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Research Article

Stability analyses of red kernel rice landraces of Tamil Nadu based on AMMI and GGE biplot methods

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Abstract
Thirty-four red kernel rice genotypes along with two check varieties were evaluated across three different locations of Tamil Nadu *viz.,* Coimbatore, Paiyur and Aduthurai during *Kharif* 2022 to assess the stability of the genotypes for single plant yield. The AMMI and GGE models were used to study the interaction between the genotypes and the environment in order to select the stable genotypes. Significant differences among the genotypes and the environment revealed the existence of variations among the genotypes and also environmental influence over the genotypes for single plant yield. Considering the overall average single plant yield performances, the genotype *Rangoon samba* recorded the highest single plant yield over the check varieties, while the genotype *Karuthakar* had the lowest single plant yield. The genotypes G24 (*Thooyala*), G25 (*Kothamalli samba*) and G34 (IG74 Check) recorded higher stable single plant yield across locations. Based on AMMI and GGE stability models, these three genotypes were identified to be highly stable over environments with less G x E interaction and these genotypes can be recommended for cultivation across the environments to obtain a higher single plant yield.

Keywords: Red rice, Stability, AMMI, GGE biplot

INTRODUCTION

Rice (*Oryza sativa* L.) is an important cereal crop that serves as the staple food for more than half of the global population. It is the chief source of major carbohydrates and some amount of protein and energy fractions. In traditionally cultivated areas like Asia, coloured rice varieties, including purple, black, red, and shades of brownish-black, have been cultivated and are commonly consumed. During ancient days, people preferred coloured rice due to its medicinal value and taste. Red rice contains a red bran layer that is comprised of anthocyanins and polyphenols, which demonstrate antioxidant properties. This leads to a decrease in the release of sugars into the bloodstream by inhibiting the activity of amylase (Silva *et al.,* 2020; Rajendran and Chandran, 2020). The decrease in amylase activity was associated with phenolic compounds binding to starch molecules and the formation of enzyme-tannin complexes, leading to a reduction in starch digestibility (Quek and Henry 2015). Additionally, red rice genotypes are rich sources of iron, zinc, and protein when compared to white rice and can be exploited for the development of nutrient-rich biofortified rice varieties. Genetic potential of landraces including red kernel genotypes were elucidated by earlier workers for traits such as 3such as resistance to brown plant hoppers (Ptb18, Ptb19, Ptb21 and Ptb33), viral diseases (Nivara) and insect resistance (Ptb 10) (Waghmode *et al.,* 2020). Besides biofortification, these genotypes can be utilized for resistance breeding programs to minimize the risk of biotic and abiotic factors. However, after the green revolution, many high yielding varieties have been introduced and released, which has not only led to a decline in the recognition of coloured rice but has also shifted preference towards white rice. Plant breeders conduct multi-location trials to choose the desirable genotype with greater single plant yield and stable performance. The environment has an influence on genotype performance in different locations. As a result, there is a need to investigate genotype-environment interactions. Various models were used to describe genotype and environmental interactions. Among these, the AMMI (Additive main effect and multiplicative interaction) model and GGE (Genotype and Genotype environment) models are commonly used. With the above information, a study was taken up to identify the stable genotype with desirable single plant yield in red rice.

MATERIALS AND METHODS

A set of 34 red rice genotypes, including 32 landraces and 2 check varieties, collected from the germplasm stock of the Paddy Breeding Station in Coimbatore, were cultivated in three different locations to assess their yield performance during the *Kharif* season of 2022. The experiments were conducted at the Paddy Breeding Station in Coimbatore (E1), the Regional Research Station in Paiyur (E2), and the Tamil Nadu Rice Research Institute in Aduthurai (E3) (**Table 1**). Each field trial was arranged in a randomized block design with two replications. The seedlings were planted with a spacing of 50 cm × 30 cm between the rows and single seedlings per hill in each replication. The single plant yield data were recorded and subjected to further stability analysis based on SES of rice. A combined analysis of variance for genotype and environmental interactions was performed using TNAUSTAT software. Additionally, AMMI analysis (Zobel *et al.,* 1988) and GGE biplot analyses (Yan *et al.,* 2001) were conducted using PB tools software (version 1.3), which was developed by the International Rice Research Institute (IRRI), Philippines.

RESULTS AND DISCUSSION

The results of the pooled ANOVA for the single plant yield trait presented in **Table 2** revealed a significant difference among the genotypes, environments, and genotype × environmental interactions. This interaction effect elucidates that the genotypes responded variably to environmental influences over the single plant yield of red rice genotypes under study. Hence, the prediction of genotype performance could be reliable and feasible based on stability models, suggesting the need to test the genotypes in different environments (Akter *et al.,* 2015).

Based on the mean single plant yield performances across different environments, the genotype *Rangoon samba* was found to record the highest single plant yield (53.78g) while *Karuthakar* had the lowest single plant yield (23.83). Among the two check varieties Jyothi recorded the highest single plant yield (g) (**Table 3**). However, different genotypes displayed inconsistent performance across environments, indicating high variation among the mean yield. Similar types of interaction results were obtained by Sharifi *et al.* (2017). The mean single plant yield performance across all three environments ranged from 21.53g to 56.94g.

The AMMI analysis results further clarify the relative contributions for the first two principal component axes, as represented in **Fig. 1 and 2**. The variance contributions for IPC1 and IPC2 components were 56.9 and 43.1 percent, respectively, and they could explain the GE interaction up to 100 percent. In the biplot, environments were denoted

Table 1. Meteorological data of different locations used in the study

Locations	Code	Latitude	Longitude	Altitude	Average Rainfall	Soil
Coimbatore	E1	11˚ N	77˚ E	427 m MSL	670 mm	Clayey
Paiyur	E2	12˚21'N	78 ˚18' E	490 m MSL	918 mm	Red loamy sand to sandy loam
Aduthurai	E3	11˚ N	79˚ E	19.5 m MSL	1139 mm	Alluvial clay

Table 2. Pooled ANOVA for G×E interactions on single plant yield in 34 red kernel rice genotypes

Source	d.f	SS	MSS	F
Genotype	33	6799.792	206.054*	39.141
Env + G×E	68	1139.740	16.761*	3.183
Environment (linear)	1	119.658	119.658*	22.729
Genotype × Environment (linear)	33	489.287	14.827*	2.816
Error (pooled)	99	1042.360	10.529	

Table 3. Average grain single plant yield of 34 red kernel rice genotypes across environments

	Genotypes	E1(g)	E2(g)	E3(g)	Mean(g)
G1	*Murugankar*	33.26	43.64	35.20	37.36
G2	*Kudai vazhai*	39.66	40.42	32.33	37.47
G3	*Sorna kuruvai*	44.59	52.60	36.75	44.65
G4	*Chinthamani*	55.12	52.55	48.59	52.09
G5	*Malayalathan samba*	27.98	40.09	31.11	33.06
G6	*Shenmolagai*	42.72	42.50	48.37	44.53
G7	*Kaatu ponni*	45.01	48.13	40.79	44.64
G8	*Sornavari*	29.33	25.24	22.62	25.73
G9	*Rama kuruvaikar*	46.76	41.16	44.01	43.97
G10	*Matta kuruvai*	47.50	37.95	39.97	41.80
G11	*Karuthakar*	26.69	23.27	21.53	23.83
G12	*Thillainayagam*	47.06	39.91	39.00	41.99
G13	*Sarapillai samba*	37.16	34.19	26.47	32.61
G14	*Manavari*	23.99	23.58	26.98	24.85
G15	*Arupatham kuruvai*	47.31	53.74	54.84	51.96
G16	*Rangoon samba*	48.32	56.09	56.94	53.78
G17	*Muthuvellai*	51.89	54.85	53.18	53.30
G18	*Chetty samba*	48.49	54.21	47.34	50.01
G19	*Karthigai samba*	41.81	31.18	38.25	37.08
G20	*Palkachaka*	51.00	52.29	42.96	48.75
G21	*Navara*	47.73	51.62	46.92	48.75
G22	*Vasanai seeraga samba*	33.86	41.31	28.81	34.66
G23	*Kuzhiyadichan*	51.79	48.35	53.05	51.06
G24	*Thooyala*	44.63	46.04	46.41	45.69
G25	*Kothamalli samba*	49.06	42.60	34.68	42.11
G26	*Kallukar*	48.85	47.05	48.83	48.24
G27	*Idly*	52.42	42.29	50.95	48.55
G28	*Karuka*	54.27	54.91	50.98	53.39
G29	*Mapillai samba*	51.46	53.24	49.25	51.32
G30	*Vellai chithiraikar*	44.92	49.05	43.76	45.91
G31	*Sivappu kavuni*	36.53	37.41	38.35	37.43
G32	*Karun kuruvai*	48.30	46.93	51.31	48.85
G33	Jyothi	45.22	40.87	41.67	42.59
G34	IG74	45.31	47.03	42.97	45.10
	OVERALL MEAN	43.82	44.01	41.62	43.15

as E1 to E3, while genotypes were represented by numbers 1 to 34. The quadrants were categorized as QI (higher mean with positive IPCA1), QII (higher mean with negative IPCA1), QIII (lower mean with negative IPCA1), and QIV (lower mean with positive IPCA1). When the genotype and environment have the same sign on the PCA1 axis, the interaction will be positive, and if they have opposite signs, their interaction will be negative. Also, genotypes with a PCA1 score near zero show a lesser interaction effect and are considered stable across varied environments. In contrast, genotypes with higher mean single plant yield and greater PCA scores are considered to be specifically adapted to their respective environments (Aryana and Wangiyana, 2016). Based on the results, genotypes G4(*Chinthamani*), G23 (*Kuzhiyadichan*), G27 (*Idly*), G32 (*Karun kuruvai*) and G26 (*Kallukar*) exhibited greater single plant yields with positive IPCA1 scores and G4 is the overall leading genotype. Meanwhile, G16 (*Rangoon samba*), G17 (*Muthuvellai*), G28 (*Karuka*), G15 (*Arupatham kuruvai*) and G29 (*Mapillai samba*) showed greater mean single plant yields with negative IPCA1 scores. Although IPCA1 for genotypes G25 (*Kothamalli samba*), G34 (IG74) and G24 (*Thooyala*) were nearer to zero, suggesting lesser environmental interactions, only

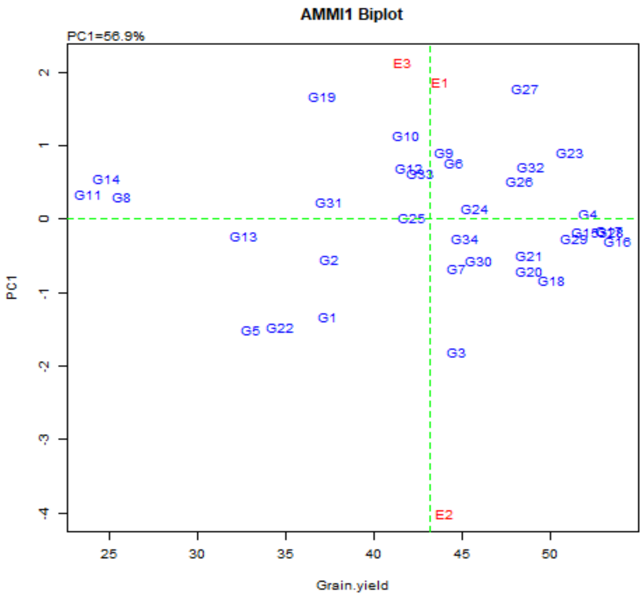

Fig. 1. The AMMI biplot of first principal component axis (PCA 1) vs grain mean single plant yield of 34 red kernal rice genotypes across three environments

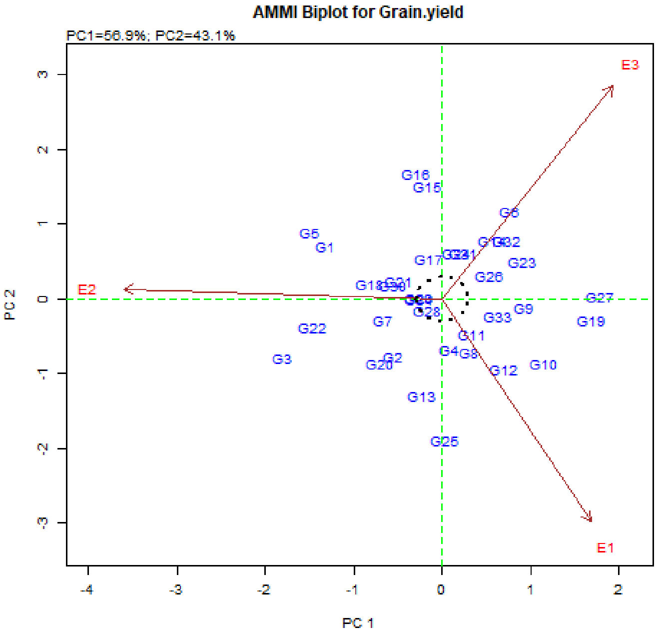

Fig. 2. The AMMI biplot of first principal component axis (PCA 1) *vs* second principal component axis (PCA 2) of 34 red kernal rice genotypes across three environments

G34 (check IG74) and G24 were found to have above-average single plant yield performance.

Unlike AMMI biplot 1, AMMI 2 (**Fig. 2**) biplot didn't provide main effects as it displayed the G × E interaction alone. The genotypes positioned near the origin showed lesser interaction on both axes, and *vice versa*. Therefore, the genotypes placed nearer to the origin were stable compared to the remaining ones. Meanwhile, those genotypes away from the origin, with long spokes, were considered highly interactive genotypes. Based on these criteria, environment E2 exhibited longer spoke, showing strong interaction force, followed by E1 and E3. The genotypes G27 (*Idly*), G25 (*Kothamalli samba*), G3 (*Sorna kuruvai*), G5 (*Malayalathan samba*) and G16 (*Rangoon samba*) were more responsive as they were located away from the origin, while G28 (*Karuka*) and G24 (*Thooyala*) were near the origin, indicating they are less sensitive to environmental forces. Based on AMMI1 and AMMI2, it was concluded that the genotype G24 (45.69 g) showed lesser G × E interaction and was highly stable with greater mean single plant yield. Similar yield stability performance was reported by Lee *et al.* (2023); Kumar and Purushottam (2020), and Kulsum *et al.* (2013) in Rice.

The GGE biplot approach is preferred to AMMI as it provides both genotype (G) and genotype and environmental interactions (GE) components simultaneously, thus helping in mega-environment identification. In **Fig. 3,** the IPC1 and IPC2 components represented relatively 87.4 percent and 7.4 percent of the variance, respectively. The environments E1 and E2, E3 and E2 were found to be positively correlated as they showed acute angles with each other. Longer environmental vector distances demonstrate genotype discrimination. The environments E1 and E3 were identified to be quite close to each other and formed a single group, whereas E1 and E2, E3 and E2 formed two separate groups, indicating variations in location. The longest environmental vector, E3, signified the environment with the highest variability, followed by E2 and E1. This indicated that the Aduthurai environment exhibited greater discriminative potential than the other locations.

Choosing the optimal test environment is essential for effective breeding, ensuring the selection of superior genotypes. The suitability of a test environment is determined by two key factors: its ability to differentiate between genotypes (discriminativeness) and its capacity to accurately represent the characteristics of all other environments under evaluation (representativeness). These factors collectively indicate the ideal nature of the tested environments (Khan *et al.,* 2021). In the present study, the GGE biplot (**Fig. 4**) demonstrated the ‘discriminativeness vs. representativeness’. An environment characterized by a longer vector that makes a smaller angle with the AEA (Average Environmental Coordination) line is optimal for identifying superior genotypes. Therefore, the environment E3, followed by E1, exhibited a small angle along with a longer vector in relation to the AEC abscissa, suggesting that these environments were the ideal testing environments, possessing high representativeness and discriminativeness. However, the environment E2 had discriminativeness but not representativeness.

In **Fig. 5**, a single arrow line represented the average environmental coordination (AEA) abscissa, which indicated greater single plant yield, and the double projectile line in the AEA coordinate displaying greater variation in either direction (Manivannan *et al.,* 2023). An ideal genotype is one that has both a high abscissa (mean single plant yield) and a high ordinate (stability). Therefore, genotypes G16 (*Rangoon samba*), G28 (*Karuka*), G29 (*Mapillai samba*) and G4 (*Chinthamani*), which fell into the center of concentric circles, were identified as ideal in terms of higher- yielding ability and stability compared to the rest of the genotypes. Also, genotypes G24 (*Thooyala*) and G25 (*Kothamalli samba*),

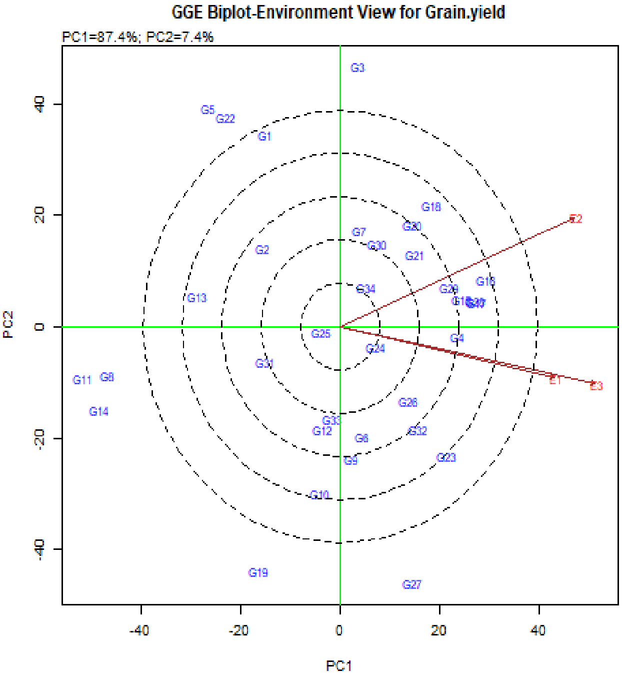

Fig. 3. The GGE biplot - Environment vector view showing the relationships among three environments

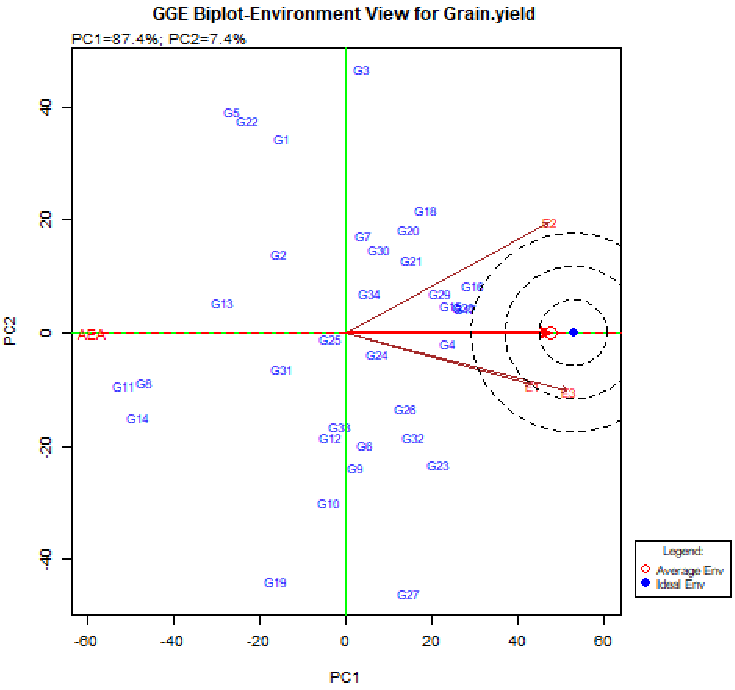

Fig. 4. The GGE biplot - Environment vector view for the grain single plant yield of 34 red kernal rice genotypes

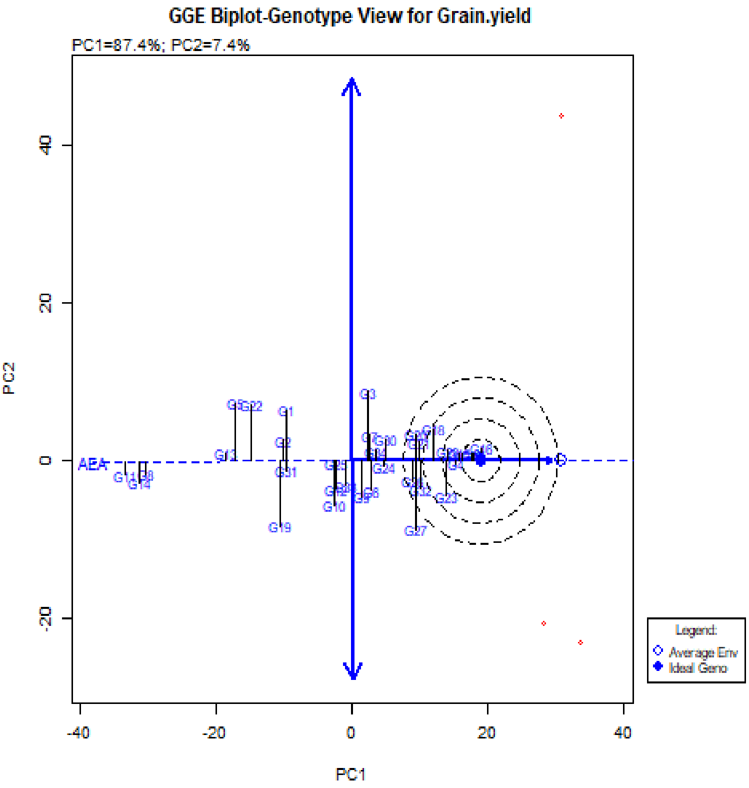

Fig. 5. The GGE biplot of stability and mean performance of 34 red kernal rice genotypes across average environments

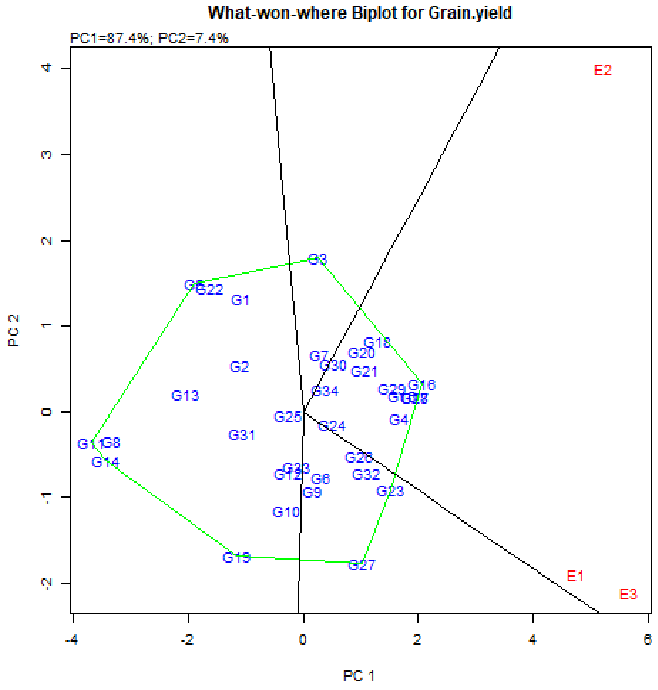

Fig. 6. What-won-where GGE biplot of 34 red kernal rice genotypes across three environments

placed outside the circle, possessed greater mean single plant yield and were found to have less interaction with environmental factors. In addition, G15 (*Arupatham kuruvai*), G17 (*Muthuvellai*) and G26 (*Kallukar*) were located on the next concentric circle and may be regarded as desirable genotypes.

The polygonal view of the represented biplot in **Fig. 6** visualizes the interaction patterns between the environments and genotypes, helping to efficiently interpret the biplot. The vertex genotypes for each sector are considered the best performers for that particular environment. In this study, the vertex genotypes were G16 (*Rangoon samba*), G27 (*Idly*), G19 (*Karthigai samba*), G11 (*Karuthakar*) and G5 (*Malayalathan samba*). The GGE biplot also showed environmental groupings, which further recommend the probable existence of different mega-environments. Chandrashekhar *et al.* (2020) stated that the existence of two or more environments in the same sector resulted in the highest single plant yield of a single genotype in those environments. Similarly, in our study, based on the biplot analysis of three environmental data, all three environments were grouped into a single mega-environment with the winning genotype G16 (*Rangoon samba*).

The study revealed that yield stability was influenced by genotype and environmental interactions, as explained by the first two principal components in the AMMI models. When compared to the check varieties, the genotype *Rangoon samba* produced the highest mean single plant yield (53.78g), whereas the genotype *Karuthakar* single plant yielded the lowest (23.83g). Based on the AMMI and GGE stability models, it can be concluded that the red kernel genotypes G24 (*Thooyala*), G25 (*Kothamalli samba*), and G34 (IG74 check), with average single plant yields of about 45.69g, 42.11g, and 45.10g, respectively, were the stable ones. Hence, these lines may be advanced for further investigation and utilization in rice breeding programmes.

REFERENCES

Akter, A., Hasan, M. J., Kulsum, U., Rahman, M. H., Khatun, M. and Islam, M. R. 2015. GGE biplot analysis for single plant yield stability in multi-environment trials of promising hybrid rice (*Oryza sativa L.*). *Bangladesh Rice Journal*, **19**(1): 1-8. [Cross Ref]

Aryana, I. M. and Wangiyana, W. 2016. Single plant yield performance and adaptation of promising amphibious red rice lines on six growing environments in Lombok, Indonesia. *AGRIVITA, Journal of Agricultural Science*, **38**(1): 40-46. [Cross Ref]

Chandrashekhar, S., Babu, R., Jeyaprakash, P., Umarani, R., Bhuvaneshwari, K. and Manonmani, S. 2020. Single plant yield stability analysis in multi-environment trials of hybrid rice (*Oryza sativa* L.) in Northern India using GGE Biplot Analysis. *Electronic Journal of Plant Breeding*, **11**(02): 665-673. [Cross Ref]

Khan, M.M.H., Rafii, M.Y., Ramlee, S.I., Jusoh, M. and Al

Mamun, M., 2021. AMMI and GGE biplot analysis for single plant yield performance and stability assessment of selected Bambara groundnut (*Vigna subterranea L. Verdc.*) genotypes under the multi-environmental trials (METs). *Scientific reports*, **11**(1): p.22791. [Cross Ref]

Kulsum, M., Hasan, M. J., Akter, A., Rahman, H. and Biswas, P. 2013. Genotype-environment interaction and stability analysis in hybrid rice: an application of additive main effects and multiplicative interaction. *Bangladesh J. Bot.*, **42**(1): 73-81. [Cross Ref]

Kumar, B. D. and Purushottam, AP. 2020. Genotype environment interaction and stability for single plant yield and its components in advanced breeding lines of red rice (*Oryza sativa* L.). *Bangladesh J. Bot.*, **49**(3): 425-435. [Cross Ref]

Lee, S. Y., Lee, H. S., Lee, C. M., Ha, S. K., Park, H. M., Lee, S. M., ... and Mo, Y. 2023. Multi-environment trials and stability analysis for single plant yield-related traits of commercial rice cultivars. *Agriculture*, **13**(2): 256. [Cross Ref]

Manivannan, N., Mahalingam, A., Bharathikumar, K. and Rajalakshmi, K. 2023. Stability analyses using regression and AMMI models for seed single plant yield in blackgram. *Legume Research-An International Journal*, **46**(2): 148-153.

Quek, R. and Henry, C. J. 2015. Influence of polyphenols from lingonberry, cranberry, and red grape on in vitro digestibility of rice. *International Journal of Food Sciences and Nutrition*, **66**(4): 378-382. [Cross Ref]

Rajendran, M. and Chandran, K. R. 2020. Grain dimension, nutrition and nutraceutical properties of black and red varieties of rice in India. *Current Research in Nutrition & Food Science*, **8**(3). [Cross Ref]

Sharifi, P., Aminpanah, H., Erfani, R., Mohaddesi, A. and Abbasian, A. 2017. Evaluation of genotype × environment interaction in rice based on AMMI model in Iran. *Rice science*, **24**(3): 173-180. [Cross Ref]

Silva, A. D. A., Ferreira, M. V. D. S., Lima, R. H. P., Barbosa Junior, J. L., Moreira, L. B. M., and Barbosa, M. I. M. J. 2020. Chemical characterization of the antioxidant, antihyperglycemic and antihypertensive capacities of red rice (*Oryza sativa* L.) whole flour *Revista chilena de nutrición*, **47**(2): 238-246. [Cross Ref]

Waghmode, B.D., Chavan, M.R., Sonone, N.G. and Bhave, S.G., 2020. AMMI biplot analysis for stability of grain single plant yield and single plant yield contributing traits in promising biofortified red kernel genotypes of rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci*, **9**(03): 1820-1832. [Cross Ref]

Yan, W. 2001. GGE biplot—A Windows application for graphical analysis of multienvironment trial data and other types of two-way data. *Agronomy journal*, **93**(5): 1111-1118. [Cross Ref]

Zobel, R. W., Wright, M. J. and Gauch Jr, H. G. 1988. Statistical analysis of a single plant yield trial. *Agronomy journal*, **80**(3): 388-393. [Cross Ref]