



Stability analysis of short duration rice genotypes in Telangana using AMMI and GGE Bi-plot models

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ABSTRACT

In order to identify stable short duration rice genotypes across different agro-climatic zones in Telangana state, Additive Main Effects and Multiplicative Interaction Models (AMMI) and GGE Bi-plot analyses was performed. Analysis of variance clearly revealed that genotypes contributed highest (34.57 %) followed by environments (32.31 %) and genotype environment interaction (17.10 %) in total sum of squares indicating very greater role played by genotypes, environments and their interactions in realizing final grain yield. AMMI analysis revealed that rice genotypes viz., KNM 2305 (G12), KNM 2307 (G16) and JGL 20776 (G9) were recorded higher mean grain yield with positive interactive principal component analysis 1 (IPCA1) scores whereas, KNM 2307 (G16) and RNR 23595 (G5) were plotted near to zero IPCA1 axis indicating relatively more stable performance across locations. However, the GGE Bi-plot genotype view depicts that the genotypes viz., RDR 1188 (G6) and KNM 2305 (G12) were known as highly unsteady across locations. Among environments, Rudrur (E4), Kunaram (E2) and Rajendranagar (E5) locations were identified as relatively ideal to realize good yields whereas Jagtial (E1), Kampasagar (E3) and Warangal (E6) locations were poor and most discriminating. Among the six locations, the performance of genotypes was relatively similar in Kunaram (E2), Kampasagar (E3) and Rudrur (E4), Warangal (E6) though they belong to different agro-climatic zones of Telangana state, whereas Jagtial (E1) location seems to be little divergent. Further, KNM 2305 (G12) and US 314 (G17) were performed better at Jagtial (E1) and Rajendranagar (E5) while MTU 1010 (G8) was found to have good performance in Rudrur (E4) and Warangal (E6) locations. The results conclude that KNM 2305 was high yielder but found to be unstable across locations whereas KNM 2307 (G16) and KPS 6251 (G15) were identified as good with reasonably higher grain yield and stable performance over locations.

Introduction

Rice (*Oryza sativa* L.) is a staple crop for more than half of the world's population, supplying roughly 20% of dietary energy requirements. Rice is grown on roughly 116 million hectares throughout the world every year, yielding over 700 million tons (Anonymous, 2019). Rice is one of the most predominantly grown crops in Telangana state during rainy and post rainy seasons. Rice is being grown in an area of 41.89 lakh hectares with the production and productivity of 218 lakh tons and 5215 kg/ha, respectively (Anonymous, 2021). In view of delayed release of canal irrigation water, existence of mostly light textures soils and varied temperatures, short duration varieties (115 to 125 days) suits well in the region. Rice productivity must be increased to address the problems of higher cost of cultivation, population expansion, climate change and limited arable land (Cordero, 2020). Rice is grown in a range of environments, including temperate, subtropical and tropical climates. Several yield-related parameters influence rice yield, including panicle number, spikelet number per panicle and grain weight. Previous research has shown that, in addition to genotypic effect, environmental effects and genotype environment interaction (GEI) have a significant impact on rice production (Balakrishnan *et al.*, 2016). The adaptation response of various genotypes to each environmental condition is represented by GEI (Olivoto *et al.*, 2019). To correctly evaluate the yield performance of different rice genotypes, GEI must be identified in specific or broad environments (Kempton *et al.*, 2012). Wide adaptation is defined as the ability to produce stable high yields across diverse environments (Gauch *et al.*, 2008; Yan, 2016) and a major goal in rice breeding programs is to achieve stability of yield performance in different agricultural environments (Xu *et al.*, 2020).

The AMMI model has recently been popular for interpreting the $G \times E$ interaction, with a biplot often used to interpret the AMMI result, with yield on one axis and principal component analysis (PCA) scores on the other, or two PCA axes scores on two axes (Crossa *et al.*, 1990). Regular analysis of variance for additive effects is combined with PCA for multiplicative structure within the interaction in the AMMI model. AMMI also provides a visual representation of trends in the

data through a biplot that makes use of the first interaction principal component axis (IPCA1) and the mean yields of both the genotypes and environments (Nachit *et al.*, 1992). To enhance the selection method, it is important to take advantage of the possibility of finding genotypes that are less influenced by $G \times E$ interaction (GEI). Genotypic main effect plus GEI (GGE) biplot analysis is a statistical method that has been widely employed to detect the GEI of target traits in multiple environments. GGE biplots graphically indicate the GEI of multiple environmental trials in a way that facilitates the evaluation of varieties. GGE biplots are constructed using first and second symmetrically scaled principal components derived from singular value decomposition of environment-centered multiple environment trial data, facilitating genotype evaluation and mega-environment delineation (Yan *et al.*, 2000). Under this context, present investigation was carried out to identify stable short duration genotypes suitable for Telangana state through AMMI and GGE biplot models.

Material and Methods

The investigation was carried out on eighteen short duration genotypes of rice (Table 1). The experiment was conducted at six locations of Telangana comprising different agro-climatic zones as detailed in Table 2 during *kharif* 2017. Crop was raised by sowing the nursery during first fortnight of July and 25-30 days age seedlings were planted in main field under irrigated farming system at all the six locations. The spacing adopted was 15×15 cm between rows and hills with plot size of 10-15 m² replicated thrice in Randomized Complete Block Design. Crop was well managed by adopting recommended agronomic package and suitable plant protection measures to realize potential yields. Grain yield was recorded in each plot and expressed in kg/ha. Statistical analyses like, combined ANOVA and AMMI analysis were conducted to understand the pattern of genotypic performance across the locations. ANOVA was used to partition genotypic deviations, environmental deviations and $G \times E$ deviations from the total variation.

Table 1: Details of 18 rice genotypes used in the study along with parentage

Code	Genotypes	Parentage	Source	Duration (Days)	Grain Type
G1	JGL 24497	JGL 17004 × NLR 3042	RARS, Jagtial, PJTSAU	115	Long Slender
G2	RDR 1162	JGL 11727 × JGL 17004	RS&RRS, Rudrur, PJTSAU	115	Medium Slender
G3	RNR 15048	MTU 1010 × JGL 3855	RRC, Rajendranagar, PJTSAU	125	Short Slender
G4	JGLH 169	CMS 64A × JMBR2	RARS, Jagtial, PJTSAU	120	Long Slender
G5	RNR 23595	Yamini × BM 71	RRC, Rajendranagar, PJTSAU	120	Medium Slender
G6	RDR 1188	JGL 17653 × RP 2421	RS&RRS, Rudrur, PJTSAU	110	Long Slender
G7	IBT R9	MTU 1010 × 2/GPP2	RRC, Rajendranagar, PJTSAU	120	Long Slender
G8	MTU 1010	Varietal Check	RARS, Maruteru, ANGRAU	115	Long Slender
G9	JGL 20776	MTU 1010 × JGL 13595	RARS, Jagtial, PJTSAU	120	Long Bold
G10	WGL 1119	WGL 32100 × RP-1 (B 95-1 × Abhaya)	RARS, Warangal, PJTSAU,	120	Medium Slender
G11	RNR 26241	WGL 505 × RNR 15048	RRC, Rajendranagar, PJTSAU	125	Medium Slender
G12	KNM 2305	JGL 11470 × Himalaya 741	ARS, Kunaram, PJTSAU	120	Long Bold
G13	IBT R4	Tellahamsa × 2/GPP2	IBT, Rajendranagar, PJTSAU	115	Long Slender
G14	WGL 962	BPT 5204 × GEB 24// BPT 5204 × Shatabdi	RARS, Warangal, PJTSAU,	125	Medium Slender
G15	KPS 6251	MTU 1010 × Chittimutyalu	ARS, Kampasagar, PJTSAU	115	Medium Slender
G16	KNM 2307	JGL 11727 × JGL 17004	ARS, Kunaram, PJTSAU	115	Long Bold
G17	US 314	Hybrid check	US Agriseeds Pvt. Ltd	115	Medium Bold
G18	IBT R8	Tellahamsa × 2/GPP2// Tellahamsa × 2/NLR145	IBT, Rajendranagar, PJTSAU	115	Long Slender

Further, multiplication effect analysis (AMMI) was used to partition GE deviations into different interaction principal component axes (IPCA). Genstat 15th Edition (GenStat, 2012) and P B Tools (IRRI, 2014) were used to analyze the AMMI and GGE biplot for eighteen genotypes.

The AMMI model used in the stability analysis is as follows:

$$Y_{ij} = \mu + g_i + e_j + \sum \lambda_k a_{ik} \gamma_{jk} + \varepsilon_{ij}$$

where

Y_{ij} = mean of a trait of i^{th} genotype in j^{th} environment;

μ = the grand mean;

g_i = genotypic effect;

e_j = environmental effect;

λ_k = eigen value of Interaction Principal Components Axes (IPCA) k ;

a_{ik} = eigen vector of genotype i for PC k ;

γ_{jk} = eigen vector for environment j for PC k ;

ε_{ij} = error associated with genotype i in environment j .

The GGE biplots were generated to predict the which-won-where pattern and to identify the genotypes best suited across environments as well as for specific environment.

Results and Discussion

An experiment was formulated to identify stable rice genotypes across different agro-climatic zones of Telangana state through Bi-plot analyses. The mean grain yield ranged varyingly from 2121 kg/ha to 9140 kg/ha (Table 3). Mean grain yield across locations showed that the KNM 2305 (6803 kg/ha) was recorded highest mean grain yield followed by MTU 1010 (6443 kg/ha) and KNM 2307 (6393 kg/ha), whereas RDR 1188 (3744 kg/ha) was the poorest yielder. Likewise, among locations, Jagtial (E1) was found to be ideal location with highest mean grain yield (6451 kg/ha) across genotypes followed by Kammasagar (E3) (6262 kg/ha), whereas Warangal (E6) was poorest location with least mean grain yield (4324 kg/ha). Genotypic performance of rice and other crops in relation to different environments has been estimated by worker like Xing *et al.* (2021), Amiri *et al.* (2015), Rakshit *et al.* (2012) and Mohammadi *et al.* (2012) all of them identified varieties suitable for a defined production system.

Analysis of variance

Analysis of variance elucidated that significant difference existed among genotypes, environments and genotypes \times environment interactions and witnessed the considerable influence of environments and interaction of genotypes with environments in expression of the grain yield (Table 4). Further, genotypes contributed highest (34.57 %) in total sum of squares followed by environments (32.31%) and genotype environment interaction (17.10 %) revealing that genetic architecture of the genotypes play greater role apart from environment and their interaction in manifestation of the trait. Xing *et al.* (2021) reported similar finding that the grain yield was more influenced by genotype, genotype \times environment interactions and environment with contribution of 35.6, 37.1 and 16.5 percent of total variance, respectively.

AMMI analysis

The significant $G \times E$ interactions were further partitioned into five significant principal component axes explaining 34.4, 31.3, 18.1, 12.2 and 4.0 of GEI variation, respectively (Table 5). The first two interaction PCAs accounted for maximum of 65.7 %. Similarly, Das *et al.* (2010)

and Umma *et al.* (2013) earlier reported that first two PCAs explained the maximum GEI. Zewdu *et al.* (2020) had similar findings that the two IPCA axes together accounted for 69.17% of the genotype by environment interaction mean squares. The IPCA score of a genotype in the AMMI analysis is a signal of the adaptability over environments and relationship between genotypes and environments (Gauch *et al.*, 1996 and Mahalingam *et al.*, 2006).

The mean grain yield and IPCA1 (interaction effects) were plotted on x and y axes, respectively for the construction of AMMI1 Bi-plot (Fig. 1). A genotype with IPCA1 score near to zero is considered to be steadier across environments. In opposition, a genotype with high IPCA1 score is highly variable among environments (Rao *et al.*, 2020). The genotypes, KNM 2305 (G12), KNM 2307 (G16) and JGL 20776 (G9) were recorded higher mean grain yield with positive IPCA1 scores (Fig. 1). The genotypes, MTU 1010 (G8), KPS 6251 (G15) and JGL 24497 (G1) had high mean grain yield and found more adaptable to Kammasagar (E3) location. However, KNM 2307 (G16) and RNR 23595 (G5) were plotted near to zero IPCA1 axis indicating that these genotypes are relatively more stable across locations. The remaining genotypes had less than the mean grain yield and found specific adaptation to few tested environments. Similarly, Balakrishnan *et al.* (2016) exhibited G8, G2, G3, G14, G11 and check Swarna (G15) had high yield with high main (additive) effects showing positive PC1 score.

GGE Bi-plot analysis

GGE Bi-plot offers effective assessment of genotypes and allow for complete understanding of the target and test atmospheres through various IPCAs. The genotype \times environment interactions were partitioned into six significant interaction PCAs and 81.2% variance was explained by first two IPCAs together (Table 6). Similarly, Zewdu *et al.* (2020) partitioned the genotype \times environment interactions into six rays which divided the biplot into seven sections.

GGE Bi-plot genotype view depicts that the genotype WGL 1119 (G10) was inside the first concentric circle and found to be more stable across environments (Fig. 2). However, the genotype RDR 1188 (G6) and KNM 2305 (G12) were known as highly unsteady across locations with longest

Table 2: Details of six locations in Telangana state used for evaluation of genotypes

Code	Location name	District	Agroclimatic Zone	Latitude (N)	Longitude (E)	Altitude (m)	Normal cultivated area (ha)
E1	Regional Agricultural Research Station, Polasa, Jagtial	Jagtial	Northern Telangana	18.49°	78.56°	243.4	85584
E2	Agricultural Research Station, Kunaram	Peddapally	Northern Telangana	18.32°	79.32°	231.0	78969
E3	Agricultural Research Station, Kampasagar	Nalgonda	Southern Telangana	16.59°	79.28°	152.0	139410
E4	Regional Sugarcane and Rice Research Station, Rudrur	Nizamabad	Northern Telangana	18.01°	85.01°	404.0	143778
E5	Rice Research Center, ARI, Rajendranagar	Rangareddy	Southern Telangana	17.33°	78.40°	586.6	21773
E6	Regional Agricultural Research Station, Warangal	Warangal	Central Telangana	15.50°	79.28°	268.5	47237

Table 3: Mean grain yield (kg/ha) of 18 rice genotypes across six locations

Code	Details of Genotype/ Environment	Environments						Mean across locations
		E1	E2	E3	E4	E5	E6	
G1	JGL 24497	7269	5096	7318	7052	5725	5181	6274
G2	RDR 1162	5153	5565	5761	6012	5461	5378	5555
G3	RNR 15048	6164	3903	5865	5110	4851	3575	4911
G4	JGLH 169	6568	3093	5134	4568	6144	3760	4878
G5	RNR 23595	6283	4003	6538	5617	6719	4553	5619
G6	RDR 1188	4551	3608	3587	4294	4301	2121	3744
G7	IBT R9	4332	3942	6242	5511	4792	3821	4773
G8	MTU 1010	6958	5004	7511	6362	6554	6267	6443
G9	JGL 20776	7824	5434	7668	5044	6424	5649	6340
G10	WGL 1119	6257	4870	6691	4921	5755	5035	5588
G11	RNR 26241	7269	3868	6087	5454	4655	2868	5033
G12	KNM 2305	9140	6378	7842	6082	6479	4895	6803
G13	IBT R4	5668	3522	5118	4951	3285	2894	4240
G14	WGL 962	5834	3847	5764	5670	5336	3592	5007
G15	KPS 6251	6998	5040	7893	6287	6729	5128	6346
G16	KNM 2307	7454	5223	7754	6541	6313	5074	6393
G17	US 314	7097	4528	5096	5343	7442	4179	5614
G18	IBT R8	5298	3924	4845	4303	5575	3864	4635
	Mean across genotypes	6451	4492	6262	5507	5697	4324	
	SE (m)±	CD (0.05)						
Genotypes	204.02	568.18						
Environments	122.07	340.12						

Table 4: Analysis of variance for grain yield over 18 rice genotypes and 6 locations

Source of variation	df	SS	MMS	P Value	% Explained
Treatments	107	548843832	5129382**	0.0000	
Block	12	17040747	1420062*	0.0017	
Genotypes	17	225912375	13288963**	0.0000	34.57
Environments	5	211160152	42232030**	0.0000	32.31
Genotypes x Environments	85	111771306	1314957**	0.0000	17.10
Residuals	45	38302099	851158**	0.0099	
Error	204	104742731	513445		
Total	323	670627310	2076246		

*Significant at $P \leq 0.05$, **Significant at $P \leq 0.01$ **Table 5: Partitioning of genotype x environment interaction with AMMI model for grain yield in rice**

Source of variation	df	SS	MMS	% Explained
Varieties x Environments	85	111771306	1314957**	
IPCA1	21	25652925	1221568**	34.4
IPCA2	19	23326828	1227728**	31.3
IPCA3	17	13478753	792868**	18.1
IPCA4	15	9101972	606798**	12.2
IPCA5	13	2954188	227245**	4

Significant at $P \leq 0.01$ **Table 6: Partitioning of genotype x environment interaction with GGE model for grain yield in rice

Source of variation	df	SS	MMS	% Explained
IPCA1	21	157418863	7496136**	69.9
IPCA2	19	25446919	1339312**	11.3
IPCA3	17	22943248	1349603**	10.2
IPCA4	15	9109878	607325**	4
IPCA5	13	7251639	557818**	3.2
IPCA6	11	2953691	268517**	1.3

**Significant at $P \leq 0.01$

vector from origin. GGE Bi-plot environment view depicted that Rudrur (E4), Kunaram (E2) and Rajendranagar (E5) locations were relatively ideal indicating that they were poor and most discriminating. The lengths of environment vectors from the biplot origin are proportional to the standard deviation within each environment and thus represent the discriminating ability of the environments (Yan and Tinkler, 2006). Similarly, Zewdu *et al.* (2020) revealed that E6, E1, E3 and E2 with short environmental vectors, did not exert strong interactive forces and had a strong contribution to the stability of the genotype, while those with long spokes (E4 and E5) indicate the high discriminating ability of these environments. The angle between the environment line and the average-environment axis (AEA), which passes through the average environments and biplot origin,

(Fig. 3) with less vector length from origin. Conversely, Jagtial (E1), Kampasagar (E3) and Warangal (E6) locations had longest vectors and indicates the representativeness of each environment. Depending on direction of environments dispersion, more similarities were noticed among Kunaram (E2), Kampasagar (E3) and Rudrur (E4), Warangal (E6) whereas Jagtial (E1) location seems to be little divergent. Yan and Kang (2003) reported that the distances from the biplot origin were indicative of the amount of interaction exhibited by genotypes over environments or environments over genotypes.

Mean performance and stability of genotypes

The genotype KNM 2307 (G16) was identified as ideal genotype followed by KPS 6251 (G15) and

Table 7: Mean grain yield and principal component scores of AMMI and GGE for rice genotypes

Genotype/ Environment code	Details of Genotype/ Environment	Mean Grain yield (kg/ha)	Interaction Principal Component Scores			
			AMMI		GGE	
			IPCA1	IPCA2	IPCA1	IPCA2
G1	JGL 24497	6274	-5.36	-15.25	-1941.49	464.22
G2	RDR 1162	5555	-30.55	4.99	-37.31	1748.46
G3	RNR 15048	4911	3.54	-7.34	1282.78	-203.52
G4	JGLH 169	4878	16.49	18.99	1367.74	-1140.52
G5	RNR 23595	5619	-1.27	13.00	-399.70	17.04
G6	RDR 1188	3744	-1.50	8.25	4385.11	-185.79
G7	IBT R9	4773	-26.19	-6.54	1698.61	1544.45
G8	MTU 1010	6443	-12.32	1.79	-2469.68	843.33
G9	JGL 20776	6340	8.75	-1.22	-2416.91	-348.56
G10	WGL 1119	5588	-6.47	1.98	-453.31	437.48
G11	RNR 26241	5033	21.54	-18.90	973.95	-1208.47
G12	KNM 2305	6803	24.76	-13.86	-3383.38	-1259.27
G13	IBT R4	4240	0.88	-21.85	2938.26	-25.48
G14	WGL 962	5007	-2.42	-1.02	1176.14	82.22
G15	KPS 6251	6346	-3.43	-2.63	-2235.62	324.95
G16	KNM 2307	6393	0.80	-9.94	-2325.29	105.94
G17	US 314	5614	16.32	31.63	-196.06	-1222.04
G18	IBT R8	4635	-3.55	17.91	2036.17	25.54
E1	Jagtial	6451	49.36	-10.49	-0.45	-0.78
E2	Kunaram	4492	-9.38	-4.48	-0.34	0.16
E3	Kampasagar	6262	-5.15	-28.69	-0.53	0.20
E4	Rudrur	5507	-17.15	-13.81	-0.27	0.28
E5	Hyderabad	5697	8.19	46.34	-0.36	-0.22
E6	Warangal	4324	-25.87	11.14	-0.45	0.45

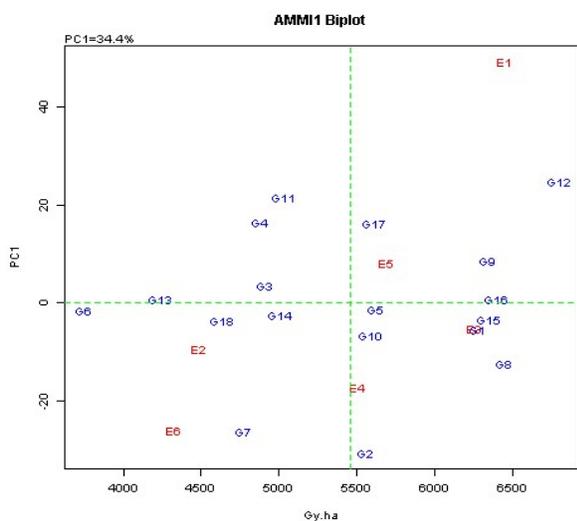


Figure 1: Means of genotypes (G) and environments (E) against their respective IPCA1 scores for grain yield in rice using AMMI-1 model.

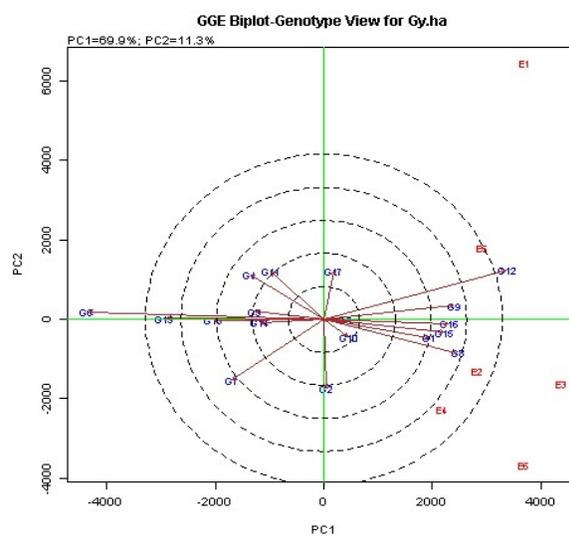


Figure 2: GGE biplot genotype view for grain yield in rice.

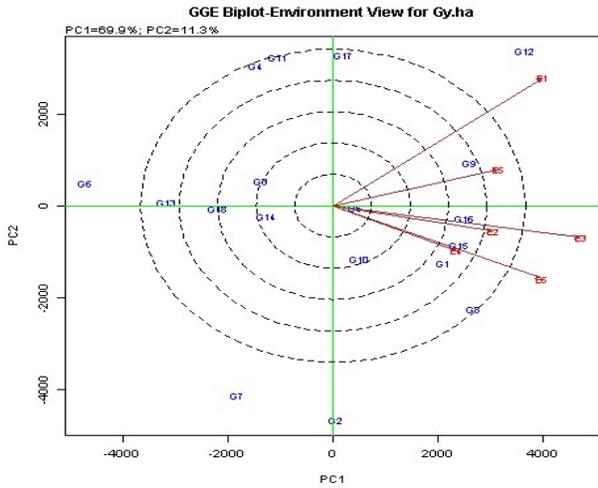


Figure 3: GGE biplot environment view for grain yield in rice.

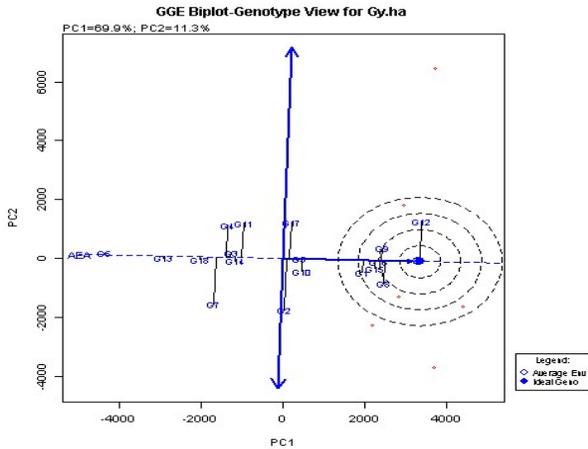


Figure 4: GGE biplot genotype view with AEA axis for grain yield in rice.

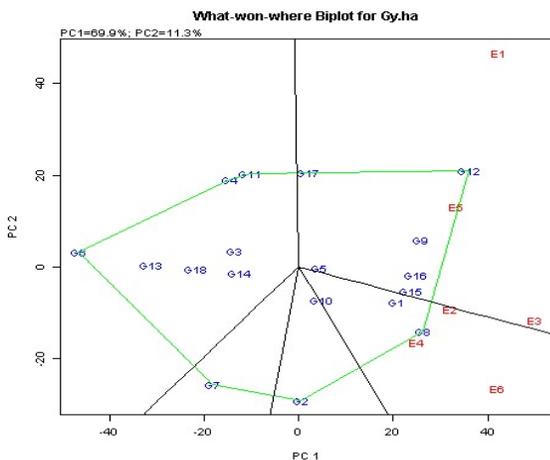


Figure 5: What-won-where biplot for 18 genotypes and six locations in rice.

JGL 20776 (G9) with relatively higher mean yield and good stability. Though the genotype, KNM 2305 (G12) had highest mean grain yield, found to be relatively not stable across locations falling out of the 2nd concentric circle (Table 7 & Fig. 4). Further, the genotypes RDR 1162 (G2) and US 314 (G17) were found to be unstable across locations with more dispersion from AEA axis and also recorded relatively less mean grain yield. Xing *et al.* (2021) reported that Suwon-2010 (temperate) and IRRI-2010 (tropical) locations were the most representative for thousand grain weight and grain yield, respectively.

What-won-where Bi-plot

What-won-where view of the GGE Bi-plot is the best model for multi-environment data for classifying the environments and also to select best performing genotype in each (Yan *et al.*, 2000). Genotypes located on the vertices of the polygon performs either the best or the poorest in one or more environments. The biplot view classified that KNM 2305 (G12) and US 314 (G17) were the best performing genotypes in Jagtial (E1) and Rajendranagar (E5) locations (Fig. 5). Similarly, the genotypes MTU 1010 (G8) was found to have good performance in Rudrur (E4) and Warangal (E6) locations. Earlier Chandramohan *et al.* (2021) found that the hybrids, JGLH 337 (G3), JGLH 275 (G11) at Jagtial (E1) whereas RNRH 98 (G7), JGLH 373 (G12) at Warangal (E6) locations were performed well while the hybrids, RNRH 99 (G4) and Bio 799 (G5) fall in separate group with poor performance in many of the locations. Comparably, Mary *et al.* (2019) reported that the biplot for yield during the wet season showed that G10 was the winner genotype in E4 and G7 in E8 and E9.

Conclusion

The results clearly conclude that expression of the grain yield was affected significantly by environments and interaction of genotypes with environments. The genotypes, KNM 2305 (G12), KNM 2307 (G16) and JGL 20776 (G9) were recorded higher mean grain yield with positive IPCA1 scores whereas KNM 2307 (G16) and RNR 23595 (G5) were plotted near to zero IPCA1 axis indicating that these genotypes were relatively more stable across locations. However, GGE Bi-plot genotype view depicts that the genotypes *viz.*, RDR 1188 (G6) and KNM 2305 (G12) were known

as highly unsteady across locations with longest vector from origin. Further, among environments Rudrur (E4), Kunaram (E2) and Rajendranagar (E5) locations were relatively identified as ideal to realize good yield whereas Jagtial (E1), Kampasagar (E3) and Warangal (E6) locations were poor and most discriminating. Among the six locations, more similarities were depicted among Kunaram (E2), Kampasagar (E3) and Rudrur (E4), Warangal (E6) though they belong to different agro-climatic zones of Telangana state and hence among them, two locations could be eliminated as testing centres to save resources. What-won-where Bi-plot clearly demonstrated that the genotypes, KNM 2305 (G12) and US 314 (G17) were performed better at Jagtial (E1) and Rajendranagar (E5) while MTU 1010 (G8) was found to have good performance in Rudrur (E4) and Warangal

(E6) locations. Considering grain yield and stability over locations, KNM 2307 (G16) and KPS 6251 (G15) were identified as promising and need to be advanced for testing at farmers' fields to enable for commercial release.

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Conflict of interest

The authors declare that they have no conflict of interest.

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