International Journal of Advanced Biochemistry Research

**ISSN Print:** 2617-4693
**ISSN Online:** 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(10): 656-659
www.biochemjournal.com
Received: 02-07-2025
Accepted: 06-08-2025

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# Genetic analysis of $M_3$ mutants of rice (*Oryza sativa* L.) *var*. Wada Kolam

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**DOI:** https://www.doi.org/10.33545/26174693.2025.v9.i10Sh.5902

**Abstract**
Rice (*Oryza sativa* L.) is a vital cereal crop which supports the food security in India. Wada Kolam, a widely grown local variety in konkan region especially in Palghar district of Maharashtra is highly valued but constrained by tall stature, susceptibility to lodging, and vulnerability to blast disease, leading to yield losses. Mutation breeding provides a practical strategy to introduce useful variability for traits such as dwarf plant type, blast resistance, and improved yield potential. The present study evaluated 150 $M_3$ mutant lines of Wada Kolam, along with four checks, during *Kharif* 2024 at the Research and Educational Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, using an Augmented Block Design. Genetic analysis revealed significant phenotypic and genotypic variation, particularly for number of filled grains per panicle, plant height, and yield attributes. Moderate genotypic and phenotypic coefficients of variation were observed for productive tillers, grain yield, and test weight, while other traits exhibited lower variability. High heritability coupled with high genetic advance was recorded for filled grains per panicle, indicating additive gene action and strong potential for direct selection. Notably, mutant lines such as M2-11, M2-123, M2-29, M2-2, and M2-76 showed reduced plant height, superior yield components, and blast resistance.

**Keywords:** Rice, Wada Kolam, variability, heritability, genetic advance, GAM

## Introduction
Wada Kolam, a popular and well-established local rice variety grown majorly in konkan region especially in Palghar district of Maharashtra. Wada Kolam fetches a good market price and has heavy demand in market due to its fine grain type but is particularly vulnerable to lodging due to its tall plant height. Lodging in Wada Kolam rice variety, results in a substantial reduction in the yield, grain quality, etc. leading to significant losses in crop productivity. To overcome, this lodging problem in popular rice variety Wada Kolam, mutation breeding aims at developing suitable varieties with enhanced seed yield and nutrients, earliness in maturity, tolerance to disease and pests, etc. Induced mutagenesis is an important source to produce mutations in higher frequencies in cultivated crops especially in diploids (Kharkwal *et al*. 2004) [10]. In Wada Kolam rice variety a trait related to dwarf height is introduced by using gamma rays for developing improved yield potential, lodging resistant along with the blast disease resistance lines.

In India, Rice is grown in about 45.15 M ha area, procuring a yield of 135.70 million tonnes with productivity of 3028 kg/ha (Anonymous (a), 2024) [2]. Maharashtra ranks 12$^{th}$ in rice cultivation producing 3.50 million tonnes produce on 1.53 Mha of land in with a productivity of 2287.4 kg/ha in 2023-24 (Anonymous (b), 2024) [3]. Konkan region has 3.31lakh ha and has 52.03 lakh tonnes of production and 3.30 t/ha of rice productivity (Anonymous (c), 2024) [4].

In recent years, rice blast disease has been consistently resulting in substantial losses when climatic conditions favour its spread. Chemical control measures are effective, but their environmental implications and potential to foster resistant pathogen strains render them undesirable. Consequently, cultivating resistant crop varieties emerges as the most viable solution to mitigate yield losses and ensure sustainable rice production.

The objectives of the present research is to select high yielding, dwarf statured and blast resistant lines. Genetic variability studies on rice variety Wada Kolam can effectively identify and quantify the traits contributing to yield and blast resistance.

## Materials & Methods

The material for the present study consists of 150 lines of $M_2$ population of local rice variety Wada Kolam was taken for research purpose and was carried out at Research and Educational Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri. The selected $M_3$ populations were studied for short stature, blast resistance along with yield and yield attributing characters. The material comprised of one hundred and fifty mutant lines with 4 check *viz*., Wada kolam, Bangalia, Botvel, Ghansal was grown in *Kharif* 2024. The list of treatments used in study is given in Table 1.The seedlings were raised in wet nursery method by following required agronomic practices and thirty days old seedlings from each treatment were transplanted to the well-prepared puddled field on 14th July 2024 at a spacing of 20 cm × 15 cm between row to row and plant to plant respectively, at the rate of one seedling per hill in Augmented Block Design (Federer, 1975) [7]. The observations were recorded for individual plants from each row.

**Table 1:** Experimental material and treatments

| Sr. No. | Lines | Sr. No. | Lines | Sr. No. | Lines | Sr. No. | Lines | Sr. No. | Lines |
|---|---|---|---|---|---|---|---|---|---|
| 1 | M2-1 | 32 | M2-32 | 63 | M2-63 | 94 | M2-94 | 125 | M2-125 |
| 2 | M2-2 | 33 | M2-33 | 64 | M2-64 | 95 | M2-95 | 126 | M2-126 |
| 3 | M2-3 | 34 | M2-34 | 65 | M2-65 | 96 | M2-96 | 127 | M2-127 |
| 4 | M2-4 | 35 | M2-35 | 66 | M2-66 | 97 | M2-97 | 128 | M2-128 |
| 5 | M2-5 | 36 | M2-36 | 67 | M2-67 | 98 | M2-98 | 129 | M2-129 |
| 6 | M2-6 | 37 | M2-37 | 68 | M2-68 | 99 | M2-99 | 130 | M2-130 |
| 7 | M2-7 | 38 | M2-38 | 69 | M2-69 | 100 | M2-100 | 131 | M2-131 |
| 8 | M2-8 | 39 | M2-39 | 70 | M2-70 | 101 | M2-101 | 132 | M2-132 |
| 9 | M2-9 | 40 | M2-40 | 71 | M2-71 | 102 | M2-102 | 133 | M2-133 |
| 10 | M2-10 | 41 | M2-41 | 72 | M2-72 | 103 | M2-103 | 134 | M2-134 |
| 11 | M2-11 | 42 | M2-42 | 73 | M2-73 | 104 | M2-104 | 135 | M2-135 |
| 12 | M2-12 | 43 | M2-43 | 74 | M2-74 | 105 | M2-105 | 136 | M2-136 |
| 13 | M2-13 | 44 | M2-44 | 75 | M2-75 | 106 | M2-106 | 137 | M2-137 |
| 14 | M2-14 | 45 | M2-45 | 76 | M2-76 | 107 | M2-107 | 138 | M2-138 |
| 15 | M2-15 | 46 | M2-46 | 77 | M2-77 | 108 | M2-108 | 139 | M2-139 |
| 16 | M2-16 | 47 | M2-47 | 78 | M2-78 | 109 | M2-109 | 140 | M2-140 |
| 17 | M2-17 | 48 | M2-48 | 79 | M2-79 | 110 | M2-110 | 141 | M2-141 |
| 18 | M2-18 | 49 | M2-49 | 80 | M2-80 | 111 | M2-111 | 142 | M2-142 |
| 19 | M2-19 | 50 | M2-50 | 81 | M2-81 | 112 | M2-112 | 143 | M2-143 |
| 20 | M2-20 | 51 | M2-51 | 82 | M2-82 | 113 | M2-113 | 144 | M2-144 |
| 21 | M2-21 | 51 | M2-52 | 83 | M2-83 | 114 | M2-114 | 145 | M2-145 |
| 22 | M2-22 | 53 | M2-53 | 84 | M2-84 | 115 | M2-115 | 146 | M2-146 |
| 23 | M2-23 | 54 | M2-54 | 85 | M2-85 | 116 | M2-116 | 147 | M2-147 |
| 24 | M2-24 | 55 | M2-55 | 86 | M2-86 | 117 | M2-117 | 148 | M2-148 |
| 25 | M2-25 | 56 | M2-56 | 87 | M2-87 | 118 | M2-118 | 149 | M2-149 |
| 26 | M2-26 | 57 | M2-57 | 88 | M2-88 | 119 | M2-119 | 150 | M2-150 |
| 27 | M2-27 | 58 | M2-58 | 89 | M2-89 | 120 | M2-120 | C1 | Wada kolam |
| 28 | M2-28 | 59 | M2-59 | 90 | M2-90 | 121 | M2-121 | C2 | Bangalia |
| 29 | M2-29 | 60 | M2-60 | 91 | M2-91 | 122 | M2-122 | C3 | Botvel |
| 30 | M2-30 | 61 | M2-61 | 92 | M2-92 | 123 | M2-123 | C4 | Ghansal |
| 31 | M2-31 | 62 | M2-62 | 93 | M2-93 | 124 | M2-124 | | |

## Results and Discussion

### Components of variation

Components of variation was estimated using the formula given by Cochran and Cox (1957) [6]. The total variation observed in the population was attributed to phenotypic, genotypic, and environmental components. For various yield attributing traits, the phenotypic, genotypic, and environmental variations varied from 1.52 (No. of productive tillers) to 711.28 (No. of filled grains per panicle), 0.32 (Days to fifty% flowering) to 616.82 (No. of filled grains per panicle) and 0.55 (Harvest Index) to 94.46 (No. of filled grains per panicle) respectively. In general, phenotypic variance exhibited greater magnitude than genotypic and environmental components across all traits. The highest phenotypic variance was recorded for number of filled grains per panicle, followed by plant height, spikelet fertility, straw yield per plant, grain yield per plant, days to 50% flowering, test weight, harvest index, and number of productive tillers. The maximum genotypic variance was recorded for number of filled grains per panicle, followed by plant height, straw yield per plant, grain yield per plant, spikelet fertility, test weight, harvest index, Number of productive tillers, and days to 50% flowering. The highest environmental variance was observed for number of filled grains per panicle, closely followed by plant height, spikelet fertility, straw yield per plant, days to 50% flowering, grain yield per plant, test weight, number of productive tillers, and harvest index. Similar results were reported by Mahantashivayogayya *et al*. (2016) [13] and Kumari *et al*. (2019) [11]. Luz *et al*. (2016) [12] also identified plant height as highly responsive to mutation. The estimates of phenotypic ($\sigma^2p$), genotypic ($\sigma^2g$) and environmental ($\sigma^2e$) variances for 9 quantitative characters is given in table 2.

**Table 2:** Estimates of phenotypic ($\sigma^2p$), genotypic ($\sigma^2g$) and environmental ($\sigma^2e$) variances for 9 quantitative characters of rice *var*. Wada Kolam

| Genetic parameters | $\sigma^2$ Environmental | $\sigma^2$ Genotypical | $\sigma^2$ Phenotypical |
|---|---|---|---|
| DFF | 4.34 | 0.32 | 4.66 |
| PH | 94.44 | 124.46 | 218.89 |
| PT | 0.59 | 0.93 | 1.52 |
| FG | 94.46 | 616.82 | 711.28 |
| SF | 22.59 | 2.97 | 25.56 |
| GY | 3.58 | 5.58 | 9.15 |
| SY | 11.12 | 7.39 | 18.51 |
| HI | 0.55 | 1.64 | 2.18 |
| TW | 1.31 | 2.02 | 3.33 |

**Coefficient of variation**

The genotypic and phenotypic coefficient of variation was calculated as per the formula given by Burton and Devane (1953) [5]. The PCV and GCV are classified as suggested by Sivasubramanian and Menon (1973) [17]. In general, phenotypic coefficients of variation (PCV) were greater in magnitude than the corresponding genotypic coefficients of variation (GCV) and environmental coefficients of variation (ECV). The characters number of filled grains per panicle, Number of productive tillers, grain yield per plant, test weight, straw yield per plant and plant height recorded moderate levels of phenotypic coefficient of variation. The traits spikelet fertility, harvest index, and days to 50% flowering exhibited low PCV values. Genotypic coefficient of variation (GCV) is a quantitative measure of the level of genetic variation exists within a population. The characters number of filled grains per panicle, number of productive tillers, grain yield per plant and test weight recorded moderate levels of genotypic coefficient of variation, indicating appreciable genetic variability for these traits. The remaining traits such as plant height, straw yield per plant, harvest index, spikelet fertility, and days to 50% flowering exhibited low GCV. Mahantashivayogayya *et al*. (2016) [13] reported narrow differences between PCV and GCV for days to 50% flowering. Moderate GCV and PCV for number of productive tillers per plant and number of filled grains per panicle align with the findings of Mahantashivayogayya *et al*. (2016) [13], who observed substantial variability for these traits. Sjahril (2021) [18] results reported similar findings for Spikelet fertility which recorded low GCV and PCV. Siddiqui and Singh (2010) [16] observed moderate variability for Grain yield per plant. Sjahril (2021) [18] observed low GCV & PCV for harvest index, while Sjahril (2021) [18] results reported moderate GCV and PCV for test weight.

**Heritability and Genetic advance**

In the present investigation, high heritability was recorded for number of productive tillers per plant, number of filled grains per panicle, grain yield per plant, harvest index, and test weight, indicating a predominant role of genetic control in the expression of these traits. These findings are in agreement with the reports of Mahantashivayogayya *et al*. (2016) [13] and Sjahril (2021) [18], who also observed high heritability for these traits in rice mutants. Moderate heritability was observed for plant height and straw yield per plant, which is consistent with the findings of Mahantashivayogayya *et al*. (2016) [13] in rice mutant population. Thus, the high heritability noted for key yield-contributing traits in the present study suggests that these characters are largely controlled by additive gene action and can be effectively improved through direct selection. The genetic advance (GA) among the studied traits ranged from 0.30 to 47.64, indicating varied potential for genetic improvement through selection. The highest genetic advance was recorded for number of filled grains per panicle, followed by plant height, grain yield per plant, straw yield per plant, harvest index, test weight, number of productive tillers, spikelet fertility, and the lowest for days to 50% flowering.

In the present investigation, high genetic advance was recorded for number of filled grains per panicle, indicating the predominance of additive gene action and high potential for improvement through direct selection. This observation is in agreement with the findings of Mahantashivayogayya *et al*. (2016) [13] and Sadimantara *et al*. (2021) [15], who reported high genetic advance for similar yield-contributing traits in rice mutants. Moderate genetic advance was observed for plant height, suggesting moderate genetic variability, which aligns with the results of Mahantashivayogayya *et al*. (2016) [13] in rice mutant populations. In contrast, all other traits-number of productive tillers per plant, grain yield per plant, test weight, straw yield per plant, harvest index, spikelet fertility, and days to 50% flowering exhibited low genetic advance.The genetic advance as percent of mean (GAM) among the studied traits ranged from 0.30 to 30.66. The highest genetic advance as percent of mean was observed for number of filled grains per panicle, followed by number of productive tillers, grain yield per plant, test weight, plant height recorded moderate genetic advance as percent of mean. Straw yield per plant, harvest index, spikelet fertility, and days to 50% flowering has lowest genetic advance as percent of mean.

In the present study, the trait number of filled grains per panicle exhibited high heritability coupled with high genetic advance, suggesting the predominance of additive genetic effects and a high potential for improvement through selection. Estimates of genetic parameters for 9 quantitative characters is given in table 3.

**Table 3:** Estimates of genetic parameters for 9 quantitative characters in rice *var*. Wada Kolam

| Genetic parameters | GCV | PCV | $h^2$ (Broad Sense) | GA | GAM |
|---|---|---|---|---|---|
| DFF | 0.57 | 2.21 | 6.77 | 0.30 | 0.30 |
| PH | 8.20 | 10.88 | 56.86 | 17.33 | 12.74 |
| PT | 11.99 | 15.32 | 61.21 | 1.55 | 19.32 |
| FG | 15.98 | 17.16 | 86.72 | 47.64 | 30.66 |
| SF | 2.29 | 6.72 | 11.64 | 1.21 | 1.61 |
| GY | 11.39 | 14.6 | 60.93 | 3.79 | 18.32 |
| SY | 7.02 | 11.11 | 39.92 | 3.53 | 9.14 |
| HI | 3.65 | 4.22 | 74.93 | 2.28 | 6.52 |
| TW | 10.72 | 13.77 | 60.57 | 2.27 | 17.18 |

This classification of heritability, genetic advance, and genetic advance as a percentage of the mean was made based on the standard criteria established by Johnson *et al*. (1955) [9].

## Conclusion

In the present investigation, high genotypic coefficient of variation, heritability, and genetic advance were recorded for trait number of filled grains per panicle indicating predominance of additive gene action and potential for effective direct selection. The investigation also indicated the presence of substantial genetic variability among the mutants lines for agronomic and yield contributing traits. Superior performance was observed in M2-11, M2-123, M2-29, M2-2, M2-76 promising lines for lesser plant height, number of filled grains per panicle, spikelet fertility, grain yield per plant, harvest index, test weight along with blast resistance such as indicating their potential for advancement through further selection.

## References


1. Allard RW. Selection under self-fertilization. In: Principles of Plant Breeding. New York (USA): John Wiley & Sons, Inc.; 1960.
2. Anonymous (a). Third advance estimates. Ministry of Agriculture and Farmers Welfare, Government of India; 2024. Available from: https://www.indiastatagri.com
3. Anonymous (b). Districtwise third advance estimate-2023-24. Department of Agriculture, Government of Maharashtra; 2024. Available from: https://krishi.maharashtra.gov.in
4. Anonymous (c). Final advance estimate during 2023-24 in Maharashtra State; 2024.
5. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron J. 1953;45(10):478-481.
6. Cochran WG, Cox GM. Experimental designs. New York (USA): John Wiley & Co.; 1957.
7. Federer WT. Augmented designs with one-way elimination of heterogeneity. Biometrics. 1975;17(3):447-473.
8. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating population of Korea Lespedeza. Agron J. 1956;48(6):267-282.
9. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. J Agron. 1955;47(1):314-318.
10. Kharkwal MC, Pandey RN, Pawar SE. Mutation breeding for crop improvement. In: Plant Breeding: Mendelian to Molecular Approaches. New Delhi: Springer; 2004. p. 601-645.
11. Kumari N, Kumar R, Kumar A. Genetic variability and association of traits in mutant lines of rice (*Oryza sativa* L.) for submergence tolerance. Curr J Appl Sci Technol. 2019;33(2):1-7.
12. Luz VKD, Silveira SFDS, Fonseca GMD, Groli EL, Figueiredo RG, Baretta D, *et al*. Identification of variability for agronomically important traits in rice mutant families. Bragantia. 2016;75(1):41-50.
13. Mahantashivayogayya K, Lakkundi BS, Kuchunur PH, Vishwanath J. Genetic variability studies on rice (*Oryza sativa* L.) mutants for yield and yield components in normal and saline stress soil. Electron J Plant Breed. 2016;7(4):1162-1168.
14. Raghuvanshi RS, Anuradha D, Tiwari D, Swetha S. Qualitative characters of red rice and white rice procured from local market of Uttarakhand: A comparative study. J Rice Res. 2017;10(1):49-53.
15. Sadimantara GR, Yusuf DN, Febrianti E, Leomo S, Muhidin M. The performance of agronomic traits, genetic variability, and correlation studies for yield and its components in some red rice (*Oryza sativa* L.) promising lines. Biodivers J. 2021;22(9):1-9.
16. Siddiqui SA, Singh S. Induced genetic variability for yield and yield traits in basmati rice. World J Agric Sci. 2010;6(3):331-337.
17. Sivasubramanian S, Madhavamenon P. Genotypic and phenotypic variability in rice. Madras Agric J. 1973;60(9):1093-1096.
18. Sjahril R. Correlation and path coefficient analysis of grain yield and its components in Toraja land-race aromatic rice mutants induced by heavy ion beam. Asian J Plant Sci. 2021;20(3):1-7.
19. Tabasum A, Cheema AA, Hameed A, Rashid M, Ashraf M. Radiosensitivity of rice genotypes to gamma radiation based on seedling traits and physiological indices. J Nat Appl Sci. 2011;43(2):1211-1222.
20. Wattoo JI, Aslam K, Shah G, Shabir M, Naveed SA. Ethyl methane sulphonate (EMS) and gamma rays induced mutagenic attempts to create genetic variability in basmati rice. J Plant Breed Crop Sci. 2012;4(7):101-105.