

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 18th 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^{th} genotype in the j^{th} environment. μ is the general mean, G_i and E_j represent the effects of the genotype and environment, respectively. λ_k is the singular value of the k^{th} axis in the principal component analysis. α_{ik} is the eigen vector of the i^{th} genotype for the k^{th} axis γ_{jk} is 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.

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

	Grain yield per hectare (kg/ha)					
Sl. No.	Genotype	Gangavati	Malnoor	Kawadimatti	Dhadesugur	Mean
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 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
	CD @ 5%	1081	1125	884	876	
	CV %	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%
ENV	3	22412959	158113871.21**	137.86121	5.38363	
GEN	21	3332508	7470986.35**	437.80096	79.75635	
ENV*GEN	63	61864782	9819801.77**	73.4766	14.86002	
IPCA1	23	44495487	19345863.19**	154.60763	71.92378	71.92
IPCA2	21	15503702	738271.53**	121.75835	25.06063	25.06
Residuals	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 sona (GNV 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

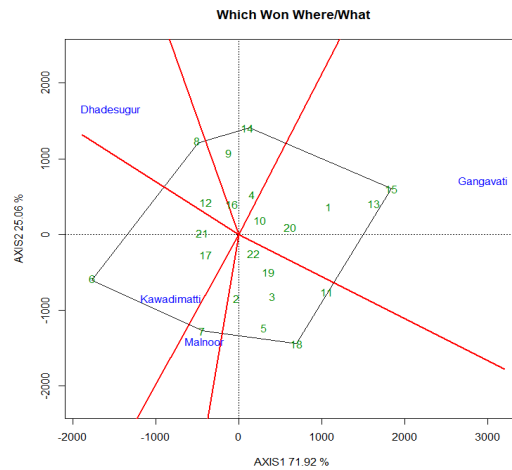
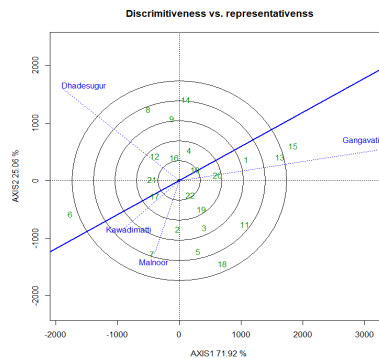


Fig.2 Discriminateness vs. Representativeness view of GGE biplot for grain yield per hectare in four environments



References

Ashwini, G. L., Rajanna, M. P., Deepak, C. A., Chethana, B. S., Shobha, D., Gouda, T. H., Dushyanthkumar, N. G., Ramesh, S., Nagaraj, M. S. and Mahantashivayogayya, K. H. 2019, Stability analysis for grain yield and quality traits in selected traditional and improved varieties of rice over

different Zones of Karnataka. *Oryza*, 56(2): 193-203.

Chethana, B. S., Deepak, C. A., Rajanna, M. P., Ramachandra, C. and Shivakumar, N. 2016, Current scenario of rice diseases in Karnataka. *IJSN*, 7(2): 405-412.

Crossa, J., Fox, P. N., Pfeiffer, W. H., Rajaram, S. and Gauch, H. G. 1991, AMMI adjustment for statistical

- analysis of an international wheat yield trial. *Theoret. Applied Genet.*, 81: 27-37.
- Dewi, A. K., Chozin, M. A., Triwidodo, H. and Aswidinnoor, H., 2014, Genotype \times environment interaction, and stability analysis in lowland rice promising genotypes. *IJAAR*, 5(5): 74-84.
- Farshadfar, E., 2008, Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. *Pakistan J. Biol. Sci.*, 11: 1791-1796.
- Gauch, H. G., 1992, Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Amsterdam, *Elsevier*, 3: 51-56.
- Kumar, K. V. K., Reddy, M. S., Kloepper, J. W., Lawrence, K. S., Zhou, X. G., Groth, D. E., Zhang, S., Sudhakara, R., Wang, Q., Raju, M. R. B., Raju, S, K., Fernando, W. G. D., Sudini, H., Du, B. and Miller, M. E., 2011, Commercial potential of microbial inoculants for sheath blight management and yield enhancement of rice, In: Bacteria in agrobiology. *Crop Ecosystem*, 4(1): 237-264.
- Prashanth, C., Mahantashivayogayya, K., Diwan, J. R., Kuchunur, P, H., and Vishwanath, J., 2019, G \times E interaction and yield stability analysis of BPT-5204 based rice mutants using AMMI analysis under saline stress soil. *Crop genomics and Data science*, 50(1):49-50.
- Purchase, J. L., Hatting, H. and Vandeventer, C. S., 2000, Genotype \times environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. *South Afric. J. Plant Soil*, 17(1): 101-107.
- Yan, W. and Rajcan I., 2002, Biplot analysis of test sites and trait relations of soyabean in Ontario. *Crop Sci.*, 42(3): 11-20.
- Yan, W. and Tinker, N. A., 2006, Biplot analysis of multi environment trial data: Principles and applications. *Canadian J. Plant Sci.*, 86: 623-645.