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RESEARCH ARTICLE

Comprehensive analysis of stability in rice genotypes for dry weight and grain yield under multi-environment stress

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Abstract

Increasing agricultural productivity and efficient use of limited nutrient resources with significant yield improvement is vital for sustainable agriculture. Phosphorus is the second most important macronutrient for crop growth next to nitrogen and its uptake varies under water-limited and irrigated conditions. However, identifying stable and high-yielding rice genotypes under varied phosphorus levels in combination with differences in water level is vital for current strategies on sustainability. Given this, 145 rice genotypes were raised in four different environments and characterized for phosphorus uptake traits, as well as grain yield and its related traits. Studies on correlation revealed that plant height and number of productive tillers exhibited a positive association with grain yield. Performed stability analysis and calculated stability parameters for dry weight and grain yield. Additive Main effects and Multiplicative Interaction (AMMI) model exposed the best performers as G115 and G47 for dry weight whereas G14 and G1 for grain yield. Based on the Genotype-by-Environment interaction (GGE) biplot, the winning genotypes for dry weight and grain yield were G14 and G1 respectively. Based on the Yield Stability Index (YSI) parameter, the best performer for dry weight was G27 and grain yield was G14. Ideal ranking of environments revealed that E1 for dry weight and E3 for grain yield can discriminate the genotypes. According to our results, the genotypes identified could be utilized to develop sustainable varieties.

Keywords: AMMI; dry weight; grain yield; low phosphorus; rice; sustainable

Introduction

Rice (*Oryza sativa* L.) is a semi-aquatic crop of the Gramineae family cultivated in varied agroclimatic zones. It plays a crucial role in sustainable development by providing a staple food source for a large portion of the global population. Currently, the global population is 7.6 billion and by 2050, it is anticipated to rise to 9.8 billion, with an annual increment of about 83 million people (1). At present, the global land area under paddy cultivation spans approximately 162 million hectares, yielding a production of 755 million metric tons (2). Over the past decade, international rice consumption has exhibited a steady upward trend, rising from 437.18 million metric tons in 2008-09 to 520.14 million metric tons in 2022-23 (3). This increasing demand places significant pressure on agricultural systems to increase food production and the gradual deterioration in the soil fertility status is a critical challenge in this context (4). Despite the limited nutrient resources, the prime focus in sustainable agriculture is to increase the grain yield per unit area.

Phosphorus (P) is a key element that plays a vital role in plant metabolism, root development, maturity and yield in all crops. Conventionally, P fertilizer is applied near the root zone of rice crop as a single basal dose contrary to nitrogen fertilizer which is applied in several split doses (5). In comparison with other macronutrients, available plant P is often the prime limiting nutrient for crop growth in most agricultural soils either due to P fixation or P occlusion (6). In tropical conditions, P is fixed in the soil in the form of organic and inorganic compounds, hence reduces the available P and in turn impacts the P acquisition efficiency of rice crop (7). Nevertheless, P fertilizer recovery efficiency is merely 15 to 25 %, much lower than that of nitrogen at 40 to 65 % in major cereal crops (8). Soil moisture status has a direct effect on P nutrition in rice crop and an increase in P uptake is proportional to an increase in dry matter production (9). The application of nitrogen to rice crop did not significantly increase crop production in low soil moisture conditions, but it did ameliorate plant Phosphorus deficit (10). To overcome this, a large amount of P fertilization is a continuous practice to increase the grain yield. However, limited access to rock phosphate resources and the high cost of P fertilizer are major constraints faced by rice farmers in developing countries. Undeniably, stable rice genotypes having tolerance to low soil P conditions or capable of high P uptake from fixed soils under varied soil moisture levels could reduce the P requirement in agricultural production systems.

Inheritance of grain yield coupled with yield related traits is polygenic in nature. High grain yield is dependent on suitable environmental conditions during the crop growth stages (11). When a genotype or variety grown in a varying environmental condition and has a high mean yield with little variation in yielding capacity over time, it is said to have broad environmental adaptability and stability (12). In crop plants, close association between varieties and their environment envisages the fact that there is a genetic component that helps the crop to adapt to that area. In order to produce elite varieties, matching genotypes with its habitats are an essential step in plant breeding. Thus, the emergence of a specific variety in a particular region is not merely a coincidence; rather it is the result of Genotype Environment Interactions (GEI) towards a phenotype (13, 14). Based on GEI, genotypes are classified as widely adapted (performs well in a wide range of conditions) and specifically adapted (outperform other genotypes in a set of restricted conditions). A significant portion of crop breeding resources are allocated to calculate GEI through replicated multilocation trials and choose the best-performing genotypes tailored to each stress condition. Current scenario of minimal fertility status (stress environment), limited water resources and sustainability the way forward, it's imperative to identify stable genotypes with high grain yield for various stress environments.

Plant breeders employ several strategies to raise genotypes under varying soil fertility regimes that correspond to rising or falling levels of a certain stress, or a mixture of stresses, where the experiments are aptly labeled as "Managed Stress Trials" (MST). These experiments are designed so that, with the exception of the specific stress, most of the variables affecting the phenotype are as similar as possible (15). The data from the MST are subjected to various non-parametric and parametric stability analysis models that are univariate and multivariate in nature. The AMMI model is one of this kind that is frequently utilized and appreciated (16). The additive variance and multiplicative variance are distinguished by the AMMI model. The AMMI model employs the ranking of genotype and environment to provide potent graphical representations known as biplots, which can speed up the interpretation of GEI. Biplots are widely utilized as a visual graphical representation for studying the interrelationships between Genotypes (G), Environments (E) and GEIs (17). They are also used to show interaction patterns and discover stable genotypes that are appropriate for various environments. The environment-centric Singular Value Decomposition (SVD) is the basis for the GGE biplots (18). The genotype and genotype by environment are displayed in the graph according to the main sources of variance associated with genotype evaluation. For rice varietal stability research, genotype assessment, environmental assessment and GGE biplots-based Multi Environment Trial (MET) can be used with success (19). Therefore, the current investigation is the first of its kind to examine how GEI affected grain yield and dry weight in diverse rice genotypes under varying P regimes and water levels. The study provides valuable insights on stability pattern of rice genotypes that could be utilized in future breeding schemes aimed at sustainable agriculture.

Materials and Methods

Plant material

The genetic material comprised of 145 rice genotypes including landraces, varieties from various geographical regions and germplasm accessions collected from different sources. The seeds of all 145 genotypes were maintained at Paddy Breeding Station, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu (Supplementary Table 1).

Experiment particulars

The experiment was conducted at the Research Farm of Paddy Breeding Station, Tamil Nadu Agricultural University (TNAU), Coimbatore, India, at 10°09' N latitude and 76°91' E longitude, at a height of 420 m above mean sea level, for two seasons (2019-20, 2020-21) and climatic conditions as mentioned in supplementary Table 2. During the cropping period, the different soil characteristics were recorded as presented in Table 1. The experiment was conducted in two fields that were under different soil P regimes as categorized by Olsen P method (<11 kg/ha as Low Soil P - LSP; >22 kg/ha as Normal Soil P - NSP), thus accomplishing two different soil P regimes. Sowing was done during the second fortnight of September. Under the two soil P regimes, limited irrigation conditions and normal irrigated conditions were accomplished to attain four different environments (E1 - LSP in water limited conditions and E2 - NSP in water limited conditions; E3 - LSP in normal irrigated conditions and E4 - NSP in normal irrigated conditions).

Raised nursery beds were prepared for sowing the seeds in LSP and NSP. Before sowing, N fertilization was uniformly given to both LSP and NSP raised nursery beds, whereas P fertilization was done only for NSP. All 145 genotypes were sown in raised nursery beds both in LSP and NSP so that exactly from the seedling stage, the difference in soil P level was maintained. Plant protection measures were implemented to ensure disease-free and healthy seedlings. On twenty fifth day, the healthy seedlings were shifted and transplanted in LSP (no basal P application) and NSP (basal P application done at the rate of 60 kg ha^{-1} of muriate of potash) main field in a Randomized Complete Block Design (RCBD) in three replication by adopting 6 m row length, 20 cm spacing between rows, 15 cm spacing between plants. The recommended dose of nitrogen (120 kg/ha) as urea was applied in three splits: one-third

Table 1. Soil properties

	Environment LSP	LSP Category	Environment NSP	NSP Category
Soil type	Black	-	Black	-
Soil texture	Sandy clay loam	-	Sandy clay loam	-
Electrical conductivity	0.41 dS m^{-1}	Non saline	0.39 dS m^{-1}	Non saline
Soil pH	7.8	Slightly alkaline	7.92	Slightly alkaline
Available N	218 kg ha^{-1}	Low	210 kg ha^{-1}	Low
Available P (Olsen)	9.8 kg ha^{-1}	Low	23.0kg ha^{-1}	High
Available K	424 kg ha^{-1}	High	411 kg ha^{-1}	High

N - Nitrogen; P - Phosphorus; K - Potash; LSP - Low Soil Phosphorus; NSP - Normal Soil Phosphorus as basal dose at the time of transplanting, one-third during initial tillering phase and another one-third during the active tillering phase. Crop stand was maintained by timely weed management and need-based plant protection measures in the transplanted field for healthy crop production. In water limited conditions the field was irrigated whenever cracks appeared on the soil surface until the desired amount of water was reached. In normal irrigated conditions the field was irrigated such that 3 cm water level was maintained above the soil surface.

Measurement of grain yield and component traits

Phenotypic data for P uptake traits, Yield Related Traits (YRT) and yield were recorded for all 145 rice genotypes. Data on P uptake traits viz., Root Length (RL), Shoot Length (SL) and single plant Dry Weight (DW) were recorded on 56th Day After Sowing (DAS) from three plants in all the entries. Data on Single Plant grain Yield (SPY) followed by YRT such as Plant Height (PH), number of Productive Tillers (NPT), Flag leaf Length (FL), Panicle Length (PL), number of Grains Per Panicle (GPP), Hundred Seed Weight (HSW), were recorded at maturity in all the genotypes as per Standard Evaluation System (SES) for Rice (20).

Statistical analysis

Correlation coefficients were calculated as per the standard method given by Karl Pearson. The statistical software R version 4.1.1 was utilized for all statistical analyses (21). The mean package was used to assess the performance of genotypes across two consecutive years by applying various stability models (22). These included AMMI and GGE Biplot analyses, which utilize Principal Component Analysis (PCA) to evaluate genotype-environment interactions and yield stability (23-25). The GEI effects in AMMI model were attained from biplot of genotype and environment effects whereas in GGE, the genotype and GEI effect using environment-centered PCA were presented. ANOVA (Analysis of Variance) is used to estimate the main effects while PCA decomposes the interaction into PCA axes. The following mathematical formula was used to compute AMMI analysis:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Y_{ij} is the mean yield of i th genotype in j th environment,

μ is the overall mean,

G_i and Ej is the genotype and environment deviation from overall mean,

λ_k is the eigenvector value for PC axis k,

α_{ik} and γ_{jk} is the genotype and environment PC scores for axis k,

ε_j is the residual error presumed to be normally and independently distributed (0, $\sigma 2/r$),

$\sigma 2$ is the pooled error variance and

r is the number of replications.

The mathematical formula to test homogeneity of error variances (Bartlett's test)

$$B = (N - k) * \ln(s^2p) - \Sigma [(n_i - 1) * \ln(s^2_i)]$$

Where N is the total sample size, k is the number of groups, s^2p is the pooled variance and s^2i is the variance of the i-th group.

The mathematical formula for the GGE model is as follows (25):

$$Y_{ij} = \mu + \beta_j + \sum_{k=1}^{n} \lambda_k \delta_{ik} \beta_{jk} + \varepsilon_{ij}$$

AMMI stability value (ASV) was calculated as per the following formula (26).

$$ASV = \sqrt{\left[\frac{ipcass1}{ipcass2}(ipcass1)\right]^2 + (ipcass2)}$$

The YSI was computed using the formula (27):

YSI = rASV + rY,

Where,

rASV is the rank of the ASV

rY represents the rank of the mean of genotypes across environments.

Results and Discussion

Mean performance and correlation among the studied traits

The mean performance for P uptake traits, YRT and SPY of the 145 genotypes evaluated across the four environments exhibited wide variations for all the traits under study (Supplementary Table 3). The mean performance for DW and SPY across the four environments was 6.76 g plant^{-1} and 14.96 g plant^{-1} respectively. The highest SPY (26.54 g plant^{-1}) was achieved by G50. The highest DW (10.44 g plant^{-1}) was recorded by G115. Average performance for DW and SPY of the genotypes in the four different environments is presented in Supplementary Table 4. Comparative insight of mean performance for SPY in the four environments showed an increased SPY in E4 (17.42 g plant^{-1}) followed by E3 (16.39 g plant^{-1}), E2 (13.03 g plant^{-1}) and E1 (13.02 g plant^{-1}). Whereas for DW, mean performance was in the order E2 (7.88) > E1 (7.66) > E3 (5.80) > E4 (5.70). The best performing genotypes in the four environments based on mean performance of the various studied traits is presented in Table 2. The association among all traits, along with SPY in the four different environments is presented in Fig. 1(a-d), respectively. In E1, SPY exhibited a significant positive correlation with RL, DW, PH, NPT and GPP, however, SPY had a significant positive correlation with PH, PL and NPT in E2. Significant positive correlation was observed for SPY with the traits *viz.,* SL, DW, PH, FL, NPT and GPP in E3 environment. SPY recorded a positive significant correlation with PH, PL, FL, NPT

Table 2. Winner genotype within each environment for SPY and other traits studied based on mean performance

Environment	RL	SL	DW	PH	FL	PL	NPT	GPP	HSW	SPY
E1	G74	G74	G70	G63	G63	G110	G98	G117	G56	G47
E2	G75	G15	G113	G63	G94	G75	G8	G89	G43	G8
E3	G17	G108	G17	G47	G2	G1	G129	G117	G130	G85
E4	G15	G145	G4	G106	G20	G11	G50	G135	G43	G50

RL- root length; SL- shoot length; DW- single plant dry weight; PH- plant height; FL- flag leaf length; NPT- number of productive tillers; GPP- number of grains per panicle; HSW- hundred seed weight; SPY- single plant grain yield.

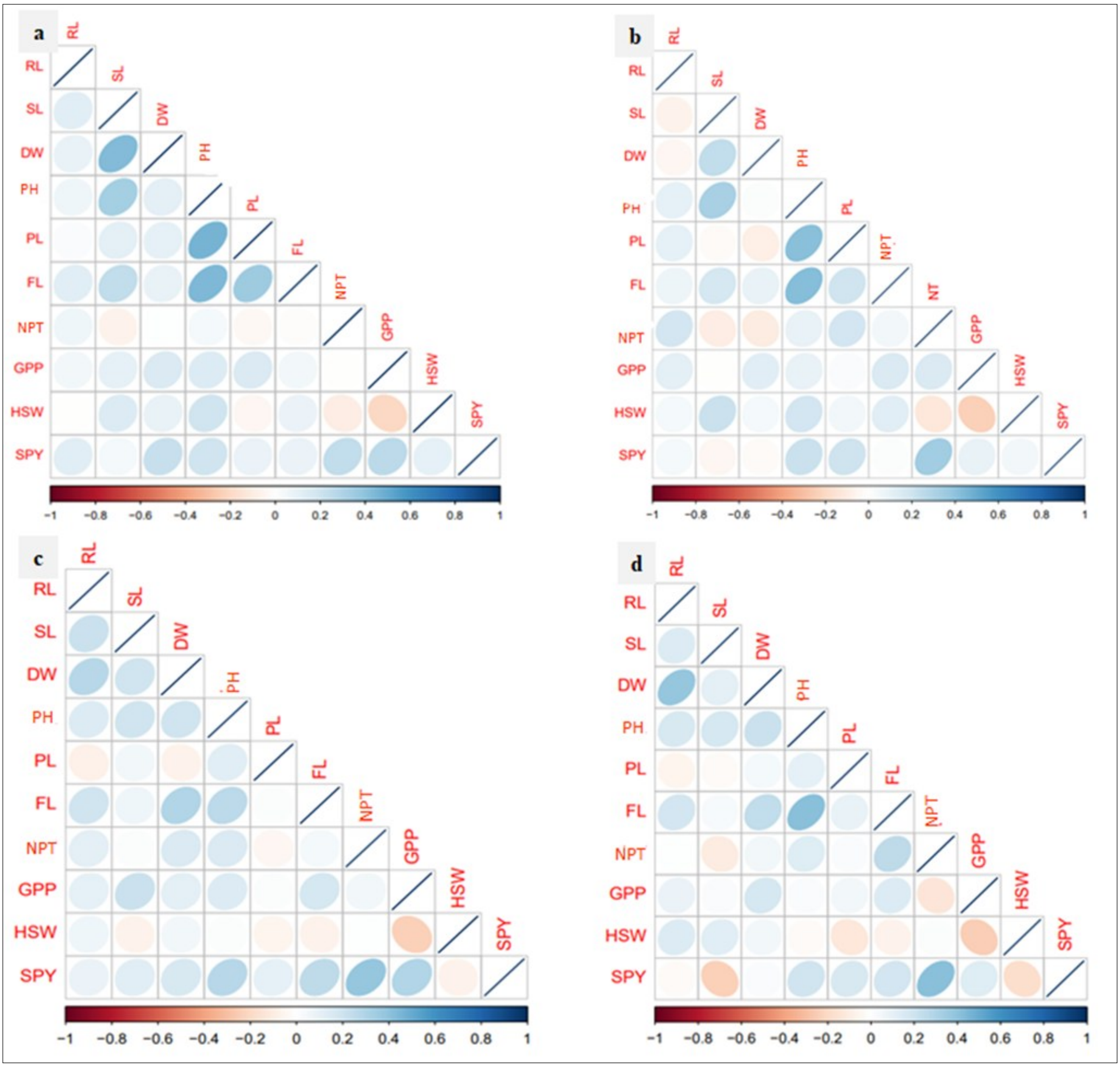

Fig. 1. Phenotype correlation coefficient for the ten traits studied across the four environments- a) E1; b) E2; c) E3; d) E4.

*The intensity of the blue color indicates a positive correlation, while the intensity of the pink color indicates a negative correlation.

and GPP in E4 environment. In all four environments PH and NPT exhibited positive association with SPY. Comparable outcomes were reported for individual plant yield, exhibiting a substantial positive correlation with PL across six conditions (28). Also, PH and PT were found to be positively correlated with yield over years (29). In both the LSP environments (E1 and E3), the DW exhibited a significant positive correlation with SPY and similar findings were already reported (30). DW is an important P uptake trait in rice during the active tillering stage (31). Hence, stability was assessed for DW in addition to SPY in all four environments.

Combined ANOVA for DW and SPY

High significant differences in genotypes, environment and GEI were noticed for both DW and SPY, which could be explained by variations in environmental factors, genetic composition and their interactions among them (Table 3). The percentage split of G, E and GEI was calculated from the sum of squares, which explains the percentage variation of both traits. Environmental and genotypic variability was higher for DW (13.36 %, 29.89 %) trait than SPY (7.04 %, 24.24 %) and GEI was higher for SPY (30.78 %) than DW (25.81 %). Three significant PCs for each of the attributes were obtained from the AMMI analysis used to break down the GEI effect. These three PCs were significant for both traits and contributed to 100 % of the overall GEI effects discussed. A parallel investigation showed that the environment had a 29.07 % fluctuation in grain yield (32). The notable variation observed in G×E interaction and their genotypic differences points to the existence of unique multi-environments that are characterized by genotypic diversity and significant yield potential. However, in order to elucidate the key elements of GEI, variance component analysis only is insufficient. Hence, multivariate analysis using additional statistical approaches like AMMI can explain GEI significantly much better (33).

Interpretation of AMMI biplot

In AMMI1 biplot, the main effects of the genotypes are depicted against their PC1 scores. The vector closer to zero is less interactive and the vector far away from the origin is more interactive. All four environments were highly interactive for both DW and SPY,

Table 3. AMMI analysis of variance for DW and SPY for the tested 145 genotypes under 4 different environments

Sl. No	Source of variation	df	DW			SPY		
			Mean Sq.	**Proportion**	**% SS**	**Mean Sq.**	**Proportion**	**% SS**
1	Environment	3	397.24**	NA	13.36	1508.38**	NA	7.04
2	Replication × Environment	6	1.18	NA	-	31.28	NA	-
3	Genotypes	144	18.51**	NA	29.89	108.14**	NA	24.24
4	Genotypes × Environment	432	5.32**	NA	25.81	45.76**	NA	30.78
5	PC1	146	10.49**	66.5		72.73**	53.7	
6	PC2	144	3.38**	21.2		42.17**	30.7	
7	PC3	142	1.98**	12.3		21.67**	15.6	
8	Pooled error	576	0.78	NA		7.76	NA	
9	Total	1593	5.60	NA		40.37	NA	

**Significant at 1 %; AMMI- Additive Main effects and Multiplicative Interaction; DF- Degrees of Freedom; DW- Single Plant Dry Weight; SPY- Single Plant Grain Yield; %SS - % of Sum of Square; PC- Principal Component

comparatively E1 and E3 were more stable for DW and SPY respectively based on their proximity to the centre of origin. G113 and G129 recorded higher mean values and positive PC1 scores for DW, hence interactive with E1 and E3 which also recorded positive PC1 scores (Fig. 2a). The genotypes G115 and G47 possessed higher mean and less interactive as it was placed near the PC1 axis. For SPY, the genotypes that lie near the origin G14 and G1 were less interactive, hence stable and recorded above average mean values. The genotypes G47, G27, G97 and G100 recorded higher mean with positive PC1 were highly interactive (Fig. 2b). The above results are comparable to earlier findings in rice and in Bambara groundnut where interactive environments were observed (17, 31).

The AMMI2 is a graphical representation of GEI based on principal component scores (PC1 and PC2). AMMI2 model explained the genotype stability and performance, genetic variations between genotypes and its relationship with environments (33). Environments located far from the origin have a low contribution to genotype stability but a high contribution to GEI (34). The first two principal component interactions of the AMMI 2 biplot model accounted for 87.7 % and 84.4 % of the G+GEI variation for DW (Fig. 3a) and SPY (Fig. 3b), respectively. Our result agreed with the earlier research studies stating that the first two PCs are acceptable for AMMI2 model projection (35). The biplot's center (0, 0) is divided into four separate sections by crossing the vertical line and horizontal line. Likewise, within a GGE biplot, genotypes positioned far from the biplot origin are considered successful genotypes in the environments located within that specific sector. The distance of the environment and genotype vectors from the biplot's origin is used to calculate the level of interaction shown by the environment over the genotype and reciprocal. In our investigation, we observed E3 for DW and E1 for SPY had shorter vector compared to other environments (Fig. 3a, 3b). Thus, the environment indicator with a shorter vector, closer to the biplot origin is less interactive and can be used as an ideal criterion to choose a genotype with average performance and adaptability (36). The majority of rice genotypes gathered near the biplot's origin. In comparison to genotypes that are separated from one another, these genotypes behave similarly to all four environments. Meanwhile, the genotypes positioned away generated a polygon that revealed that these genotypes were highly interactive and possess a narrow sense of adaptability to specific environments. Thus, certain variations in the environment may have a bigger effect on some genotypes than others. This finding reiterated with an earlier study (37).

Interpretation of which-won-where biplot

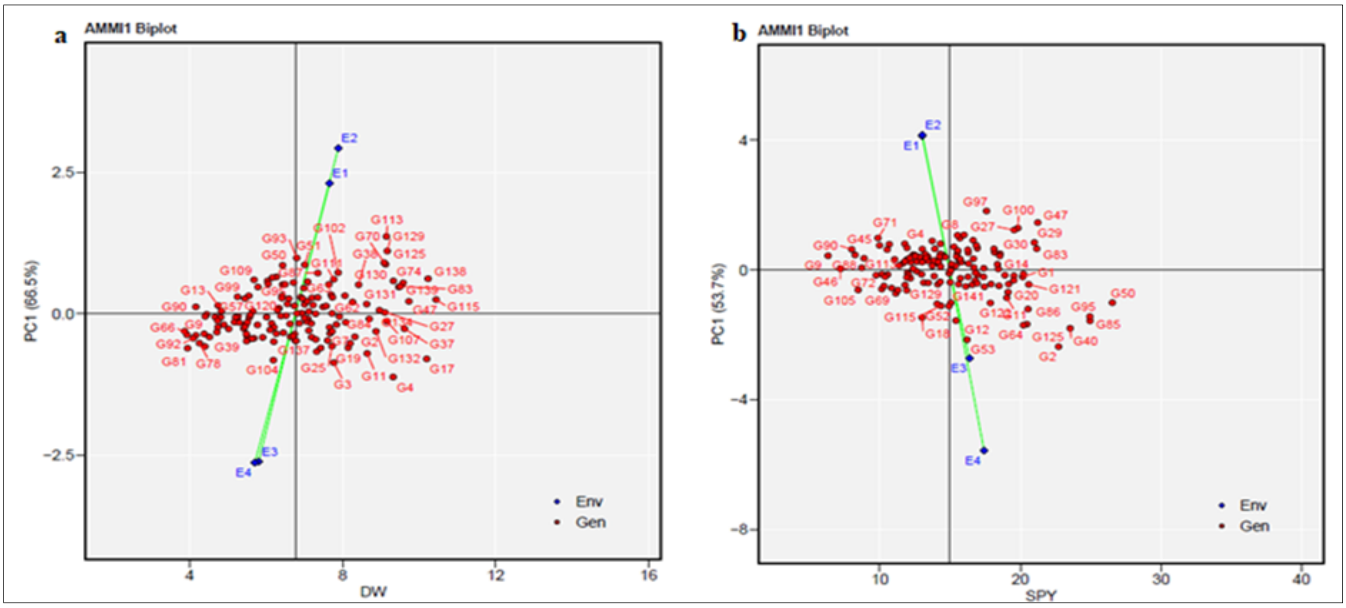

Fig. 2. AMMI1 Biplot. a) DW (Dry Weight); b) SPY (grain yield).

*Biplot indicating the expressivity and stability of the genotypes.

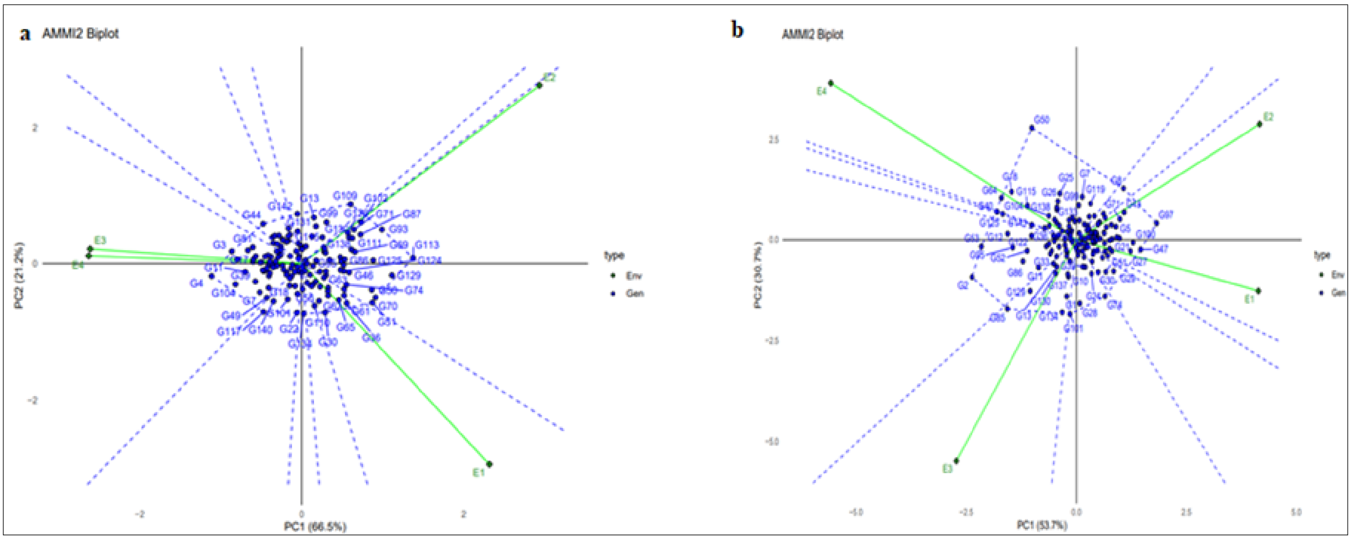

Fig. 3. AMMI II Biplot. a) DW (Dry Weight); b) SPY (grain yield).

*Biplot indicating the genotype-environment interaction.

A graphical representation of which-won-where biplot is created by joining the genotypes at the vertex and those farthest from the biplot origin. The genotypes at the vertex were represented as the winning ones in the particular sector that contained environments. Two mega environments M1 (comprising of E1 and E2) and M2 (comprising of E3 and E4) visualized for DW (Fig. 4a). G4 and G104 were vertex genotypes in M1; G138, G113 and G93 vertex genotypes in M2. For SPY, the four environments divide into three sectors. E1 and E2 in the same sector formed one mega environment (M1), whereas E3 and E4 in different sectors hence two mega environments M2 and M3 respectively (Fig. 4b). The winning genotype in M1 was G47, hence best genotype for the environment E1 and E2, whereas genotypes G50 and G85 performed best in consisted environment E3 (M2). The vertex genotypes in M3 were G2 and G53 hence the best performing genotypes in E4. Results confirmed the presence of a distinct interaction between genotype and environment for SPY and DW. Conversely, in a biplot section without an environment, the genotypes positioned at the polygon vertex are regarded as underperforming in every tested environment; additionally, the genotypes within the polygon exhibit reduced interaction with the environment. Therefore, different genotypes can arise as the best performers in different mega environments for different traits (31).

GGE biplot for 'mean vs. stability' and assessment of ideal genotype

The 'Mean vs. stability' biplot view often explains average environment coordinate (AEC) and single value portioning (SVP), which makes genotype assessment easier by using average performance and stability across a wide range of environments. Identification of stable genotypes with superior mean performance was done by AEC method (Fig. 5a, 5b). A ray drawn that passes through the average environment and the biplot origin with one direction indicated to a larger genotype main effect. Deviating both way from AEC ordinate and from the biplot origin depicts a larger GEI effect and decrease in stability. The genotypes were categorized as below-average means and above-average means based on AEC ordinate. For DW, G115, G138 and G47 were highly interactive with higher mean in E1 and E2. G17, G37 and G4 possessed greater mean and responsive in E3 and E4. The genotype G50, G85 and G95 were

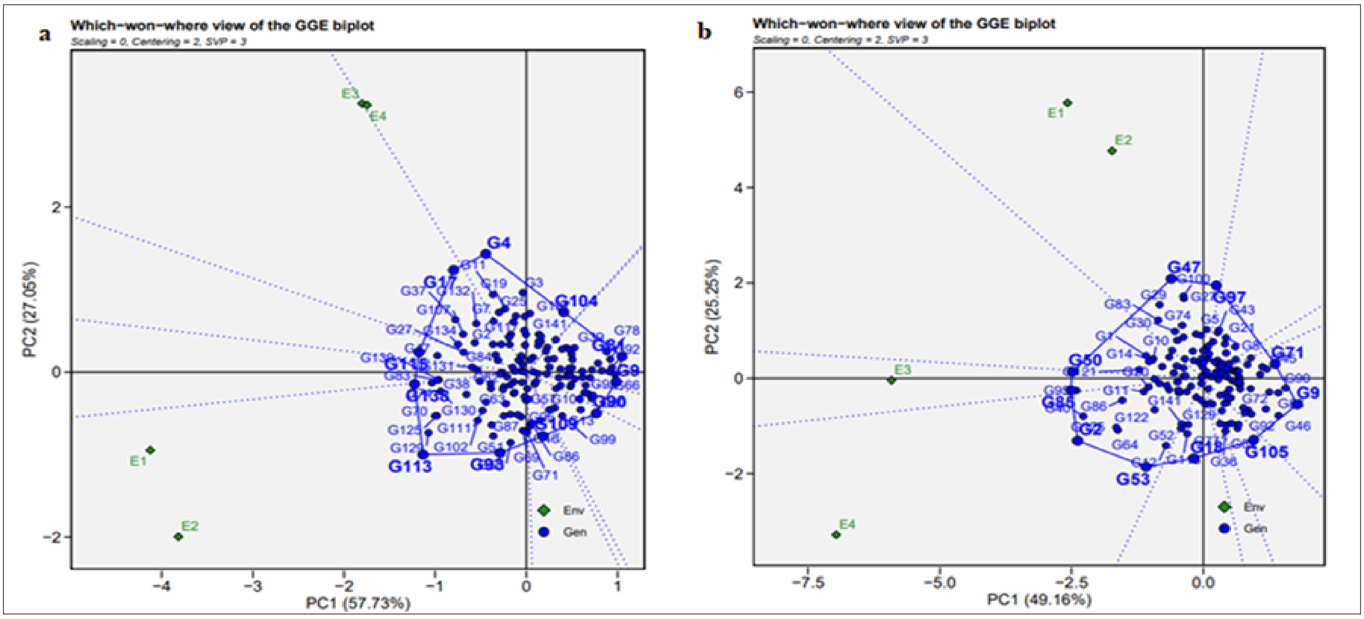

Fig. 4. Classification of Environments. a) DW (Dry Weight); b) SPY (grain yield).

*Classification of environments into mega-environment and extreme genotypes are placed in the peaks of blue.

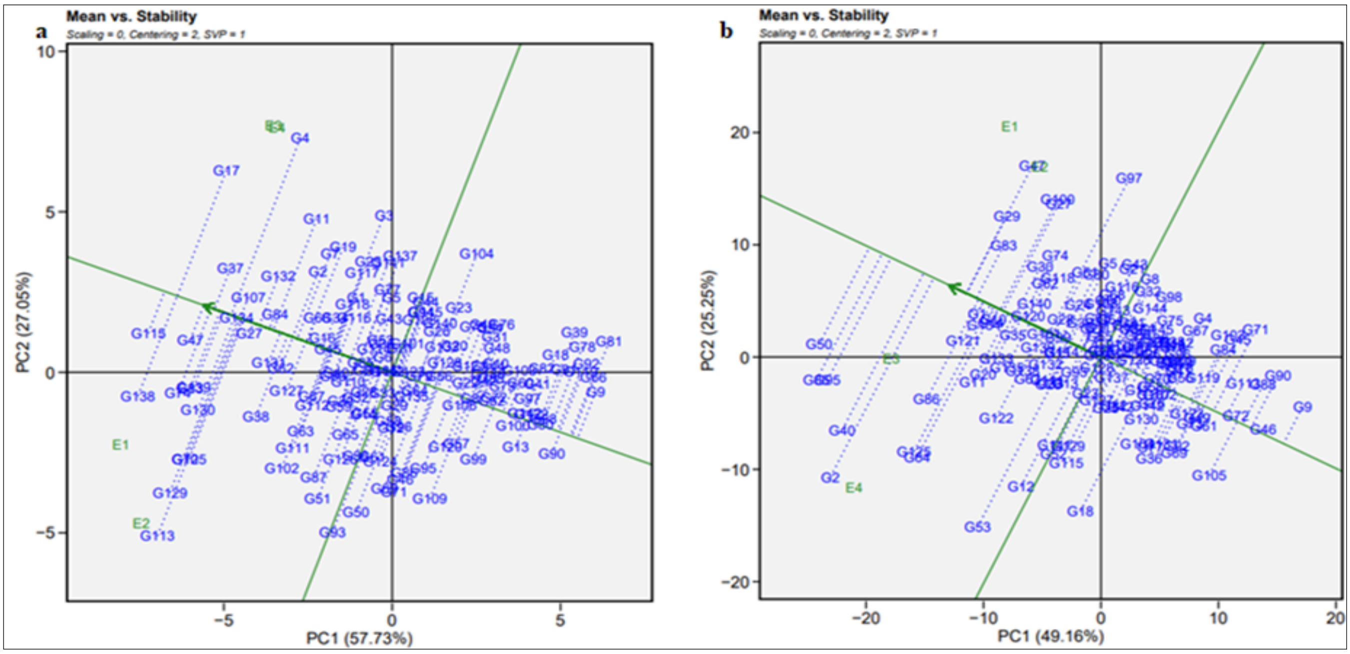

Fig. 5. Biplot for Mean *vs* stability. a) DW (Dry Weight); b) SPY (grain yield).

*Dotted blue lines away from AEC ordinate indicate greater GEI effect and reduction in stability.

interactive with higher mean for SPY in E3 and E4. Meanwhile, G47, G29 and G83 possessed higher mean and were interactive in E1 and E2 environments for SPY. Genotypes on the AEC abscissa are highly stable though they do not record a higher mean. Similar results for stable and interactive genotypes with higher means were reported in earlier studies on rice (13, 17).

Ranking genotypes

An ideal genotype can be realized by genotype ranking biplot based on the genotype's location in the innermost concentric circle and nearness to the arrow point. If the innermost concentric circle lacks genotypes, then the genotypes in the subsequent concentric ring are chosen as ideal ones. In the present study, for DW genotype G115 is regarded as an ideal genotype due to their nearness to concentric circle followed by G47> G37> G134 (Fig. 6a). G50 was observed as the ideal genotype for SPY as it was located near to the concentric circle, followed by G14>G30>G121>G83> G29> G95>G85 (Fig. 6b). However, it is better to include stability parameters likewise for ranking of ideal genotypes (38).

Ranking environments

Ranking of the environment is based on its nearness to concentric rings, revealed that environment E1 for DW (Fig. 7a) and environment E3 for SPY (Fig. 7b) was the ideal environment. Similar another finding reported that among the four tested environments for yield per hectare a single environment was sufficient for selection of ideal genotype (39). A successful breeding strategy in the choice of superior genotypes depends on the identification of a best suitable (ideal) test environment. The twofold features, discriminativeness (the capability of an environment to differentiate genotype) and representativeness (the capability of an environment to represent all other evaluated environment), imply the idealness of the tested

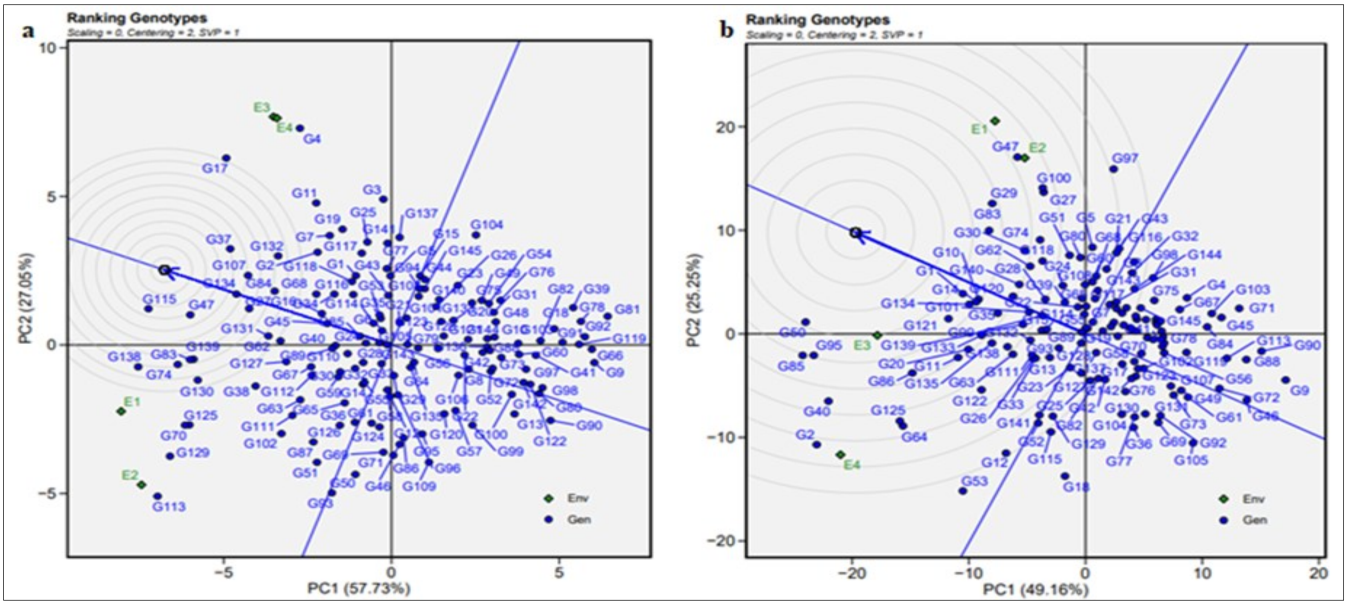

Fig. 6. GGE biplot for genotypes ranking pattern. a) DW (Dry Weight); b) SPY (grain yield).

*An ideal genotype is shown by a circle within the innermost concentric rings on average environment coordinate (AEC) abscissa passing through biplot origin.

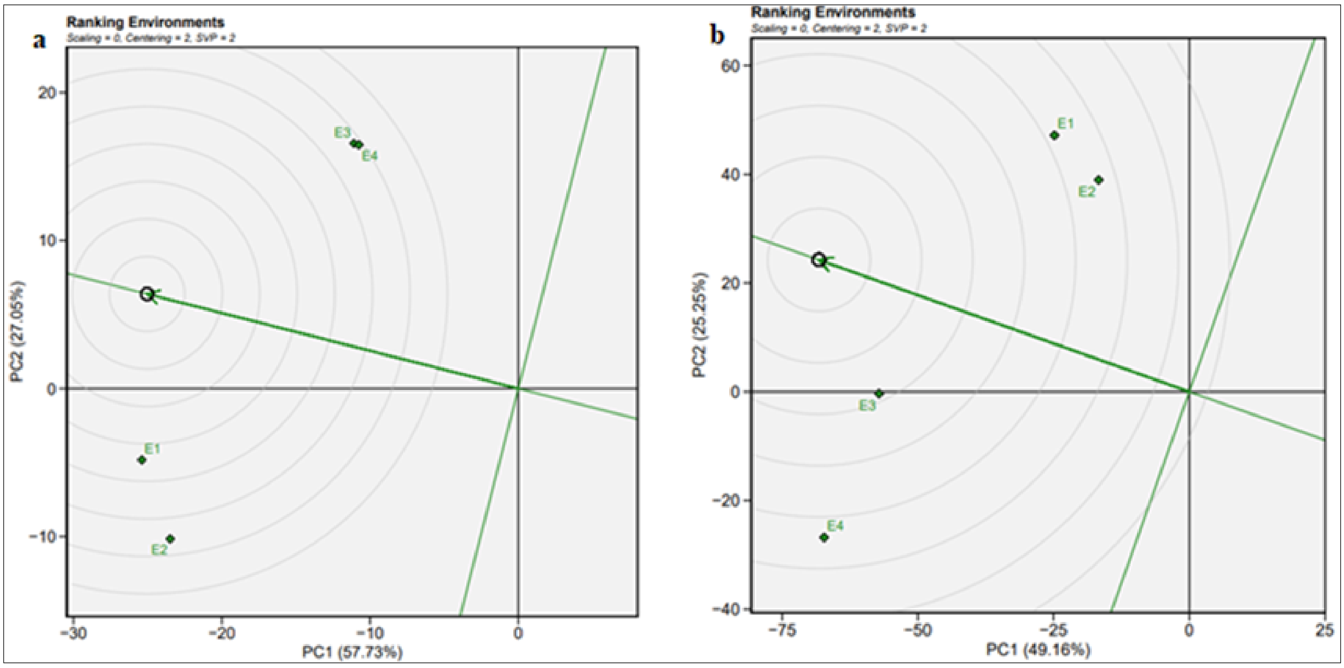

Fig. 7. GGE biplot for environment ranking pattern. a) DW (Dry Weight); b) SPY (grain yield).

*A circle within the innermost concentric circles on the AEC abscissa, passing through the biplot origin, represents the ideal environment.

environments, which are depicted as a biplot (Fig. 8a, 8b). The environments with the long vector are more suitable in distinguishing the rice genotypes, hence E2 for DW (Fig. 8a) and E4 for SPY (Fig. 8b), due to their long vectors, are regarded as distinctive and exclusive study locations. But the best conditions for the selection of superior genotypes are those when a lengthy vector makes a narrow angle with the AEC abscissa line. Therefore, E1 for DW and E3 for SPY exhibited narrow angle along with lengthy vector with AEC abscissa indicating that the test environment was better representative and discriminative. Though E1 and E3 were less in P content but water level in E3 was in irrigated condition, thus P requirement of the plants was met by P solubilization (40).

Stability parameters

The AMMI model lacks in quantification of stability which is a criterion to rank genotypes according to yield stability, hence stability parameters that aid in quantifying the results were calculated (Supplementary Table 5). ASV was calculated as the distance from zero in a two-dimensional scatterplot of PC scores (PC1 *vs* PC2). Thus, the variation in the GEI is well explained in ASV for all genotypes, since it takes into account both IPCA1 and IPCA2. The least ASV score corresponds to the most stable genotype. Consequently, genotypes G105>G143>G106>G123>G79 were ranked as top five stable genotypes for DW, whereas G46 >G102>G94>G89>G19 were observed for SPY. The stability parameter ASV cannot be used as the sole selection standard because the most stable genotypes may not produce higher yields (41, 42). Therefore, a single selection model that incorporates both mean and stability is required. The ranks of ASV and yield mean are arranged so that the lowest ASV is ranked one, the highest yield mean is ranked one and the ranks are then added to produce the YSI. The genotype with least YSI value is considered the most stable

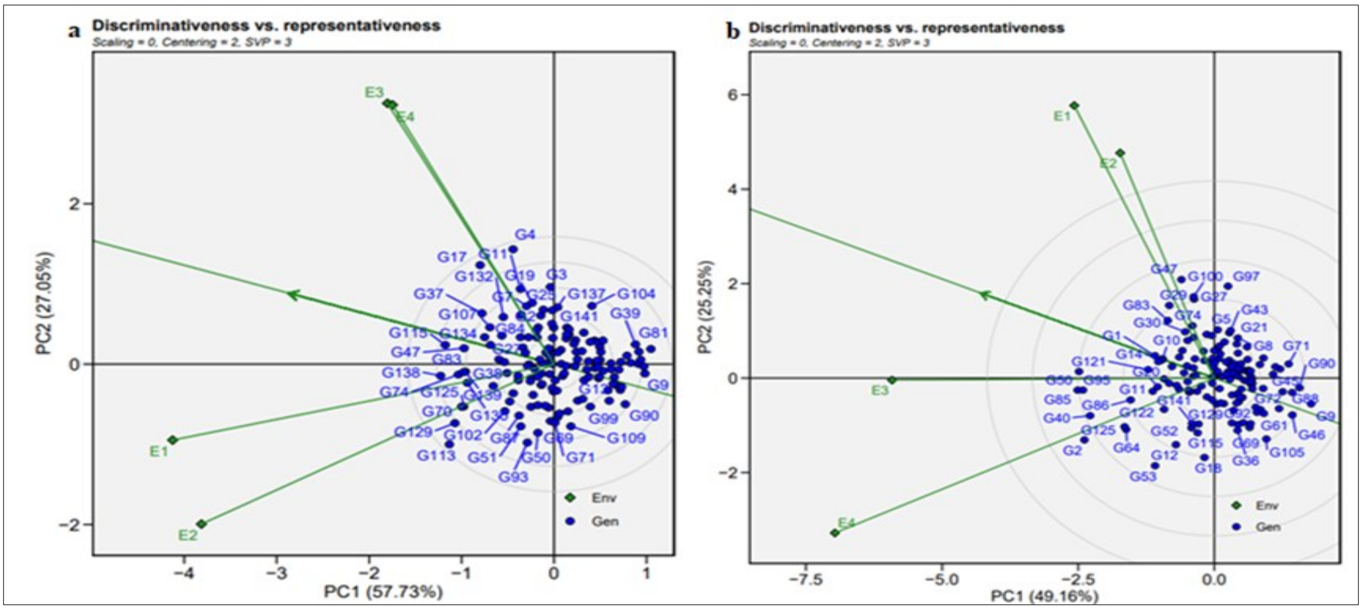

Fig. 8. GGE biplot for ‘Discriminativeness vs. Representativeness’ pattern for genotype comparison with ideal genotype. a) DW (Dry Weight); b) SPY (grain yield).

*An environment with a lengthy vector that forms a narrow angle with the AEC abscissa is apt for the selection of superior genotypes.

and high grain yielding (17). Based on YSI, the top five most stable genotypes for DW were G27>G84>G107>G16>G47; for SPY were G14>G120>G35>G140>G139. Therefore, the selection of genotypes with high yield coupled with stability in performance reduces the GEI effect.

Thus the 145 rice genotypes utilized in the present investigation were found to exhibit variations in their responses to the four environments studied. The AMMI1 biplot explained that E1 was stable for DW and E3 was stable for SPY. Additionally, both the low P environments, E1 (water-limited condition) and E3 (irrigated condition), were representative and distinctive in distinguishing the rice genotypes. The genotype G47 was the best genotype for the environments E1 and E2, whereas genotypes G50 and G85 performed best in E3, with above average value for SPY. G47 was also found to rank among the top five genotypes for YSI. The present study emphasized the importance of environment-specific trait expression under P-deficient conditions, revealing that low P water-limited conditions were best for evaluating dry weight, whereas low P irrigated conditions provided a better platform for assessing single plant yield. These findings are especially important in the context of breeding rice for low-input and climate-stressed regions where nutrient and water scarcity are common.

Conclusion

These results could be deployed in the selection of stable genotypes with higher mean that are specific to the environments (narrow sense adaptability) as well as across environments (broad sense adaptability) that can be effectively used for multi-environment stress (combinations of phosphorus level and water level). Genotype evaluations (winning genotypes) for SPY and DW can also be used as a source to further study the mechanism of P uptake traits under water-limited conditions and to generate sustainable cultivars. In addition, the identification of stable genotypes using the stability parameters (ASV and YSI) would enable the breeders to choose ideal parents that accomplish the various purposes of rice breeding. The crux of the investigation based on both stability analysis and stability parameters identified the best performing genotypes G27 and G47 for DW, G14 and G1 for SPY. These genotypes have enormous potential in sustainable rice breeding programs, allowing the development of geographic region-specific cultivars and climate resilient varieties.

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Authors' contributions

DN and JP acquired funding, conceptualized, carried out the formal analysis, investigation and project administration. DN and VBS framed the methodology. DN and MK drafted the manuscript. AS and VBS reviewed and edited the manuscript. AL and RSN performed data curation and statistical analysis. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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