



Genotype × Environment Interaction and Yield Stability of UiTM Advanced Rice Lines Across Two Malaysian Environments

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Abstract: Genotype × Environment (G×E) interaction is a key determinant of yield stability and adaptability in rice under varying agro-ecological conditions. This study evaluated five gamma-irradiation-derived UiTM advanced rice mutant lines alongside six commercial varieties across two Malaysian locations to assess yield performance, phenotypic variability, and preliminary adaptability. Although we detected significant genotype × environment interactions, the limited number of test sites constrains stability inference and highlights the need for broader multi-location trials. Two-way ANOVA detected significant ($p < 0.001$) effects of genotype, environment, and the G×E interaction for most agronomic traits, with genotypic variation prominent in flowering and yield traits, while environmental factors mainly influenced plant height and spikelet number. Significant crossover interactions for yield-related traits indicated differential genotype performance across environments. Several UiTM mutant lines exhibited stable flowering and yield, suggesting broad or specific adaptability. Correlation analysis revealed strong positive relationships among yield components, and principal component analysis identified yield traits as the primary contributors to phenotypic variability. Cluster analysis categorized genotypes into early-maturing, high-yielding, and late-maturing types with larger spikelet numbers. Overall, the results highlight the importance of multi-location testing for varietal selection and demonstrate the potential of UiTM mutant lines as stable, climate-resilient candidates for sustainable rice production in Malaysia.

Keywords: Genotype × environment interaction; rice mutant lines; yield stability; phenotypic variability; multi-location trials

1. Introduction

Rice (*Oryza sativa* L.) remains the cornerstone of global food security, nourishing over half of the world's population and shaping the socio-economic fabric of Asia, where more than 90 % of the crop is produced and consumed [1]. In Malaysia, rice is a strategic commodity underpinning rural livelihoods and national food sovereignty. Yet, the sector faces increasing vulnerability due to climate change, rapid urbanization, and resource degradation. Recent assessments by the Intergovernmental Panel on Climate Change predict that rising temperatures, erratic rainfall, and more intense drought and flood

episodes could lower rice yields by 10–15% by 2050 if adaptive measures are not implemented [2, 3]. Malaysia's 2024 agricultural statistics indicate a rice self-sufficiency ratio of about 63%, reflecting persistent yield gaps and reliance on imports to meet domestic demand [4].

Extreme weather events have become more frequent in recent years, with the 2022–2024 monsoon floods in Kedah, Perak, and Kelantan damaging thousands of hectares of paddy land, while intermittent dry spells in northern Peninsular Malaysia have constrained irrigation schedules and disrupted planting [5]. Beyond climatic factors, declining soil fertility, poor nutrient-use efficiency, and the resurgence of major rice diseases such as bacterial leaf blight (*Xanthomonas oryzae* pv. *oryzae*), rice blast (*Magnaporthe oryzae*), and sheath blight (*Rhizoctonia solani*) have compounded productivity losses [6, 7]. Global outbreaks of blast disease, particularly in South and Southeast Asia, have caused yield reductions of up to 50 % during severe epidemics [8]. These challenges underscore the urgent need for resilient, high-yielding rice cultivars that maintain stable performance under complex environmental and biotic stress conditions [9, 10].

Induced mutation breeding has long been recognized as a powerful tool for crop improvement, creating novel allelic variations that are difficult to obtain through conventional breeding or transgenic approaches [11]. Among mutagenic techniques, gamma irradiation is the most widely used because it is reproducible, cost-effective, and can generate stable, heritable mutations [12]. Globally, more than 830 mutant crop varieties have been officially released through nuclear-assisted breeding programs, with over 250 being rice [13]. Notable examples include the high-yielding Japanese variety Reimei, the semi-dwarf Shwewartun in Myanmar, and Binadhan-7 and Binadhan-8 in Bangladesh, developed via gamma-ray mutagenesis [14, 15]. These mutants exhibit improved traits such as early maturity, short stature, lodging resistance, and tolerance to salinity or drought, attributes essential for sustaining production under changing climates [16, 17]. In Malaysia, induced mutation breeding has been championed by collaborative programs between Universiti Teknologi MARA (UiTM) and the Malaysian Nuclear Agency. Through gamma-irradiation of elite local cultivars such as MR219 and MR297, UiTM has successfully developed advanced mutant lines exhibiting early maturity (≤ 100 days), enhanced resistance to bacterial leaf blight, and stable grain quality [18]. Despite these promising traits, the yield stability and adaptability of these lines across Malaysia's diverse agroecological regions ranging from the irrigated granary schemes of MADA (Kedah) and KADA (Kelantan) to the rainfed systems in Sarawak have not been systematically assessed.

A major bottleneck in varietal deployment arises from the genotype $\times$ environment (G $\times$ E) interaction, which governs how genotypes respond to spatial and temporal variations in climate, soil fertility, and management [19,20]. Strong G $\times$ E interactions can mask genetic potential, alter genotype rankings, and reduce selection efficiency, limiting the identification of stable, high-performing cultivars [21]. Conversely, understanding G $\times$ E patterns allows breeders to dissect phenotypic plasticity and to target genotypes for either wide adaptation (stability across sites) or specific adaptation (superior performance in defined environments) [22]. Several statistical approaches have been developed to quantify G $\times$ E interactions and yield stability. Traditional two-way ANOVA provides a baseline assessment of significance. In rice, studies by Akinwale et al. [26] and Nguyen et al. [27] showed that grain yield, days to flowering, and spikelet fertility are particularly sensitive to G $\times$ E variation, underscoring the need for multi-location trials before varietal release. Because Malaysia's 12 major granary areas differ markedly in rainfall patterns, soil nutrient status, and disease pressure, a comprehensive G $\times$ E evaluation of newly developed mutant rice lines is crucial to ensure consistent productivity under real-field conditions. Integrating multi-environment data with principal component and cluster analyses can further elucidate the underlying structure of phenotypic variability and help classify genotypes by adaptation domains [28, 29].

Therefore, this study aims to (i) evaluate the magnitude and pattern of G $\times$ E interaction for yield and related agronomic traits in UiTM advanced rice mutant lines across 3 diverse Malaysian environments; (ii) determine the stability and adaptability of these genotypes using robust statistical models; and (iii) identify candidate lines combining high yield potential with environmental resilience for further multi-location trials. The outcomes will contribute to the selection of elite UiTM lines suitable for large-scale cultivation and provide valuable insight into breeding strategies for climate-resilient rice in Malaysia. Ultimately, this work aligns with

national goals to enhance rice self-sufficiency, promote sustainable intensification, and strengthen food security under increasing climatic uncertainty.

2. Materials and Methods

2.1 Plant Materials

This study evaluated five advanced rice mutant lines developed by Universiti Teknologi MARA (UiTM), Malaysia, through gamma-ray irradiation of the elite Malaysian variety MR219, and six commercial check varieties widely cultivated across the country (Table 1). Gamma irradiation was performed using a ^{60}Co source at the Malaysian Nuclear Agency, following protocols adapted from IAEA [1]. The selected UiTM mutant lines (UiTM 1–5) represent advanced stabilized lines (Technology Readiness Level 6) that previously exhibited superior yield potential, early maturity, and improved tolerance to abiotic stresses under controlled field conditions [2]. The control varieties included popular high-yielding and climate-resilient cultivars such as MR219, MR297, MR220 CL2, NMR152, and two Putra series cultivars developed by Universiti Putra Malaysia.

Table 1. List of rice varieties/lines used in this study.

Code	Line/Variety	Status	Method of Development	Development stage
1	NMR 152	Commercial check variety	Gamma-ray Irradiation	Release variety
2	MR 219	Commercial check variety	Crossbreed	Release variety
3	MR 220 CL2	Commercial check variety	Crossbreed	Release variety
4	MR297	Commercial check variety	Crossbreed	Release variety
5	Putra 1	Commercial check variety	Crossbreed	Release variety
6	Putra 2	Commercial check variety	Crossbreed	Release variety
19	UiTM 1	Advanced mutant line	Gamma-ray Irradiation	TRL 6
20	UiTM 2	Advanced mutant line	Gamma-ray Irradiation	TRL 6
21	UiTM 3	Advanced mutant line	Gamma-ray Irradiation	TRL 6
22	UiTM 4	Advanced breeding line	Gamma-ray Irradiation	TRL 6
23	UiTM 5	Advanced breeding line	Gamma-ray Irradiation	TRL 6

All plant materials were sourced from the UiTM Laboratory and maintained under appropriate seed-storage conditions before planting.

2.2 Research Locations and Environmental Conditions

Field evaluations were conducted across three agroecologically distinct rice-growing areas in Malaysia between March and September 2024 to capture a wide range of climatic and edaphic conditions (Table 2). The selected sites Sungai Haji Dorani (Selangor), Titi Serong (Perak), and Sanglang (Kedah) represent coastal, inland, and northern granary ecosystems, respectively, differing in rainfall, temperature, and soil fertility [3]. We synchronized transplanting schedules with local farmer practices in each region to ensure representativeness. However, data from Titi Serong, Perak were excluded from the final statistical analysis because severe blast disease infection during the reproductive stage caused non-uniform plant stands and unreliable yield performance. Therefore, only two environments (Selangor and Kedah) were included in the final genotype $\times$ environment (G $\times$ E) interaction and stability analyses.

Table 2. Location and timing of field trials.

Time of Transplanting	Field Evaluation Period	Location (Coordinates)
March 2024	May–July 2024	3.654832° N, 101.035347° E (Sg Haji Dorani, Selangor)
April 2024	April–July 2024	5°06'18.4" N, 100°27'36.4" E (Titi Serong, Perak)
May 2024	May–September 2024	6°20'27.7" N, 100°15'37.4" E (Sanglang, Kedah)

Average monthly temperatures across sites ranged from 28–32 °C, with annual rainfall ranging from 1,500–2,800 mm. Soils were characterized as silty clay loam with moderate organic matter (1.2–2.1%) and near-neutral pH (6.0–6.8).

2.3 Experimental Design and Field Management

The experiment used a Randomized Complete Block Design (RCBD) with three replications per location. Each plot measured 2 m × 2 m and was arranged in an 8 × 8 hill matrix, with 25 cm × 25 cm spacing between hills and rows. Three pre-germinated seedlings were transplanted per hill at the three-leaf stage (21 days old). Genotypes were randomized within each block to minimize positional bias. We followed standard agronomic practices according to MARDI rice cultivation guidelines [4]. Basal fertilization comprised 80 kg N ha⁻¹, 60 kg P₂O₅ ha⁻¹, and 60 kg K₂O ha⁻¹, applied in three splits: at transplanting (40%), tillering (40%), and panicle initiation (20%). Pest and disease control followed an integrated management approach using *Bacillus thuringiensis*-based biocontrol and minimal pesticide input. Fields were maintained under continuous flooding (5–10 cm water depth) until grain maturity, except for brief drainage before harvest.

2.4 Data Collection

Morpho-agronomic data were recorded from five randomly selected representative plants per genotype per replication following the Standard Evaluation System for Rice (SES, IRRI 2022) [5]. Observations included:

- Days to 50% flowering (DTF): number of days from sowing to 50% of plants flowering.
- Days to maturity (DTM): days from sowing to physiological maturity.
- Plant height (PH): measured from ground level to the tip of the tallest panicle (cm).
- Number of tillers per plant (NT) and number of panicles per plant (NP).
- Panicle length (PL) and number of filled spikelets (NFS).
- Grain yield per plant (YLDPLT): weight of filled grains after drying to 14% moisture content (g).
- Thousand-grain weight (TGW) and seed length-to-width ratio (SLWR) were used to evaluate grain quality.

Pre-harvest measurements (DTF, PH, NT) and post-harvest yield traits (YLDPLT, TGW) were used to assess each component's contribution to final yield.

2.5 Statistical Analyses

All data were analyzed using descriptive and inferential statistics in R (version 4.3.2) and Minitab 21.2. We computed descriptive statistics, including mean, standard deviation, and coefficient of variation (CV%), to evaluate phenotypic variability across genotypes and environments.

A two-way Analysis of Variance (ANOVA) was performed to determine the effects of genotype (G), environment (E), and G×E interaction on each trait using the linear model:

$$Y_{ijk} = \mu + G_i + E_j + (G \times E)_{ij} + \varepsilon_{ijk}$$

where Y_{ijk} is the observation for the i th genotype in the j th environment and k th replication, μ is the overall mean, and ε_{ijk} is the random error.

Pearson's correlation analysis was performed to determine relationships among key agronomic traits and yield components, while Principal Component Analysis (PCA) and hierarchical cluster analysis were used to classify genotypes based on multivariate performance [8]. Statistical significance was set at $p < 0.05$.

2.6 Data Availability and Ethical Statement

All raw and processed datasets generated in this study will be deposited in the UiTM Institutional Repository (<https://ir.uitm.edu.my>) and the FAO/IAEA Plant Mutation Database (MVDdb) upon acceptance. No human or animal subjects were involved; thus, ethical approval was not required.

3. Results and Discussion

3.1 Analysis of Variance

The two-way ANOVA (Table 1) showed highly significant ($p < 0.001$) main effects of genotype (G) and environment (E) for nearly all 15 traits, with significant G×E for several key traits. Genotypic differences were most pronounced for DTF50 (SS = 261.81) and DTM85 (SS = 270.9), while NFS (SS = 2220.8) and YLDPLT (SS = 181.8) also exhibited substantial genotypic variation. Environmental effects dominated PH (SS = 2897.9), NOS (SS = 4348), and YLD (SS = 81.1), underscoring strong location-specific influences. Significant G×E was detected for NFS, YLDPLT, SLSWR, TSW, DTF50/DTM85, NOS, and NSS, indicating rank changes across test sites.

3.2 Descriptive Statistics and Trait Stability

Substantial phenotypic variability was observed (Table 2). NSS showed the highest dispersion (CV = 54.91%), followed by YLD (30.18%) and YLDPLT (28.26%), reflecting strong environmental sensitivity. Conversely, SL (CV = 5.48%) and DTF50 (CV = 8.28%) were most stable across environments.

3.3 Correlation Analysis

The correlation matrix (Figure 1) revealed strong positive associations among NOS, NFS, and NP (>0.90), and significant positive links between YLDPLT and TSW and NFS, indicating that sink size and grain filling jointly drive productivity. DTF50/DTM85 showed weak associations with yield traits, suggesting scope to combine earliness with high yield.

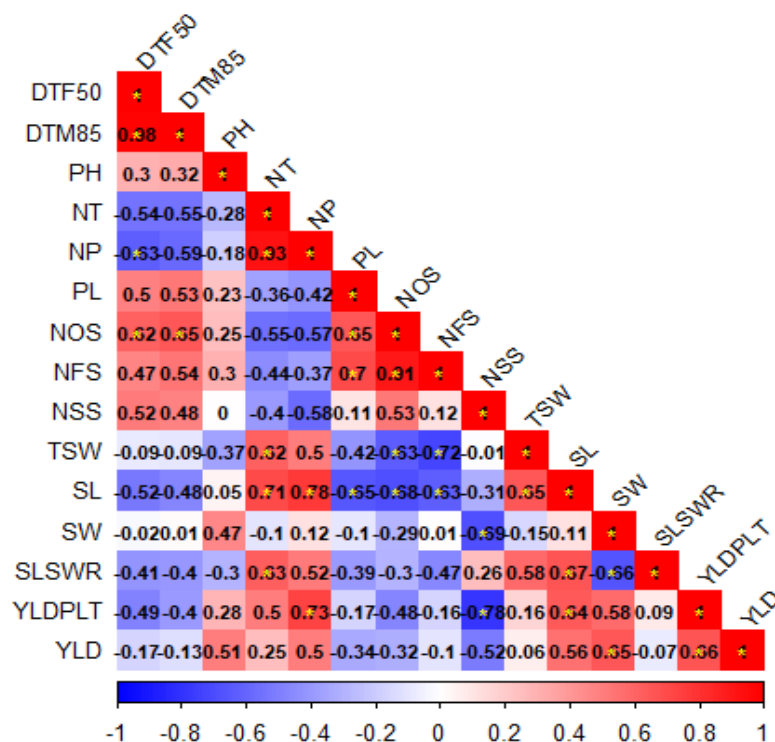


Figure 1. DTF50: days to 50% flowering, DTM85: 85% maturity, PH: plant height, NT: number of tillers per plant, NP: number of panicles per plant, PL: panicle length, NOS: number of spikelets per panicle, NFS: number of filled spikelets, NSS: number of sterile spikelets. TSW: thousand-seed weight (g), SL and SW: seed length and seed width (mm), SLSWR: seed length-to-width ratio, YLDPLT: yield per plant (g), YLD: grain yield per hectare (t ha⁻¹).

Table 1. Analysis of variance for yield and yield component traits across two locations. (*p<0.01; ***p<0.001) *

Factor	Df	DTF50	DTM85	PH	NT	NP	NOS	NFS	NSS	TSW	SL	SW	SLSWR	YLDPLT	YLD
E	1	33.47	33.47	2897.9	47.52	167.05	4348	1630.1	578.1	45.21	0.427	0.313	0.604	1203.5	81.1
G	10	261.81	270.9	460.7	36.59	35.4	3187	2220.8	622.3	15.08	1.045	0.057	0.364	181.8	15.81
E × G	10	17.5	17.5	108.1	7.12	11.79	704	923.7	250.2	4.43	0.38	0.039	0.156	191.4	5.78
R	44	0.45	0.45	37.4	11.57	10.21	310	249.8	135.7	1.65	0.094	0.02	0.075	99.4	2.79
Mean		79.92	110.29	112.28	23.21	21.73	153.29	125.18	27.92	25.23	9.82	2.39	4.14	42.35	8.42
SD		6.62	6.72	12.55	3.91	4.09	29.58	26.04	15.33	2.19	0.54	0.18	0.37	11.97	2.54
CV (%)		8.28	6.1	11.17	16.84	18.83	19.3	20.8	54.91	8.7	5.48	7.63	9.05	28.26	30.18
Min		66	96	80.33	15	13.33	103.3	75.67	6.33	18.67	8.53	1.87	3.33	17.4	3.08
Max		90	120	135	33.33	32.67	220.7	178	81	30	10.99	2.75	5.52	67.7	15.46

In the analysis of variance tables, E stands for environment (different locations), G for genotype (rice varieties or mutant lines), E × G for the environment × genotype interaction, and R for replication (experimental block within each site). DTF50: days to 50% flowering, DTM85: 85% maturity, PH: plant height, NT: number of tillers per plant, NP: number of panicles per plant, PL: panicle length, NOS: number of spikelets per panicle, NFS: number of filled spikelets, NSS: number of sterile spikelets. TSW: thousand-seed weight (g), SL and SW: seed length and seed width (mm), SLSWR: seed length-to-width ratio, YLDPLT: yield per plant (g), YLD: grain yield per hectare (t ha⁻¹).

3.4 Principal Component Analysis

PCA identified two major components explaining 68.6% of total variation (PC1 = 45.8%, PC2 = 22.9%; Table 3). PC1 loaded positively on NOS, NFS, DTF50, and DTM85, capturing reproductive capacity and phenology; PC2 was associated with SLSWR, SW, and PH, reflecting grain morphology and plant stature. The biplot (Figure 2) separated yield-related axes from grain-quality axes, facilitating multi-trait selection.

Table 3. The results of the principal component analysis (PCA) for all traits

Component	PC1	PC2
Standard deviation	2.706	1.9119
Proportion of Variance	0.4577	0.2285
Cumulative Proportion	0.4577	0.6861
DTF50	0.2796	-0.0612
DTM85	0.2709	-0.0945
PH	0.0537	-0.353
NT	-0.2962	0.1208
NP	-0.33	-0.0097
PL	0.2346	-0.1514
NOS	0.3125	-0.0677
NFS	0.2485	-0.2331
NSS	0.2305	0.306
TSW	-0.2051	0.2536
SL	-0.3258	0.0463
SW	-0.0964	-0.4428
SLSWR	-0.1822	0.3571
YLDPLT	-0.2764	-0.2981
YLD	-0.2763	-0.2981

DTF50: days to 50% flowering, DTM85: 85% maturity, PH: plant height, NT: number of tillers per plant, NP: number of panicles per plant, PL: panicle length, NOS: number of spikelets per panicle, NFS: number of filled spikelets, NSS: number of sterile spikelets. TSW: thousand-seed weight (g), SL and SW: seed length and seed width (mm), SLSWR: seed length-to-width ratio, YLDPLT: yield per plant (g), YLD: grain yield per hectare (t ha^{-1}).

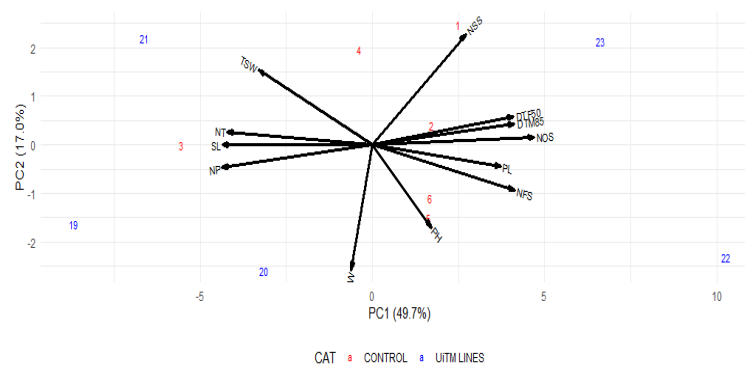


Figure 2. Principal Component Analysis (PCA) biplot of the 11 genotypes evaluated

3.5 Cluster Analysis

Hierarchical clustering partitioned genotypes into two groups (Table 4; Figure 3). Cluster I (genotypes 3, 19, 20, 21) combined earlier flowering (DTF50 = 72.33 d) with higher YLDPLT (45.76 g) and YLD (8.97 t ha⁻¹)—suited to tighter calendars or stress-prone sites. Cluster II had more spikelets (NOS = 166.74) but longer maturity and slightly lower yield (8.11 t ha⁻¹), suggesting value under longer seasons with optimized management.

Table 4. Comparison of cluster mean values for all traits

CLUSTER	I	II
NO. OF GENOTYPES	4	7
LIST OF GENOTYPES	3,19,20,21	2,4,5,6,22,23
DTF50	72.33	84.26
DTM85	102.33	114.83
PH	109.93	113.63
NT	24.89	22.25
NP	23.57	20.68
PL	24.65	25.97
NOS	129.75	166.74
NFS	108.50	134.71
NSS	20.97	31.89
TSW	25.65	24.98
SL	10.10	9.66
SW	2.41	2.37
SLSWR	4.23	4.08
YLDPLT	45.76	40.40
YLD	8.97	8.11

DTF50: days to 50% flowering, DTM85: 85% maturity, PH: plant height, NT: number of tillers per plant, NP: number of panicles per plant, PL: panicle length, NOS: number of spikelets per panicle, NFS: number of filled spikelets, NSS: number of sterile spikelets. TSW: thousand-seed weight (g), SL and SW: seed length and seed width (mm), SLSWR: seed length-to-width ratio, YLDPLT: yield per plant (g), YLD: grain yield per hectare (t ha⁻¹).

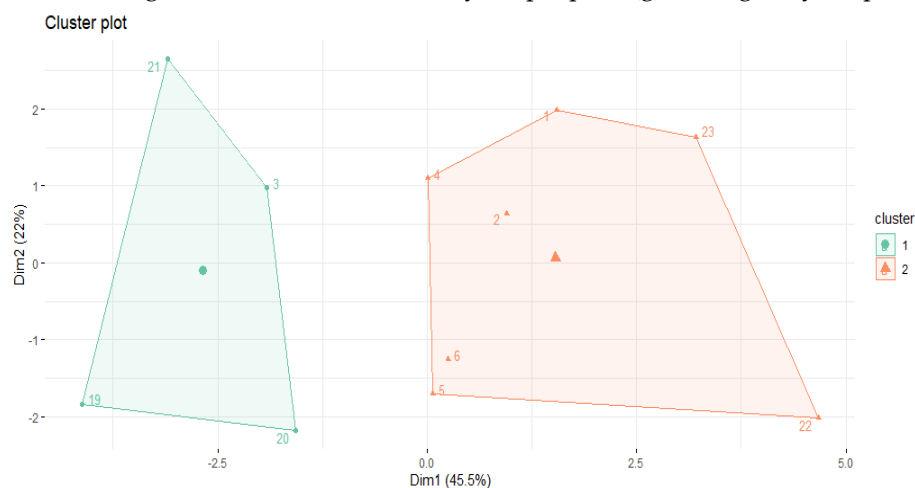


Figure 3. Dendrogram and cluster membership of genotypes

3.6 Discussion

Our analysis confirms that both genetic divergence and heterogeneous environments jointly shape rice phenotypes, consistent with earlier reports that flowering time, maturity, and yield components are under strong genetic control. In contrast, stature and spikelet number are more sensitive to environmental variation [12, 13, 21]. The pronounced genotypic effects for days to 50% flowering (DTF50), days to maturity (DTM85), and yield-related traits such as number of filled spikelets (NFS) and yield per plant (YLDPLT) highlight their

importance as selection criteria for Malaysia's double-cropping and variable monsoon systems [10, 11, 26, 27]. In contrast, the dominant environmental effects observed for plant height (PH), number of spikelets (NOS), and yield (YLD) reflect the influence of rainfall distribution, soil nutrient availability, and field management, all of which strongly modulate productivity in Southeast Asian rice ecosystems [3, 6]. Notably, we excluded data from the Perak site (Titi Serong) from the final analysis because a technical error caused by a severe disease outbreak compromised plant stand uniformity and yield reliability. This location experienced heavy blast disease (*Magnaporthe oryzae*) infection during the reproductive phase, consistent with recent observations in Malaysia's humid lowland areas where high rainfall and poor drainage create ideal conditions for pathogen proliferation [6, 7]. Similar outbreaks have been reported by Dorairaj and Govender [6] and Miah et al. [14], where disease severity reduced grain yield by up to 60%. Therefore, to preserve the integrity of the dataset and ensure valid statistical interpretations, only two locations (Selangor and Kedah) were included in the final genotype $\times$ environment (G $\times$ E) and stability analyses, following recommendations by Crossa et al. [22] and Yan and Kang [24] to exclude anomalous environments affected by extreme biotic stress.

Significant G $\times$ E interactions for NFS, YLDPLT, SLSWR, TSW, and phenological traits indicate crossover responses among genotypes across sites, suggesting that certain lines performed inconsistently under varying environmental conditions. Such genotype re-ranking may result from spatial differences in water availability, soil fertility, or temperature regimes, as noted in earlier multi-location studies [19, 20]. This pattern contrasts with results from more uniform environments such as those reported by Akinwale et al. [19], where minimal crossover was detected due to controlled irrigation and uniform soil conditions. From a breeding perspective, genotypes exhibiting high mean yield with low G $\times$ E variance are desirable for broad adaptation and varietal release [22]. In this study, several UiTM mutant lines showed stable flowering and yield performance, indicating adaptability across distinct Malaysian environments and potential for climate-resilient rice development. Similar results have been observed in gamma-irradiated mutant lines from Bangladesh (Binadhan-7) and Vietnam, where improved stress tolerance and yield stability were reported under fluctuating climatic conditions [14, 17]. Conversely, some commercial check varieties such as MR219 and MR297 displayed greater environmental sensitivity, reinforcing the advantage of mutation breeding in generating allelic diversity that enhances adaptive stability [15,18].

The trait variability observed in this study reinforces the importance of integrating genetic and environmental insights into selection strategies. High coefficients of variation (CVs) for sterile spikelets (NSS), yield (YLD), and yield per plant (YLDPLT) indicate that local conditions highly influence these yield components, underscoring the need for targeted nutrient and water management to mitigate performance instability [27]. In contrast, the low CVs recorded for seed length (SL) and days to flowering (DTF50) suggest these traits are more stable, governed primarily by genetic control and less affected by environmental variation, making them reliable targets for early-generation selection [12, 26]. Correlation analysis further revealed strong positive relationships among spikelet number (NOS), filled spikelets (NFS), and panicle number (NP), all of which contribute to the sink capacity that determines yield potential. The strong correlation between YLDPLT, TSW, and NFS supports the classical sink–source relationship model, emphasizing that improved grain-filling efficiency and sink strength drive yield improvement [17,27]. The weak correlation between flowering or maturity duration and yield indicates that early-maturing, high-yielding genotypes can be developed, giving breeders flexibility to create varieties that fit multiple cropping seasons and help mitigate climate-related risks such as terminal drought or flood events [22].

Multivariate analysis further clarifies the key traits driving genotype differentiation. Principal Component Analysis (PCA) showed that PC1 was associated with yield-related and reproductive traits, while PC2 represented grain morphology and plant architecture, confirming that productivity and grain quality traits are largely independent dimensions under genetic control [15,25]. This finding agrees with Kim and Reinke [27], who reported distinct clustering of yield and grain-type traits due to separate genetic regulation mechanisms. The cluster analysis grouped genotypes into two main clusters, providing useful insights for breeding strategy. Cluster I included early-flowering, high-yielding genotypes suited to stress-prone or short-season environments, while Cluster II included late-maturing genotypes with higher spikelet numbers and potential for yield maximization under favorable conditions. Nguyen et al. [20] and Bui and Nguyen [17]

reported similar genotype stratification, demonstrating the practical utility of cluster-based selection in matching genotype performance with environmental conditions.

Overall, the results validate that mutation breeding using gamma irradiation is a powerful approach for enhancing rice genetic diversity, yield potential, and resilience under variable Malaysian agroecologies. The stable performance of several UiTM mutant lines supports their potential for national varietal registration and inclusion in large-scale adaptive trials. These findings align with international evidence showing that induced mutations contribute significantly to the diversification of stress-tolerant rice varieties [11–13, 15, 17]. Future work should integrate AMMI and GGE biplot analyses with environmental covariates such as rainfall, temperature, and soil nitrogen to refine mega-environment classification and guide selection for stability. Incorporating physiological and molecular markers linked to flowering and spikelet fertility genes will further accelerate marker-assisted breeding, while on-farm participatory validation will ensure the relevance and scalability of UiTM lines. The integration of yield stability, grain quality traits, and economic performance will be vital to support Malaysia's goals of sustainable and climate-resilient rice self-sufficiency under intensifying climate variability [2–5, 9, 10]

4. Conclusions

This study identified several UiTM mutant rice lines that matured early, produced high yields, and performed stably across different Malaysian environments. Mutation breeding through gamma irradiation effectively improved yield, maturity, and stress tolerance. The findings highlight the potential of these lines for climate-resilient rice production. Future work should combine GGE biplot and AMMI analyses with physiological and molecular markers to select stable, high-yielding cultivars for sustainable rice improvement in Malaysia.

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