

AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.)

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Abstract

In order to determine stable bread wheat genotypes with high grain yield via a single parameter, field experiments were conducted with 14 genotypes for 3 consecutive years (2008-2011) under two different conditions (irrigated and rainfed) in a complete randomized block design with three replications in each environment. Combined analysis of variance showed highly significant differences for the GE (genotype-environment) interaction indicating the possibility of selection for stable entries. The results of AMMI (additive main effect and multiplicative interaction) analysis indicated that the first four AMMI (AMMI1–AMMI4) were highly significant ($P < 0.01$). The partitioning of TSS (total sum of squares) exhibited that the environment effect was a predominant source of variation followed by GE interaction and genotype effect. The GE interaction was ~5 times higher than that of the genotype effect, suggesting the possible existence of different environment groups. AMMI stability value discriminated genotypes 10 and 6 as the stable accessions, respectively. Based on the YSI (yield stability index) and new RS (rank-sum) the most stable genotypes with high grain yield were genotypes 13 and 10. The results of this investigation proved that SI (sustainability index) and I (stability index) are not suitable stability indices for discriminating stable genotypes with high grain yield.

Keywords: Bread wheat, AMMI model, AMMI stability value, yield stability index, rank-sum.

Abbreviations: AMMI-additive main effect and multiplicative interaction; ANOVA- analysis of variance; ASV- ammi stability value; GE- genotype-environment; GEI- genotype-environment interaction; I- stability index; IPCA- interaction principal component axes; PCA- principal component analysis; RS- rank-sum; SDR- standard deviation of rank; SI -sustainability index; TSS- total sum of squares; YSI -yield stability index.

Introduction

It is apparent that the phenotype of wheat is a joint contribution of both genes as well as environment. 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 (Farshadfar et al., 2000). The existence of genotype-environment interaction (GEI) complicates the identification of superior genotypes for a range of environments and calls for the evaluation of genotypes in many environments to determine their true genetic potential (Yaghotipoor and Farshadfar, 2007). The importance of $G \times E$ interactions in national cultivar evaluation and breeding programs have been demonstrated in almost all major crops, including wheat genotypes (Najafian et al., 2010; Zali et al., 2011). Various statistical methods (parametric and non-parametric) have been proposed to study Genotype \times environment interactions (Lin et al., 1986; Becker and Léon, 1988; Crossa, 1990; Lin and Binns, 1994; Hussein et al., 2000; Mohammadi and Amri, 2008; Mohammadi et al., 2010). Different concepts and definitions of stability have been described over the years. Lin et al. (1986) identified three concepts of stability (Type 1, 2, 3), later Lin and Binns (1988b) proposed a fourth type (Type 4). Type 1 is also called a static or a biological concept of stability (Becker and Léon, 1988). Parameters used to

describe this type of stability are coefficient of determination (R_i^2) (Pinthus, 1973), coefficient of variability (CV_i) (Francis and Kannenberg, 1978) and the genotypic variances across environments (S^2_{ij}) (Roemer (1917) cited in Becker and Leon (1988)]. Type 2 is also called the dynamic or agronomic concept of stability (Becker and Léon, 1988). A regression coefficient (bi) (Finlay and Wilkinson, 1963) and Shukla's (1972) stability variance (σ_i^2) can be used to measure type 2 stability. Type 3 is also a part of the dynamic or agronomic stability concept (Becker and Léon, 1988). Methods that describe type 3 stability are the regression coefficient (bi) and deviation from regression (S^2_{di}) (Eberhart and Russell, 1966; Perkins and Jinks, 1968). Becker and Léon (1988) stated that all stability procedures based on quantifying GEI effects belong to the dynamic concept. This includes the procedures for partitioning the GEI of Wricke's (1962) ecovalence as well as non-parametric stability statistics. Lin & Binns (1988a, 1988b) proposed the cultivar performance measure (Pi) and within location variance ($MS_{y/l}$) as type 4. The main problem with stability statistics is that they don't provide an accurate picture of the complete response pattern (Hohls, 1995). The reason is that a genotype's response to varying environments is multivariate (Lin et al., 1986) whereas the stability indices are usually univariate (Gauch, 1988; 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; Gauch and Zobel, 1996). Purchase (2000) developed the AMMI stability value (ASV) based on the AMMI model's IPCA1 and IPCA2 (interaction principal components axes 1 and 2, respectively) scores for each genotype. The ASV is comparable with the methods of Shukla, Wricke and Eberhart & Russell stability methods. Various nonparametric methods have also been used based on the ranks of genotypes in each environment. Genotypes with similar rankings across environments are classified as stable. Nassar and Huehn (1987) proposed four nonparametric statistics of phenotypic stability ($S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$ and $S_i^{(6)}$) based on the classification of the genotypes in each environment and defined stable genotypes as those whose position in relation to the others remained unaltered in the set of environments assessed. Fox et al. (1990) suggested a nonparametric superiority measure for general adaptability. They used stratified ranking of the cultivars in each environment to determine the proportion of sites in which each cultivar occurred in the top, middle (MID), and bottom third of the ranks, forming the nonparametric measures TOP, MID and LOW, respectively. Thennarasu (1995) proposed non-parametric statistics $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ based on ranks of adjusted means of the genotypes in each environment and defined stable genotypes using Nassar and Huehn (1987)'s definition. Regardless of type of stability statistics, 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. A few methods that simultaneously estimate yield and stability have been proposed. Stability statistics that consider deviations from a hypothetical, desired genotype (Sepahi, 1974) are considered associated primarily with yield level and show little correlation with stability (Leon, 1986); therefore, they are not suitable for simultaneous selection of yield and stability. The concept of risk aversion was adapted by Barah et al. (1981). They indicated that only the stability component was relevant for farmers in their adoption decision. They used measures of farmers' risk aversion to rank genotypes according to preferences that took account of both yield and stability. They found no significant differences between yield-based ranking and ranking obtained from both yield and stability. Eskridge (1990) advocated the use of a decision theory concept known as safety-first to develop an index that incorporates mean yield and stability. He indicated that safety-first selection indices can be useful to plant breeders when the GE interaction is large and poor yield results in severe consequences such as bankruptcy or starvation. Huhn (1996) proposed two non-parametric statistics that combine yield and stability. These statistics are $S_i^{(3)}$ and $S_i^{(6)}$. These two statistics showed significant correlation with yield and stability statistics W_i (ecovalence) and S_{di}^2 (deviation from regression) (Leon, 1986). $S_i^{(6)}$ is more strongly correlated with grain yield and less with stability statistics than is $S_i^{(3)}$. A choice between $S_i^{(3)}$ and $S_i^{(6)}$ gives the opportunity to weight yield or yield stability (Leon, 1986). Kang and Pham (1991) discussed several methods of simultaneous selection for yield and stability and relationships among them. The development and use of yield-stability statistic (YSi) has enabled incorporation of stability in the selection process (Kang, 1993). Kang's yield-stability statistic has been evaluated and found to be useful for recommending varieties (Pazdernik et al., 1997). However, Bajpai and Prabhakaran (2000) observed that Kang's rank-sum method has an inherent weakness that it is weighing heavily towards yield performance, apart from the

arbitrariness in the scoring procedure. Therefore, this method is not fit for drawing general conclusions. Accordingly, they proposed an improved stability index (I) that is free from all the aforesaid drawbacks and found to be superior to Kang (1993) indices. Rao and Prabhakaran (2005) proposed selection index (I) consists of (i) a yield component, measured as the ratio of the average performance of the jth genotype to the overall mean performance of the genotypes under test, and (ii) a stability component, measured as the ratio of stability information (I/ASTAB) of the jth genotype to jth mean stability information of all the genotypes under test. This stability parameter defines stability with dynamic concept. A new approach known as genotype selection index (GSI) was recommended by Farshadfar (2008). Using AMMI stability value and mean yield, GSI incorporates both mean yield and stability in a single criterion. Low value of this parameter shows desirable genotypes with high mean yield and stability. The objectives of this study were (i) to identify bread wheat genotypes that have both high mean yield and stable yield performance across different environments for semiarid areas of Iran, (ii) to study the relationships, similarities and dissimilarities among yield – stability statistics.

Results and discussion

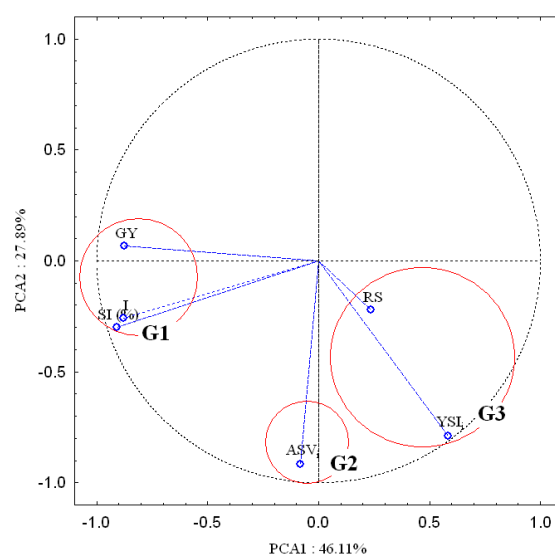
Yield adaptation across environment

Combined analysis of variance (Table 2) over locations (stress and non-stress) and years resulted in highly significant differences ($P < 0.01$) in the interaction of genotypes × environments (locations and years). The significant interactions of genotypes × environments (locations and years) suggest that grain yield of genotypes varied across irrigated and rainfed conditions. Significant differences for genotypes, environments and GE interaction indicated the effect of environments in the GE interaction, genetic variability among the entries and possibility of selection for stable genotypes. Chandra et al. (1974) reported that GE interaction with location is more important than GE interaction with year. As GE interaction was significant, therefore we can further proceed and estimate phenotypic stability (Farshadfar and Sutka, 2006).

The average grain yield of the genotypes ranged from 614.64g for genotype 11 to 214.36g in genotype 14. Genotypes of annual crops evaluated for grain yield on a multi-locational, multi-year basis frequently show GE interaction that complicates the selection or recommendation of materials. Coping with genotype-year or genotype-location-year interaction effects is possible only by selection for yield stability across environments defined as location-year combinations (Annicchiarico, 1997). There are two possible strategies for developing genotypes with low GE interactions. The first is sub-division or stratification of heterogeneous area into smaller, more homogeneous sub-regions, with breeding programs aimed at developing genotypes for specific sub-regions. However, even with this refinement, the level of interaction can remain high, because breeding area does not reduce the interaction of genotypes with location on years (Eberhart and Russell, 1966; Tai, 1979). The second strategy for reducing GE interaction involves selecting genotypes with a better stability across a wide range of environments in order to better predict behavior (Yaghotipoor and Farshadfar, 2007).

Table 1. Pedigree of investigated genotypes

Code	Pedigree
1	Croos alborz
2	Aazar-2
3	Sardari
4	Shi#4414.Crow"S"..Fow-1
5	Ww33G.Vee"S".Mrn.3.Atilla.Tjn
6	Shi#4414.Crow"S"..Vee"s:.Nac
7	Ww33G.Vee"S".Mrn.4.HD2172.Bloudan ..Azd.3..san.Ald"s"..Avd
8	Azd.HD2172..Kayson.Glenson.3.170-28.Ning8201
9	TEVEE S. KARAWAN S
10	Ww33G.Vee"S".Mrn.3.Atilla.Tjn
11	CHAM-8.MAYON"S'.CW93-0031-1AP-OL-OBR-2AP-1AP-OAP
12	T.AEST..SPRW"S"..CA8055.3.BACANORA88.CW92-0477-...
13	T.AEST..SPRW"S"..CA8055.3.BACANORA88ICW92-0477-...
14	AZD.HD2172..Pltoma.Cucurp88

**Fig 1.** Biplot of yield – stability statistics investigated in wheat genotypes over rainfed and irrigated conditions.

AMMI analysis of GE interaction

The advantages of the AMMI model or its variants are that, they use overall fitting, impose no restrictions on the multiplicative terms and result in least square fit (Freeman, 1990). Within limits, any model may be expected to fit the data from which it was derived. However, the AMMI model has a good chance of being able to predict for new sites and new years, thus contributing a real advance (Gauch, 1988). Gauch and Zobel (1996) showed that AMMI1 with IPCA1 and AMMI2 with IPCA1 and IPCA2 are usually selected and the graphical representation of axes, either as IPCA1 or IPCA2 against main effects or IPCA1 against IPCA2 is generally informative. The AMMI method is used for three main purposes. The first is model diagnoses, AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular data sets (Gauch, 1988). Secondly, AMMI clarifies the $G \times E$ interaction and it summarizes patterns and relationships of genotypes and environments (Zobel et al., 1988; Crossa et al., 1990). The third use is to improve the accuracy of yield estimates. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of

replicates by a factor of two to five (Zobel et al., 1988; Crossa, 1990). Such gains may be used to reduce testing cost by reducing the number of replications, to include more treatments in the experiments or to improve efficiency in selecting the best genotypes. Using ANOVA, yield sum square was partitioned into genotype, environment and GE interaction. GE interaction was further partitioned by principal component analysis (Table 3). It is evident from Table 3 that the use of biplots to explain efficiently the interaction is very much limited, since the first two PCA axes explain only 32% of the total interaction variation. Hence it may not be advisable to conclude either on stability or simultaneous selection based on these two axes. It is evident that at least 4 axes must be retained for explaining stability or using the proposed simultaneous selection indices. Accordingly, the index values and stability values are calculated by retaining 4 PCA axes in the model (AMMI1-AMMI4) (Rao and Prabhakaran, 2005). The results of AMMI analysis indicated that the first four AMMI (AMMI1-AMMI4) were found to be highly significant ($P < 0.01$) (Table 3). The partitioning of TSS indicated that the environment effect was a predominant source of variation

Table 2. Combined analysis of variance for grain yield under different rainfed and irrigated conditions

Source of variation	df	F-values
Location (L)	6	3.74*
Year (Y)	2	3.66*
L × Y	12	4.28**
Error 1	42	-
Genotype (G)	13	9.22**
G × L	78	6.22**
G × Y	26	4.02**
G × L × Y	156	5.33**
Error 2	546	-
% C.V	-	15.24

*, ** significant at the 5% and 1% probability levels, respectively

Table 3. AMMI analysis of grain yield in bread wheat over rainfed and irrigated conditions

Source	df	MS	TSS explained %
Genotypes (G)	13	154.32**	12.98
Environments (E)	5	5347.83**	267.35
G×E	65	88.47**	57.20
Model	35	564.29**	197.4
AMMI1	17	81.11**	17.00
AMMI2	15	73.14**	15.00
AMMI3	13	64.92**	13.00
AMMI4	11	61.58*	11.00
Residual (noise)	49	14.18ns	1
Error	168	23.16	-

**significant at 1% probability level; Ns; non- significant

followed by GE and genotype effect. The GE interaction was ~5 times higher than that of the genotype effect, suggesting the possible existence of different environment groups (Mohammadi et al., 2011).

IPCA crossover and non-cross over interaction

IPCA scores of genotypes and environments displayed positive and negative values (Table 4). A genotype with large positive IPCA score in some environments must have large negative interaction in some other environments. Thus, these scores presented a disproportionate genotype response (Yan and Hunt, 2001; Mohammadi et al., 2007), which was the major source of variation for any crossover (qualitative) interaction. This disproportionate genotype response is referred to as crossover GE interaction for convenience. Diversely, scores with the same sign or near zero represent a non- crossover (quantitative) GE interaction or a proportionate genotype response (Mohammadi and Amri 2008; Farshadfar, 2008).

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 to their yield stability, the ASV measure was proposed by Purchase et al. (2000) to cope with this problem. In fact, ASV is the distance from zero in a two dimensional scattergram of IPCA1 (interaction principal component analysis axis 1) 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. 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 is the most stable, accordingly, genotype 10 followed by 6 were the most stable. Adjusted yield can be obtained by AMMI1, AMMI2, AMMI3 and AMMI4 for each environment by the formula:

$$\bar{Y}_{i0} + \bar{Y}_{0j} - \bar{Y}_{00}$$

Where \bar{Y}_{i0} = mean of genotype i;

$$\bar{Y}_{0j} = \text{mean of environment } j; \bar{Y}_{00} = \text{grand mean, and used}$$

as a selection criterion in breeding programs. In general the importance of AMMI model is in reduction of noise even if principal components do not cover much of the GESS (Gauch and Zobel, 1996; Gauch, 1992).

Yield stability index (YSI)

Stability *per se* should however not be the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance (Mohammadi et al., 2007; Mohammadi and Amri, 2008), hence there is a need for approaches that incorporate both mean yield and stability in a single index, that is why various authors introduced different selection criteria for simultaneous selection of yield and stability (Eskridge, 1990; Kang, 1993; Dashiell et al., 1994; Bajpai and Prabhakaran, 2000; Rao and Prabhakaran, 2005; Farshadfar, 2008; Babarmanzoor et al., 2009). In this regard, as ASV takes into account both IPCA1 and IPCA2 that justify most of the variation in the GE interaction, therefore the rank of ASV and yield mean in such a way that 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.

Table 4. First and second IPCA, mean yield and various yield-stability statistics investigated in wheat genotypes over rainfed and irrigated conditions

Genotypes	IPCA1	IPCA2	GY	ASVi	YSIi	SI (%)	I	RS
G1	3.697	0.293	431.43	5.968	17	65.6	1.23	11.63
G2	4.663	-3.357	463.61	8.228	18	66.2	1.19	11.08
G3	-3.737	6.257	413.41	8.688	23	65.7	1.25	10.07
G4	4.897	4.253	472.44	8.968	19	76.7	1.54	12.40
G5	3.903	5.213	498.24	8.168	14	78.8	2.10	10.51
G6	2.113	1.513	391.08	3.728	15	69.5	1.84	12.50
G7	2.633	-1.617	445.10	4.538	14	67.8	1.36	13.56
G8	3.033	1.633	541.81	5.148	7	77.6	2.08	10.53
G9	2.563	-1.887	473.06	4.538	10	76.1	1.95	12.75
G10	0.653	2.413	498.37	2.638	5	69.2	1.32	9.6
G11	3.163	3.303	614.64	6.068	8	91.3	2.94	10.55
G12	-8.037	5.953	452.56	14.248	22	78.8	2.21	11.24
G13	-2.507	-5.697	531.58	6.998	11	64.3	1.32	5.75
G14	1.847	3.013	214.36	4.238	17	60.7	1.15	12.32

Based on YSI the most stable genotype with high grain yield is genotype 10 which is in accordance with the result of AMMI stability value.

Sustainability index (SI)

Various authors used SI for selecting stable genotypes (Singh & Agarwal, 2003; Gangwar et al., 2004; Tuteja, 2006). The values of sustainability index were divided arbitrarily into 5 groups viz. very low (upto 20%), low (21-40%), moderate (41-60%), high (61-80%) and very high (above 80%) (Babarmanzoor et al., 2009). The sustainability index of each genotype has been given in the Table 4. Very high sustainability index (%) was estimated in the case of genotype 11 (91.03%), while the rest of genotypes showed high sustainability index (61-80%). These results prove that SI is not a suitable stability index for discriminating stable genotypes with high grain yield.

Stability index (I)

Rank sum method has an inherent weakness, that it weighs heavily in the direction of yield performance, apart from the arbitrariness in the scoring involved. Therefore, this method is not fit for drawing general conclusions. Keeping these points in view, 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. According to Bajpai and Prabhakaran (2000), 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 14th rank in the present study involving 14 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, which showed high mean performance (5, 8, 11, 12) were not stable across rainfed and irrigated conditions as indicated by high

magnitudes of (I) for grain yield (Rao et al., 2004). Rank-sum (RS) introduced genotype 13 (RS=5.75) followed by genotype 10 (RS=9.6) as the most stable genotypes with high grain yield. Both YSI and RS introduced genotype 10 as stable with high grain yield.

Principal components

To better understand the relationships, similarities and dissimilarities among the yield-stability statistics, principal component analysis (PCA), based on the rank correlation matrix was used. The main advantage of using PCA over cluster analysis is that each statistics can be assigned to one group only. The relationships among different stability parameters are graphically displayed in a biplot of PCA₁ and PCA₂ (Fig. 1). The PCA₁ and PCA₂ axes which justify 74% of total variation, mainly distinguish the statistics in different groups. Mean yield groups with I and SI and we refer to group 1= G₁ stability measures. The PCs axes separated AMMI stability value in a single group (G₂). Rank-sum (RS) and Yield stability index (YSI) were separated from the other groups (We refer to as group 3 = G₃) (Fig. 1). The statistics of G₃ (RS and YSI) distinguished genotypes 13 and 10 as the most stable genotypes with high grain yield. The advantage of YSI over RS is that a genotype's response to varying environments is multivariate and YSI is based on AMMI stability value which is multivariate whereas, RS is a univariate statistics.

Materials and methods

Plant genetic materials and experimental design

Fourteen genotypes of bread wheat (*Triticum aestivum* L.) listed in Table 1 were received from Dryland Agriculture Research Sub_Institute (Sararood Station). They were assessed using a randomized complete block design with three replications under both rainfed and irrigated conditions during 2008–2011 growing season in the experimental field of the College of Agriculture, Razi University, Kermanshah, Iran (47° 20' N latitude, 34° 20' E longitude and 1351.6 m altitude). Climate in the region is classified as semi-arid with mean annual rainfall of 378 mm. Minimum and maximum temperature at the research station were -27 and 44°C,

respectively. Each genotype was planted in 2-m rows and at 15 × 25 cm inter-plant and inter-row distances. Fertiliser application was 41 kgNha⁻¹ and 46 kg P2O5 ha⁻¹ at planting. The soil of experimental field was clay loam with pH 7.1. The seeding rate was 400 seeds per m² for all plots. At the rainfed experiment, water stress was imposed after anthesis. Non-stressed plots were irrigated three times after anthesis, while stressed plots received no water. The seeds were planted in early October and harvested in early July. At harvest time, yield potential (Yp) and stress yield (Ys) were measured from 2 rows 1m in length. The environments were considered as random factors, while genotypes as fixed factors.

Statistical analysis

AMMI analysis

The grain yield data were subjected to combined analysis of variance and AMMI analysis which is a combination of analysis of variance and multiplication effect analysis. Briefly, analysis of variance is used to partition variance into three components: genotype deviations from the grand mean, environment deviations from the grand mean, and GE deviations from the grand mean. Subsequently, multiplication effect analysis is used to partition GE deviations into different interaction principal component axes (IPCA), which can be tested for statistical significance through ANOVA. The IRRISTAT software was used for combined analysis of variance and AMMI analysis.

AMMI stability value (ASV)

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

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

Where $\frac{SS_{IPCA1}}{SS_{IPCA2}}$ is the weight given to the IPCA1-value by

dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the IPCA score, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV scores indicate a more stable genotype across environments.

Sustainability index (SI)

The sustainability index was estimated by the following formula (Babarmanzoor et al., 2009).

$$S.I = [(Y - \sigma_n) / YM] \times 100$$

where Y = Average performance of a genotype, σ_n = Standard deviation and YM = Best performance of a genotype in any year. The values of sustainability index were divided arbitrarily into 5 groups viz. very low (upto 20%), low (21-40%), moderate (41-60%), high (61-80%) and very high (above 80%).

Stability index (I)

Subsequently, the data were subjected to Bajpai and Prabhakaran (2000) non-parametric stability analysis to identify stable and high yielding genotypes. The stability index (I) was computed as follows:

$$I = \left(\frac{\bar{y}_i}{\bar{y}_{..}} + \frac{1}{\sigma_i^2} \right) / \left[\frac{1}{n} \sum_i \left(\frac{1}{\sigma_i^2} \right) \right]$$

(Rao et al., 2004) where, \bar{y}_i = average performance of the *i*th genotype, $\bar{y}_{..}$ = the overall mean, σ_i^2 = Shukla's (1972) stability variance of the *i*th genotype, n = number of environment. According to Bajpai and Prabhakaran (2000), 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 14th rank in the present study involving 14 genotypes.

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

The new approaches known as YSI and RS were calculated by the following formulas:

$$YSI = RASV + RY$$

Where RASV is the rank of AMMI stability value and RY is the rank of mean grain yield of genotypes (RY) across environments. YSI incorporate both mean yield and stability in a single criterion. Low value of this parameter shows desirable genotypes with high mean yield and stability. Rank sum (RS) = Rank mean (R) + Standard deviation of rank (SDR). RS incorporate both yield and yield stability in a single non-parametric index. Genotypes with the least RS are considered stable with high grain yield under rainfed and irrigated conditions. Standard deviation of rank (SDR) was measured as:

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

where R_{ij} is the rank of X_{ij} within the *j*th environment, \bar{R}_i (R) is the mean rank across all environments for the *i*th genotype and $SDR = (S_i^2)^{0.5}$.

Principal component analysis (PCA)

To better understand the relationships among the yield-stability statistics, principal component analysis (PCA), based on the rank correlation matrix was used by the software STATISTICA.

Conclusion

Genotype-by-environment (GE) interaction has been an important and challenging issue among plant breeders, geneticists and agronomists 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 of this investigation proved that SI and I are not suitable stability indices for discriminating stable genotypes with high grain yield. YSI which incorporate ASV and mean grain yield in a single non-parametric index and RS (R+SDR) were the most desirable indices for discriminating the most stable genotypes with high grain yield. Based on the YSI and RS the most stable genotypes with high grain yield were genotypes 13 and 10. The only advantage of YSI over RS is that a genotype's response to varying environments is multivariate and YSI is based on AMMI stability value which is multivariate, whereas, RS is a univariate statistics.

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