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ASSESSMENT OF DROUGHT TOLERANCE AND YIELD STABILITY OF RICE MUTANTS IN DROUGHT-PRONE AREAS OF BANGLADESH

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Abstract

Drought is a major abiotic stress severely limiting rice production, especially in rain-fed ecosystems. The present study evaluated the drought tolerance and yield stability of four advanced rice mutants developed by the Bangladesh Institute of Nuclear Agriculture (BINA), alongside drought-tolerant BRRI dhan56 and susceptible Binadhan-7 checks, across three different drought-prone environments in Bangladesh. A twenty-one-day irrigation withdrawal was imposed post-transplanting to simulate drought stress during the early to maximum tillering stage. Results revealed an average yield reduction of 51.84% for grain and 51.17% for straw under drought. Among the genotypes, mutants M-3 and M-4 showed superior resilience, with minimal reductions in key yield components like filled grains panicle^{-1}, and effective tillers number. Correlation and Principal Component Analysis (PCA) identified filled grains panicle^{-1} as a critical trait for selection under stress. Stability analyses using phenotypic indices, regression coefficients, and GGE biplot confirmed M-3 and M-4 as high-yielding and stable mutants across environments. GGE biplot also highlighted Rangpur's high discriminative power for evaluating drought responsiveness. The susceptible check Binadhan-7 showed the poorest performance and the highest environmental sensitivity. These findings demonstrate the genetic potential of M-3 and M-4 as drought-resilient genotypes and as valuable donors in future breeding programmes.

Keywords: *Oryza sativa* L., Water stress, SPAD, Genotype plus GE interaction, GGE biplot

Introduction

Grown across varied ecosystems worldwide, rice (*Oryza sativa* L.) is one of the most important cereal crops and nourishes over 50% of the world's population (USDA, 2025). In Bangladesh, rice holds significant importance, occupying approximately 76% of the total cropped area and providing around 60% of total calories and 50% of protein intake for adults (Biswas *et al.*, 2022). The country has witnessed a remarkable increase in rice production, reaching 4.10 crore tonnes in the fiscal year 2023–24, marking a 4.1% year-on-year growth (Parvez, 2024). The rise in rice production is due to better varieties, practices, and favorable climate, but challenges like drought, salinity, floods, and temperature extremes especially drought in rainfed areas remain major threats (Sagar *et al.*, 2025). It affects plant growth, reduces tillering, inhibits panicle formation and grain filling, and ultimately decreases yield

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(Farooq *et al.*, 2014). Drought stress also disrupts physiological processes such as photosynthesis, water relations, and nutrient uptake, leading to poor plant performance (Seleiman *et al.*, 2021). Developing drought-tolerant rice varieties is therefore essential to sustain productivity under water-limited conditions (Hallajian *et al.*, 2024).

Drought-tolerant rice varieties can be developed using conventional and mutation breeding with the aid of marker-assisted selection, and genome editing to introduce traits such as deep rooting, osmotic adjustment, and improved water-use efficiency. Mutation breeding creates novel alleles for stress tolerance, which can be combined with high-yielding cultivars through selection and molecular approaches (Hasibuzzaman *et al.*, 2025). Conventional breeding and mutation breeding has been basic approach for a long time and some successes have been achieved in case of introducing drought tolerance in rice (Serraj *et al.*, 2009; Anilkumar *et al.*, 2023), wheat (Bapela *et al.*, 2022) and jute (Kar *et al.*, 2022; Atiq *et al.*, 2023). Genetic improvement for adaptation to drought stress is addressed through the conventional approach by selecting for yield and its stability over the locations and years. Agro-morphological and physiological screening under field conditions further ensures stable performance under water-limited environments (Gaballah *et al.*, 2022). Breeding for drought tolerance in rice is challenging due to strong genotype-environment interactions and limited understanding of tolerance mechanisms. Effective field evaluation is crucial, focusing on identifying genotypes with stable reproductive performance and minimal yield loss under drought, assessed through multi-environment trials (Shah *et al.*, 2020). Multi-environment trials (METs) are crucial for evaluating rice genotype performance and stability under diverse environmental conditions. They help analyze genotype x environment interactions and identify key traits linked to yield and stress tolerance. Correlation analysis helps reveal the strength and direction of associations between traits. In contrast, principal component analysis (PCA) reduces dimensionality and highlights significant variation patterns and helps to identify suitable genotypes (Hasibuzzaman *et al.*, 2024).

Additionally, multivariate techniques, such as cluster analysis and GGE biplots, facilitate the evaluation of genotype performance and stability across environments. Advanced statistical models such as AMMI (Additive Main effects and Multiplicative Interaction) and GGE (Genotype plus Genotype x Environment) biplot analysis are applied to identify stable and high-yielding genotypes (Haque *et al.*, 2024). These trials help breeders to select rice varieties with stable yields and drought tolerance under varying conditions.

The study aims to evaluate rice mutants for drought tolerance, stable performance, and high yields across diverse water-limited environments in Bangladesh, highlighting key traits contributing to resilience. Ultimately, this study will identify superior rice mutants with stable performance and drought resilience that can support sustainable production, enhance food security, and serve as valuable resources in future breeding programmes.

Materials and methods

Four advanced rice mutants developed by the Plant Breeding Division of BINA, Headquarters, Mymensingh-2202, were evaluated in this study, along with two check varieties: BRRI dhan56 as the drought-tolerant check and Binadhan-7 as the drought-susceptible check. The experiments were conducted in three drought-prone locations of Bangladesh: Magura, Rangpur, and Rajshahi. Two treatments were applied: (i) Regular irrigation as the control and (ii) Twenty one day irrigation withdrawal to impose drought stress. The experiments were laid out in a randomized complete block design (RCBD) with three replications. Twenty-six-day-old seedlings were transplanted at a spacing of 20 cm between rows and 15 cm between plants. Irrigation was withdrawn entirely three weeks after transplanting to induce drought stress. The field–managed drought screening protocol was followed as described by IRRI 2008. To prevent interference from rainfall, polyhouses were erected over the experimental plots, while the control plots were maintained under regular irrigation. From the early tillering to the maximum tillering stage, the stressed plots exhibited severe drought symptoms, including leaf rolling and leaf drying. Other necessary interculture operations including two times weeding and fertilizer applications were applied at a similar dose as FRG-2018.

Data were recorded on plant height (cm), culm length (cm), number of effective tillers (no.), SPAD readings during stress imposition, panicle length (cm), number of filled grains panicle^{-1} (no.), number of unfilled grains panicle^{-1} (no.), thousand-seed weight (g), grain yield (tha^{-1}), straw yield (tha^{-1}), biological yield (tha^{-1}), and harvest index (%). The relative changes (%) of each parameter under drought stress, compared to the control were calculated using the following formula:

$$\frac{Trait\ in\ stress - Trait\ in\ control}{Trait\ in\ control}\ x\ 100$$

Techniques of statistical analysis for estimating response and stability

i) Phenotypic index (Pi)

The formula calculates the phenotypic index:

$$P_i = \overline{Y}_i - \overline{Y}$$

Where, $\overline{Yi}$ = Mean of ith genotype over the environments;
$\overline{Y}$ .. = Grand mean and Pi = Phenotypic index for ith genotype.

ii) Environmental index (Ij)

The formula calculates the environmental index as Ij = $\overline{Y}$ .j – $\overline{Y}$ ..

Where, $\overline{Y}$ .j = Mean at jth environment,
$\overline{Y}$ ..= Grand mean and Ij = Environmental index.

iii) Regression coefficient/linear component (b_i)

Linear regression analyses calculated as-

b_i= regression coefficient that measures the response of ith genotype on the environmental index to varying environments, that is– b_i = SPXY/SSX

Where, SS_x is the sum of squares of the environmental means, and SP_{xy} is the sum of the products of the genotype mean (Y) and the environmental index (E).

iv) Deviation from regression/non–linear component ($\bar{S}^2di$)

Mean square deviation ($\bar{S}^2di$) from linear regression was calculated using the following formula-

$$\bar{S}^2di = \text{Remainder MS} - \text{Error MS}$$

Where, Remainder MS = Remainder SS/n–2 (n = number of environments);
Remainder SS = SS (Y) – Regression SS and Regression SS = SP $(XY)^2$/SS(X).

b) Hypotheses of the study

The hypothesis that there is no response of the genotypes to different environments (H_0: bi =1) and there is no deviation from regression (H_0: S^2di=0) were tested approximately by F–test.

H_0: b_i = 1 (F= MS due to linear regression/Error MS)

H_0: $\bar{S}^2di$ = 0 (F= MS due to deviation/Error MS).

The individual genotype response (regression co–efficient, bi) and their mean deviation from regression, S^2di were tested by using t–test and F–test against the hypotheses that it did not differ significantly from unity and zero, respectively as,

t= 1– bi/S_E (bi) and t= bi/S_E (bi) with n–1 df, n= number of genotypes

Where, $S_E (b_i) = \sqrt{SSY - SPXY.bi/SSX}$; F= [∑δij2/(S–2)]/pooled error and S= Environments.

c) Graphical analysis

Graphical analyses were conducted using RStudio version 4.5.1, employing several R packages to visualize and interpret the relationships among traits, genotypes, and environments under drought conditions. Trait correlation analysis was performed using the *GGally*, *ggplot2*, and *dplyr* packages, with the *ggpairs* function from *GGally* providing a comprehensive correlation matrix that revealed key associations among drought-related traits. Principal Component Analysis (PCA) was carried out using the *factoextra*, *ggplot2*, and *dplyr* packages to reduce dimensionality and illustrate the contribution of each trait to the overall variation, enabling apparent genotype clustering based on multivariate performance. To assess the physiological impact of drought stress, *ggplot2* was used to generate boxplots depicting the percent reduction in each trait, highlighting variability and trait-specific sensitivity. Multi-environment trial data were analyzed using the GGE biplot methodology through the gge and *ggplot2* packages, which enabled the visualization of genotype performance and stability across environments. The GGE biplot included "which-won-where" plots for identifying winning genotypes and mega-environments, mean vs. stability plots to select high-performing and stable genotypes, and environment ranking plots to evaluate the discriminating power and representativeness of each test location. Collectively, these graphical tools supported by the *GGally*, *ggplot2*, *dplyr*, *factoextra*, and GGE-related packages provided robust visual insights into genotype behavior, trait dynamics, and genotype-by-environment interactions under drought stress.

Results

Overall reduction of the studied traits under drought stress

Relatively lower degree of decreasing trend was observed for plant height (2.62%), culm length (6.55%), effective tillers (19.36%), SPAD value (9.88%), panicle length (25.73%), filled grains panicle^{-1} (23.61%), unfilled grain panicle^{-1} (20.9%) and for 1000 grain weight (18.61%) under drought. But grain yield tha^{-1} and straw yield tha^{-1} declined drastically, which were recorded as 51.84% and 51.17% for grain and straw yield, respectively under drought conditions (Fig. 1). On average, both grain and straw yields were reduced by approximately 50% relative to irrigated conditions, indicating a severe impact of drought on rice yield.

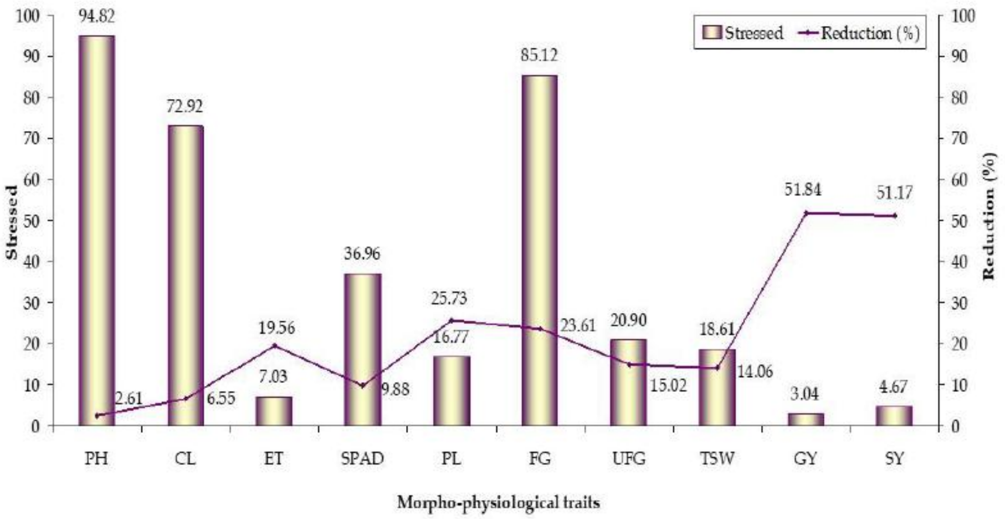

Fig. 1. Overall relative performance and reduction percentages of quantitative characters in rice genotypes under drought.

PH= Plant height (cm), CL= Culm length (cm), ET= Number of effective tillers hill^{-1}, SPAD = SPAD value, P= Panicle length (cm), FG= Number of filled grains panicle^{-1}, UFG= Number of unfilled grains panicle^{-1}, TSW= Thousand seed weight (g), GY= Grain yield (tha^{-1}) and SY = Straw yield (tha^{-1}).

Genotype-wise reduction of the traits under drought stress

Under drought stress, a noticeable reduction was observed in all measured traits across the studied genotypes. Plant height and culm length declined moderately (5–15%) with the highest reduction in Binadhan-7, whereas BRRI dhan56 and the mutants, particularly M-3 and M-4, showed comparatively smaller losses. Effective tillers, SPAD values, and panicle length exhibited a 20–40% reduction, with M-3 maintaining superior tiller number and chlorophyll content under stress. A sharp decline (30-50%) was recorded in filled grains panicle^{-1}, accompanied by a marked increase in unfilled grains panicle^{-1}, most prominently in Binadhan-7, whereas M-3 showed the least increase, reflecting better reproductive resilience. Thousand seed weight decreased by 10-25%, but M-4 and BRRI dhan56 experienced relatively lower reductions. Grain yield suffered the most severe losses (50–80%) with the susceptible check (Binadhan-7) being most affected, while M-2 and M-3 displayed higher yield stability. Straw yield and biological yield followed a similar trend, and harvest index declined slightly (2-6%) with M-3 maintaining a higher proportion of grain to total biomass. Overall, mutants M-2 and M-3 consistently outperformed the susceptible check and maintained better performance than the tolerant check in most traits (Fig. 2).

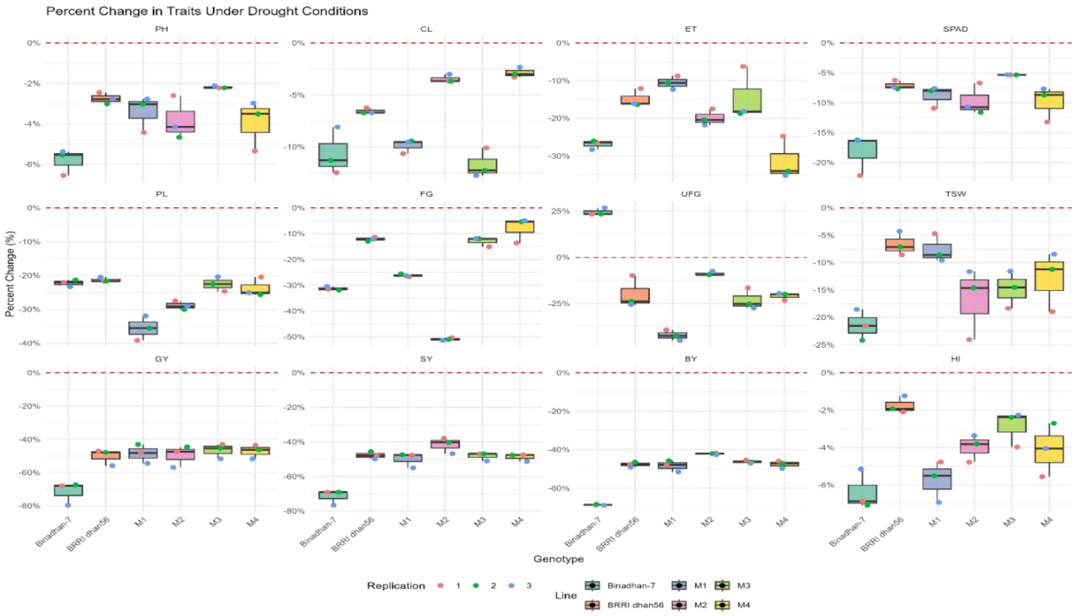

Fig. 2. Genotype-wise percentage reduction of quantitative traits in rice genotypes under drought stress.

PH= Plant height (cm), CL= Culm length (cm), ET= Number of effective tillers hill^{-1}, SPAD = SPAD value, PL= Panicle length (cm), FG= Number of filled grains panicle^{-1}, UFG= Number of unfilled grains panicle^{-1}, TSW= Thousand–seed weight (g), GY= Grain yield (tha^{-1}), SY= Straw yield (tha^{-1}) and HI= Harvest index.

Trait association studies

The trait association of the traits for control and drought conditions along with overall relations are presented in Fig. 3. Correlation analysis showed that PH was positively and significantly associated with all studied traits except HI across all three observations: overall, control, and drought. For ET, SY was insignificant under control, but under drought stress, tillering capacity increased and showed a significant positive association (0.486*). Conversely, ET was positively significant with HI (0.476*) under control, while under drought it was nonsignificant. Variations in SPAD were observed with UFG, which showed a strong positive correlation under control (0.741***) but became nonsignificant under drought. FG consistently exhibited a significant positive correlation with GY, SY, and BY across all three observations. The main impacts of drought were evident for UFG, which was positively significant with GY, SY, and BY under control, but these associations became nonsignificant under stress. Under drought, TSW showed a significant positive association with SY (0.629***), whereas under control it was nonsignificant. For HI, these relationships were reversed: it was positively significant under control (0.645***) but nonsignificant under drought. Similarly, the association between GY and HI was significant in control (0.622***) but nonsignificant under drought. BY was positively significant with HI under control (0.491*) but became nonsignificant under drought conditions.

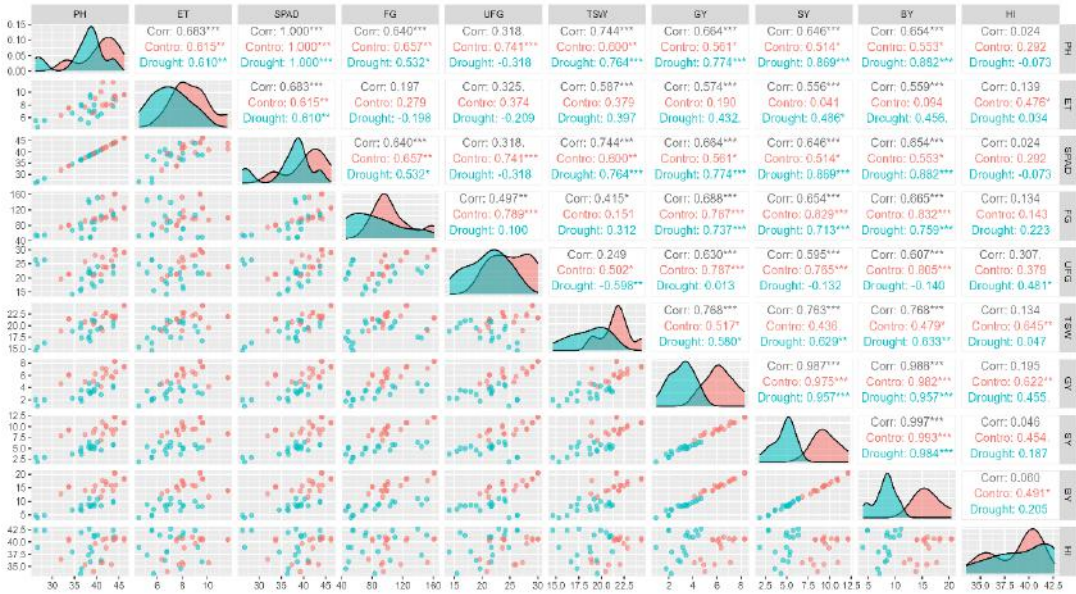

Fig. 3. Trait association studies of the traits under both control and drought stress.

PH = Plant height (cm), CL = Culm length (cm), ET = Number of effective tillers hill^{-1}, SPAD = SPAD value, PL= Panicle length (cm), FG = Number of filled grains panicle^{-1}, UFG = Number of unfilled grains panicle^{-1}, TSW= Thousand–seed weight (g), GY=Grain yield (t ha^{-1}) and SY= Straw yield (tha^{-1}), BY= Biological Yield (t ha^{-1}), HI= Harvest index

Principal component analysis

The PCA biplot (Fig. 4) reveals a clear segregation of the rice genotypes, forming two distinct eclipses corresponding to the experimental treatments: stress and control. The first principal component (Dim1, 59.7%) overwhelmingly captures the drastic phenotypic shift induced by drought stress. Within the drought-stressed eclipse, genotypic performance varied significantly along Dim2 (13.9%), allowing for the identification of superior and inferior performers. Under control conditions, all genotypes were observed on the right side of the biplot, except the susceptible check Binadhan-7. Among these, mutants M-1 and M-2 were the top performers, along with the tolerant check BRRI dhan56. Under drought conditions, mutant M-3 was the best performer, also alongside the tolerant check BRRI dhan56. In contrast, the susceptible check Binadhan-7 exhibited the most inferior performance under drought stress, located far apart from the tolerant clusters.

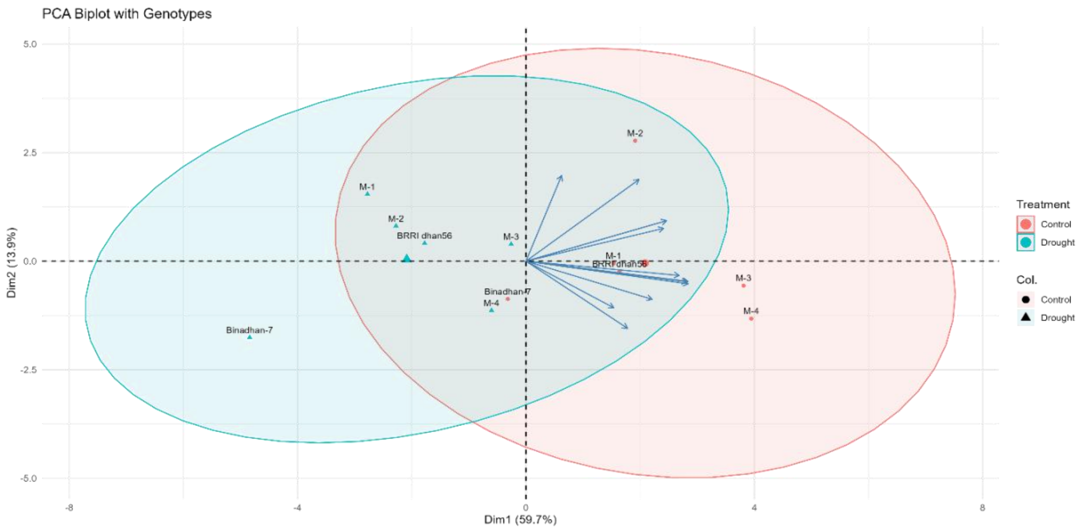

Fig. 4. Principal component analysis of the studied genotypes and their associated traits under two stress conditions.

Trait stability and response analysis

Significant G×E interactions for yield traits enabled identification of adaptable genotypes under drought, using four stability parameters: mean, phenotypic index, regression coefficient, and deviation from regression. The number of effective tillers per plant averaged 7.79 across locations, ranging from 4.67 (Binadhan-7) to 10.5 (M-4). Genotypes M-2, Binadhan-7, and BRRI dhan56 had lower tiller numbers with negative phenotypic indices. Regression coefficients (bi) ranged from 0.795 to 1.561, showing varied environmental responses Binadhan-7 (bi > 1) was highly responsive, while M-1 and BRRI dhan56 ($S^2di \approx 0$) showed greater stability (Table 1).

Panicle length varied significantly across genotypes and environments, ranging from 15.33 cm (Binadhan-7) to 22.55 cm (M-4). The highest mean was recorded at L_3 (Rajshahi). Genotypes M-3, M-4, and BRRI dhan56 showed high performance with positive phenotypic indices and bi ≈ 1, indicating stable performance. M-2 (bi = 1.312) was the most responsive to environmental changes, while M-2, M-4, and BRRI dhan56 had low S^2di values, indicating greater stability.

Table 1. Stability parameters of drought tolerance in rice genotypes for number of effective tillers hill^{-1} and panicle length

Genotypes	Number of effective tillers hill^{-1}							Panicle length (cm)						
	L_1	L_2	L_3	Mean	P_i	b_i	S^2_{di}	L_1	L_2	L_3	Mean	P_i	b_i	S^2_{di}
M-1	8.99	9.01	7.44	8.48b	0.69	1.011	0.171	22.01	20.33	21.65	21.33b	-1.29	0.872	-0.390
M-2	6.40	6.4	6.88	6.56d	-1.23	1.131	-0.564	20.22	19.81	19.81	19.95c	-0.62	1.312	0.105
M-3	8.99	7.98	10.06	9.01ab	1.22	0.911	-0.514	19.46	21.02	20.99	20.49bc	4.93	0.809	-0.218
M-4	11.23	10.99	9.28	10.5a	2.71	1.012	-0.675	21.64	22.89	23.12	22.55a	0.12	1.086	0.016
Binadhan-7	3.99	5.01	5.02	4.67e	-3.12	1.561	2.115	14.99	16.01	14.99	15.33e	-3.88	0.678	-1.137
BRRI dhan56	7.23	8.01	7.23	7.49c	-0.3	0.795	0.179	20.12	16.19	21.11	19.14d	0.71	1.053	0.045
Env. Mean	7.81	7.9	7.64	7.79				19.74	19.38	20.28	19.80			
Env. Index	0.02	0.11	-0.15					-0.06	-0.43	0.48				

L_1= Magura; L_2= Rangpur; L_3= Rajshahi

Number of filled grains per panicle showed significant variation across genotypes, environments, and their interactions, averaging 91.57 grains. Counts ranged from 67.63 (Binadhan-7) to 123.3 (M-4). M-1, M-2, and Binadhan-7 had negative phenotypic indices, indicating fewer grains. Binadhan-7 had the highest environmental response (bi = 2.108), while M-1 showed a lower response (bi = 0.608). Only BRRI dhan56 demonstrated stable performance with S^2di near zero; others showed variable stability (Table 2).

Table 2. Stability parameters of drought tolerance in rice genotypes for the number of filled gains and unfilled grains per panicle

Genotypes	Number of filled grains panicle^{-1}							Number of unfilled grains panicle^{-1}						
	L_1	L_2	L_3	Mean	P_i	b_i	S^2_{di}	L_1	L_2	L_3	Mean	P_i	b_i	S^2_{di}
M-1	85.22	81.11	85.76	84.03d	-7.54	0.608	-37.28	22.65	23.21	20.95	22.27c	-1.51	1.301	1.467
M-2	73.85	73.86	74.89	74.20e	-17.37	0.897	-27.54	25.05	25.05	26.01	25.37ab	1.59	1.134	2.209
M-3	105.1	106.1	105.9	105.7b	14.13	1.214	-12.44	25.0	22.40	24.10	23.83b	0.05	0.878	0.008
M-4	120.8	125.2	124.1	123.3a	31.73	1.101	-10.21	23.07	22.26	23.07	22.80cd	-0.98	1.147	1.649
Binadhan-7	68.11	68.06	66.72	67.63f	-23.94	2.108	-18.32	25.89	28.14	26.22	26.75a	2.97	1.457	5.221
BRRI dhan56	94.87	93.92	94.87	94.56c	2.99	0.911	-.0911	22.01	21.50	21.50	21.67d	-2.11	0.902	0.039
Env. Mean	91.33	91.35	92.04	91.57				23.95	23.76	23.64	23.78			
Env. Index	-0.25	-0.23	0.47					0.17	-0.02	-0.14				

L_1= Magura; L_2= Rangpur; L_3= Rajshahi

Number of unfilled grains per panicle were significantly affected by genotypes, environments, and their interactions, with means ranging from 21.67 (BRRI dhan56) to 26.75 (Binadhan-7). Binadhan-7 was the most sensitive and had poor drought yield. M-1, M-4, and BRRI dhan56 had fewer unfilled grains under drought. Regression coefficients ranged from 0.878 to 1.457, and stability varied, with R-3027 showing the greatest stability (S^2di = 0.008).

Yield stability analysis

The GGE biplot (Fig. 5A) illustrates genotype-by-environment interactions across Magura, Rangpur, and Rajshahi. PC1 (78.2%) reflects genotype performance, while PC2 (15.4%) captures interactions. Rangpur, with the longest vector, best differentiates genotypes; Magura and Rajshahi have shorter, closely aligned vectors, showing lower discrimination and strong positive correlation. M-1 performs the best in Rangpur, while BRRI dhan56 shows stable, favorable performance in Magura and Rajshahi.

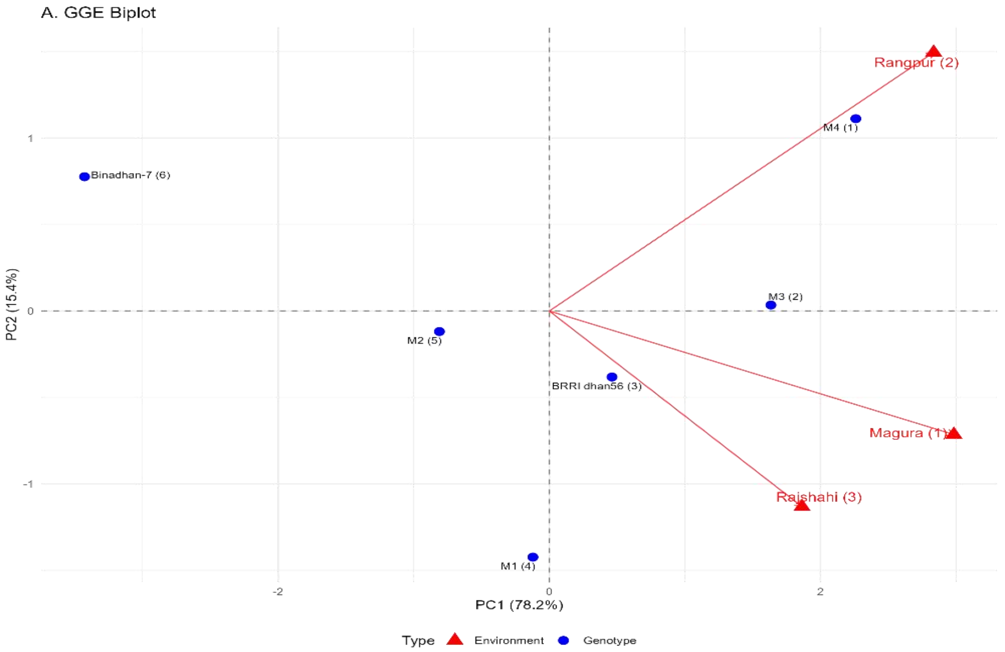

Fig. 5A. GGE biplot showing genotype performance and stability across environments

Fig. 5B appears to be a scatter plot where the mean performance of genotypes is plotted against a stability parameter. The axes show a mean performance scale from 3 to 6 on the X-axis and a stability index from 0.4 to 1.0 on the Y-axis, where a higher value likely indicates greater instability. This figure suggests that two genotypes, M-4 and M-3, offer the best compromise between high mean yield and acceptable stability.

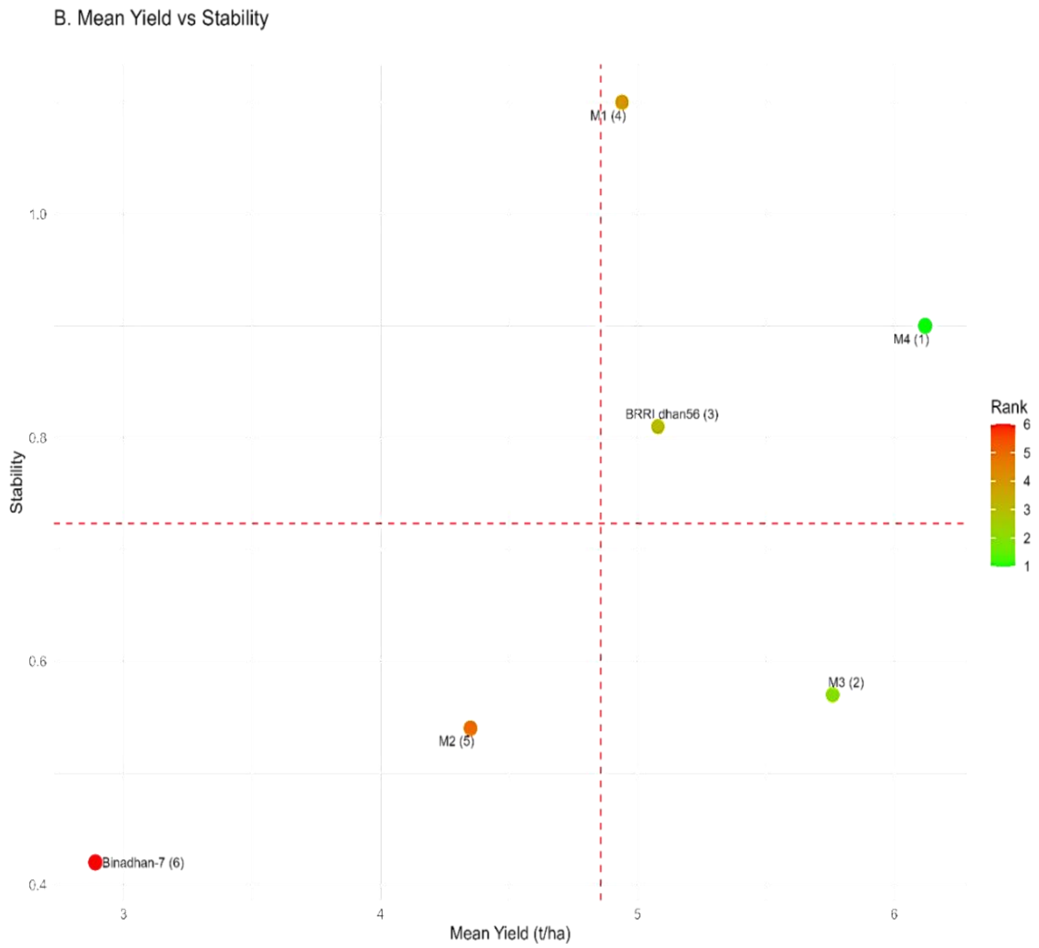

Fig. 5B. Mean yield vs stability of the genotypes

The Which-Won-Where plot in Fig. 5D is a key visualization to visualize which genotypes performed the best in which locations. The plot displays genotypes and environments on a plane defined by the first two principal components, which together explain 93.6% of the total variation. For Rangpur, M-4 is the best genotype, while M-1, M-3, and BRRI dhan56 perform better in both Magura and Rajshahi under drought conditions. Binadhan-7 is the worst performer for cultivating in drought-prone areas.

Fig. 5C presents an environment analysis depicting the standard deviation values for a large set of entries. Magura exhibited the best stable environments in the case of cultivating these genotypes, followed by Rangpur and Rajshahi.

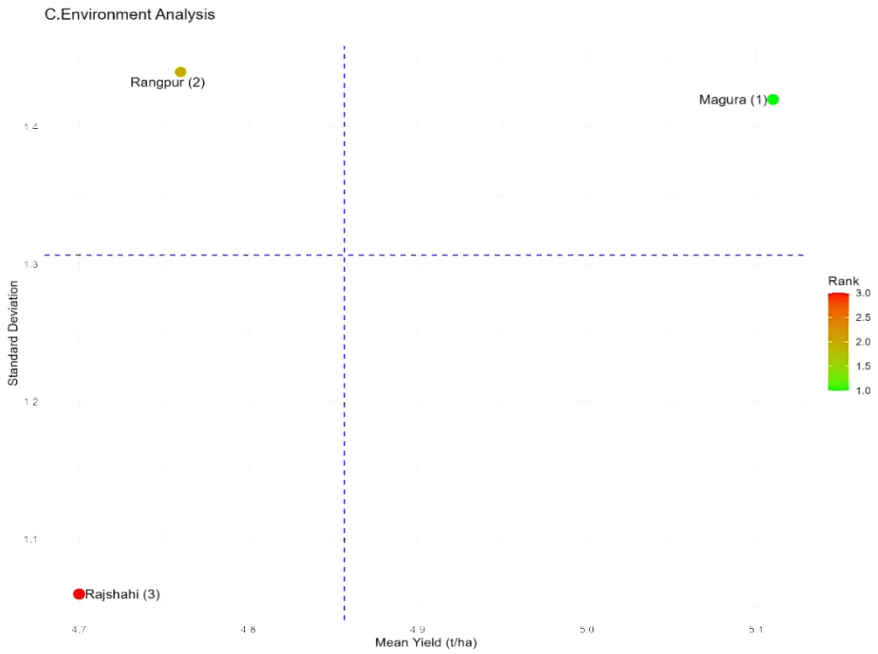

Fig. 5C. Environmental analysis with standard deviations

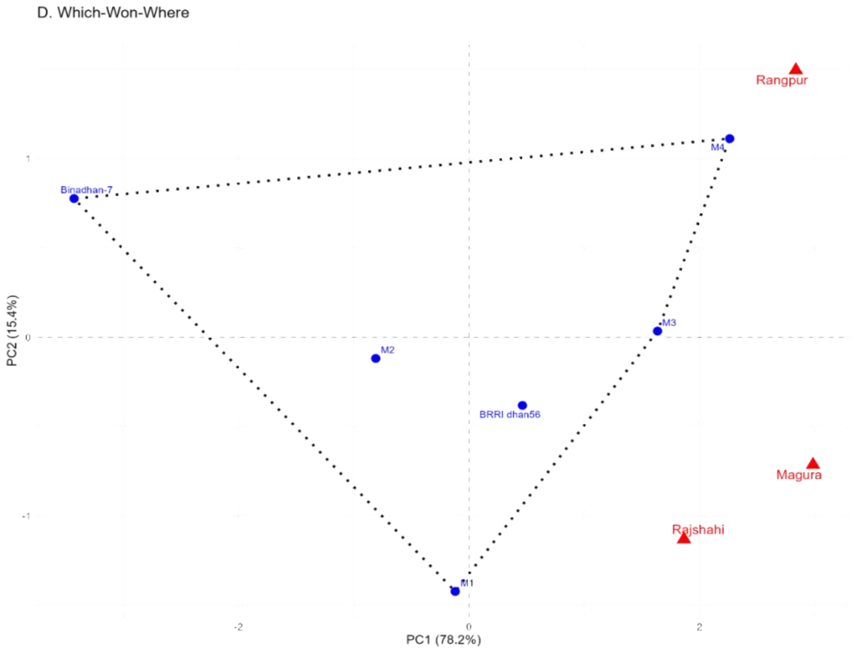

Fig. 5D. The Which-Won-Where plot illustrates genotype performance across environments

Discussion

Drought is one of the most significant abiotic stresses limiting agricultural productivity worldwide. It adversely affects plant growth, development, and yield by disrupting physiological and metabolic processes (Oshunsanya *et al.*, 2019). Developing drought-tolerant crops is vital for food security, with stable traits serving as key indirect selection criteria in breeding. This highlights the need to select genotypes that sustain yield under stress. Although all characteristics declined under drought, mutants M-3 and M-4 showed greater resilience, likely due to better root architecture, water-use efficiency, osmotic adjustment or genes controlling spikelet fertility and stress-responsive pathways (Ruggiero *et al.*, 2017).

From a plant breeding perspective, the consistent positive correlation of filled grains with grain yield (r = 0.792***) under both control and drought highlights it as a key selection trait for drought tolerance. In contrast, traits like harvest index and unfilled grains lost their associations under stress, indicating genotype-specific responses that breeders must account for during selection (Richards *et al.*, 2010). The PCA biplot (Fig. 4) clearly distinguishes genotypic responses to drought, with Dim1 (59.7%) capturing the significant variation caused by stress. Mutants M-1 and M-2 performed the best under control conditions, while M-3 showed superior performance under drought, clustering with the tolerant check BRRI dhan56, highlighting their potential use in developing drought-resilient rice varieties. The analysis of trait stability revealed that M-4 recorded the highest mean effective tillers (10.5) with a phenotypic index (Pi) of 2.71 and stable performance (S^2di = -0.675). It also had the longest panicle length (22.55 cm) with a regression coefficient (bi = 1.086) and low deviation (S^2di = 0.016). For number of filled grains penicle^{-1}, M-4 led with a mean of 123.3, Pi of 31.73, while Binadhan-7 showed poor response (bi = 2.108) and low mean (67.63). BRRI dhan56 and M-3 had stable filled grain numbers. Binadhan-7 had the highest unfilled grains (26.75, Pi = 2.97) indicating poor drought adaptability, whereas M-3 and BRRI dhan56 showed low S^2di and better control. Overall, M-4 and M-3 exhibited strong genetic stability and performance for drought tolerance.

The GGE biplot analyses provided valuable insights into the adaptability and yield stability of the tested genotypes under drought-prone environments (Mohammadi *et al.*, 2023). The high explained variation (93.6%) highlights strong genotype and G×E effects, stressing the need for environment-specific selection. Rangpur’s superior discriminating ability makes it ideal for identifying drought-responsive genotypes. Stable performance of BRRI dhan56 in Magura and Rajshahi reflects broad adaptability and resilience, while M-3 and M-4 combine high yield with moderate stability, likely due to stress-responsive traits like deeper roots and better assimilate partitioning (Peer *et al.*, 2024).

This study highlights significant genotype-by-environment interactions affecting drought tolerance and yield stability in rice mutants. M-3 and M-4 showed superior yield and stability under drought, likely due to favorable genetics. GGE biplot identified Rangpur as the key environment for selecting drought-responsive genotypes. Combining stability parameters with G×E analysis offers valuable insights for breeding drought-resilient rice varieties.

Conclusion

Drought stress caused substantial reductions in rice growth and yield, with grain and straw yields declining by approximately 50%. Among the tested genotypes, mutants M-3 and M-4 consistently demonstrated superior performance, maintaining higher effective tillers, filled grains, and chlorophyll content under stress. Stability and G×E analyses, including GGE biplots, identified these mutants as drought-resilient, with Rangpur being the most discriminating environment for selection. The study highlights the potential of M-3 and M-4 as promising candidates for developing drought-tolerant rice varieties with stable performance across diverse environments.

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