
**E-ISSN:** 2788-9297
**P-ISSN:** 2788-9289
https://www.agrijournal.org
SAJAS 2024; 4(1): 115-120
Received: 22-10-2023
Accepted: 29-11-2023

**Deepak Verma**
Department of Genetics and Plant Breeding, Faculty of Agriculture Science and Technology, AKS University, Satna, Madya Pradesh. India

**Ayodhya Prasad Pandey**
Department of Genetics and Plant Breeding, Faculty of Agriculture Science and Technology, AKS University, Satna, Madhya Pradesh, India

**Rajbeer Singh Gaur**
Department of Genetics and Plant Breeding, Faculty of Agriculture Science and Technology, AKS University, Satna, Madhya Pradesh, India

**Ankit Bhagat**
Department of Genetics and Plant Breeding, Faculty of Agriculture Science and Technology, AKS University, Satna, Madhya Pradesh, India

**Correspondence Author:**
**Deepak Verma**
Department of Genetics and Plant Breeding, Faculty of Agriculture Science and Technology, AKS University, Satna, Madhya Pradesh, India

# Variability, heritability and genetic advance studies of mustard [*Brassica juncea* (L.)] Genotypes at Satna District of Madhya Predesh

**Deepak Verma, Ayodhya Prasad Pandey, Rajbeer Singh Gaur and Ankit Bhagat**

**Abstract**
Twenty diverse cultivars of mustard in a Completely Randomized block design (CRBD) at AKS University, Satna, during *Rabi* season on November 2022. The twelve quantitative characters studied *viz*., days to 50% flowering, plant height (cm), primary branches per plant, secondary branches per plant, length of main raceme (cm), siliquae on main raceme, days to maturity, length of siliqua, seeds per siliqua, test seed weight (g), biological yield per plant (g) and seed yield per plant. Data were collected for twelve quantitative traits and estimated for variance, genetic variability, heritability and genetic advance. The design of the experiment indicated highly significant differences for all the characters due to treatments. The analysis of variance indicated the existence of sufficient amount of variability among genotypes for all the studied characters. PCV was higher than GCV for all the studied characters. The maximum GCV and PCV was observed for secondary branches per plant followed by seed yield /per plant, primary branches per plant, biological yield /plant, length of main raceme and siliquae on main raceme. High heritability ($h^2b$) >80% were observed for all the studied characters except siliquae on main raceme and seeds per siliqua. High estimate of expected genetic advance at 5% were found for secondary branches per plant followed by seed yield per plant, biological yield per plant and primary branches per plant. High heritability coupled with high genetic advance indicated the predominance of additive gene action in the expression of these traits.

**Keywords:** Mustard, variance, variability, heritability and genetic advance

## Introduction
Oilseed crops are the strong backbone of agricultural economy of India. Most of edible oils are obtained from rapeseed and mustard. The oil content of seeds of different forms ranges from 30 to 46 percent. Canola and mustard belong to the *cruciferous* (*Brassicaceae*) family. In the regional Indian languages rapeseed-mustard is called as Rai, Banarasi rai Kalee sarson, in Sanskrit it is called as Asuri, Bimbata. Indian subcontinent, accounting for more than 80% of the total area of rapeseed mustard in the country. *Brassica juncea* (2n=36) is an allopolyploid species obtained from natural interspecific cross between *Brassica nigra* (2n=18) and *B. campestris/rapa* (2n=20) (Nagaharu, U. 1935) [10].
The origin of B. juncea is controversial. The Middle East seems to be the origin of the parent species; *B. nigra* and *B. campestris* are crossed (Olson 1960) [12]. Biochemical and molecular studies support this finding and provide further evidence for the existence of two races, Chinese and Indian (Vaughan *et al.* 1963, Vaughan and Gordon 1973) [18, 19]. It is expected that, 19$^{th}$ century Indian mustard [*B. juncea* (L.) Czern & Coss] originated in China and may have traveled to India.
Among different oilseeds crops, rapeseed and mustard are important both for human consumption and for industrial purposes. In human diet, they provide not only essential fatty acids as a good source of energy, but also help in metabolism of fat-soluble vitamins A, D, E and K. In each gram of oil supplies 5 kilo calories. The leaves of young plants are used as green vegetables locally known as (Sarson ka saag) and plants are used as green fodder for cattle. Oil of rapeseed and mustard are used for cooking and for the preparation of various food products and pickles.
Worldwide, *Brassica species* are mainly grown in the temperate and subtropical zones of Europe, Asia and North America. India, China, Pakistan, Europe, Canada and Russia are the principal oilseeds growing countries. India contributes 6.30 million hectares area and 7.20 million tones of production of rapeseed and mustard in 2018-19.

The chief oilseeds producing states are Rajasthan, Madhya Pradesh, Uttar Pradesh, Punjab, Haryana, Assam, Bihar, West Bengal and Orissa.

Genetic variability is a basic feature of a crop improvement programme. The assessment of genetic variability for yield and its components is a pre–requisite for improvement of the crop to the desired level and the effectiveness of selection depends upon its nature and magnitude in genetic material. The concept of heritability explains whether differences observed between individuals due to the differences in genetic constitution or because of environmental forces. Genetic advance gives the impression or idea of possible improvement of new individuals through selection as compared to the original populations.

The genetic gain depends upon the quantity of genetic variability and magnitude of masking effect of the environment. Therefore, the analysis of variability, heritability, and genetic advance are of exquisite significance for creating a success breeding programme in mustard crop. This may assist in selecting proper line for hybridization which may also give better segregants in Indian mustard.

## Material and Method

The present investigation was conducted during *Rabi*, 2022-23 at Research farm, Genetics and Plant Breeding, AKS University, Sherganj, Satna, Madhya Pradesh. The material consists 20 varieties/strains of Mustard (*Brassica juncea* L.) germplasm comprising indigenous genotypes, evaluated in Completely Randomized Block Design. The entire experimental field divided in 3 blocks of equal size and each block had 20 plots. Each plot was consisted of three rows 2 meters length, following row to row spacing of 45 cm. and plant to plant spacing of 15 cm. These genotypes exhibiting wide spectrum of variability for various agronomic and morphological characters were obtained from the, eleven from Bundelkhand University Jhansi, U.P. eight from local market Satna, M.P. one from Farmers field, Satna, M.P.

Twelve observations on yield and yield contributing characters were recorded. In each plot, five competitive plants were randomly selected for recording observations for all the twelve quantitative characters, which were recorded on the plot basis.

The analysis of variance for the design of the experiment was carried out according to the procedure outlined by Panse and Sukhatme, (1967) [13]. The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) was estimated by the formula suggested by Burton and de Vane, (1953) [4]. Heritability in broad sense ($h^2b$) was estimated using the formula suggested by Burton and de Vane, (1953) [4]. Genetic advance was calculated by the method suggested by Johnson *et al*., (1955) [8].

## Result and Discussion

The analysis of variance for the design of the experiment involving 20 strains/varieties of mustard was evaluated in Randomized Block Design with three replications for the twelve quantitative characters. The design of the experiment indicated highly significant differences for all the characters presented in Table 1. indicating thereby the presence of sufficient genetic variability in the genotypes. All the twelve characters selected for study showed highly significant inter-varietal variation and hence these characters can be used for selection in formulating breeding programmes. The similar results were found by Raliya *et al*., (2018) [16], Gadi *et al*., (2020) [6], Priyanka and Pandey, (2021) [14], Gupta *et al*., (2022) [7], Nishad *et al*., (2022) [11], Vanukuri and Pandey, (2022) [17], Yadav *et al*., (2022) [20].

The mean performance, grand means, range, GCV, and PCV of 20 genotypes of mustard for 12 quantitative characters are presented in Table: 2 and Table: 3. The magnitude of phenotypic coefficients of variation (PCV) was slightly higher than corresponding genotypic coefficients of variation for all the seed quality parameters due to the environmental influence. The magnitude of GCV ranged from secondary branches per plant (35.668) to days to maturity (4.673). The magnitude of PCV ranged from seed yield /per plant (38.569) to days to maturity (5.213). The high GCV and PCV were recorded for secondary branches per plant (35.668) followed by seed yield /per plant (35.219), primary branches per plant (28.858), biological yield /plant (28.159), length of main raceme (15.541) and siliquae on main raceme (14.595). This is an indicative of less amenability of these characters to environmental fluctuations and hence, greater emphasis should be given to these traits. The traits with high environmental coefficient of variation (ECV) indicated more influence of environmental factors. Therefore, caution has to be exercised during the selection programme because the environmental variations are unpredictable in nature and may mislead the results. Earlier researchers also observed high amount of PCV and GCV values for plant height Akkenapally and Chetariya, (2022) [1], for primary branches per plant Chakraborty *et al.* (2021) [5], Akkenapally and Chetariya (2022) [1], Gupta *et al.* (2022) [7], Reddy and Shrivastav, (2022) [15], Vanukuri and Pandey, (2022) [17], for secondary branches per plant Chakraborty *et al.* (2021) [5], Priyanka and Pandey, (2022) [14], Akkenapally and Chetariya (2022) [1], Gupta *et al.* (2022) [7], Reddy and Shrivastav, (2022) [15], Yadav *et al*., (2022) [20], for length of main raceme Akkenapally and Chetariya, (2022) [1], Gupta *et al*., (2022) [7], for biological yield per plant Akkenapally and Chetariya, (2022) [1], Gupta *et al*., (2022) [7], Yadav *et al*., (2022) [20] and for seed yield per plant Chakraborty *et al.* (2021) [5], Akkenapally and Chetariya (2022) [1], Gupta *et al.* (2022) [7], Nishad *et al*., (2022) [11], Reddy and Shrivastav, (2022) [15], Vanukuri and Pandey, (2022) [17], Yadav *et al.* (2022) [20].

Heritability estimates are used to predict expected advance under selection so that breeders are able to anticipate improvement from different of selection intensity. The major function of heritability estimates is to provide information on transmission of characters from parents to the progeny. Such estimates facilitate evaluation of hereditary and environmental effect in phenotypic variation and thus aid in selection. Burton and De Vane (1953) [4] suggested that the GCV along with heritability estimate could provide better picture of the genetic advance to be expected by phenotypic selection. Heritability $h^2$ (Broad Sense), $h^2$ (Broad Sense) %, Genetic Advancement @ 5%, Genetic Advancement @1%, Genetic Advance as % of Mean 5%, Genetic Advance as % of Mean 1%, and Variation was estimated for all the characters and has been presented in Table 4.

The heritability value ranged from lowest seeds per siliqua (77.00%) to highest plant height (97.7%). plant height (97.7%) followed by days to 50% flowering (95.9%),

biological yield /plant (93.4%), length of siliqua (90.6%), length of main raceme (88.7%), seed yield /per plant (83.4%), primary branches per plant (82.2%), test seed weight (81.7%) and days to maturity (80.4%) suggested that the characters are least influenced by the environmental factors and also indicates the dependency of phenotypic expression which reflect the genotypic ability of strains to transfer the gene to their offspring.

Genetic advance is a measure of genetic gain under selection which depends upon main factors *viz*., genetic variability, heritability, and selection index Allard RW, (1960). The expected genetic advance as percent of mean at 5% ranged from days to maturity (8.63%) to secondary branches per plant (69.788%). High estimate of expected genetic advance as percent of mean at 5% were found for secondary branches per plant (69.788%) followed by seed yield /per plant (66.249%), biological yield /plant (56.075%) and primary branches per plant (53.915%). High heritability coupled with high genetic advance observed for biological yield per plant, seed yield per plant, primary branches per plant and secondary branches per plant indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement. Similar results were reported earlier by Chakraborty *et al*., (2021) [5], Gadi *et al*., (2020) [6] reported high heritability for days to flowering. High heritability for days to maturity was also reported by few workers like Gadi *et al*., (2020) [6]. High heritability for plant height was also reported by Akkenapally and Chetariya, (2022) [1], Gupta *et al*., (2022) [7]. High heritability along with high genetic advance was also recorded for primary branches per plant by Gupta *et al*., (2022) [7], Reddy and Shrivastav, (2022) [15], Chakraborty *et al*., (2021) [5]. High heritability along with high genetic advance was also recorded for secondary branches per plant by Akkenapally and Chetariya, (2022) [1], Gupta *et al*., (2022) [7], Reddy and Shrivastav, (2022) [15], Chakraborty *et al*., (2021) [5] Kumar, (2008) [9]. Akkenapally and Chetariya, (2022) [1], Reddy and Shrivastav, (2022) [15], reported high heritability along with high genetic advance for length of main raceme in this crop. High heritability along with high genetic advance was also recorded for 1000- grain weight by Akkenapally and Chetariya, (2022) [1], Reddy and Shrivastav, (2022) [15]. High heritability coupled with high genetic advance was also reported for biological yield per plant by Akkenapally and Chetariya, (2022) [1], Gupta *et al*., (2022) [7], Reddy and Shrivastav, (2022) [15]. High heritability coupled with high genetic advance was also reported by a number of workers such as Akkenapally and Chetariya, (2022) [1], Chakraborty *et al*., (2021) [5] for seed yield.

## Conclusion

In the light of above findings it may be concluded that wide spectrum of exploitable variability in the material studied with respect to seed yield per plant and its component characters. As per mean performance the maximum yield was recorded by varieties/genotypes *viz*., Gold star, Varuna, Vasundhra, NRDR-2 and Mahiko gold-plus. The maximum GCV and PCV was observed for secondary branches per plant followed by seed yield /per plant, primary branches per plant, biological yield /plant, length of main raceme, and siliquae on main raceme. Higher estimates ($h^2b$) >80% were observed for all the characters except number of seed per siliqua, harvest index (%) and seed yield per plant (g). High heritability coupled with high genetic advance observed for biological yield per plant, seed yield per plant, primary branches per plant and secondary branches per plant indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement and will help in improving the seed yield in mustard.

**Table 1:** Analysis of variance for 12 quantitative characters in Mustard

| S. No. | Traits | Replications (DF = 2) | Treatments (DF = 19) | Error (DF = 38) |
|---|---|---|---|---|
| 1. | Days to 50% flowering | 75.37 | 208.46** | 8.63 |
| 2. | Plant height | 2.97 | 889.64** | 25.21 |
| 3. | Primary branches per plant | 2.66 | 12.19** | 2.16 |
| 4. | Secondary branches per plant | 82.22 | 103.37** | 10.11 |
| 5. | Length of main raceme | 53.6 | 231.93** | 26.19 |
| 6. | Siliquae on main raceme | 219.06 | 167.61** | 34.81 |
| 7. | Days to maturity | 331.69 | 119.55** | 23.47 |
| 8. | Length of siliqua | 1.01 | 1.42** | 0.13 |
| 9. | Seeds per siliqua | 1.29 | 3.32** | 0.76 |
| 10. | Test seed weight | 2.02 | 1.49** | 0.27 |
| 11. | Biological yield /plant | 185.55 | 1258.83** | 82.49 |
| 12. | Seed yield /per plant | 308.28 | 340.97** | 56.66 |

*Significant at 5% probability level.
**Significant at 1% probability level.

**Table 2:** Mean performance of 12 characters of mustard genotypes

| S.N. | Genotypes | Days to 50% flowering | Plant height (cm) | Primary branches per plant | Secondary branches per plant | Length of main raceme (cm) | Siliquae on main raceme | Days to maturity | Length of siliqua (cm) | Seeds per siliqua | Test seed weight (g) | Biological yield /plant (g) | Seed yield / per plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1. | NRDR-2 | 61.29 | 159.81 | 6.08 | 18.74 | 66.05 | 53.59 | 117.52 | 5.23 | 12.81 | 5.33 | 53.48 | 38.72 |
| 2. | RVM-3 | 64.05 | 178.59 | 5.63 | 15.56 | 57.76 | 42.69 | 123.75 | 4.12 | 13.35 | 4.15 | 78.67 | 33.69 |
| 3. | JM-3 | 67.03 | 176.57 | 5.68 | 12.06 | 55.08 | 42.61 | 126.40 | 6.50 | 14.25 | 5.25 | 70.12 | 22.12 |
| 4. | PM-26 | 55.75 | 165.56 | 6.06 | 13.40 | 44.01 | 46.51 | 124.56 | 5.35 | 13.21 | 4.01 | 54.00 | 22.94 |
| 5. | Sej-2 | 64.58 | 165.26 | 6.29 | 14.84 | 56.44 | 47.10 | 121.11 | 4.78 | 13.70 | 5.55 | 54.31 | 16.43 |
| 6. | Vasundhra | 59.75 | 183.33 | 9.55 | 24.88 | 62.38 | 44.63 | 116.11 | 4.96 | 13.27 | 5.18 | 90.42 | 41.44 |
| 7. | Maya | 50.64 | 163.09 | 6.01 | 16.86 | 46.04 | 49.83 | 126.66 | 5.38 | 13.24 | 4.68 | 60.44 | 26.79 |
| 8. | Varuna | 66.00 | 191.49 | 11.49 | 24.00 | 58.91 | 63.45 | 125.42 | 6.26 | 15.26 | 5.14 | 113.53 | 42.01 |
| 9. | Rohini | 49.24 | 177.99 | 6.07 | 12.46 | 36.58 | 42.23 | 104.36 | 5.28 | 12.64 | 4.58 | 50.65 | 23.14 |
| 10. | Pusa vijay | 69.18 | 181.30 | 8.46 | 19.24 | 64.95 | 45.44 | 108.89 | 5.93 | 13.87 | 5.12 | 83.81 | 30.74 |
| 11. | MS-2 | 67.58 | 171.03 | 6.11 | 11.17 | 57.48 | 61.73 | 125.68 | 5.79 | 13.64 | 3.99 | 80.74 | 21.61 |
| 12. | Kaliya-92 | 63.31 | 171.81 | 4.59 | 11.74 | 51.94 | 45.57 | 125.25 | 4.82 | 12.93 | 4.43 | 62.22 | 16.58 |
| 13. | Krishna Gold | 48.21 | 166.08 | 5.85 | 11.57 | 58.15 | 43.40 | 123.56 | 4.85 | 13.19 | 5.53 | 61.79 | 25.23 |
| 14. | Basanti | 65.08 | 152.74 | 5.98 | 12.25 | 45.81 | 30.95 | 122.71 | 4.53 | 12.20 | 4.47 | 66.54 | 17.31 |
| 15. | Kalawati | 67.60 | 150.77 | 5.37 | 12.93 | 55.91 | 39.30 | 122.34 | 4.89 | 12.46 | 3.46 | 64.13 | 17.39 |
| 16. | Gold star | 71.54 | 209.78 | 9.80 | 33.31 | 53.73 | 38.72 | 123.58 | 5.83 | 14.01 | 4.54 | 126.18 | 55.99 |
| 17. | Mahiko gold-plus | 57.11 | 137.99 | 3.65 | 10.69 | 35.29 | 37.79 | 118.25 | 4.83 | 13.01 | 4.65 | 48.61 | 35.52 |
| 18. | Chutki sarson | 73.08 | 176.87 | 6.06 | 14.28 | 50.19 | 45.48 | 128.77 | 3.85 | 10.58 | 3.32 | 66.82 | 21.34 |
| 19. | Karuna | 70.70 | 142.31 | 4.03 | 11.90 | 45.51 | 45.96 | 124.01 | 4.79 | 12.28 | 3.96 | 55.45 | 26.77 |
| 20. | Local variety(L1) | 44.59 | 149.38 | 3.97 | 10.77 | 63.53 | 44.74 | 113.13 | 4.36 | 11.03 | 3.33 | 64.49 | 17.07 |

**Table 3:** Mean, Range, Genotypic, Phenotypic and environmental variances, and coefficient of variation for 12 quantitative characters in mustard

| S.N. | Characters | Grand mean | Range | | GCV | PCV | ECV | C.D. @ 5% |
|---|---|---|---|---|---|---|---|---|
| | | | Max | Min. | | | | |
| 1. | Days to 50% flowering | 61.82 | 73.08 | 44.59 | 13.203 | 13.485 | 4.754 | 4.86 |
| 2. | Plant height | 168.59 | 209.78 | 137.99 | 10.069 | 10.215 | 2.978 | 8.30 |
| 3. | Primary branches per plant | 6.34 | 11.49 | 3.65 | 28.858 | 31.82 | 23.22 | 2.43 |
| 4. | Secondary branches per plant | 15.63 | 33.31 | 10.69 | 35.668 | 37.552 | 20.345 | 5.26 |
| 5. | Length of main raceme | 53.29 | 66.05 | 35.29 | 15.541 | 16.501 | 9.604 | 8.46 |
| 6. | Siliquae on main raceme | 45.59 | 63.45 | 30.95 | 14.595 | 16.396 | 12.942 | 9.75 |
| 7. | Days to maturity | 121.10 | 128.77 | 104.36 | 4.673 | 5.213 | 4.001 | 8.01 |
| 8. | Length of siliqua | 5.12 | 6.50 | 3.85 | 12.819 | 13.465 | 7.137 | 0.60 |
| 9. | Seeds per siliqua | 13.05 | 15.26 | 10.58 | 7.075 | 8.064 | 6.702 | 1.45 |
| 10. | Test seed weight | 4.53 | 5.55 | 3.32 | 14.085 | 15.58 | 11.534 | 0.86 |
| 11. | Biological yield /plant | 70.32 | 126.18 | 48.61 | 28.159 | 29.13 | 12.916 | 15.01 |
| 12. | Seed yield /per plant | 27.64 | 55.99 | 16.43 | 35.219 | 38.569 | 27.233 | 12.44 |

**Table 4:** Heritability (%) in broad sense, Genetic advance and genetic advance as percent of mean for 12 quantitative characters in mustard

| S.N. | Characters | Heritability ($h^2b$) | Heritability ($h^2b$ %) | Genetic Advancement 5% | Genetic Advancement 1% | Gen. Adv. as % of Mean 5% | Gen.Adv as % of Mean 1% |
|---|---|---|---|---|---|---|---|
| 1 | Days to 50% flowering | 0.959 | 95.90 | 16.461 | 21.095 | 26.629 | 34.126 |
| 2 | Plant height | 0.972 | 97.70 | 34.469 | 44.174 | 20.446 | 26.203 |
| 3 | Primary branches per plant | 0.822 | 82.20 | 3.416 | 4.378 | 53.915 | 69.095 |
| 4 | Secondary branches per plant | 0.902 | 90.20 | 10.909 | 13.981 | 69.788 | 89.438 |
| 5 | Length of main raceme | 0.887 | 88.70 | 16.068 | 20.591 | 30.153 | 38.643 |
| 6 | Siliquae on main raceme | 0.792 | 79.20 | 12.2 | 15.635 | 26.762 | 34.296 |
| 7 | Days to maturity | 0.804 | 80.40 | 10.451 | 13.394 | 8.63 | 11.060 |
| 8 | Length of siliqua | 0.906 | 90.60 | 1.286 | 1.649 | 25.139 | 32.217 |
| 9 | Seeds per siliqua | 0.77 | 77.0 | 1.668 | 2.138 | 12.788 | 16.388 |
| 10 | Test seed weight | 0.817 | 81.70 | 1.189 | 1.524 | 26.232 | 33.618 |
| 11 | Biological yield /plant | 0.934 | 93.40 | 39.433 | 50.535 | 56.075 | 71.863 |
| 12 | Seed yield /per plant | 0.834 | 83.40 | 18.312 | 23.468 | 66.249 | 84.901 |

**Acknowledgement**
This paper and the research behind it would not have been possible without the exceptional support of my supervisor, Mr. Ayodhya Prasad Pandey. I acknowledge to all the faculty of Department of Genetics and plant breeding and AKS University, Satna (M.P.) for providing the essential facilities during the research.

**Reference**

1. Akkenapally JS, Chetariya CP. Variability, Correlation, Path Coefficient and Genetic Diversity Analysis in Indian mustard. International Journal of Environment and Climate Change. 2022;12(10):1116-1125. DOI: 10.9734/IJECC/2022/v12i1030907.
2. Allard RW. Principles of Plant Breeding. New York: John Wiley and Sons, Inc.; c1960. p. 20-24, 88-89.
3. Economic Survey. Government of India, Ministry of Finance, Department of Economic Affairs Government of India; c2021-22.
4. Burton GW, De Vane EM. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
5. Chakraborty S, Kumar A, Kishore C, Anand Kumar A, Kumar RR, De N. Genetic Variability and Character Association Studies in Indian Mustard (*Brassica juncea* L.). International Journal of Environment and Climate Change. 2021;11(11):100-105. DOI: 10.9734/IJECC/2021/v11i1130519.
6. Gadi J, Chakraborty NR, Imam Z. To Study the Genetic Variability, Heritability and Genetic Advance for Different Quantitative Characters in Indian mustard (*Brassica juncea* L. Czern & Coss). International Journal of Current Microbiology and Applied Sciences. 2020;9(10):1557-1563. DOI:10.20546/ijcmas.2020.910.186.
7. Gupta A, Tyagi SD, Chauhan S, Johari A, Singh S. Genetic variability, correlation, path coefficient and cluster analysis in Indian mustard (*Brassica juncea* L.). The Pharma Innovation Journal. 2022;11(11):2401-2406.
8. Johnson HW, Robinson HE, Comstock RE. Estimates of genetic and environmental variability in soyabean. Agronomy Journal. 1955;47:314-318.
9. Kumar A. Genetic parameters and path coefficient analysis in Indian mustard [*Brassica juncea* (L.) Czem & Coss] under late sown and unirrigated condition [M.Sc. (Ag.) Thesis]. Jaunpur: V. B. S. Purvanchal University; c2008. p. 56.
10. Nagaharu U. Genome-analysis in Brassica with special reference to the experimental formation of B. napus and peculiar mode of fertilization. Japan Journal of Botany. 1935;7:389-452.
11. Nishad C, Salam JL, Singh S, Singh DP. Studies of genetic variability in Indian mustard (*Brassica juncea* L. Czern and Coss). The Pharma Innovation Journal. 2022;11(2):261-263.
12. Olsson G. Species crosses within genus Brassica. I. Artificial *Brassica juncea*. Hereditas. 1960;43:171-223.
13. Panse VG, Sukhatme PV. Statistical Methods for Agriculture Workers. New Delhi: Indian Council of Agriculture; c1967.
14. Priyanka N, Pandey MK. Genetic variability and Genetic diversity study in Indian mustard (*Brassica juncea* L.). The Pharma Innovation Journal. 2021;10(10):1133-1135.
15. Reddy SNK, Shrivastav SP. Studies on Genetic Variability and Divergence in Mustard (*Brassica juncea* L.). International Journal of Plant & Soil Science. 2022;34(20):565-574. DOI: 10.9734/IJPSS/2022/v34i2031189.
16. Raliya B, Kumar K, Ramesh P, Meena HS, Mundiyara R. Genetic variability and character association in Indian mustard (*Brassica juncea* L.). International Journal of Agricultural Sciences. 2018;10(9):5993-5996.
17. Vanukuri AR, Pandey MK. Genetic variability and genetic diversity studies in Indian mustard (*Brassica juncea* L.). The Pharma Innovation Journal. 2022;11(7):1357-1360.
18. Vaughan JG, Hemingway JS, Schofield HJ. Contribution to a study of variation in *Brassica juncea* Coss. & Czern. Botanical Journal of the Linnean Society. 1963;58:435-447.
19. Vaughan JG, Gordon EL. A taxonomic study on *Brassica juncea* using the techniques of electrophoresis, gas-liquid chromatography and serology. Annals of Botany. 1973;37:167-184.
20. Yadav D, Singh L, Jafri SKF, Singh A, Singh V. Study on genetic variability and principal component analysis in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. The Pharma Innovation Journal. 2022;11(4):2166-2169.