



Genetic Diversity in *Brassica integrifolia*

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ABSTRACT

Background: Because of the large genetic variation, local varieties of *Brassica integrifolia* serve as a good germplasm resource for developing new varieties. This study was conducted to assess the level of genetic diversity through heritability coefficients, clustering collected samples and selecting clusters with the highest growth and yield traits.

Methods: The experiment was conducted at the College of Agriculture, Can Tho University from October 2023 to January 2024. The experimental materials included 36 accessions of *B. integrifolia* collected from different areas of Can Giuoc district, Long An province, Vietnam. The experiment was arranged in a completely randomized block design with one factor, 36 treatments and three replications. The parameters of 11 quantitative traits were recorded to calculate genetic parameters.

Result: All collected local sources of *B. integrifolia* accession showed differences for most of the traits. The results of the study showed that the heritability was very high (>80%) combined with high genetic advance (>20%) for 11 quantitative traits, indicating that these traits are under the control of genetics and are not affected by environmental factors, while the remaining traits showed a tendency to change due to environmental factors. Through hierarchical cluster analysis, the quantitative traits of 36 *B. integrifolia* accession were divided into 4 clusters. Cluster III contained bestest germplasm sources. This study showed a great diversity in growth, yield and yield component traits, contributing a valuable genetic source for *B. integrifolia* breeding.

Key words: *Brassica integrifolia*, Cluster analysis, Genetic advance, Genetic diversity.

INTRODUCTION

Brassica integrifolia also named *Cai Ngot* in Vietnam belongs to the Brassicaceae family. This family contains about 350 genus and 3,500 species. *B. integrifolia* is originates to India and China and is often grown as a vegetable. In Vietnam, the cultivation area of *B. integrifolia* is very large and it is one of the main crops because it brings high economic efficiency. By 2024, the area of *B. integrifolia* cultivation nationwide will reach 200,000 hectares, with a productivity of about 3,000,000 tons/year. Therefore, research related to *B. integrifolia* breeding is very interested.

Can Giuoc District, Long An Province is a large vegetable farm in Vietnam with an area of over 2000 hectares. Can Giuoc district is a rare place in Vietnam that still cultivation local *B. integrifolia* varieties with large farm. Because this is a local germplasm source mainly produced by farmers the *B. integrifolia* variety is currently morphologically degraded. Evaluation of the genetic diversity parameters of this local *B. integrifolia* variety is the first step in improving *B. integrifolia* populations to conserve and develop local *B. integrifolia* germplasm.

Nowadays plant breeders are exerting to develop new varieties. For this, breeders must have a good knowledge of genetic variability and heritability. In addition, locally collected *B. integrifolia* varieties are also a good source of genetic material to start breeding programs because they have higher genetic variability. This genetic variation can be improved during breeding to develop varieties with high yield potential (Sidra Iqbal *et al.*, 2014).

Certain morphological traits serve as tools for estimating genotypic variance (Ali *et al.*, 2013) and heritability (Azam

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et al., 2013). Environmental factors can influence these parameters due to the polygenic inheritance of the genes involved. The heritability coefficient can calculate the relative influence of genetic and environmental effects. This indicates the extent to which a trait will be transmitted to the next generations. Thus, the expression of the next generations can be predicted and selection can be carried out Khan *et al.* (2003).

Heritability and response to selection show a direct relationship to genetic progress. The expected response to selection is also known as genetic advance (GA). Therefore, to estimate genetic advances breeders often use heritability to calculate, which measures the extent of increase in any trait under a particular selection pressure. Therefore, genetic advance is one of the important parameters that help breeders select genotypes (Shukla *et al.*, 2004). To select effectively for certain traits high genetic advance along with high heritability is required. Heritability along with selection efficiency should be considered in breeding processes.

The genetic variability present in the available germplasm of a particular crop determines the success of any breeding program in general and the improvement of specific traits through selection. The traits for variability traits must have high heritability because the selection process depends on the heritability and genetic advance and helps the breeder to select an appropriate selection programme in the crop improvement process (Yadava *et al.*, 2011). High heritability in the initial breeding material ensures better chances of producing new desirable crops (Raturi *et al.*, 2014).

MATERIALS AND METHODS

The experiment was conducted at the College of Agriculture, Can Tho university from October 2023 to January 2024. The experimental materials were 36 samples of *B. integrifolia* collected from different areas of Can Giuoc district, Long An province, Vietnam. The criteria for selecting 36 samples were from farmers with seed production areas of over 500 m² and using locally *B. integrifolia* resources for seed production. The experiment was arranged in a completely randomized block design with 36 treatments corresponding to 36 accession of *B. integrifolia* collected and 3 replications. Eleven quantitative traits were collected and evaluated (Table 1) as such as seed weight (g/plant), seed weight at the bottom of

the panicle (g), number of seeds/10 silique at the bottom of the panicle, number of seeds/10 silique at the top of the panicle, number of seeds/10 silique at the middle of the panicle, number of seeds per 10 silique/plant, seed filling time (day), plant width (cm), number of secondary branches, number of primary branches, thousand seed weight (g) were collected to assess genetic diversity. The method of collecting morphology criteria is shown through (Table 1). After the traits were collected, variance will be estimated and calculate genetic parameters (Table 2). Correlation coefficient analysis 11 quantitative trait (Pearson, 1939). Cluster analysis (Ward, 1963). The data are presented in a statistical format SPSS 22.0.

RESULTS AND DISCUSSION

Genetic diversity parameters of 36 *B. integrifolia* accessions

The parameter of genetic variance (GV), phenotypic variance (PV), genetic coefficient variation (GCV), Phenotypic coefficient variation (PCV), heritability (h²) and Genetic advance (GA) were calculated for all 11 quantitative traits under study are presented in (Table 3), showing that genotypic variance (GV) ranges from 0.006 for thousand seed weight to 1,674.98 for number of seed.10 siliques at

Table 1: Description of the method of recording morphological indicators.

Trait	Trait data recording method	Stage
Plant width (cm)	Average of two diagonal lines of the plant wide.	28 day after sowing
Grain filling day (days)	From the plant finished flowering until 90% of the fruit on the plant is ready to harvest.	From finished flower to fruit ripe
Number of primary branches	Total number of branches distributed from the main branch of the plant.	After harvest
Number of secondary branches	Count the total number of branches from the primary branches of the plant.	After harvest
Number of seed of 10 silique at top of panicle	Count the total number of seeds of 10 silique at the top of the panicle.	After harvest
Number of seed of 10 silique at middle of panicle	Count the total number of seeds of 10 silique at the middle of the panicle.	After harvest
Number of seed of 10 silique at bottom of panicle	Count the total number of seeds of 10 silique at the bottom of the panicle.	After harvest
Number of seed of 10 silique per plant	Average number of seeds of 10 silique/plant.	After harvest
Seed weight at bottom of panicle	Total weight of grain at the bottom of the panicle (seed at 8% moisture content).	After harvest
Seed weight (g/plant)	Weight and record the weight of seeds/plant, then convert to standard moisture content of 8% (TCVN 319 - 69) according to the formula:	After harvest
$W_q = W_t \frac{100 - H_t}{100 - H_q}$		
Thousand seed weight (g)	Record the weight of 1,000 seed at 8% moisture	After harvest

the top of panicle. Phenotypic variance (PV) ranges from 0.007 for thousand seed weight to 1,693.47 for number of seed/10 siliques at the top of panicle. The low difference between genotypic and phenotypic variance in a trait indicates that these traits are less influence of environment factor. Genetic variation is one of the most important requirements for crop improvement because it provides a wider range of choices (Pal *et al.*, 2019).

The genotypic coefficient of variation (GCV) ranged from 15.96 (medium) for thousand seed weight to 67.05 (high) for seed weight (g). According to the classification of Deshmukh *et al.* (1986), all traits had high genotypic coefficients of variation, except for thousand seed weight which had a medium genotypic coefficient of variation. The genotypic coefficient of variation is considered a measure used to compare genetic variations occurring in different

types of traits and a high genotypic coefficient of variation helps in more effective selection and improvement of traits.

The phenotypic coefficient of variation (PCV) ranged from 16.58 (medium) for thousand seed weight to 67.27 (high) for seed weight. Overall, all 11 quantitative traits had high phenotypic coefficients of variation according to the classification of Deshmukh *et al.* (1986), except the thousand seed weight (16.58) which was average. The results of high genotypic coefficients of variation and phenotypic coefficients of variation in this experiment were similar of Patel *et al.* (2021); Nishad *et al.* (2022); Mandal *et al.* (2022) and Sur *et al.* (2023) on seed weight/plant of *B. juncea* L.

High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) also help in the effective selection and improvement of traits. In this experiment, high phenotypic coefficient of variation and

Table 2: The formulas of genetic parameter.

Parameter	Formula	Source
Genetic variance	$GV = \frac{(MS_g - MS_e)}{r}$	Singh and Chaudhary, (1985)
Phenotypic variance	$PV = GV + MS_e$	
Genetic coefficient variation	$GCV = \left(\frac{\sqrt{GV}}{\bar{X}} \right) \times 100$	
Phenotypic coefficient variation	$PCV = \left(\frac{\sqrt{PV}}{\bar{X}} \right) \times 100$	Allard, (1960)
Heritability	$h^2 = \frac{GV}{PV} \times 100$	
Genetic advance	$GA = K \times PCV \times \frac{h^2}{\bar{X}}$	
Genetic advance as per cent of mean	$GAM = \frac{GA}{\bar{X}}$	

Where, MS_g : Mean square of genotype; MS_e : Mean square of error; r = Repeat; $\bar{X}$: means. K = Intensity of selection, the value of which is 2.06 when 5 per cent of the individual are selected from the population.

Table 3: Genetic diversity parameter of 11 quantitative traits of 36 accession collected *Brassica integrifolia*.

Traits	GV	PV	GCV	PCV	H ²	GA	GAM
Seed weight (g/plant)	4.95	4.98	67.05	67.27	99.0	4.58	100.00
Seed weight at bottom of panicle	0.20	0.20	60.99	61.91	97.0	0.90	100.00
Number of seed of 10 silique at bottom of panicle	1,631.77	1,680.07	37.81	38.37	97.0	82.13	76.88
Number of seed of 10 silique at top of panicle	1,674.98	1,693.47	35.93	36.13	99.0	83.97	73.72
Number of seed of 10 silique at middle of panicle	1,550.25	1,566.26	34.56	34.74	99.0	80.81	70.93
Number of seed of 10 silique per plant	1,324.78	1,331.51	32.63	32.71	99.0	74.90	67.14
Grain filling day (day)	71.78	75.44	30.44	31.21	95.0	17.05	61.25
Plant width (cm)	34.81	35.25	25.88	26.05	99.0	12.09	53.06
Number of secondary branches	23.95	26.15	25.36	26.50	92.0	9.66	50.07
Number of primary branches	4.43	5.54	20.56	22.99	80.0	3.88	37.93
Thousand seed weight (g)	0.06	0.07	15.96	16.58	93.0	0.50	31.69

GV: Genotypic variance; PV: Phenotypic variance; GCV: Genotypic coefficient variance; PCV: Phenotypic coefficient variance; h²: Heritability; GA: Genetic advance; GAM: Genetic advance as percent of mean *: Significant at 5% level of probability.

genotypic coefficient of variation were observed for all quantitative traits, which shows that environmental factors have little impact on trait expression and that traits are mainly controlled by genotype (Jagaonkar *et al.*, 1990).

The heritability (h^2) in this experiment was very high for 11 quantitative traits such as seed weight (99.0%), seed weight at the bottom of the panicle (97.0%), number of seeds/10 silique at the end of the panicle (97.0%), number of seeds/10 silique at the top of the panicle (99.0%), number of seeds/10 silique at the middle of the panicle (99.0%), number of seeds/10 silique/plant (99.0%), grain filling time (95.00%), plant width (99.0%), number of secondary branches (92.0%), number of primary branches (80.0%), thousand seed weight (93.0%). Thus, based on the classification of very high heritability, population improvement is possible because these traits are mainly determined by genotype and are less affected by the environment. The heritability reflects the contribution rate of the genotype to the quantitative trait. The heritability was higher the less influenced the trait by environmental factors (Singh, 2001).

The percentage of genetic advance for all quantitative traits ranged from 31.69% for thousand seed weight (g) to 100% for seed weight and Seed weight at bottom of panicle was rated high according to the classification of as according to the classification of Johnson *et al.* (1955). This result is consistent with the study of Yadava *et al.* (2011); Kumar *et al.* (2013); Rout *et al.* (2019); Patel *et al.* (2019); Jat *et al.* (2019); Yadav *et al.* (2020); Patel *et al.* (2021); Nishad *et al.* (2022); Mandal *et al.* (2022) và Sur *et al.* (2023) reported high heritability and genetic advance values for seed/plant weight in *Brassicaceae*. High heritability and high genetic advance across traits suggest that direct selection can improve through breeding programs (Pal *et al.*, 2019). According to Burton (1951) suggested that combining the genotypic coefficient of variation with heritability allows for a better assessment of genetic variation. Johnson *et al.* (1955) suggested that combining heritability with genetic advance as a percent of means (GAM) would help evaluate the selected phenotypes more effectively. Thus, combining

heritability and genetic advance, all 11 quantitative traits showed that selection through these traits would be useful in improving the *B. integrifolia* population.

High heritability coefficients show that these traits are not affected by environmental factors. High GA shows that the ability to select the desired *B. integrifolia* lines is very high. Thus, high heritability combined with a high genetic advance for local *B. integrifolia* varieties in this study is very useful for breeding local *B. integrifolia* varieties.

Cluster analysis

The results of hierarchical cluster analysis of 36 *B. integrifolia* accessions collected based on 11 quantitative traits such as seed weight, seed weight at the bottom of the panicle, the number of seeds/10 silique at the bottom of the panicle, the number of seeds/10 silique at the top of the panicle, the number of seeds/10 silique at the middle of the panicle, the number of seeds/10 silique per plant, grain filling time, plant width, the number of secondary branches, the number of primary branches and thousand seed weight were divided into 4 clusters (Fig 1).

Cluster I consist of 9 accessions (3, 5, 12, 28, 34, 2, 13, 16, 30) accounting for 25% of the total number of accessions. Cluster II consists of 14 accessions (6, 10, 4, 14, 8, 36, 29, 7, 19, 15, 35, 17, 33, 1) accounting for 39% of the total number of accessions. Cluster III consists of 2 accessions (31, 32) accounting for 5.6% of the total number of accessions. Cluster IV consists of 11 accessions (9, 20, 11, 25, 23, 18, 26, 27, 21, 24, 22) accounting for 30.5% of the total number of accessions.

Thus, based on the means of quantitative traits of 4 clusters (Table 4), it shows that Cluster III has the highest growth, yield components and yield such as plant width (27.7 cm), number of secondary branch (22.8), number of primary branch (13.5), seed weight (9.1 g/plant), number of 10 seeds/plant (157.2), thousand seed weight (1.7 g). Cluster I, Cluster II have the average growth, yield components and yield. Cluster IV has the lowest growth, yield components and yield. It is possible to use germplasm resources from Cluster III as materials for future breeding programmes.

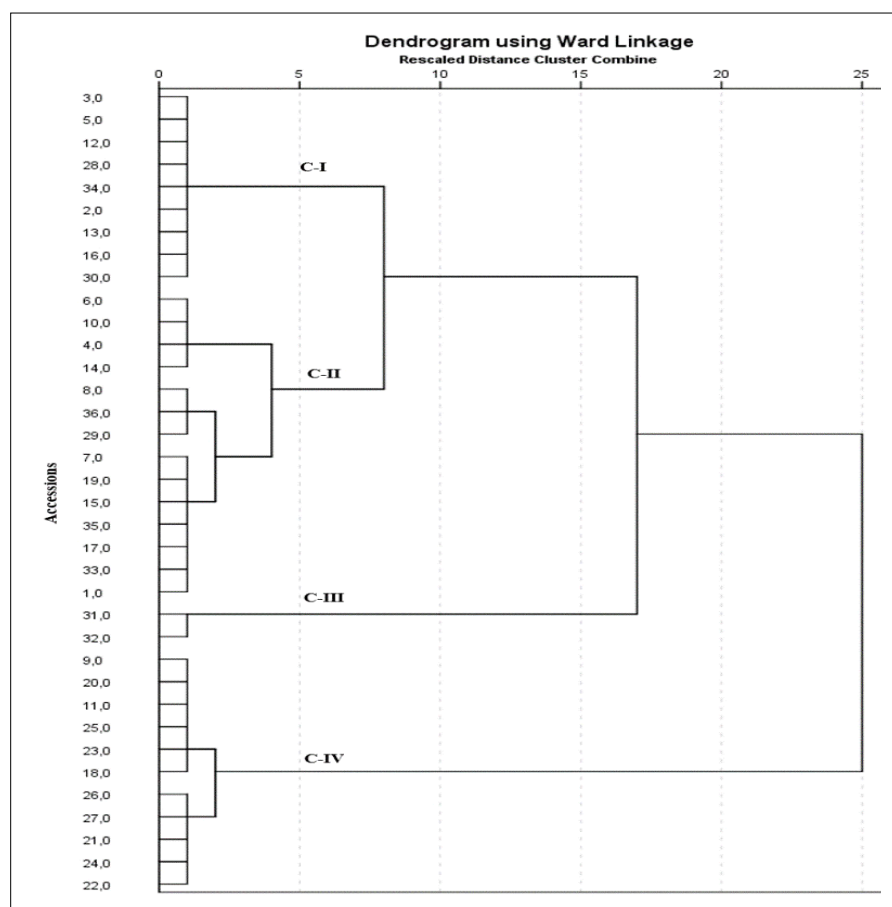
Table 4: Means of quantitative traits of 4 cluster.

Traits	Cluster I	Cluster II	Cluster III	Cluster IV
Plant width (cm)	25.4 ^{ab}	24.3 ^{ab}	27.7 ^a	17.9 ^b
Grain filling time (day)	24.9	25.0	30.5	33.3
Number of secondary branches	20.6	18.8	22.8	18.2
Number of primary branches	10.7 ^b	9.6 ^b	13.5 ^a	10.0 ^b
Seed weight (g/plant)	4.6 ^b	3.1 ^b	9.1 ^a	1.5 ^c
Number of seed of 10 silique at top of panicle	137.6 ^a	129.2 ^a	150.3 ^a	68.5 ^b
Number of seed of 10 silique at medium of panicle	135.3 ^{ab}	121.3 ^b	166.8 ^a	77.5 ^c
Number of seed of 10 silique at bottom of panicle	127.5 ^b	112.9 ^{ab}	154.5 ^a	73.5 ^b
Number of seed of 10 silique per plant	133.4 ^{ab}	121.1 ^b	157.2 ^a	73. ^c
Seed weight at the bottom of panicle (g)	0.9 ^{ab}	0.7 ^b	1.4 ^a	0.4 ^c
Thousand seed weight (g)	1.7 ^a	1.6 ^{ab}	1.7 ^{ab}	1.4 ^b

Table 5: Correlations between quantitative traits.

Traits	SW	SWB	NSB	NST	NSM	NSP	GFT	PW	NSP	NPB
SWB	0.73**									
NSB	0.59**	0.37**								
NST	0.49**	0.32**	0.69**							
NSM	0.57**	0.37**	0.79**	0.66**						
NSP	0.61**	0.39**	0.92**	0.87**	0.99**					
GFT	-0.14	-0.03	-0.25**	-0.33**	-0.41**	-0.37**				
PW	0.45**	0.45**	0.5**	0.45**	0.45**	0.52**	-0.46**			
NSB	0.13	0.12	0.06	0.24*	-0.04	0.10	0.25**	-0.07		
NPB	0.27**	0.24*	0.17	0.05	0.17	0.14	0.07	-0.02	0.20*	
TSW	0.49**	0.48**	0.31**	0.26**	0.42**	0.36**	-0.26**	0.17	-0.18	0.27**

** : Correlation is significant at the 0;01 (2 tailed); * : Correlation is significant at the 0;05 (2 tailed); SW: Seed weight; SWB: Seed weight at bottom of panicle; NSB: Number of seed of 10 silique at bottom of panicle; NST: Number of seed of 10 silique at top of panicle; NSM: Number of seed of 10 silique at medium of panicle; NSP: Number of seed of 10 silique per plant; GFT: Grand filling time; PW: Plant width; NSB: Number of secondary branches; NPB: Number of primary branches; TSW: Thousand seed weight.

**Fig 1:** Dendrogram using ward linkage.

Correlations between quantitative traits

The correlation coefficients between quantitative traits are presented in (Table 5), showing that some traits have good correlation coefficients ($r > |0.5|$). Seed weight trait has a

good correlation with seed weight at bottom of panicle, number of seed of 10 silique at bottom of panicle, number of seed of 10 silique at top of panicle, number of seed of 10 silique at medium of panicle, number of seed of 10 silique

per plant, thousand seed weight. Number of seed of 10 siliques at bottom of panicle positive correlation with number of seed of 10 siliques at top of panicle, number of seed of 10 siliques at medium of panicle, number of seed of 10 siliques per plant. Correlation analysis shows that yield components and yield are positively correlated, the higher the yield component, the higher the yield.

CONCLUSION

All collected local sources of *B. integrifolia* showed differences for most of the traits. The results of the study showed that the heritability was very high (>80%) combined with high genetic advance (>20%) for 11 quantitative traits, indicating that these traits are under the control of genetics and are not affected by environmental factors, while the remaining traits showed a tendency to change due to environmental factors. Through hierarchical cluster analysis, the quantitative traits of 36 *B. integrifolia* accession were divided into 4 clusters. Cluster III contained good germplasm sources. This study showed a great diversity in growth, yield and yield component traits, contributing a valuable genetic source for *B. integrifolia* breeding.

Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Informed consent

All animal procedures for experiments were approved by the Committee of Experimental Animal Care and Handling Techniques were approved by the University of Animal Care Committee.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish or preparation of the manuscript.

REFERENCES

- Ali, Y., Farhatullah, Rahman, H., Nasim, A., Azam, S.M. and Khan, A. (2013). Heritability and correlation analysis for morphological and biochemical traits in *Brassica carinata*. *Sarhad J. Agric.* **29**(3): 359369.
- Allard, R.W. (1960). Principles of Plant Breeding. John Wiley Sons, New York.
- Azam, S.M., Farhatullah, Nasim, A., Shah, S. and Iqbal, S. (2013). Correlation studies for some agronomic and quality traits in *Brassica napus* L. *Sarhad J. Agric.* **29**(4): 547-550.
- Burton, G.W. (1951). Quantitative inheritance in pearl millet (*P. glaucum*). *Agron Journal*. **43**: 409-417.
- Deshmukh, S.N.N., Basu, M.S., Reddy, P.S. (1986). Genetic variability, character association and path co-efficients of quantitative traits in *Virginia Bunch* varieties of groundnut. *Indian J. Agric. Sci.* **56**: 816-821.
- Jagaonkar R.B.M. Jamadagni, M.J. Salvi (1990). Genetic variability and correlation studies in turmeric. *Ind Cocoa, Arecanut Spices Journal*. **14**(1): 20-22.
- Jat, L., Rai, S.K., Choudhary, J.R., Bawa, V., Bharti, R., Sharma, M. and Sharma, M. (2019). Phenotypic evaluation of genetic diversity of diverse Indian mustard [*Brassica juncea* (L.) Czern and Coss] genotypes using correlation and path analysis. *International Journal of Bio-resource and stress Management*. **10**(5): 467-471.
- Johnson, H.W., Robinson, H.F., Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybeans. *Agron. J.* **47**: 314-318.
- Khan, A.S., Salim, I. and Z. Ali. (2003). Heritability of various morphological traits in wheat. *Intl. J. Agric. Bio.* **5**(2): 138-140.
- Kumar, B., Pandey, A. and Singh, S.K. (2013). Genetic diversity for agro-morphological and oil quality traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *The Bioscan*. **8**(3): 771-775.
- Mandal, K., Ghosh, A., Dasgupta, T. and Kundagrami, S. (2022). Genetic variability and trait association in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Agricultural Science Digest*. **42**(5): 580-585. doi: 10.18805/ag.D-5550.
- Nishad, C., Salam, J.L., Singh, S. and Singh, D.P. (2022). Studies of genetic variability in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *The Pharma Innovation Journal*. **11**(2): 261-263.
- Pal, S., Dubey, N., Avinash, H., Khan, S. and Reddy, J.P. (2019). Estimation of genetic variability, correlation and path analysis for yield and yield contributing characters in Indian mustard (*Brassica juncea* L.). *Journal of Pharmacognosy and Phytochemistry*. **8**(15): 102-105.
- Patel, J.R., Prajapati, K.P., Patel, P.J., Patel, B.K., Patel, A.M., Jat, A.L. and Desai, A.G. (2019). Genetic variability and character association analysis for seed yield and its attributes in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *The Pharma Innovation Journal*. **8**(4): 872-876.
- Patel, P. B. Patel, P.J. Patel, J.R. and Patel, P.C. (2021). Elucidation of genetic variability and inter-relationship studies for seed yield and quality traits in Indian mustard *Brassica juncea* (L.) Czern and Coss. *Electronic Journal of Plant Breeding*. **12**(2): 589-596.
- Pearson, E.S. (1939). Student's as statistician. *Biometrika*. **30**(3/4): 210-250. doi: 10/1093/biomet/30.3-4.210.
- Rout, S. Kerkhi, S.A. and Gupta, A. (2019). Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard *Brassica juncea* (L.) Czern and Coss. *Journal of Pharmacognosy and Phytochemistry*. **8**(3): 4119-4123.
- Raturi, A., Singh, S.K., Sharma, V. and Pathak, R. (2014). Genetic variability and interrelationship among qualitative and quantitative traits in mungbean. *Legume Research*. **37**(1): 1-10. doi: 10.5958/j.0976-0571.37.1.001.

- Shukla, S., Bhargava, A., Chatterjee, A. and Singh, S.P. (2004). Estimates of genetic parameters to determine variability for foliage yield and its different quantitative and qualitative traits in vegetable amaranth (*A. tricolor*). *J. Genet. Breed.* **58**: 169-176.
- Sidra, I., Farhatullah, Sikandar, S., Mehwish, K., Laila, F. and Afzal, M. (2014). Genetic variability and heritability studies in indigenous *Brassica rapa* accessions. *Pak. J. Bot.* **46**(2): 609-612.
- Singh, B.D. (2001). Plant Breeding: Principles and Methods, 6th ed. Kalyani Publishers, New Delhi, India.
- Singh, R.K. and Chaudhary, B.D. (1985). Biometrical Methods in Quantitative Genetic Analysis. 2nd ed. Kalyani Publishers, New Delhi-Ludhiana.
- Sur, B., Rout, S., Singla, S., Mandal, R., Nath, S., Maying, B. *et al.* (2023). Evaluation of mustard genotypes *Brassica juncea* (L.) Czern and Coss for quantitative traits and character association of seed yield and yield components at sub Himalayan region of West Bengal (India). *Plant Science Today.* **10**(1): 166-178.
- Ward, J.H. (1963). Hierarchical grouping to optimize an objective function. *Journal of the American Statistical Association.* **58**: 236-244.
- Yadav, R.K. and Yadav, R.G. (2020). Genetic variability and path coefficient analysis for seed yield and its related attributes in Indian mustard [*Brassica juncea* (L.) Czern and Coss.] under late sown condition. *Progressive Agriculture.* **20** (1,2): 117-122.
- Yadava, D.K., Giri, S.C., Vignesh, M., Vasudev, S., Kumar Yadav, A., Dass, B. *et al.* (2011). Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). *Indian Journal of Agricultural Sciences.* **81**(8): 712.