

Genetic Analysis of Some Genotypes of Indian Mustard (*Brassica juncea* L.) for Yield and Yield Attributing Traits

A. M. Pradhan ^a, M. Roy Choudhury ^a, A. Sawarkar ^{a*} and S. Das ^b

^a *School of Agriculture and Rural Development, Integrated Rural Development & Management (IRDM), Ramakrishna Mission Vivekananda Educational and Research Institute, Narendrapur-700 103, Kolkata, West Bengal, India.*

^b *Mali Agritech Pvt. Ltd., Ranaghat, Nadia-741201, West Bengal, India.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/CJAST/2021/v40i3531573

Editor(s):

(1) Dr. Ashish Anand, GV Montgomery Veteran Affairs Medical Center, USA.

Reviewers:

(1) Seyede Roghie Ghadirnezhad Shiade, Sari Agricultural Science and Natural Resources University, Iran.

(2) Purendra Singh, India.

Complete Peer review History, details of the editor(s), Reviewers and additional Reviewers are available here:

<https://www.sdiarticle5.com/review-history/72924>

Original Research Article

Received 14 September 2021

Accepted 28 August 2021

Published 04 December 2021

ABSTRACT

The current investigation was carried out to examine the selection criteria for yield improvement in selected genotypes of Indian mustard. Twenty-four genotypes of Indian mustard were evaluated for seed yield and yield attributing characters with randomized block design with three replications. The analysis of variance showed significant differences among all the 24 genotypes against all the characters. The phenotypic and genotypic coefficient of variation were higher for most of the traits like seed yield per plant, number of secondary branches per plant and number of siliquae per plant. High heritability coupled with high genetic advance in percent of mean was registered for number of siliquae per plant, number of primary and secondary branches per plant, plant height, 1000 seed weight, siliqua length per plant and seed yield per plant suggesting predominant role of additive gene action for expression of these traits. The correlation study revealed that seed yield per plant was positively and significantly correlated with number of primary and secondary branches per plant, number of siliquae per plant, siliqua length per plant and 1000 seed weight at both phenotypic and genotypic level. The traits namely, number of secondary branches per plant recorded as highest

*Corresponding author: E-mail: annu.sawarkar@gmail.com;

positive direct effect followed by number of seeds per siliqua, number of siliquae per plant and plant height. Therefore, they may be carried out further evaluation in multilocal trials, biotic and abiotic stress like environmental conditions to check their stability and adaptability.

Keywords: Mustard; genetic variability; heritability; genetic advance; correlation; path analysis.

1. INTRODUCTION

Rapeseed and mustard (*Brassica species*) group of crops is the second most important oilseed crop after groundnut, contributing nearly about 25-30% of the total oilseed production in the country. Indian Mustard (*Brassica juncea* L.) belongs to the family *Cruciferae*, commonly known as rai or laha. It is pre-dominantly a self-pollinated crop, but out crossing rates of 20-30% [1]. Rapeseed-mustard is the third most important oilseed crop in the world after soybean and palm [2]. In India this crop is the second most important edible oilseed after groundnut sharing about 28% in the Indian oilseed economy. It is grown for oil as well as vegetable, green manure, forage, medicines, pharmaceutical, industries, biodiesel and components of many other products. Mustard seed contains 30% - 46% oil content which is one of the most important and popular oil in India. Seed protein content ranges from 17.8% - 22.0%.

Though India is fourth largest contributor of oilseeds, but its average productivity is less than 50% of the world's average productivity. Being the natural repository of oilseed crop, yet Indian subcontinent is importing about 40% of the Country's edible oil [3]. It leads as major vegetable oil importing Country, though during the November-March period of 2019-20 oil year, total edible oils imports declined to 53,91,807 tonnes from 60,05,067 tonnes in the year-ago period (Data released by SEA,2020). The performance of available land races and introduced varieties are poor due to fluctuating environment and pest-disease incidence. In order to exploit and explore consumer demand, introduction of high grain yielding varieties is indispensable. Henceforth, to meet out the present oil requirements, there is an urgent need to break the yield barrier, by increasing the yield potential of *B. juncea* through genetic interventions. Yield is complex trait and the increasing seed yield is depending upon several factors including various yield attributing traits. [4] as well as [5] also investigated mustard genotypes to understand the variability. The development of an intensive breeding and

improvement programme needs detailed biological information and understanding of nature and magnitude of variability of the yield and its components. Hence the present investigation is undertaken to estimate the genetic parameters viz. variability, heritability, genetic advance, genotypic and phenotypic coefficient of variation for different yield attributing characters among mustard genotypes and also to assess direct and indirect effects of different traits on seed yield per plant using path analysis.

2. MATERIALS AND METHODS

Experiment involved twenty-four genotypes (Table 1) including two checks Pusa Bold and Gujarat Local. The experiment was conducted at Agricultural Experimental Farm, Integrated Rural Development Management (IRDM), Faculty Centre, Ramakrishna Mission Vivekananda Educational and Research Institute (RKMVERI), Narendrapur, Kolkata during *Rabi* season, 2019. The Farm is situated at an elevation of 8m above mean sea level at approximately 22° 43'Nlatitude and 88° 40'Elongitude in New Alluvial Zone of West Bengal. The experiment conducted with randomized block design (RBD) with three replications. The row length kept was two metres with standard spacing (30cm x 10cm). All the recommended cultural practices were followed throughout the crop season to raise a good crop.

The characters under studies were days to 50% flowering (D50%F) was recorded as number of days taken from the date of sowing to the date when 50% plant population showed blooming condition. Days to maturity (DM) was recorded from days from sowing upto the date at which maximum siliquae of the selected plant reach physiological maturity *i.e.* yellowing of siliqua which is considered as maturity period. Plant height (PH) was recorded from its base up to the end of main raceme in centimeter. The number of primary branches per plant (NPBPP) were counted from the branches emerging directly from the main shoot of the plant and bearing siliqua were counted at maturity whereas number of secondary branches per plant (NSBPP) were counted emerging from the primary branches at

Table 1. List of genotypes of Indian mustard

Sr. No.	Name of Genotypes	Source	Sr. No.	Name of Genotypes	Source
1	PM-21	Mali Agritech Private Ltd. Ranaghat, West Bengal	13	Pusa Karisma	Mali Agritech Private Ltd. Ranaghat, West Bengal
2	PM-22	-----do-----	14	Pusa Vijay	-----do-----
3	PM-24-4	-----do-----	15	Bhagirathi	-----do-----
4	PM-25	-----do-----	16	Seeta	-----do-----
5	PM-26	-----do-----	17	Sarna	-----do-----
6	PM-27	-----do-----	18	NRCHB-101	-----do-----
7	PM-28	-----do-----	19	Bankura Black	-----do-----
8	PM-29	-----do-----	20	Shivani	-----do-----
9	PM-30	-----do-----	21	Bullet	Sasya Shyamala Krishi Vigyan Kendra, Arapanch, West Bengal
10	PusaTarak	-----do-----	22	Kranti	Mali Agritech Private Ltd. Ranaghat, West Bengal
11	DRMR -150-35	-----do-----	23	Gujarat Local (Check)	-----do-----
12	Sanjuktaasech	-----do-----	24	Pusa Bold (Check)	-----do-----

maturity. The number of siliquae per plant (NSPP) were counted from the seed bearing siliqua of the tagged plants at maturity. Length of siliqua (LS) (cm) was measured by taking five siliqua from each selected plants at random. The number of seeds per siliqua (NSPS) were taken by considering five siliqua from each selected plant randomly, threshed and counted their seeds. 1000-seed weight (1000 SW) (g) was weighed from the produce of each selected plant. Finally, the seed yield per plant (SYPP) (g) was taken from the selected plants and weighed. The data were recorded on the basis of five randomly selected competitive plants excluding border plants in each genotype.

2.1 Statistical Analysis

The components of variance were calculated by [6] and coefficient of variation, Correlation coefficient between different characters as per [7] and Path coefficient analysis suggested by [5]. The data recorded for various traits were statistically analysed through software 'OPSTAT' and 'Genres'.

3. RESULTS AND DISCUSSION

The analysis of variance showed significant differences among all the 24 genotypes against all the characters viz., days to 50% flowering, days to maturity, plant height, primary and secondary branches per plant, number of siliquae per plant, siliqua length per plant, number of seeds per siliqua, 1000 seed weight and seed yield per plant (Table 2) indicating wide spectrum of variation among the genotypes under study and had wide scope for improvement.

Genetic parameters are presented in Table 3. Wide range of variability present among the genotypes for almost all the traits. This would offer a great scope for selection of desirable traits of genotypes. Phenotypic Variances (PV) are found higher than the corresponding Genotypic Variances (GV) against all the characters. Number of siliquae per plant was found to be highest PV and GV followed by plant height, days to maturity, days to 50% flowering and seed yield per plant. Similarly, lowest Environmental Variance was found in primary branch per plant, followed by 1000 seed weight, siliqua length, days to 50 % flowering and secondary branch per plant. It indicates that these characters were less interaction with environment. In the present investigation, all the

Phenotypic Coefficient of Variation (PCV) are higher than the Genotypic Coefficient of Variation (GCV) which indicates that effect of environment on the expression of different characters. It was found that seed yield per plant recorded highest PCV's and GCV'S which was followed by secondary branch per plant, number of siliquae per plant, number of seeds per siliqua and siliqua length and lowest for days to maturity. Similar findings were recorded by [8,9,10,11,12,13,14] and [15].

From the present investigation almost all the characters had high heritability i.e., more than 60 per cent (Table 4) except number of seeds per siliqua. The highest heritability was recorded by number of siliquae per plant and it was followed by plant height, primary branch per plant, days to 50% flowering and 1000 seed weight. Similar results were corroborated with [15,16,17,18,19] and [20]. Large variation was observed for Genetic Advance (GA) for all the characters among the genotypes of the investigation. The highest GA was observed in number of siliquae per plant and it was followed by plant height. Rest of the characters estimated low GA. Among them, 1000 seed weight was found lowest GA and it was followed by siliqua length per plant and primary branches per plant. This finding was also recorded by [12,15] and [19].

The highest GA as a percent of mean was observed in number of siliquae per plant and it was followed by secondary branches per plant, seed yield per plant and siliqua length per plant. Similar results were obtained by [8,12,14,15,19,21] and [22]. Other characters like days to maturity were observed as the lowest GA as percent of mean followed by number of seeds per siliqua and days to 50% flowering. High heritability couple with moderate GA as a percent of mean was observed in days to 50% flowering and number of seeds per siliqua. It indicated that these characters were predominantly controlled by additive and non-additive gene action. i.e., it might be dominance or epistatic gene effects and the high heritability is being exhibited due to the influence of environmental rather than genotypes. This result was in agreement with [8,12,15] and [20]. High heritability accompanied with high genetic advance as a per cent of mean was recorded for number of siliquae per plant, primary and secondary branches per plant, plant height, 1000 seed weight, siliqua length per plant and seed yield. This indicated that these characters were governed by additive gene action.

Table 2. Analysis of variance for different characters in Indian mustard genotypes (Mean sum of square)

Source of variation	DF	D50%F	DM	PH	NPBPP	NSBPP	NSPP	LS	NSPS	1000 SW	SYPP
Replication	2	5.895	42.341	42.374	0.245	1.307	117.250	0.151	14.311	0.453	19.699
Treatment	23	56.262**	114.230**	1467.616**	2.405*	27.038**	6536.132**	2.319*	14.491**	2.047*	29.380**
Error	46	1.443	8.991	23.661	0.053	2.508	21.578	0.150	4.971	0.071	3.148

** Significant at 1% level, *Significant at 5% level, degree of freedom (DF), days to 50% flowering (D50%F), days to maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), number of siliquae per plant (NSPP), length of siliqua (LS) (cm), number of seeds per siliqua (NSPS), 1000-seed weight (1000 SW) (g) and seed yield per plant (SYPP) (g)

Table 3. Variability and genetic parameters for different characters of Indian mustard genotypes

Characters	Mean	Range	Variance			G.C.V.	P.C.V.	h ² (%) (BS)	G.A.	G.A. as % of mean
			Phenotypic	Genotypic	Environmental					
D50%F	49.816	43.000-59.500	19.716	18.273	1.443	8.581	8.913	92.679	8.477	17.017
DM	129.379	111.500-138.500	44.068	35.085	8.983	4.578	5.131	79.599	10.885	8.414
PH	171.216	127.700-213.500	504.979	481.320	23.659	12.814	13.125	95.314	44.123	25.770
NPBPP	5.531	3.967-7.062	0.837	0.784	0.053	16.008	16.540	93.675	1.765	31.917
NSBPP	11.983	7.096-16.100	10.684	8.177	2.507	23.863	27.278	76.530	5.153	43.005
NSPP	196.651	123.900-320.500	2193.095	2171.530	21.565	23.697	23.814	99.016	95.522	48.574
LS	4.976	2.969-6.962	0.873	0.723	0.150	17.087	18.776	82.826	1.594	32.035
NSPS	14.370	10.414-18.460	8.144	3.173	4.971	12.397	19.860	38.963	2.291	15.941
1000 SW	5.236	3.802-6.893	0.730	0.659	0.071	15.501	16.319	90.227	1.588	30.332
SYPP	12.314	7.860-17.920	11.892	8.744	3.148	24.013	28.005	73.525	5.223	42.416

days to 50% flowering (D50%F), days to maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), number of siliquae per plant (NSPP), length of siliqua (LS) (cm), number of seeds per siliqua (NSPS), 1000-seed weight (1000 SW) (g) and seed yield per plant (SYPP) (g)

Table 4. Phenotypic (P) and Genotypic (G) correlation among yield and other characters of Indian mustard genotypes

Characters		DM	PH	NPBPP	NSBPP	NSPP	LS	NSPS	1000 SW	SYPP
D50%F	P	0.287*	0.739**	0.17	0.198	0.350**	0.179	-0.114	0.026	0.153
	G	0.193	0.737**	0.142	0.237*	0.339**	0.134	-0.376**	-0.008	0.110
DM	P		0.336**	-0.223	-0.122	-0.067	0.383**	0.333**	-0.332**	-0.042
	G		0.297*	-0.330**	-0.164	-0.123	0.342**	0.263*	-0.457**	-0.185
PH	P			0.335**	0.173	0.389**	0.430**	-0.069	0.118	0.172
	G			0.326**	0.202	0.384**	0.460**	-0.280*	0.110	0.166
NPBPP	P				0.545**	0.575**	0.163	-0.076	0.501**	0.452**
	G				0.672**	0.584**	0.172	-0.208	0.506**	0.500**
NSBPP	P					0.556**	0.167	-0.00	0.473**	0.528**
	G					0.637**	0.177	-0.029	0.577**	0.692**
NSPP	P						0.106	-0.071	0.626**	0.552**
	G						0.093	-0.178	0.650**	0.623**
LS	P							0.328**	0.015	0.254*
	G							0.389**	0.025	0.255*
NSPS	P								-0.048	0.202
	G								-0.111	0.283*
1000 SW	P									0.424**
	G									0.495**

** Significant at 1% level, *Significant at 5% level, days to 50% flowering (D50%F), days to maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), number of siliquae per plant (NSPP), length of siliqua (LS) (cm), number of seeds per siliqua (NSPS), 1000-seed weight (1000 SW) (g) and seed yield per plant (SYPP) (g)

Table 5. Path coefficient (Genotypic) analysis showing direct and indirect effects of different characters of Indian mustard genotypes

Characters	D50%F	DM	PH	NPBPP	NSBPP	NSPP	LS	NSPS	1000 SW	SYPP
D50%F	-0.075	-0.060	0.175**	-0.009	0.115*	0.147**	-0.004	-0.178**	0.001	0.110
DM	-0.014	-0.313	0.070*	0.023**	-0.079	-0.053	-0.011**	0.125*	0.067**	-0.185
PH	-0.055**	-0.092*	0.237	-0.022**	0.098	0.166**	-0.015**	-0.133*	-0.016	0.166
NPBPP	-0.010	0.103**	0.077**	-0.070	0.327**	0.253**	-0.006	-0.099	-0.075**	0.500**
NSBPP	-0.017*	0.051	0.047	-0.047**	0.487	0.276**	-0.006	-0.013	-0.085**	0.692**
NSPP	-0.025**	0.038	0.091**	-0.041**	0.310**	0.433	-0.003	-0.084	-0.096**	0.623**
LS	-0.010	-0.107**	0.109**	-0.012	0.086	0.040	-0.033	0.185**	-0.004	0.255*
NSPS	0.028**	-0.082*	-0.066*	0.014	-0.014	-0.077	-0.013**	0.476	0.016	0.283*
1000 SW	0.001	0.143**	0.026	-0.035**	0.281**	0.281**	-0.001	-0.053	-0.149	0.495**

** Significant at 1% level, *Significant at 5% level, days to 50% flowering (D50%F), days to maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), number of siliquae per plant (NSPP), length of siliqua (LS) (cm), number of seeds per siliqua (NSPS), 1000-seed weight (1000 SW) (g) and seed yield per plant (SYPP) (g)

Therefore, these characters could be improved through direct selection. Similar results were obtained by [8], [12], [14], [15] and [19]. High heritability along with low GA as a per cent of mean was found in days to maturity, suggested that the character was governed by non-additive gene action and the improvement of the character could not possible through direct selection.

The characters which showed positive and significant genotypic and phenotypic correlation with yield were number of primary and secondary branches, number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua and 1000 seed weight (Table 5). Similar results were reported by [8],[23-26]. In contrast, [27] and [28] in their finding reported that 1000-seed weight had a positive but non-significant correlation with seed yield. Therefore, these are the main determining characters for the improvement of yield in Indian mustard. Number of secondary branches per plant showed maximum positive direct effect on seed yield per plant as reported previously by [29] and it was followed by number of seeds per siliquae, number of siliquae per plant respectively while minimum positive direct effect on seed yield was recorded by plant height indicating greater scope for genetic improvement of grain yield based on selection through these traits. In contrast, [30] observed negative direct effect of plant height for seed yield. Similarly, maximum negative direct effect imparted from days to maturity followed by 1000 seed weight, primary branches per plant while minimum negative direct effect was showed by siliqua length per plant. Similar result was also reported by [21]. The path analysis helps in the analysis of the association of seed yield with direct and indirect components to decipher a cause-and-effect relationship. If the correlation between yield and a character is due to the direct effect of a character, it reveals the true relationship between them and direct selection for this trait will be effective for yield improvement [30]. However, if the correlation coefficient is mainly due to the indirect effects of the character through another component trait, indirect selection through such trait will be effective in yield improvement. From the path coefficient studies (Table 5) indicated that number of primary and secondary branches per plant, number of siliquae per plant, length of siliqua, number of seeds per siliqua, 1000 seed weight were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization

program. These results were in agreed with [8] and [31].

4. CONCLUSIONS

From the present investigation, the only genotype NRCHB-101 was surpassed their yield potential to the both check varieties. Other genotypes like Bullet, PM 22, DRMR-150-35, Seeta, PM-27 were also showed superior yield performance to nearby check varieties. In addition to this, other yield attributing characters like days to 50% flowering, primary branch per plant, number of siliquae per plant, siliqua length, number of seeds per siliqua and 1000 seed weight were also found outstanding in these superior genotypes. Therefore, they may be carried out further evaluation in multi-location trials, biotic and abiotic stress like environmental conditions to check their stability and adaptability.

DISCLAIMER

The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Gulden RH, Shirliffle JS, Thomas AG. Secondary seed dormancy prolongs persistence of volunteer canola in western Canada. *Weed Science*. 2003;51:904-913.
2. Shekhawat K, Rathore SS, Premi OP, Kandpal BK, Chauhan JS. Advances in agronomic management of Indian Mustard (*Brassica juncea* (L.) Czernj. Cosson): An Overview. *International Journal of Agronomy*. 2012;1-14. DOI:10.1155/2012/408284.
3. Yadava DK, Vasudev S, Singh N, Mohapatra T. Breeding major oil crops: present status and future research needs.

- In: S.K. Gupta (ed.), Technological Innovations in Major World Oil Crops, Volume 1: Breeding; 2013.
DOI 10.1007/978-1-4614-0356-2_2.
4. Dawar S, Kumar N, Mishra SP. Genetic variability, correlation and path coefficient analysis in the Indian Mustard (*Brassica juncea* L. Czern and Coss) varieties grown in Chitrakoot, India. International Journal of Current Microbiology and Applied Sciences. 2018;7(3):883-890.
DOI:https://doi.org/10.20546/ijcmas.2018.7.03.103.
 5. Rout S, Kerkhi SA, Chauhan C. Character association and path analysis among yield components in Indian Mustard [*Brassica juncea* (L.) Czern and Coss]. International Journal of Current Microbiology and Applied Sciences. 2018;7(1):50-55.
DOI:https://doi.org/10.20546/ijcmas.2018.7.01.007.
 6. Synrem GJ, Rangare NR, Myrthong I, Bahadure DM. Variability studies in intra specific crosses of Indian mustard [*Brassica juncea* (L.) Czern and Coss.] genotypes. IOSR Journal of Agriculture and Veterinary Science. 2014;7(9):29-32.
 7. Maurya JK, Singh AK, Singh A, Singh DR, Singh PK and Sriom. Studies on character association and path analysis of vigour and vigour contributing traits in Indian mustard (*Brassica juncea* L. Czern & Coss.) germplasm. 2019;7(3): 4708-4712.
 8. Mahla HR, Jambhulkar SJ, Yadav DK, Sharma R. Genetic variability, correlation and path analysis in Indian mustard [*Brassica juncea* (L.) Czernand Coss]. Indian Journal of Genetics and Plant Breeding. 2003;2:171-172.
 9. Singh A, Avtar R, Singh D, Sangwan O, Balyan P. Genetic variability, character association and path analysis for seed yield and component traits under two environments in Indian mustard. Journal of Oilseed Brassica. 2013;4(1): 43-48.
 10. Shekhawat N, Jadeja GC, Singh J. Genetic variability for yield and its components in Indian mustard (*Brassica juncea* L. Czern & Coss). Electronic Journal of Plant Breeding. 2014;5(1): 117-119.
 11. Bind D, Singh D, Dwivedi VK. Genetic variability and character association in Indian mustard. Agricultural Science Digest. 2014;34(3):183-188.
 12. Akabari RV, Niranjana M. Genetic variability and trait association studies in Indian mustard. International Journal of Agricultural Science. 2015;11(1):35-39.
 13. Rauf A, Rahim A. Genetic variability studies among yield and its contributing traits in mustard (*Brassica napus* L.). Advances in Zoology and Botany. 2018;6(4):101-108.
 14. Tripathi N, Kumar K, Tiwari R, Verma OP. Assessing genetic variability in Indian mustard (*Brassica juncea* L. Czern and Coss.) for seed yield and it's contributing attributes under normal and saline/alkaline condition. Journal of Pharmacognosy and Phytochemistry. 2019;8(2):1322-1324.
 15. Ray J, Singh OP, Pathak VN, Verma SP. Assessment of genetic variability, heritability, genetic advance and selection indices for yield contributing traits in Indian mustard [*Brassica juncea*]. International Journal of Chemical Studies. 2019; 7(4):1096-1099.
 16. Sikarwar RJ, Dixit SS, Hira CD. Genetic association, path analysis, heritability and genetic advance studies in mustard [*Brassica juncea* (L.) Czern and Coss]. Journal of Oilseeds Research. 2000; 17(1):11-16.
 17. Prasad L, Singh M, Dixit RK. Analysis of heritability and genetic advance in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. Journal of Advanced Plant Science. 2001;14(2): 557-581.
 18. Swarnakar GB, Singh M, Prasad L, Lallu. Analysis of heritability and genetic advance in relation to yields and its contributing traits in Indian mustered (*Brasica juncea* (L.) Czern & Coss). Plant Archives. 2002;2(2):305-308.
 19. Kumar S, Misra MN. Study on genetic variability, heritability and genetic advance in populations in Indian mustard [*B. juncea* (L.) Czern & Coss.]. International Journal of Plant Science. 2007;2:188–90.
 20. Yadava DK, Giri SC, Vignesh M, Vasudev S, Yadav AK, Das B, et al. Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). Indian Journal of Agricultural Science. 2011; 81(8):712–6.
 21. Singh P, Singh DN. Path coefficient analysis in Indian mustard (*Brassica juncea* L.). Journal of Research. Birsa Agricultural University. 2004;16(2):293-295.
 22. Pawar PD, Nair B, Charjan SU, Manojkumar D. Evaluation of induced

- genetic variability, heritability and genetic advance in Indian mustard (*Brassica juncea* L.). Soils and Crops. 2018;28(1):115-120.
23. Gangapur DR, Prakash BG, Salimath PM, Kumar R, Rao MS. Correlation and path analysis in Indian mustard (*Brassica juncea* (L. Czern & Coss.)). Karnataka Journal of Agricultural Science. 2009;22(5):971-977.
 24. Lodhi B, Thakral NK, Ramavtar, Singh A. Genetic variability, association and path analysis in Indian mustard (*B. juncea*). Journal of Oilseed Brassica. 2014;5:26-31.
 25. Mustafa H, Mahmood T, Hasan E, Aftab M, Rehman H. Yield evaluation and interrelationship between yield related traits in advance lines of mustard through correlation studies. The Journal of Agricultural Science. 2018;13(1):66-71.
 26. Prasad G, Patil BR. Association and path coefficient analysis in Indian mustard genotypes. International Journal of Chemical Studies. 2018;6(5):362-368.
 27. Roy SK, Haque S, Kale VA, Asabe DS, Dash S. Variability and character association in rapeseed-mustard (*Brassica sp.*). Journal of crop and weed. 2011; 7(2):108-112.
 28. Shweta. Correlation and path coefficient analysis of yield and yield components of Indian mustard (*Brassica juncea* L.). Journal of Hill Agriculture. 2013;4(1): 44-46.
 29. Roy RK, Kumar A, Kumar S, Kumar A, Kumar RR. Correlation and path analysis in Indian mustard (*Brassica juncea* L. Czern and Coss) under late sown condition. Environment & Ecology. 2017;36(1A):247-254.
 30. Kumar N, Sarkar S, Bhattacharya PK. Association studies for yield components in mustard (*Brassica juncea* and *Brassica rapa*) in Gangetic alluvium zone of West Bengal. Journal of Pharmacognosy and Phytochemistry. 2019;8(4):3057-3063
 31. Mahak S, Singh HL, Satyendra and Dixit RK. Studies on genetic variability, heritability, genetic advance and correlation in Indian mustard (*Brassica juncea* (L.) Czern. and Coss.). Plant Archives. 2004;4(2):291-294.

© 2021 Pradhan et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/72924>