

AMMI analysis of rice yield trials (*Oryza sativa* L.)

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ABSTRACT

Rice (*Oryza sativa* L.) is one of the world's most important staple cereal food crop growing in at least 114 countries under diverse conditions such as irrigated, rainfed lowland, rainfed upland and flood prone ecosystems. The considerable variation in environment has resulted in significant variation in the yield performance of rice genotypes. Thus, genotype x environment interaction (GEI) is an important issue faced by the plant breeders and agronomists. There are different approaches for studying GEI i.e. parametric, non-parametric and multivariate statistical methods. The objective of the present investigation was to analyze the pattern of genotype x environment interaction (GEI) for grain yield of 21 rice genotypes by Additive Main effect and Multiplicative Interaction (AMMI) model using the data generated from the four different locations (Nawagam, Vyara, Dabhoi and Thasra) of Gujarat state, India. The results revealed that the genotypes (G), environments (E) and genotypes x environments interaction (GEI) were highly significant and contributed 7.8, 80.1 and 12.1 per cent of trial variation, respectively. The partitioning of GEI variation into principal component axis indicated that the first two axis were found significant and contributed 63.13 and 27.97 per cent, respectively to the GEI variance. The genotypes viz. NWGR-3199 was winner and high yielding for Dabhoi and Thasra locations, IET-19132 for vyara location and IET-19143 for Nawagam location. Genotypes NWGR-3026, NWGR-3006, IET-19147 and IET-19160 were close to the origin in biplot and hence, they were non-sensitive to environmental interactive forces. Therefore, they possess general adaptation due to better mean grain yield. Nawagam environment was high yielding potential location, whereas Vyara, Dabhoi and Thasra were observed low yielding environments. According to AMMI Stability Value (ASV), $W_{i(AMMI)}$ and $ASTAB_i$, Genotypes NWGR-3026, IET-19147 and NWGR-3006 were found stable whereas genotypes IET-19132 and IET-19143 were unstable.

Key words: Rice, yield, trials

Rice is one of the world's most important staple cereal food crop growing in at least 114 countries under diverse conditions such as irrigated, rainfed lowland, rainfed upland and flood prone ecosystems. The considerable variation due to environment has resulted in significant variation in the yield performance of rice genotypes. Thus, genotype x environment interaction (GEI) is an important issue faced by the plant breeders and agronomists. There are the different approaches for studying GEI i.e. parametric (regression equation) univariate, non-parametric and multivariate statistical methods (AMMI). The analysis of variance is useful for identifying and testing sources of variability, it

provides no insight into the particular pattern of the underlying interaction. The ANOVA model effectively describes the main additive effects, while interaction (residuals from the additive model) is non-additive and requires alternative techniques, such as principal component analysis (PCA) to identify interaction pattern. Thus, ANOVA and PCA models combined to constitute the Additive Main effects and Multiplicative Interaction (AMMI) model (Gauch and Zobel, 1997; Zobel *et al.*, 1988). AMMI is, therefore, a hybrid concept of statistical model incorporating both ANOVA (for additive component) and PCA (for multiplicative component) for analyzing two way genotype x environment data structure. The present investigation was carried out to analyze the pattern of genotype x environment interaction (GEI) for grain yield and to select the stable genotypes of rice. Three stability

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measures (1) $W_{(AMMI)}$ measure (Raju, 2002) (2) ASV (AMMI Stability Value) proposed by Purchase (1997) and (3) ASTAB_i (AMMI based Selection Index.) (Rao *et al.*, 2004) were also calculated from AMMI analysis to find out stable genotypes.

MATERIALS AND METHODS

Twenty one rice genotypes were evaluated at multilocations (Nawagam, Vyara, Dabhoi and Thasra) of different agro-climatic zones of Gujarat under RBD with three replications. Yield data of rice collected from Main Rice Research Station, Anand Agricultural University, Nawagam were subjected to combined analysis of variance and AMMI model.

Statistical Model :

$$\text{ANOVA : } Y_{ij} = \mu + \alpha_g + \beta_e + \alpha\beta_{ge} + \rho_{ij} + \varepsilon_{ijk}$$

$$\text{PCA : } Y_{ij} = \mu + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ij} + \varepsilon_{ijk}$$

$$\text{AMMI : } Y_{ij} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ij} + \varepsilon_{ijk}$$

Where

- μ = grand mean
- α_g = deviations of genotype(g)
- β_e = deviations of environment(e)
- λ_n = singular value for Interaction Principal Component Axis n (IPCA)
- γ_{gn} = genotype eigenvector for axis n
- δ_{en} = environment eigenvector
- ρ_{ij} = residual
- ε_{ijk} = error term or uncontrolled variation

The bi-plot is a graphical representation from AMMI analysis which is a useful tool to understand more complex specific pattern of genotypes and GEI or both genotypes and environments. The concept of bi-plot was first developed by Gabriel (1971). It is a scatter plot that graphically displays the genotype (entries) and the environments (testers) of a two-way data and allows visualization of the interrelation among the entries (genotypes) and interaction between entries and testers (environments).

$W_{(AMMI)}$
 $W_{(AMMI)}$ a measure of stability is as good as Wruck's ecovalence (W_i^2) was estimated as per Raju (2002)

$$W_{i(AMMI)} = \sum_{m=1}^M \lambda_m^2 \gamma_{mi}^2$$

λ_m^2 = singular value for Interaction

Principal Component Axis m (IPCA)

γ_{mi}^2 = genotype eigenvector for axis n

AMMI Stability Value (ASV)

The AMMI model does not make provision for a quantitative stability measure, such a measure is essential in order to quantify and rank genotypes according their yield stability, the following measure proposed by Purchase (1997) was estimated as under.

$$\text{ASV} = \sqrt{\left(\frac{\text{IPCA1 SS}}{\text{IPCA2 SS}} \times (\text{IPCA1 score})^2 \right) + (\text{IPCA2 score})^2}$$

AMMI based Selection Indices

Rao *et al.* (2004) proposed a new stability measure and incorporated as a stability component. When more than two axis are retained in AMMI model, the biplot formulation of interaction is failed. When n' of N axis are retained in the AMMI model to explain GEI, then the stability measure of i^{th} variety can be determined as the end point of its vector a_{1i}^* , a_{2i}^* , ..., a_{ni}^* from the origin $O_{n \times 1}^*$. This is a squared Euclidean distance and was calculated as under.

$$\text{ASTAB}_i = \alpha_{1i}^{2*} + \alpha_{2i}^{2*} + \dots + \alpha_{ni}^{2*} = \sum_{n=1}^{n'} \alpha_{ni}^{2*} = \sum_{n=1}^{n'} \lambda_n \alpha_n^2$$

A genotype is considered as highly stable when the value of ASTAB_i is small or closer to zero.

RESULTS AND DISCUSSION

The combined analysis of variance (ANOVA) of 21 rice genotypes over 4 locations according to AMMI model is presented in Table 1.

In AMMI model, additive effects for main effects i. e. genotypes and environments and multiplicative effects for G x E interaction are considered. The results presented in Table 1 indicated that mean square for genotypes and locations (environments) were found significant and highly significant, respectively. This suggested existence of broad range of diversity among genotypes and locations and the differential performance of genotypes over locations i.e. G x E interaction was significant. Of the total treatment

Table 1 Analysis of variance (ANOVA) according to AMMI model for rice genotypes.

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	% SS
Trials	83	238.2129	2.8700	5.96**	—
Genotypes	20	18.4842	0.9242	1.92*	7.76
Environments	3	190.8184	63.6061	132.01**	80.10
GxE Interaction	60	28.9160	0.4819	5.04**	12.14
PCA I	22	18.2527	0.8297	8.68**	63.13
PCA II	20	8.0882	0.4041	4.23**	27.97
Residual	18	2.5751	0.1431	1.50	8.90
Pooled error	80	7.6496	0.0956		

*, and ** significant at $P < 0.05$ and $P < 0.01$, respectively

variation (trial SS), the proportion of variance due to locations was the largest (80.10 per cent) followed by the variance due to G x E interaction (12.14 per cent) and genotypes (7.76 per cent). ANOVA provided no insight into the particular pattern of genotypes or environments that gave rise to interactions, but described only main effects effectively. These results confirmed to the observations made by Zobel *et al.* (1988). Since G x E interaction was highly significant (Table 1), ANOVA model was combined with PCA model to further analyze the residuals (GEI) of the ANOVA model.

The GEI was highly significant and was further partitioned into two PCA axes (IPCA) which jointly contributed 91.1 per cent of GEI. The first and second PCA were found highly significant ($P < 0.01$) and contributed 63.13 and 27.97 per cent to the total GEI variance, respectively and both the IPCA jointly 91.1 per cent of GEI. The two PC components accounted 70 % of the df for GEI. The residual SS accounted 8.90% of the interaction SS and 30% of df for GEI. (Gauch and Zobel, 1997).

The results of AMMI analysis can also be easily comprehended with the help of AMMI 1 biplot as presented in Fig. 1. The mean performance of genotypes and environments vs IPCA 1 score were used to construct the biplot in Table 2. According to AMMI model, the genotypes which are characterized by mean higher than the grand mean and the IPCA scores nearly zero are considered as generally adapted to all environments. However, the genotypes with high mean performance with large value of IPCA scores are considered to have specific adaptability to the environments (Crossa *et al.* (1991), Sharma *et al.* (1998) and Shinde *et al.* (2002)). Biplot assay presented in Fig. 1 identified three high yielding genotypes viz., G7, G13 and G14 having general adaptability, having mean yield > 4.336 kg plot⁻¹ and

close to IPCA 1 = 0 line. Genotypes G10, G12 and G17 were higher yielding and specially adapted to favourable environments. Genotypes G1, G2, G5, G9 and G16 had low mean yield and positioned near to IPCA I = 0 line indicated that they were poorly adapted to all environments.

Similar sign of IPCA I score for both genotypes and environment imply positive interaction and thus it attributed to higher yield of genotype at particular environment (Anandan *et al.*, 2009). Accordingly IPCA scores of genotypes G4, G7, G10, G12, G14 G17, G18 and G20 and of Nawagam (E1) location were positive, which indicated that these genotypes attributed higher yield at this location having positive GEI.

Environments were widely spread over scatter diagram which indicated high variability was among the locations. The environment E1 (Nawagam) was high yielding potential location, whereas, E2, E3, and E4 were found low yielding environments (Mahalingam *et al.*, 2006).

Genotypes located near the plot of origin were less responsive than the vertex genotypes. In this study, genotypes G1 and G14 were close to the origin and hence, they were non-sensitive to environmental interactive forces therefore, have general adaptation with different mean grain yield. Similarly the environment close together i.e. E3 and E4 were found to have similar interaction pattern in genotypes.

Visualization of which-won-where pattern of MLT data is important for studying the possible existence of different mega-environments. The polygon is drawn by connecting the markers of the genotypes that are far away from the biplot origin such that all other genotypes were contained in the polygon. The rays in Figure 2 were lines that were perpendicular to all the sides of the polygon. Ray 1 was perpendicular to the line connecting genotypes G17 and G18. Rays 2

is perpendicular to the line connecting G18 and G5, similar way Ray 3 and 4 were perpendicular to line connecting G5 to G15 and G15 to G17, respectively. These four rays divided the biplot into four sectors and the environments were distributed in the three sectors. The interesting feature of this view of GGE biplot is that the vertex genotype(s) for each sector was/were the best for the environment fall in the same sector than the others in all environments (Yan, 2002). Thus, environment E3 and E4 fell into sector II delineated by Rays 2 and 3 and the vertex genotypes for this sector was G5 suggesting that G5 was the winner high yielding genotype for Dabhoi (E3) and Thasra (E4) locations. Similarly, for environment E2 (sector III) the vertex genotypes was G15 which was the best for Vyara location (E2). Sector IV delineated by Rays 4 and 1 contained the environment E1 and the winning genotypes for Nawagam (E1) location was G17, which was higher yielding genotype. The discrepancy between the results of vertex genotype and higher yielding one may be because of the biplot

explained 91.1% to variation of GEI and the remaining 8.90 % variation was unaccounted (Mohammadi *et al.*, 2007).

AMMI Stability Value (ASV)

The ASV is the distance from the co-ordinate point to the origin in two dimensions of IPCA 1 scores against IPCA 2 scores in the AMMI model.

It was weighted by the proportional difference between IPCA 1 and IPCA 2 scores to compensate for the relative contribution of IPCA 1 and IPCA 2 to total GE sum of square. The distance from zero is then determined using the theorem of Pythagoras (Purchase *et al.*, 2000). In ASV method, a genotype with least ASV score was considered as the most stable. Accordingly, genotype G1 followed by G13, G7 and G14 were the most stable, while genotype G15, G17 and G21 were undesirable in terms of stability (Table 3). These results were in confirmation with the results of biplot analysis. Among the stable genotypes, mean yield of all genotypes were higher than over all mean of grain yield except genotype G1.

Table 2 IPCA1 and IPCA2 scores of different rice genotypes and locations.

Sr. No.	Genotypes	Mean yield (kg plot ⁻¹)	Rank	IPCA1	IPCA2
G1	NWGR-3026	4.165	17	0.036	-0.018
G2	NWGR-3113	4.017	18	-0.073	-0.196
G3	NWGR-3215	3.288	21	-0.197	-0.113
G4	NWGR-3132	4.534	7	0.124	-0.297
G5	NWGR-3199	4.265	16	-0.069	-0.343
G6	NWGR-3213	4.334	11	-0.143	-0.057
G7	NWGR-3006	4.470	8	0.055	0.088
G8	NWGR-2018	4.410	10	-0.160	0.231
G9	NWGR-2032	3.910	19	-0.033	0.275
G10	IET-19140	5.426	1	0.165	-0.184
G11	IET-19148	4.278	15	0.165	0.217
G12	IET-19123	5.351	2	0.092	-0.226
G13	IET-19147	4.634	3	-0.057	0.043
G14	IET-19160	4.579	4	0.079	-0.027
G15	IET-19132	4.327	12	-0.672	0.230
G16	IET-19114	4.322	13	0.022	-0.145
G17	IET-19143	4.574	5	0.464	0.406
G18	IET-19189	4.565	6	0.146	-0.322
G19	IET-19117	4.292	14	0.109	0.347
G20	IET-19146	4.424	9	0.208	0.069
G21	GR-103	3.515	20	-0.260	0.019
	Over all Mean	4.366			
E1	Nawagam	6.922	1	0.837	0.196
E2	Vyara	3.017	4	-0.448	0.722
E3	Dabhoi	3.799	2	-0.089	-0.555
E4	Thasra	3.725	3	-0.301	-0.364

Correlation between PC1 and PC2 = -3.45E-11 ns

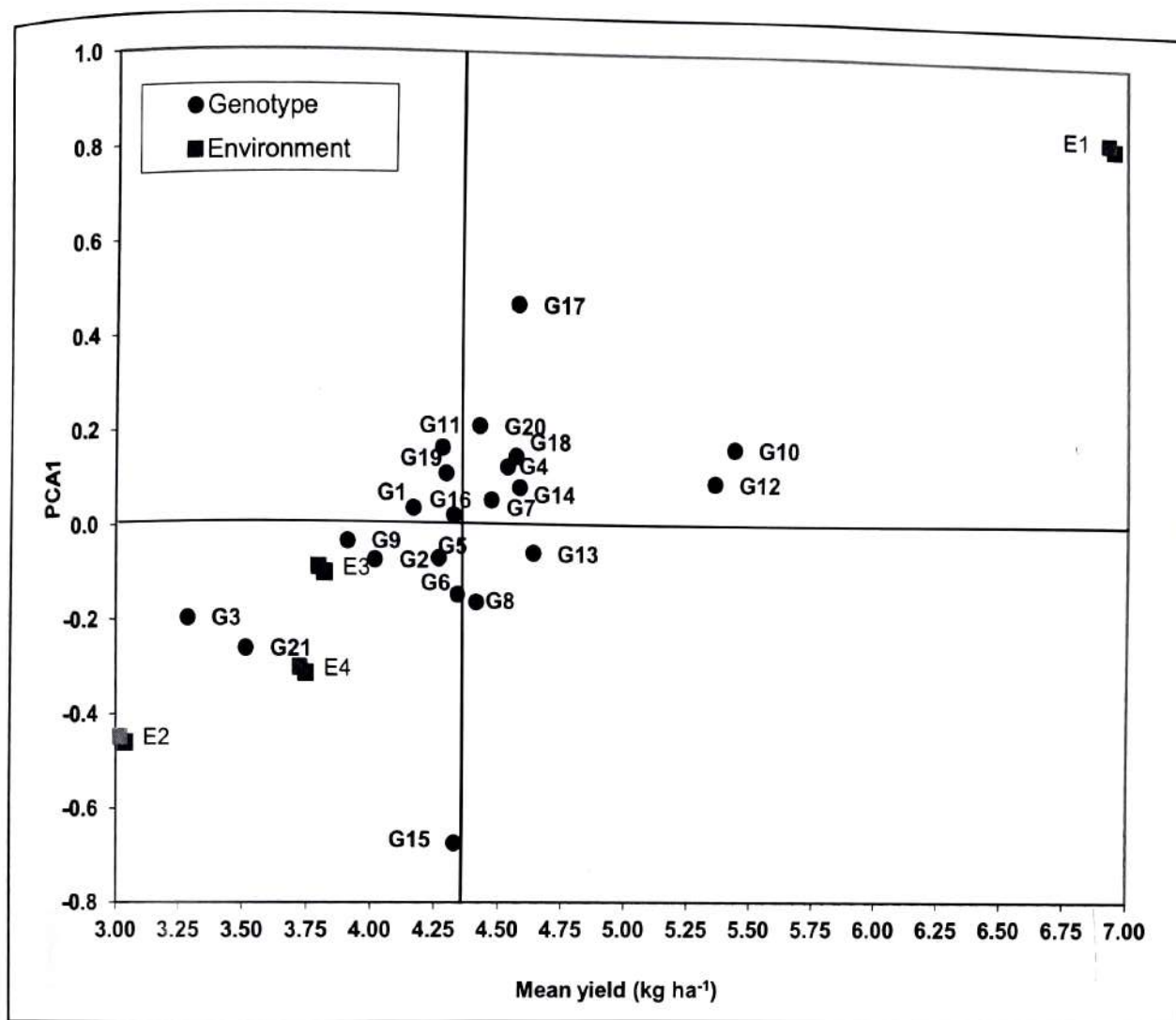


Fig.1 AMMI1 biplot for rice genotypes and locations.

Similarly in unstable genotypes G17 and G21 had higher grain yield while G15 had lower grain yield than mean grain yield (Farshadfar, 2008). This Index (ASV) was also worked out by different researcher to assess stability in different crops (Pourdad, and Mohammadi (2008) and Hugo-Ferney *et al.* (2006)). Thus, present findings are in accordance with those reported by different workers.

$W_{(AMMI)}$ measure
 $W_{(AMMI)}$, a measure of stability may be viewed as Wricke's ecovalence (W_i^2) in terms of AMMI parameters and may be denoted as $W_{(AMMI)}$ (Raju, 2002). The different $W_{(AMMI)}$ values presented in Table 3 indicated that ranks of $W_{(AMMI)}$ superimposed on ranks of AVS measures. According to the value of $W_{(AMMI)}$, G1, G13, G7 and G14 were the most stable,

while genotype G15, G17 and G21 were most unstable. (Raju and Bhatia, 2003).

AMMI based selection Index (ASTABi)

ASTABi (Rao *et al.*, 2004) stability measures (squared Euclidean distance) were calculated using the retained 'n' axis out of 'N' total axis and presented in Table 3. Genotype G1 had the lowest value of ASTABi followed by G13, G7 and G14 and considered as stable. Among these genotypes, only G1 had lower grain yield than overall mean grain yield. The highest values of ASTABi were observed for G15, G17 and G21 which indicated their unstability over environments.

Thus, overall results suggested that genotypes G 7 (NWGR-3006), G 13 (IET-19147) and G 14 (IET-19160) were high yielding stable genotype which can be recommended for all four locations.

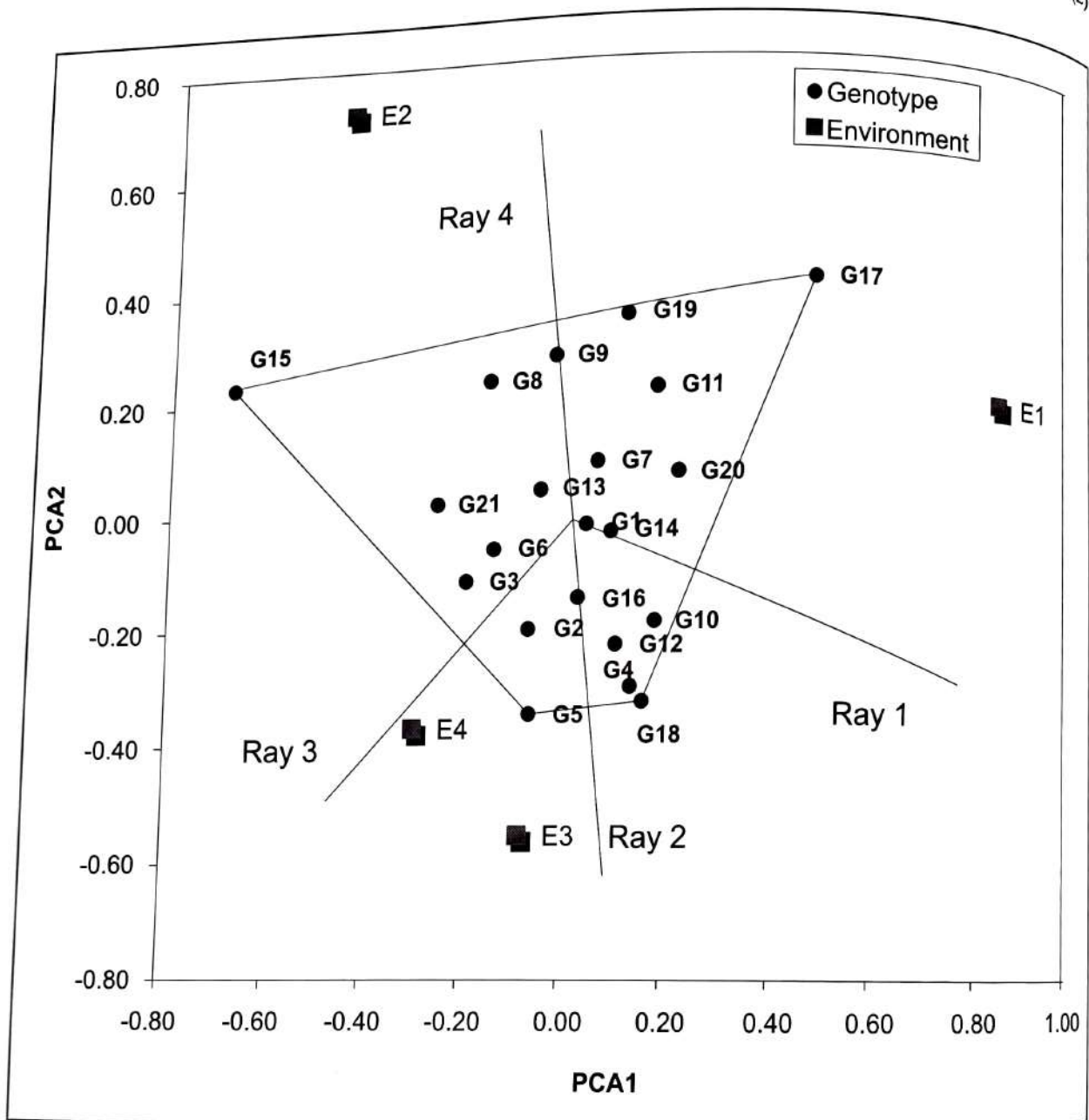


Fig. 2 AMMI2 biplot for rice genotypes and locations

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Table 3 Selection of genotypes based on different indices based on AMMI model for rice genotypes.

Sr.No.	Genotype	Mean yield (kg plot ⁻¹)	Rank	$W_{(AMMI)}$	Rank	ASV	Rank	ASTABi	Rank
G1	NWGR-3026	4.165	17	0.026	1	0.056	1	0.03	1
G2	NWGR-3113	4.017	18	0.407	7	0.224	7	0.41	7
G3	NWGR-3215	3.288	21	0.811	11	0.317	11	0.81	11
G4	NWGR-3132	4.534	7	0.996	15	0.351	15	1.00	15
G5	NWGR-3199	4.265	16	1.036	16	0.358	16	1.04	16
G6	NWGR-3213	4.334	11	0.401	6	0.223	6	0.40	6
G7	NWGR-3006	4.470	8	0.118	3	0.121	3	0.12	3
G8	NWGR-2018	4.410	10	0.900	14	0.334	14	0.90	14
G9	NWGR-2032	3.910	19	0.630	9	0.279	9	0.63	9
G10	IET-19140	5.426	1	0.770	10	0.309	10	0.77	10
G11	IET-19148	4.278	15	0.879	13	0.330	13	0.88	13
G12	IET-19123	5.351	2	0.568	8	0.265	8	0.57	8
G13	IET-19147	4.634	3	0.074	2	0.096	2	0.07	2
G14	IET-19160	4.579	4	0.121	4	0.122	4	0.12	4
G15	IET-19132	4.327	12	8.682	21	1.036	21	8.68	21
G16	IET-19114	4.322	13	0.178	5	0.148	5	0.18	5
G17	IET-19143	4.574	5	5.258	20	0.807	20	5.26	20
G18	IET-19189	4.565	6	1.225	18	0.389	18	1.22	18
G19	IET-19117	4.292	14	1.189	17	0.384	17	1.19	17
G20	IET-19146	4.424	9	0.831	12	0.321	12	0.83	12
G21	GR-103	3.515	20	1.235	19	0.391	19	1.24	19

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