

## Original Research Article

# Tungabhadra Sona (GNV 1801) - Stable High Yielding Mutant Rice Variety for Tungabhadra Command Area of Karnataka

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## ABSTRACT

Rice (*Oryza sativa* L.) is a staple food source for nearly 3.5 billion people and has occupied an enviable prime place among the food crops cultivated around the world, which contributes significantly to global food security and with China and India as lead producers. Measurement of G x E interaction has always remained an intriguing problem in the past. Now a day, the use of biplot to quantify the genotype environment interaction (GEI) is widespread since the GE effects can be visualized in a single graph, which facilitates the comparison of genotypes and their interaction with the environments. More recently, Yan *et al.*, (2000) proposed a new technique in the GEI analysis using biplots similar to the AMMI technique, which has the advantage of decomposing the joint effect of genotype (G) and GE (G + GE) by principal component analysis, differing from the original AMMI analysis that decomposes only GE and method was called GGE biplot by Yan *et al.*, (2000). The main objective of this study was to evaluate rice genotypes and to apply GGE biplot to identify better performance and stability on grain yield and hence to recommend the best genotype for rice farmers of tungabhadra command area of Karnataka. The experimental material for the present study consisted of twenty-two medium slender rice genotypes used from previous study Prashant *et al.*, (2019) including BPT 5204 based mutants along with local checks BPT 5204 and Gangavati sona, These varieties were evaluated in four locations of Karnataka *viz.*, Agriculture Research Station, Gangavati, Agriculture Research Station, Dhadesugur, Agriculture Research Station, Malnoor and Agriculture Research Station, Kawadimatti of Karnataka state during *kharif* 2019. Evaluation of these rice genotypes along with four checks was carried out using randomized complete block design with three replications at four locations selected under study. Each genotype was planted in 13 rows of 4 m row length with a spacing of 20 cm between the rows and 15 cm between the plants was followed in all locations and recommended package of practices for rice cultivations in respective locations were followed, AMMI model and GGE bi-plot methodology was used for the stability analysis.

## Keywords

Rice, Stability analysis, AMMI model, Rice mutant, BPT-5204

## Introduction

Rice (*Oryza sativa* L.) is a staple food source for nearly 3.5 billion people and has occupied an enviable prime place among the food crops cultivated around the world, which

contributes significantly to global food security and with China and India as lead producers, more than 90 % of rice is produced in Asia (Kumar *et al.*, 2011). Rice has occupied the central position in Indian agriculture with 24 per cent of gross cropped

area of the country under its cultivation and contributing 42 per cent of total food grain production and 45 per cent of total cereal production of the country (Chethana *et al.*, 2016).

The phenotypic value (P) measured on an appropriate scale is not equal to genotypic value (G) when the genotype is grown under more than one environment (E), therefore,  $P = G + E + (G \times E)$ . Since, G x E interactions greatly affect the phenotype therefore, stability analysis is required to characterize the performance of genotypes in different environments, so as to assist plant breeders in selecting stable genotypes. Measurement of G x E interaction, however, has always remained an intriguing problem in the past. Now a days, the use of biplots to quantify the genotype environment interaction (GEI) is widespread since the GE effects can be visualized in a single graph, which facilitates the comparison of genotypes and their interaction with the environments (Gauch and Zobel 1989). More recently, Yan *et al.*, (2000) proposed a new technique in the GEI analysis using biplots similar to the AMMI technique, which has the advantage of decomposing the joint effect of genotype (G) and GE (G + GE) by principal component analysis, differing from the original AMMI analysis that decomposes only GE and method was called GGE biplot by Yan *et al.*, (2000).

The basic ANOVA model describes main effects effectively and determines if genotype  $\times$  environment is a significant source of variation, but it does not provide an insight into the patterns of genotypes or environments that give rise to the interaction, besides PCA (multiplicative model) contains no sources of variation for additive main effects, genotype and environment and does not analyze the interactions effectively (Zobel *et al.*, 1988). However, the probability of

successful selection is significantly improved by AMMI analysis (Gauch and Zobel, 1988) and has been used to analyze genotype  $\times$  environment interaction with greater precision in many crops (Gauch, 1992, Crossa *et al.*, 1991). The GGE biplot are often used effectively to identify the GEI pattern of the data. It clearly simplifies mega environment identification.

The main objective of this study was to evaluate rice genotypes and to apply GGE biplot to identify better performance and stability on grain yield and hence to recommend the best genotype for rice producers in the region and also for familiar agro ecologies of the country.

## **Materials and Methods**

The experimental material for the present study consisted of twenty-two medium slender rice genotypes along with four checks which includes both early and medium maturing, advanced BPT 5204 based mutants (M8 Generation) and advanced breeding lines identified and developed at AICRP-Rice breeding, ARS, Gangavati. These varieties were evaluated in four locations of Karnataka viz., Agriculture Research Station (ARS) Gangavati (Zone 1), Agriculture Research Station (ARS) Dhadesugur (Zone 4), Agriculture Research Station (ARS) Malnoor (Zone 2), Agriculture Research Station (ARS) Kawadimatti (Zone 3) during *kharif* 2019.

Evaluation of these rice genotypes along with four checks was carried out using randomized complete block design with three replications at four locations selected under study. Nursery was raised during July-August, 2018 and 25-30 days old seedlings were transplanted and each genotype was planted in 13 rows of 4 m row length with a spacing of 20 cm between the rows and 15 cm

between the plants was followed in all locations and recommended package of practices for rice cultivations in respective locations were followed.

### Statistical analysis: AMMI analysis

The G X E interaction of twenty two rice genotypes over four locations were assessed by AMMI model as proposed by Gauch and Zobel, 1989, using the statistical program GenStat 18<sup>th</sup> edition. First, an ANOVA model was used with main effects of genotype and environment (without the interaction), then a principal component analysis (PCA) was fitted using the standardized residuals. These residuals include the experimental error and the effect of the G×E interaction. The equation was:

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

Where,  $Y_{ij}$  is the observed mean yield of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment.  $\mu$  is the general mean,  $G_i$  and  $E_j$  represent the effects of the genotype and environment, respectively.  $\lambda_k$  is the singular value of the  $k^{\text{th}}$  axis in the principal component analysis.  $\alpha_{ik}$  is the eigen vector of the  $i^{\text{th}}$  genotype for the  $k^{\text{th}}$  axis  $\gamma_{jk}$  is the eigen vector of the  $j^{\text{th}}$  environment for the  $k^{\text{th}}$  axis.  $n$  is the number of principal components in the model,  $e_{ij}$  is the average of the corresponding random errors.

### Stability parameters

Two stability parameters were calculated viz., AMMI stability value (ASV) and genotypic stability index (GSI). The AMMI model does not make provision for a quantitative stability measure, and as such a measure is essential in order to quantify and rank genotypes in terms of yield stability (Gauch and Zobel, 1989; Gauch, 1992). Therefore, the AMMI stability value (Purchase *et al.*, 2000) was used to

quantify and rank genotypes based on their stability for a trait. AMMI stability value (ASV) is the distance from zero in a two dimensional scatter diagram of IPCA1 scores against IPCA2 scores. AMMI stability value was calculated using sum of squares and scores of both IPCA1 and IPCA2. The genotype recording the lowest ASV was the most stable one across the tested environments and genotype recording highest ASV was the most unstable across the tested environments. In the same manner, the genotype having IPCA2 score near zero reveals more stability while large values indicate more responsive and less stable genotypes. Genotypic selection index (GSI), also called as Yield Stability Index (YSI) was used for simultaneous selection for stability and performance of the genotypes. Low values of GSI show desirable genotypes with high mean yield and stability (Farshadfar, 2008). AMMI stability value (ASV) and Genotypic stability index (GSI) were calculated (Purchase *et al.*, 2000) as:

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

Where  $SS_{IPCA1}$  and  $SS_{IPCA2}$  are the sum of squares of IPCA1 and IPCA2 respectively. IPCA1 score and IPCA2 score are the scores of the genotype in those particular PCAs.

$$GSI = RASV + RY$$

Where, RASV is the rank of AMMI stability value, and RY is the rank of mean yield of genotypes (RY) across environments.

### Results and Discussions

Mean yield performance of all twenty two varieties over four locations for grain yield per hectare are represented in Table 1.

Analysis of variance as per AMMI model revealed that there was significant contribution for variation by main effects (genotypes and environments) and interaction effects for the trait yield (Table 2). Significant mean sum of squares due to genotypes indicate that there existed genotypic differences and significance of environment explains that environmental effects differ across different locations and test locations were diverse. Further, G×E interaction effects signify that genotypes behave differently across different environments.

Large sum of squares due to environments for yield indicated that differences among environmental means were very high and environments were diverse in nature (Zobel *et al.*, 1988). It was found in present study that environmental mean variations were very higher than genotypic mean variations for yield (Table 2). Hence, test locations were diverse. Present results are in agreement with Prashant *et al.*, (2019) who evaluated twelve rice mutants for grain yield stability under saline soil at four locations, AMMI analysis revealed that the mutants BPT-5204 Mutant-653, BPT-5204 Mutant-1807 were found to be stable genotypes for grain yield.

CD-critical difference, CV-coefficient of variation

Alike Ashwini *et al.*, (2019) evaluated traditional along with improved varieties of rice over five different locations of Karnataka using AMMI model and biplots were developed following GGE bi-plot methodology for grain yield and quality traits. In contrast to this, Dewi *et al.*, (2014) observed that mean sum of square due to genotype main effect was high for grain yield when rice genotypes were evaluated in different growing seasons. These results suggest that variations in environment means are majorly due to location differences than

seasonal variations.

The multiplicative variance of the treatment sum of squares due to G×E interaction was further partitioned into interaction principal component axis (IPCA) as it was significant. IPCA I and IPCA II scores explained 71.92 per cent and 25.06 per cent of the interaction respectively. These two PCA axes cumulatively captured 96.98 per cent of the total GEI for the trait grain yield per hectare.

### **Stability parameters**

According to AMMI stability value (ASV) Tungabhadra sona (BPT mutant GNV 1801) (8637 kg/ha) was the most stable genotype for yield since it recorded lowest ASV (0.31) followed by BPT mutant 1804 (8003 kg/ha) and BPT mutant 1811 (8071 kg/ha) with 0.39 and 0.41 ASV respectively. Alike, according to Genotypic selection index (GSI) Tungabhadra sona (BPT mutant GNV 1801) was found to be the best variety since it recorded lower value for it (Table 3).

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

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

A polygon is drawn on the genotypes that are farthest from the bi-plot origin so that all other genotypes fall within the polygon. The perpendicular lines starting from GGE bi-plot origin are drawn to each side of the polygon. The perpendicular lines are equality lines between adjacent genotypes on the polygon. The genotypes located on the vertices of the polygon perform either the best or poorest in one or more locations. The equality lines divide the bi-plot into sectors. The vertex genotype in each sector is the winning genotype at locations whose markers (points) fall into the respective sector (Yan *et al.*, 2000). Locations within the same sector share

the same winning genotype, and locations in different sectors have different winning genotypes. Thus, polygon view of a GGE biplot indicates presence or absence of cross-over GEI (Yan and Rajcan, 2002).

Which won where' pattern of GGE biplots for grain yield of selected varieties (Fig. 1) indicated that genotypes *viz.*, IET-27870, IET-26241, Gangavati sanna, BPT mutant 1809, BPT mutant 1806 and IET-27438 occupied vertices of polygon and unstable for grain yield per hectare, since they were located on vertices of polygon. The four environments were divided into four sub-groups by the radiating lines from the biplot origin to intersect each of the polygon sides at right angle. First sub-group consisted of environment Dhadesugur (E4) in which IET-27438 was winning genotype. Kawadimatti (E3) formed the second sub-group, in which the genotype IET-27870 was winner. Third sub group consisted of environment Malnoor (E2) where IET-26241 was the winner. Fourth sub group consisted of environment Gangavati (E1) where BPT mutant 1809 was the winner. Rest of the genotypes *viz.*, GNV 10-89, Tungabhadra sona (BPT mutant GNV 1801), BPT mutant 1811, BPT mutant 1804, RNR-15048, BPT-5204, Rp Bio 226 and GGV-05-01 were found to be stable according to GGE biplots since they are located near origin and among them Tungabhadra sona (BPT mutant GNV 1801) was most stable genotype because it is located very closer to the origin and have high yield potential combined with the better and wide adaptability over different agro-climatic conditions.

'Discriminateness vs. representativeness' pattern of GGE biplot for grain yield per hectare (Fig. 2) indicated that the environment Kawadimatti (E3) had shortest vector, so this environment was unable to

discriminate the genotypes, while the environments Malnoor (E2), Dhadesugur (E4) and Gangavati (E1) were having longer vectors than Kawadimatti (E3) depicting that environments were able to discriminate the genotypes for grain yield per hectare. Low discrimination ability of the location Kawadimatti (E3) could be due to environmental or human effect.

Environments Gangavati (E1) and Malnoor (E2) formed smaller angle with AEA contemplated best representative environments for grain yield per hectare than other environments. The environment Gangavati (E1) had longest vector and formed smallest angle with AEA followed by Malnoor (E2) indicating best representative environment for discriminating the genotypes, while the environments Kawadimatti (E3) is having shortest vector and Dhadesugur (E4) forms the bigger angle with AEA, so these environments cannot be used for discriminating the genotypes but can be used for culling of unstable genotypes.

In conclusion, genotype-Environment (GE) interaction is a complex phenomenon in nature which needs to be understood by breeders in order to identify locations that are suitable for better yield of a given variety. It was revealed by AMMI analysis in present investigation that there existed significant GE interaction among twenty-two rice varieties evaluated across four different locations. Analysis revealed that Tungabhadra sona (BPT mutant GNV 1801), BPT mutant 1804 and BPT mutant 1811 were found to be most stable varieties. Among these varieties, Tungabhadra sona (BPT mutant GNV 1801) was found to be best variety since it recorded highest grain yield and also it was stable performer for grain yield across four different locations and could be released for commercial cultivation.

**Table.1** Mean yield performance of varieties in four locations

| Sl. No. | Genotype                       | Grain yield per hectare (kg/ha) |         |             |            | Mean |
|---------|--------------------------------|---------------------------------|---------|-------------|------------|------|
|         |                                | Gangavati                       | Malnoor | Kawadimatti | Dhadesugur |      |
| 1       | GNV -1905                      | 3390                            | 2932    | 2774        | 3156       | 3063 |
| 2       | GNV-1906                       | 6303                            | 6042    | 6356        | 6261       | 6240 |
| 3       | GNV-1907                       | 6283                            | 6667    | 6158        | 6938       | 6511 |
| 4       | IET-27904                      | 8257                            | 6768    | 6482        | 7819       | 7332 |
| 5       | IET-27416                      | 5297                            | 5591    | 5654        | 5857       | 5600 |
| 6       | IET-27870                      | 7964                            | 7231    | 6946        | 6128       | 7067 |
| 7       | IET-26241                      | 7080                            | 7092    | 7236        | 6600       | 7002 |
| 8       | IET-27438                      | 8069                            | 6662    | 6954        | 7394       | 7270 |
| 9       | IET-25520                      | 8427                            | 7390    | 7146        | 7798       | 7690 |
| 10      | Tungabhadra<br>sona (GNV 1801) | 9434                            | 8305    | 8132        | 8678       | 8637 |
| 11      | BPT mutant 1802                | 6301                            | 6424    | 6628        | 7754       | 6777 |
| 12      | BPT mutant 1804                | 8828                            | 7742    | 7449        | 7995       | 8003 |
| 13      | BPT mutant 1805                | 7347                            | 6739    | 7054        | 9222       | 7590 |
| 14      | BPT mutant 1806                | 8444                            | 7549    | 7136        | 7793       | 7731 |
| 15      | BPT mutant 1809                | 7371                            | 6781    | 6958        | 9504       | 7654 |
| 16      | BPT mutant 1811                | 8667                            | 7799    | 7586        | 8231       | 8071 |
| 17      | RNR - 15048                    | 8598                            | 7856    | 7684        | 6109       | 7562 |
| 18      | Gangavati sanna                | 6018                            | 6458    | 6756        | 7161       | 6598 |
| 19      | Rp-Bio 226(C)                  | 8073                            | 7707    | 7432        | 7944       | 7789 |
| 20      | GNV 10-89 (C)                  | 7882                            | 7239    | 6744        | 7394       | 7315 |
| 21      | GGV-05-01 (C)                  | 8004                            | 7645    | 7796        | 8093       | 7884 |
| 22      | BPT-5204 (C)                   | 8248                            | 7042    | 7256        | 7075       | 7405 |
|         | <b>CD @ 5%</b>                 | 1081                            | 1125    | 884         | 876        |      |
|         | <b>CV %</b>                    | 9.22                            | 10.47   | 8.31        | 7.69       |      |

**Table.2** ANOVA table for AMMI model for grain yield (kg/ha.)

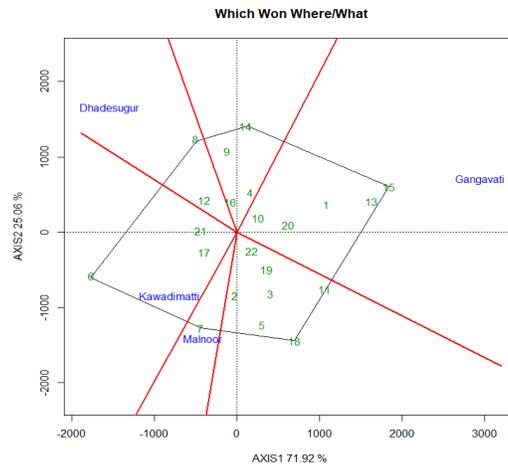
| Source           | df  | SS       | MSS            | F ratio   | %TSS     | G×E%  |
|------------------|-----|----------|----------------|-----------|----------|-------|
| <b>ENV</b>       | 3   | 22412959 | 158113871.21** | 137.86121 | 5.38363  |       |
| <b>GEN</b>       | 21  | 3332508  | 7470986.35**   | 437.80096 | 79.75635 |       |
| <b>ENV*GEN</b>   | 63  | 61864782 | 9819801.77**   | 73.4766   | 14.86002 |       |
| <b>IPCA1</b>     | 23  | 44495487 | 19345863.19**  | 154.60763 | 71.92378 | 71.92 |
| <b>IPCA2</b>     | 21  | 15503702 | 738271.53**    | 121.75835 | 25.06063 | 25.06 |
| <b>Residuals</b> | 176 | 73617287 | 418280.41      |           |          |       |

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

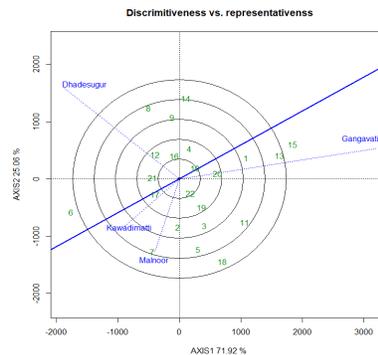
**Table.3** AMMI stability parameters for grain yield (kg/ha)

| Sl. No. | Genotype                          | IPCA 1 | IPCA 2 | ASV  | Rank ASV | Mean | Rank of mean | GSI |
|---------|-----------------------------------|--------|--------|------|----------|------|--------------|-----|
| 1       | GNV -1905                         | -0.03  | -0.08  | 4.32 | 22       | 3063 | 22           | 44  |
| 2       | GNV-1906                          | -0.27  | 0.51   | 1.84 | 19       | 6240 | 20           | 39  |
| 3       | GNV-1907                          | 0.58   | -0.32  | 2.81 | 21       | 6511 | 19           | 40  |
| 4       | IET-27904                         | -0.17  | 0.27   | 0.89 | 11       | 7332 | 12           | 23  |
| 5       | IET-27416                         | 0.88   | 0.17   | 2.42 | 20       | 5600 | 21           | 41  |
| 6       | IET-27870                         | -0.12  | 0.23   | 1.18 | 14       | 7067 | 15           | 29  |
| 7       | IET-26241                         | 1.00   | 0.25   | 1.32 | 16       | 7002 | 16           | 32  |
| 8       | IET-27438                         | -0.05  | 0.17   | 1.24 | 15       | 7270 | 14           | 29  |
| 9       | IET-25520                         | -0.96  | -0.25  | 0.76 | 8        | 7690 | 7            | 15  |
| 10      | Tungabhadra<br>sona (GNV<br>1801) | 0.38   | -0.61  | 0.31 | 1        | 8637 | 1            | 2   |
| 11      | BPT mutant 1802                   | -0.11  | 0.13   | 1.63 | 18       | 6777 | 17           | 35  |
| 12      | BPT mutant 1804                   | -0.01  | -0.35  | 0.39 | 2        | 8003 | 3            | 5   |
| 13      | BPT mutant 1805                   | -0.09  | 0.12   | 1.11 | 13       | 7590 | 9            | 22  |
| 14      | BPT mutant 1806                   | -0.06  | 0.03   | 0.53 | 6        | 7731 | 6            | 12  |
| 15      | BPT mutant 1809                   | -0.33  | 0.10   | 0.72 | 7        | 7654 | 8            | 15  |
| 16      | BPT mutant 1811                   | 0.22   | -0.34  | 0.47 | 3        | 8071 | 2            | 5   |
| 17      | RNR - 15048                       | 0.07   | 0.59   | 0.93 | 12       | 7562 | 10           | 22  |
| 18      | Gangavati sanna                   | 0.16   | -0.52  | 1.54 | 17       | 6598 | 18           | 35  |
| 19      | Rp-Bio 226(C)                     | -0.67  | -0.11  | 0.49 | 4        | 7789 | 5            | 9   |
| 20      | GNV 10-89 (C)                     | -0.24  | -0.53  | 0.78 | 9        | 7315 | 13           | 22  |
| 21      | GGV-05-01 (C)                     | -0.08  | 0.28   | 0.52 | 5        | 7884 | 4            | 9   |
| 22      | BPT-5204 (C)                      | -0.10  | 0.26   | 0.84 | 10       | 7405 | 11           | 21  |

**Fig.1** Polygon view of GGE bi-plot based on the symmetrical scaling for ‘which won-where’ pattern of genotypes and locations for grain yield per hectare



**Fig.2** Discriminateness vs. Representativeness view of GGE biplot for grain yield per hectare in four environments



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