)

Character	Seed yield per plot (Kg)	Days to Flowering	Days to Maturity	Plant Height (cm)	Number of primary branches	Number of Secondary branches	Number of Siliqua per plant	Siliqua Length (cm)	Seeds per Siliqua
Seed yield per plot (Kg)	**0.9989**	0.3606	0.3057	0.1293	-0.4112	-0.1811	-0.2371	0.2984	-0.3178
Days to Flowering	-0.0014	0**.0039**	-0.002	-0.0034	0.0006	-0.0003	-0.0012	-0.0015	-0.0002
Days to Maturity	0.0006	0.0011	**0.0020**	0.0007	0.0003	0.0004	0.0007	0.0002	0.0002
Plant Height (cm)	0.0005	0.0032	0.0013	**0.0037**	0.0001	0.0007	0.0020	0.0004	-0.0003
Number of primary branches	0.0008	0.0003	-0.0003	0.0000	**-0.0019**	-0.0014	-0.0009	0.0003	0.0002
Number of Secondary branches	-0.0004	0.0001	0.0004	0.0004	0.0015	0**.0021**	0.0015	-0.0002	0.0003
Number of Siliqua per plant	0.0005	-0.0007	-0.0008	-0.0012	-0.0010	-0.0016	**-0.0021**	0.0004	-0.0001
Siliqua Length (cm)	0.0002	0.0003	0.0001	0.0001	-0.0001	-0.0001	-0.0002	**0.0008**	0.0002
Seeds per Siliqua	0.0003	0.0000	-0.0001	0.0001	0.0001	-0.0001	0.0000	-0.0002	**-0.0008**
Seed yield/ plant (gm)	**1.000**	**0.3610**	**0.3060**	**0.1296**	**-0.4117**	**-0.1812**	**-0.1812**	**0.2986**	**-03184**
Partial R^2	0.9989	-0.0014	0.0006	0.0005	0.0008	-0.0004	0.0005	0.0002	0.0003

R SQUARE=1.0000

Genotypic and phenotypic correlation coefficient among different characters in Indian mustard are presented in Table 4 suggested that the genotypic correlation coefficient was higher than their corresponding phenotypic correlation, revealing that there was less influence of the environment and that the association between these traits is not only due to genes but also due to favorable influence of environment. Seed yield per plot showed positive correlation with all the traits except number of secondary branches (-0.18) at genotypic level. It showed positive and significant correlation with days to 50% flowering (0.36), days to maturity (0.30) while it showed positive and highly significant correlation with number of siliqua per plant (0.92), number of primary branches (0.58), length of siliqua (0.53) and number of seeds per siliqua (0.66) suggesting that the association between these traits with seed yield per plot is high. At genotypic level the seed yield per plot showed strong correlation plant height (0.86) and moderately strong correlation with days to 50% maturity (0.56), while for siliqua length (0.32), number of seeds per siliqua (0.22) and seed yield per plot (0.36) it showed moderately weak correlation. For all the others it showed weak correlation. The traits which showed strong correlation with seed yield per plot can be used for selection for increasing seed yield.

At phenotypic level the seed yield per plot showed positive correlation with all the traits. Seed yield per plot showed positive and significant correlation with siliqua length (0.26), number of primary branches (0.52), number of seeds per plant (0.59) and number of siliqua per plant (0.69). It showed very strong correlation with siliqua per plant (0.69) and moderately strong correlation with primary branches (0.52), seeds per siliqua (0.59). It showed very weak correlation with days to flowering (0.16), days to maturity (0.15), plant height (0.10) and number of secondary branches (0.07). Yadava *et al.* (2011) also reported that seed yield was positively associated with 1000-seed weight and siliqua length at phenotypic level. Dhavar *et al.* (2018) had also reported that seed yield per plant showed significant and positive correlation with plant height, number of primary branch and number of siliqua per plant and 1000-seed weight at genotypic level and at phenotypic level. Plant height, number of siliqua per plant, 1000-seed weight and number of primary branch exhibited significant and positive correlation with seed yield per plant.

The genotypic path analysis was carried out considering seed yield per plant as dependent character and other yield attributing characters as independent characters (Table 5). The path coefficient analysis revealed that seed yield per plant exhibited positive direct effect with days to flowering (0.0039), days to maturity (0.0020), plant height (0.0037), number of secondary branches per plant (0.0021) and average siliqua length (0.0008). Seed yield per plant exhibited negative direct effect with number of primary branches per plant (0.0019), number of siliqua per plant (0.0021) and seeds per siliqua, (0.0008). Highest positive direct effect on seed yield per plant was exhibited by seed yield per plot, followed by days to 50% flowering (0.0039) and plant height (0.0037) while lowest was reported by siliqua length (0.0008).Highest negative direct effect on seed yield per plant was exhibited by number of primary branches (-0.0019) and lowest by seeds per siliqua (0.0008). Residual effect value was high indicating that other yield attributing traits must be included in the path analysis study. Dawar *et al.* (2018) also reported that, the high positive direct effect on seed yield (g) was exhibited by plant height.

High values of heritability in broad sense, genotypic coefficient of variation and expected genetic advance was recorded for days to 50% flowering, number of primary branches, length of siliqua and seed yield while moderate heritability was noted in plant height and number of siliqua per plant. Direct selection by selecting these traits may be effective for yield improvement because traits are highly heritable and less affected by environment. Selection for few generations will be sufficient for improvement of such traits. Correlation studies indicated seed yield per plot had positive correlation with all the traits except number of secondary branches at genotypic level. Hence, for improvement of seed yield per plot indirect selection should be done using these traits. The path coefficient analysis revealed that seed yield per plot, days to 50% flowering and plant height has positive direct effect on seed yield per plant which suggests that direct selection for these traits can be done for improvement of yield.

References

Al-Jibouri HA, Miller PA and Robinson HF.1958. Genetic and environmental variances and co-variances in an upland cotton cross of interspecific origin. *Agron J* 50: 633-636.

Burton GW and Devane EH. 1953. Estimating Heritability in Tall Fescue (*Festuca arundinacea*) from Replicated Clonal Material. *Agronomy J* 45(10): 478-481.

Dewey DR and Lu KH. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy J* 51: 515-518.

Kardam DK and Singh VV. 2005. Correlation and path analysis in Indian mustard [*Brassica juncea* (L.) Czern & Coss] grown under rainfed condition. *J Spices Aromatic Crop* 14(1): 56–60.

Kumar S and Mishra MN. 2007. Study on genetic variability, heritability and genetic advance in populations in Indian mustard (*Brassica juncea* L. Czern and Coss). *Int J Pl Sci* 2(1): 188–190.

Johanson HW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in Soybean. *Agronomy J* 47(7): 314-315.

Panse VG and Sukhatme PV. 1967. Statistical methods for research workers. ICAR, New Delhi, 220-40.

Dawar S, Kumar N and Mishra SP. 2018. Genetic Variability, Correlation and Path Coefficient Analysis in the Indian Mustard (*Brassica juncea* L. Czern and Coss) Varieties Grown in Chitrakoot, India. *Int J Current Microbiology Applied Sci* 7(3): 883-890.

Singh B. 2004. Character association and path analysis under dry land condition in Indian mustard (*Brassica juncea* L.). *Cruciferae Newsletter* 25: 99–100.

Yadava DK, Giri SC, Vignesh M, Vasudev S, Yadav AK, Dass B, Singh R, Singh N, Mohapatra T. and Prabhu KV. 2011. Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). *Indian J Agric Sci* 81(8): 712-716.

How to cite this article:

Anand Lakra, Girish Tantuway, Aditi Eliza Tirkey and Kartikeya Srivastava. 2020. Genetic variability and Trait association studies in Indian mustard (*Brassica juncea* L. Czern & Coss). *Int.J.Curr.Microbiol.App.Sci.* 9(01): 2556-2563. doi: https://doi.org/10.20546/ijcmas.2020.901.290