



Use of parametric and non-parametric stability indices for selection of high yielding stable lowland rice genotypes

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Abstract : Twenty two rainfed lowland rice genotypes were evaluated at five locations in Eastern India to identify stable and high yielding genotypes. The experiment was conducted using Randomized Complete Block Design with three replications. Combined analysis of variance showed highly significant differences among genotypes, environments and genotype by environment interactions for grain yield. The additive main effects and multiplicative interaction (AMMI) analysis of variance indicated that the genotype-by-environment interaction sum of squares was about 5 times larger than that for genotypes, which determined substantial differences in genotypic response across environments. The presence of genotype-by-environment interaction was clearly demonstrated by the AMMI model, when the interaction was partitioned among the first three interaction principal component axis (IPCA) which cumulatively captured 97.73 per cent of the total GEI. In this study, environments (testing locations) fell into three sections, where most of the tested genotypes showed specificity. AMMI stability value discriminated genotypes 17 and 18 as the stable genotypes based on YSI (yield stability index) and the RS (rank sum).

Key Words : Additive main effects and multiplicative interaction, Rice, Stability, Genotype-by-environment interaction

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INTRODUCTION

Rice (*Oryza sativa* L.) is the most important cereal crop of India. As this crop is grown under a varied range of agro-climatic conditions ranging from upland to lowland and irrigated to rainfed situations, their phenotypic responses vary greatly in accordance with the environment. Rainfed lowland environments are mostly unfavourable and characterized by variable water regimes, occurrence of submergence and water logging. Nearly 38 million hectares in the world are rainfed lowland out of which 35 million ha are in South-east Asia. Water depth in rainfed fields is mostly variable depending on rainfall distribution, pattern and soil topography. The rice growing environments were analyzed and have been reported on decline in rice production that was due to physical environmental constraints (Ray and Panwar, 1994). The major

efforts in crop technology, under unfavourable environment should be yield stabilizing, cost reducing, risk minimizing and returns enhancing (Nanda and Tomar, 1981). The genotypes should, therefore, be high stability cultivars besides high yielding cultivars. Many methods are available for assessing the stability of performance of crop varieties (Finley and Wilkinson, 1963; Eberhart and Russel, 1966; Perkins and Jinks, 1968; Freeman and Perkins, 1971).

Identification of superior genotypes through genotype-environment interaction (GEI) became complicated for a range of environments in order to determine their true genetic potential (Yaghotipoor and Farshadfar, 2007). The importance of G × E interactions has been demonstrated in almost all major crops (Najafian *et al.*, 2010; Zali *et al.*, 2011). Various statistical methods / models (parametric and non-parametric) and concepts have been described by many researchers (Lin

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et al., 1986; Becker and Leon, 1988; Crossa, 1990; Lin and Binns, 1986; Hussein *et al.*, 2000; Mohammadi and Amri, 2008; Mohammadi *et al.*, 2008). Different models have been used for G×E interaction like static or a biological concept of stability (Becker and Leon, 1988). Another model is also called the dynamic or agronomic concept of stability (Becker and Leon, 1988) where parameters used like regression co-efficient (bi) (Finlay and Wilkinson, 1963) and Shukla (1972) stability variance (σ^2), the regression co-efficient (bi) and deviation from regression (S2di) (Eberhart and Russel, 1966; Perkins and Jinks, 1986). The main problem with stability statistics is that a single model could not provide an accurate picture because of genotype's response to varying environments is multivariate (Lin *et al.*, 1986) whereas the stability indices are usually univariate (Gauch, 1992; Crossa, 1990). One of the multivariate techniques is the AMMI model. The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the G × E interaction (Zobel *et al.*, 1988; Gouch and Zobel, 1996). Therefore, based on the AMMI models (IPCA1 and IPCA2) the AMMI stability value (ASV) has been used (Purchase *et al.*, 2000). The development and use of yield-stability index statistic (YSI) was also being used for recommending varieties (Kang, 1993; Pazdernik *et al.*, 1997). A new approach known as genotype selection index (GSI) was used taking into consideration of AMMI stability value and mean yield for yield stability (Farshadfar, 2008). The objectives of this study was (i) to identify rice genotypes that have both high mean yield and stable yield performance across different environments (ii) to study the relationships, similarities and dissimilarities among yield – stability statistics.

MATERIAL AND METHODS

The present experiment was conducted to determine the yield stability of 22 lowland rice genotypes in five locations during wet season 2002. Seeds of those rice genotypes were sown in wet seed beds. Twenty one day-old healthy seedlings were transplanted in well puddle plots of 3m x 4m size. The plant density was maintained at 33 plants m² with spacing of 20 x 15 cm line to plant basis. Fertilizer was applied @ 80:40:20 of N: P: K kg ha⁻¹. The entire dose of P and K along with 30 kg of N was applied as basal dose, while the rest of the 50 kg of N was applied in two split doses, one 21 days after transplanting and the other at flowering stage of the crop. The maximum water depth in the plots during the experimental period was 50-60 cm. Appropriate cultural practices like weeding and need based plant protection measures were undertaken in order to raise a healthy crop. The experiment was conducted in a randomised completely block design with three replications. The replication wise plot yield data of individual entries were recorded and computed in tons per hectare. For statistical analysis the grain yield data were subjected to combined analysis of variance and AMMI

analysis (SAS Institute, 2010).

Statistical analysis :

The grain yield data were subjected to combined analysis of variance and AMMI analysis. Analysis of variance was used to partition into genotype deviations from the grand mean, environment deviations from the grand mean, and GE deviations from the grand mean. Subsequently, multiplication effect analysis (AMMI) was used to partition GE deviations into different interaction principal component axes (IPCA). The SAS 9.2 (SAS Institute, 2010) software was used for the Analysis purpose.

AMMI analysis :

The AMMI model was applied, with additive effects for the 12 rice genotypes (G) and five locations (Environments=E), and multiplicative term for G×E interactions. The AMMI analysis first fits additive effects for host genotypes and environments by the usual additive analysis of variance procedure and then fits multiplicative effects for G×E by principal component analysis (PCA). The AMMI model is

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

where, Y_{ij} is the yield of the i^{th} genotype in the j^{th} environment,

g_i is the i^{th} genotype mean deviation,

e_j is the j^{th} environment mean deviation,

λ_k is the square root of the eigen value of PCA axis k

α_{ik} and γ_{jk} are the principal component scores for PCA axis k of the i^{th} genotype and the j^{th} environment, respectively and

ε_{ij} is the residual.

The environment and genotypic PCA scores are expressed as unit vector times the square root of λ_k *i.e.* environment PCA score = $\lambda_k^{0.5} \gamma_{jk}$; genotype PCA score = $\lambda_k^{0.5} \alpha_{ik}$ Zobel *et al.* (1988).

The AMMI stability index 'D_i', which is the distance of interaction principal component (IPC) point with origin in space, was estimated according to the formula suggested by Zhang *et al.* (1998).

$$D_i = \sqrt{\sum_{s=1}^c Y_{is}^2}$$

where, c is the number of significant IPCs,

Y_{is} is the scores/yield of the rice genotype i in IPCs.

To assess fitting AMMI model, predictive and post-predictive approaches offered by Zobel *et al.* (1988) were applied to the data.

In addition to the above stability parameters, several yield-stability statistics were also calculated as follows:

AMMI stability value (ASV) :

The AMMI stability value (ASV) as described by Purchase *et al.* (2000) was calculated as follows :

$$ASV = \sqrt{\left[\frac{IPCA1_{\text{sum of square}}}{IPCA2_{\text{sum of square}}} (IPCA1_{\text{score}})^2 \right] + (IPCA2_{\text{score}})^2}$$

where, $\frac{SS_{IPCA1}}{SS_{IPCA2}}$ is the weight given to the IPCA1-value by dividing the IPCA1 sum of square by the IPCA2 sum of square. The larger the IPCA score, either negative or positive, the more specifically adapted a genotype is to the certain environments. Smaller ASV scores indicate a more stable genotype across environments.

Sustainability index (SI) :

The sustainability index was calculated by the following formula as suggested by Babarmanzoor *et al.* (2009):

$$S.I. = [(Y - \bar{Y}) / \sigma Y] \times 100$$

where, Y = Average performance of genotype,
 σY = Standard deviation and

YM = Best performance of a genotype in any year.

The values of SI were classified arbitrarily into five groups *viz.*, very low (up to 20%), low (21-40%), moderate (41-60%), high (61-80%) and very high (above 80%)

Stability index (I) :

The stability index (I) was computed by the nonparametric stability analysis Bajpai and Prabhakaran (2002) to identify stable and high-yielding genotypes as follows :

$$I = \left[\frac{\bar{y}_i}{\bar{y}_..} + \frac{1}{2} \right] / \left[\frac{1}{n} \sum_i \left(\frac{1}{i} \right) \right] \text{ Rao } et al. (2004)$$

where, \bar{y}_i = average performance of the i^{th} genotype

$\bar{y}_..$ = overall mean

$\hat{\sigma}_i^2$ = Shukla's (1972) stability variance of the i^{th} genotype

and

n = number of environment.

Yield stability index (YSI) and Rank-Sum (RS) :

The YSI and RS were calculated as :

$$YSI = RASV + RY \text{ (Farshadfar } et al., 2011)$$

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

$$RS = \text{Rank mean (R)} + \text{Standard deviation of rank (SDR)}$$

The RS incorporates both yield and yield stability in a single non-parametric index, while YSI incorporates both mean yield and stability in a single criterion. Low values of both the parameters show desirable genotypes with high mean yield

and stability.

The standard deviation of rank (SDR) was measured as:

$$S_i^2 = \frac{\sum_{j=1}^m (R_{ij} - \bar{R}_i)^2}{I - 1}$$

where, R_{ij} is the rank of X_{ij} within the j^{th} environment,

\bar{R}_i is the mean rank across all environments for the i^{th} genotype and $SDR = (S_i^2)^{0.5}$

RESULTS AND DISCUSSION

The results obtained from the present investigation as well as relevant discussion have been summarized under following heads :

Analysis of variance :

The combined analysis of variance is presented in Table 2. Environment (E) and genotype \times environment interaction (GEI) were significant ($P = 0.01$) for grain yield. Such statistical interaction resulted from the changes in the relative ranking of the genotypes from one environment to another. The significant genotype \times environment interaction effects demonstrated that genotypes responded differently to the variation in environmental conditions of location which indicated the necessity of testing rice varieties at multiple locations. The factors explained (%) show that rice grain yield

Table 1: Tested genotypes

Genotype no.	Genotype name
1.	NDR 40001-1-2
2.	NDR 40055-2-1
3.	NDR 40059-6-5
4.	Rayada B ₃
5.	Borjohingia
6.	LPR 106
7.	Panikekoa
8.	PSR 1209-2-3-2
9.	RAU 1306-3-2-2
10.	CN 1035-61
11.	Sabita
12.	Purnendu
13.	Hanseswari
14.	Ambika
15.	CR 778-95
16.	CR 662-2211
17.	CR 661-236
18.	CR 780-1937
19.	CR 682-162
20.	OR 1334-16
21.	OR 1358-RGA-4
22.	OR 877-ST-4-2

was affected by environment (26.22%), genotype (20.57%) and their interaction (52.45%). The mean grain yield of the 22 genotypes ranged from 2.460 to 4.65 t ha⁻¹ and the highest grain yield was obtained from genotypes GEN18, GEN17 and GEN16 (Table 1). The AMMI analysis of variance for lowland rice grain yield (t ha⁻¹) of 22 genotypes tested in five environments showed that 26.41 per cent of the total sum of squares was attributed to environmental effects, while only 20.73 per cent to genotypic effects and 52.84 per cent to genotype × environment interaction effects (Table 3). The environments were diverse and caused the greatest variation in grain yield. The genotype × environment interaction sum of squares was about 5 times larger than that for genotypes, which determined substantial differences in genotypic response across environments. The presence of GEI was clearly demonstrated by the AMMI model, when the interaction was partitioned among the first three interaction principal component axis (IPCA) as they were significant P = 0.01 in a postdictive assessment. The IPCA1 explained 58.32 per cent of the interaction sum of squares in 24 per cent of the interaction degree of freedom (DF). Similarly, the second and third principal component axis (IPCA 2-3) explained a further 24.52 and 14.89 per cent of the GEI sum of square, respectively (Table 3). They cumulatively captured 97.73 per cent of the total GEI using 66 DF. This implied that the interaction of the 22 lowland rice genotypes with five environments was predicted by the first three components of genotypes and environments, which is in agreement with the recommendation of Sivapalan *et al.* (2000). However, this contradicted the

findings of Gauch and Zobel (1996) which recommended that the most accurate model for AMMI can be predicted using the first two IPCAs. These results indicate that the number of terms to be included in an AMMI model cannot be specified a priori without first trying AMMI predictive assessment (Kaya *et al.*, 2002). In general, factors like type of crop, diversity of the germplasm and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa *et al.*, 1990). The AMMI analysis provided a biplot (Fig. 1) of main effects and the first principal component scores of interaction (IPCA1) of both genotypes and environments. The differences among genotypes in terms of direction and magnitude along the X-axis (yield) and Y-axis (IPCA1 scores) are important. In the biplot display, genotypes or environments that appear almost on a perpendicular line of a graph had similar mean yields and those that fall almost on a horizontal line had similar interactions (Crossa *et al.*, 1990). Thus, the relative variability due to environments was greater than that due to genotypic differences. Genotypes or environments on the right side of the midpoint of the perpendicular line have higher yields than those on the left side. As a result, genotypes including GEN18, GEN17, GEN16 and GEN21 were generally high yielding (4.65, 4.37, 3.99 and 3.81 t/ha, respectively) (Fig. 1). Environments ENV4 and ENV5 were on the right hand side of the midpoint of the main effect axis, seemed to be favourable environments, while ENV2, ENV1 and ENV3 were generally less favourable environments. Genotypes or environments with large negative or positive IPCA scores have high interactions, while those with IPCA1 scores near zero (close

Table 2 : Combined analysis of 22 lowland genotypes in rainfed condition

Source	df	SS	MS	Explained SS (%)
Replication	2	0.127697	0.063849	
Environment (E)	4	117.3986	29.34965**	26.22117
Genotype (G)	21	92.13918	4.38758**	20.57944
G*E	84	234.8534	2.795874**	52.45489
Error	218	3.205636	0.014705	
Total	329	447.7245		

* and ** indicate significance of values at P=0.05 and P=0.01, respectively
NS= Non significant

Table 3: AMMI analysis of 22 lowland genotypes in rainfed conditions

Source	df	ms	TSS explained %
Genotypes	21	1.463 ns	20.734
Environments	4	9.783 **	26.418
G×E	84	0.932 **	52.848
Model	25	2.794 **	47.152
AMMI1	24	5.707 **	58.321
AMMI2	22	2.618 **	24.522
AMMI3	20	1.749 **	14.892
Error	218	0.015	

* and ** indicate significance of values at P=0.05 and P=0.01, respectively
NS = Non significant

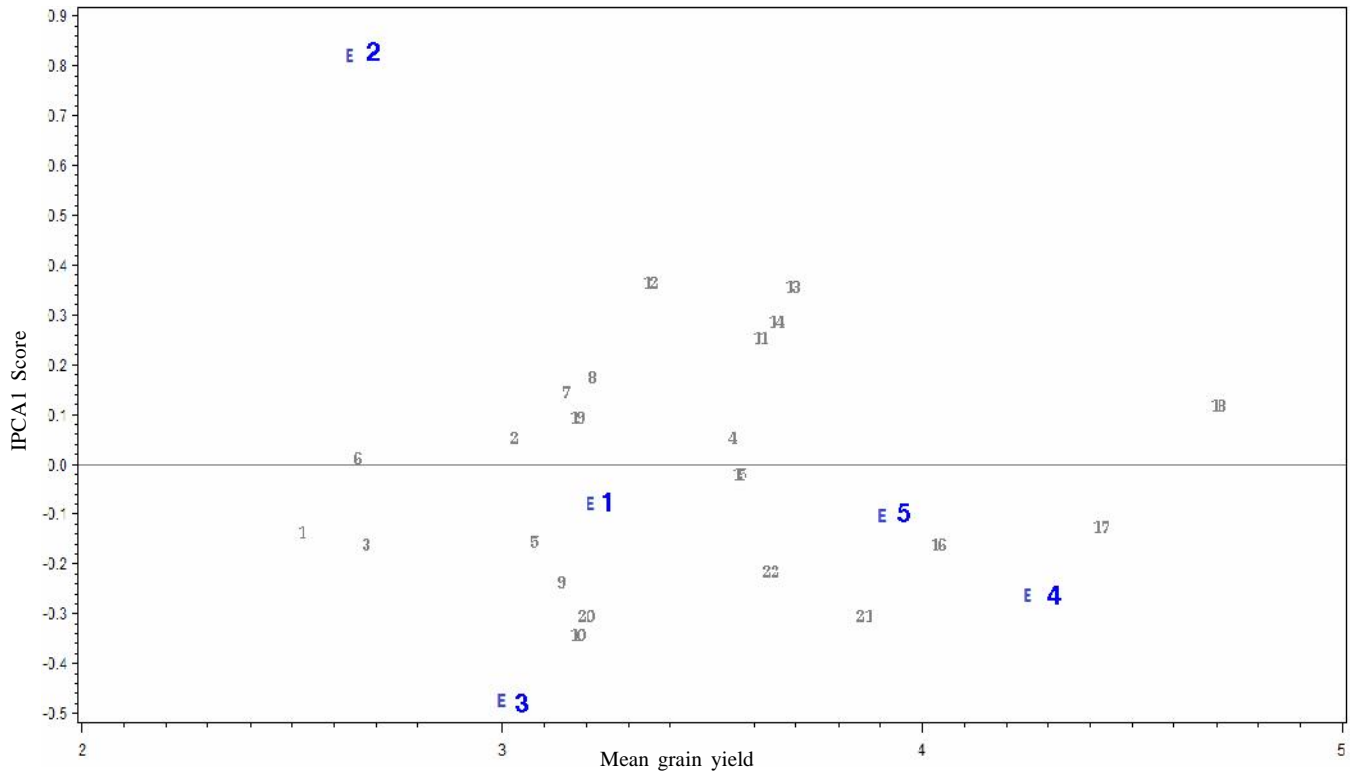


Fig. 1 : AMMI biplot of 22 rice genotypes and five environments for grain yield (t ha⁻¹) using genotypic and environmental scores

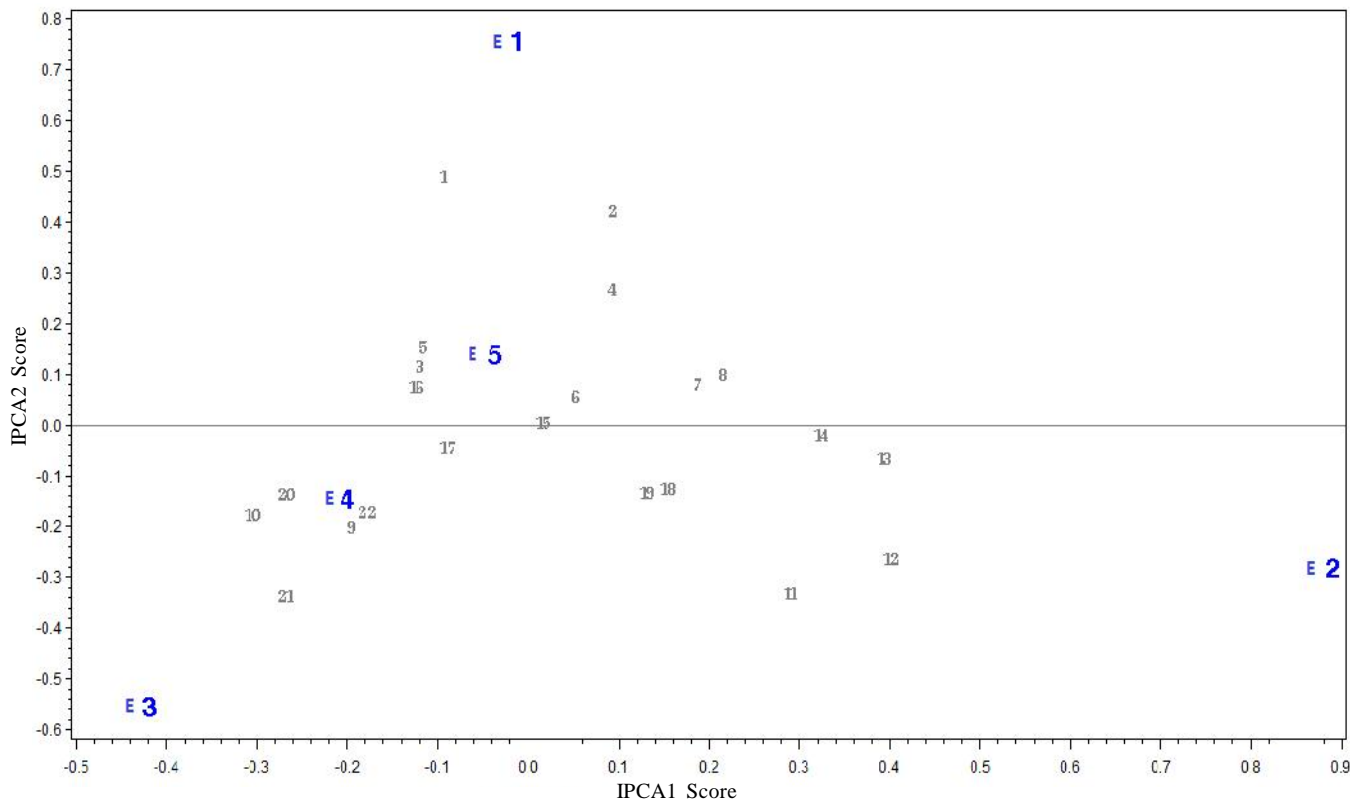


Fig. 2 : Biplot of the second interaction principal component axis (IPCA2) against the first interaction principal component axis (IPCA1) scores for grain yield of 22 rice genotypes in five environments

to horizontal line) have little interaction across environments and vice versa for environments (Crossa *et al.*, 1990) and are considered more stable than those further away from the line. In the biplot, genotypes GEN16, GEN17 and GEN18 were vertically distant apart; however, they did not fall close to the horizontal line. This implies that these genotypes lack stability but had high yield potential in favourable environments. Since, IPCA2 scores were also important (24.52% of $G \times E$ SS) in explaining genotype \times environment interaction, the biplot of the first two IPCAs was also used to demonstrate the relative magnitude of the GEI for specific genotypes and environments (Fig. 2). The IPCA scores of genotypes in the AMMI analysis is an indication of stability or adaptation over environments (Gouch and Zobel, 1996). The greater the IPCA scores, the more specifically adapted is a genotype to certain environments (Saini *et al.*, 2009). The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled. The biplot of the first two IPCA show GEN6 and GEN15 were adapted genotype to most environments but were low yielders. However, GEN18 were well adapted to high yielding environment of ENV2 while GEN17 was well adapted to high yielding environment of ENV3 and ENV4. In Fig. 2, the environments divided into three sections; the genotypes favourable in ENV4 were GEN3, GEN5, GEN16 and in ENV5 were GEN9, GEN10, GEN20, GEN21, GEN22. On the other hand, genotypes GEN2, GEN4, GEN7

and GEN8 were not found to be suitable in any of the testing locations. Considering the environments tested in this study, only GEN15 and GEN6 had both IPCA 1 and IPCA2 scores close to zero line. This indicates that all the environments had potential for large GEI in most of the genotypes. Since 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 (Gouch and Zobel, 1996; Gouch, 1992). Therefore, the AMMI stability value (Purchase *et al.*, 2000) was used to quantify and rank genotypes based on their yield stability. AMMI stability value (ASV) is the distance from zero in a two dimensional scatter diagram of IPCA1 scores against IPCA2 scores. Since the IPCA1 score contributes more to GE sum of square (Table 2), it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 total GE sum of squares. In ASV method, a genotype with least ASV score is the most stable, accordingly, genotype 15 followed by 6 were the most stable. Another approach known as yield stability index (YSI) is calculated by ranking the mean grain yield of genotypes (RY) across environments and rank of AMMI stability value (RASV). YSI incorporates both mean yield and stability in a single criterion. Another approaches known as YSI calculated by the formula $YSI = RASV + RY$ (Farshadfar *et al.*, 2011) was also used. Low value of this

Table 4: First and second IPCA, mean yield and various yield-stability statistics

Genotype No.	IPCA1	IPCA2	GY	ASV	YSI	SI%	I	RS
1.	-0.322	1.046	2.46	1.297	34	23.682	0.101	28.715
2.	0.167	0.905	2.96	0.988	29	42.613	0.131	24.283
3.	-0.388	0.267	2.61	0.960	28	36.915	0.250	21.555
4.	0.164	0.581	3.48	0.700	13	56.765	0.238	18.329
5.	-0.376	0.345	3.01	0.959	25	32.037	0.166	21.726
6.	0.059	0.143	2.59	0.200	22	39.071	0.490	20.927
7.	0.408	0.192	3.08	0.988	25	45.171	0.189	21.639
8.	0.483	0.229	3.15	1.172	24	60.163	0.212	21.140
9.	-0.585	-0.400	3.08	1.447	31	41.922	0.154	19.725
10.	-0.860	-0.347	3.12	2.074	34	34.746	0.113	22.981
11.	0.687	-0.670	3.56	1.765	24	44.252	0.118	23.266
12.	0.978	-0.530	3.30	2.387	33	42.543	0.105	25.217
13.	0.959	-0.114	3.64	2.283	26	50.714	0.120	20.589
14.	0.776	-0.020	3.60	1.845	24	59.131	0.143	16.963
15.	-0.021	0.031	3.51	0.059	10	60.056	2.634	11.899
16.	-0.387	0.181	3.98	0.938	10	63.928	0.252	12.927
17.	-0.298	-0.069	4.37	0.713	7	71.610	0.379	7.782
18.	0.335	-0.237	4.65	0.832	7	82.170	0.244	7.982
19.	0.276	-0.257	3.12	0.705	18	64.199	0.112	24.408
20.	-0.762	-0.262	3.14	1.832	30	29.964	0.124	23.316
21.	-0.764	-0.682	3.80	1.941	23	38.715	0.125	19.481
22.	-0.528	-0.335	3.58	1.301	21	53.308	0.174	16.449

GY - Grain yield; ASV - AMMI stability value; YSI - Yield stability index; SI - Sustainability index; I - Stability index; RS - Rank sum

parameter shows stable genotypes with high mean yield. Using these measures, suitable rice varieties for varying environmental conditions existing can be identified. In this method ASV was taken into account along with IPCA1 and IPCA2 for generating variation in the GE interaction as a result of which the lowest ASV takes the rank one, while the highest yield mean takes the rank one and then the ranks are summed in a single simultaneous selection index of yield and yield stability named as: yield stability index (YSI). The least YSI is considered as the most stable with high grain yield. Based on YSI the most stable genotype with high grain yield is genotype 18 and 17 (Table 2). Another stability index *i.e.* Sustainability index (SI) was used for selecting stable genotypes (Singh and Agarwal, 2003; Gangwar, 2004; Tuteja, 2006). The values of sustainability index were divided arbitrarily into 5 groups *viz.*, very low (up to 20%), low (21-40%), moderate (41-60%), high (61-80%) and very high (above 80%) (Babarmanzoor, 2009). Very high sustainability index (%) was estimated in the case of genotype 18 (82.17%) and genotype 17 (71.61). These results prove that SI is also provides a suitable stability index for discriminating stable genotypes with high grain yield. Bajpai and Prabhakaran (2000) proposed a new index that is free from all the aforesaid drawbacks. The basic element in the construction of this proposed index is that the levels of achievement of genotypes and their stability are quantified by expressing the individual achievements relative to the mean performance in the set of genotypes evaluated. The proposed index has an inbuilt integration of both stability and mean performance and genotypes were ranked based on the stability index (I). Ranks were assigned in increasing order to the genotypes whose stability indices varied in decreasing order *i.e.*, the genotype which had highest stability index (I) received first rank and the one with the lowest 'I', received 22nd rank in the present study involving 22 lowland genotypes. Results (Table 4) indicated that the ranking of genotypes, in general, were more or less similar based on stability index (I). However, the same was not true with respect to mean performance. Further, the genotypes performances (Gourch, 1992; Eberhart and Russell, 1966) were stable indicating by high magnitudes of (I) for grain yield (Rao *et al.*, 2004). Whereas, Rank-sum (RS) introduced genotype 18 (RS=7.982) followed by genotype 17 (RS=7.782) as the most stable genotypes with high grain yield. For better understanding of the relationships, similarities and dissimilarities among the yield-stability statistics, principal component analysis (PCA), based on the rank correlation matrix was used. The relationships among different stability parameters were graphically displayed in a biplot of PCA1 and PCA2 (Fig. 3). The PCA1 and PCA2 axes which justify 85.92 per cent of total variation, mainly distinguish the statistics in different groups. Mean yield as group 1 (G1) stability measures. YSI, RS and SI in a single group (G2). ASV and I were separated from the other groups as group 3 (G3) (Fig. 3). The statistics of G2 (YSI, SI and RS) distinguished

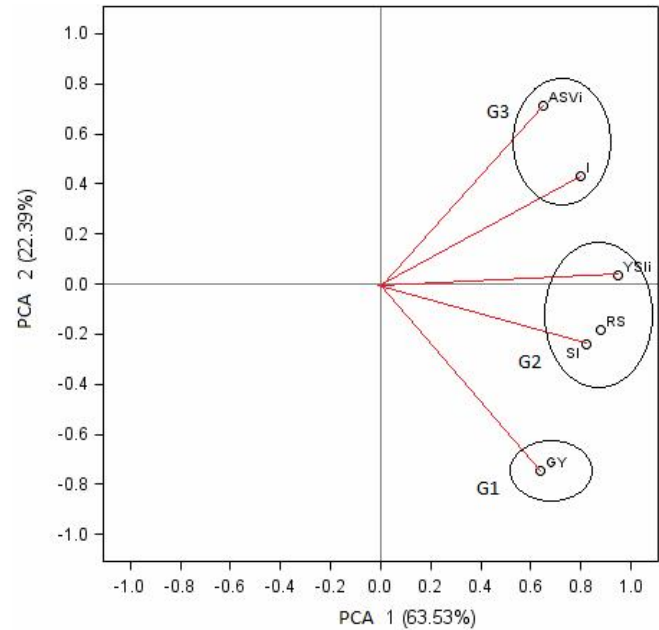


Fig. 3 : Biplot of yield - stability statistics investigated in lowland rice genotypes

genotypes 18 and 17 as the most stable genotypes with high grain yield.

Conclusion :

Genotype \times environment interaction (GEI) has been an important issue among the researchers who are engaged in performance testing. The genotype-environment interaction reduces association between phenotypic and genotypic values and leads to bias in the estimates of gene effects and combining ability for various characters sensitive to environmental fluctuations. Such traits are less amenable to selection. Both yield and stability of performance should be considered simultaneously to reduce the effect of GE interaction and to make selection of genotypes more precise and refined. The results show that based on AMMI stability value (ASV) and stability index (I) the GEN15 and GEN6 were more stable with moderate to low yielder; based on RS, SI and YSI genotypes GEN18 and GEN17 were more stable with high yield across the locations. The approaches like YSI incorporates both the components ASV which is based on AMMI and grain yield which is based on high yield potential in a single stability index; and RS (R+SDR) were the most desirable indices for discriminating the most stable genotypes with high grain yield. The advantage of YSI is that genotype's response to varying environments is multivariate and is based on AMMI stability value whereas, RS is a univariate statistics. These indices may be well used in identifying superior genotypes for commercial production. Hence, those indices which include both, the yield and stable performance in different location may be considered.

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