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STABILITY ANALYSIS FOR GRAIN YIELD USING AMMI MODEL IN ELITE LINES OF RICE (*ORYZA SATIVA* L.)

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ABSTRACT

The genotype × environment interaction and stability performance on grain yield was studied with 51 elite lines of rice across six environments using the additive mean effects and multiplicative interaction (AMMI) analysis. The ANOVA for grain yield revealed highly significant ($P<0.01$) for genotypes, environments and their interactions. It was evident from AMMI analysis that first two principal components accounted for 80.60%, which is enough to explain the variability among the genotypes. The mean grain yield value of genotypes averaged over environments indicated that G17 (R2756-61-1) had the highest (3902 kg ha^{-1}) and G28 (R2736-71-1) the lowest yield (2580 kg ha^{-1}), respectively. In the AMMI analysis, AMMI 1 biplot showed that the genotypes G2 (R2733-1-1), G4 (R2737-74-1), G24 (R2723-23-1) and G17 (R2756-61-1) had high mean grain yields and positive IPCA1 scores indicating strong additive effects but the genotype G17 (R2756-61-1) being the overall best. Hence, the genotype G17 would be considered more adapted to a wide range of environments than the rest of genotypes. The AMMI 2 biplot showed that, the genotypes G20 (R2739-85-1), G10 (R2734-34-1) and G40 (R2743-73-1) are close to the origin indicating non sensitive nature of these genotypes and highly stable genotypes across the environments with low yield potential when compared to others.

According to the polygon view of GGE biplot, the genotypes G16 (R2738-12-1) and G13 (R2745-118-1) were the winner in the environment E5 & E6 whereas the genotypes G38 (R2735-46-1) and also G4 (R2737-74-1) were the winners in the environment E2 & E3. The genotype, G17 (R2756-61-1), has high mean yield with stable performance over six environments being the overall best and it may be considered for the direct seeded rice cultivation in the rainfed ecosystem.

***Key words*: AMMI analysis, Stability, GGE biplot, G × E interaction**

Introduction

Rice is not just a grain-it's a global cornerstone of sustenance, tradition and economic significance. As a primary food source for more than half the world's population, rice cultivation plays a crucial role in food security and agricultural economies. From the terraced paddies of Southeast Asia to the floodplains of India, rice cultivation is deeply intertwined with local agriculture and livelihoods. Following China, India is ranked second with 121 million metric tons of rice consumption in the same period. Total Rice production during 2023-24 is estimated at record 1378.25 LMT. It is higher by 20.70 LMT than previous year's Rice production of 1357.55 LMT. The world population is projected to reach a peak of 10.4 billion by the 2080s, with approximately 9.7 billion people anticipated by 2050 (Norrman *et al*., 2023). This possesses a significant challenge in feeding the world's population within the planet's ecological boundaries (Rockström *et al*., 2020).

The demand that is expected to arise by 2025 is staggering because, in the major Asian countries, rice consumption is increasing day by day but production rate is slower so new technique adoption is compulsory to expand faster than population growth. The development of cultivars, which can be adapted to a wide range of diversified environments, is the ultimate goal of plant breeders in a crop improvement programme.

Chhattisgarh, one of the largest paddy producer states in India, has ideal weather conditions and soil for growing paddy. Central plains of Chhattisgarh are known as "Rice Bowl of Central India". To start, Chhattisgarh conserves 23,250 different types of rice. Rice agriculture is the main source of control for the peasants, who make up around 80% of the state's population.

Rice's resilience and performance over a wide range of environments go hand in hand with its increased output. The adaptation of a cultivar over different environments is usually tested by the level of its interaction with different environments under which it is cultivated. A variety or genotype is considered to be more adaptive or stable one, if it has a high mean yield but a low degree of variation in yielding capacity when grown over varied environments (Ashraf *et al*., 2003).

The stability study is crucial to assess the performance of varieties under different situations and to help plant breeders select appropriate varieties since G × E interactions have a substantial impact on the phenotype of the varieties. Whether a variety's performance was good in comparison to that of one or more conventional cultivars grown over crop seasons is typically the main consideration when deciding whether to release it. Selection for superior genotypes based on yield per se at a single site in a year may not be very efficient because yield is a complicated quantitative trait that is heavily influenced by variable environmental conditions.

Additive main effect and multiplicative interaction (AMMI) model or consideration of cumulative main effects and multiplicative interactions is a multivariate method for the consideration of genotype stability that has comprehensively been used for the estimation of genotype ×environment interaction and a number of stable genotypes (Askarinia *et al*., 2009). The reason behind comprehensive usage of AMMI method is that this model considers a great part of sum of squares in interactions and separates main effects and interactions (Ebdon and Gauch, 2002). Moreover, the results of this method can be used for breeding programs with specific adaptation and desirable environmental selection.

Materials and Methods

The experiments were conducted at six research stations namely Raipur (E1), Bilaspur (E2), Ambikapur (E3), Jagdalpur (E4), Kawardha (E5) and Raigarh (E6) representing six different agro-climatic zones of Chhattisgarh. The experimental material consists of 51 elite lines of rice including 8 checks such as Samleshwari, Bastar Dhan 1, Danteshwari, Sahbhagi Dhan 1, Narendra 97, Annada, Vandana and Protezin. The experiment was set up in a Randomized Block Design with two replications during *kharif* 2024.

Data Collection and Statistical Analysis

Data were collected for days to 50 % flowering, panicle length, plant height, number of filled grains/panicle, number of unfilled grains/panicles, spikelet fertility, test weight, biological yield per plot and grain yield per plot. The grain yield and other agronomic parameters were subjected to analysis of variance using the OPSTAT software. The grain yield data were also subjected to the Additive Main Effect and Multiplicative Interaction (AMMI) analysis. The GGE-biplot analysis was also used for ranking genotypes based on grain yield performance and stability and also for detecting wider and /or specifically adapted genotype(s).

AMMI Analysis

The G × E interaction was examined using the additive main effects and multiplicative interactions (AMMI) model, which combines principal component analysis and standard analysis of variance. In order to explain the pattern in the GE interaction or residual matrix, this method isolated the main effects of genotype and environment. Principal component analysis (PCA) was then used to generate a multiplicative model, which was then utilized to examine the interaction effect from the additive ANOVA model.

Gauch and Zobel (1998) compared the performance of AMMI analysis with ANOVA approach and regression approach and found that ANOVA fails to detect a significant interaction component and regression approach accounts only a small portion of the interaction sum of squares only when the pattern fits a specific regression model. The AMMI model for T genotypes and S environment is given as:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n-1}^{n!} \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij}$$

$$\theta_{ij} \sim N(0, \sigma^2); i = 1,2, \ldots ..T; j = 1,2, \ldots ..S$$

Where,

Y_{ij} = mean yield of the i^{th} genotype in the j^{th} environment

n= general mean

g_i= i^{th} genotypic effect

e_j= j^{th}location effect

λ_n=eigen value of the PCA axis n

α in and γ_{jn}= i^{th} genotype j^{th} environment PCA scores for the PCA axis n

θ^{ij} = residual

Table 1: List of Environments used in the study.

S.	Planting place	Environment code
1.	Research cum Instructional Farm, College of Agriculture, Raipur.	E1(RPR)
2.	Barrister Thakur Chhedilal College of Agriculture and Research Station, Sarkanda, District Bilaspur.	E2(BSP)
3.	Rajmohini Devi College of Agriculture and Research Station, Ambikapur.	E3(AMBK)
4.	Shaheed Gundadhur College of Agriculture and Research Station, Kumharawand, District Jagdalpur.	E4(JGD)
5.	Sant Kabir College of Agriculture and Research Station, Kawardha.	E5(KWD)
6.	College Research of Agriculture Station and Boirdadar, District Raigarh	E6(RGH)

n = number of PCA axis retained in the mode

Calculation of ASV (AMMI Stability Value)

The AMMI Stability Value (ASV) is a widely used quantitative stability measure in AMMI analysis. It provides a single value that ranks genotypes based on their stability across environments, using the Interaction Principal Component Axes (IPCA1 and IPCA2) from the AMMI model.

$$ASV = \sqrt{\frac{SS(IPCA1)}{SS(IPCA2)} \times (IPCA\ 1)^2 + (IPCA\ 2)^2}$$

- LOW value = More stable
- HIGH value = less stable and more interaction effect.

Results and Discussion

AMMI analysis of variance

The AMMI analysis of variance for grain yield (kg/ha) revealed significant effects for genotype, environment, and genotype × environment (G×E) interaction (Table 2). Together, these sources of variation accounted for 80.6 % of the total trial sum of squares, indicating that they are the major contributors to the total variation in grain yield. The mean squares for both IPCA1 and IPCA2 were highly significant, explaining 39.9 % and 28.4 % of the total G×E interaction sum of squares, respectively and the cumulative variance was about 68.3 % for PCA1 and PCA2. This implies that the interaction of the 51 genotypes of rice with six environments was predicted by the first two components of genotypes and environments and these two interaction principal components will be used for further analysis and interpreting the biplots.

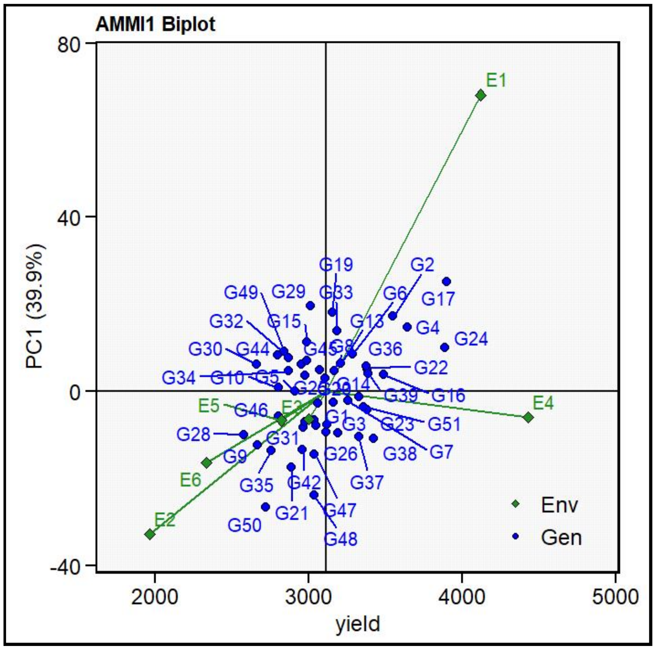

Fig. 1: AMMI 1 biplot between mean yield Vs. PC1.

Stability analysis by AMMI model

Biplot analysis is possibly the most powerful interpretive tool for AMMI models. There are two basic AMMI biplots, the AMMI 1 biplot where the main effects (genotype mean and environment mean) and IPCA1 scores for both genotypes and environments are plotted against each other. On the other hand, the second biplot is AMMI 2 biplot where scores for IPCA1 and IPCA2 are plotted (Table 3). The mean grain yield value of genotypes averaged over environments indicated that the genotypes, G17 (R2756-61-1) and G28 (R2736-71-1), had the highest (3902 kg/ha) and the lowest (2580 kg/ha) yield, respectively. Different genotypes showed inconsistent performance across all the environments. The environmental mean grain yield range was found to 1964 kg/ha for E2 (BSP) to 4429 kg/ha for E4 (JGD)

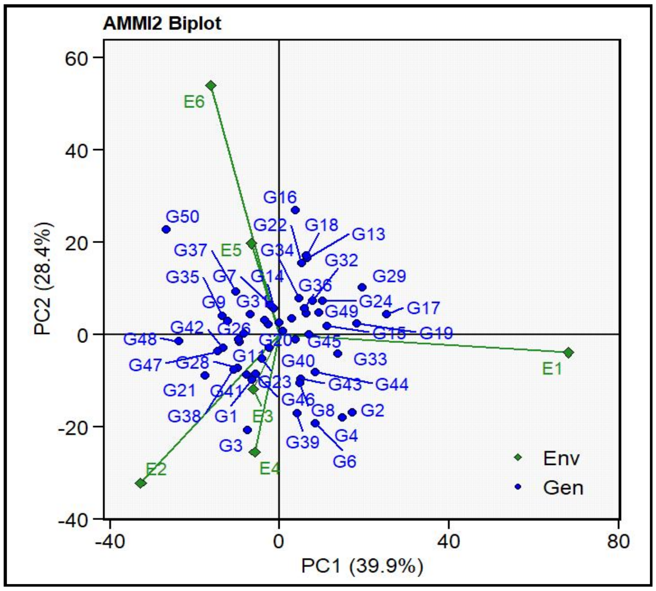

Fig. 2: AMMI 2 biplot between PC1 Vs. PC2.

Table 2: AMMI ANOVA and the proportional sources of sum of squares, per cent variation and mean squares from AMMI analysis of grain yield of 51 rice genotypes across six locations.

Source of Variation	Degree of freedom	TSS	MSS	Percentage	F value
Environment	5	**487057474.2****	**97411494.84****	-	**284.22****
REP(ENV)	6	2056405.255	342734.20	-	1.53
Genotype	50	**50112525.27****	**1002250.5****	-	**4.48****
Genotype × Environment	250	**186322761.5****	**745291.05****	-	**3.34****
IPCA 1	54	74351091.46	**1376872.06****	**39.9**	**6.17****
IPCA 2	52	52831882.13	**1015997.73****	**28.4**	**4.55****
IPCA 3	50	27928811.38	558576.23	15	2.5
IPCA 4	48	20551819.02	428162.9	11	1.92
IPCA 5	46	10659157.46	231720.81	5.7	1.04
Residuals	300	66994821.75	223316.07	-	
Total	861	978866749.4	1136895.18	-	

** Significant at P<0.01

and mean grain yield over environment and genotype was 3111 kg/ha. On the basis of environmental index value in terms of negative and positive, E2 (BSP), E3 (AMBK), E5 (KWD) and E6 (RGH) are poor, and E4 (JGD) and E1 (RPR) are rich environment.

AMMI 1 biplot display

In the AMMI 1 biplot (Fig. 1), the primary axis (abscissa) represents the mean (additive) effects of genotypes and environments, while the ordinate (vertical axis) represents the interaction effects as captured by the first Interaction Principal Component Axis (IPCA1). Displacements along the horizontal axis reflect differences in mean performance, whereas displacements along the vertical axis indicate the magnitude of genotype × environment (G×E) interaction (Kempton, 1984).

Genotypes or environments that cluster together in the biplot are considered to have similar adaptation patterns or similar influences, respectively. A genotype with an IPCA1 score near zero is considered to have minimal interaction with the environment, indicating high stability across different environments. Such genotypes are often preferred in breeding programs aiming for broader adaptability.

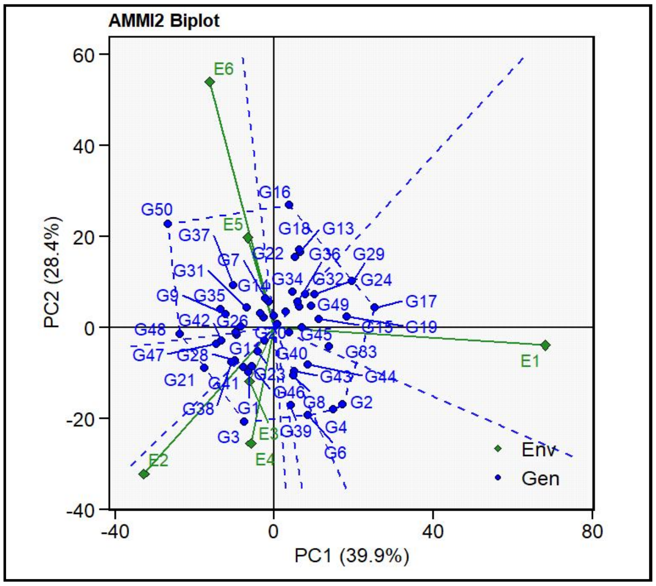

Fig. 3: GGE biplot (What-won-where) display

The mean grain yields of rice landraces along with their IPCA1 and IPCA2 scores are presented in Table 3. Genotypes or environments located on the right side of the origin typically indicate higher mean grain yields compared to those on the left. In the present study, the landraces G10 (R2734-34-1), G5 (R2739-30-1), G31 (R2733-6-1), G46 (R2733-132-1), G40 (R2743-73-1), G25 (R2735-130-1) and G20 (R2739-85-1) are positioned near the origin, indicating high stability, recorded IPCA1 scores close to zero and were located near the origin in the AMMI biplot, suggesting stable yield performance across all the environments.

Genotypes with high mean grain yields and positive IPCA1 scores indicating strong additive effects include G2 (R2733-1-1), G4 (R2737-74-1), G6 (Samleshwari (ch)), G16 (R2738-12-1), G24 (R2723-23-1), G17 (R2756-61-1), G51 (*Protezin* (ch)). These genotypes combine high mean yield with positive interaction effects, meaning they respond well under favourable environments.

However, due to higher IPCA1 values, they are not stable across all environments but can be excellent performers in targeted, responsive locations. E1 (RPR) is the most discriminating environment, as it is far from the origin and has a long vector. Among these genotypes, G17 (R2756-61-1) exhibited the highest overall grain yield and demonstrated strong adaptability to environments E1 (RPR) and E4 (JGD).

Additionally, Environments plotted on the left side have below-average environmental means. Genotypes located near these environments on the left side perform

Table 3: Mean performance for grain yield (kg/ha), IPCA axes scores for genotypes and environments, AMMI stability value (ASV) of 51 rice genotypes grown at six locations during *Kharif*-2024 season.

S.	Genotypes	E1	E2	E3	E4	E5	E6	Mean	Y Rank	IPCA1	IPCA2	ASV	ASV Rank
1	R2749-5-1	3641	2542	3106	4258	3126	1528	3034	30	-6.58	-9.93	13.58	23
2	R2733-1-1	5713	2125	3475	5638	2697	1656	3551	4	17.19	-16.92	29.53	48
3	R2733-114-1	3633	2892	2969	4912	3425	878	3118	22	-7.63	-20.72	23.34	42
4	R2737-74-1	5833	2717	4238	5088	1886	2104	3644	3	14.78	-18.15	27.60	46
5	R2739-30-1	3673	1217	2769	4408	3680	1712	2910	39	0.00	2.43	2.43	2
6	Samleshwari (ch)	4863	2250	3144	5488	2664	1303	3286	14	8.50	-19.37	22.77	41
7	R2765-17-1	4044	1875	3031	4532	3299	2756	3256	15	-2.17	6.29	6.99	9
8	R2749-33-1	4594	2333	3346	4460	2466	1794	3166	19	4.74	-10.65	12.56	19
9	R2733-118-1	2831	1833	2594	3955	2583	2201	2666	49	-12.21	2.80	17.40	33
10	R2734-34-1	3766	1333	2819	4352	2540	2015	2804	44	0.84	0.61	1.33	1
11	R2737-12-1	3421	2083	2963	5068	2561	2581	3113	23	-9.42	-1.70	13.37	21
12	R2739-6-1	3189	1500	2744	5189	2913	2267	2967	36	-8.31	0.09	11.70	16
13	R2745-118-1	4305	658	3000	4544	3997	2765	3212	16	6.51	16.50	18.87	35
14	Annada (ch)	4222	2008	2794	4840	3171	2925	3327	12	-1.28	5.62	5.90	8
15	R2723-12-1	4905	1708	2631	4144	2095	2454	2990	33	11.30	1.75	15.94	29
16	R2738-12-1	4768	1625	3194	3721	3382	4233	3487	5	3.82	26.76	27.30	45
17	R2756-61-1	6684	2000	3238	4909	3655	2924	3902	1	25.21	4.25	35.74	50
18	R2763-2-1	4181	625	2600	4424	2810	3079	2953	38	6.30	17.09	19.23	37
19	R2736-1-1	5319	1083	2644	4935	2572	2365	3153	21	18.17	2.28	25.67	43
20	R2739-85-1	4161	2542	2700	4521	2587	2461	3162	20	-2.54	-2.99	4.65	4
21	R2735-8-1	2804	2708	2950	4557	2180	2106	2884	40	-17.48	-9.02	26.20	44
22	R2736-44-1	4705	1625	2819	4346	3492	3314	3384	8	5.24	15.35	17.04	31
23	R2735-100-1	4160	2450	3444	5299	1994	2931	3380	9	-4.19	-5.32	7.95	10
24	R2723-23-1	5594	2208	2781	5667	3524	3556	3889	2	10.10	7.19	15.93	28
25	R2735-130-1	3806	1667	3350	4531	2425	2598	3063	26	-2.67	2.05	4.28	3
26	R2739-134-1	3821	2992	2919	4264	2178	2956	3189	17	-9.60	-1.14	13.56	22
27	R2734-2-1	4466	2275	3269	3213	3236	2203	3110	24	2.98	3.42	5.41	6
28	R2743-37-1	2805	1625	2906	4395	2237	1509	2580	51	-9.90	-7.35	15.75	27
29	R2733-100-1	5482	1375	2556	3359	2871	2417	3010	31	19.58	10.01	29.33	47
30	R2736-71-1	4146	1333	3013	3249	2148	2067	2659	50	6.26	4.40	9.84	11
31	R2733-6-1	3641	2292	2844	3812	2619	2643	2975	35	-6.97	4.21	10.68	15
32	R2736-70-1	4311	1083	3050	3799	2734	2248	2871	42	7.73	7.16	13.03	20
33	R2733-65-1	5101	1625	2875	4658	3062	1798	3187	18	13.83	-4.18	19.91	39
34	R2754-1-1	4024	958	2944	4184	2773	2347	2872	41	4.63	7.68	10.07	14
35	R2733-125-1	3049	2450	2919	3363	2066	2678	2754	47	-13.56	3.99	19.50	38
36	R2741-79-1	4856	2108	3044	4297	3089	2853	3375	10	5.82	5.56	9.90	13
37	Narendra 97 (ch)	3620	2292	3238	4310	3290	3204	3326	13	-10.33	9.30	17.26	32
38	R2735-46-1	3539	2458	3831	5094	3527	2101	3425	6	-10.82	-7.61	17.02	30
39	Bastar Dhan 1(ch)	4844	2917	3101	5054	2766	1653	3389	7	4.12	-17.23	18.18	34
40	R2743-73-1	4223	1708	2750	4385	2788	2014	2978	34	3.71	-1.16	5.35	5
41	R2736-52-1	3453	2183	2994	4964	2910	1799	3051	27	-7.83	-8.77	14.08	25
42	R2742-59-1	3058	2342	2613	4609	3010	2135	2961	37	-13.35	-2.91	19.02	36
43	R2736-51-1	4476	2125	3000	4564	2597	1676	3073	25	4.98	-9.70	11.97	18
44	Danteshwari (ch)	4275	1417	3875	3460	2753	990	2795	46	8.38	-8.25	14.39	26
45	R2736-92-1	4657	2067	2813	3776	2410	2223	2991	32	7.00	-0.12	9.86	12
46	R2733-132-1	3629	2542	2945	3818	2087	1785	2801	45	-5.68	-8.64	11.77	17
47	R2743-53-1	3082	2458	2850	4818	2590	2434	3039	28	-14.51	-3.71	20.75	40
48	Sahabhagi Dhan 1 (ch)	2480	2875	3025	4336	2990	2514	3037	29	-23.84	-1.50	33.58	49
49	R2738-130-1	4410	1167	2694	3864	2959	1933	2838	43	9.30	4.62	13.88	24
50	Vandana (ch)	1815	1667	2681	3590	2957	3626	2723	48	-26.63	22.62	43.77	51
51	Protezin (ch)	4090	2208	2781	4844	3572	2638	3356	11	-3.48	3.00	5.75	7
	Mean yield							**3111**					

well specifically in low-yielding or marginal environments. Landraces such as G48 (Sahabhagi Dhan 1 (ch)), G50 (Vandana (ch)), G21 (R2735-8-1), G9 (R2733-118-1) and G47 (R2743-53-1) showed better performance in environments E2 (BSP), E3 (AMBK), E5 (KWD) and E6 (RGH). These genotypes showed better performance in the left-side environments, which are generally low-yielding or stress-prone. They may not have high overall yield but can be suitable for cultivation under challenging conditions like drought or poor soils.

AMMI 2 biplot display

In the AMMI 2 biplot (Fig No.2), environmental scores are connected to the origin by spokes. The length of these spokes reflects the strength of the interaction effects. Short spokes indicate that a particular environment does not exert strong interaction, whereas long spokes signify greater interactive forces.

Environments E1 (RPR) and E6 (RGH) appear to be the most discriminative and interactive as they are positioned farthest from the origin, indicating that they exert strong selective pressure on genotype performance. In contrast, E3 (AMBK) and E5 (KWD) are nearer to the origin, implying lower interaction effects and possibly more average or neutral environments.

Genotypes that cluster near the origin tend to have consistent performance across all the six environments, indicating stability in their yield value. Thus, genotypes such as G20 (R2739-85-1), G10 (R2734-34-1), G40 (R2743-73-1), G31 (R2733-6-1), and G5 (R2739-30-1) exhibited minimal interaction with environments and can be considered stable across diverse conditions. Conversely, genotypes that are positioned far from the origin show a high degree of interaction with the environment, reflecting sensitivity and variability in performance. In the current study, genotypes such as G50 (Vandana (ch)), G48 (Sahabhagi Dhan 1 (ch)), G19 (R2736-1-1) and G15 (R2723-12-1) were identified as highly sensitive to environmental variations.

GGE biplot (What-won-where) display

A key feature of the “What-Won-Where” pattern in the GGE biplot is its capacity to vividly illustrate the interaction between genotypes and environments. In constructing this biplot, a polygon is formed by connecting the genotypes that are farthest from the origin, thereby enclosing all other genotypes within it.

From the origin of the biplot, perpendicular lines (or rays) are then drawn to each side of the polygon. These rays divide the biplot into several sectors, each containing one or more environments. The genotype located at the vertex of a sector is considered the “winner” in the environments that fall within that sector. This graphical approach makes it easy to identify which genotypes perform best in specific environments.

Table 4: Environment wise PC1 and PC2 scores.

Environment	PC1	PC2	Mean yield(kg/ha)
E1(RPR)	68.07	-3.96	4121
E2(BSP)	-32.78	-32.22	1964
E3(AMBK)	-6.318	-11.85	2998
E4(JGD)	-5.95	-25.54	4429
E5(KWD)	-6.66	19.67	2822
E6(RGH)	-16.36	53.9	2332

In the present study, a total of six sectors were identified in the polygon view of the GGE biplot (Fig. 3 and Fig. 4), out of which the environments fall into four sectors, thus forming four mega-environments (MEs). This visualisation approach aligns with the method described by Muthuramu and Ragavan (2022).

The polygon view of GGE biplot (Fig. 4) is the best way for the identification of winning genotypes with visualizing the interaction patterns between genotypes and environments. There are four mega environments one with E1 (RPR) that lies in a separate sector where G17 (R2756-61-1) dominates and also G19 (R2736-1-1) and G15 (R2723-12-1) will also give good performance but specifically in E1 (RPR). The second one consisting of E2 (BSP) and E3 (AMBK), where G38 (R2735-46-1) and also G4 (R2737-74-1) are the winners, third with E4 (JGD) where G3 (R2733-114-1) and G39 (Bastar Dhan 1(ch)) probably are the good performers and another mega environment consists of E5 (KWD) and E6 (RGH) where the winning genotypes are G50 (Vandana (ch)) which may show specific performance and also G16 (R2738-

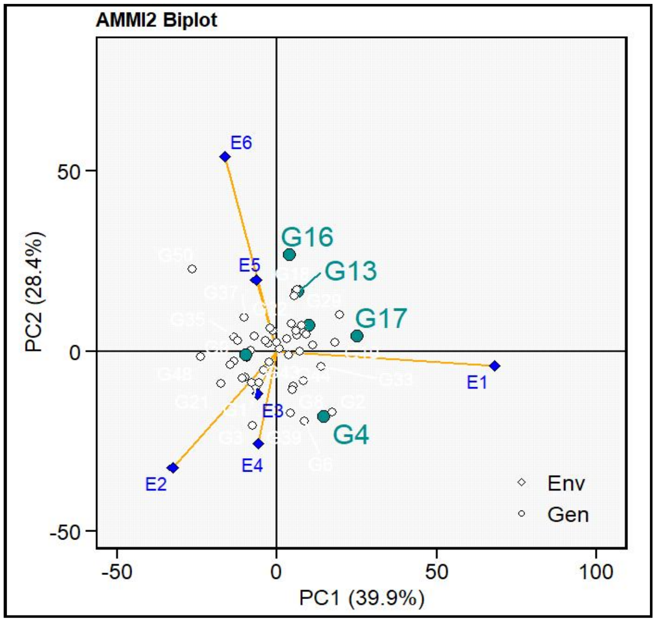

Fig. 4: GGE biplot display (Marked).

12-1) and G13 (R2745-118-1) will show better yield performance. These genotypes, located at the vertices or edge of the polygon and farthest from the origin, exhibited the highest interaction with the environments within their respective sectors. They are thus considered specifically adapted to the conditions of the environments falling within those sectors.

Discussion

The AMMI 1 biplot display helped us to identify the most stable genotype and also the genotypes with positive yield scores. Similar findings are also obtained by Akter *et al.*, (2014) who showed that the hybrids BRRI 1A/ BRRI 827R (G1), IR58025A/ BRRI 10R(G2), BRRI 10A/BRRI 10R(G3) and BRRI hybrid dhan1(G4) have higher average mean yields with high main (additive) effects with positive IPCA1 score, but the hybrid BRRI 10A/BRRI 10R(G3) being the overall best. These results align closely with the results of Lingaiah *et al.*, (2020), Das *et al.*, (20016) and with Vaezi *et al.*, (2017).

Similarly, the AMMI 2 biplot display helped us to find out the most and least discriminating genotypes as well as the environments. The results are aligned with the study of Wang *et al.*, (2023) in which he showed that distance of G3 from the biplot origin was the shortest demonstrating that the G3 variety had the strongest adaptability of all test varieties. Devi *et al.*, (2020) and Jeberson *et al.*, (2017) also had the similar findings.

The GGE biplot helped us to find out the winners in respective environments and also the genotypes which are specifically adapted to specific environments. The results go similar with the findings of Pagi *et al.*, (2017) found the genotypes G4 in E1 are the vertex genotype, which had the highest grain yield and also with the results given by Akinwale *et al.*, (2014) and Lingaiah *et al.*, (2020).

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