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GENETIC VARIABILITY FOR YIELD-RELATED TRAITS AND BLAST RESISTANCE AMONG M_4 MUTANT LINES OF RICE (*Oryza sativa* L.) *VAR.* WADA KOLAM

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ABSTRACT

Rice (*Oryza sativa* L.) is a vital cereal crop that underpins food security in India. Wada Kolam, an economically prominent traditional cultivar grown widely in the Konkan region of Maharashtra, is favoured for its fine grain and pleasant eating quality but is severely constrained by tall stature, lodging susceptibility, and blast disease (*Pyricularia oryzae*). Mutation breeding provides a practical approach to induce beneficial alterations such as dwarf stature, blast tolerance, and improved yield attributes without compromising consumer grain quality. The present study evaluated 105 M_4 mutant lines of Wada Kolam alongside four standard checks (Wada Kolam, Bangalia, Botvel, and Ghansal) during Rabi 2024–25 at the Agricultural Research Station, Shirgaon, Ratnagiri, using an Augmented Block Design. Analysis of variance demonstrated significant genetic differences among treatments for 11 out of 12 quantitative traits, confirming the generation of wide, exploitable variability. Moderate genotypic and phenotypic coefficients of variation were observed for productive tillers per plant, spikelet fertility, panicle length, harvest index, and grain yield per plant. Broad-sense heritability was high (>60%) for almost all characters. High heritability coupled with high genetic advance as per cent of mean (GAM) was recorded for productive tillers per plant, spikelet fertility, and harvest index, indicating the predominance of additive gene action and strong potential for direct phenotypic selection. Field screening under natural epiphytotic blast conditions categorized 39.0% of lines as moderately susceptible and 40.0% as susceptible. Promising mutant lines—specifically M_4-3, M_4-15, M_4-20, M_4-52, M_4-66, and M_4-92 exhibited reduced plant height, superior yield attributes, and favourable field blast reactions, demonstrating strong merit for advancement into pureline selection and station trials.

***Key words*:** Rice, Wada Kolam, M_4 mutants, genetic variability, heritability.

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops and serves as a major staple food for more than half of the world's population. Rice belongs to the family *Poaceae* and has a chromosome number of 2n = 24. It is cultivated under diverse agro-ecological conditions and contributes substantially to global food and nutritional security. In Maharashtra, rice is predominantly cultivated during the *Kharif* season, and the Konkan region is particularly rich in traditional rice diversity. Wada Kolam is one of the important traditional rice varieties of the region and is highly preferred because of its fine grain quality, cooking characteristics, soft texture and pleasant eating quality. However, its tall plant stature makes it vulnerable to lodging under the high-rainfall conditions of Konkan. The variety is also susceptible to blast disease and has comparatively poor responsiveness to fertilizer application, limiting its yield potential (Vaughan *et al.*, 2008).

Induced mutation breeding provides an effective means of generating novel genetic variability and improving specific undesirable characters while retaining the desirable characteristics of an established variety. In rice, mutation breeding has been successfully utilized for modifying plant architecture, improving lodging resistance, increasing yield and developing resistance to biotic and abiotic stresses. Wada Kolam is a popular and well-established local rice variety grown extensively in the Konkan region, particularly in the Palghar and coastal districts of Maharashtra. It commands high market demand and premium prices due to its fine grain quality, excellent cooking characteristics, and pleasant aroma. However, the variety is tall-statured, rendering it highly prone to lodging under heavy rainfall and stormy monsoon winds. Lodging causes substantial losses in grain yield and quality while impairing harvesting efficiency. In addition, Wada Kolam is vulnerable to rice blast disease (*Pyricularia oryzae*) and displays poor responsiveness to nitrogenous fertilizers. Rice blast causes severe yield reductions whenever climatic conditions favour disease spread. While fungicidal applications offer chemical control, associated environmental concerns, input expenses, and the potential emergence of fungicide-resistant pathogen strains necessitate the development of host-plant resistance or field tolerance as the most viable, sustainable strategy (Ahloowalia *et al.*, 2004).

Induced mutagenesis represents an effective breeding tool to broaden the genetic base and generate novel variations in self-pollinated diploid crops like rice. By using physical mutagens such as gamma rays, specific deficiencies- such as tall height and disease vulnerability - can be altered while preserving the desirable grain and eating quality traits of a traditional landrace. Evaluating advanced mutant generations such as the M_4 is critical, as segregation diminishes, mutant traits become relatively fixed, and genetic parameters can be estimated with high biometrical precision. The primary objective of the present research was to estimate the extent of genetic variability, heritability, genetic advance, and blast resistance among 105 M_4 mutant lines of Wada Kolam to select superior, dwarf, high-yielding, and blast-tolerant purelines (Shu *et al.*2012)

Materials and Methods

The field experiment was conducted at the Agricultural Research Station, Shirgaon, Ratnagiri, Maharashtra, situated in the South Konkan Coastal Zone (MH-1) at 16°59' N latitude and 73°18' E longitude during Rabi 2024–25. The soil was typically lateritic, and the climate was tropical and humid.

The experimental material comprised 105 M_4 mutant lines derived from mutagenized Wada Kolam alongside four standard check varieties: untreated Wada Kolam, Bangalia, Botvel, and Ghansal. Seedlings were raised using the wet nursery method and 30-day-old single seedlings were transplanted on January 21, 2025, in an Augmented Block Design across five blocks at a spacing of 20 cm × 15 cm. Each experimental plot measured 3.0 m × 1.0 m, accommodating 30 plants per row. Standard recommended agronomic and crop protection packages were followed. Observations were recorded from individual plants on twelve characters - Days to 50% flowering, Plant height (cm), Panicle length (cm), Number of productive tillers per plant, Number of filled grains per panicle, Number of unfilled grains per panicle, Spikelet fertility (%), Test weight (g), Straw yield per plant (g), Grain yield per plant (g). The observations were recorded following the procedures described in the experimental methodology. Grain yield and straw yield were recorded separately from selected plants, while harvest index was calculated from economic and biological yield. Blast reaction was evaluated using the 0–9 scale of IRRI (1996). The data were analysed according to the Augmented Block Design. Analysis of variance was performed to determine differences among treatments. Environmental, genotypic and phenotypic variances were estimated, followed by estimation of GCV, PCV, broad-sense heritability, genetic advance and genetic advance as per cent of mean (GAM).

Results and Discussion

Components of variation

Components of variation were estimated using the method of Cochran and Cox (1957). Across all twelve characters, phenotypic variance (σ^2 p) exceeded genotypic (σ^2 g) and environmental (σ^2 e) variances.

For the components of variation in the M_4 mutant population of rice var. Wada Kolam, the phenotypic variance (σ^2 p) ranged from 0.711 for blast score to 80.087 for number of filled grains per panicle, followed by plant height (36.663) and spikelet fertility (23.351). Similarly, the genotypic variance (σ^2 g) was highest for number of filled grains per panicle (76.471), followed by plant height (36.278) and spikelet fertility (19.818), while the lowest genotypic variance was recorded for blast score (0.636), followed by test weight (1.026) and grain yield per plant (2.012). The environmental variance (σ^2 g) reached its maximum for number of filled grains per panicle (3.617), followed closely by spikelet fertility (3.533) and harvest index (1.800), whereas the minimum environmental variance was observed for blast score (0.075), followed

Table 1: Experimental material and treatments.

Sr.	Lines	Sr.	Lines	Sr.	Lines	Sr.	Lines
1	M_4-1	28	M_4-28	55	M_4-55	82	M_4-82
2	M_4-2	29	M_4-29	56	M_4-56	83	M_4-83
3	M_4-3	30	M_4-30	57	M_4-57	84	M_4-84
4	M_4-4	31	M_4-31	58	M_4-58	85	M_4-85
5	M_4-5	32	M_4-32	59	M_4-59	86	M_4-86
6	M_4-6	33	M_4-33	60	M_4-60	87	M_4-87
7	M_4-7	34	M_4-34	61	M_4-61	88	M_4-88
8	M_4-8	35	M_4-35	62	M_4-62	89	M_4-89
9	M_4-9	36	M_4-36	63	M_4-63	90	M_4-90
10	M_4-10	37	M_4-37	64	M_4-64	91	M_4-91
11	M_4-11	38	M_4-38	65	M_4-65	92	M_4-92
12	M_4-12	39	M_4-39	66	M_4-66	93	M_4-93
13	M_4-13	40	M_4-40	67	M_4-67	94	M_4-94
14	M_4-14	41	M_4-41	68	M_4-68	95	M_4-95
15	M_4-15	42	M_4-42	69	M_4-69	96	M_4-96
16	M_4-16	43	M_4-43	70	M_4-70	97	M_4-97
17	M_4-17	44	M_4-44	71	M_4-71	98	M_4-98
18	M_4-18	45	M_4-45	72	M_4-72	99	M_4-99
19	M_4-19	46	M_4-46	73	M_4-73	100	M_4-100
20	M_4-20	47	M_4-47	74	M_4-74	101	M_4-101
21	M_4-21	48	M_4-48	75	M_4-75	102	M_4-102
22	M_4-22	49	M_4-49	76	M_4-76	103	M_4-103
23	M_4-23	50	M_4-50	77	M_4-77	104	M_4-104
24	M_4-24	51	M_4-51	78	M_4-78	105	M_4-105
25	M_4-25	51	M_4-52	79	M_4-79	C1	Wada kolam
26	M_4-26	53	M_4-53	80	M_4-80	C2	Bangalia
27	M_4-27	54	M_4-54	81	M_4-81	C3	Botvel
						C4	Ghansal

by test weight (0.161) and straw yield per plant (0.197). A similar predominance of genotypic over environmental variance for major yield components in mutant rice populations has been reported by Kole *et al.*, (2010) and Oladosu *et al.*, (2014).

Coefficient of variation

Estimates of GCV and PCV are presented in Table 2. On the classification scale of low (<10%), moderate (10-20%) and high (>20%) proposed by Sivasubramanian and Menon (1973), In all characters, phenotypic coefficients of variation were slightly higher than genotypic coefficients of variation. The close correspondence between PCV and GCV across most characters indicated minimal environmental influence on trait manifestation.

Spikelet fertility (15.60%), number of productive tillers (14.74%), harvest index (11.77%), grain yield per plant (11.25%) and panicle length (10.22%), recorded moderate genotypic coefficients of variation, while days to 50 per cent flowering (2.12%), unfilled grains per panicle (2.81%), blast score (4.25%), plant height

Table 2: Components of variance for different characters in M_4 mutant lines of rice var. Wada Kolam.

Character	σE	σG	σ P
Days to 50% flowering	0.970	2.472	3.447
Plant height (cm)	0.292	36.278	36.663
Panicle length (cm)	0.717	2.881	3.597
No. of productive tillers	0.417	2.618	3.035
Filled grains/panicle	3.617	76.471	80.087
Unfilled grains/panicle	1.038	5.080	6.180
Spikelet fertility (%)	3.533	19.818	23.351
Test weight (g)	0.161	1.026	1.187
Straw yield/plant (g)	0.197	2.312	2.509
Grain yield/plant (g)	0.608	2.012	2.620
Harvest index (%)	1.800	3.060	4.860
Blast score	0.075	0.636	0.711

σE: σ^2 Environmental; σG: σ^2 Genotypical; σP: σ^2 Phenotypical

(6.28%), straw yield per plant (7.36%), filled grains per panicle (7.60%) and test weight (8.37%) recorded low GCV.

The phenotypic coefficients of variation followed a similar trend but was marginally higher in magnitude than the respective GCV for every character. The narrow gap between GCV and PCV recorded for filled grains per panicle (7.60 vs 7.78), spikelet fertility (15.60 vs 16.93), number of productive tillers (14.74 vs 15.87) and harvest index (11.77 vs 12.45) indicates that environmental influence on the expression of these traits was comparatively limited and that a large part of the observed phenotypic variability is genetic in origin. A relatively wider PCV-GCV gap noted for panicle length (10.22 vs 11.42) and grain yield per plant (11.25 vs 11.72) points to a somewhat greater, though still moderate, contribution of the environment to their phenotypic expression. Siddiqui and Singh (2010) similarly observed moderate genotypic variability for grain yield per plant in mutant rice, while Arunachalam *et al.*, (2019) reported a comparable pattern of slightly higher PCV than GCV across yield-attributing traits in EMS-derived M_4 rice mutants,

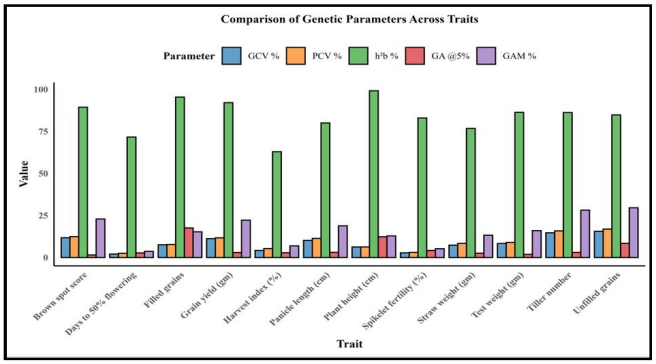

Fig. 1: Graphical representation of genotypic and phenotypic coefficient of variation, heritability and genetic advance as a percentage of the mean.

Table 3: Estimates of GCV, PCV, heritability and genetic advance for different characters.

Character	GCV (%)	PCV (%)	h^2 (bs)%	GA	GAM (%)
Days to 50% flowering	2.117	2.500	71.71	2.743	3.693
Plant height (cm)	6.278	6.303	89.20	12.370	12.880
Panicle length (cm)	10.220	11.420	80.08	3.129	18.840
No. of productive tillers	14.740	15.870	86.27	3.096	28.210
Filled grains/panicle	7.602	7.780	95.48	17.600	15.300
Unfilled grains/ panicle	2.812	3.086	83.04	4.231	5.279
Spikelet fertility (%)	15.600	16.930	84.87	8.448	29.600
Test weight (g)	8.367	9.002	86.40	1.939	16.020
Straw yield/plant (g)	7.356	8.394	46.80	2.561	7.280
Grain yield/plant (g)	11.250	11.720	72.14	3.007	18.250
Harvest index (%)	11.770	12.450	89.46	1.554	22.940
Blast score	4.249	5.355	62.97	2.860	6.946

indicating only a mild role of environment in their expression, a finding broadly consistent with the present study.

Heritability and genetic advance

Broad-sense heritability, genetic advance and genetic advance expressed as per cent of mean, computed following Johnson *et al.,* (1955), are presented in Table 3. Heritability, classified as low (<30%), moderate (30-60%) and high (>60%) following Robinson *et al.* (1949), was high for all twelve characters, ranging from 62.97 per cent for blast score to 95.48 per cent for filled grains per panicle, reflecting the predominant role of the genotype over the environment in the expression of these traits under the present experimental conditions. High heritability for most of these yield-attributing characters in mutant rice populations has similarly been reported by Arunachalam *et al.,* (2019) and Oladosu *et al.,* (2014).

High heritability alone, however, is not a dependable indicator of the response expected from selection unless it is accompanied by high genetic advance expressed as per cent of mean (GAM). In the present study, high heritability coupled with high GAM was recorded for number of productive tillers (86.27%, 28.21%), spikelet fertility (84.87%, 29.60%) and harvest index (89.46%, 22.94%), indicating that these three characters are governed predominantly by additive gene effects and can be improved reliably through simple, direct phenotypic selection in the succeeding generations. High heritability coupled with high genetic advance for number of grains per panicle, panicle weight and single-plant yield in EMS-derived M_4 rice mutants was similarly documented by Arunachalam *et al.,* (2019), who attributed it to the predominance of additive gene action, a conclusion consistent with the present findings for number of productive tillers, spikelet fertility and harvest index.

Table 4: Reaction of M_4 mutant lines of Wada Kolam to blast disease under artificial inoculation conditions in the field during the 2026 cropping season.

Disease reaction grade	PDI range(%)	NML	PP
Moderately susceptible (MS)	55.56 - 66.67	41	39.0
Susceptible (S)	73.33 - 77.78	42	40.0
Highly susceptible (HS)	88.89 - 100.00	22	21.0
Total mutant lines screened	-	105	100.0
NML: No. of mutant lines; PP: Per cent of population			

High heritability accompanied by moderate GAM was recorded for panicle length (80.08%, 18.84%), filled grains per panicle (95.48%, 15.30%), test weight (86.40%, 16.02%) and grain yield per plant (72.14%, 18.25%), suggesting an appreciable, though somewhat less dominant, additive component for these traits, so that direct selection would still be expected to yield reasonable genetic gain. In contrast, high heritability combined with low GAM was observed for days to 50 per cent flowering (71.71%, 3.69%), unfilled grains per panicle (83.04%, 5.28%), straw yield per plant (46.80%, 7.28%) and blast score (62.97%, 6.95%), implying that the apparently high heritability recorded for these characters is likely inflated by non-additive (dominance and epistatic) gene effects, and that phenotypic selection alone may not translate into proportionate genetic gain for these traits; selection would need to be deferred to more advanced, largely homozygous generations or combined with progeny testing. A comparable combination of high heritability with low or moderate genetic advance for such traits, attributed to the influence of non-additive gene action, has also been noted in induced mutants of rice by Riadi *et al.,* (2018).On the whole, the pattern of high heritability coupled with high GAM recorded for number of productive tillers, spikelet fertility and harvest index, together with the moderate GAM noted for grain yield per plant itself, identifies these characters as the most dependable and rewarding criteria for direct phenotypic selection in advancing this M_4 mutant population of Wada Kolam.

Reaction of M_4 Mutant Lines to Blast Disease

All 105 M_4 mutant lines, together with the four checks, were screened against blast under the natural epiphytotic that developed in the field at Shirgaon, and graded on the 0-9 scale of IRRI (1996). The disease reaction, expressed as per cent disease index (PDI), is summarised in Table 4. None of the 105 mutant lines, nor any of the four checks, displayed an immune, resistant or even moderately resistant reaction to blast. Of the mutant population, 41 lines (39.0%) were graded moderately

susceptible, 42 lines (40.0%) susceptible and the remaining 22 lines (21.0%) highly susceptible, while all four checks – Wada Kolam, Bangalia, Botvel and Ghansal were rated susceptible. The complete absence of a resistant reaction confirms that Wada Kolam and its induced mutants remain broadly vulnerable to *Pyricularia oryzae* under conducive epiphytotic conditions, in line with the well-documented blast susceptibility of this traditional variety.

Even so, the mutant lines recording the comparatively lower per cent disease index within the moderately susceptible group, such as M_4-20, M_4-71, M_4-80 and M_4-94, represent the best available combination of reduced blast severity currently present in the population. Since these lines have not been confirmed as stable sources of tolerance over more than one season, they should be re-screened under artificial or repeated natural epiphytotic conditions in the next generation before being used as donors for blast tolerance in further breeding.

Conclusion

The investigation confirmed the presence of substantial genetic variability among the M_4 mutant lines of Wada Kolam for plant height, panicle length, number of productive tillers, filled grains per panicle, spikelet fertility, harvest index and grain yield per plant. Mutant lines M_4-3, M_4-15, M_4-20, M_4-52, M_4-66 and M_4-92 combined reduced plant height with superior yield, harvest index, spikelet fertility and a comparatively favourable blast reaction, and are recommended for advancement to the further generation. High heritability coupled with high genetic advance as per cent of mean was recorded for number of productive tillers, spikelet fertility and harvest index, indicating the predominance of additive gene action for these traits and the scope for effective improvement through direct phenotypic selection. Correlation and path coefficient analyses consistently identified harvest index, spikelet fertility and straw yield per plant, supported by panicle length, number of productive tillers and filled grains per panicle, as the key traits contributing to grain yield per plant, and these should be prioritised as selection criteria in subsequent breeding cycles. The significant negative association of plant height and blast score with grain yield indicates that taller, more blast-susceptible plant types are less desirable; selection should therefore favour moderately short-statured, comparatively blast-tolerant mutant lines with high harvest index and spikelet fertility for sustained improvement of grain yield in Wada Kolam. On the basis of performance, following mutant lines *viz.*, M_4-3, M_4-15, M_4-20, M_4-52, M_4-66 and M_4-92 are found promising for further as a pureline selection and station trial.

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