



Stability Analysis of Rice Hybrids for Grain Yield in Telangana through AMMI and GGE Bi-plot Model

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Citation: Mohan et al., 2021. Stability Analysis of Rice Hybrids for Grain Yield in Telangana through AMMI and GGE Bi-plot Model. *International Journal of Bio-resource and Stress Management* 2021, 12(6), 687-695. [HTTPS://DOI.ORG/10.23910/1.2021.2575](https://doi.org/10.23910/1.2021.2575).

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

Acknowledgement: The authors are obliged to PJTSAU and ICAR-IIRR, Hyderabad, India for funding under AICRIP programme to different Rice Research Centers of Telangana, India.

Abstract

An investigation was carried out on fifteen rice genotypes to identify stable rice hybrids across six different agroclimatic zones in Telangana state using AMMI and GGE bi-plot analyses during July to November, 2020. Analysis of variance clearly showed that environments contributed highest (65.47%) in total sum of squares followed by genotypes \times environments (21.19%) indicating very greater role played by environments and their interactions in realizing final grain yield. AMMI analysis revealed that rice hybrids viz., RNRH 39 (G6), 27P31 (G14) and RNRH 15 (G1) were recorded higher mean grain yield with positive IPCA1 scores. The hybrids, JGLH 275 (G11) and JGLH 365 (G15) were plotted near to zero IPCA1 axis indicating that these hybrids are relatively more stable across locations. GGE bi-plot genotype view depicts that the hybrids, JGLH 365 (G15) and US 314 (G8) were inside the first concentric circle and found to be more stable across environments. GGE bi-plot environment view showed that Rudrur (E4) location was the most ideal environment. However, Warangal (E6) and Jagtial (E1) locations were poor and most discriminating. Depending on dispersion of environments in different directions, six locations were partitioned into three mega zones as first zone comprised of four locations viz., Kunaram (E2), Kampasagar (E3), Rudrur (E4) and Rajendranagar (E5) whereas highly dispersed Jagtial (E1) and Warangal (E6) were identified as two separate mega environments. The bi-plot view identified that 27P31 (G14), JGL 24423 (G2) and RNRH 39 (G6) were the best performing genotypes in first zone comprising four locations.

Keywords: Rice hybrids, GE interaction, GGE biplot, AMMI, stability

1. Introduction

Rice (*Oryza sativa* L.) is the staple food for a large proportion of the world's population. Globally rice is cultivated in an area of 162.06 million ha, with 755.47 million t paddy production and 4.66 t ha⁻¹ productivity (Anonymous, 2019a). In India, rice has occupied an area of 43.79 million ha with 116.42 million t production and 2659 kg ha⁻¹ productivity (Anonymous, 2019b). Whereas in Telangana state, rice is grown in an area of 2.01 million ha with a production of 7.43 million t and an average

Article History

RECEIVED on 20th August 2021

RECEIVED in revised form on 28th November 2021

ACCEPTED in final form on 24th December 2021



productivity of 3694 kg ha⁻¹ (Indiastat, 2020).

Human selection and adaptation to diverse environments has resulted in numerous cultivars. Although more than 900 rice varieties have been released in India, many of them were no longer cultivated within a few years due to inconsistent performance in diverse environments and only a few varieties with stable performance continue under cultivation after 15 to 20 years of their release (Nitiprasad et al., 2015). Nevertheless, there is still a large gap between production and demand. To meet this challenge, there is a need to develop rice varieties with higher stability. In order to meet the domestic demand of the increasing population, the expected requirement of rice in India would be 130 and 168 million t with reduced cultivated area of only 42 and 40 million ha by 2030 and 2050, respectively (Gupta et al., 2020). Since the yield of high yielding varieties (HYVs) of rice is plateauing, it is rather difficult to achieve this target with the present day inbred varieties. Among the limited options available, hybrid rice production is the only practically proven, sustainable and eco-friendly technology currently available for stepping up rice production significantly. Hybrid rice has clearly shown a yield advantage of 1-1.5 t ha⁻¹ (20 to 30%) over conventionally bred modern varieties. Therefore, the introduction of hybrids and popularization of their production technology are feasible and readily adoptable to achieve targeted production.

So far in our country, an excellent progress has been made in hybrid rice research and development. As a result of concerted efforts over the last three decades, 127 hybrids have been released for commercial cultivation in different rice growing states across the country. Among these, 38 hybrids have been developed by the public sector, while remaining 89 are developed by the private sector (Anonymous, 2021). During the year, 2020, hybrid rice was planted in an area of 3.5 million ha and more than 80% of the total hybrid rice area is in the states of Uttar Pradesh, Jharkhand, Chhattisgarh, Madhya Pradesh, Odisha and Haryana. It's a matter of concern to note that area under hybrid rice remains @ 3 million ha since 2016 and major reason would be inadequate yield heterosis and unstable performance across environments.

Telangana state is being identified as seed hub of the country and producing huge quantities of quality seed in different crops. Especially in hybrid rice, about 80 percent of the total hybrid rice seed production of India is taken up in the three districts of Telangana viz., Warangal, Medak, and Karimnagar (Nirmala, 2015). Though the Telangana state is producing large quantities of hybrid seed, very limited area is being grown with hybrids in rice due to their poor stability and low heterosis over available inbred varieties.

Yield is a complex character that depends on a number of other characters and is highly influenced by genetic and environmental factors. Identification of superior genotypes through GEI became complicated for a range of environments to determine their true genetic potential. Various statistical

methods/ models (parametric and non-parametric), concepts, and definitions of stability have been described over the years by many researchers (Becker and Leon, 1988; Crossa et al., 1990).

The additive main effects and multiplicative interaction (AMMI) model proposed by Gauch (1992) is a multivariate method widely used for GEI investigation. This method uses analysis of variance (ANOVA) and principal component analysis (PCA) to compute additive main effects and interaction effects, respectively. It refers to double-centered PCA. The effectiveness of AMMI procedure has been clearly demonstrated by various authors using multi-location data (Yan and Hunt, 2001). The GGE biplot model uses one-way ANOVA for estimating genotypic effects and G×E interactions. In AMMI, G×E effects is plotted in a biplot, whereas, in GGE, the genotype and G×E effects are presented using environment-centered PCA.

The AMMI and GGE biplot analyses have been extensively used to identify promising stable cultivars with high yield in a wide variety of crops in diverse production environments. In the present investigation, an attempt was made to identify stable hybrids suitable for Telangana state through AMMI and GGE biplot models.

2. Materials and Methods

The present investigation was carried out on fifteen genotypes of rice during crop season of July to November 2020. The list of hybrids and checks used in the present investigation is provided in Table 1 along with their parentage and source of the material. The study was conducted at six different locations of Telangana covering different agroclimatic zones as detailed in Table 2. Crop was raised by sowing the nursery during first week of July and 25–30 days age seedlings were planted in mail field under irrigated ecosystem at all the six locations. The spacing adopted was 15×15 cm² between hills and rows with plot size of 12 m² replicated thrice in Randomized Complete Block Design.

Crop was managed by adopting recommended agronomic package and suitable plant protection measures to enable for realizing potential yields in all genotypes. Grain yield was recorded in each plot and expressed as kg ha⁻¹.

Statistical analyses for grain yield were subjected to combined ANOVA and AMMI analysis to understand the pattern of genotype performance across the six locations. ANOVA was used to partition genotype deviations, environment deviations, and G×E deviations from the grand mean. Subsequently, multiplication effect analysis (AMMI) was used to partition GE deviations into different interaction principal component axes (IPCA). The AMMI stability value (ASV) was calculated as described by Purchase et al. (2000). PB tool software (IRRI, Philippines) was used to analyze the AMMI and GGE biplot for fifteen genotypes.

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



Table 1: Details of 15 genotypes used in the study along with parentage

Code	Genotypes	Parentage	Source	Duration (Days)	Grain Type
G1	RNRH 15	CMS 59 A×SN 232	RRC, Rajendranagar, PJTSAU	120-125	Long Slender
G2	JGL 24423	Variety check	RARS, Jagtial, PJTSAU	125-130	Long Bold
G3	JGLH 337	CMS 23A×IRTON 270	RARS, Jagtial, PJTSAU	120-125	Long Bold
G4	RNRH 99	CMS 64A×SN 233	RRC, Rajendranagar, PJTSAU	125	Long Slender
G5	Bio 799	Hybrid check	Bioseeds Research India Pvt. Ltd	130-135	Long Bold
G6	RNRH 39	CMS 59 A×SN 596	RRC, Rajendranagar, PJTSAU	125-130	Long Slender
G7	RNRH 98	CMS 64A×SN 232	RRC, Rajendranagar, PJTSAU	125	Long Slender
G8	US 314	Hybrid check	US Agriseeds Pvt. Ltd	120-125	Medium Bold
G9	RNRH 78	CMS 59 A×SN 470	RRC, Rajendranagar, PJTSAU,	130	Long Slender
G10	RNRH 18	CMS 59 A×SN 233	RRC, Rajendranagar, PJTSAU,	125	Long Slender
G11	JGLH 275	CMS 59A×JR 70	RARS, Jagtial, PJTSAU	125	Long Slender
G12	JGLH 373	JMS 18A×JGL 24440	RARS, Jagtial, PJTSAU	125-130	Medium Slender
G13	RNR 15048	Variety check	RRC, Rajendranagar, PJTSAU,	130	Short Slender
G14	27P31	Hybrid check	Bayer Crop Sciences Pvt. Ltd.	125-130	Long Bold
G15	JGLH 365	JMS 18A×JGL 24502	RARS, Jagtial, PJTSAU	125	Medium Slender

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

$$Y_{ij} = \mu + g_i + e_j + \sum \lambda_k a_{ik} v_{jk} + \epsilon_{ij}$$
 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 = eigenvalue of Interaction Principal Components Axes (IPCA) k ;
 a_{ik} = eigenvector of genotype i for PC k ;
 v_{jk} = eigenvector for environment j for PC k ;
 ϵ_{ij} = error associated with genotype i in environment j .
 The GGE biplots were generated to ascertain the which-won-where pattern and to identify the genotypes best suited across environments as well as for specific environments.

3. Results and Discussion

An effort was made to identify stable rice hybrids across different agroclimatic zones in Telangana state using AMMI and GGE bi-plot analyses. The mean grain yield ranged from 1997 kg ha⁻¹ to 8680 kg ha⁻¹ (Table 3). Mean grain yield across locations revealed that the JGLH 337 (6275 kg ha⁻¹) was the top ranked hybrid followed by RNRH 39 (6053 kg ha⁻¹), JGLH 275 (5945 kg ha⁻¹) and 27P31 (6053 kg ha⁻¹). However, among locations, Rudrur (E4) was found to be best location with highest mean grain yield (7509 kg ha⁻¹) across genotypes followed by Rajendranagar (E5) (7018 kg ha⁻¹), whereas Warangal (E6) was poorest location with least mean grain yield (3959 kg ha⁻¹). Jat et al., (2020) reported that Arize

Table 3: Mean grain yield (kg ha⁻¹) of 15 rice genotypes across six locations

Code	Details of genotype/ Environment	Environments						Mean across locations
		E1	E2	E3	E4	E5	E6	
G1	RNRH 15	4177	5771	5244	7234	7633	3423	5580
G2	JGL 24423	3893	6787	4830	6716	7679	2975	5480
G3	JGLH 337	5186	6766	5063	8680	6545	5407	6275
G4	RNRH 99	2392	5434	3519	8297	7603	2958	5034
G5	Bio 799	1997	5756	4604	8176	7476	3145	5192
G6	RNRH 39	5594	5647	5356	7645	7984	4091	6053
G7	RNRH 98	2375	3745	3641	7114	7771	7215	5310
G8	US 314	4439	4425	3674	8091	7199	3344	5195
G9	RNRH 78	3233	4612	3067	7182	7241	3010	4724
G10	RNRH 18	3438	4313	4270	6786	6412	3035	4709
G11	JGLH 275	5904	5912	4467	7706	7041	4642	5945
G12	JGLH 373	3937	5193	2993	7242	4058	4693	4686
G13	RNR 15048	4192	5634	3033	6590	5990	4647	5014
G14	27P31	5731	6202	4289	7668	8431	3227	5925
G15	JGLH 365	4289	6391	3259	7513	6202	3574	5205
	Mean across genotypes	4052	5506	4087	7509	7018	3959	

6444 hybrid recoded higher grain yield compared to PHB 71. According to Islam et al. (2014) the average productivity of all the genotypes across environments was 6.84 t ha⁻¹. On the basis of environmental index value considering negative and positive, E4 and E3 were poor, E5 was medium and E2 and E1 were rich environments.

3.1. Analysis of variance

Analysis of variance clearly showed that grain yield was significantly different among genotypes, environments and genotypes×environment interactions depicting the presence of significant variability among genotypes, considerable influence of environments and interaction of genotypes with environments in expression of the trait (Table 4). Further,

Table 4: Analysis of variance for grain yield over 15 rice genotypes and 6 locations

Source of variation	df	SS	MS	% Explained
Treatments	89	820715361	9221521**	
Blocks	12	3755044	312920	
Genotypes	14	65351296	4667950**	7.50
Environments	5	570691092	114138218**	65.47
Genotypes× Environments	70	184690049	2638429**	21.19
Error	180	50836717	282426	
Total	269	871569155	3239974	

***p*<0.01 probability level

environments contributed highest (65.47%) in total sum of squares followed by genotypes×environments (21.19%) indicating very greater role played by environments and their interactions in realizing final grain yield. Zewdu et al. 2020 observed highly significant difference for grain yield in upland rice by genotype (6.97%), environment (61.64%), and their interaction (20.86%). Further Fentie et al. (2013) and Islam et al. (2014) also reported the similar results in rice production.

3.2. AMMI analysis

The significant G×E interactions were further partitioned by PCA (Gollob, 1968) into five significant principal component axes explaining 39.6, 31.7, 14.8, 8.0 and 5.9% of GEI sum of squares, respectively (Table 5). The first two interaction PCAs accounted for maximum of 71.3%. The IPCA score

Table 5: Partitioning of genotype×environment interaction with AMMI model for grain yield in rice

Source of variation	df	SS	MS	% Explained
Varieties× Environments	70	184690049	2638429**	
IPCA1	18	48742075	2707893**	39.6
IPCA2	16	39045068	2440317**	31.7
IPCA3	14	18241173	1302941**	14.8
IPCA4	12	9835592	819633**	8.0
IPCA5	10	7255488	725549**	5.9

***p*<0.01 probability level



of a genotype in the AMMI analysis is an indication of the adaptability over environments and association between genotypes and environments (Gauch and Zobel, 1996 and Mahalingam et al., 2006). Farshadfar and Sutka (2003), Asenjo et al. (2003), Das et al. (2010) and Umma et al. (2013) analyzed G×E interaction in rice by AMMI model and found significant G×E interaction for grain yield stating the usefulness of AMMI analysis for selection of genotypes for specific location/environment.

The mean grain yield and IPCA1 (interaction effects) were plotted on x and y axis, respectively for the construction of AMMI1 bi-plot (Figure 1). The four quadrants (Q) of the bi-plot corresponded to higher mean (Q I, II), lower mean (QIII, IV), +ve IPCA1 score (QI, IV) and -ve IPCA1 score (QII, III) and a genotype falling in same quadrant denote positive interaction and vice-versa. A genotype with IPCA1 score near to zero is considered to be more stable across environments. Conversely, a genotype with high IPCA1 score is highly variable among environments (Rao et al., 2020).

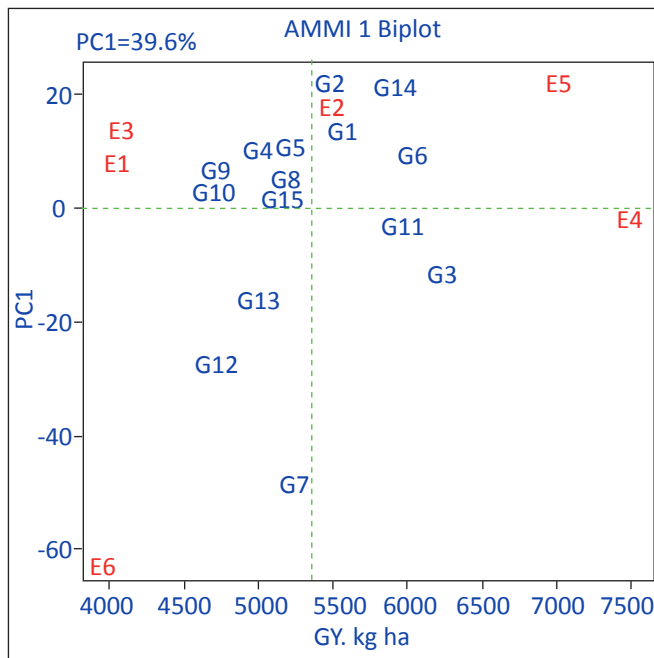


Figure 1: AMMI-1 model for grain yield showing the means of genotypes (G) and environments (E) against their respective IPCA1 scores in rice

Rice hybrids, RNRH 39 (G6), 27P31 (G14), RNRH 15 (G1) and varietal check, JGL 24423 (G2) were recorded higher mean grain yield with positive IPCA1 scores (Figure 1). The hybrid, JGLH 337 (G3) had high mean grain yield and found more adaptable to Rudrur (E4) location. However, JGLH 275 (G11) and JGLH 365 (G15) were plotted near to zero IPCA1 axis indicating that these hybrids are relatively more stable across locations. The remaining hybrids had less than the mean grain yield and found specific adaptation to few tested environments. Likewise Mary et al. (2019) reported that genotypes with PC1 scores close to zero are usually widely

adapted and they were considered more stable in their performance across test environments.

3.3. GGE bi-plot model analysis

GGE bi-plots provide effective evaluation of genotypes and allow for comprehensive understanding of the target and test environments through various IPCAs. The genotypexenvironment interactions were partitioned into six significant interaction PCAs and 61.8% variance was explained by first two IPCAs together (Table 6). Similarly Zewdu et al. (2020) partitioned the genotypexenvironment interactions into six rays which divided the biplot into seven sections.

Table 6: Partitioning of genotypexenvironment interaction with GGE model for grain yield in rice

Source of variation	df	SS	MS	% Explained
IPCA1	18	58581823	3254546**	35.1
IPCA2	16	44487758	2780485**	26.7
IPCA3	14	32378572	2312755**	19.4
IPCA4	12	15142981	1261915**	9.1
IPCA5	10	8874022	887402**	5.3
IPCA6	8	7218688	902336**	4.3

**p<0.01 probability level

GGE bi-plot genotype view depicts that the hybrid JGLH 365 (G15) and US 314 (G8) were inside the first concentric circle and found to be more stable across environments (Figure 2). However, the hybrid RNRH 98 (G7) and JGLH 373 (G12) were known as highly unstable across locations with longest vector from origin.

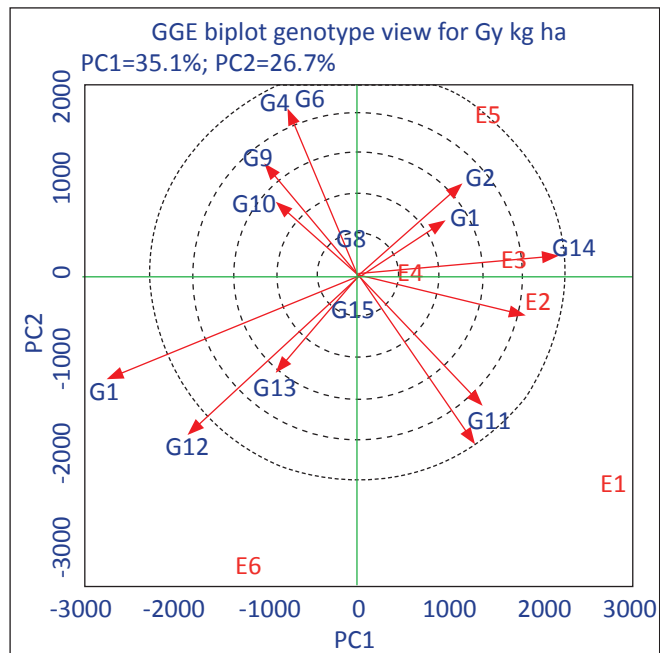


Figure 2: GGE biplot genotype view for grain yield in rice

GGE bi-plot environment view showed that Rudrur (E4) location was the most ideal environment (Figure 3) with least vector length from origin. Conversely Warangal (E6) and Jagtial (E1) locations had longest vectors and indicating that they were poor and most discriminating. Correspondingly, Zewdu et al., 2020 reported that E6, E1, E3, and E2 environments were ideal with short vectors, while E4 and E5 had long spokes and indicated as high discriminating ability of these environments. Similarly, Kripa et al. (2020) reported that the most powerful interpretive tool for AMMI models is Bi-plot analysis and identified that environment E6 and E5 had short vectors and they did not exert strong interactive forces while E1, E2, E3 and E4 with long vectors were more differentiating environments.

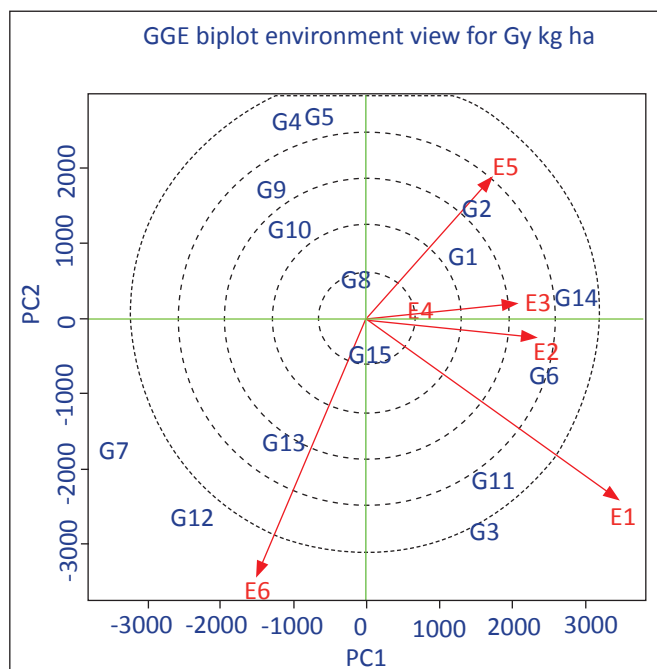


Figure 3: GGE biplot environment view for grain yield in rice

Depending on dispersion of environments in different directions, six locations were partitioned into three mega zones. First zone comprised of four locations viz., Kunaram (E2), Kampasagar (E3), Rudrur (E4) and Rajendranagar (E5) with less than 60° angle among the respective vectors, whereas highly dispersed Jagtial (E1) and Warangal (E6) were identified as two separate mega environments. Keeping in view of similarity among the locations and cost reduction of genotype testing, one environment either E2 (Kunaram) or E4 (Rudrur) pertaining to Northern Telangana Zone and likewise E3 (Kampasagar) or E5 (Rajendranagar) from Southern Telangana Zone might be ignored as a testing location to ascertain hybrid performance. In parallel, Krishnamurthy et al. (2017), the biplot showed four sectors containing all the test environments in 2011 and accordingly four mega-environments were identified, whereas three mega-environments were identified in 2012 and 2013.

3.4. Mean performance and stability of genotypes

The magnitude of interaction can be visualized for each genotype and each environment using IPCA vs. mean yield and IPCA1 vs. IPCA2 biplot model (Yan et al., 1998). The hybrid RNRH 39 (G6) was identified as ideal genotype followed by JGLH 275 (G11) with higher mean yield and good stability. Though the hybrids, JGLH 337 (G3) and 27P31 (G14) had high mean grain yield, found to be relatively not stable across locations falling out of the concentric circle (Table 7 and Figure 4). Considering AMMI stability value and respective rank, US 314 (G8), RNRH 18 (G10) and RNRH 78 (G9) were found to be highly stable across environments whereas RNRH 98 (G7) and JGLH 375 (G12) as most unstable. Similarly, among locations, Rudrur (E4) was identified as best location for realizing higher grain yields.

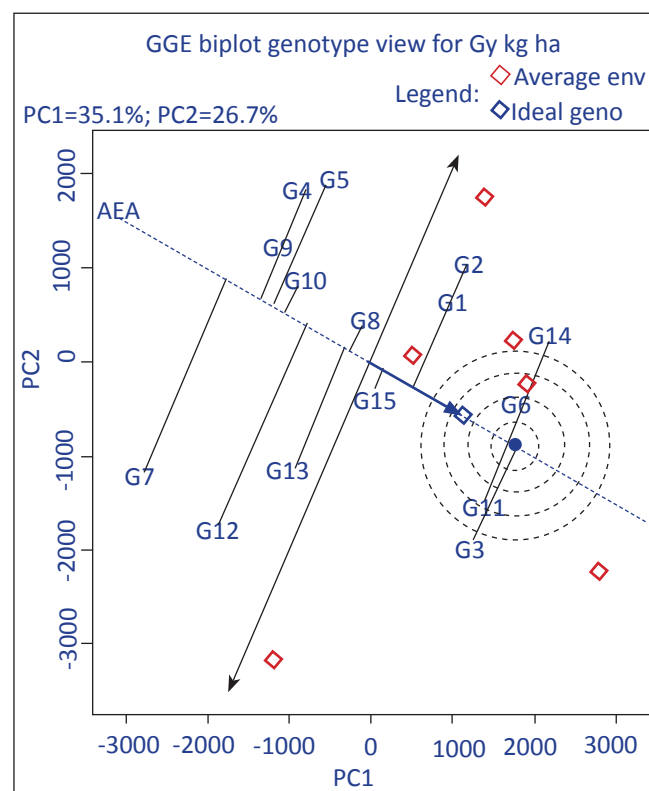


Figure 4: GGE biplot genotype view for grain yield in rice

Further, the hybrid JGLH 365 (G15) was identified as highly stable with least dispersion from AEA axis and also recorded reasonably good mean grain yield. However, the hybrid, JGLH 373 (G12) and RNRH 98 (G7) were found to be most unstable across locations. Similarly, Mary et al., 2019 found G10 and G9 as ideal genotypes having the highest mean yield, followed by G2 and were also considered the most stable genotype due to its close proximity to AEA, whereas genotype G3 was considered unstable and the poorest yielder.

3.5. What-won-where bi-plot

The what-won-where view of the GGE bi-plot (Yan et al., 2000) is the best model for multi-environment trial data for grouping

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 ⁻¹)	Interaction Principal Component Scores					
			AMMI			GGE		
			IPCA1	IPCA2	ASV	ASV Rank	IPCA1	IPCA2
G1	RNRH 15	5580	14.03	-4.37	18.05	6	-994.33	-623.32
G2	JGL 24423	5480	21.92	-1.19	27.39	11	-1175.42	-1034.84
G3	JGLH 337	6275	-11.27	15.48	20.92	8	-1289.34	1869.34
G4	RNRH 99	5034	10.50	-22.60	26.13	10	779.41	-1839.98
G5	Bio 799	5192	11.18	-26.30	29.77	13	556.84	-1885.02
G6	RNRH 39	6053	9.44	4.86	12.75	4	-1889.15	444.76
G7	RNRH 98	5310	-47.86	-34.42	68.95	15	2783.35	1151.88
G8	US 314	5195	4.10	-1.71	5.40	1	100.04	-383.69
G9	RNRH 78	4724	5.50	-10.58	12.61	3	1055.17	-1221.47
G10	RNRH 18	4709	4.14	-3.37	6.17	2	893.53	-819.86
G11	JGLH 275	5945	-2.85	18.99	19.32	7	-1388.67	1463.84
G12	JGLH 373	4686	-27.12	27.11	43.37	14	1881.02	1753.46
G13	RNR 15048	5015	-15.54	14.75	24.37	9	926.47	1083.36
G14	27P31	5925	21.52	7.46	27.88	12	-2185.19	-227.45
G15	JGLH 365	5205	2.33	15.88	16.14	5	-53.73	268.98
E1	Jagtial	4052	8.27	46.59	47.72	4	-0.65	0.52
E2	Kunaram	5506	17.70	18.16	28.60	3	-0.45	0.06
E3	Kampasagar	4087	14.09	-8.47	19.52	2	-0.41	-0.05
E4	Rudrur	7509	-0.50	-9.13	9.15	1	-0.12	-0.02
E5	Hyderabad	7018	22.48	-41.62	50.20	5	-0.33	-0.42
E6	Warangal	3959	-62.05	-5.54	77.66	6	0.28	0.74

the environments and also to identify best performing genotype in each. Many researchers found this biplot intriguing, as it graphically addresses important concepts such as crossover GE, mega environment differentiation, specific adaptation (Yan and Tinker, 2006).

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 27P31 (G14), JGL 24423 (G2) and RNRH 36 (G6) were the best performing genotypes in Kampasagar (E3), Rajendranagar (E5), Kunaram (E2) and Rudrur (E4) locations (Figure 5). Similarly, the hybrids JGLH 337 (G3), JGLH 275 (G11) were found to have good performance in Jagtial (E1) and RNRH 98 (G7), JGLH 373 (G12) in Warangal (E6) locations. Whereas 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. Rukmini Devi et al., (2020) reported the rice genotypes, G2 (WGRH-6) and G3 (WGRH-10), had better performance in mega environment E3 and the genotype, G9 (WGRH-18), exhibited better

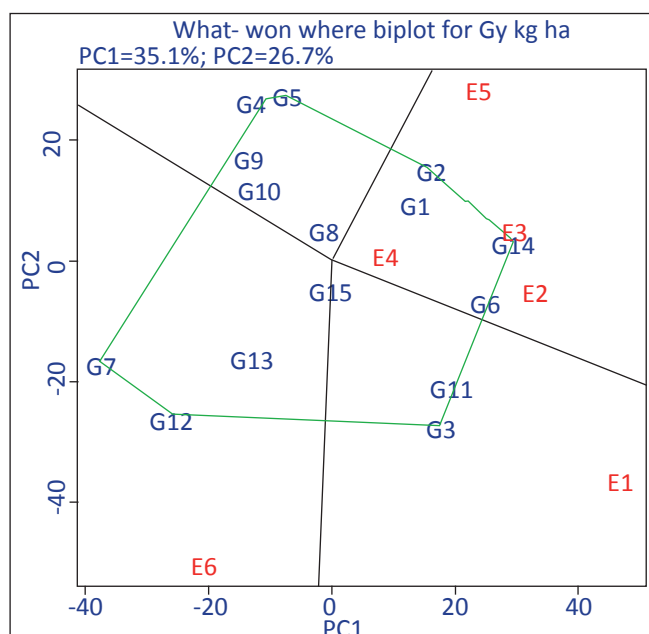


Figure 5: What-won-where biplot for 15 genotypes and six locations in rice

performance in the second mega environment consisting of E1 and E2.

4. Conclusion

Rice hybrids, US 314 (G8) and RNRH 39 (G6) were more stable across locations with higher grain yields. GGE bi-plot environment view and ASV ranks confirmed that Rudrur (E4) location as the most ideal environment to obtain higher grain yields. Six locations were partitioned into three mega zones and to economize the genotype testing. One environment each from Northern and Southern Telangana Zone might be ignored as a testing location to ascertain hybrid performance. Further, 27P31 (G14) and RNRH 39 (G6) were the best performing genotypes in first mega zone.

5. Acknowledgement

The authors are obliged to PJTSAU and ICAR-IIRR, Hyderabad, India for funding under AICRIP programme to different Rice Research Centers of Telangana, India.

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