*Original Research Article*

# Assessment of genetic stability of medium slender rice genotypes for yield trait using AMMI model and GGE biplot methodology over different locations of Karnataka


## ABSTRACT

Medium slender grain varieties of rice are one of the most preferred among the south Indian rice consumers and has a high demand in both national as well as international markets. In the study, 18 medium slender rice genotypes were examined along with four individual checks in Karnataka across four different locations to assess genetic stability using additive main effects and multiplicative interaction (AMMI) model and GGE bi-plot methodology. The genotype environment interaction (G×E interaction) were partitioned into two principal components and were found highly significant. Together, IPCA1 and IPCA2 explained more than 75 percent of G×E interactions for yield trait, with IPCA I explaining maximum G×E interaction. Gangavati and Malnoor were found to be favorable environments. AMMI analysis indicated that the BPT mutant 1801, BPT mutant 1804 and BPT mutant 1811 were found to be most stable genotypes for grain yield across locations over check GGV-05-01. Among rice genotypes, the best elite genotype, BPT mutant 1801 recorded highest grain yield and was also the most stable in grain yield across four locations.



*Keywords*: Rice, stability analysis, AMMI, GGE bi-plot


## 1. INTRODUCTION

A staple food for more than 3.5 billion people worldwide, rice (*Oryza sativa* L.) holds an enviable position among the food crops that are grown around the globe, making a significant contribution to global food security. Most rice is produced in Asia, primarily in China and India (Kumar *et al*., 2011). As India's largest agricultural crop, rice accompanies 42% of its total food grain production and 45% of its total cereal production, accounting for 24% of the country's gross cropped land (Chethana *et al*., 2016).

An evaluation of phenotypic traits (P) assessed upon multiple environments (E) will be different from an assessment of genotypic traits (G), so P = G + E + (G×E). Due to the huge impact that G×E interactions have on phenotype, it is imperative to conduct stability analyses to assess genotype performance in various environments and make the process easier for plant breedersThe estimation of the G×E interaction, on the other hand, has continuously been a intriguing issue within the past. Biplots are presently broadly utilized to evaluate genotype environment interaction (GEI) since the G×E impacts can be envisioned in a single chart, making genotypes and their intelligent with situations less demanding to compare (Gauch and Zobel 1989). Yan *et al.* (2000) proposed a modern GEI examination procedure based on biplots, comparative to the AMMI method, that has the advantage of breaking down the joint impact of genotype (G) and G×E (G + GE) by central component examination, as restricted to the initial AMMI investigation, which as it were breaks down G×E.

The essential ANOVA depicts fundamental impacts and determines whether genotype × environment may be a critical source of variety, but it does not give knowledge into the designs of genotypes or environments that provide rise to intuitive. Besides, PCA (multiplicative show) contains no sources of variations for genotype or environment, and does not viably dissect interactions (Zobel *et al.,* 1988). AMMI analysis (Gauch and Zobel, 1988) improves the likelihood of effective selection and has been used to assess genotype × environment interaction with greater precision in various crops (Gauch, 1992, Crossa *et al*., 1991). The GGE biplot is habitually utilized to discover the GEI design in information. It clearly simplifies the location of huge environments.

The goal of this study was to figure out how different agro-climatic zones (environments) affect yield in specific genotypes and to find sites that are best suited for higher production. As a result, to offer the optimum genotype for rice growers in the region, as well as for the country's familiar agro ecologies.

## 2. MATERIAL AND METHODS

During this study, 18 medium slender rice genotypes were used, along with four yield checks (Rp-Bio 226, GNV 10-89, GGV-05-01, and BPT-5204), which included both early and medium maturing mutants (M8 Generation) and advanced breeding lines developed at AICRP-Rice breeding, ARS, Gangavati (Table 1).

**Table 1. List of 22 genotypes used in the study**

| Sl. No. | Genotypes | Sl. No. | Genotypes |
|---|---|---|---|
| 1 | GNV-1905 | 12 | BPT mutant 1804 |
| 2 | GNV-1906 | 13 | BPT mutant 1805 |
| 3 | GNV-1907 | 14 | BPT mutant 1806 |
| 4 | IET-27904 | 15 | BPT mutant 1809 |
| 5 | IET-27416 | 16 | BPT mutant 1811 |
| 6 | IET-27870 | 17 | RNR - 15048 |
| 7 | IET-26241 | 18 | Gangavati sanna |
| 8 | IET-27438 | 19 | Rp-Bio 226(C) |
| 9 | IET-25520 | 20 | GNV 10-89 (C) |
| 10 | BPT mutant 1801 | 21 | GGV-05-01 (C) |
| 11 | BPT mutant 1802 | 22 | BPT-5204 (C) |



### 2.1 Field experiments

Four locations in Karnataka were used to test these genotypes during the *Kharif* of 2019, namely Agriculture Research Station Gangavati (Zone 3), Agriculture Research Station Dhadesugur (Zone 3), Agriculture Research Station Malnoor (Zone 2), and Agriculture Research Station Kawadimatti (Zone 2). A randomized complete block design with three replications at four study sites was used to evaluate these rice genotypes with four checks. At each location, 25-30-day-old seedlings were transplanted into 13 rows of 4 m row length, planted 20 cm apart, and the recommended package of procedures for rice production in the region was followed.

### 2.2 Additive main and multiplicative interaction (AMMI) analysis

Using the statistical program GenStat 18th edition, the G X E interaction of 22 rice genotypes in four locations was assessed using the AMMI model proposed by Gauch and Zobel in 1988. After fitting an ANOVA model with main effects of genotype and environment (without

interaction), the standardized residuals were used to fit a principal component analysis (PCA). The experimental error as well as the influence of the G×E interaction are included in these residuals. The equation was:

$$Y_{ij} = \mu + G_i + E_j + \Sigma\lambda_k \alpha_{ik} \gamma_{jk} + e_{ij}$$

$Y_{ij}$ is the observed mean yield of the i $^{th}$ genotype in the j $^{th}$ environment, m is the general mean, $G_i$ represents the effects of genotypes and environments for the $k^{th}$ axis, $a_{ik}$ is the eigen vector of the i $^{th}$ genotype for the k $^{th}$ axis, $g_{jk}$ represents the eigen vector of the j $^{th}$ environment for the k $^{th}$ axis, n is the number of principal components in the model. $e_{ij}$ is the average of the corresponding random errors.

**2.3 Stability parameters**

The AMMI stability value (ASV) and the genotypic stability index were calculated as two stability parameters (GSI). AMMI does not include a quantitative stability measure, which is crucial to quantifying and ranking genotypes according to their yield stability (Gauch and Zobel, 1996; Gauch, 1992). To quantify and rank genotypes based on their trait stability, the AMMI stability value (Purchase et al., 2000) was utilised.

The distance from the origin in the two-dimensional scatter plot of IPCA1 against IPCA2 scores is the AMMI stability value (ASV). The contribution of IPCA1 and IPCA2 sums of squares to the interaction sum of squares was used to compute it for each genotype (Purchase, 2000). The formula for calculating the AMMI stability value is as follows:

$$\mathbf{ASV} = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}(\mathbf{IPCA1score})\right]^2 + [\mathbf{IPCA2\ score}]^2}$$

Where,

$SS_{IPCA1}$ and $SS_{IPCA2}$ are the sum of squares of $IPCA_1$ and $IPCA_2$ respectively.

$IPCA_1$ score and $IPCA_2$ score are the scores of the genotype in those particular PCAs.

Genotype having low ASV is considered as widely adapted genotype. In the same manner, the genotype having IPCA2 score near zero reveals more stability while large values indicate more responsive and less stable genotypes.

$$\mathbf{GSI = R_{ASV}+R_Y}$$

Low values of GSI indicate desirable genotypes with high mean yield and stability, RASV is the rank of AMMI stability value, and RY is the rank of mean yield of genotypes (RY) across environments.

### 2.4 GGE bi-plot analysis

In order to interpret GEI patterns, we used GGE bi-plot methodology, which is a combination of AMMI bi-plot and GGE concepts (Yan *et al.*, 2000). An average-environment coordination (AEC) view of biplot based on environment-focused scaling was used to interpret mean genotype performance vs. their adaptability patterns based on a polygon view of genotype-environment interaction biplot based on symmetrical scaling.

## 3. RESULTS AND DISCUSSION

Mean yield performance of all 22 genotypes over four locations for grain yield per hectare are represented in Table 2. The trait yield had a considerable contribution from main factors (genotypes and environments) and interaction effects, according to the AMMI model (Table 3). Significant mean sums of squares attributable to genotypes suggested that there were genotypic differences, and relevance of environment explains why environmental effects change across different sites and test locations. Furthermore, genotype-environment interaction results indicate that genotypes behave differently in different settings.

The large sum of squares owing to environments for yield suggested that there were significant variances in environmental means and that the environments were diversified (Zobel et al. 1988). In this study, it was discovered that environmental mean differences in yield were much higher than genotypic mean variations (Table 3). As a result, the test locations were varied. AMMI study demonstrated that the mutants BPT-5204 Mutant-653 and BPT-5204 Mutant-1807 were stable genotypes for grain yield, which agrees with Prashant et al. (2019) who examined twelve rice mutants for grain yield stability under saline soil at four locations.

Similarly, Ashwini *et al.* (2019) used the AMMI model to analyze conventional and enhanced rice varieties in five distinct Karnataka locales, and biplots were created using GGE bi-plot approach for grain yield and quality attributes. In the case of yield, it was discovered that environmental mean fluctuations were far higher than genotypic mean variations. In contrast, Dewi et al. (2014) found that when rice genotypes were examined in different growing seasons, the mean sum of square due to genotype main effect was high for grain yield. These findings show that seasonal variations in environment mean are less important than geographical differences.

The multiplicative variance of the treatment sum of squares due to the GE interaction was significant, it was further partitioned into the interaction principal component axis (IPCA). The IPCA I and IPCA II scores, respectively, explained 71.92 percent and 25.06 percent of the interaction. The total GEI for the trait grain yield per hectare was captured by these two PCA axes, which accounted for 96.98% of the total GEI.

**3.1 Stability parameters**

BPT mutant 1801 (86.37 q/ha) had the lowest AMMI stability value (0.31), followed by BPT mutant 1804 (80.03 q/ha) and BPT mutant 1811 (80.71 q/ha) with 0.39 and 0.41 ASV, respectively. Similarly, according to the Genotypic Selection Index (GSI), BPT mutant 1801 was discovered to be the best genotype because it had a lower value (Table 4).

**3.2 Pattern of genotype-environment interaction display using graphical tool**

On the genotypes that are farthest from the bi-plot origin, a polygon is constructed, and all other genotypes fall within the polygon. Each side of the polygon has perpendicular lines drawn from the GGE bi-plot origin. The perpendicular lines on the polygon are equality lines between adjacent genotypes. In one or more locations, the genotypes positioned on the polygon's vertices perform the best or the worst. The bi-plot is divided into sections by the equality lines. At sites whose markers (points) fall inside the relevant sector, the vertex genotype is the winning genotype (Yan *et al*., 2000).

Locations within the same sector share. The winning genotype is the same, but winning genotypes in different areas are different. The presence or absence of cross-over GEI is indicated by the polygon view of a GGE bi-plot (Yan and Rajcan, 2002).

**Table 2. Mean yield performance of varieties in four locations.**

| Grain yield per hectare (q/ha.) | | | | | | |
|---|---|---|---|---|---|---|
| **Sl. No.** | **Genotype** | **Gangavati** | **Malnoor** | **Kawadimatti** | **Dhadesugur** | **Mean** |
| 1 | GNV -1905 | 33.90 | 29.32 | 27.74 | 31.56 | 30.63 |
| 2 | GNV-1906 | 63.03 | 60.42 | 63.56 | 62.61 | 62.40 |
| 3 | GNV-1907 | 62.83 | 66.67 | 61.58 | 69.38 | 65.11 |
| 4 | IET-27904 | 82.57 | 67.68 | 64.82 | 78.19 | 73.32 |
| 5 | IET-27416 | 52.97 | 55.91 | 56.54 | 58.57 | 56.00 |
| 6 | IET-27870 | 79.64 | 72.31 | 69.46 | 61.28 | 70.67 |
| 7 | IET-26241 | 70.80 | 70.92 | 72.36 | 66.00 | 70.02 |
| 8 | IET-27438 | 80.69 | 66.62 | 69.54 | 73.94 | 72.70 |
| 9 | IET-25520 | 84.27 | 73.90 | 71.46 | 77.98 | 76.90 |
| 10 | BPT mutant 1801 | 94.34 | 83.05 | 81.32 | 86.78 | 86.37 |
| 11 | BPT mutant 1802 | 63.01 | 64.24 | 66.28 | 77.54 | 67.77 |
| 12 | BPT mutant 1804 | 88.28 | 77.42 | 74.49 | 79.95 | 80.03 |
| 13 | BPT mutant 1805 | 73.47 | 67.39 | 70.54 | 92.22 | 75.90 |
| 14 | BPT mutant 1806 | 84.44 | 75.49 | 71.36 | 77.93 | 77.31 |
| 15 | BPT mutant 1809 | 73.71 | 67.81 | 69.58 | 95.04 | 76.54 |
| 16 | BPT mutant 1811 | 86.67 | 77.99 | 75.86 | 82.31 | 80.71 |
| 17 | RNR - 15048 | 85.98 | 78.56 | 76.84 | 61.09 | 75.62 |
| 18 | Gangavati sanna | 60.18 | 64.58 | 67.56 | 71.61 | 65.98 |
| 19 | Rp-Bio 226(C) | 80.73 | 77.07 | 74.32 | 79.44 | 77.89 |
| 20 | GNV 10-89 (C) | 78.82 | 72.39 | 67.44 | 73.94 | 73.15 |
| 21 | GGV-05-01 (C) | 80.04 | 76.45 | 77.96 | 80.93 | 78.84 |
| 22 | BPT-5204 (C) | 82.48 | 70.42 | 72.56 | 70.75 | 74.05 |
| | CD @ 5% | 10.81 | 11.25 | 8.84 | 8.76 | |
| | CV % | 9.22 | 10.47 | 8.31 | 7.69 | |

q/ha= quintal per hectare, CD=critical difference, CV=coefficient of variation, C= Check

**Table 3 ANOVA table for AMMI model for grain yield (q/ha.)**

| Source | d.f. | Sum of squares | Mean squares | F ratio | %TSS | G*E% |
|---|---|---|---|---|---|---|
| ENV | 3 | 23417 | 7470.98** | 86.9 | 53.83 | |
| GEN | 21 | 34325 | 15811.38** | 37.8 | 14.86 | |
| ENV*GEN | 63 | 62864 | 981.98** | 7.35 | 29.76 | |
| IPCA1 | 23 | 7449 | 1934.58** | 15.46 | 21.92 | 71.92 % |
| IPCA2 | 21 | 3264 | 738.27** | 3.17 | 7.84 | 25.06 % |
| Residuals | 168 | 6901 | 418.4 | | | |

**Significance @ p=0.001, %TSS= % of total sum of squares, IPCA= interaction principle component Axes, %G*E= % of genotype and environment interaction.

**Table 4. AMMI stability parameters for grain yield (q/ha.)**

| Sl. No. | Genotype | IPCA 1 | IPCA 2 | ASV | Rank ASV | Mean | Rank of mean | GSI | Rank of GSI |
|---|---|---|---|---|---|---|---|---|---|
| 1 | GNV -1905 | -0.04 | -0.09 | 4.33 | 22 | 30.63 | 22 | 44 | 22 |
| 2 | GNV-1906 | -0.27 | 0.51 | 1.84 | 19 | 62.40 | 20 | 39 | 19 |
| 3 | GNV-1907 | 0.58 | -0.32 | 2.81 | 21 | 65.11 | 19 | 40 | 20 |
| 4 | IET-27904 | -0.17 | 0.27 | 0.89 | 11 | 73.32 | 12 | 23 | 12 |
| 5 | IET-27416 | 0.88 | 0.17 | 2.42 | 20 | 56.00 | 21 | 41 | 21 |
| 6 | IET-27870 | -0.12 | 0.23 | 1.18 | 14 | 70.67 | 15 | 29 | 15 |
| 7 | IET-26241 | 1.00 | 0.25 | 1.32 | 16 | 70.02 | 16 | 32 | 16 |
| 8 | IET-27438 | -0.05 | 0.17 | 1.24 | 15 | 72.70 | 14 | 29 | 14 |
| 9 | IET-25520 | -0.96 | -0.25 | 0.76 | 8 | 76.90 | 7 | 15 | 7 |
| 10 | BPT mutant 1801 | 0.38 | -0.61 | 0.31 | 1 | 86.37 | 1 | 2 | 1 |
| 11 | BPT mutant 1802 | -0.11 | 0.13 | 1.63 | 18 | 67.77 | 17 | 35 | 17 |
| 12 | BPT mutant 1804 | -0.01 | -0.35 | 0.39 | 2 | 80.03 | 3 | 5 | 3 |
| 13 | BPT mutant 1805 | -0.09 | 0.12 | 1.11 | 13 | 75.90 | 9 | 22 | 10 |
| 14 | BPT mutant 1806 | -0.06 | 0.03 | 0.53 | 6 | 77.31 | 6 | 12 | 6 |
| 15 | BPT mutant 1809 | -0.33 | 0.10 | 0.72 | 7 | 76.54 | 8 | 15 | 8 |
| 16 | BPT mutant 1811 | 0.22 | -0.34 | 0.47 | 3 | 80.71 | 2 | 5 | 2 |
| 17 | RNR - 15048 | 0.07 | 0.59 | 0.93 | 12 | 75.62 | 10 | 22 | 11 |
| 18 | Gangavati sanna | 0.16 | -0.52 | 1.54 | 17 | 65.98 | 18 | 35 | 18 |
| 19 | Rp-Bio 226 (C) | -0.77 | -0.12 | 0.47 | 4 | 77.89 | 5 | 9 | 5 |
| 20 | GNV 10-89 (C) | -0.24 | -0.53 | 0.78 | 9 | 73.15 | 13 | 22 | 13 |
| 21 | GGV-05-01 (C) | -0.08 | 0.28 | 0.52 | 5 | 78.84 | 4 | 9 | 4 |
| 22 | BPT-5204 (C) | -0.10 | 0.26 | 0.84 | 10 | 74.05 | 11 | 21 | 9 |

ASV-AMMI stability value, GSI- Genotypic selection index, IPCA- interaction principle component axes

'Which won where' pattern of GGE biplots for grain yield of chosen varieties revealed that genotypes IET-27870, IET-26241, Gangavati sanna, BPT mutant 1809, BPT mutant 1806 and IET-27438 occupied vertices of polygon and were unstable for grain yield per hectare because they were placed on vertices of polygon (Fig. 1). The radiating lines from the biplot origin intersected each of the polygon sides at right angles, dividing the four environments into four sub-groups. The first sub-group included the Dhadesugur (E4) habitat where IET-27438 was the winning genotype. The genotype IET-27870 won the second sub-group which was produced by Kawadimatti (E3). Environment Malnoor (E2) was the third subgroup and IET-26241 was the winner. The Gangavati (E1) environment formed the fourth subgroup where BPT mutant 1809 was the winner. According to GGE biplots, BPT mutant 1801, BPT mutant 1811, BPT mutant 1804, RNR-15048, BPT-5204, Rp Bio 226 and GGV-05-01 are stable genotypes because they are close to the origin, with BPT mutant 1801 being the most stable genotype because it is located very close to the origin and has high yield potential combined with better and wider adaptability over various agro-climatic conditions.

The GGE biplot for grain yield per hectare (Fig. 2) revealed that the environment Kawadimatti (E3) had the shortest vector, indicating that this environment was unable to discriminate genotypes, whereas the environments Malnoor (E2), Dhadesugur (E4), and Gangavati (E1) had longer vectors than Kawadimatti (E3), indicating that environments were able to discriminate genotypes. The location Kawadimatti (E3) has a limited ability to discriminate, which could be due to environmental or human factors.

Environments Gangavati (E1) and Malnoor (E2) formed smaller angle with AEA contemplated best representative environments for grain yield per hectare than other environments. In terms of genotype discrimination, Gangavati (E1) had the longest vector and formed the smallest angle with AEA, followed by Malnoor (E2), whereas Kawadimatti (E3) has the shortest vector and Dhadesugur (E4) forms the biggest angle with AEA, so these environments are not suitable for genotype discrimination, but can be used for culling unstable genotypes.

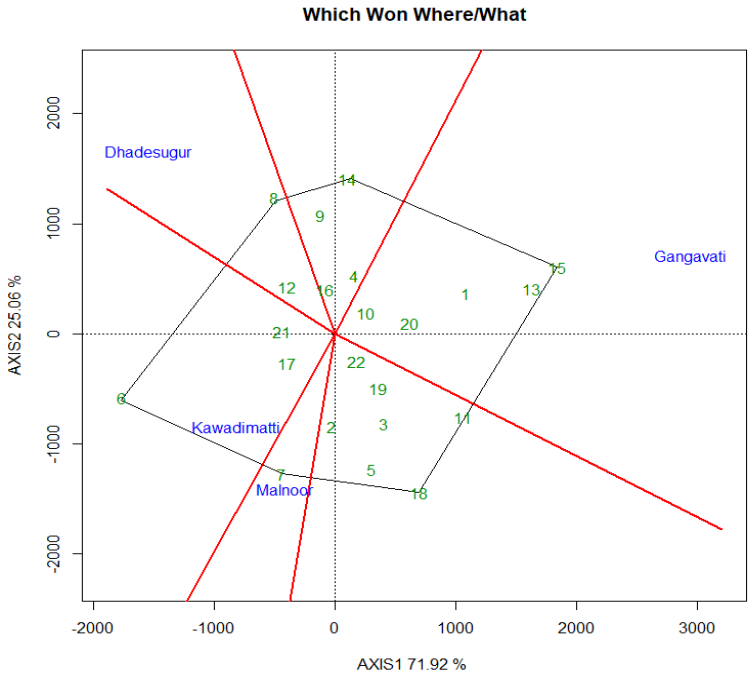


**Fig 1. 'which won-where' pattern of genotypes and locations for grain yield per hectare.**

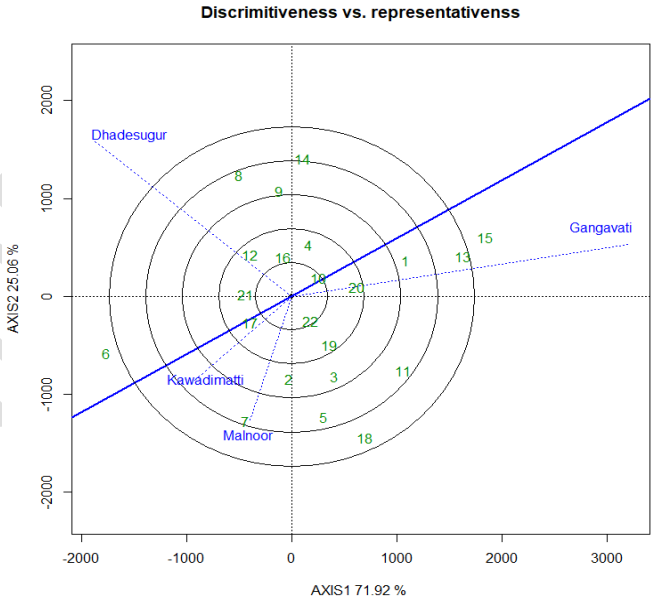


**Fig 2. Discrimitiveness vs. Representativeness view of GGE biplot for grain yield per hectare.**

## 4. CONCLUSION

Significant Genotype × Environment interaction among 22 rice genotypes evaluated across four different locations was revealed by AMMI analysis. There were a wide range of genotypes and environments, IPCA1 and IPCA2 jointly accounted more than 75% of GE interaction for yield traits, with IPCA1 accounting for the most GEI.

The most stable genotypes were discovered to be BPT mutant 1801, BPT mutant 1804, and BPT mutant 1811, BPT mutant 1801 was found to be the best of these genotypes, since it had the highest grain yield and was also the most consistent in terms of grain yield across four distinct locations. Although in the present study, both the AMMI model and GGE biplots have been found to be great tools for understanding GE interactions, however GGE biplots may provide more meaningful information with regard to genotype-environment relationships. The high yielding stable genotypes found can be recommended for release or used in breeding programmes to improve rice yield and grain quality attributes.

**COMPETING INTERESTS DISCLAIMER:**

Authors have declared that no competing interests exist. The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

## REFERENCES

Ashwini GL, Rajanna MP, Deepak CA, Chethana BS, Shobha D, Gouda TH, Dushyanthkumar, NG, Ramesh S, Nagaraj MS, Mahantashivayogayya, KH. Stability analysis for grain yield and quality traits in selected traditional and improved varieties of rice over different Zones of Karnataka. Oryza. 2019; 56(2):193-203.

Chethana BS, Deepak CA, Rajanna MP, Ramachandra C, Shivakumar N. Current scenario of rice diseases in Karnataka. International Journal of Science and Research. 2016; 7(2):405-412.

Crossa J, Fox PN, Pfeiffer WH, Rajaram S, Gauch HG. AMMI adjustment for statistical analysis of an international wheat yield trial. Theoretical and Applied Genetics. 1991; 81:27-37.

Dewi AK, Chozin MA, Triwidodo H, Aswidinnoor H. Genotype × environment interaction, and stability analysis in lowland rice promising genotypes. International Journal of Agronomy and Agricultural Research. 2014; 5(5):74-84.

Farshadfar E. Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. Pakistan Journal of Biological Sciences. 2008; 11:1791-1796.

Gauch, HG, Zobel RW. Accuracy and selection success in yield trial analyses. Theoretical and Applied Genetics. 1989; 77:473-481.

Gauch HG. Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier. 1992; 3:51-56.

Kumar KVK, Reddy MS, Kloepper JW, Lawrence KS, Zhou XG, Groth DE, Zhang S, Sudhakara R, Wang Q, Raju MRB, Raju SK, Fernando WGD, Sudini H, Du B, Miller ME. Commercial potential of microbial inoculants for sheath blight management and yield enhancement of rice, In: Bacteria in agrobiology. Crop Ecosystem. 2011; 4(1): 237-264.

Prashanth C, Mahantashivayogayya K, Diwan JR, Kuchunur PH, Vishwanath J. G × E interaction and yield stability analysis of BPT-5204 based rice mutants using AMMI analysis under saline stress soil. Crop genomics and Data science. 2019; 50(1):49-50.

Purchase JL, Hatting H, Vandeventer CS. Genotype × environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: Π. Stability analysis of yield performance. South African Journal of Plant and Soil Science. 2000; 17(1): 101-107.

Yan W, Rajcan I. Biplot analysis of test sites and trait relations of soyabean in Ontario. Crop Science. 2002; 42(3): 11-20.

Yan W, Tinker NA. Biplot analysis of multi environment trail data: Principles and applications. Canadian Journal of Plant Science. 2006; 86: 623-645.

Yan W, Hunt LA, Sheng Q, Sziavnics Z. Cultivar evaluation and mega environment investigation based on GGE biplot. Crop Science. 2000; 40: 597- 605.

Zobel RW, Wright MJ, Gauch HG. Statistical analysis of a yield trial. Journal of Agronomy. 1988; 80(3): 388-393.