Original Research Article

Evaluation of rice genotypes for yield stability and adaptability across multiple environments using AMMI and GGE Biplot analysis

Abstract

The study aimed to identify elite rice genotypes with the highest yield response and broad adaptability, as well as those with specific adaptability to individual or groups of environments. Three different environments were selected for the experimentwith 23 rice genotypes in Dharwad, Malagi, and Sirsi, Karnataka, during the year 2020 (Kharif season). The ANOVA revealed that environments contributed the highest (33.5%) to the total sum of squares, followed by genotypes × environments (21.7%), indicating a major role played by environments and their interactions in realizing final yield.The AMMI 1 analysis identified rice genotypes BA04, BA07, BA10, BA09, and BD07 as highly stable, positioned near the origin of the biplot with smaller ASV and Di values.The AMMI2 model revealed a positive association of genotype BD08 with the Dharwad environment and BD05 with the Sirsi environment, consistent with the recorded grain yield data. The GGE biplot genotype view identified genotype BD08 as the ideal genotype, followed by BA08, with higher mean yield and good stability, while D6-2-2 and BD10 were found to be the most unstable. The GGE biplot environment view showed that Dharwad was the most ideal and discriminating environment, followed by Sirsi, while Malagi was the least discriminating. What-won-where biplot indicated that all the three environments fell into two mega environments. Hence, BD08 was the winning genotype in mega environment 1 consisting of Dharwad and Malagi. While the genotype BD05 was the winner in mega environment 2 i.eSirsi.

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Keywords: AMMI, GGE-biplot, adaptability, ASV, Yield

INTRODUCTION

Rice (*Oryza sativa* L.) is a short dayannual self-pollinated angiosperm within the genus *Oryza*of family Poaceae with chromosome number 2n=2x=24. More than 40 per cent of the world's population depends on rice as one of the major source of calories. Asia is considered as Rice basket of the world, as more than 90 per cent of the rice is produced and consumed in Asia, a region with high population density. To meet the food demand of the growing population and to achieve self-sufficiency of food in the country, the present production levels should be increased by two million tonnes every year. Globally, rice is cultivated in an area of 167.2 mha with an annual production of 769.6mtand productivity of 4,600Kg ha^{-1}. Rice is grown on 43.77 mhawith an annual production of 117.47mtand productivity of 2,570 Kg ha^{-1} in India. In Karnataka it has the area of 1.24mha and production of 3.54 mt with a productivity of 2,670Kg ha^{-1}(INDIA STAT 2019-20).India occupied second place in the rice area however, its productivity per unit area is low in India. So, efforts are needed to increase rice productivity along with stability of performance under diverse environments. A genotype with smaller variance among different environments is known as stable. If a genotype exhibiting mean performance at different environments equal to its overall mean over different environments is known as stable genotype. Stability in

Comment [Ec1]: What is this? Metric ton or million ton? Please specify it performance of a genotype over a wide range of environmental conditions is assessed for a genotype to be released for cultivation along with high yield. Yield is a complex quantitative trait and highly influenced by the G X E interactions. Developing a stable genotype with high yield along with good grain quality is the main aim of a plant breeder. A specific genotype may not show the same phenotypic expression under all environments and different genotypes exhibit different expression to a specific environment.

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Phenotypic value of a trait such as yield has a dependency on the genetic architecture of the plant or the genotype (G), the growing environment (E) and an array of GE interactions (GEI) (Malosetti*et al.,* 2013). Out of these three terms (G, E and GEI), GEI plays an important role in the variable performance of the same genotype in different environments. Presence of strong GEI leads to cross over interactions or reversal of genotype ranks for trait variable such as yield in different environment (Yan and Tinker, 2006). Therefore, GEI imposes an impediment which complicates the selection of elite stable genotypes with wide adaptability & superior performance across a range of environments (Malosetti*et al.,* 2013). This complexity makes it challenging to select stable and adaptable genotypes with consistent performance across diverse environments. Thus, understanding GEI patterns is crucial for effectively evaluating crop varieties which are adaptable and stable across different environments and seasons (Simmonds, 1991; Malosetti*et al.,* 2013; Yan and Tinker, 2006). Various methods and models, such as joint regression regression (Finlay and Wilkinson, 1963, Eberhart and Russell, 1966; Perkins and Jinks, 1968), AMMI, and GGEBiplot analysis, have been developed to study GEI patterns. In our work, we have used AMMI regression (Finlay and Wilkinson, 1963, Eberhart and Russell, 1966; Perkins and Jinks, 1968) and GGEBiplot (Yan and Tinker, 2006) tools to investigate how GEI influences the adaptability and stability of grain yield in rice genotypes cultivated in different agroclimatic conditions in Karnataka, India.

The AMMI analysis is a statistical method used in analysing multi-location trials data, particularly in studying genotype by environment interactions (GEI). It integrates ANOVA and principal component analysis (PCA) to examine the main effects of genotypes and environments, as well as the residual multiplicative interactions between them (Gauch and Zobel, 1996; Zobel *et al.*1988 and Crossa *et al.* 1990). It facilitates the simultaneous assessment of each genotype and environment contribution to GEI, aiding in identifying elite genotypes with broad adaptability or zoning genotypes based on specific adaptability. Through graphical biplot representations, AMMI simplifies the classification of genotypes and environments, offering advantages in agricultural research and experimental design (Kempton, 1984; Silveira *et al.*, 2013).Similarly, in GGEBiplot analysis, which relies on singular value decomposition (SVD) as a mathematical technique (Pearson, 1901; Yan, 2002), both genotype (G) and genotype by environment (GE) contributions are visually depicted in a biplot. This method, pioneered by Yan and Kang (2003) and further developed by Yan and Tinker (2006), aids in evaluating genotypes and test environments concurrently, enhancing insights into genetic performance and environmental suitability.

This study aimed to examine the Multitrait Environment Trait (MET) data regarding yield for 23 rice genotypes cultivated across three distinct environments (Dharwad, Malagi, and Sirsi) in Karnataka during the *Kharif* season of 2020. The objectives included pinpointing elite genotypes with the highest yield response and broad adaptability, identifying genotypes with specific adaptability to individual or groups of environments, and characterizing the three test environments by analysing their interrelationships and the efficacy of different environments in discriminating and representing genotypes based on yield response using tools like AMMI and GGEBiplot.

MATERIALS AND METHODS

The present investigation was carried out on 23 genotypes consists of 20 advanced breeding lines and 3 parents of rice during the kharif season 2020. The list of genotypes used in the present study is provided in Table 1 along with their parentage and source of the material. All the 23 rice genotypes were sown during *kharif* 2020 in three locations i.e., Sirsi (Zone IX- Hilly zone-high rainfall area, transplanted), Malagi (Zone IX Hilly zone - low rainfall area, direct seeded) and Dharwad (Zone VIII- Northern transition zone, direct seeded) of Karnataka State. Experiment layout was a Completely Randomized Block Design consisted of 23 genotypes with two replications, each experimental plot comprised of five rows of five metres length, with a spacing of 20 x 15 cm between rows and plants respectively. The field was ploughed until fine tilth of soil was obtained in case of Dharwad and Malagi, puddled in cases of Sirsi. The crop was raised under rainfed conditions during *kharif* 2020. Then 25 days old seedlings were transplanted with the application of recommended dose of fertilizers.

Table 1. List of 20 advanced breeding lines used under present investigation along with parents

Genotypes	Pedigree/Parentage	Genotypes	Pedigree/Parentage	Developed / Identified
BA – 1	BPT 5204/ ANTHRASALI-1	BD – 1	BPT 5204/DODDIGA -07	GPB, AICRIP (VC) ARS (Paddy), Banavasi Road, Sirsi -581 401, (UASD)
BA – 2	BPT 5204/ ANTHRASALI-4	BD – 1	BPT 5204/DODDIGA -08	
BA – 3	BPT 5204/ ANTHRASALI-7	BD – 3	BPT 5204/DODDIGA -10	
BA – 4	BPT 5204/ ANTHRASALI-8	BD – 4	BPT 5204/DODDIGA -11	
BA – 5	BPT 5204/ ANTHRASALI-9	BD – 5	BPT 5204/DODDIGA -12	
BA – 6	BPT 5204/ ANTHRASALI-27	BD – 6	BPT 5204/DODDIGA -13	
BA – 7	BPT 5204/ ANTHRASALI-31	BD – 7	BPT 5204/DODDIGA -15	
BA – 8	BPT 5204/ ANTHRASALI-32	BD – 8	BPT 5204/DODDIGA -16	
BA – 9	BPT 5204/ ANTHRASALI-34	BD – 9	BPT 5204/DODDIGA -36	
BA - 10	BPT 5204/ ANTHRASALI-36	BD – 10	BPT 5204/DODDIGA -41	
BPT5204	GEB-24 x TN1 x Mahsuri			ARS, Bapatla, ANGRAU
D6-2-2	Local Selection from Doddiga			ARS Mugad, UASD
A-67	Local Selection from Anthrasali			ARS Mugad, UASD

Analysis of variance (ANOVA)

The average grain yield performance of each genotype during kharif 2020 was calculated and was used for individual-environment wise analysis of variance (ANOVA). Multi-environmental trial data for grain yield were pooled after testing the homogeneity of error variance across three different test sites using Bartlett test (Bartlett, 1937) which yielded a significant chi square statistic. A combined ANOVA analysis was performed after transformation of average grain yield data of each genotype at different locations to know the contribution of genotype (G), environment (E) and their interaction (GEI) using R-scripts by considering the effect of genotypes and environment as fixed and random, respectively, using following statistical model:$Y_{gsb}=\mu+E_{sb}+G_g+E_s+GE_{gs}+\varepsilon_{gsb}$, Where, Y_{gsb} : Grainyield response of gth genotype in sth environment andbth block, μ: Grand mean, E_{sb}: Effect of block withinthe sth environment and bth block, Gg: Effect of gthgenotype, Es: Effect of sth environment, GE_{gs}: Effectdue to the interaction of gth genotype and sthenvironment, and ε_{gsb} : Experimental error.

AMMI Analysis and GGEBiplot

All statistical analyses were conducted in the statistical software R (R Core Team) version 4.3.1. The "metan" package (Olivoto and Lúcio, 2020) was employed to conduct the analysis of variance, AMMIanalysis of variance (George and Lundy, 2019), genotype plus genotype by environment (GGE) biplot analysis (Team,2012) stability statistical analysis, and weighted average of absolute scores (Koutroubas and Ntanos, 2003). The AMMI analysis was conducted based on the following mathematical formula:

$$y_{ij}^{N} = \mu + g_i + e_j + \Sigma\lambda_k Y_{ik}\alpha_{jk} + \varepsilon_{ij}$$

where y_{ij} is the yield of the ith genotype in the jth environment, N is the number of PCI in the AMMImodel, μis the overall mean of the genotypes, and g_i and e_j are the genotype and environment diversions from the overall mean. λ_k is the eigenvalue of the PCA axis k, $Y_{ik}$and α_{jk} are the GE-PCs scores for axis k, and Σij is the remaining value. Meanwhile, the GGEmodelwasconsidered by the following formula:

$$y_{ij}^{N} = \mu + e_j + \Sigma\lambda_k Y_{ik}\alpha_{jk} + \varepsilon_{ij}$$

RESULTS AND DISCUSSION

Results of individual environment-wise analysis of variance revealed significant differences among genotypes for grain yield response at all the locations (Table 2a). Among all the environments, higher yield performance has been recorded in Dharwad environment while poor yield was recorded for genotypes in Malagi environment (Table 3a). Further, to know the significance of interaction between genotypes and environments, a combined analysis of variance was performed using grain yield response data which revealed that genotypes (G), environments (E), and GE interaction (GEI) contributed 17.3%, 33.5% and 21.7%, respectively, to the total sum of squares (TSS) (Table 2b). Combined ANOVA analysis revealed that environmental factor (E) followed by GEI contributed to the maximum variability in the yield performance of genotypes which may be attributed to the diverse nature of three environments representing different zones of Karnataka and differential sensitivities of different genotypes to the different test environments, respectively. High degree of GEI is in line with the variable yield performance of genotypes including cross-over interactions or reversal of genotype ranking in three different test environments.

AMMI ANALYSIS

To deepen the understanding of GE interaction (GEI), an AMMI analysis was performed which retained two interaction principal component axes (IPCAs) namely IPCA1, and IPCA2 explaining 86.9% and 13.1% of total sum of squares due to interactions, respectively (Table 2c). Cumulatively, both IPCA1 and IPCA2 captured most of the structural patterns of SSGxE representing 100 % of total interaction variations in AMMI analysis and were statistically significant ($P \leq 0.001$) (Table 2c). Therefore, IPCA1 and IPCA2 were used for construction of AMMI1 and AMMI2 biplots.

Table 2a: Individual environment wise analysis of variance

Source of Variation		M.S of Environments		
	D.F	**Dharwad**	**Malagi**	**Sirsi**
Replication	1	189811.8ns	1122490.6ns	18610452.6ns
Genotypes	22	7871607.5**	150727.3**	1386764.8**
Error	22	42367.6	34962.1	374719.5
Mean (kg/ha)		5084.2	2368.1	3214.3

**Significant at P≤ 0.001, NS: Non-significant, DF: Degrees of freedom

Table 2b: Combined analysis of variance for grain yield response

Source	DF	Sum Sq	Mean Sq	Explained % of TSS
Environment (E)	2	177708999.2	88854500**	33.54
Replication (Environment)	3	19922755.1	6640918ns	3.76
Genotypes (G)	22	91834298.4	4174286**	17.33
G x E	44	115165896.8	2617407**	21.73
Error	66	9945086.5	150683.1	

**Significant at P≤ 0.001, NS: Non-significant, DF: Degrees of freedom, TSS: Total Sum of Squares

Table 2c: Analysis of variance and partitioning of multiplicative interaction component by AMMI method.

Source	DF	Sum Sq	Mean Sq	Explained % of ISS*	Cumulative %
Environment (E)	2	177708999.2	88854500**		
Genotypes (G)	22	91834298.4	4174286**		
G x E	44	115165896.8	2617407**		
PC1	23	100125509.5	4353283**	86.9	86.9
PC2	21	15040387.35	716208.9**	13.1	100
Error	66	9945086.5	150683.1		

**Significant at P ≤ 0.001, *ISS: Interaction sum of squares

AMMI biplot analysis

AMMI1 biplot model is a graphical representation of AMMI analysis in which main effects are represented in the abscissa while IPCA1 scores of genotypes and environments, simultaneously represented on the ordinate to describe the interaction effects. Displacement along the abscissa and along the ordinate is an indicative of the differences in the main effects and variation in the interaction effects, respectively (Bose *et al.*, 2014). The score and sign of IPCA1 reflect the magnitude of the contribution of both varieties and environments to GEI, where scores near zero are characteristic of stability, whereas higher score (absolute value) considered as unstable and specific adapted to environment. Based on AMMI1 biplot model (Fig. 1a), out of 23 genotypes tested BD08, BA08 and BD09 are generally showed high yield above the mean yield of the varieties with IPCA1 score. This indicated that these varieties are high yielding in high potential areas.Also, it was found that genotypes BA04, BA07, BA10, BA09 and BD07were highly stable genotypes as they were positioned near to the origin of the biplot with smaller ASV values of 3.7, 11.8, 15.2,26.7 and 30.5, respectively and relatively smaller Di values (Fig. 1a and 1b, Table 3b). Similar findings have been reported in literature in rice crop (Bose *et al.,* 2014 and Akter *et al.,* 2016). Genotypes with smaller AMMI Stability Values (ASVs) and AMMI stability index (ASI) values are generally stable genotypes (Bose *et al.,* 2014). Therefore, these genotypes are least influenced by the environments due to their smaller degree of interactions with the environment. In contrast, D6-2-2, BPT 5204, BA01 and BD01 genotypes were the most unstable as they were distantly positioned from the biplot origin and hence, they seemed to have environment-specific adaptations (Fig. 1a and 1b, Table 3b). Similar findings have been reported in sugarcane crop (Silveira *et al.,* 2013) and in hybrid rice (Akter *et al.,* 2016).

Overall, among all the genotypes, BD07 had the highest yield of 4141.0 kg/ha with moderately smaller ASV and Di value of 30.5 and 3.9, respectively, was adjudged as the best genotypes followed by BA09 due to their higher yield response with wider adaptability among all the genotypes (Fig. 1a, 1c, Table 3a and 3b). All the three environments like Dharwad, Malagi and Sirsi environments were highly responsive to the GEI. All these findings are in agreement with their respective IPCA1 scores as depicted in AMMI1 biplot (Fig. 1a). Among the environments, Dharwad environment had witnessed a large positive IPCA1 score and relatively high above average yield compared to other environments while, Malagienvironment had the lowest mean yield with high negative IPCA1 score. These findings are consistent with the prevalence of favourable and unfavourable climatic regimesat Dharwad and Malagi, respectively.

Comment [Ec3]: Add supporting previous finding

Table 3a: Mean yield performance (kg/ha) of each genotype in 3 different environments of Karnataka

Genotypes	Dharwad	Malagi	Sirsi
A 67	4054.84	2019.92	3503.86
BA01	2244.91	2019.92	3266.37
BA02	4424.83	2119.92	3416.87
BA03	2674.90	2319.91	2753.39
BA04	4899.81	2329.91	2909.89
BA05	6697.24	3079.88	3003.38
BA06	4107.34	2359.91	2223.41
BA07	5024.80	2699.89	3053.38
BA08	8027.19	2479.90	3594.36
BA09	5979.77	2439.90	4231.83
BA10	5387.29	2599.90	4013.34
BD01	2269.91	2599.90	2439.90
BD02	6999.73	2199.91	2092.92
BD03	6969.73	2039.92	2927.89
BD04	6579.74	2079.92	2999.88
BD05	4074.84	2079.92	4736.82
BD06	6892.23	2639.90	4133.34

BD07	5969.77	2519.90	3933.35
BD08	8534.67	2679.90	3693.36
BD09	7337.21	2399.91	3796.35
BD10	2774.89	2319.91	1929.92
BPT 5204	2412.41	2399.91	3942.85
D6-2-2	2599.90	2039.92	1333.45
Mean	5084.25	2368.16	3214.35

Table 3b: Ranking of genotypes based on yield response and stability

Genotype	ASI	YSI	ASV	ASV_R	Y_R	Y (kg/ha)
A 67	8.4	24	64.6	8	16	3192.8
BA01	22.7	40	173.6	20	20	2510.4
BA02	5.4	22	41.2	7	15	3320.5
BA03	18.2	35	139.7	16	19	2582.7
BA04	0.5	15	3.7	1	14	3379.8
BA05	11.5	15	88.1	10	5	4260.1
BA06	4.5	24	34.3	6	18	2896.8
BA07	1.5	15	11.8	2	13	3592.6
BA08	22.8	23	174.5	21	2	4700.4
BA09	3.5	10	26.7	4	6	4217.1
BA10	1.9	11	15.2	3	8	4000.1
BD01	21.6	40	165.7	19	21	2436.5
BD02	21.6	29	165.1	18	11	3764.1
BD03	18.5	26	141.7	17	9	3979.1
BD04	14.7	24	112.9	14	10	3886.5
BD05	13.9	24	106.4	12	12	3630.5
BD06	10.3	12	79.3	9	3	4555.1
BD07	3.9	12	30.5	5	7	4141.0
BD08	25.8	24	197.5	23	1	4969.3
BD09	16.5	19	126.4	15	4	4511.1
BD10	14.2	35	108.4	13	22	2341.5
BPT 5204	25.7	39	196.8	22	17	2918.3
D6-2-2	12.1	34	92.8	11	23	1991.0

Closer positioning of genotypes andenvironments to each other in biplots has been reportedto have positive association between them, which helpsin agronomic zoning of genotypes for specificenvironments (Silveira *et al.,* 2013). In AMMI2 biplot(Fig. 1b), we found the closer association between BD08 genotype with Dharwad environment,BD10 genotype with Malagienvironment and, BD05 genotype with Sirsienvironment. All these findingsare in congruence with the recorded yield in differentenvironment in terms of high yield winning genotypes withspecific adaptation for a particular environment. OurAMMI2 model was clearly explained thepositiveassociation BD08 genotype withDharwad environment and BD05genotype with Sirsi environment, which wereconsistent with the recorded yield data. In the AMMI2 biplot, environmental vectors are joined to the origin by sidelines. The locations with short spokes do not exert strong interactive forces and had strong contribution to the stability of the variety, while those with long spokes have strong interaction. From the Fig. 1b environments like Dharwad, Malagi and Sirsi had the long spokes which indicated the high discriminating ability of these environments. The distances from the biplot origin are indicative of the amount of interaction that was exhibited by genotypes over environments or environments over genotypes (Peyman *et al.*, 2017 and Yan and Kang, 2002).

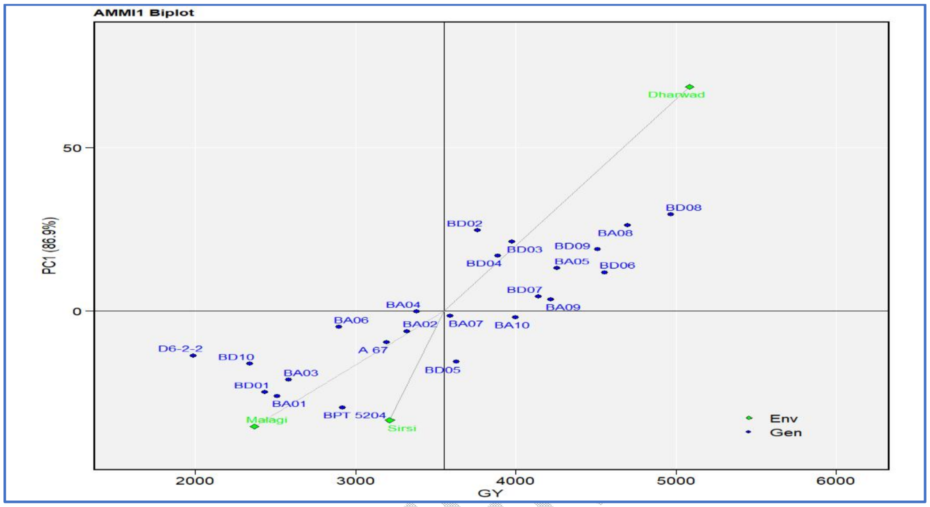

Fig. 1a: AMMI 1 biplot showing the means of genotypes and environments for grain yield against their respective IPCA1 scores.

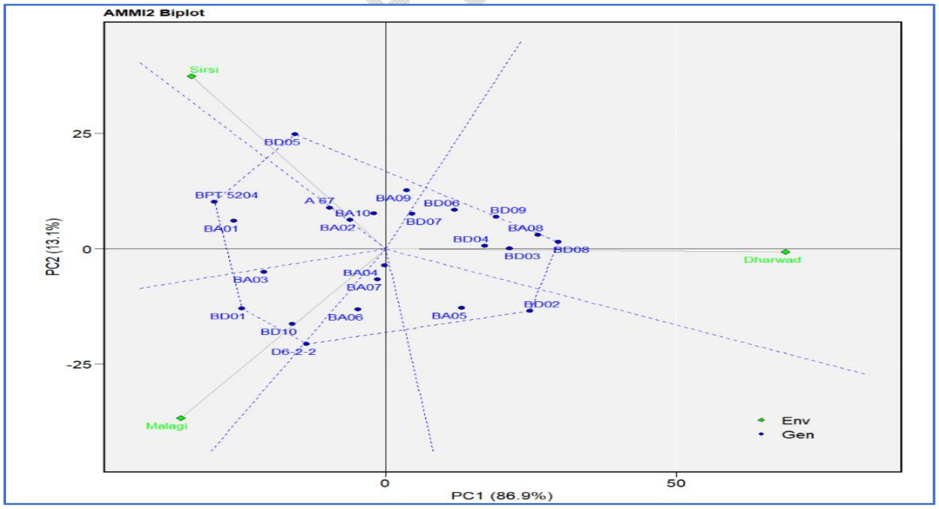

Fig 1b:AMMI2 biplot showing interaction of IPCA2 against IPCA1 scores for grain yield of 23 rice genotypes in three environments

GGEBiplot analysis

In addition to AMMI, GGE biplot analysis was performed to evaluate both genotypes and environments in order to select the elite stable genotypes, to identify the best responsive and adaptive genotypes for each environments or group of environments through the ranking of the genotypes and "Which-Won-Where" pattern analysis and to dissect the interrelationship among the different test environments in terms of their discriminatory power and representativeness ability in terms of graphical visualization for better interpretation. GGEBiplot explained 98.6% of total G and GE interaction effects for the yield data by its two principal components (PC1 and PC2). PC1 explained 85.78% while PC2 accounted for the 12.82% of total G and GE interaction effects.

Mean Grain Yield and Stability Performance

The magnitude of interaction can be visualized for each genotype and each environment using IPCA1 vs. mean yield and IPCA1 vs. IPCA2 biplot model (Yan and Hunt, 1998). "An ideal genotype is one with large PC1 scores representing the high yielding ability and small PC2 scores representing high stability" (Yan *et al.,* 2000). The concentric circles help to rank the genotype based on their distances to the ideal genotype, and the genotypes evaluated in multi-environmental trials, shifts in the relative ranking of genotype by environment interaction occur (Alam *et al.*, 2014; Parihar *et al.*, 2017; Mohan *et al.*, 2021, Siddi *et al.*, 2022). Thus, Fig 2a and 2b indicated that genotype BD08was identified as ideal genotype followed by BA08 with higher mean yield and good stability whereas, D6-2-2and BD10 were found to be most unstable. Similarly, among environments Dharwad was identifies as the best location for realizing higher grain yields. Further, the genotype BD09 was identified as highly stable with the least dispersion from AEA axis and also recorded reasonably good mean grain yield. These results are in close correspondence with the results reported by Mohan *et al.* (2021) and Siddi *et al.* (2022).

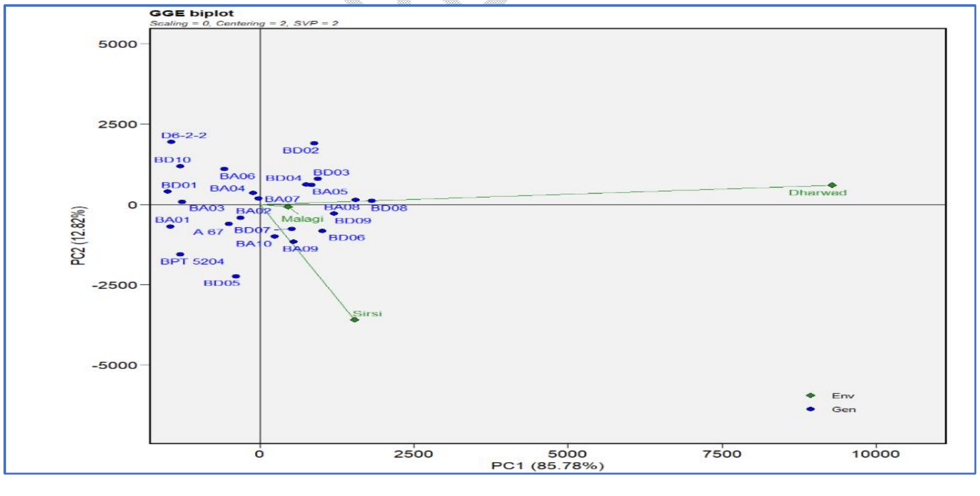

Fig 2a: GGE Biplot for grain yield of rice

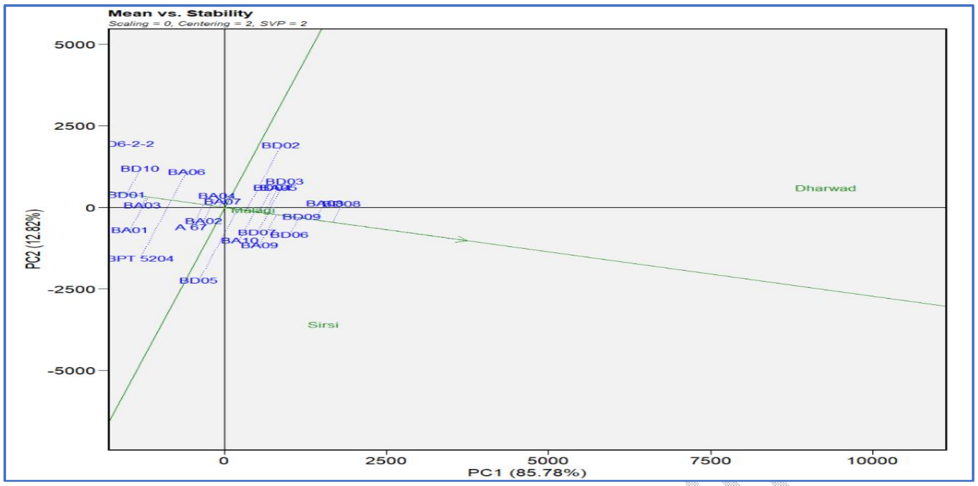

Fig 2b: GGE biplot of stability and mean performance of genotypes across average environments.

Ranking of genotypes

An ideal genotype is characterized by high average performance and a high level of stability across various environments. Such a genotype is situated at a point in the positive direction of the Average Environment Axis (AEA), aligning with the centre of concentric circles indicating "absolute stability." Additionally, it has the longest genotypic vector length, indicating superior mean genotypic performance, from the biplot origin compared to all other genotypes (Yan and Tinker, 2006).

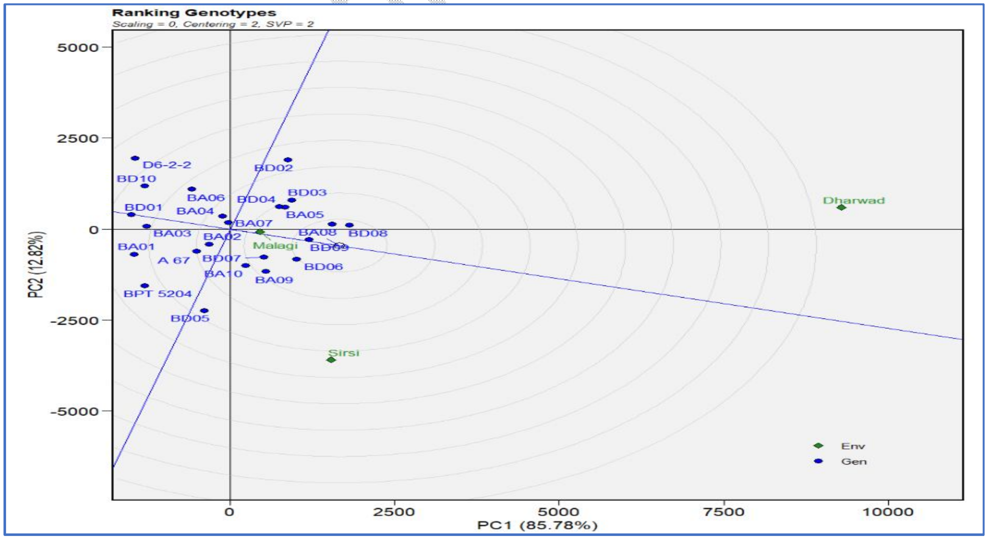

Fig 3: Ranking of genotypes based on mean grain yield and stability across environments

In the present study, BD08, BD09 and BA08 were found to be an ideal genotype which were positioned in the centre of concentric circles compared to other genotypes among 23 genotypes studied (Fig.3).

The genotypes like D6-2-2, BD10, BD01, BA01, BA03 and BPT 5204 are showing poor performance with low mean yield across all the environments. These are unstable genotypes and are not suitable for further crop improvement.

Environment evaluation

Discriminating power and representativeness behaviour of environments

The angles between environment vectors in biplots reveal their relationships, with the cosine of these angles indicating their correlation. An acute angle between two environment vectors signifies a positive correlation, an obtuse angle signifies a negative correlation, and a right angle indicates no correlation. Environments exhibit complex interrelationships. The ideal environment is represented by a small circle at the centre of the concentric rings.

The concentric circle in the GGE biplot are used to visualize the magnitude of the length of environment vector that is proportional to the standard deviation within the concerned environment. Environment vector length has the discriminating power, viz. longer the vector length more the discriminating ability between genotype and small angle between environment vector and AEA line make it the best representative environment for discriminating the genotype. In the present study (Fig.4a) Dharwad was found to be the most discriminating environment followed by Sirsi whereas, Malagi were found to be least discriminating. AEA which passes through the average environment containing average coordinates of all the test environments, and the biplot origin. A test environment having smaller angle with the AEA is the most representative environment compared to other test environments (Yan and Tinker, 2006). Thus, Dharwad and Malagi is showing smaller angle so, these two environments are considered as most representative compared to Sirsi. Similarly, Zewdu *et al.* (2020) found that environments E6, E1, E3, and E2 were ideal, having short vectors, while environments E4 and E5 had long spokes, indicating their high discriminating ability. Likewise, Kripa *et al.* (2020) noted that biplot analysis is the most effective interpretive tool for AMMI models. They identified that environments E6 and E5 had short vectors, suggesting they did not exert strong interactive forces, whereas environments E1, E2, E3, and E4, with long vectors, were more differentiating.

Ranking of environment

An ideal test environment is defined by its high discriminating ability and high degree of representativeness. It is located on the Average Environment Axis (AEA) in the positive direction, indicating it is the "most representative," and its distance to the biplot origin equals the longest vector of all environments, making it the "most informative" (Yan and Tinker, 2006) and sits at the centre of the concentric circles. In our analysis, no environment was identified as the ideal test environment. However, the Dharwad environment was relatively closer to the ideal test environment compared to others (Fig. 4b). Therefore, the Dharwad environment is suitable for selecting genotypes with general adaptability across all test environments. Conversely, Sirsi and Malagi environments are less suitable for selecting such genotypes, as they are positioned far from the ideal test environment.

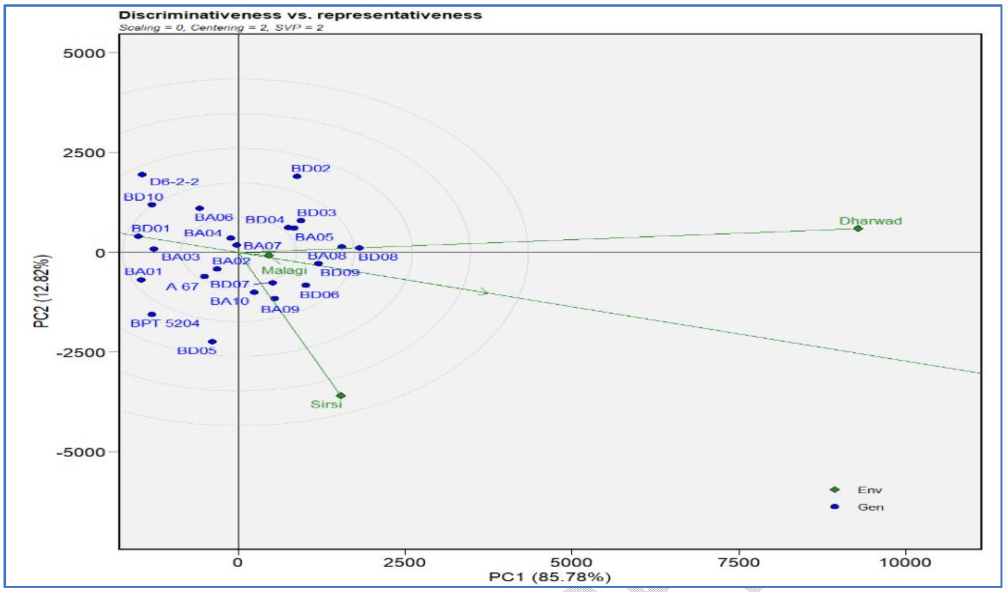

Fig 4a:Discriminating ability and representativeness behaviour of environments.

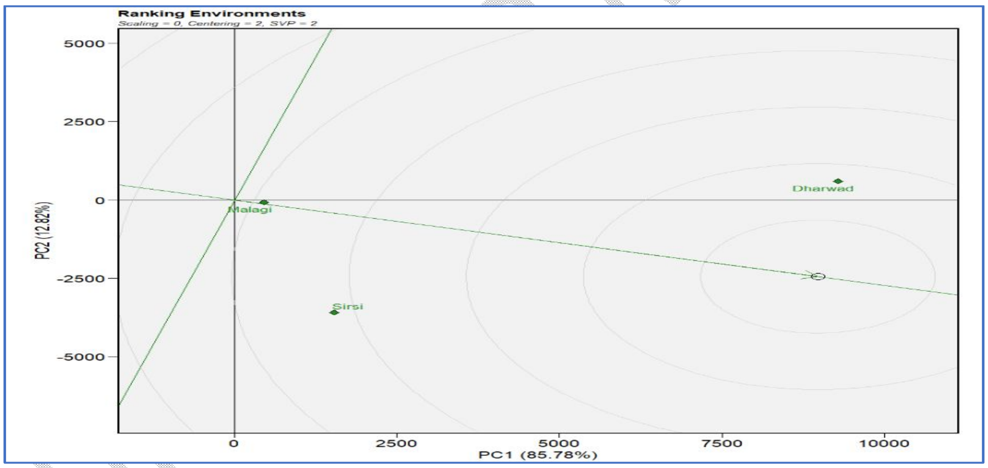

Fig 4b: Ranking of environments w.r.t an ideal environment

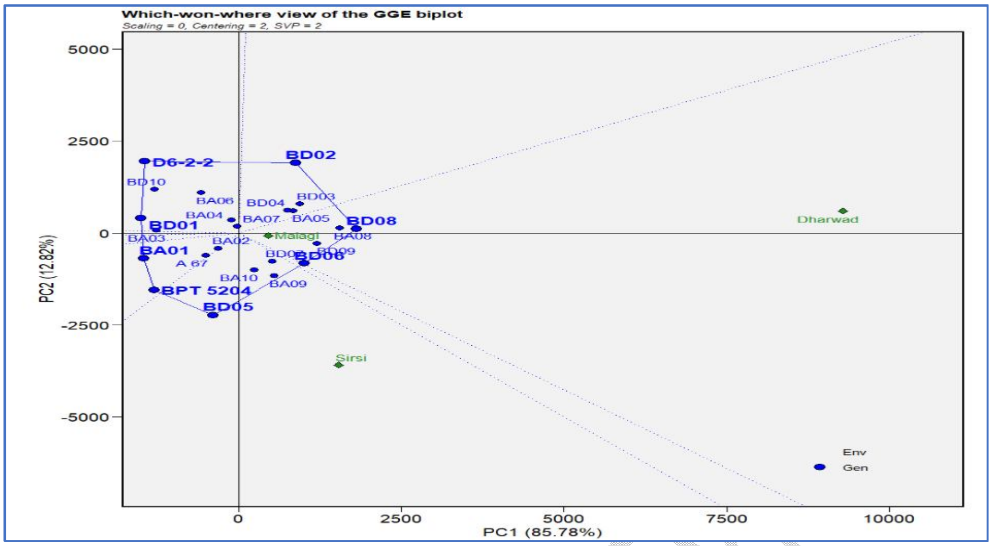

Fig 4c: Which-Won-Where GGE biplot for yield

Which-Won-Where Biplot

"The what-won-where view of the GGE bi-plot (Yan and Hunt, 2020) is the best model for multi-environment trial data for grouping the environments and also identifying best performing genotype in each". "Many researchers found this biplot intriguing, as it graphically addresses important concepts such as crossover GE, mega environment differentiation, and specific adaptation. A polygon is first drawn on genotypes that are furthest from the biplot origin so that all other genotypes are contained within the polygon. The perpendicular lines to each side of the polygon are drawn, starting from the biplot origin" (Yan and Tinker, 2006). It divided the biplot into seven sections and three environments fall into two mega environments viz., Dharwad and Sirsi for grain yield (Fig. 3). Genotypes located on the vertices of the polygon performs either the best or the poorest in one or more environments. Vertex genotype BD08 was the winning genotype in mega environment 1 consisting of Dharwad and Malagi. While the genotype BD05 was the winner in mega environment 2 *i.e*Sirsi (Fig. 4c). It concludes that "different cultivars should be selected and deployed for each different environment". Similar results were reported by the rice workers viz., Akter *et al.*(2015), Rukmini Devi *et al.*(2020), Lingaiah *et al.*(2020), Mohan *et al.*(2021) and Siddi *et al.*(2022). Whereas other vertex genotypes BD02, D6-2-2, BD01, BA01 and BPT 5204 fall in separate groups with poor performance in all the environments.

Conclusion

This study indicated the significance difference exhibited among the tested genotypes and its interaction with environments for grain yield. This is an indication of a wide variability among genotypes. The GGE and AMMI biplots are useful techniques that were able to effectively detect the existence of a significant amount of GE interaction between23upland rice genotypes across three environments. As AMMI model revealed that genotypes like BA04, BA07, BA10, BA09 and BD07 are the stable genotypes across the environments. GGE biplotmodel revealed genotypesBD08 and BA08 outperformed amongthe tested genotypes and can be used for specific siteproduction. In variety selection, genotypes with high meanyield and high stability is preferred. As a result, genotypes BD08, BA08, BA09, BD07 and BD09 gave high yieldand good stability across environments and can berecommended for testing sites.

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