GxE evaluation of salinity tolerant barley genotypes by AMMI model

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ABSTRACT

The highly significant variances due to interaction, environments and genotypes were observed by AMMI analysis of salinity tolerant barley genotypes under multi location trials. The genotypes G6 and G13 with negative IPCA1 values showed positive IPCA2, IPCA3, IPCA4 values. Genotype G1 showed lowest value of D with smallest negative IPCA1 score (-0.013). Genotype G18 followed by G8, G1 and G5 were the stable performer based on ASV. Yield stability index advocated G8 followed by G5, G10, G4 and G12. The results of MASV indicated that genotypes G5, G1, G15, G17, G9 and G19 were stable, whereas genotypes G5, G9, G8 and G11 were the stable genotypes with relatively more average yield. Overall mean ranks of all of the AMMI estimates, genotypes G5, G1 and G8 were the most stable genotypes followed by genotypes G17 and G18.

Key words : AMMI models, AMMI stability value (ASV), D(AMMI distance), Modified AMMI stability value (MASV), Yield stability index(YSI)

INTRODUCTION

The low productivity of cereal crops due to salinisation of cultivable land had attracted the attention of policy makers. Total area of saline soils and sodic soils at global level were estimated by FAO up to 397 and 434 million hectare, respectively. The increasing population of world often led to the use of marginal salt affected soils (Verma *et al*., 2011). Barley is known to be one of the most salt tolerant crops having high level of variability in tolerance among cultivars (Kharab *et al*., 2013). Soil salinity is a major abiotic stress which not only delays but also reduces flowering and yield for barley crops (Kumar *et al*., 2014). To mitigate this problem, one of the cheap alternatives is to grow salinity tolerant varieties. The continuous efforts of barley workers under coordinated system have resulted in the development and release of tolerant varieties. These varieties produce good yield under unfavorable conditions (Anonymous 2014).

Genotype by environment interaction (GxE) refers to the differential responses of genotypes across environments (Bavandpori *et al*., 2015). The repeatable GxE interactions, change the ranking of genotypes across environments, are meaningful for the specific breeding strategy (Sabaghnia *et al*., 2008). Several statistical models have been used to understand interactions of different crops for identifying suitable genotypes (Bose *et al*., 2014). Usually for multi location trials analysis of variance (ANOVA), principal component analysis (PCA) and linear regression (LR) analysis methods are used (Mohammadi *et al*., 2010). The additive main effects and multiplicative interaction

(AMMI) model, describes interaction effects more effectively (Mortazavian *et al*., 2014). Kandus *et al*. (2010) found the AMMI model was the best model to describe the GxE interaction in maize cereal. Mohammadi *et al* (2015) established the more usefulness of AMMI analysis for durum wheat genotypes. The main objectives of the present investigation was to study (i) stratification of salinity tolerant barley genotypes based on interaction effects by AMMI estimates (ii) to compare the ranking of genotypes by various methods (iii) to identify similar or redundant measures to streamline GxE interaction analysis in MET data.

MATERIALS AND METHODS

The AMMI model is defined for main effects and GxE interaction effects as per Silveira *et al.,* 2013:

$$Y_{ij} = \mu + gi. + e.j + \sum_{k=1}^{n} \lambda_k \, \gamma_{ik} \, \delta_{jk} + \rho_{ij} \qquad (i)$$

where Y_{ij} is the yield of the i-th genotype in the j-th environment; μ is the grand mean; gi. and e.j are the genotype and environment deviations from the grand mean, respectively ; λ_k is the eigen value of the Principal Component analysis axis k; γ_{ik} and δ_{jk} are the genotype and environment principal component scores (eigenvectors) for axis k; n is the number of principal components retained in the model and ρ_{ij} is the error term.

AMMI Stability Value (ASV)

The ASV is the distance from the coordinate point to the origin in a two-dimensional scatter graph of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase *et al*., 2000). Because the IPCA1 score contributes more to

the GxE interaction sum of squares, a weighted value is needed. This weight is calculated for each genotype and environment according to the relative contribution of IPCA1 to IPCA2 to the interaction SS as follows:

AMMI Stability Value (ASV) =

$$\sqrt{\left[\frac{SSIPCA1}{SSIPCA2} * IPCA1 \text{ score}\right]^2 + IPCA2 \text{ score}^2} \qquad (ii)$$

where SSIPCA1 and SSIPCA2 are sum of squares by the IPCA1, IPCA2 respectively and the weight given to the IPCA1value 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 IPCA scores indicate a more stable genotype across environments. Similarly, IPCA2 score near to zero revealed more stable, while large values indicated more responsive and less stable genotypes.

Modified AMMI's stability value (MASV)

Adugna and Labuschange had introduced in the year 2002 new parameter as modified AMMI's stability value for effective interpretation of GE interactions as follows:

$$MASV = \sqrt{\sum_{n=1}^{N-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}}\right)(IPC_n^2) + (IPC_{n+1}^2)}$$

In this modified AMMI stability parameter, all significant IPCs were used.

The AMMI distance statistic coefficient (D) (Zhang *et al.*, 1998) was calculated as the distance of the interaction principal component (IPC) from the origin

$$\text{AMMI Distance (D}_i) = \sqrt{\sum_{i=1}^{n} \gamma_{is}^2} \qquad (i = 1,2,3,.. n) \qquad (iv)$$

Yield stability index (YSI) considered the rank of yield of genotypes across environments and rank of AMMI stability value. This index incorporate mean and stability index in a single criteria and calculated as (Farshadfar *et al.*, 2011):

$$YSI = RASV + RY \qquad (v)$$

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

Twenty barley genotypes were evaluated during crop season 2013-14 across 6 environments viz: Hisar, Faizabad-1, Faizabad-2, Rampura, Bawal and DWR-Hisar. The details of pedigrees for evaluated genotypes along with environmental conditions are presented in Table 1. The randomized complete block design employed with four replications for field experimentation. Recommended agronomical practices were carried out to harvest the good yield. AMMI and correlation analysis were carried out by Genstat software version 17.1 (VSN international).

RESULTS AND DISCUSSION

The yield of the 20 genotypes tested over the six environments indicated highly significant effects due to genotypes (G), environments (E) and the G×E interaction (Table 2). The environmental main effect (E) emerged as the most important source of variation due to its largest contribution (54.4 %) to the total sum of squares (TSS). The contribution of GxE interaction to the TSS was observed to be 21.9% which was more than main effects of genotypes (7.67%). This indicates the differences in yield and rank of genotypes was largely due to environmental effect (Abdipur

Table 1: Details of salinity tolerant barley genotypes, parentage and environmental conditions

Code	Genotype	Parentage	Code	Environment	Latitude	Longitude
G1	NDB1592	IBCB-S(2008-09)-31	E1	Hisar	29° 10'N	75° 46'E
G2	KB 1370	JYOTI/RD2552	E2	Faizabad-1	26° 87'N	80° 97'E
G3	RD 2552	RD2035/DL472	E3	Faizabad-2	26° 87'N	80° 97'E
G4	DWRB 131	IBYT-LRA-M -11 (2011 -12)	E4	Rampura	24° 46'N	75° 44'E
G5	NDB 1586	(IBYT-MRA-24-2008-09)	E5	Bawal	28° 10'N	76° 59'E
G6	RD 2886	RD2715 / K750 // PETUNIA- 1	E6	DWR- Hisar	29° 17'N	75° 67'E
G7	NDB 1173	BYTLRA 3-(1 994-95)/NDB217				
G8	RD 2888	RD2683/RD2503//RD2683				
G9	BH 984	2005EIBGN-4/BH646				
G10	BH 972	29'" EIBGN-22/BH 646				
G11	RD 2860	RD2552/ADABELLA/M-1 1 1 /CANELA				
G12	RD 2889	RD2552 /UBL-9//GLORIA-BAR				
G13	RD 2890	BH393/RD2360//RD271 5				
G14	RD 2887	R D2670/RD2683// BLLU / PINON				
G15	NDB 1600	NDB2OB/ALFA93				
G16	BH 986	RD2670/K792				
G17	BH 985	JB47/K792				
G18	RD 2794	RD2035/RD2683				
G19	NDB 1587	IBON-HI-31(2008-09)				
G20	KB 1375	K551/HUB158				

Table 2: AMMI analysis of salinity tolerant barley genotypes over locations

Source of variation	Degree of freedom	Sum of squares	Mean Sum of squares	Variance ratio	% TSS	% GxE
Treatments	119	33233	279.3	18.33***	84.02	
Genotypes	19	3035	159.7	10.49***	7.67	
Environments	5	21519	4303.7	69.58***	54.40	
Block	18	1113	61.8	4.06***		
Interactions	95	8680	91.4	6.00***	21.94	
IPCA 1	23	3893	169.3	11.11		44.85
IPCA 2	21	2173	103.5	6.79		25.03
IPCA 3	19	1499	78.9	5.18		17.27
IPCA 4	17	729	42.9	2.82		8.40
Residuals	15	386	25.7	1.69		
Error	342	5209	15.2			
Total	479	39556	82.6			

%TSS, percentage of total sum of squares, % GxE, percentage of GxE total sum of squares
*** denotes significant at 0.001 level of significance

and Vaezi, 2014). Partitioning of GxE interaction indicated the AMMI4 model described the interaction patterns significantly by the first four IPCA's based on cross-validation. The first four principal component axes of the interaction captured 44.8%, 25.0%, 17.3% and 8.4% of the interaction sum of squares.

Average yield: The range for yield in the present investigation varied from minimum of 19.8 to 33.5 q/ha with genotype NDB 1173 recorded the highest yield followed by RD 2888 and BH 972 (Table 3). Genotypes with lower yield were observed as KB 1375, BH 986 and KB 1370. The magnitude of the genotype x environment interaction sum of squares was less than that for environments indicated substantial differences in environments as compared to GxE interaction toward genotypes.

Crossover and non-crossover IPCAs interactions: IPCA scores of genotypes showed both positive and negative values. Nine out of 20 genotypes showed negative IPCA1 score with some environments as well as showed positive interactions with other environments. Genotypes with negative IPCA1 score i.e G1(NDB 1592), G6(RD 2886), G13(RD 2890), G14(RD 2887) showed positive IPCA4 values (Table 3). The genotypes G6(RD 2886), G13(RD 2890) with lower IPCA1 scores showed positive IPCA2, IPCA3, IPCA4 values respectively. These genotypes would produce a lower absolute G×E interaction effect and had less variable yields (more stable).

AMMI stability index (D): The ranking of genotypes in ascending order of 'D' values were those in G1 (0. 97) < G5 (1.11) < G15 (1.42) < G17 (1.47). Genotypes with lowest yield G20(KB 1375) and G16(BH 986) exhibited D values 2.06 and 2.09, respectively. Genotype G1(NDB 1592) showed lowest value of D and smaller negative IPCA1 score (-0.013). This genotype recognized as possessing stable yield of lowest magnitude for studied environments.

AMMI stability value (ASV): In ASV method, a genotype with least ASV score is the most stable. Accordingly genotypes G18 (RD 2794) followed by G8(RD 2888), G1(NDB1592) and G5(NDB 1586) were the most stable, while genotypes G6(RD 2886), G13(RD 2890), G3(RD 2552) and G14(RD 2887) would be undesirable.

Yield Stability index (YSI): Genotypes with least YSI are considered as the stable with high yield. The most desirable genotype for selection of both stability and high yield was G8(RD 2888) followed by G5(NDB 1586), G10(BH 972), (G4(DWRB 131) and G12(RD 2889).

Modified AMMI stability value (MASV): The visual interpretation of GxE interaction through biplot is not valid for situations with more than two significant IPCs (Gauch, 2006). The AMMI model in this study indicated that there was a more complex interaction of GxE and it could not facilitate graphical visualization of the genotypes in low dimensions and so it is essential to use an alternative procedure to interpretation of GE interaction using AMMI parameters (Sabaghnia et al., 2012).

Although, ASV parameter was reported to produce a balanced measurement as parameter uses IPC1 and IPC2 scores as well as magnitude of their sum of squares and so is different from the other AMMI parameters which use only genotypic or environmental IPCs scores or their modifications (Sabaghnia et al., 2012). The modified AMMI's stability value (MASV) used all four significant IPCs. The results of MASV indicated that genotypes G5, G1, G15, G17, G9,G19, G16, G5, G14, G8 and G11 were most stable, whereas genotypes G5, G9, G8 and G11 were the stable genotypes which had relatively more average yield (Table 3). Therefore, MASV parameter introduced some of the high mean yielding genotypes (G5 and G9) as the most stable ones. As per AMMI estimates computed from four significant IPCs were more useful and introduced relatively

Table 3: Ranking of salinity tolerant barley genotypes as per AMMI estimates

Code	Genotype	Gm	R_{Gm}	IPCA1	IPCA2	IPCA3	IPCA4	YSI	R_{YSI}	D	R_D	ASV	R_{ASV}	MASV	R_{MASV}
G1	NDB1592	27.56	14	-0.0132	0.8610	0.4369	0.0898	17	9	0.97	1	0.86	3	1.55	2
G2	KB 1370	26.72	18	1.1503	-0.4773	1.3610	-0.3876	29	16	1.89	8	2.12	11	2.96	11
G3	RD 2552	29.20	5	1.1400	-2.9375	-0.3167	0.5528	23	12	3.21	20	3.58	18	4.91	20
G4	DWRB 131	28.39	8	0.7231	-1.2701	0.9173	-1.5001	14	4	2.29	15	1.81	6	3.12	12
G5	NDB 1586	28.41	7	0.5046	0.0753	0.2587	-0.9455	11	2	1.11	2	0.91	4	1.25	1
G6	RD 2886	28.27	10	-2.7886	0.0051	0.8168	0.0095	30	19	2.91	19	5.00	20	4.00	19
G7	NDB 1173	33.51	1	1.0587	1.4506	-1.5714	0.2873	15	6	2.40	17	2.39	14	3.85	18
G8	RD 2888	31.09	2	-0.2032	-0.7452	-1.4417	-0.9321	4	1	1.88	7	0.83	2	2.94	9
G9	BH 984	28.12	11	0.7304	0.8921	0.4587	-1.0654	16	7	1.64	5	1.58	5	2.16	5
G10	BH 972	30.98	3	-0.3211	1.9368	0.2953	-0.4620	12	3	2.04	10	2.02	9	3.14	13
G11	RD 2860	29.42	4	-1.5118	0.0095	-1.1303	-0.8296	19	10	2.06	12	2.71	15	2.95	10
G12	RD 2889	28.43	6	-1.0332	-0.3960	-1.9033	-0.2491	14	5	2.22	14	1.89	8	3.66	16
G13	RD 2890	28.34	9	-2.3342	0.5700	1.0848	0.0926	28	14	2.64	18	4.22	19	3.76	17
G14	RD 2887	27.88	12	-1.6224	-0.2517	0.2200	1.6725	29	16	2.35	16	2.92	17	2.80	8
G15	NDB 1600	27.31	17	1.2489	0.2288	0.4027	-0.4856	30	19	1.42	3	2.25	13	1.91	3
G16	BH 986	25.96	19	1.5541	0.7229	0.3018	1.1542	35	20	2.09	13	2.88	16	2.69	7
G17	BH 985	27.77	13	0.8940	0.9925	-0.1036	0.6048	20	11	1.47	4	1.88	7	2.06	4
G18	RD 2794	27.39	16	0.2863	-0.2984	-1.7378	0.7310	17	9	1.93	9	0.59	1	3.18	14
G19	NDB 1587	27.52	15	1.2138	0.2524	0.7218	1.1359	27	13	1.83	6	2.19	12	2.38	6
G20	KB 1375	19.84	20	-0.6766	-1.6207	0.9290	0.5267	30	19	2.06	12	2.02	10	3.19	15

Gm-Genotype mean; D- AMMI stability index; ASV-AMMI stability Value; YSI- Yield stability Index ; MASV-Modified AMMI Stability Value

the high yielding genotypes as the most stable genotypes. Considering the mean ranks of all of the AMMI stability parameters, genotypes G5, G1 and G8 were the most stable genotypes followed to genotypes G17 and G18. All of these stable genotypes, G5 and G8 had the high mean yield performance over grand mean.

CONCLUSIONS

The AMMI model has been well established for understanding complex GxE interactions in multi-environmental trials for number of cereal crops. The interaction of 20 salinity tolerant barley genotypes with 6 environments was best predicted by the first four significant principal components of genotypes and environments. The AMMI model used in the present study indicated a more complex GE interaction which required as many as four IPCs. AMMI based parameters assisted breeders to have an overall picture in behavior of the genotypes, the environments and

GxE interaction. The ASV and MASV benefit dynamic concept of stability and could be useful simultaneous selection of yield and stability (Dehghani *et al.*, 2010). The results obtained by AMMI analysis indicated that genotypes G5 (NDB 1586), G1 (NDB1592), G8 (RD 2888) and G17 (BH 985) were as the stable genotypes and would be recommended salinity tolerant barley for saline areas of the country.

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