

GENOTYPE ENVIRONMENT INTERACTION AND STABILITY FOR YIELD AND ITS COMPONENTS IN ADVANCED BREEDING LINES OF RED RICE (*ORYZA SATIVA* L.)

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Abstract

Effects of genotype, environment and their interaction for grain yield and yield attributing characters in 20 advanced breeding lines of rice across six environments was investigated. Yield stability and adaptability of yield performance were analyzed by Eberhart and Russel model and (GGE) bi-plot. The AMMI analysis of variance indicated that mean squares due to genotypes, location and genotype location contributed per cent 59.08, 5.79 and 21.63, respectively for total variability in grain yield per hectare. Estimates of GGE bi-plot revealed that the lines G1, G3, G11, G13, G15, G12, G16, G7 and G10 were positioned near GGL bi-plot origin indicating wider adaptation for the trait grain yield per hectare. Eberhart and Russel Model and GGE biplot model showed the advanced breeding lines *viz.*, JB 1-11-7 (G1) and JA 6-2 (G15) exhibited wider adaptability across the tested environments for number of productive tillers per plant and yield per hectare.

Introduction

Rice is the most important cereal crop and staple food for more than one third of the world population. An alarming increase in the population throughout the world will continuously increase the demand for rice in near future. Therefore, rice breeders across the world aim at increasing grain yield of rice (Song *et al.* 2007), but existence of genotype by environment interaction hinders the selection of genotype for wider adaptability which makes the variety development process more complex and expensive. Thus, evaluation of genotypes for stable performance under varying environmental conditions for yield and yield attributing characters has become an essential part of any breeding programme. Understanding the causes of genotype \times environment interaction can help in identifying the traits and the environments for better cultivar evaluation. Plant breeders perform multi-environment trials (MET) to select favourable genotypes based on both mean yield and performance stability and to determine whether a test environment is homogenous should be divided into various mega environments (Yan and Kang 2003). For developing stable varieties, different statistical model were used to describe GE interactions such as stability variance (Shukla 1972), coefficient of variability (Francis and Kanneberg 1978), regression coefficient (bi) and deviation from regression coefficient (S^2_{di}) (Eberhart and Russell model 1966) and additive main effects multiplicative interaction model (AMMI) (Gauch and Zobel 1988, Zobel *et al.* 1988, Gauch 2006) have been commonly used to analyse multi-environmental data to reveal patterns of GE interaction. The AMMI model is a hybrid model involving both additive and multiplicative components of two-way data structure. The model separates the additive variance from the multiplicative variance then applies principle component analysis (PCA) to the interaction portion to a new set of coordinate axes that explains detail the interaction pattern and estimation accomplished using the least squares principle. Further, Yan

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et al. (2000) proposed another methodology known as genotype and genotype by environment (GGE) biplot analysis which considers both genotype (G) and GE interaction effects and graphically displays GE interaction in two-way table. This method is based on the principle component analysis (PCA) to fully explore multi-environment data and it also allows visual examination of the relationships among the test environments, genotypes and the GE interactions. The main objectives of the present study are to develop rice cultivar with high yield for different environments which is one of the existing research which leads to successful release of stable genotype with high yield across the environments. Therefore, the present investigation was carried out for identifying high yield, stable genotype with desirable grain yield using Eberhart and Russell model and GGE biplot model.

Material and Methods

Twenty advanced breeding lines of F_6 developed from Jyothi \times Biliya, Jyothi \times KHP-2, Jyothi \times Akkalu, Jyothi \times Tunga (Table 1) with three checks *viz.*, Jyothi, KHP-2 and Tunga collected from Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga, Karnataka, India were sown on 17, 21 and 22 June, 2016 at College of Agriculture (CoA) Shivamogga, ZAHRS Mudigere and AHRS Kattalagere, respectively whereas 5, 6 and 7 July, 2016 at AHRS Honnavile, AHRS Bhavikere and AHRS Ponnampet, respectively (Table 2) in raised beds of one sq m each. Twenty days old seedlings were transplanted to the main field at the rate of one seedling per hill by following Randomized Complete Block Design with two replications in puddle field at all the six locations. Five plants were selected at random in each advanced breeding lines from each replication, and the observations were recorded on days to 50% flowering, plant height (cm), number of productive tillers per plant, grain yield (kg/ha). The mean data of five randomly selected plants in each of twenty advanced breeding lines with three checks from each of the two replications of six environments were applied to assess the pooled analysis of variance (Mather and Jinks 1971). The pooled ANOVA was carried out to detect genotype \times environments interaction. If the existence of significant genotype \times environments interaction, the data were further subjected to different stability models *i.e.* stability model proposed by Eberhart and Russel (1966) using Windostat version 9.2 software. Additive main effect and multiplicative interactions model (AMMI) and genotype, environment and genotype + environment (GGE) interaction biplot model using 'CIMMYT- R' software to unravel the pattern of interaction of genotype with environment (Gauch and Zobel 1988).

The magnitude of $G \times E$ interaction was assessed for each character and each genotype. This was worked out as per the procedure suggested by Eberhart and Russel (1966). The joint consideration of three parameters, the mean performance of the genotypes over environments (locations) \bar{X}_i , regression coefficient b_i and the deviation from linear regression S^2d_i is used to determine stability of genotype (variety). The estimate of deviation from regression suggests the degree of reliance that should be put to linear regression in interpretation of data. If these values are significantly deviating from zero, the expected phenotype cannot be predicted satisfactorily. When deviations are non-significant, the conclusions may be drawn by joint consideration of mean yield and regression values (Finlay and Wilkinson 1963 and Eberhart and Russel 1966). Regression value of unity is interpreted as average stability since the average slope over all varieties on the environment index will be unity.

The AMMI model combines the analysis of variance for main effects of inbred line and environment with principal component analysis (PCA) of the genotype (inbred line)-environment interaction (GEI). The additive main effect of inbred lines and environments were fitted by univariate ANOVA followed by fitting GEI using PCA. Visual criteria were used to interpret GEI

patterns of inbred lines. The criterion was based on genotype + genotype environment (GGE) bi-plot (Yan *et al.* 2000).

Table 1. List of advanced breeding lines (F₆) used in the present investigation with checks.

Cross combinations	Code	Advanced breeding lines	Grain shape	Grain colour
Jyoti × Biliya	G1	JB-1-11-7	Medium slender	Light red
	G2	JB-1-20-2	"	"
	G3	JB-1-22-1	"	"
	G4	JB-1-22-2	"	"
	G5	JB-1-22-3	"	"
Jyoti × KHP-2	G6	JK-1-7-5	Medium bold	Dark red
	G7	JK-1-11-8	"	Light red
	G8	JK-1-12-1	"	"
	G9	JK-1-13-1	"	"
	G10	JK2-2-1-8-1	"	"
	G11	JK2-1-12-1	"	"
Jyoti × Akkalu	G12	JA-4-1	Medium slender	"
	G13	JA-4-2	"	"
	G14	JA-4-3	"	"
	G15	JA-6-2	"	"
	G16	JA-6-3	"	"
	G17	JA-6-4	"	"
Jyoti × Tunga	G18	JT-2-15-1	"	"
	G19	JT-2-16-1	"	"
	G20	JT-2-22-5	"	White
Jyothi (Check)	G21		Bold	Red
KHP-2 (Check)	G22		Long bold	White
Tunga (Check)	G23		Medium slender	"

Table 2. Description of the experimental locations.

Particulars	Tested locations					
	E1	E2	E3	E4	E5	E6
Locations	AHRS, Kattalagere	UAHS, Shivamogga	AHRS, Honnavile	ZAHRS, Mudigere	AHRS, Bhavikere	AHRS, Ponnampete
Latitude	16°12' N	13.054° N,	13.9299° N,	13°8'3"N	12.50° N,	12.14907° N
Longitude	74°54' E	75.03930° E	75.5681° E	75°38'30"E	77.35° E	75.94052 °E
Elevation	598 meters	569 meters	570 meters	915 meters	566.7 meters	851 meters
Av. temperature	25.5 °C	24.8 °C	24.6 °C	23.2 °C	36 °C	22.6 °C
Av. rainfall	567 mm	909 mm	863 mm	610 mm	1104.2 mm	2173 mm

GGE-biplot, which is a combination of AMMI bi-plot and GGE concepts (Yan *et al.* 2000) was used for visual interpretation of patterns of GEI. There are numerous ways to use a GGE bi-plot, but the polygon view of the bi-plot is most relevant. Genotype and environment interaction PC 1 (IPC-1) scores were plotted against their IPC-2 scores to visually identify the accessions with specific/wide adaptation and similarity between advanced breeding lines and environments. The lines that are more similar to each other in terms of their morphological characters are more close to each other in the GGE bi-plot than those that are less similar. The advanced lines placed near origin of IPC 1 vs. IPC 2 bi-plot are regarded as better adaptable across environments than those located far from the origin. The breeding lines that are further from bi-plot origin are connected

with straight lines so that a polygon is formed with all other inbred lines contained within the polygon. A set of lines were drawn from the bi-plot origin perpendicular to each side of polygon. The perpendicular lines to the polygon sides divide the polygon into sectors, each having its own winning genotype which is the vertex genotype for that sector (Yan *et al.* 2000).

Results and Discussion

The pooled analysis of variance revealed that significant genotypes \times locations ($G \times L$) differences for all the traits studied across the six tested locations. The important source of variations such as varieties or genotypes, environment + (varieties \times environment) and environment (linear) and pooled deviation are statistically significant for majority of the traits. The advance breeding lines G4, G15 and G13 recorded less mean value than the population mean for days to 50% flowering i.e. 93.92, 92.58 and 93.25 days, respectively and regression coefficient is unity ($b_i = 1$) and least deviation from regression, indicated these advanced breeding lines showed stable performance across the environments. Therefore, these advanced breeding lines can be utilized in breeding programmes to develop short duration stable cultivars. The line G18 showed high mean value (102.75) and regression coefficient greater than the unity ($b_i = 1.22$) and less deviation from the regression coefficient concluded that this line can be specifically adopted to the favourable environments (Table 4). The present results are in conformity with the reports of Ganesh and Soundarapandian (1987), Amrithadevarathnam (1987) and Koli *et al.* (2015) and thus confirmed that days to flowering is a stable character.

Table 3. Analysis of variance for stability based on Eberhart and Russel model.

Source of variations	df	Days to 50% flowering	Plant height	Number of productive tillers	Yield per hectare
Replication within environment	6	0.821	4.625	0.519	57622.57
Varieties	22	337.8**	1024.00**	10.58**	6665733.00**
Env. + (Var. \times Env.)	115	51.621**	74.93**	1.719	296132.081**
Environments	5	1736.1**	2587.20**	17.12	2875758
(Var. \times Env.)	110	29**	39.10**	2.81**	488469.00**
Environments (Lin.)	1	4340.31**	6468.11**	42.815**	7189396.53**
(Var. \times Env.) (Lin.)	22	18.42	3.4	1.249	435198.68**
Pooled deviation	92	12.94	22.544**	1.384**	187950.23*
Pooled error	132	15.5	17.4	1.75	248170
Total	137	70.45	146.77	2.293	783782.87

The advanced breeding line G9 (78.91 cm) and G16 (80.38 cm) showed dwarf plant type compared to population mean with regression coefficient near unity (1) and less deviation from regression coefficient (S^2_{di} G9 = 4.02 and G 16 = 5.07) indicates that these two lines are of sd^2 moderate height with stable performance across the locations which intern helps to develop non-lodging and stable lines over the environments. The line G2 had lowest mean plant height and regression coefficient less than the unity ($b_i = 0.67$) indicating specific adaptation of the line to that favorable environment (Table 4). G1 (19.21) and G11 (20.00) showed higher number of productive tillers per plant as compared to mean number of productive tillers of the population. The regression coefficient is near to unity (G1 = 0.91 and G2) and deviation from regression coefficient is less (G1 = 0.62 and G11 = 0.04) which reveals that these two advance breeding lines showed stable performance across the locations (Table 4). These findings are in agreement with the results reported by Vishnuvardhan *et al.* (2015). Among twenty advanced breeding line JA-6-2 (mean = 6865.83 kg/ha) had more mean value than population mean which also had regression coefficient value ($b_i = 0.94$) around unity and less deviation from the regression ($Sd^2 = -344.27$).

Table 4. Stability parameters with respect to yield and yield attributing characters over the six locations as per Eberhart and Russel model.

Sl. No.	Line	Days to 50% flowering			Plant height (cm)			Productive tillers/plant			Grain yield (kg/ha)		
		Mean	S ² di	bi	Mean	S ² di	bi	Mean	S ² di	bi	Mean	S ² di	bi
1	G1	96.83	1.61*	1.14	67.08	19.20*	0.77	19.21	0.62	0.91	6026.63	-92232.61	0.83
2	G2	97.33	10.99**	1.14	77.66	12.65*	0.67	18.67	-0.61	1.20	6466.69	277102.89*	0.44
3	G3	96.83	27.02**	1.07	82.44	6.05	1.06	18.24	-0.16	2.17	6490.38	-102165.83	0.30*
4	G4	93.92	5.91**	1.10	82.67	2.45	0.90	18.08	-0.21	1.79	6530.04	175040.21*	0.22
5	G5	96.25	8.15**	1.14	83.91	0.91	1.06	18.78	1.22	0.99	6459.36	303364.99**	-0.43
6	G6	95.50	0.65	0.40*	80.89	-3.71	1.15	19.33	-0.79	1.54*	6875.67	176756.09*	-0.43
7	G7	94.75	13.74**	1.37	81.68	-4.17	1.11	18.73	-0.17	1.55	6397.34	-12557.51	1.24
8	G8	95.00	7.75**	1.30	81.29	3.51	1.04	18.98	-0.51	0.93	6575.67	95776.87	1.26
9	G9	96.67	11.30**	1.28	78.91	4.02	0.98	19.13	1.66*	1.79	6549.13	244994.25*	1.54
10	G10	97.58	16.72**	0.87	82.11	1.25	0.99	18.72	-0.35	1.88	6352.49	-26221.86	1.29
11	G11	98.58	-0.47	0.94	78.59	-3.55	1.17	20.00	0.04	1.01	6177.71	54428.55	0.61
12	G12	99.83	7.46**	0.81	84.12	5.95	0.86	18.95	-0.23	1.31	6634.93	-11067.75	0.46
13	G13	93.25	1.77*	1.03	81.18	-5.31	0.90	19.88	0.09	0.70	6584.93	-45167.91	0.63
14	G14	95.67	9.55**	1.00	80.87	-2.02	0.94	19.58	1.50*	0.55	6696.80	66107.04	0.21
15	G15	92.58	4.91**	0.98	82.58	0.08	0.84	21.10	1.99*	-1.03	6865.83	-344.27	0.94
16	G16	95.17	7.29**	0.68	80.38	5.70	1.01	19.40	0.61	0.64	6477.90	-69897.93	1.36
17	G17	96.92	19.00**	0.05*	82.15	0.27	1.01	18.84	0.04	2.05	6456.39	-2367.73	2.27
18	G18	102.75	11.46**	1.22	100.85	36.12**	1.08	19.88	3.63**	1.42	7059.60	242504.26*	3.78
19	G19	100.92	9.70**	0.84	107.89	71.88**	0.95	19.23	1.06	0.15	6827.72	248044.72*	3.41
20	G20	98.83	6.71**	0.87	102.12	102.80**	1.07	20.31	3.21**	0.26	7177.53	110844.45	2.81
21	G21	96.83	8.63**	1.21	78.16	19.08*	0.94	16.50	0.86	0.78	4093.06	52475.53	0.91
22	G22	109.92	9.67**	0.81	82.84	35.39**	1.22	17.58	0.56	0.53	4881.40	-81675.58	0.53
23	G23	116.00	26.21**	1.06	98.78	26.14**	0.97	18.35	-0.75	1.62	4788.67	-68369.08	1.15*
Total mean		98.17			84.31			19.04			6323.73		

Table 5. ANOVA of F₆ advanced breeding lines of rice for productivity traits based on AMMI.

Source of variations	Days to 50% flowering						Plant height (cm)					
	DF	SS	MSS	F CAL	P \geq F	% variation	DF	SS	MSS	F CAL	P \geq F	% variation
Genotype	22	7433	337.8	259.8	0.001	38.13	22	22536	1024.3	58.86	0.001	53.50
Location	5	8681	1736.1	1335.38	0.001	44.53	5	12936	2587.2	147.84	0.001	30.71
Interaction	110	3192	29	22.307	0.001	16.37	110	4298	39.1	2.24	0.001	10.20
IPC1	26	1493	57.4	44.138	0.001	46.77	26	2135	82.1	4.71	0.001	49.67
IPC2	24	770	32.1	24.69	0.001	24.12	24	1102	45.9	2.63	0.001	25.63
Residual	60	929	15.5	11.92	0.001		60	1060	17.7	1.01	0.001	
Error	132	176	1.3	1.3	0.001		132	2294	17.4			
Source of variation	Number of productive tillers						Grain yield (kg/ha)					
	DF	SS	MSS	F CAL	P \geq F	% variation	DF	SS	MSS	F Cal	P \geq F	% variation
Genotype	22	232.9	10.58	6.04	0.001	26.97	22	146646129	6665733	26.85	0.001	59.08
Location	5	85.6	17.12	9.78	0.001	9.89	5	14378791	2875758	11.58	0.001	5.79
Interaction	110	309.7	2.81	1.60	0.0045	35.78	110	53731588	488469	1.96	0.001	21.63
IPC1	26	119.6	4.59	2.62	0.001	38.61	26	24664295	948627	3.82	0.001	45.96
IPC2	24	96.2	4	2.28	0.0016	31.06	60	12676754	528198	2.12	0.0037	23.59
Residual	60	93.9	1.56	0.88			132	16390539	273176	1.1	0.321	
Error	132	231	1.75					32758431	248170			

It indicates that the presence of advanced breeding lines had stable performance across the environments and can adapt to diverse environments. Hence, these can be used as stable lines for wider environments and proposed in the zone 7 for large scale trials. Similar results were also reported by Mall *et al.* (2013).

The AMMI analysis of variance indicated that mean squares due to genotypes, location and GLI contributed 38.13, 44.53 and 16.37% , respectively for total variability of days to fifty percent flowering. The Genotypes, Location and GLI contributed 53.50, 30.71 and 10.20% to total variation for plant height respectively. For number of productive tillers 26.97, 9.78 and 1.6% of total variation was contributed by genotypes, location and GLI respectively. Similarly, for Grain yield (kg/ha) 59.08, 5.79 and 21.63% contributed to total variations from genotypes, locations and GLI respectively. Further, the GLI was partitioned into two interactions principal component (IPC) axes (IPC1 and IPC 2) which together explains 70.89, 75.30, 69.67 and 69.55% variations for days to 50% flowering, Plant height, number of productive tillers and grain yield per hectare, respectively towards total GLI variance (Table 6). Similarly, stability of rice hybrids were studied using AMMI analysis by Kulsum *et al.* (2013).

It is a multivariate analytical tool that graphically displays interaction between each genotype and environment in a two-dimensional biplot (Yan and Hunt 2002) and allows visualization of the inter-relationship among environments, and between genotypes and environments. The model with first few IPC axes that capture most of the GLI variation is considered as the best one for extracting GGE pattern from the data (Yan *et al.* 2000). The first two IPCs explained > 75% of G + GE sum of squares of the traits studied. The near origin positioning of the advanced breeding lines G1, G11, G2 and G20 in the bi-plot suggested their wide adaptation to all the six locations for days to 50 per cent flowering (Fig. 1a). For plant height most of the genotypes were widely adapted across six environments as indicated by their near origin position in GGI biplot. (Fig. 1b). For productive tillers per plant the lines G10, G6, G17, G7, G12, G1, G23 and G2 are positioned near GGL bi-plot origin (Fig. 1c). For yield per hectare G1, G3, G11, G13, G15, G12, G16, G7 and G10 are positioned near GGL bi-plot origin (Fig. 1d). The approximate positioning of G10 near to the origin in GGL bi-pot indicated wider adaptation for all the traits studied except days to 50% flowering. These results are in close correspondence with the results reported by Susanto *et al.* (2015) in rice while studying G × E interaction for Fe content.

Which-won-where graph was constructed by joining the farthest genotypes and forming a polygon. Later perpendicular lines were drawn from the biplot origin to each side of the polygon, then dividing the biplot into several sectors with one genotype at the vertex of the polygon. These lines are referred as equality lines (Yan *et al.* 2001). Genotypes which fall on the vertices of the polygon are either the best or poorest in one or more environments (Yan and Tinker 2006). Where biplot of days to 50% flowering, plant height, number of productive tillers and grain yield per hectare are presented in Fig.1a-d, respectively. Polygon view of the days to 50% flowering, plant height and grain yield per hectare indicates that all the tested locations could not segregate the advanced breeding lines effectively in different sectors of the biplot.

The polygon view of number of productive tillers per plant is the most informative and it could discriminate both environments and genotypes effectively and also well distributed (Fig. 2c). Perpendicular lines are equality lines between the adjacent genotypes on the polygon, which facilitate visual comparison among the lines. In number of productive tillers per plant equality line between the G18 and G15, G18 was better in environment E4, E5 and E6. Whereas G15 was better in E3 and E2. Equality line between G20 and G21 indicates that genotype G20 is better in E1 environments than G1. The other vertex genotype G21 which was located far away from all of test environments implied that it did not performed well at any of the test environments. This indicates that the target environments may consists of three mega environments for above trait

(E4, E6 and E5), (E3 and E2) and (E1). This conclude different cultivar should be selected and deployed for each different environment. Similar results were reported by Akter *et al.* (2015)

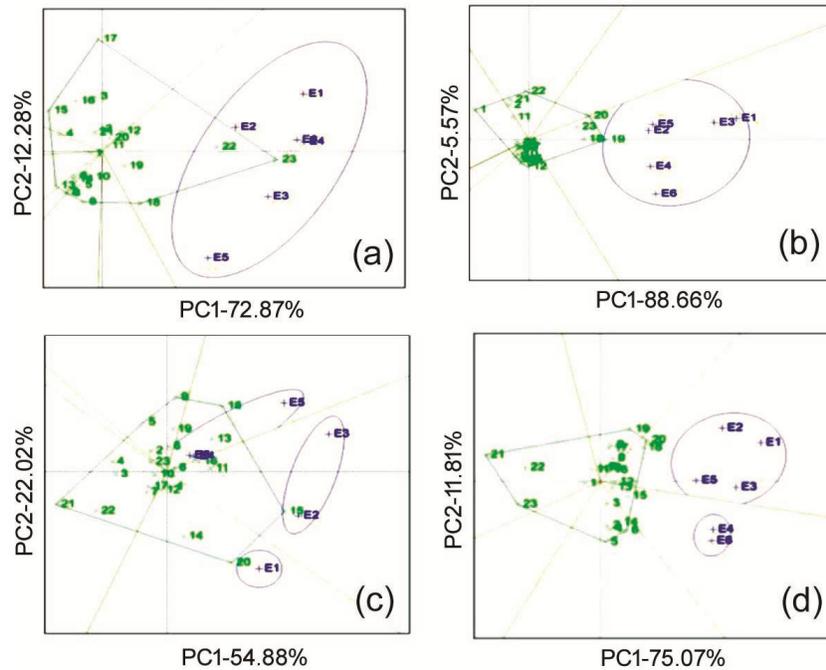


Fig. 1. Polygon view of GGE biplot for identification of stable advanced breeding lines across the tested environments. (a) Days to 50% flowering, (b) plant height (cm), (c) productive tillers per plant, (d) yield per hectare (kg/ha).

Environmental vector view of GGE biplot is based on an environment-centred (Centring = 2) G by E without any scaling (Scaling = 0 and its environment-metric preserving (SVP = 2) and its axes are drawn to scale (Default feature of GGE biplot). Line which connects between the environment and origin called as environmental vectors. Angle between the vector of two environments correlate the relationship between them. Presence of acute and obtuse angle between the two environments represents the positive and negative correlation, respectively GGE biplot showed wider acute angle between the E1 and E3 environments for the trait days to 50% flowering (Fig. 3a) and number of productive tillers (Fig. 3b) where as E5 and E6 environments for plant height (Fig. 3c), E6 and E2 environments for grain yield per hectare (Fig. 3d) which represent weak interactions of genotype \times environments. Narrow acute angle between the remaining environments for all the four character studied represents the weaker interaction of genotype \times environments. Angle between E1 and E5 environments for the days to 50 per cent flowering and productive tillers per plant shown slightly smaller angle than acute angle represents moderate G \times E interactions. Distance between the two environment vectors represents dissimilarities in discriminating the genotypes, for example in days to 50% flowering E4 E6 and E2 has formed one group while other three tested locations formed solitary group. Presence of close association between the tested environments indicated that there is no potentiality of environment to discriminate the tested genotypes with respect to the trait days to 50% flowering. Avoiding non-discriminating tested environments (E4, E6 and E2) can reduce the cost of testing and increases the breeding efficiency. Similar results were reported by Akter *et al.* (2015).

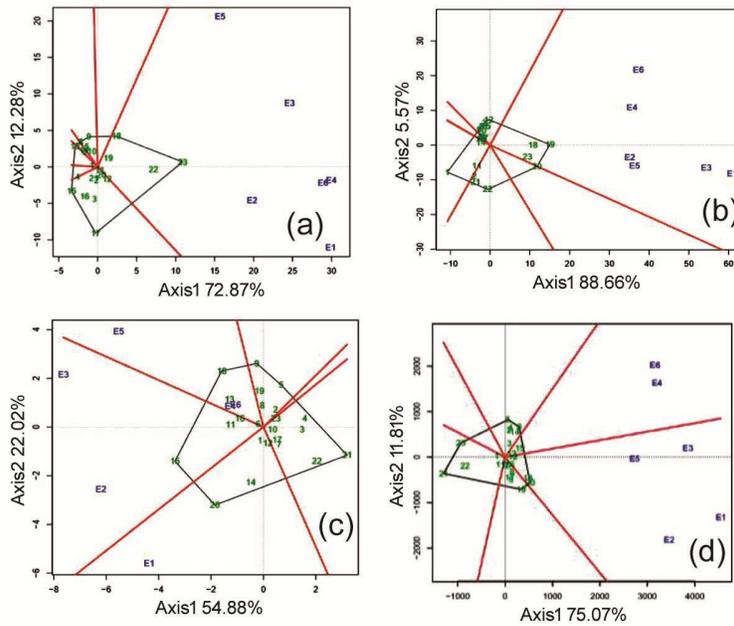


Fig. 2. Biplot view to identify adaption of advanced breeding lines to specific environments. (a) Days to 50% flowering, (b) plant height (cm), (c) productive tillers per plant, (d) yield per hectare (kg/ha).

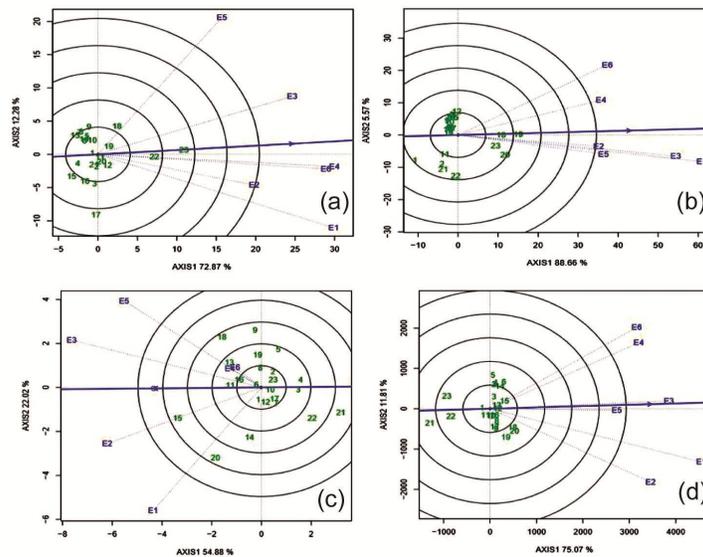


Fig. 3. GGE biplot indicating relationship between the tested environments for yield and its related traits. (a) Days to 50% flowering, (b) plant height (cm), (c) productive tillers/plant, (d) yield per hectare (kg/ha).

Length of the environment vector is visualized by the concentric circles (Average environment point) present on the biplot which intern helps to measure the discriminating ability of the environments (Fig. 4). Shorter the environmental vector has least discriminating ability

whereas, longer vector has highest discriminating ability. For example, in biplot view for productive tillers per plant (Fig. 4c), environment E3 and E1 is most discriminating where as E2 and E6 are least discriminating. The test environment which has smaller angle with the AEA (average environmental axis - line passes through the average environmental point and biplot origin) representing more representativeness.

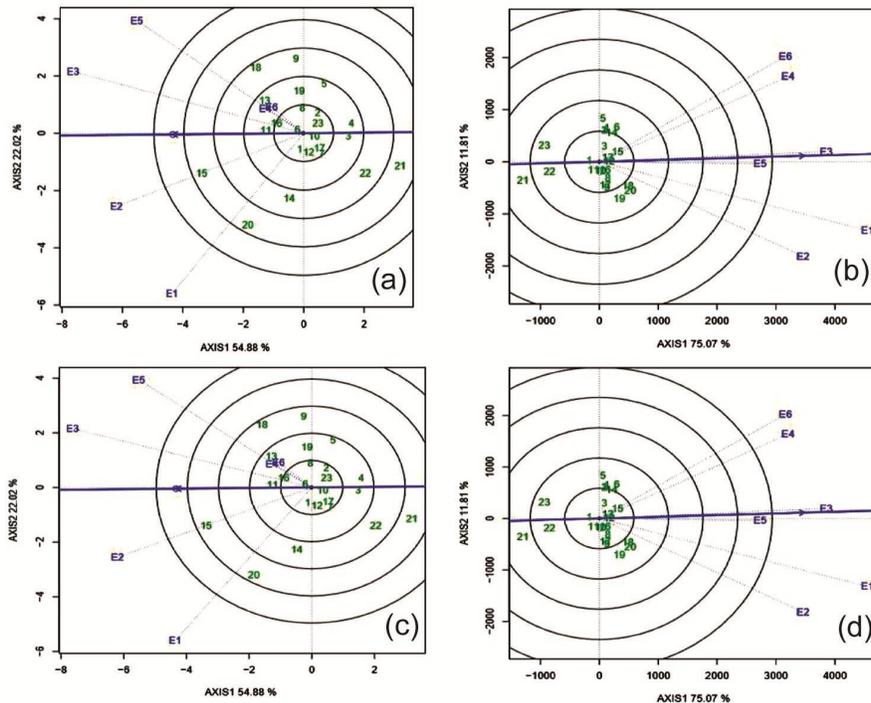


Fig. 4. Discriminating and representativeness of tested environments towards advanced breeding lines for yield and its related traits. (a) Days to 50% flowering, (b) plant height (cm), (c) number of productive tillers/plant, (d) yield per hectare (kg/ha).

In the polygon view of productive tillers per plant (Fig. 4c) E3 and E2 are highly representativeness whereas E5 and E1 are least representativeness. From Fig. 4c there is no any such tested environments which has both discriminating and representativeness for the trait productive tillers per plant. The presence of both discriminating and representativeness depicts good test environments for generally adapted genotypes. Environments E3 and E1 are most discriminating but non-representativeness resulted that the test environment may good for selecting the specifically adaptable genotypes. These results are in agreement with those of Susanto *et al.* (2015).

The investigated stability analysis parameters in Eberhart and Russel model and GGE biplot analysis enabled to classify genotypes and environments for their stability. Above two models identified JA 6-2 (G15) and JB 1-11-7 (G1) as relatively low interaction accompanied with higher grain yield performance as compared to local checks. These lines could be tested in largescale demonstration at farmer's field and further proposed for release in zone 7 and zone 9 of Karnataka, India as supplement to old red rice variety Jyothi.

References

- Aktar A, Hasan MJ, Kulsumu, Rahman MH, Khatun M and Islam MR 2015. GGE Bipolt Analysis for Yield Stability in Multi-Environment Trials of Promising Hybrid Rice (*Oryza sativa* L.). Bangladesh Rice J. **19**(1): 1-8.
- Amrithadevarathinam A 1987. Stability analysis of some released varieties and local cultivars in dry and semidry condition. Madras Agric. J. **24**(10-11): 434-439.
- Eberhart SA and Russell WA1966. Stability parameters for comparing varieties. Crop Sci. **6**(1): 36-40.
- Finlay KW and Wilkinson GN1963. The analysis of adaptation in a plant breeding programme. Australian J. of Agric. Res. **14**(7): 742-754.
- Francis TR and KannenbergLW 1978. Yield stability studies in short season maize. I. A descriptive method for grouping genotypes. Can. J. Plant Sci. **58**: 1029-1034.
- Ganesh SK and Soundarapandian G1987. Association studies for stability parameters in short duration varieties of rice (*Oryza sativa* L.). Madras Agric. J. **74**: 208-212.
- Gauch HG and Zobel FW1988. Predictive and postdictive success of statistical analysis of yield trials. Theor. Appl. Genet. **76**:1-10.
- Gauch HG2006. Statistical analysis of yield trials by AMMI and GGE. Crop Sci. **46**: 1488-1500.
- Koli NR and Prakash C. 2013. Genotype × environment interactions and adaptability with sustainability index their comparison in aromatic rice (*Oryza sativa* L.) under transplanted condition. Int J. Agric, Envi and Biotech. **5**(4): 401-404.
- KulsumMU, Hasan MJ, AkterA, Rahman H and Biswas P 2013. Genotype-environment interaction and stability analysis in hybrid rice: an application of additive main effects and multiplicative interaction. Bangladesh J. Bot. **42**(1): 73-81.
- Mall AK, Swain P, Singh ON and Baig MJ 2013. Use of Genotype x Environment interactions and drought susceptibility index for identification of drought tolerant genotypes at vegetative stage in upland Rice. Indian J. Dryland Agric. Res. Development **27**: 73-78.
- Mather K and Jinks JL1971. Biometrical Genetics, 2nd edition, Chapman and Hall, London. Heredity **29**: 237-245.
- Song XJ, Huang W, Shim ZM and Lin H2007. A QTL for rice grain width and weight encodes a previously unknown RING- type E3 Ubiquitin ligase. Nat. Genet. **39**(5): 623-630.
- Shukla GK1972. Some statistical aspects of portioning genotype-environmental components of variability. Genet. **3**(9): 623-630.
- Susanto U, Rohaeni WR, Johnson SB and Jamil A 2015. GGE biplot analysis for genotype x environment interaction on yield trait of high Fe content rice genotypes in Indonesian irrigated environments. Agriveta, **37**(3) 265-275.
- Vishnuvardhan BR, Payasi K, Devendra and Anwar Y2015. Stability analysis for yield and its components in promising rice hybrids. Int Quarterly J. Environ. Sci. **9**(1-2): 311-321.
- Yan W, Hunt LA, Sheng Q and Sziavnic Z 2000. Cultivar evaluation and mega environment investigation based on GGE biplot. Crop Sci. **40**: 597605.
- Yan W, Cornelius PL, Crossa J and Hunt LA 2001. Two types of GGE biplots for analysing multi-environment trial data. Crop Science **41**: 656-663.
- Yan W and KangMS 2003. GGE biplot analysis: a graphical tool for breeders, Geneticists and Agronomists. 1st Edn., CRC Press LLC., Boca Raton, Florida pp. 271.
- Yan W and Hunt LA 2002. Biplot analysis of diallele data. Crop Sci. **42**: 21-30.
- Yan W and Tinker NA 2006. Biplot analysis of multi-environment trial data: Principles and applications. Can. J. Plant Sci. **86**: 623-645.
- Zobel RW, Wright MJ and Gauch HG 1988. Statistical analysis of a yield trial. Agron. J. **80**: 388-393.

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