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Research Article

Stability analysis in rice (*Oryza sativa* L.) through AMMI and GGE biplots

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Abstract
Rice (*Oryza sativa* L.) is a major staple known for fulfilling our dietary requirements. Continuous breeding efforts for widening its genetic base are essential to develop climate-resilient varieties in the future. In view of this, a stability analysis among 81 genotypes comprising of traditional landraces and released varieties was done to evaluate their yield-attributing traits across three seasons namely, *Kharif* 2022, *Rabi* 2023, and *Kharif* 2024. The AMMI and GGE biplot exhibited seven genotypes *viz.,* KRG 45 (*Sithiraikar*), KRG 33 (*Kulipadichan*), KRG 21 (JGL), KRG 40 (*Norungan*), KRG 46 (*Sivapu Kavuni*), KRG 2 (*Aanaikomban*) and KRG 12 (CO 51) as the stable genotypes with high yield across seasons. Considering the *per se* performance for yield, KRG 2 and KRG 46 had the highest yield across seasons than the two checks *viz.,* CO 51 and CO 55. Among the three seasons, *Kharif* 2022 was found to be ideal and exhibited a favorable influence on the genotypes for yield. Since, the three seasons were found to interact independently on the genotypes, they could be used to evaluate the upcoming breeding trials for testing stability in rice. The identified stable genotypes from this study could be advanced for further evaluation to develop climate-resilient rice varieties in future.

Keywords: Rice landraces, AMMI, GGE biplot, yield attributing traits

INTRODUCTION

Rice is considered a "Millennium Crop" since it helps to sustain the global food security. This staple cereal crop serves as the main food supply for more than 60% of the population (Quadri *et al*., 2023). Rice is cultivated in an area of 158 million hectares worldwide with an annual production of 700 million tons. More than 90 per cent of rice production and consumption is observed to be from Asian countries (Palanog *et al*., 2014). The annual rice production in Asia is about 533.80 million tons. India has the maximum rice area of 43.19 million hectares with a production of 145 million tons and a productivity of 2550 kg/ha (Rice Outlook, 2024). However, there has been a 25.40% reduction in the total yield owing to the impact of unpredictable environmental factors (Zhang *et al*., 2019). To combat the alarming climatic conditions, it is essential to broaden the genetic base and identify potential and stable donors for climate smart rice production (Habib *et al*.,2024).

For novel alleles, the landraces in rice serve as a major source, and characterizing them leads to tapping the unexploited variability (Rahim *et al*., 2023). In India, around one lakh accessions of rice landraces were conserved prior to green revolution and still the exploration for their variability, heritability and adaptability across seasons is expected to provide us a novel genetic resource for developing climate smart rice in future (Eliazer *et al*.,2019). Earlier reports on these rice landraces and traditional varieties portrays them as a novel source of donors for drought, salinity and high yield attributing traits (Nachimuthu *et al*.,2014; Chandramohan *et al*., 2023). This is due to the fact that, these rice landraces are reported to be rich in phenol, flavonoids, antioxidants, and phytochemicals which often render them the resilience and tolerance against abiotic and biotic stresses. The identified potential donors for novel traits from traditional landraces and varieties could be used for developing climate resilience rice with higher nutrition (Azrai *et al*., 2023).

Stability for a landrace depends upon its adaptability across seasons and locations. However, they are also affected by the varying management practices during cultivation. A study involving the stability of rice landraces was recently conducted by Jain *et al.* (2018). This study evaluated six basmati genotypes in varying conditions like transplanted rice (TPR), dry direct seeded rice (Dry DSR), wet direct seeded rice (Wet DSR), and system of rice intensification (SRI). It revealed four genotypes to be ideal and stable across various cultivation systems (Das *et al*., 2018). Followed by this, Ritu *et al.* (2021) analyzed the stability of sixty landraces and two checks under water stress conditions and identified four genotypes, *viz.,* Jhitpiti, Angurguchcha, E-1702, and Layachi as stable under three different water stress conditions. The drought intensity index highlighted that there was a significant stress in the rainfed and TSD (Terminal stage drought) conditions. Despite these challenges, these above four genotypes were found to produce a stable yield and they could be valuable for developing drought-tolerant lines in rice.

Habib *et al.* (2024) identified five genotypes of rice as stable under flooding and alternate wetting and drying conditions. These identified genotypes exhibited a superior and stable performance of yield attributing traits which was emphasized to be an essential parameter in analyzing the stability in rice. Thus, it is understood that the stability analysis in traditional landrace and varieties is essential and this would enable the identification of stable and potential donors for climate resilience. Owing to this, the current study was conducted with 29 landraces and 52 rice varieties, which includes two checks, *viz*., CO 51 and CO 55. These genotypes were evaluated for their stability across three seasons from 2022 to 2024 for their yield-attributing characters with a major objective of focusing on identifying stable genotypes for yield.

MATERIALS AND METHODS

In this study, 79 rice genotypes and two check varieties, namely CO 51 and CO 55, were evaluated for their stability for yield across seasons. The genotypes were raised in a randomized block design with three replications in the south farm of Karunya Institute of Technology and Sciences (**Table 1**). It is located at a latitude of 10.9380° N, and longitude of 76.7522° E, and at an altitude of 467 m above the mean sea level of Tamil Nadu. These 81 lines were evaluated across three seasons in two years from 2022-2024. The seasons of experimentation in the current study were *Kharif* 2022 (S1), *Rabi* 2023 (S2), and *Kharif* 2024 (S3), and these were considered as distinct environments. The genotypes were evaluated for five yield attributing traits *viz.*, number of productive tillers (nos), panicle length (cm), 100 seed weight (g), number of grains per panicle (nos) and single plant yield (g) in the three seasons. The list of the genotypes and the codes for genotypes are mentioned in **Table 1**. The stability analysis was performed with the single plant yield as the response variable and pooled mean performance was recorded for analyzing the yield-attributing traits (**Table 3**).

Statistical analysis: The recorded observations were subjected to stability analysis in AMMI and GGE biplot. The data was analyzed in the PB Tools 1.4 package from IRRI. The ANOVA for stability analysis for AMMI was calculated by using the following formula in the R package 4.4.3

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + t_{ger}$$

Where μ is the grand mean estimated by $\bar{Y}$, genotype deviation from the grand mean ag by $\bar{Y}g$ - $\bar{Y}$, and the environment deviation α_g by $\bar{Y}_g$ -$\bar{Y}$ and the environment deviation β_e by $\bar{Y}e$ -$\bar{Y}$. λ_n represents the singular value for PCA axis n. γ_{gn} is the genotype eigenvector for axis n and δ_{en} is the environment eigenvector. Pge is the residual of PCA axes 1 to N (Dessie *et al.,* 2018).

The graphs of GGE depicting (1) the "what won-where" pattern, (2) cultivar rating based on yield and stability, (3) season vectors, and (4) comparison of locations for the ideal environment were generated from PCA scores obtained from AMMI model which is used for capturing the stable genotypes (Khatun *et al*., 2024).

RESULTS AND DISCUSSION

The analysis of variance revealed significant G × E interaction for the 81 genotypes raised across three environments. Thus, the three environments were found to exhibit a significant influence on the genotypes and they can be further utilized for analyzing the stability parameters in rice (**Table 2**).

Based on the *per se* performance, 28 genotypes exhibited high yield (>35 g) in all the environments (**Table 3**). Out of these, seven genotypes, *viz*, KRG 47, KRG 50, KRG 46, KRG 42, KRG 40, KRG 29 and KRG 2 were found to establish the highest yield with higher *per se* performance for the yield-attributing traits. Considering the *per se* performance, the genotypes, KRG 40, KRG

17, KRG 31, KRG 12 and checks, CO 51 (KRG 14) and CO 55, (KRG 18) were found to be stable. Similar findings for the stable and high *per se* performance of the two checks were reported by Nachimuthu *et al.,* (2015) and Borule *et al.* (2024). The highest pooled mean performance for 100 seed weight was observed in KRG 47 and followed by this, it was found in KRG 50 and KRG 26. The genotypes namely KRG 18 followed by KRG 47, KRG 13 and KRG 79 were found to exhibit a higher *per se* performance for the number of grains per panicle. Based

Table 1. List of genotypes used in the present study

S. No	Accession No	Genotype	Code	S. No	Accession No	Genotype	Code
1	KRG 2	*Anai komban*	G01	42	KRG 51	TPS 5	G42
2	KRG 3	*ADT 45*	G02	43	KRG 52	*Vellakar*	G43
3	KRG 4	*Amman ponni*	G03	44	KRG 60	ADT 53	G44
4	KRG 6	*Arumpatham Kuruvai*	G04	45	KRG 61	BABTLA	G45
5	KRG 7	ASD 16	G05	46	KRG 62	ADT 38	G46
6	KRG 8	*Chinnar*	G06	47	KRG 63	Super ponni 43	G47
7	KRG12	CO 51	G07	48	KRG 64	IR 50	G48
8	KRG13	CO 52	G08	49	KRG 67	*Gundu*	G49
9	KRG14	CO 53	G09	50	KRG 68	RLR	G50
10	KRG16	CO 50	G10	51	KRG 69	LLR	G51
11	KRG17	CO 54	G11	52	KRG70	*Nootripathu*	G52
12	KRG18	CO 55	G12	53	KRG71	*Renjini*	G53
13	KRG19	CR1009 *Sub1*	G13	54	KRG72	*Pavithra*	G54
14	KRG21	JGL	G14	55	KRG73	*Makom*	G55
15	KRG23	*Kalasar*	G15	56	KRG74	*Mysore malli*	G56
16	KRG24	*Karudan samba*	G16	57	KRG75	IG 18	G57
17	KRG25	*Karumkuruvai*	G17	58	KRG76	KRG 76	G58
18	KRG26	*Karppu kavuni*	G18	59	KRG77	KRG 77	G59
19	KRG27	*Keerai samba*	G19	60	KRG78	*Prathyasa*	G60
20	KRG29	*Kichili samba*	G20	61	KRG79	*Pisni*	G61
21	KRG30	*Kollan samba*	G21	62	KRG80	KRG 80	G62
22	KRG31	*Kothamalli samba*	G22	63	KRG81	KRG 81	G63
23	KRG32	*Kottaram samba*	G23	64	KRG82	KRG 82	G64
24	KRG33	*Kuliadichan.*	G24	65	KRG83	CO 53	G65
25	KRG34	*Kullakar*	G25	66	KRG84	KRG 84	G66
26	KRG35	*Kuttakar*	G26	67	KRG85	ADT 45	G67
27	KRG36	*Kuzhaiyadi samba*	G27	68	KRG86	JCL NEL	G68
28	KRG37	*Mapillai samba*	G28	69	KRG87	ArB6072	G69
29	KRG38	*Milagu samba*	G29	70	KRG88	Coimbatore Local	G70
30	KRG39	*Navara*	G30	71	KRG89	Tenkasi Local	G71
31	KRG40	*Norungan*	G31	72	KRG90	Kanyakumari Local	G72
32	KRG41	*Poongar*	G32	73	KRG 91	KRG 91	G73
33	KRG42	*Rajae samba*	G33	74	KRG92	KRG 92	G74
34	KRG43	*Rakthasali*	G34	75	KRG93	KRG 93	G75
35	KRG44	*Seerga samba*	G35	76	KRG94	KRG 94	G76
36	KRG 45	*Sithiraikar*	G36	77	KRG95	KRG 95	G77
37	KRG 46	*Sivapu kavuni*	G37	78	KRG 101	Kanyakumari Local 1	G78
38	KRG 47	*Sornamasuri*	G38	79	KRG102	Tenkasi Local 2	G79
39	KRG 48	*Thanga samba*	G39	80	KRG103	Erode Local	G80
40	KRG 49	*Thooyamalli*	G40	81	KRG112	Tirunelveli Local	G81
41	KRG 50	TPS 3	G41				

Table 2. ANOVA for G × E interaction

	Degrees of freedom	Sum of Squares	Mean Sum of Squares
Genotype	80.00	51489.00	643.61**
Environment	2.00	597.00	298.60**
G × E	160.00	13632.00	85.20**
Heterogeneity	80.00	7467.00	93.33
Residual	80.00	6166.00	77.00
Pooled error	19200.00		1.25
Total	242.00	65719.00	

Table 3. Pooled mean performance of genotypes for yield & its attributing traits

S. No	Accession no	Genotypes	No. of productive tillers (Nos)	Panicle length (cm)	No. of grains per panicle (nos)	100 seed weight (g)	Single plant yield (g)
1	KRG 2	*Aanai Komban*	20.10	29.53	157.93	2.28	48.73
2	KRG 3	ADT 45	21.73	17.17	102.77	2.61	38.83
3	KRG 4	*Amman Ponni*	12.60	21.93	109.03	1.96	26.80
4	KRG 6	*Arumpatham Kuruvai*	22.43	15.83	120.63	2.50	43.57
5	KRG 7	ASD 16	13.60	23.80	147.73	2.37	39.73
6	KRG 8	*Chinnar*	13.10	16.23	119.60	2.11	28.20
7	KRG 12	CO 51	16.50	18.50	152.77	1.86	38.54
8	KRG 13	CO 52	14.07	22.80	155.43	2.38	41.27
9	KRG 14	CO 53	13.13	19.10	152.06	2.41	37.49
10	KRG 16	CO 50	16.27	23.50	149.63	2.58	43.17
11	KRG 17	CO 54	12.30	18.60	92.50	2.20	24.50
12	KRG 18	CO 55	10.33	18.70	157.90	2.08	28.37
13	KRG 19	CR1009Sub 1	18.43	21.53	145.27	2.74	44.80
14	KRG 21	JGL	19.87	16.07	124.63	2.60	40.37
15	KRG 23	*Kalasar*	6.13	18.33	96.70	1.68	14.20
16	KRG 24	*Karudan Samba*	13.03	21.33	128.50	2.21	28.37
17	KRG 25	*Karumkuruvai*	20.67	21.43	131.87	2.53	44.63
18	KRG 26	*Karuppu Kavuni*	22.03	25.43	149.73	2.80	48.73
19	KRG 27	*Keerai Samba*	16.40	31.28	102.80	2.13	29.57
20	KRG 29	*Kichili Samba*	17.13	26.47	144.03	2.77	46.33
21	KRG 30	*Kollan Samba*	12.20	23.63	112.27	2.01	27.80
22	KRG 31	*Kothamalli Samba*	20.30	24.43	112.43	2.41	42.20
23	KRG 32	*Kottaram Samba*	19.80	19.47	111.60	2.45	38.27
24	KRG 33	*Kuliadichan*	19.60	23.33	120.21	2.60	39.47
25	KRG 34	*Kullakar*	18.43	19.30	92.73	2.03	27.69
26	KRG 35	*Kuttakar*	22.10	23.13	115.33	2.64	39.63
27	KRG 36	*Kuzhaiyadi Samba*	11.27	20.77	138.67	2.31	29.13
28	KRG 37	*Mapillai Samba*	13.63	23.13	108.33	2.01	26.87
29	KRG 38	*Milagu Samba*	16.07	26.07	118.00	2.17	30.43
30	KRG 39	*Navara*	18.47	19.60	123.70	2.46	36.93
31	KRG 40	*Norungan*	23.05	23.80	113.87	2.69	46.10
32	KRG 41	*Poongar*	19.00	21.70	134.98	2.58	38.47
33	KRG 42	*Rajae Samba*	22.40	20.37	121.63	2.68	45.53
34	KRG 43	*Rakthasali*	15.43	15.20	117.60	2.42	30.80
35	KRG 44	*Seeraga Samba*	13.93	21.63	100.67	2.51	17.83

S. No	Accession no	Genotypes	No. of productive tillers (Nos)	Panicle length (cm)	No. of grains per panicle (nos)	100 seed weight (g)	Single plant yield (g)
36	KRG 45	*Sithiraikar*	18.60	23.90	102.90	2.39	37.17
37	KRG 46	*Sivapu Kavuni*	21.70	23.13	139.33	2.73	47.27
38	KRG 47	*Sornamasuri*	22.23	17.37	156.33	3.16	50.20
39	KRG 48	*Thanga Samba*	12.80	15.27	100.63	1.84	26.20
40	KRG 49	*Thooyamalli*	13.33	17.37	134.74	2.38	30.37
41	KRG 50	TPS 3	26.73	18.23	144.03	2.85	50.73
42	KRG 51	TPS 5	21.90	15.43	144.00	2.61	44.10
43	KRG 52	*Vellakar*	10.20	22.60	137.67	2.02	26.83
44	KRG 60	ADT 53	12.50	17.90	122.40	2.43	22.50
45	KRG 61	BABTLA	11.00	15.33	76.33	1.97	18.46
46	KRG 62	ADT 38	14.80	20.10	92.50	2.20	28.50
47	KRG 63	SUPER PONNI 43	6.67	19.67	90.00	1.57	9.47
48	KRG 64	IR50	15.00	18.33	89.00	1.77	23.68
49	KRG 65	*Gundu*	9.67	17.67	91.00	1.61	14.16
50	KRG 68	RLR	6.67	22.67	123.33	1.58	14.82
51	KRG 69	LLR	6.33	22.67	145.00	1.75	16.13
52	KRG 70	*Nootri pathu*	8.00	10.00	80.00	1.85	18.50
53	KRG 71	*Renjini*	7.00	21.00	115.00	1.71	13.81
54	KRG 72	*Pavithra*	11.00	16.33	88.00	2.03	21.93
55	KRG 73	*Makom*	10.00	20.33	90.00	1.80	29.50
56	KRG 74	*Mysore malli*	7.67	16.33	100.00	1.60	12.27
57	KRG 75	IG 18	11.50	18.50	105.70	1.78	18.70
58	KRG 76	KRG76	10.20	17.50	88.90	2.10	19.60
59	KRG 77	KRG77	14.50	21.40	115.70	2.30	30.10
60	KRG 78	*Prathyasa*	4.33	29.67	153.33	1.96	18.73
61	KRG 79	*Pisini*	3.00	20.67	150.00	2.54	8.64
62	KRG 80	KRG 80	8.00	17.40	85.70	2.10	20.50
63	KRG 81	KRG 81	6.67	19.33	108.00	2.68	12.72
64	KRG 82	KRG 82	10.50	17.40	100.50	2.10	18.45
65	KRG 83	CO 53	4.00	15.33	82.33	2.56	6.76
66	KRG 84	KRG 84	14.80	20.10	94.50	2.10	30.20
67	KRG 85	ADT 45	5.00	18.00	86.67	1.78	12.23
68	KRG 86	JCL NEL	5.00	20.00	140.00	1.70	17.67
69	KRG 87	ArB6072	6.33	19.67	79.00	2.45	18.56
70	KRG 88	Coimbatore Local	10.80	17.60	121.50	1.90	38.91
71	KRG 89	Tenkasi Local	12.20	16.50	110.36	2.02	27.68
72	KRG 90	Kanyakumari Local	12.40	17.72	131.87	1.78	44.63
73	KRG 91	KRG 91	9.40	16.46	140.23	1.74	25.93
74	KRG 92	KRG 92	9.56	20.84	129.56	1.71	19.71
75	KRG 93	KRG 93	12.00	17.60	110.23	1.17	32.52
76	KRG 94	KRG 94	11.00	16.24	132.40	1.89	21.84
77	KRG 95	KRG 95	13.00	18.12	102.50	1.63	34.12
78	KRG 101	KRG 101	15.00	22.22	125.00	1.90	34.56
79	KRG 102	KRG 102	16.50	19.50	110.00	1.85	30.50
80	KRG 103	Erode local	13.40	18.40	122.00	1.75	28.69
81	KRG 112	KRG 112	13.40	19.50	110.00	1.85	22.80

on the pooled mean performances of the landraces and the varieties, it was observed that the genotypes *viz.,* KRG 47, KRG 50 and KRG 2 could be utilized as potential donors for yield and its contributing traits. Similar findings for the performance of these genotypes were also recorded by Nachimuthu *et al.* (2014) and Nachimuthu *et al.* (2015).

Stability analysis by AMMI biplot : The Additive Main Effects and Multiplicative Interaction (AMMI) model is a statistical tool crucial in plant breeding for analyzing genotype by environment (G x E) interactions (Rahayu, 2020). The variance contribution for PC1 and PC2 components were 54.80 and 45.20 percent, respectively. Among the 81 genotypes, 21 genotypes were found to be placed near the center of the origin. Thus, these genotypes were found to exhibit a lower interaction with the environment in the AMMI biplot (Habib *et al*., 2024).

Although 21 genotypes were stable, their adaptability to the environment depended on their mean yield. Considering this, nine genotypes, namely, KRG 2, KRG 45, KRG 82, KRG 46, KRG 49, KRG 91, KRG 33, KRG 17, and KRG 13 had established a higher and stable yield across locations. The biplot also revealed that the environments *viz*., S2 and S1 had a favorable positive influence on the genotypes. However, environment S3 had a negative interaction as it fell on the negative quadrant of the biplot. Also, S3 (*kharif* 2024) had the highest interaction with the genotypes and it could be concluded that, among all the environments S3 was found to be interactive towards the genotypes for yield (**Fig. 1**). Similar, interaction of environment in the negative quadrant was also reported by Pramitha *et al.* (2020). An earlier report comparing temperatures during the *kharif* and *rabi* seasons in India also indicates that the *kharif* season has been experiencing a significantly greater year-on-year increase in temperature compared to the *rabi* season (Madhukar *et al.,*2022). Thereby, these further projects the strong G X E interaction across three environments and they could be further utilized for evaluating other breeding trials.

Stability analysis by GGE biplots: The GGE biplot is a powerful visualization tool used in multi-environmental trials (METs) to analyze genotype-by-environment interaction (G×E), This aids in identifying stable and high-performing genotypes across environments (Pramitha *et al*., 2020). The GGE biplot 1 comprised 82.70% of the variation contributed by PC1 and 11.50% of the variation was contributed by PC2. Among all, six genotypes were found to exhibit a lower interaction with lower PC scores (**Table 4 and Fig. 2**).

These genotypes were found to have lower axis lengths from the center of origin. The identified stable genotypes in the GGE biplot were, KRG 45, KRG 82, KRG 21, KRG 40, KRG 12, KRG18 and KRG 19. Among two checks, CO 55 (KRG 18) was found to be stable than CO 51 (KRG 14). Moreover, in the GGE biplot, KRG 40 and KRG 21 were found to be placed far away from the center with a longer axis and were found to be unstable. Similar results for stability parameters were reported by Krishna *et al*. (2023). From **Fig. 3** in the GGE biplot, the ideal environment was observed to be S1 (*kharif* 2022). Thus, it could be observed that the *kharif*, 2022 was found to have a favorable interaction with the genotypes. The monsoon report on *kharif* 2022 by Kumar *et al.* (2022) also projects this season as a desirable season for rice production due to greater monsoon and amenable temperatures throughout the season for higher productivity. A similar identification of favorable seasons from the GGE biplot was reported by Wang *et al*. (2023). Hence, *kharif* season could be identified as a desirable season under optimum precipitation for the multiplication of these landraces and varieties.

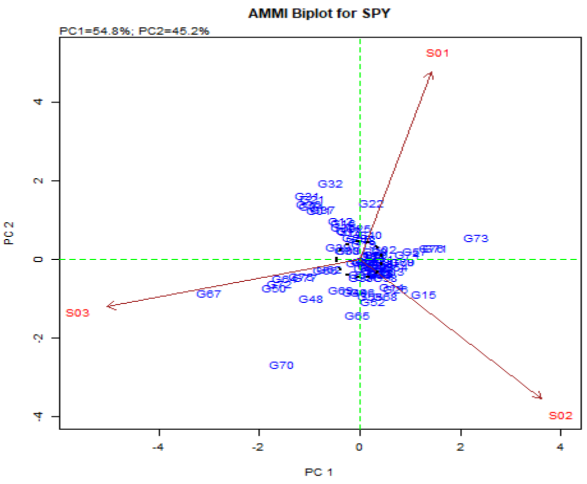

Fig. 1. AMMI biplot for SPY

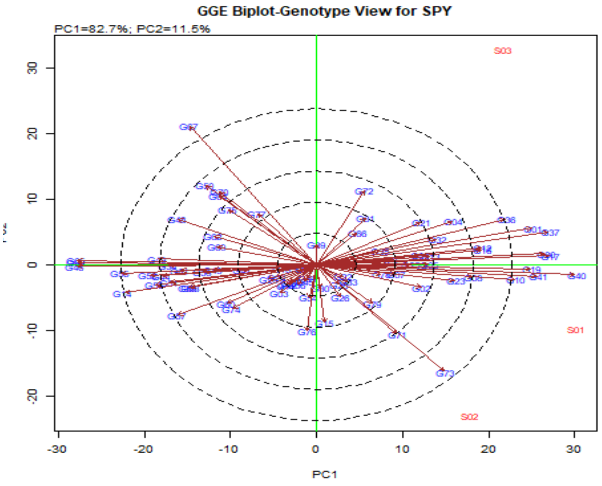

Fig. 2. GGE Biplot genotypes view for SPY

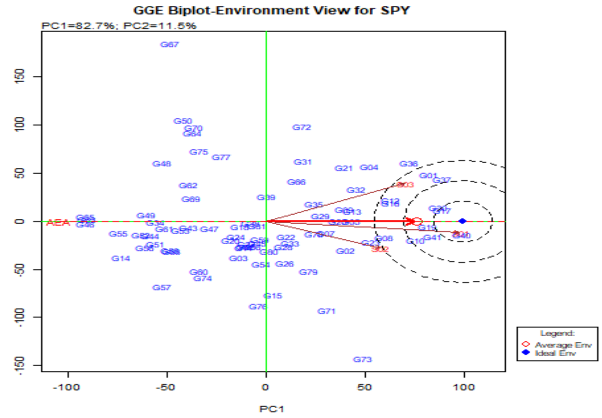

Fig. 3. GGE Biplot- Environment view for SPY

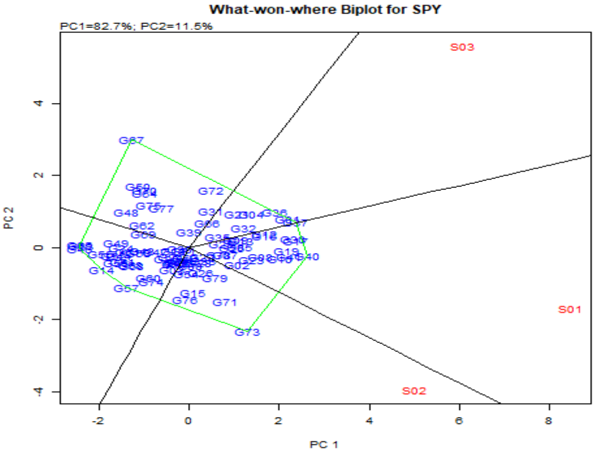

Fig. 4. What-Won-Where biplot for SPY

*Biplots of AMMI and GGE biplot for single plant yield (SPY). AMMI biplots depicting the stable genotypes near the center of origin. GGE biplots for classification of environments and identification of ideal environment.

Table 4. PC scores of Genotypes in Stability analysis

S. No.	Codes	SPY	PC1	PC2
1	G01	48.73	-25.18	-5.6
2	G02	38.83	-12.24	3.46
3	G03	26.80	4.26	4.33
4	G04	43.57	-15.94	-6.57
5	G05	39.73	-13.13	-0.06
6	G06	28.20	2.27	2.98
7	G07	38.54	-9.18	1.39
8	G08	41.27	-18.23	1.90
9	G09	37.49	-12.00	-1.48
10	G10	43.17	-23.21	2.25
11	G11	24.50	3.56	3.11
12	G12	28.37	-19.35	-2.22
13	G13	44.80	-13.28	-1.48
14	G14	40.37	22.51	4.28
15	G15	14.20	-0.96	8.82
16	G16	28.37	-19.31	-2.22
17	G17	44.63	-27.22	-1.38
18	G18	48.73	4.09	0.60
19	G19	29.57	-25.05	0.62
20	G20	46.33	5.61	2.19
21	G21	27.80	-12.18	-6.50
22	G22	42.20	-3.14	1.81
23	G23	38.27	16.14	2.46
24	G24	39.47	4.68	1.85
25	G25	27.69	-10.99	-0.02
26	G26	39.63	-2.79	4.97
27	G27	29.13	3.11	2.71
28	G28	26.87	-2.64	2.98
29	G29	30.43	-8.35	-0.65
30	G30	36.93	-26.71	-1.68

S. No.	Codes	SPY	PC1	PC2
31	G31	46.10	-5.70	-7.20
32	G32	38.47	-13.98	-3.89
33	G33	45.53	-3.67	2.57
34	G34	30.80	17.31	0.08
35	G35	17.83	-7.33	-2.14
36	G36	37.17	-22.09	-7.01
37	G37	47.27	-27.18	-5.01
38	G38	50.20	2.45	0.20
39	G39	26.20	0.04	-3.02
40	G40	30.37	-30.28	1.56
41	G41	50.73	-25.80	1.79
42	G42	44.10	3.36	2.99
43	G43	26.83	12.00	0.69
44	G44	22.50	18.08	1.68
45	G45	18.46	1.48	2.54
46	G46	28.50	28.14	0.26
47	G47	9.47	8.73	0.79
48	G48	23.68	16.23	-7.01
49	G49	14.16	18.62	-0.85
50	G50	14.82	12.94	-12.11
51	G51	16.13	17.14	2.71
52	G52	18.50	19.57	1.64
53	G53	13.81	13.22	1.07
54	G54	21.93	0.86	5.04
55	G55	29.50	22.89	1.32
56	G56	12.27	18.88	3.07
57	G57	18.70	16.17	7.76
58	G58	19.60	14.97	3.45
59	G59	30.10	1.11	2.09
60	G60	18.73	10.49	5.95
61	G61	8.64	15.85	0.88
62	G62	20.50	12.01	-4.41
63	G63	12.72	27.92	-0.28
64	G64	18.45	11.39	-10.6
65	G65	6.76	28.04	-0.62
66	G66	30.20	-4.70	-4.87
67	G67	12.23	14.89	-21.23
68	G68	17.67	14.71	3.49
69	G69	18.56	11.65	-2.73
70	G70	38.91	11.34	-11.21
71	G71	27.68	-9.36	10.61
72	G72	44.63	-5.53	-11.32
73	G73	25.93	-15.00	16.42
74	G74	19.71	9.84	6.72
75	G75	32.52	10.36	-8.40
76	G76	21.84	1.17	10.12
77	G77	34.12	6.90	-7.79
78	G78	34.56	-7.47	1.44
79	G79	30.50	-6.53	5.89
80	G80	28.69	-0.44	3.56
81	G81	22.80	1.42	0.54

What-Won-Where Plot for Environment : Further, the what-won-where biplot indicated the absence of any distinct mega-environment. Thus, we could observe that each environment *i.e*., the *kharif* and *rabi* seasons from 2022-2024 had interacted independently with genotypes. Therefore, all these environments could be used to evaluate stability for the upcoming breeding trials. Similar results for independent interaction of environments were reported by Ahmed *et al*. (2020) and Zewdu *et al. (*2020). Among all, three genotypes, *viz*., KRG 46, KRG 49, and KRG 91 could be recommended for cultivation in S1 and S2. These genotypes had a desirable and higher mean performance for yield in the respective environments. Moreover, for S3, the genotypes namely KRG 45, KRG 82, and KRG 46, could be recommended for their cultivation. Although these genotypes were not stable, the seed multiplication trials for the above-mentioned genotypes could be effectively carried out in these respective environments, where they exhibited a desirable performance. Similar results for independent interaction of environments were reported by Assefa *et al*., (2021) (**Fig. 4**).

The stability analysis for rice landraces and varieties is essential to identify potential donors for climate resilience. The data emphasized the role of yield-attributing traits in 81 genotypes across three environments. Based on AMMI and GGE biplot, seven genotypes namely, KRG 45, KRG 33, KRG 21, KRG 40, KRG 46, KRG 2 and KRG 12 were identified to be high yielding with stable performance for yield across environments. These genotypes could be effectively forwarded for evaluating their yield and climate-resilient traits in future. Although this serves as a preliminary study for identifying stable lines, further investigations for identifying stress tolerance could be explored by forwarding these genotypes to trait-specific breeding programs.

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