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AMMI ANALYSIS TO ESTIMATE GENOTYPE X ENVIRONMENT INTERACTION OF MALT BARLEY GENOTYPES

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ABSTRACT

AMMI analysis of seven malt barley genotypes evaluated at number of locations in north western plains zone had expressed highly significant variations due to environments (60.7%), G x E interactions (20.5%), and genotypes (11%). Further Interaction effects partitioned into seven Interactions principal components. AMMI Stability Value (ASV) and Modified AMMI Stability Value (MASV) measures based on two components utilized 80% variations and significant interaction components accounted for 94.5% respectively. Higher values of Genotypic Adaptability Index (GAI) values were achieved by G7 & G6, the values for Harmonic Mean of genotypic values (HMGV) had identified the G7 & G6 whereas the same pair of genotypes had also selected by Relative Performance of Genotypic values (RPGV) and Harmonic mean for Relative Performance of Genotypic values (HMRPGV) measures for across the locations. Multivariate hierarchical clustering based on Ward's method had observed higher yielder varieties G7 & G6 were assigned to cluster second along with two other genotypes. Value of standard deviation (SD) was observed a point of demarcation of studied measures of the present study into three clusters. The first group was consistent of Mean, GAI. RPGV, HMGV as IPC1 had joined with IPC3 values in second group while ASV, MASV, IPC2, IPC4, IPC5 had formed the third group.

***Keywords* :** GEI analysis, Statistical models, Environment interaction

Introduction

Barley has occupied fourth ranked among the cereal crops after maize, rice and wheat, and cultivated at larger areas across the world (Assefa *et al.,* 2021). Barley is cultivated under higher productive areas and also suitably in marginal as well as subsistence environments. On a global scale, it is the adaptability of barley to a very wide range of environments compared to other cereal crops, apart from its nutritional properties that has been the anticipated mainly as for food use (Mehraban *et al*., 2019). There has been considerable recent interest in the nutritional properties of barley, which has stemmed largely from the discovery of the cholesterol-lowering effect of β-glucan, a cell-wall polysaccharide found in barley (Ahakpaz *et al*., 2021). The overall importance of barley as a human food is very much appreciated owing to much potential of the health benefits of the whole grain and adaptability of barley has been recognised to a wide range of environments in comparison to other cereal crops (Dinsa *et al*., 2022). Reliable information about cultivar performance in different environments has been provided by genotype × environment interaction effects with the execution of multi-environment trials (Jędzura *et al.,* 2023). Picking the best crop variety (genotype) is tricky owing to different environments can affect their performance in unpredictable ways (genotype-environment interaction); by the same token, this complex interaction can weaken the influence of genes on important traits (heritability), making it harder to identify the best performers for specific areas (Karimizadeh *et al*., 2023). Literature reflected the large number of analytic approaches for the precise estimation of genotype × environment interaction effects (Aditi *et al.,* 2023). Good numbers of multivariate parametric AMMI based measures (AMMI stability value (ASV), Modified AMMI stability value (MASV) have been advocated (Pour-Aboughadareh *et al.,* 2022). The stability and adaptability of malt genotypes had been evaluated by mostly cited measures via harmonic mean of genotypic values

(HMGV), relative performance of genotypic values (RPGV), and harmonic mean of relative performance of genotypic values (HMRPGV) (Mohan *et al.,* 2025). The prime objective of the present study was to explore the similarity of the genotypes performances across the multi locations trials among the recently developed measures for adaptability and stable performance of the genotypes.

Materials and Methods

Seven promising malt barley genotypes were evaluated under field trials during 2023-24 cropping seasons at eleven major locations. The environmental conditions of the locations and parentage details of the evaluated malt barley genotypes reflected in table 1 for ready reference. Randomized complete block designs were laid out with three replications. Recommended agronomic interventions followed to harvest the yield of good crop. Important morphological traits were recorded and yield data had utilized for further statistical analysis. The popular and widely recommended software's AMMISOFT and JMP were employed for collected data sets.

ASV	$ASV = [(\frac{SSIPC\,1}{SSIPC\,2} PC1)^2 + (PC2)^2]^{1/2}$
Modified AMMI stability Value	$MASV = \sqrt{\sum_{n=1}^{N-1} \frac{SSIPC_n}{SSIPC_{n+1}} (PC_n)^2 + (PC_{n+1})^2}$
$HMGV_i$	$=$ Number of environments / $\sum_{j=1}^{k} \frac{1}{GV_{ij}}$
	GV_{ij} genetic value of ith genotype in jth environments
Relative performance of genotypic values across environments	$RPGV_{ij} = \sum GV_{ij} / \sum GV_j$
Harmonic mean of Relative performance of genotypic values	$HMRPGV_{i.} =$ Number of environments / $\sum_{j=1}^{k} \frac{1}{RPGV_{ij}}$
Geometric Adaptability Index	$GAI = \sqrt[n]{\prod_{k=1}^{n} \bar{X}_k}$

Results and Discussion

Malt barley yield was significantly impacted by both environmental factors and the genetic makeup of the genotypes, as well as their interaction, as revealed by a combined analysis of variance (ANOVA). This finding unveil that statistically highly significant at ($p < 0.05$), indicated the strong influence of these factors on yield Table 2. Highly significant variations due to environments, GxE interactions, and genotypes were observed by AMMI analysis (Table 2). This analysis also revealed about 60.7% of the total sum square of variation for yield was due to environments followed by 22.5% of GxE interactions, whereas genotypes accounted for marginally 11%. This study confirmed that genetic diversity among varieties, environmental variations across testing locations and their interaction play a crucial role in determining the variability observed in yield (Roy *et al*., 2024). The results suggest that environmental factors and genotype-environment interaction (GXE interaction) played a significantly greater role in influencing yield performance compared to the main effect of genotype alone. Interaction effects are further portioned into five Interaction principal components totalled more than 98.5% of interactions sum of square variations. AMMI1 explained a total variation of 41.5%, followed by 37.7% for AMMI2, 9.9% for AMMI3, AMMI4 accounted for 5.8% and followed by 3.6% respectively. The first two AMMI components in total showed 79.2% of the total variation indicating the two AMMI components well fit and confirm the use of AMMI model. FR-tests at the 0.01 level diagnose AMMI5. The values of estimated sums of squares for GxE signal and noise were 93.3% and 6.7% respectively. As per the analysis an early IPCs selectively capture the signal factor while the late ones account for noise factor (Rao *et al*., 2020). The sum of squares for GxE-signal was up to 1.90 times that for genotypes main effects. Hence, narrow adaptations are important for this dataset. Even just IPC1 alone expressed 0.85 times the genotypes main effects. Also it was observed that GxE-noise was to the tune of 0.14 times the genotypes main effects. Obviously by discarding the portion of noise it would improve the accuracy, increases repeatability, simplifies conclusions, and accelerates progress. The correlation coefficient had expressed significant positive relation between genotypes mean yields and IPC1 scores had 0.81** whereas the weak correlation was observed between environmental means and IPC1 scores i.e. 0.34.

Performance of genotypes based on AMMI analysis

Since the genotypes yield, the mean yield was considered an important measure to assess the genotypes.

Mean yield of genotypes expressed highly significant variations and yield potential selected G7, G6, and the consistent yield observed by least values of SD had expressed by G1, G6 genotypes (Table 3). The locations of Tabiji and SG Nagar were more productive as compared to other locations of zone. Higher values of Genotypic Adaptability values were achieved by G7 & G6, the values for Harmonic Mean of genotypic values had identified the G7 & G6 whereas the same pair of genotypes had also selected by Relative Performance of Genotypic values and Harmonic mean for Relative Performance of Genotypic values measures for given data pertaining to genotypes performance across the locations (Mohan *et al*., 2021). Consistent performance of G6 and G1 genotypes was pointed out by CV (Coefficient of Variation). Moreover the higher values for next two measures RPGV*Mean and HMRPGV*Mean were also exhibited by G7& G6 genotypes. The stable behaviour or the general and specific adaptability of genotypes had been judged by values of IPCA's in the AMMI analysis. The large values of the IPCA scores reflected the specific adaptation of genotype to the certain locations. While, the values approximated to zero were recommended for in general adaptations of the genotype (Gerrano *et al*., 2020). Absolute IPCA-1 scores pointed for G1, G5 as per minimum IPCA-2, pointed for G5, G3 genotypes would be of choice. Values of IPCA-3 favored G4, G7 genotypes. As per IPCA-4, G2, G4 genotypes would be of stable performance. As per IPCA5, G3, G5. First two IPCAs in ASV measure utilized 79.2% of G×E interaction sum of squares. Using first two IPCAs in stability analysis could benefits dynamic concept of stability in the identification of the stable high yielder genotypes. Adaptability measures MASV considered all five significant IPCAs of the AMMI analysis using 98.5% of G x E interactions sum of squares pointed towards (G1 and G5) as of stable performance.

Multivariate Hierarchical clustering

Two ways grouping of measures and barley genotypes was carried out using the multivariate hierarchical clustering as per Ward method, and the results were visualized graphically as dendrogram (Khalid *et al*., 2023). Based on the cluster analysis, the analyzed genotypes were divided into two homogeneous groups (Figure 1). The higher yielder varieties G7 & G6 were assigned to cluster no. 2 along with two other genotypes (Table 3). SD was observed a point of demarcation of measures into three clusters. The first group was consistent of Mean, GAI. RPGV, HMGV as IPC1 had joined with IPC3 values in second group while ASV, MASV, IPC2, IPC4, IPC5 had formed the third group as AMMI analysis based measures had distance from other known.

Biplot and association analysis

First two significant principal components had accounted for 69.6% of variation among the evaluated genotypes and studied measures for the study with 50% and 19.5% respective share (Table 4). Measures GAI, RPGV, HMGV RPGV* Mean along with Bathinda, Karnal, Durgapura had contributed more in first principal components whereas CV, SD, IPC2, Ludhiana, SG Nagar were of major share in second component. In terms of evaluated genotypes the % share was more in in first component by G2, G7 and for the second were G6, G4. The biplot analysis is an appropriate method to analyse interaction between genotypes and measures of their adaptability and narrowing down to the number of measures to the ones accounted for a major portion to the variability (Bocianowski *et al*., 2021). In the biplot vectors of measures or locations showing acute angles were positively correlated whereas those showing obtuse or straight angles were would exhibit negative association and those with right angles had no correlation. Unstable performance of G2, G6, G7 genotypes as compared to genotypes placed near to origin G5, G3 in biplot analysis. The largest difference between the mean yields for genotypes was obtained in 56 q/ha, and the smallest in 44 q/ha. The measures that brought the lowest variability of the interaction effects were IPC3, IPC5, ASV which was manifested by the shortest vector among all the studied measures (Figure 2). Four clusters of small and moderate sizes observed in biplot analysis (Figure 3). AMMI analysis based measures IPC3 & IPC5, ASV, MASV along with Modipuram, Pantnagar formed a cluster as placed near to the origin. Next cluster consisted of IPC1, HMGV and Durgapura, Karnal, Hissar, Bhatinda locations. Measures GAI, RPGV, HMRPGV, Mean, RPGV*Mean, HMRPGV* Mean grouped with Tabiji, Navgaon, Bawal locations. Last adjacent cluster comprised of SD, CV, IPC2 with SG Nagar locations.

Conclusions

Malt barley market has gaining momentum and grain yield with acceptable quality standards are required as raw materials for breweries and malt factories. Genotype by environment interaction complicates variety selection for wide adaptability whenever it exists and hence it is important to carefully consider stability analysis. AMMI analysis-based measures IPC3 & IPC5, ASV, MASV along with Modipuram, Pantnagar formed a cluster as placed near to the origin. Next cluster consisted of IPC1, HMGV and Durgapura, Karnal, Hissar, Bhatinda locations. Measures GAI, RPGV, HMRPGV, Mean, RPGV*Mean, HMRPGV* Mean grouped with Tabiji, Navgaon, Bawal locations. Last adjacent cluster comprised of SD, CV, IPC2 with SG Nagar locations. Varieties with required level of quality traits need, at the same time, to be stable across environments.

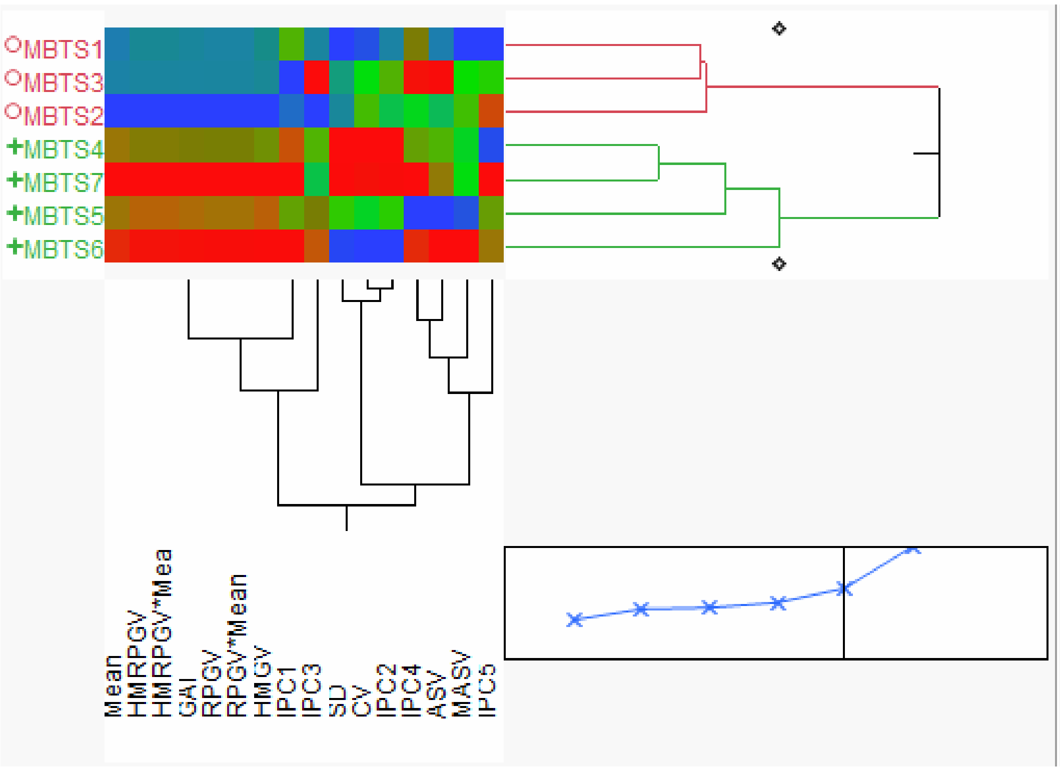

Fig. 1: Ward's method of clustering considering multivariate hierarchical

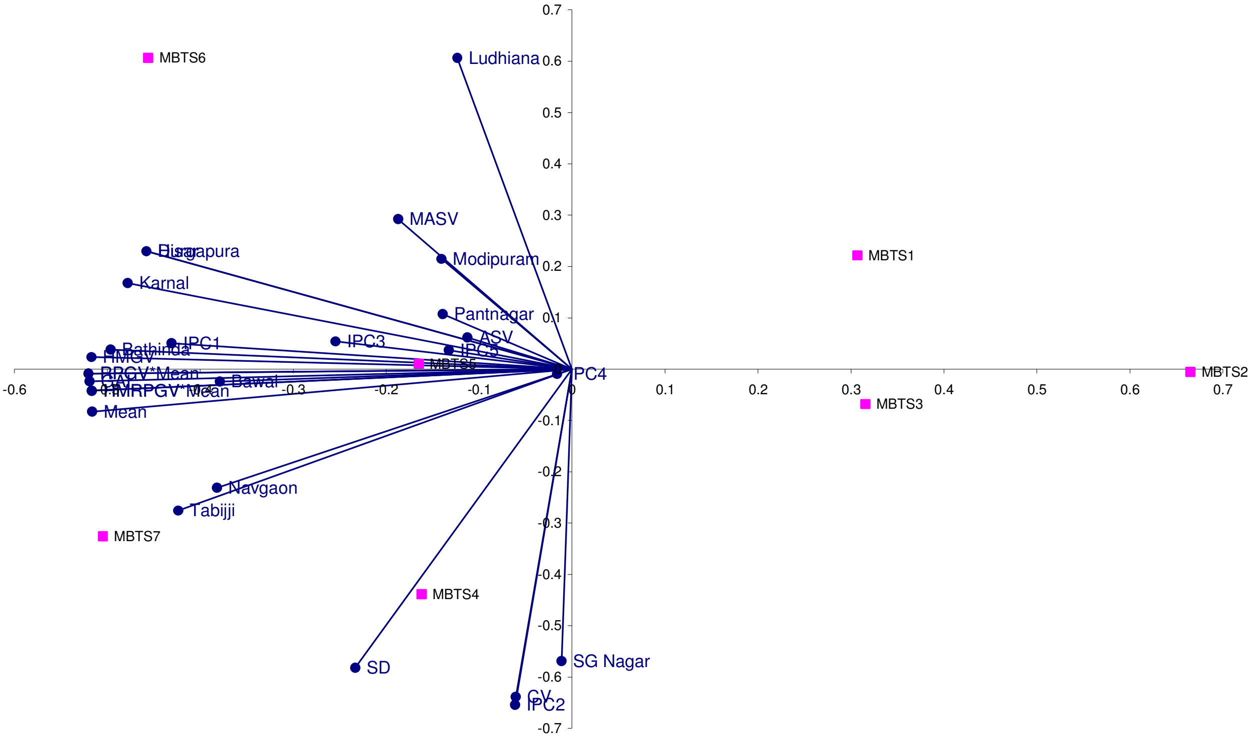

Fig. 2: Genotypes x Locations biplot analysis of malt barley genotypes

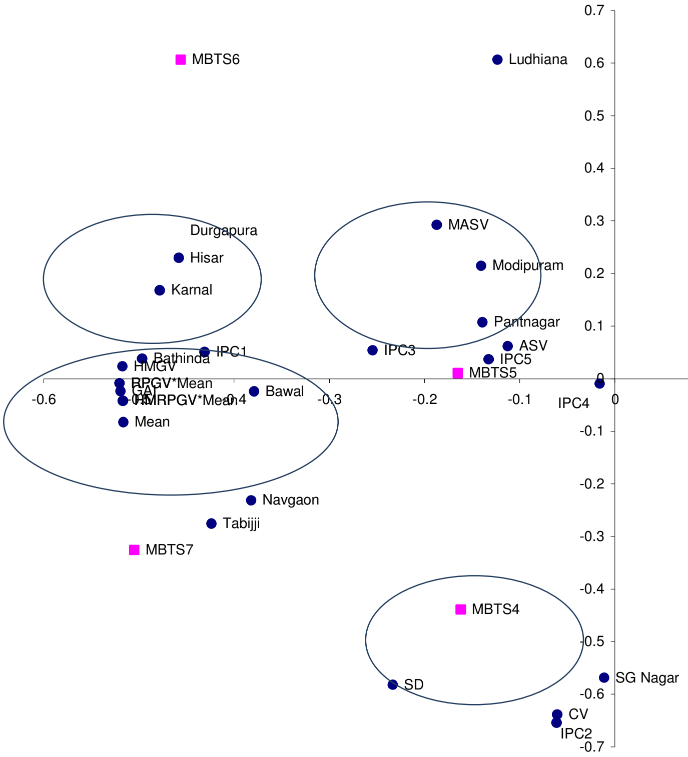

Fig. 3 : Grouping of Genotypes and Locations by biplot analysis of malt barley genotypes

Table 1 : Parentage vis-a-vis location details of malt barley genotypes

Code	Genotype	Parentage	Locations	Latitude	Longitude	Altitude
G1	RD-2849	DWRUB52/PL705	Bathinda	30 ° 09' N	74 ° 55 ’E	211
G2	DWRB-182	DWRUB52/DWRB78	Bawal	28 ° 10'N	76 ° 50’E	266
G3	DWRUB-52	DWR17/K551	Durgapura	26 °51'N	75 ° 47’E	390
G4	RD-3064	NBPGR 92 X RD 2668 X RD 2894	Hisar	29 ° 10' N	75 ° 46’E	229
G5	DWRB-238	DWRB101/DWR28	Karnal	29 ° 43' N	70 ° 58’E	245
G6	DWRB-235	DWR47/RD2035	Ludhiana	30 ° 54' N	75 ° 48 ’E	247
G7	DWRB-137	DWR28/DWRUB64	Modipuram	29 °05' N	77 °70’E	226
			Pantnagar	29 ° 02'N	79 ° 48’E	243.8
			SG Nagar	29 ° 66'N	75 ° 53’E	175.6

Table 2 : AMMI analysis of malt barley genotypes evaluated under coordinated trials

Source of variation	Degree of Freedom	Mean Sum of Squares	Significance level	% share of components	% contribution of interaction terms in G X E	Cumulative share of interaction components
Treatments	76	604.27	***	94.18		
Genotype (G)	6	894.66	***	11.01		
Environment (E)	10	2959.96	***	60.70		
GxE interactions	60	182.62	***	22.47		
IPC1	15	302.82	***		41.46	41.46
IPC2	13	318.02	***		37.73	79.19
IPC3	11	99.15	***		9.95	89.14
IPC4	9	70.16	***		5.76	94.90
IPC5	7	55.56	***		3.55	98.45
Residual	5	33.90	*			
Error	231	12.28				
Total	307	158.83				

Table 3 : AMMI based measures of GxE for malt barley genotypes

Genotype	Mean	SD	IPC 1	IPC 2	IPC 3	IPC 4	IPC 5	GAI	HMGV	CV	RPGV	RPGV *Mean	HMRPGV	HMRPGV *Mean	ASV	MASV
G1	47.83	8.53	0.33	-1.69	-1.20	0.38	-1.92	47.24	46.75	17.83	0.94	48.14	0.93	47.88	1.73	4.99
G2	44.29	10.44	-2.37	-0.45	-2.86	-0.12	0.88	43.06	41.73	23.58	0.86	44.19	0.84	43.29	2.53	6.87
G3	48.10	10.92	-4.07	0.43	2.19	0.82	0.09	47.13	46.31	22.69	0.94	48.26	0.93	47.54	4.28	6.61
G4	53.53	15.67	1.25	2.80	0.32	0.24	-1.57	51.81	50.39	29.27	1.03	52.84	1.02	52.47	3.09	6.51
G5	53.57	12.03	0.46	0.19	0.71	-3.15	0.34	52.49	51.56	22.46	1.04	53.46	1.04	53.23	0.52	5.47
G6	54.68	8.87	2.13	-3.81	1.17	0.71	0.65	54.09	53.56	16.22	1.08	55.56	1.06	54.29	4.42	9.11
G7	56.68	15.63	2.26	2.55	-0.32	1.13	1.54	55.11	53.84	27.57	1.10	56.21	1.09	55.80	3.48	6.56

Table 4 : Loadings of measures, genotypes and locations as per principal components

Locations & Measures	Principal Component 1	Principal Component 2	Measures	Principal Component 1	Principal Component 2	Genotypes	Principal Component 1	Principal Component 2
Bawal	-0.1977	-0.0160	GAI	-0.2708	-0.0156	G1	0.2860	0.2613
Hisar	-0.2389	0.1516	HMGV	-0.2698	0.0155	G2	0.6197	-0.0067
Karnal	-0.2494	0.1107	RPGV	-0.2715	-0.0059	G3	0.2939	-0.0805
Bathinda	-0.2589	0.0250	RPGV*Mean	-0.2715	-0.0059	G4	-0.1509	-0.5172
Ludhiana	-0.0644	0.4001	HMRPGV	-0.2695	-0.0279	G5	-0.1537	0.0122
Durgapura	-0.2389	0.1516	HMRPGV*Mean	-0.2695	-0.0279	G6	-0.4248	0.7144
Navgaon	-0.1994	-0.1526	ASV	-0.0588	0.0406	G7	-0.4701	-0.3836
Tabijji	-0.2210	-0.1818	MASV	-0.0976	0.1929			
SG Nagar	-0.0059	-0.3753	IPC1	-0.2248	0.0333			
Modipuram	-0.0733	0.1417	IPC2	-0.0320	-0.4317			
Pantnagar	-0.0726	0.0707	IPC3	-0.1327	0.0356			
Mean	-0.2693	-0.0545	IPC4	-0.0084	-0.0064			
SD	-0.1217	-0.3842	IPC5	-0.0692	0.0243			
CV	-0.0316	-0.4215						
% of measures (Total = 69.55%)	50.02%	19.53%						

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