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Research Article

Detection of superior rice genotypes and yield stability using AMMI and MTSI models

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Abstract

Multi-environment yield trials and multi-trait stability analyses are essential to identify the superior genotype. The aim of this research was to assess the adaptation and stability of rice genotypes using additive main effect and multiplicative interaction (AMMI) and genotype plus genotype by environment (GGE) biplot analysis and multi-trait stability index (MTSI). In this study, 20 rice genotypes were evaluated for three seasons at the same location during 2020–21. Based on AMMI analysis, the genotypes G22 (Vandana), G32 (IC-0098989), G34 (IC-0135769), G60 (ADT 36), G61 (ADT 37), and G64 (ADT 45) were found to have high yield and were more stable. GGE analysis revealed that the high-yielding and stable genotypes were G22 (Vandana), G34 (IC-0135769), G60 (ADT 36), and G64 (ADT 45). The genotypes G65 (ADT 48), G60 (ADT 36), G38 (IC-0135529), and G33 (IC-0124198) were observed to be stable based on the Multi Trait Stability Index (MTSI). Based on the above, G60 (ADT 36) could be concluded as stable across all seasons, not only based on yield but also other important agronomic traits.

Keywords: AMMI, GGE, MTSI, Stability

INTRODUCTION

Rice [*Oryza sativa* L. (2n=24)] is a cereal grain belonging to the Poaceae family, annual and self-pollinated. It is also considered as a “Millennium Crop”. It is consumed by about 50 % of the global population (Patil *et al.*, 2012 and Syed *et al.*, 2023). Rice production needs to be increased by over 60 % by 2050, as the world’s population is predicted to reach nine billion (Tester and Langridge., 2010). The goals of plant breeding programmes have been the development of high-yielding cultivars. However, current breeding methods emphasize the significance of a cultivar’s performance stability and adaptability under a wide range of environmental conditions (Li *et al.*, 2019). Rice has the ability to grow in various ecosystems such as, rainfed, irrigated lowland, upland and flooded conditions. Yield is an end product and is determined by the number

of independent variables that show variation in different environments due to genotype and environmental interaction. Analyzing genotypic performance and stability is essential in improving selection efficiency and genotype adaptability in multi-environments. The present study was formulated to find out the phenotypic stability of rice genotypes over seasons by applying Additive Main Effect and Multiplicative Interaction (AMMI) analysis (Gauch, 1992); Genotype main effect plus Genotype x Environment (GGE) biplot analysis (Gabriel, 1971) and multiple trait stability index (Olivoto *et al.*, 2019) by observing 19 yield and yield component traits. In order to achieve accuracy, AMMI distinguishes between genotype, environment, and genotype x environment models (Anandan *et al.*, 2009b). The GGE analysis, a graphical approach and multiple trait

stability index, a new multivariate stability analysis model, which considers all traits to identify stable genotypes, were employed in this study.

MATERIALS AND METHODS

During 2020 and 2021, 20 rice genotypes (**Table 1**) were evaluated for three seasons viz., Oct,2020 – Dec,2020 (S1), July,2021 – Sep,2021 (S2) and Oct,2021 – Dec,2021 (S3) at the same location.

The trial was planted in Randomized Complete Block Design (RBD) with three replications, in two row plots of three meter length and with a spacing of 20 cm between rows and 15 cm between the rows. Each plot consisted of 40 plants. The trials were conducted at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu, India (Latitude 11°23'31.4"N; Longitude 79°42'53.09"E; MSL 5 m). Observations were recorded on the 19 yield contributing traits namely Number of days to first flowering (X1), Number of days to 50% flowering (X2), Number of days to maturity (X3), Height of the plant at first flowering (X4), Height of the plant at maturity (X5), Number of leaves at first flowering (X6), Total number of tillers per plant (X7), Number of productive tillers per plant (X8), Length of primary panicle (X9), Total number of seeds per primary panicle (X10), Percentage of seed fertility (X11), Length of seeds (X12), Breadth of the seeds (X13), L/B ratio of seeds (X14), Weight of 100 seeds (X15), Total dry matter production (X16), Harvest index

(X17), Per day productivity (X18) and Seed yield per plant (X19). All the recommended agronomic practices and need-based plant protection measures were judiciously followed. Replication means for the above traits were subjected to AMMI, GGE and MTSI (Multi-Trait Stability Index) analyses.

AMMI analysis decomposes the genotype, environment, and genotype-environment interaction effects in multilocation trials. It is particularly useful for complex genotype-environment interactions, providing clear visualization through biplots and helps breeders identify stable genotypes and suitable environments for cultivation. GGE analysis aims to understand genotype-environment interactions and identify genotypes with broad or specific adaptations to different environments. MTSI is a method used to assess the stability of genotypes across multiple traits rather than just focusing on yield or performance. It quantifies stability across traits, considering not only yield but also other important agronomic traits. All the above statistical analyses were carried out using CRAN R (version 4.3.1) software.

RESULTS AND DISCUSSION

The AMMI analysis of variance for yield (**Table 2**) revealed that the main effects of genotype (G) and environment (E) accounted for 75.44% and 17.71% of the variation, respectively, while the effects of the genotype x environment (G x E) interaction effects accounted for 3.24% of the total variation. The results of the investigation

Table 1. Details of the genotypes used in the present study

| S. No | Genotype | Name | Geographical origin |
|-------|----------|-------------|---------------------|
| 1 | G40 | IC-0207992 | NRRI, Cuttack |
| 2 | G35 | IC-0123756 | NRRI, Cuttack |
| 3 | G39 | IC-0134873 | NRRI, Cuttack |
| 4 | G65 | ADT 48 | TRRI, Aduthurai |
| 5 | G42 | IC-206447 | NRRI, Cuttack |
| 6 | G41 | IC-0207955 | NRRI, Cuttack |
| 7 | G33 | IC-0124198 | NRRI, Cuttack |
| 8 | G36 | IC-0142508 | NRRI, Cuttack |
| 9 | G38 | IC-0135529 | NRRI, Cuttack |
| 10 | G63 | ADT 43 | TRRI, Aduthurai |
| 11 | G10 | Kalinga III | NRRI, Cuttack |
| 12 | G37 | IC-0123083 | NRRI, Cuttack |
| 13 | G22 | Vandana | NRRI, Cuttack |
| 14 | G60 | ADT 36 | TRRI, Aduthurai |
| 15 | G34 | IC-0135769 | NRRI, Cuttack |
| 16 | G61 | ADT 37 | TRRI, Aduthurai |
| 17 | G64 | ADT 45 | TRRI, Aduthurai |
| 18 | G32 | IC-0098989 | NRRI, Cuttack |
| 19 | G66 | ASD 16 | RRS, Ambasamudram |
| 20 | G28 | Anjali | NRRI, Cuttack |

Table 2. AMMI Analysis of variation for rice 20 genotypes for yield

| Source | Yield | | | | | |
|-----------|--------|---------|--------|---------|---------|------------------|
| | df | SS | MSS | F value | P value | Explained SS (%) |
| ENV | 2.00 | 1285.70 | 642.86 | 2032.96 | 0.00 | 17.71 |
| REP(ENV) | 6.00 | 1.90 | 0.32 | 1.39 | 0.23 | 0.03 |
| GEN | 19.00 | 5477.70 | 288.30 | 1265.89 | 0.00 | 75.44 |
| GEN:ENV | 38.00 | 235.00 | 6.18 | 27.15 | 0.00 | 3.24 |
| IPCA1 | 20.00 | 161.50 | 8.08 | 35.47 | 0.00 | 2.22 |
| IPCA2 | 18.00 | 73.50 | 4.08 | 17.92 | 0.00 | 1.01 |
| Residuals | 114.00 | 26.00 | 0.23 | NA | NA | 0.36 |
| Total | 217.00 | 7261.20 | 33.46 | NA | NA | NA |

showed that G, E, and G x E related variances were significant. The significant mean sum of squares for genotypes indicated that the performance of genotypes was uneven, with substantial fluctuations across genotypic means accounting for most of the variation in yield. In this study, the genotypes for yield and yield component traits in various contexts showed substantial differences. The selected study material consisted of a range of genotypes from landraces and improved varieties. Since landraces are able to adapt to their local environment and are a great source of genetic resources, including them in scientific investigations is vital (Anandan *et al.*, 2011; Thangavel *et al.*, 2011). When the interaction was partitioned between the first two interaction principal component axes (IPCA), which were significant in the postdictive analysis, the AMMI model clearly showed the presence of genotype-environment interaction (GEI). About 2.22% of the interaction sum of squares was explained by IPCA1 and 1.01% was explained by IPCA2. This suggested that the first two principal components of genotypes and environments were sufficient to predict the interaction of the genotypes with the three seasons. While the residual effect is low, the very first principal component factor provides significant information about the interaction sum of squares. This suggests that G x E interaction is influenced by one basic element, which may be environmental or genetic in origin (Anandan *et al.*, 2009a; 2009b; Ponsiva *et al.*, 2022)

AMMI Bi-Plots: The most potent interpretative technique for AMMI models is probably biplot analysis. There are two types of fundamental AMMI biplots: the AMMI first biplot, which compares the major impacts and IPCA1 scores for genotypes and environments. The AMMI second biplot, displays the scores for IPCA1 and IPCA2.

First biplot of AMMI: In order to visualize interrelationships, biplots are graphs where factors of both genotypes and environments are shown on a single axis. The typical interpretation of a biplot, as seen in the AMMI 1 biplot (Fig. 1), is that displacements along the ordinate denote variations in interaction effects while displacements along the abscissa denote variations in main effects

(Anandan *et al.*, 2009a; Akter *et al.*, 2014). A genotype or environment on the right side of the centroid of this axis has larger yields than those on the left. According to the procedure given by Zobel *et al.* (1988), genotypes and environments on the same straight line, related, or ordinated have similar yields. In the present study, the genotype G64 (ADT 45) was observed to be the best overall, followed by G22 (Vandana), G32 (IC-0098989), G34 (IC-0135769), G60 (ADT 36) and G61 (ADT 37). All these genotypes typically showed high yield with significant additive main effects. Thus, the genotype G64 (ADT 45) was recognized to suit the wide range of environments. Out of the three seasons, season S3 had the lowest IPCA1 score and the least interaction effects, showing that all the genotypes flourished there. Additionally, the IPCA1 scores for G33 (IC-0124198), G39 (IC-0134873), G41 (IC-0207955), G62, and G65 (ADT 48) were nearly zero, showing that they were stable and were less affected by environments. The G x E interaction had little impact on the genotypes G22 (Vandana), G32 (IC-0098989), G34 (IC-0135769), G60 (ADT 36), G61 (ADT 37), and G64 (ADT 45), which means they would perform well in a broad range of environments. Due to their consistent yields, S3 could be considered a suitable season for genotype development.

Second biplot of AMMI: The season scores are connected to their origin by straight lines in the AMMI 2 biplot (Fig. 2). If the seasons have short straight line, the interaction is considered as less and vice versa. In this study, all the seasons had long straight lines revealing significant interaction. In general, genotypes that are close to the origin are considered better for all the seasons, while genotypes that are away from the origin may not perform equally in all the seasons. In the present study, all the genotypes were close to the origin, and hence could be insensitive to environmental interactive forces except G62, G66 (ASD 16), and G37 (IC-0123083). When environments and genotypes are in the same sector, they interact positively and vice versa (Anandan *et al.*, 2009a).

GGE biplot analysis: GGE biplot is based on both genotype and environment-focused scaling. It is used to compare

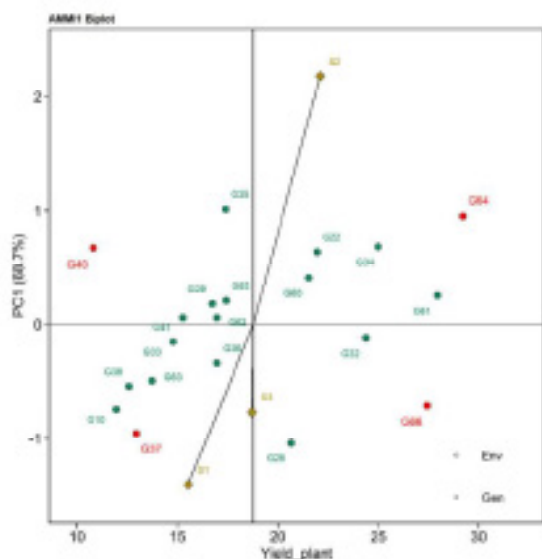


Fig. 1. First biplot of AMMI

the genotypes with the ideal genotype and estimate the patterns of reference environments. Genotypes that had positive IPCA1 scores were high yielding and those that had negative IPCA1 scores were lower yielders. IPCA2 was associated with genotypic stability. Positive IPCA2 scores for genotypes were correlated with greater stability, whereas negative IPCA2 scores correlated with less stability. In the current study, the genotypes G22 (Vandana), G34 (IC-0135769), G60 (ADT 36), and G64 (ADT 45) were more stable with higher yield. Although G28 (Anjali), G32 (IC-0098989), G61 (ADT 37), G62, and G66 (ASD 16) had high yields, they were unstable. All the three seasons had positive IPCA1 scores. As a result, it is possible that IPCA1 indicated proportionate genotype yield variations across the seasons. In seasons with higher IPCA1 scores, genotypes can be clearly distinguished (Yan *et al.*, 2000). However, IPCA2 had values that were both positive as well as negative. This indicated disproportionate yield changes between the seasons, resulting in the crossover GEI (Yan *et al.*, 2000).

The interrelationships between the seasons are briefly summarised in the GGE-biplot vector (Fig. 3). Site vectors are the lines that link the biplot origin and the site markers. The correlation coefficient between two seasons is linked to the angle between their vectors. Since none of the angles were greater than 90° between any two seasons, they could all be considered as positively correlated.

Discriminative and representativeness: The discriminative capacity and representativeness of the GGE biplot are crucial estimates of the testing seasons. The biplot in Fig. 4 had concentric circles that aid in visualizing the length of the season vectors, which is an

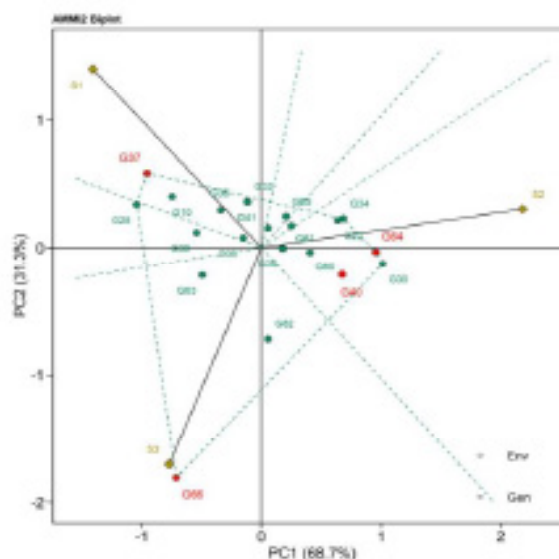


Fig. 2. Second biplot of AMMI

estimate of the seasons' capacity for discrimination and is proportionate to the standard deviation within each site. Thus, compared to S1 and S3, the S2 test setting was more discriminating. S3 had a smaller angle with the AEC abscissa than S1 and S2. Therefore, S3 is a greater representation of the wide-environment. Seasons are an ideal site to choose better genotypes since they feature lengthy vectors and modest angles with the AEC abscissa. As a result, better genotypes might be chosen from the S3 environment.

Ranking of genotypes: An ideal genotype should be stable in all the seasons and have the best mean performance. An arrow pointing to an ideal genotype in Fig. 5 denotes it as having zero GEI and the longest vector length among the high yielding genotypes. Even if such a perfect genotype could not exist, it might be utilised as a benchmark for evaluating other genotypes (Yan and Tinker, 2006). It is most preferable to have a genotype that is nearer to the ideal genotype. To interpret the gap between the ideal genotype and each of the test genotypes, concentric circles were constructed with the ideal genotype at their core. The units of the AEC abscissa (mean yield) and ordinate (stability) should be in the original unit of yield as the units of IPCA1 and IPCA2 for the genotypes are the original unit of yield in the genotype-focused scaling (Fig. 5). The initial unit of yield will now include the unit of the difference between the ideal genotype and genotypes under study. As a result, stability and mean yield are assumed to be equally essential in the ranking based on genotype-focused scaling (Farshadfar *et al.*, 2012). Among the genotypes studied, G61 (ADT 37), G66 (ASD 16), and G64 (ADT 45), which were in the core of concentric circles, were the ideal genotypes in terms of better yielding capacity and stability (Fig. 5). Additionally,

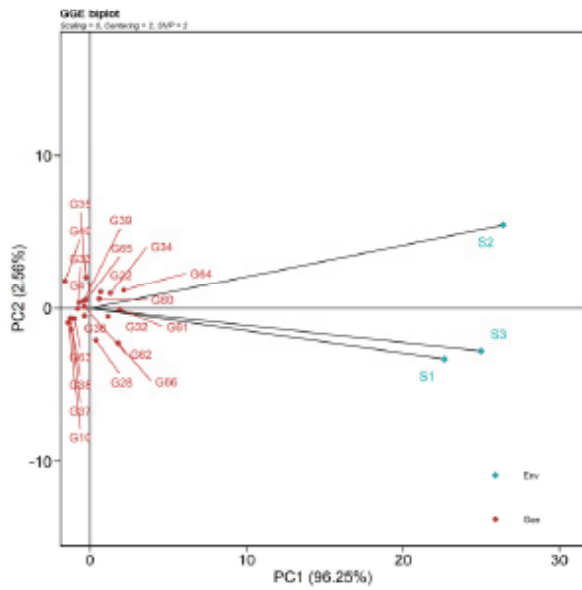


Fig. 3. GGE biplot with scale centred on both environment and genotype

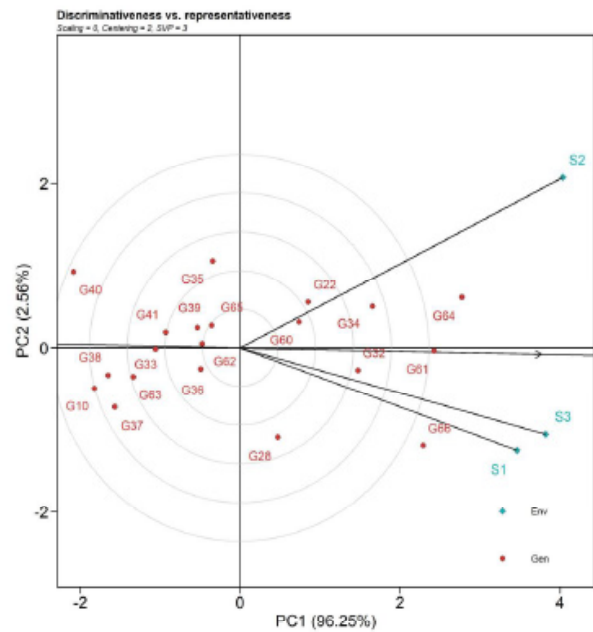


Fig. 4 GGE biplot of discriminativeness and representativeness

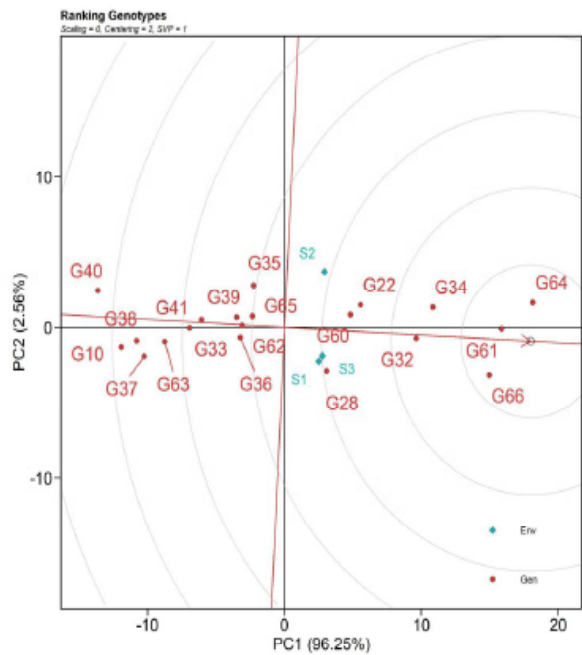


Fig. 5. GGE biplot for ranking genotypes

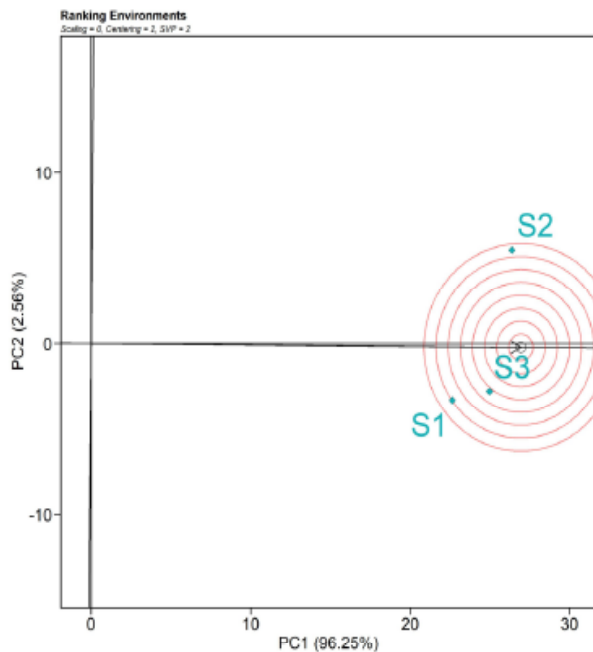


Fig. 6. GGE biplot for ranking environments

the genotypes G32 (IC-0098989) and G34 (IC-0135769), which are found on the following concentric circle, can be viewed as desirable genotypes.

Ranking environments: A location near the ideal site makes a site more appealing. To illustrate the distance

between each habitat and the ideal site, concentric circles were formed with the ideal site at their center. In **fig. 6**, an arrow pointing direction denotes the ideal site. S3 was the closest to the concentric circle and none of the settings fit the definition of an ideal site. S3 was therefore regarded as the most advantageous of the three seasons.

Mean and stable performance of genotypes: The stability and yield performance of genotypes were evaluated using the average environment coordination (AEC) approach. It is important to examine the average performance and environmental stability of the genotypes. The GGE biplot's average environment coordination (AEC) position is shown in Fig. 7. A genotype with a high ordinate (stability) and a high abscissa (mean single plant yield) is considered desirable (Kiruba *et al.*, 2023). The AEC abscissa, which is represented by the single arrow, indicates greater mean yield across seasons. The highest mean yield was observed in G64 (ADT 45), G61 (ADT 37), and G66 (ASD 16). Poor stability in either direction is shown by the AEC ordinate, the non-arrowed line. It was observed that G40 (IC-0207992), G10 (Kalinga III), and G38 (IC-0135529) had extremely low yield and were exceedingly unstable. Additionally, while having the greatest mean yield, G61 (ADT 37) was more stable than G64 (ADT 45) and G66 (ASD 16).

Which genotype won where: The which-won-where pattern is plainly displayed in the polygon view of a GGE-biplot, which provides a clear overview of the GEI pattern of yield data. By joining the markers of the genotypes that are distant from the biplot origin, the polygon is created, containing all other genotypes. In Fig.8, the lines that represent the rays are orthogonal to the polygon's sides. Rays 1 and 2 are, respectively, perpendicular to the side that joins genotypes G35 (IC-0123756)-G64 (ADT 45) and G64 (ADT 45)-G66 (ASD 16). Side G28 (Anjali)-G37 (IC-0123083) is perpendicular to Rays 3, 4, and 5. G10

(Kalinga III)-G40 (IC-0207992) are perpendicular to Ray 6. From G35 (IC-0123756) to G64 (ADT 45), Ray 7 is perpendicular.

All three seasons lie inside the seven sectors that these seven rays create in the biplot. The vertex genotypes for each sector in this perspective of a GGE biplot have better yield than the others in all the seasons that lie inside the sector (Yan, 2002), which is an attractive attribute. Therefore, one site (S2) occurred within the sector 1 constituted by Rays 1 and 2, and the edge genotype for this sector was G64 (ADT 45), indicating that higher-yielding genotypes for this site. Similarly, two seasons (S1 and S3) appeared in sector 2 between rays 2 and 3, and the apex genotypes for this sector were G28 (Anjali) and G66 (ASD 16), indicating that these two seasons' higher yielding genotypes were G28 (Anjali) and G66 (ASD 16). According to Chandrashekar *et al.* (2020), the highest single plant yield of a genotype in those environments was produced when two or more environments existed in the same sector. In contrast, S2 site was grouped into a single environment with the winning genotype G64 in the present inquiry. S1 and S3 were grouped into another single site with the winning genotypes G66 and G28.

Multiple Trait Mean Performance and Stability: The factor analysis using the WAASBY (Weighted Average of Absolute Scores Stability index) is presented in the table 4. Considering eigenvalues larger than one, the initial five components explained 79.80% of the variation in the characteristics. Four traits (Days to First Flowering, Days

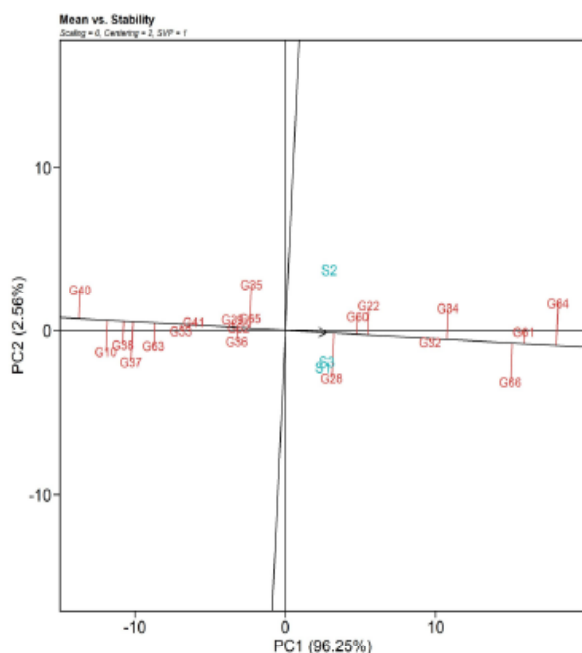


Fig. 7. GGE biplot for mean and stable performance of genotypes

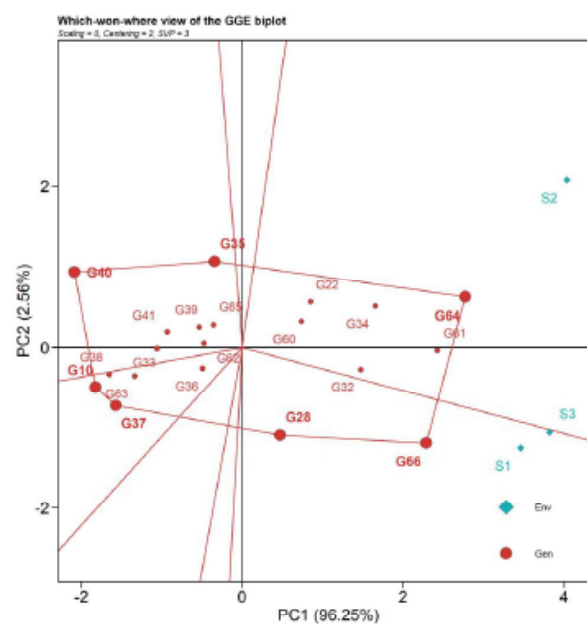


Fig. 8. GGE biplot for which won-where view

to Fifty percent Flowering, Days to Maturity, and seeds per panicle) were grouped together by FA1. Tiller number, seed weight, productivity per day, and plant yield were grouped in FA2. Plant height at maturity and plant height at first flowering were two traits that FA3 grouped together. The traits (leaf number at first flowering, panicle length, and seed width) were grouped together by FA4. Five traits were grouped together by FA5, including seed length, seed length breadth ratio, total dry matter production and harvest index (Table 4).

Fig. 9 presents the MTSI rankings for 20 genotypes. The genotypes G65 (ADT 48), G60 (ADT 36), G38 (IC-0135529), and G33 (IC-0124198) were chosen based on all the 18 traits such as days to first flowering, days to fifty percent flowering, days to maturity, plant height at first flowering, plant height at maturity, leaf number at first flowering, tiller number, panicle length, seeds per panicle, seed fertility, seed length, seed width, seed length breadth ratio, seed weight, total dry matter production, harvest index, productivity per day and yield per plant. These traits were used to calculate selection differentials. Selection Differentials (SD) quantify the change in the mean trait value of a population between pre- and post-selection. For all the traits, the top four genotypes throughout the environment had desired values. Among them, HI trait had a maximum SD percentage (Table 4).

Based on a variety of traits and multiple environments, selection using the WAASB index with MTSI produces stable and high-yielding parent lines. This study was able to identify the stable genotypes, which are highlighted in Fig. 9. With the exception of seed weight, the MTSI yields a positive SD for every one of the traits, suggesting the efficiency of MTSI in selecting stable-performing genotypes (Ramalingam et al., 2024)

Crop yield is a complicated character which is either directly or indirectly affected by the environment. The AMMI statistical model could make an excellent tool to identify the most stable, high-yielding genotypes for specific as well as general situations. The genotype G64 (ADT 45) recorded a higher yield than all other genotypes across all the seasons in the current investigation. The genotypes G22 (Vandana), G32 (IC-0098989), G34 (IC-0135769), G60 (ADT 36), G61 (ADT 37), and G64 (ADT 45) were influenced by the G x E interaction and would thus function well in a variety of contexts. The yield performance was strongly impacted by genotype, followed by environment and GEI, according to the GGE biplot results from this study. The genotypes G22 (Vandana), G34 (IC-0135769), G60 (ADT 36), and G64 (ADT 45) were selected for specific environmental adaptation based on the GGE biplot analysis. According to Multi Trait Stability Index (MTSI), the genotypes G65

Table 3. Result of factor analysis

| Factor Components | FA1 | FA2 | FA3 | FA4 | FA5 | Communality | Uniquenesses |
|---------------------------------|-------|-------|-------|-------|-------|-------------|--------------|
| Eigenvalue | 4.19 | 3.60 | 2.77 | 2.05 | 1.76 | - | - |
| Relative variance (%) | 23.30 | 20.00 | 15.40 | 11.40 | 9.81 | - | - |
| Cumulative variance (%) | 23.30 | 43.30 | 58.60 | 70.00 | 79.80 | - | - |
| Eigen vectors | | | | | | | |
| Days to First Flowering | -0.96 | 0.03 | 0.09 | -0.12 | -0.11 | 0.96 | 0.04 |
| Days to Fifty percent Flowering | -0.99 | 0.04 | 0.05 | -0.01 | -0.04 | 0.98 | 0.02 |
| Days to Maturity | -0.98 | 0.07 | 0.09 | -0.02 | 0.01 | 0.98 | 0.02 |
| Plant Height at First Flowering | -0.12 | 0.03 | 0.92 | -0.11 | 0.15 | 0.89 | 0.11 |
| Plant Height at Maturity | -0.08 | 0.03 | 0.98 | -0.06 | 0.04 | 0.97 | 0.03 |
| Leaf number at First Flowering | -0.27 | 0.11 | 0.28 | -0.71 | 0.13 | 0.69 | 0.31 |
| Tiller Number | -0.04 | -0.74 | -0.11 | -0.26 | -0.24 | 0.68 | 0.32 |
| Panicle length | 0.19 | -0.22 | 0.56 | 0.57 | -0.05 | 0.72 | 0.28 |
| Seeds per panicle | -0.67 | -0.34 | -0.07 | 0.26 | -0.31 | 0.73 | 0.27 |
| Seed fertility | -0.41 | -0.04 | -0.18 | 0.04 | -0.64 | 0.61 | 0.39 |
| Seed length | -0.02 | 0.25 | -0.01 | -0.46 | -0.56 | 0.60 | 0.41 |
| Seed width | 0.35 | -0.22 | -0.01 | -0.85 | -0.03 | 0.89 | 0.11 |
| Seed Length Breadth ratio | -0.21 | 0.38 | 0.05 | 0.33 | -0.65 | 0.72 | 0.28 |
| Seed weight | 0.36 | 0.64 | -0.05 | -0.02 | -0.15 | 0.56 | 0.44 |
| Total Dry matter Production | -0.10 | -0.52 | 0.13 | 0.15 | 0.61 | 0.69 | 0.31 |
| Harvest Index | 0.05 | -0.37 | -0.05 | 0.08 | -0.86 | 0.89 | 0.11 |
| Productivity per day | 0.18 | -0.94 | -0.01 | 0.08 | 0.09 | 0.92 | 0.08 |
| Yield per plant | 0.07 | -0.94 | 0.04 | 0.14 | 0.05 | 0.90 | 0.10 |

Table 4. The WAASBY index's selection differential

| S. No. | Variables | Factor | Xo | Xs | SD | SD% |
|--------|---------------------------------|--------|------|------|-------|-------|
| 1 | Days to First Flowering | FA1 | 67.1 | 77 | 9.95 | 14.8 |
| 2 | Days to Fifty percent Flowering | FA1 | 70.5 | 78.3 | 7.79 | 11 |
| 3 | Days to Maturity | FA1 | 69 | 77.3 | 8.27 | 12 |
| 4 | Seeds per panicle | FA1 | 83.5 | 91.4 | 7.86 | 9.41 |
| 5 | Tiller Number | FA2 | 53.3 | 66.2 | 12.9 | 24.1 |
| 6 | Seed weight | FA2 | 73.6 | 72 | -1.56 | -2.12 |
| 7 | Productivity per day | FA2 | 65.6 | 75.9 | 10.3 | 15.7 |
| 8 | Yield per plant | FA2 | 58.6 | 73.2 | 14.6 | 24.9 |
| 9 | Plant Height at First Flowering | FA3 | 67.8 | 81.8 | 14.1 | 20.8 |
| 10 | Plant Height at Maturity | FA3 | 64.3 | 84.4 | 20.2 | 31.4 |
| 11 | Leaf number at First Flowering | FA4 | 62.3 | 69.5 | 7.23 | 11.6 |
| 12 | Panicle length | FA4 | 46.9 | 53.5 | 6.59 | 14.1 |
| 13 | Seed width | FA4 | 59.3 | 60.4 | 1.09 | 1.84 |
| 14 | Seed fertility | FA5 | 54.4 | 62.4 | 7.93 | 14.6 |
| 15 | Seed length | FA5 | 49.1 | 51.5 | 2.46 | 5.02 |
| 16 | Seed Length Breadth ratio | FA5 | 60.4 | 63.8 | 3.45 | 5.71 |
| 17 | Total Dry matter Production | FA5 | 71.4 | 72.8 | 1.42 | 1.99 |
| 18 | Harvest Index | FA5 | 58.8 | 77.5 | 18.6 | 31.7 |

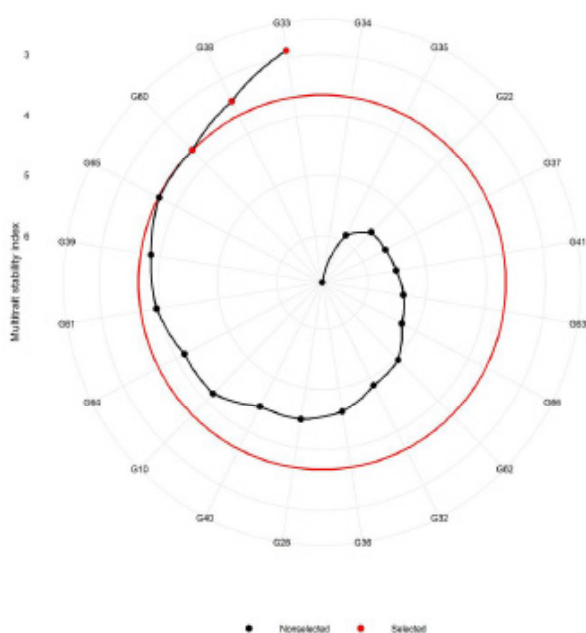


Fig. 9 MTSI rankings for 20 genotypes

(ADT 48), G60 (ADT 36), G38 (IC-0135529) and G33 (IC-0124198) were selected to identify best genotype across all the 18 traits. As a result, G60 (ADT 36) demonstrates stable performance across all environments, considering not only yield but also other important agronomic traits.

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