

Genetic Variability Studies on Induced Mutants in Indian Mustard (*Brassica juncea* L.)—Analysis of Component Characters for Better Yield

Meghna Garg¹, Anubhuti Sharma^{2*}, Sanjay Jambhulkar³, Rakesh Goel⁴, P.K. Rai², and Shoor Vir Singh¹

¹Department of Biotechnology, GLA University, Mathura–281 406, India

²ICAR-Directorate of Rapeseed Mustard Research, Bharatpur, Rajasthan–321 303, India

³Nuclear Agriculture & Biotechnology Division, Bhabha Atomic Research Centre, Mumbai–400 008, India

⁴Department of AGB, DUVASU, Mathura–281 001, India

*E-mail: Anubhuti.Sharma@icar.gov.in

ABSTRACT

The study aimed to develop elite mutants of Indian Mustard (*Brassica juncea* L.) with improved seed yield by studying the correlation of various morphological characters with seed yield. Low erucic acid varieties of Indian Mustard (PM21 and PM30) were irradiated with different doses of gamma rays (1000 Gy, 1200 Gy & 1500 Gy) and also treated in combination with different concentration of chemical mutagen EMS (0.25 %, 0.50 % & 0.75 %) to induce the genetic variability. The stable true breeding lines were evaluated for the heritability, genetic variability, genetic advance & correlation studies for 8 different parameters. The ANOVA confirms the existence of significant amount of genetic diversity in mutant genotypes. The primary, secondary & tertiary branches, total siliqua and seed yield of the selected superior mutants possessed higher values of GCV while the phenotypic coefficient of variation was found to be moderate for all of the characters. A significant positive correlation exists between primary, secondary & tertiary branches & total siliqua of a plant. The value of heritability ranged between 0-0.6 (h^2) for various parameters; seed number per siliqua being the most genetically variant among the traits studied. Seed yield is positively correlated with seed number per siliqua, primary & secondary branches which indicates that selection of these traits could improve seed yield. Mutation breeding is used to broaden the genetic variability in the germplasm. Novel mutants with high seed yield were isolated. The identification of component characters which have positive or negative association with seed yield has helped in designing of a breeding program to produce stable true breeding lines in Indian Mustard with high seed yield.

Keywords: *Brassica juncea*; Heritability; PCV-GCV; Correlation coefficient; Genetic advance

NOMENCLATURE

| | |
|-------------|-------------------------------------|
| GCV | Genotypic coefficient of variation |
| PCV | Phenotypic coefficient of variation |
| ANOVA | Analysis of variance |
| PM21 & PM30 | (Pusa Mustard 21 & 30) |
| EMS | Ethyl Methane sulphonate |

1. INTRODUCTION

The *Brassica oleiferous* species, often referred to as rapeseed-mustard, are a commercially significant agricultural commodity. It is a key oilseed crop in India, ranking second only to soybean production. The global rapeseed-mustard cultivation area, production, and yield are expected to be 36.59 million hectares (mha), 72.37 million tonnes (mt), and 1980 kg/ha, respectively¹. On a global scale, India encompasses around 19.8 % of the total geographical area and contributes approximately 9.8 % to the overall output²⁻³. Indian mustard comprises around 75-80 % of the total cultivated area of 6.23 million hectares dedicated to these specific crops in India⁴.

Variability in germplasm is a pedestal in crop improvement

programme. Analysis of its components and selection based on the same leads to identification of superior genotype. The different genotypic constitution of the individuals in a population accounts for genotypic variance. Whereas, environmental variance comprises of all the variations of non-genetic origin. Moreover, the variable characters selected, should be highly heritable as the success of the program depends on the character's heritability, selection intensity & genetic advance.

Heritability is a measure of a trait's transmissibility to offspring. Estimates of heritability and genetic progress aid in determining the best breeding methods for any crop improvement operation. The correlation coefficient determines the relationship between economically significant quantitative characteristics. Correlation coefficients can be divided into two categories using path coefficient analysis: direct and indirect impacts. It aids in elucidating the intrinsic nature of observed associations for complicated characteristics such as grain yield. The analysis of the aforesaid characteristics aids in clarifying the relationship between distinct morphological qualities and yield. As a result, understanding the direct and indirect impacts of various components on yield is critical in the selection

of high yielding genotypes¹.

Induced mutations have been used mainly to generate variations of desirable trait in an otherwise high yielding popular variety. Large spectrum of variation in Brassica crops have been generated through induced mutation and been used to develop high yielding varieties⁵⁻⁶.

Seed number/silique, silique on main shoot, Number of primary, secondary, and tertiary branches, Total silique on whole plant, Height (cm) and seed yield are important parameters which are focused upon while designing any breeding program in mustard. However, reports on genetic analysis of variability generated through induced mutagenesis are scanty. The studies conducted so far have only analysed the relation of one or two parameters with the seed yield^{14,15}. This research studied the association of total 7 parameters with seed yield and moreover mutant varieties of the Indian Mustard were used. Therefore, the current investigation was up-taken to estimate the genetic variability of selected mutant genotypes isolated from parents PM21 & PM30 using Gamma rays & Ethyl Methane Sulphonate (EMS).

2. METHODOLOGY

The study material consisted of 57 stable mutant genotypes isolated from 22 different treatments on two zero erucic acid varieties of Indian mustard (*Brassica juncea*) i.e. PM 21 and PM 30. Initially, the seeds of PM21 and PM 30 were irradiated with three doses of gamma rays (1000 Gy, 1200 Gy & 1500 Gy) and also treated in combination with different concentration of chemical mutagen EMS (0.25 %, 0.50 % & 0.75 %). The seeds were then sown to obtain the M₁ generation. The experiment was carried out at ICAR-DRMR, Sear, Bharatpur, Rajasthan. The recommended fertilizers and cultural practices were used to maintain a healthy crop growth. Desirable genotypes for seed yield were selected in M₂ generation and their progenies were raised in M₃ and M₄ generations. The stable true breeding mutants were characterised for seed yield and their components. The genotypes of each experiment were raised in Randomized Block design with 2 replications. The distance between two rows was 30cms or 45cms and the distance between two plants was 10cms respectively. The genotypes were individually harvested when they were 80 % mature. The data was recorded on selective genotypes with high seed yield for 8 parameters i.e., seed number (CH1), silique on main shoot (CH2), primary branches (CH3), secondary branches (CH4), tertiary branches (CH5), total silique on whole plant (CH6), height in cms (CH7) and seed yield in grams (CH8).

The analysis of variance (ANOVA) was conducted using established standard operating procedures (SOPs). The approach outlined in the study included the estimation of phenotypic and genotypic coefficients of variation (PCV, GCV). The examination of path coefficients was conducted by using correlation coefficients, specifically focusing on heritability⁷, phenotypic correlation coefficients, and genomic correlation coefficients^{1,8,9}.

The calculation of heritability (h²) in a wide context included determining the ratio between genotypic variation and phenotypic variance.

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

where

σ^2_p Phenotypic variance
 σ^2_g Genotypic variance
 h^2 Heritability in broad sense

$$G.A. = h^2 \times \sigma_p \times k$$

where

$h^2(b)$ Heritability in broad sense;

G.A. Expected genetic advance;

K Intensity of selection

σ_p Phenotypic standard deviation

The genetic advancement, expressed as a percentage of the mean, was computed for each characteristic by using following formula:

$$\text{Genetic advance as percent of means} = \frac{GA}{\text{Mean}} \times 100$$

The GCV and PCV were calculated as:

$$GCV = \frac{\text{Genotypic standard deviation} \times \sqrt{\sigma_g^2}}{\text{Mean}} \times 100$$

$$PCV = \frac{\text{Phenotypic standard deviation} \times \sqrt{\sigma_p^2}}{\text{Mean}} \times 100$$

3. RESULTS AND DISCUSSION

3.1 Variability Studies

Total 8 characters for which variability studies were conducted are: Seed number (CH1) per silique, silique on main shoot (CH2), primary branches (CH3), secondary branches (CH4), tertiary branches (CH5), total silique on whole plant (CH6), height (CH7) and seed yield (CH8).

Table 1 displays the analysis of variance conducted on eight characteristics related to yield and yield attributes of 57 genotypes of *B. juncea*.

The total mean square due to genotypes was found to be more significant in all of the traits except main shoot, total silique on whole plant & height. This signifies that a considerable amount of genetic variation exists in the maximum characters. The results were in agreement with previously published work in *B. juncea*.^{4,10}

The results of coefficient of variation studies are reported in Table 2. The values of PCV are higher than GCV in all of the traits which signifies that not only genotypes but environment has also played a significant role in generating variability through induced mutagenesis.

The values of GCV & PCV between 10 to 20 % are considered as moderate. Primary branches per plant (27.62 %), secondary branches (24.92 %), tertiary branches (24.42%), total silique on whole plant (11.17 %) and seed yield (15.64 %) possess moderate values of GCV. Interestingly, all of the characters possess moderate magnitude of phenotypic coefficient of variation i.e., Seed number/silique (13.38 %), silique on main shoot (20.07 %), primary branches per plant (55.93 %), secondary branches (43.55 %),

Table 1. ANOVA for *B. juncea* genotype yield and yield-attributing traits

| Source | d.f | CH1 | CH2 | CH3 | CH4 | CH5 | CH6 | CH7 | CH8 |
|-------------|-----|-----------|----------|---------|-----------|-----------|-----------|----------|----------|
| Replication | 1 | 21.5517* | 304.6897 | 3.8017 | 37.5517* | 178.7586 | 283141.04 | 193.9655 | 0.5272 |
| Treatment | 57 | 7.11736** | 158.3823 | 6.2542* | 15.9800** | 783.7677* | 257873.94 | 419.1924 | 1.0999** |
| Error | 57 | 3.3061 | 104.8476 | 3.8017 | 8.0956 | 449.8814 | 243377.06 | 509.3164 | 0.5399 |

CH1: Seed number/silique; CH2: silique on main shoot; CH3: primary branches; CH4: secondary branches; CH5: tertiary branches
CH6: total silique on whole plant; CH7: height (cm); CH8: seed yield (g); (*, **): significant at 0.05 and 0.01 levels

Table 2. Genetic yield and yield attributing traits parameter estimation in *Brassica juncea* genotypes

| Trait | Mean | Range | GCV | PCV | h ² | GA |
|-------|---------|----------|---------|---------|----------------|---------|
| CH1 | 17.052 | 10-22 | 8.0956 | 13.3882 | 0.6047 | 2.8437 |
| CH2 | 57.362 | 36-85 | 8.8493 | 20.0757 | 0.4408 | 10.4569 |
| CH3 | 4.009 | 1-13 | 27.6246 | 55.9373 | 0.4938 | 2.2812 |
| CH4 | 7.966 | 2-19 | 24.9262 | 43.5572 | 0.5723 | 4.0901 |
| CH5 | 52.897 | 12-140 | 24.4263 | 46.9519 | 0.5202 | 26.6165 |
| CH6 | 761.922 | 150-2700 | 11.1741 | 65.7055 | 0.1701 | 17.3838 |
| CH7 | 189.483 | 135-250 | 0 | 11.3713 | 0 | 0 |
| CH8 | 3.382 | 1.1-5.48 | 15.6456 | 26.776 | 0.5843 | 1.0899 |

PCV (phenotypic coefficient of variation); GCV (Genetic coefficient of variation);
GA (Genetic Advance); h² (Heritability)

tertiary branches (46.95 %), total silique on whole plant (65.70 %), height (11.37 %) and seed yield (26.776 %). These qualities have been identified as the primary yield-contributing characteristics¹¹. For many characteristics, including seed yield/plant, similar conclusions regarding the occurrence of considerable variability were revealed.¹²

High estimate of heritability is observed for seed number per silique (0.647). The high heritability for this trait indicates that selection gain to improve this trait would be higher. Number of silique on main shoot (10.45 %), tertiary branches (17.38 %) & total silique on whole plant (17.38 %) have high genetic advance magnitudes which predicts that these traits are regulated by additive genes and their selection is beneficial. Similar results for total silique on whole plant and high GA (genetic advance) values for number of silique on main shoot have also been reported earlier in *B. juncea*^{3,13}.

3.2 Association Studies Between Traits

The phenotypic and genotypic correlation coefficients between different traits were estimated and presented in Table 3. The primary diagonal (1.00), which runs from top left to bottom right, demonstrates that each variable always precisely correlates with itself. The first row of each character shows its genotypic correlation with another variable and the second line depicts its phenotypic correlation with another variable.

Results of coefficient analysis suggest that the seed number per silique is negatively correlated with silique on main shoot (-0.06), branches (-0.01), branches (-0.04) & total silique on whole plant (-0.05) while positively

related with branches (0.05), height (0.08) & seed yield (0.05). It exhibits positive phenotypic correlation with silique on main shoot (0.13), tertiary branches (0.02), total silique on whole plant (0.09) & seed yield (0.15) & negative phenotypic correlation with primary branches (-0.09), secondary branches (-0.1) & height (-0.02). The silique on main shoot shows negative genotypic correlation with all of the characters except the seed yield (0.09) & is also negatively correlated with secondary branches (-0.05) & seed yield (-0.08), rest all characters are positively correlated.

The primary branches are negatively correlated with secondary branches (-0.3), tertiary branches (-0.22) & total silique on whole plant (-0.27) and positively with height (0.16) & seed yield (0.07). The primary branches show significant positive phenotypic correlation with secondary branches (0.786) and tertiary branches (0.557). The secondary branches exhibit negative genotypic correlation with tertiary branches (-0.25) & total silique on whole plant (-0.28) and positive correlation with height (0.23) & seed yield (0.07). Phenotypically, it is positively correlated with seed yield (0.05) & total silique on whole plant (0.4) while negatively with CH7 (-0.08). The secondary branches have significant positive phenotypic correlation with the tertiary branches (0.53).

The tertiary branches show negative genotypic correlation with total silique on whole plant (-0.3) & seed yield (-0.01) while positive correlation with height (0.09). Also, tertiary branches show positive phenotypic correlation with height (0.05) and seed yield (0.3) and significant phenotypic correlation with total silique on

whole plant (0.53). The total siliqua on whole plant is negatively correlated with all of the characters except height (0.12) & seed yield (0.18) while it shows positive phenotypic correlation with all of the traits except seed yield (-0.06).

The height is positively correlated with all of the characters except siliqua on main shoot (-0.02) & seed yield (-0.08) & shows positive phenotypic correlation with all characters except seed number per siliqua (-0.02), primary branches (-0.02) & secondary branches (-0.08). The seed yield exhibits positive genotypic correlation with all characters except tertiary branches (-0.01) & height (-0.09). It also shows positive phenotypic correlation with all characters except siliqua on main shoot (-0.08)

& total siliqua on whole plant (-0.06). The findings presented here are consistent with previous studies^{1-2,13}.

Only the nature and degree of association between any two variables are described by correlation coefficients, whereas path analysis allows for the interpretation of cause and effect relationships. While other traits were taken into consideration as independent variables, the seed yield is treated as the dependent variable. The path coefficient analysis findings (Table 4) showed the indirect and direct impacts of several features on production of seed. The seed yield is seen to be positively correlated by the number of seeds per siliqua (0.181). The main shoot's siliqua exhibits a direct negative correlation (-0.128) with the seed yield. Together with the primary branches, the

Table 3. Phenotypic and genotypic correlations for various traits in *Brassica juncea* genotypes

| | CH1 | CH2 | CH3 | CH4 | CH5 | CH6 | CH7 | CH8 |
|-----|----------|----------|----------|----------|----------|----------|----------|----------|
| CH1 | 1 | -0.06472 | -0.01569 | -0.04596 | 0.057842 | -0.05051 | 0.082111 | 0.058966 |
| | | 0.132 | -0.009 | -0.1 | 0.028 | 0.093 | -0.021 | 0.152 |
| CH2 | -0.06472 | 1 | -0.16075 | -0.10678 | -0.1804 | -0.33095 | -0.02917 | 0.098974 |
| | 0.132 | | 0.054 | -0.053 | 0.163 | 0.283 | 0.094 | -0.085 |
| CH3 | -0.01569 | -0.16075 | 1 | -0.35364 | -0.27335 | -0.27461 | 0.167547 | 0.073172 |
| | -0.009 | 0.054 | | 0.786 | 0.557 | 0.465 | -0.029 | 0.082 |
| CH4 | -0.04596 | -0.10678 | -0.35364 | 1 | -0.25695 | -0.28082 | 0.239028 | 0.073982 |
| | -0.1 | -0.053 | 0.786 | | 0.533 | 0.438 | -0.086 | 0.057 |
| CH5 | 0.057842 | -0.1804 | -0.27335 | -0.25695 | 1 | -0.37892 | 0.090416 | -0.0133 |
| | 0.028 | 0.163 | 0.557 | 0.533 | | 0.535 | 0.05 | 0.319 |
| CH6 | -0.05051 | -0.33095 | -0.27461 | -0.28082 | -0.37892 | 1 | 0.122513 | 0.18994 |
| | 0.093 | 0.283 | 0.465 | 0.438 | 0.535 | | 0.019 | -0.067 |
| CH7 | 0.082111 | -0.02917 | 0.167547 | 0.239028 | 0.090416 | 0.122513 | 1 | -0.09776 |
| | -0.021 | 0.094 | -0.029 | -0.086 | 0.05 | 0.019 | | 0.191 |
| CH8 | 0.058966 | 0.098974 | 0.073172 | 0.073982 | -0.0133 | 0.18994 | -0.09776 | 1 |
| | 0.152 | -0.085 | 0.082 | 0.057 | 0.319 | -0.067 | 0.191 | |

CH1: Seed number/siliqua; CH2: siliqua on main shoot; CH3: primary branches; CH4: secondary branches; CH5: tertiary branches; CH6: total siliqua on whole plant; CH7: height (cm); CH8: seed yield (g)

Table 4. Direct and indirect path coefficients for various traits in *Brassica juncea* genotypes

| Direct-indirect effects | | | | | | | |
|-------------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | CH1 | CH2 | CH3 | CH4 | CH5 | CH6 | CH7 |
| CH1 | 0.181 | 0.023892 | -0.001629 | -0.0181 | 0.005068 | 0.016833 | -0.003801 |
| CH2 | -0.016896 | -0.128 | -0.006912 | 0.006784 | -0.020864 | -0.036224 | -0.012032 |
| CH3 | 0.000135 | -0.00081 | -0.015 | -0.01179 | -0.008355 | -0.006975 | 0.000435 |
| CH4 | 0.005 | 0.00265 | -0.0393 | -0.05 | -0.02665 | -0.0219 | 0.0043 |
| CH5 | 0.014616 | 0.085086 | 0.290754 | 0.278226 | 0.522 | 0.27927 | 0.0261 |
| CH6 | -0.027993 | -0.085183 | -0.139965 | -0.131838 | -0.161035 | -0.301 | -0.005719 |
| CH7 | -0.003822 | 0.017108 | -0.005278 | -0.015652 | 0.0091 | 0.003458 | 0.182 |

CH1: Seed number/siliqua; CH2: siliqua on main shoot; CH3: primary branches; CH4: secondary branches; CH5: tertiary branches; CH6: total siliqua on whole plant; CH7: height (cm); CH8: seed yield (g)

tertiary branches have a direct effect that is favourable on seed yield (0.29). Similar to secondary branches, tertiary branches exhibit a positive direct influence on seed yield (0.278). The direct impact of the tertiary branches on seed output is similarly highly favourable (0.522). With total siliqua on the entire plant, it also demonstrates a favourable direct influence on seed yield (0.279). With regard to primary, secondary, and tertiary branches as well as an independent negative direct effect (-0.301), the total siliqua on the entire plant exhibits a negative correlation with the seed yield. Additionally, the seed yield was directly influenced by the height (0.182). The outcomes are consistent with earlier reports on mustard that have been published.^{5,14,15}

4. CONCLUSIONS

The ultimate objective of mutation breeding is the creation of mutants with genetic variability for a certain feature and the selection of economically advantageous qualities in the mutants. Novel mutants with high seed yield were isolated. The primary, secondary & tertiary branches, total siliqua and seed yield of the selected superior mutants possessed higher values of GCV while the PCV was found to be moderate for all of the characters. A significant positive correlation existed between primary, secondary & tertiary branches & total siliqua of a plant. The seed yield was also found to be positively correlated with the number of seeds per siliqua, primary & secondary branches. The identification of component characters which have positive or negative association with seed yield has helped in designing of a breeding program to produce stable true breeding lines in Indian Mustard with high seed yield.

ACKNOWLEDGEMENT

The authors are immensely grateful to Bhabha Atomic Research Centre, Trombay, Mumbai-400085 for the financial support and ICAR-DRMR, Bharatpur, Rajasthan-321303 for providing the facilities that greatly assisted the research.

REFERENCES

1. Yadava, D.K.; Giri, S.C.; Vignesh, M.; Vasudev, S.; Yadav, A.K.; Dass, B.; Singh, R.; Singh, N.; Mahapatra, T. & Prabhu, K.V. Genetic variability and trait association studies in Indian mustard (*B. juncea* L.). *Indian J. Agric. Sci.*, 2011, **81**, 712–716. doi: 10.20546/ijcmas.2020.901.290.
2. Agarwal, A.P. & Nair, S.K. Genotypic path analysis for oil and seed yield in mustard. *Indian Agric.*, 2003, **47**, 151–6.
3. Aktar, T.; Nuruzzaman; M.; Rana, M.S.; Huda, M.M.; Hossain, M.A. & Hassan, L. Genetic parameters and diversity studies of yield and yield contributing characters in Brassica genotypes. *J. Bangladesh Agric. Univ.*, 2019, **17**, 295–300. doi: 10.3329/jbau.v17i3.43200.
4. Gupta, M.; Roy, H.S. & Bhadauria, S.S. Genetic variability analysis in F2/F3 population derived through inter-specific hybridization in oilseed Brassica. *Electron. J. Plant Breed.*, 2019, **10**, 1275-1282. doi: 10.5958/0975-928X.2019.00163.7.
5. Chauhan, J.S.; Singh, K.H.; Singh, M.; Bhadauria, V.P.S. & Kumar, A. Studies on Genetic Variability and Path Analysis for Quality Characters in Rapeseed-Mustard (Brassica species). *J. Plant Genet. Res.*, 2008, **21**(2), 113-117.
6. Jambhulkar, S.J. Induced mutagenesis and allele mining. Brassica Oilseeds: Breeding and Management. CAB International, 2015, 53-67. doi: 10.1079/9781780644837.0053.
7. Prasad, G. & Patil, BR. Genetic variability and heritability studies for yield and attributes in Indian Mustard. *J. Pharmacogn. Phytochem.*, 2018, **7**(5), 519-522.
8. Kumar, S. & Misra, M.N. Study on genetic variability, heritability and genetic advance in populations in Indian mustard (*Brassica juncea* L. Czern & Coss.) *Int. J. Plant Sci.*, 2007, **2**(1), 188–90. doi: 10.20546/ijcmas.2020.910.186.
9. Yimer, O.; Mohammed, W.; Teju, E. & Pae, D.H. Correlation and path coefficient analysis studies in Ethiopian mustard. *Afr. J. Plant Sci.*, 2021, **15**(8), 250-256. doi: 10.5897/ajps2021.2156.
10. Rout S.; Kerkhi, S.A. & Gupta, A. Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard. *J. Pharmacogn. Phytochem.*, 2019, **8**, 4119-4123.
11. Kardam, D.K. & Singh, V.V. Correlation and path analysis in Indian mustard (*Brassica juncea* L. Czern&Coss.) grown under rainfed condition. *J. Spices. Aromat Crops.*, 2005, **14**(1), 56–60. <https://www.updatepublishing.com/journal/index.php/josac/article/view/4815> (accessed on date 29th April 2023).
12. Singh, B. Character association and path analysis under dry land condition in Indian mustard (*Brassica juncea* L.). *Cruciferae Newsl.*, 2004, **25**, 99–100. doi: 10.20546/ijcmas.2020.902.362.
13. Lodhi, B.; Thakral, N.K.; Avtar, R. & Singh, A. Genetic variability, association and path analysis in Indian mustard (*B. juncea*). *J. Oilseed Brassica.*, 2014, **5**, 26-31.
14. Gupta, A.; Chauhan, S.; Tyagi, S.D. & Singh, S. Genetic Variability, Heritability, Genetic Advance and Cluster Analysis in Indian Mustard (*Brassica juncea* L. Czern & Coss.) under timely and late sown conditions. *Int. J. Plant Soil Sci.*, 2023, **35**(19), 292–301. doi: 10.9734/ijpss/2023/v35i193554.
15. Gupta, A.; Tyagi, S.D.; Chauhan, S.; Johari, A. & Singh, S. Genetic variability, correlation, path coefficient and cluster analysis in Indian mustard (*Brassica juncea* L.). *Pharm. Innovation J.*, 2022, **11**(11), 2401-2406. doi: 10.13140/RG.2.2.30220.97922.

CONTRIBUTORS

Ms Meghna Garg is research scholar at GLA University, Mathura. She has worked as JRF at ICAR-DRMR, Bharatpur under the project funded by BRNS. Her main area of interest is in improvement of Mustard through chemical and physical mutations.

She has contributed in the data gathering, analysis, interpretation, and manuscript preparation.

Dr Anubhuti Sharma is Principal Scientist at ICAR-DRMR, Bharatpur, Rajasthan. Her main area of interest is nutritional, biochemical, genetic and molecular analysis of mustard.

She has contributed in the manuscript preparation, overall guidance and framing of this study.

Dr Sanjay Jambhulkar is Scientist at Bhabha Atomic Research centre (Nuclear & Agriculture Division). His main area of

interest in Plant Breeding through Mutations.

He has contributed in conceptualisation, availability of experimental material and proofreading of manuscript.

Mr Rakesh Goel is Assistant Professor (AGB) at DUVASU, Mathura. His main area of interest is Animal genetics and Breeding.

He has helped in statistical analysis of the manuscript.

Dr P.K. Rai is Director ICAR-DRMR, Bharatpur, Rajasthan. He has worked on several infectious diseases of Mustard and development of tolerant varieties for the same.

He has contributed in providing the facilities for conduction of experimental work and proof reading of the manuscript.

Dr Shoor Vir Singh is Head of the Department of Biotechnology at GLA University, Mathura. He has worked on zoonotic disease caused by agent *Mycobacterium Avium Paratuberculosis*.

He has contributed overall proof reading of the manuscript.