



Multi-location Yield Stability Analysis Involving Univariate and Multivariate (AMMI) Methods in Feed Barley

Om Veer Singh, Lokendera Kumar, Jogendera Singh, Chuni Lal and Ajay Verma 

ICAR-Indian Institute of Wheat and Barley Research, Agrasain Marg, Kunjpura Karnal, Haryana (132 001), India



Corresponding  verma.dwr@gmail.com

 0000-0001-9255-6134

ABSTRACT

The present study was conducted during the cropping season from November, 2023 to April, 2024 at eight major locations of the country to study the specific and general adaptation of feed barley genotypes by recent AMMI analysis based measures. AMMI analysis had observed highly significant variations due to environments, G×E interactions, and genotypes about 76.7% of the total sum square of variation for yield was due to environments, followed by 13.2% of G×E interactions, whereas genotypes accounted for marginal share of 7.5%. Explained variation of G×E interaction accounted by each of IPCA exploited by defined measures, as type-1 measures benefited 39.9%, type-2 measures utilized 59.8%, type 3 measures used up to 76.2%, type 5 measures benefited up to 90.6%, as observed from table. This justified the use of AMMI derived measures based on the larger numbers of IPCAs resulting in the most usage of G×E interaction variations. Biplot analysis of the measures of adaptability had observed that the first two significant principal components had accounted for 63.3% of the variation among the evaluated genotypes and studied measures for the current study with 33.4% and 29.9% respective share. Measures ASTAB3, SIPC3, SIPC2, ASTAB5 along with G20, G16, G21 genotypes, had contributed more in the first principal component whereas D5, D3, D2, ASV were of major share in second component. In terms of the evaluated genotypes share of G08, G7, G14 was significant.

KEYWORDS: G×E interactions, AMMI model, ASV, ASTAB, EV, D, MASV

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1. INTRODUCTION

Multi-environment trials (METs) are inevitable in crop improvement programs to evaluate the new genotypes' yield potential and their specific or general adaptability in diverse environmental conditions (Jedzura et al., 2023). The importance of stability and adaptability of the cultivar's performance under various environmental conditions, including a rapidly changing climate has been highlighted in breeding trials (Karimizadeh et al., 2023). Therefore, the estimation of the genotype $\times$ environment interactions in order to quantify genotypic performance and the degree of stability is an essential procedure to increase the selection efficiency. G $\times$ E interaction governs the identification of the stable yield performer genotypes suitable for a specific environment or for several environments (Roy, et al., 2024). An efficient assessment of G $\times$ E interaction is essential to determine the yield potential of genotypes along with stable yield performance (Mohan et al., 2025). The significance of interaction effects hinders the selection of high-yielding and stable genotypes, and recommendation of ideal genotypes for specific regions (PourAboughadareh, et al., 2022). Therefore, to reduce the dramatic and negative impact of GEI on the efficiency of breeding programs, a comprehensive knowledge of the GEI can provide ideal opportunities for breeders and agronomists to increase the accuracy of selection in their breeding programs (Lee et al., 2023). ANOVA analysis is useful to test the significance of interaction but this test fails to partition into total variation into simple and cross over interactions and AMMI model (Additive main effects and multiplicative interaction model) observed as choice of researchers with emphasis on main effects and interactions both (Aditi et al., 2023; Rao et al., 2020). The additive main effects and multiplicative interaction (AMMI) method and the GGE biplot are the two main statistical tools that have emerged to analyze GEI in multi environment trials. AMMI allocates the majority of GEI patterns in the first interaction principal component axis (IPCA), and most of the random errors are preserved in the final IPCAs. AMMI analysis has been observed as useful for exploring complex G $\times$ E interaction, improving selections and increasing experimental efficiency (Agahi, et al., 2020). Barley has occupied fourth ranked among the cereal crops after maize, rice and wheat, and cultivated at larger areas across the world (Mehraban et al., 2019). Barley is cultivated under higher productive areas and also suitably in marginal as well as subsistence environments (Dinsa et al., 2022). 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 for feed and food use (Akbarzai et al., 2022; Salim et al., 2024). Feed barley is a vital cereal grain that accounts for roughly 70% to 85% of global barley

production. It is highly valued for livestock nutrition due to its rich profile of starches, proteins, essential amino acids (like lysine), and fiber. Even today over 75% of total world barley production is consumed as feed. Asia is the next biggest user of feed barley with over half going to the Middle East, an area where feed barley use has significantly increased over the past 20 years. The analytic adaptability measures defined based on AMMI analysis had exhibited positive affiliation with IPC scores-based measures. Every measure relates to a different concept of stability and would be useful to barley researchers of this zone to select high and stable yield (Bocianowski et al., 2021). The prime objectives of this study were the application of different AMMI based measures and exploring the association analysis among different measures in identifying adapted genotypes.

2. MATERIALS AND METHODS

Twenty-five promising feed barley genotypes were evaluated at eight major locations of the country during cropping season November to April in 2023–2024 in field trials via a randomized complete block design with two replications as reflected in Table 1. Fields were prepared nicely and agronomic recommendations were followed to harvest a good crop. More over feed yield was analysed further to estimate the G $\times$ E interaction component by AMMI analysis. The description of widely used measures based on AMMI analysis was mentioned for Completeness (Table 2). The, greater the IPCA scores reflected the specific adaptation of genotype to certain locations. While the values approximate to zero were recommended for in general adaptations of the genotype. The AMMI stability was introduced based on the averages of the squared eigen vector (EV) values. AMGE and SIPC stability parameters of the AMMI model to describe the contribution of environments to G $\times$ E interaction. AMMI stability value (ASV) benefited from the first two IPCA of AMMI analysis. The Euclidean distance from the origin of significant interaction IPCA axes as D parameter, was also suggested. In recent studies, the agronomic concept of stability would be more preferred instead of the static concept of stability and with the use of first two IPCAs in stability analysis could benefit the dynamic concept of stability in the identification of the stable high-yielding genotypes as details were mentioned by Mohan et al. (2021).

3. RESULTS AND DISCUSSION

AMMI analysis had observed highly significant variations due to environments, G $\times$ E interactions, and genotypes as observed by Ahakpaz et al., 2021 (Table 3). This analysis revealed about 76.7% of the total sum of squares of variation for yield was due to environments, followed by 13.2% of G $\times$ E interactions, whereas genotypes accounted for a

Table 1: Details of widely used measures based on AMMI analysis

Zobel	EV1 and EVF	$EV = \sum_{n=1}^N \lambda_{in}^2 / n$
Sneller, et al	SIPC1and SIPCF	$SIPC = \sum_{n=1}^N \lambda_n^{0.5} \gamma_{in}$
Purchase	ASV	$ASV = [\frac{SSIPC\ 1}{SSIPC\ 2} (PCI)^2 + (PC2)^2]^{1/2}$
Annicchiarico	D	$D = \sqrt{\sum_{n=1}^N (\lambda_n \gamma_{in})^2}$
Rao and Prabhakaran	ASTAB	$ASTAB = \sum_{n=1}^n \lambda_n \gamma_{ni}^2$
Zali, et al	MASV	$MASV = \sqrt{\sum_{n=1}^{N-1} \frac{SSIPC_n}{SSIPC_{n+1}} (PC_n)^2 + (PC_{n+1})^2}$
Rao and Prabhakaran	I_i stability indexes	$I = \frac{Y_i}{\mu} + \alpha \frac{1/ASTAB_i}{(\sum_{n=1}^N ASTAB)/N}$
Ajay, et al	MASV1	$MASV1 = \sqrt{\sum_{n=1}^{N-1} (\frac{SSIPC_n}{SSIPC_{n+1}} * PC_n)^2 + (PC_{n+1})^2}$
	ASV1	$ASV1 = [(\frac{SSIPC\ 1}{SSIPC\ 2} * PCI)^2 + (PC2)^2]^{1/2}$
Harmonic mean of genotypic values	HMGV	HMGV= 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	$RPGV_{ij} = \sum GV_{ij} / \sum GV_j$
Harmonic mean of Relative performance of genotypic values across environments	HMRPGV	$HMRPGV_i = \text{Number of environments} / \sum_{j=1}^k \frac{1}{RPGV_{ij}}$
Geometric Adaptability Index	GAI	$GAI = \sqrt[n]{\prod_{k=1}^n \bar{X}_k}$

Table 2: Parentage details of feed barley genotypes along with environmental conditions

Code	Genotype	Parentage	Code	Environments	Latitude	Longitude	Mean sea level
G1	HUB 291	HUB113×KARAN-280	E1	Hisar	29° 10 'N	75° 46 'E	215.2
G2	DWRB 2303	DWR83/SMM83	E2	Durgapura	26° 51 'N	75° 47 'E	390
G3	RD 3093	HUB 113×BH 959	E3	Karnal	29° 43 'N	76° 58 'E	252
G4	RD2907	RD103/RD2518//RD2592	E4	Tabiji	26° 35 'N	74° 61 'E	508
G5	PL 954	BH946×DWRB137	E5	Ludhiana	30° 54 'N	75° 52 'E	247
G6	BH1059	DWRB 123/BH 885	E6	Pantnagar	29° 05 'N	79° 29 'E	236.54
G7	UPB 1123	DWRUB101/RD2552/BH976	E7	Modipuram	29° 43 'N	77° 42 'E	237
G8	BH1058	RD 2891/BH 885	E8	Dholpur			
G9	HUB 290	JYOTI×HUB113					
G10	GB1	RD2835/BH922					
G11	DWRB 2302	Alanda/5/Aths/4/Pro/TolI//Cer*2/ TolI/3/5106/6/Baca'S'/3/AC253// CI08887/CI05761/7/Ala nda-01/3/ Alanda//Lignee527/Arar					
G12	PL 956	PL426 X BH902					
G13	DWRB2319	Manal/6/P.STO/3/LBIRAN/ UNA80//LIGNEE640/4/ BLLU/5/PETUNIA 1					
G14	UPB 1122	RD2849/UPB1054					
G15	PL 955	BH946×RD2552					
G16	RD3096	NDB 1445×RD 2794					
G17	DWRB 2301	Carbo/Hamra/4/Rhn-08/3/ DeirAlla106//DL71/Strain205/6/ Rhn-03/Eldorado/5/ Rhn 03// Lignee527/NK1272/4/Lignee527/ Chn-01/3/Alanda					
G18	DWRB64						
G19	RD 3095	HUB 113×RD 2715					
G20	KB 2212	VLB 118/RD 2809					
G21	GB2	IBYT-HI-10/BH922					
G22	DWRB137	DWR28/DWRUB64					
G23	HUB113	KARAN280/C138					
G24	RD2899	RD2592/RD2035//RD2715					
G25	BH 946	BHMS22A/BH549//RD2552					

marginal share of 7.5% only. Interaction effects were further partitioned into six principal components, which augmented a total of more than 97% of the interactions' sum of square variations (Gerrano et al., 2020). AMMI1 explained a total variation of 39.9%, followed by 19.9% for AMMI2, 16.4% for AMMI3, AMMI4 accounted for 7.7% and followed by 6.8% respectively. The first two AMMI components in total showed 59.8% of the total variation indicated the two

AMMI components would fit and confirming the use of the AMMI model (Krishna et al., 2022). FR-tests at the 0.01 level diagnose AMMI4. The estimated sums of squares for G×E signal and noise were 84.7% and 15.3%, respectively. The early IPCs selectively capture signal, and late ones noise. Note that the sum of squares for G×E-signal was 1.51 times that for genotypes' main effects. Hence, narrow adaptations are important for this dataset. Even just IPC1

Table 3: AMMI analysis of feed barley genotypes

Source	df	MS	Level of significance	% of Total SS	% of G×E SS	Cumulative % SS by PCA's
Treatments	199	604.90	***	97.45		
Genotypes	24	384.19	***	7.46		
Environments	7	13534.07	***	76.70		
G×E	168	97.71	***	13.29		
IPC1	30	218.31	***		39.90	39.90
IPC2	28	116.59	***		19.89	59.78
IPC3	26	103.44	***		16.38	76.17
IPC4	24	52.47	***		7.67	83.84
IPC5	22	50.66	***		6.79	90.63
IPC6	20	52.38	***		6.38	97.01
Residual	18	27.29				
Error	200	15.75				
Total	399	309.58				

alone was 0.71 times the genotypes effects. Also note that G×E-noise was 0.27 times the genotype effects. Discarding noise improves accuracy, increases repeatability, simplifies conclusions, and accelerates progress (Kilic, 2014). The correlation coefficient between genotypes, means and IPC1 scores was 0.3621, whereas the correlation value between location means and IPC1 scores was 0.7899.

3.1. Performance of genotypes as per adaptability measures

The average yield of genotypes over the studied locations had significant variations as observed in ANOVA. More yields were achieved by G20, G15, and G06 whereas the least yielders were G10, G21 and G01 feed barley genotypes (Table 4). In plant breeding, standard deviation (SD) values can be used to assess the stability of genotypes across different environments. A lower SD value indicates a more stable genotype, as the data points are closer to the mean, implying consistent performance across environments (Assefa et al., 2021).

Consistent performance of G21, G02 and G04 had been pointed out by SD measure, as well the values of CV measures had also selected G21, G07 and G02 feed barley genotypes. In plant breeding, lower CV (Coefficient of Variation) values generally indicate greater genotype stability, meaning the genotype's performance is less variable across different environments. Conversely, higher CV values suggested lower stability, as the genotype's performance fluctuates more significantly. Some stability metrics, like Shukla's stability variance, also followed this principle, with lower values indicating greater stability.

The measure GAI (Geometric Adaptability Index) and genotype stability were related in plant breeding because

GAI was used to assess the stability of genotypes across different environments. A genotype's stability refers to its ability to maintain consistent performance (e.g., yield) under various conditions, while GAI quantifies this stability. Genotypes with high GAI values were generally considered more stable. The genotypic adaptability index had observed the higher values by G20, G06, and G15 genotypes. HMGV (Harmonic mean of genotypic values) values and genotype stability were related in that higher HMGV values generally indicate greater stability. HMGV was a measure that considered both the overall yield of a genotype and its consistency across different environments. In essence, a genotype with a high HMGV value was not only likely to produce well on average but also to maintain that performance consistently, even when faced with varying environmental condition. The relationship between RGPV (Regression genotype×Environment interaction) and genotype stability revolved around how a genotype's performance was consistent across different environments. A genotype with high RGPV values might not be as stable as one with lowered values, as higher RGPV suggested a stronger interaction between genotype and environment, leading to greater variability in performance across different settings.

Harmonic mean of genotypic values had seen maximum values for G06, G20 and G15, whereas the measure Relative performance of genotypic values had identified G20, G06 and G15 as higher yielders. The HMRPGV method calculated the average of the relative performance of a genotype across different environments, considering both the mean performance and its ranking. This approach helped to identify genotypes that consistently performed

Table 4: Performance of feed barley genotypes as per adaptability measures

	Mean	Stdev	CV	GAI	HMGV	RPGV	RPGV×Mean	HMRPGV	HMRPGV×Mean
G1	41.51	14.46	34.83	39.23	36.95	0.853	41.67	0.829	40.46
G2	46.35	12.50	26.97	44.88	43.46	0.974	47.57	0.950	46.39
G3	49.83	23.13	46.43	45.36	41.44	0.988	48.24	0.955	46.61
G4	46.32	12.92	27.89	44.80	43.35	0.966	47.15	0.954	46.60
G5	53.00	18.72	35.33	50.30	47.91	1.089	53.16	1.067	52.11
G6	55.79	17.99	32.25	53.55	51.61	1.149	56.12	1.145	55.92
G7	50.88	13.05	25.65	49.40	47.92	1.075	52.50	1.042	50.87
G8	52.38	15.39	29.38	50.36	48.36	1.097	53.55	1.062	51.88
G9	46.57	13.66	29.34	44.92	43.43	0.968	47.25	0.957	46.73
G10	39.15	15.61	39.87	36.48	34.07	0.798	38.97	0.766	37.39
G11	50.12	16.12	32.15	47.85	45.65	1.031	50.34	1.019	49.77
G12	45.18	21.94	48.57	40.53	36.20	0.889	43.40	0.845	41.24
G13	49.10	20.64	42.03	45.74	42.96	0.987	48.20	0.973	47.49
G14	44.62	16.79	37.63	42.28	40.41	0.909	44.38	0.903	44.09
G15	55.86	20.37	36.46	53.06	50.71	1.140	55.68	1.133	55.34
G16	53.19	22.70	42.68	49.49	46.42	1.068	52.17	1.052	51.37
G17	49.89	19.90	39.88	46.67	43.84	1.012	49.39	0.989	48.28
G18	46.38	17.58	37.91	43.74	41.49	0.943	46.05	0.931	45.47
G19	41.61	18.17	43.68	38.65	36.27	0.838	40.91	0.818	39.95
G20	57.53	23.61	41.03	53.99	51.17	1.159	56.61	1.154	56.36
G21	41.33	10.15	24.56	40.33	39.42	0.871	42.54	0.858	41.88
G22	53.86	20.21	37.53	50.88	48.27	1.101	53.76	1.080	52.74
G23	48.25	16.07	33.30	45.96	43.81	0.995	48.60	0.975	47.60
G24	51.16	19.15	37.42	48.07	45.16	1.045	51.03	1.014	49.50
G25	50.90	15.90	31.23	48.77	46.75	1.055	51.49	1.035	50.55

well, even when the environmental conditions changed.

HMRPGV (Harmonic mean of relative performance of genotypic values) was a method used to assess the stability and adaptability of different genotypes across various environments. Essentially, genotypes with higher HMRPGV values were considered more stable and adaptable, meaning they performed consistently well across a range of conditions. The HMRPGV method combined information about the mean genotypic value (HMGV) and the relative performance of genotypic values (RPGV) to provide a comprehensive measure of stability and adaptability.

3.2. Behavior of genotypes based on Interaction principal components

In genotype by environment interaction (GEI) studies, the stability of a genotype was not directly determined by the sign (negative, positive) of the Interaction Principal

Component (IPCA) scores, but rather by the magnitude or absolute value of these scores (Islam et al., 2020). A genotype with larger IPCA scores, whether positive or negative, was generally considered less stable, as it was more specifically adapted to certain environments and less stable across different environments. Genotypes with smaller IPCA scores, or scores closer to zero, tended to be more stable across a wider range of environments.

The stability or adaptability of genotypes had been judged by values of IPCA's in the AMMI analysis. G20 had expressed higher yield values followed by G15 and G6, while the lowest values of IPCA1 were exhibited by G24, G18 and G1, whereas genotypes G12, G10 and G11 showed the specific adaptation behaviour as evident from the lower values of IPCA2 (Table 5). Feed barley genotypes G1, G4, and G22 maintained the lower values of IPCA3 measure. G23, G20 and G16 had achieved the least values for IPCA4 measure. SIPC2 measure consider the IPCA1 and IPCA2

Table 5: Principal components analysis of feed barley genotypes

	Average	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	SIPC1	SIPC2	SIPC3	SIPC5
G1	41.51	-0.2747	-2.4167	0.1240	-1.1949	1.2296	-1.4067	-0.275	-2.691	-2.567	-2.533
G2	46.35	-1.9716	-1.1969	2.1751	1.0258	-0.3821	0.0657	-1.972	-3.169	-0.993	-0.350
G3	49.83	1.1483	2.5828	1.4777	-0.8284	0.7387	-0.0868	1.148	3.731	5.209	5.119
G4	46.32	-1.4397	-0.2739	-0.1596	1.6659	-0.6521	-1.0206	-1.440	-1.714	-1.873	-0.859
G5	53.00	0.5024	0.6272	-2.6575	-0.5931	-0.1709	-1.0414	0.502	1.130	-1.528	-2.292
G6	55.79	0.8786	-0.3358	0.7563	0.6367	0.0234	-0.7618	0.879	0.543	1.299	1.959
G7	50.88	-3.0366	0.9331	-0.2062	-1.1503	0.4653	0.0965	-3.037	-2.103	-2.310	-2.995
G8	52.38	-2.5461	1.1471	1.2155	-0.8908	-1.5048	-0.8992	-2.546	-1.399	-0.184	-2.579
G9	46.57	-0.7165	-0.9148	-1.4794	-0.1420	1.5546	0.3044	-0.716	-1.631	-3.111	-1.698
G10	39.15	-1.0771	0.1451	-1.6999	1.4107	-0.1443	2.4472	-1.077	-0.932	-2.632	-1.366
G11	50.12	-0.4202	-0.2301	1.0702	-0.9282	1.5195	-0.9042	-0.420	-0.650	0.420	1.011
G12	45.18	1.8487	0.0357	0.8461	0.4262	0.5180	-0.3609	1.849	1.884	2.730	3.675
G13	49.10	1.4039	-0.3229	0.3035	-0.5220	-0.0032	2.0725	1.404	1.081	1.385	0.859
G14	44.62	0.3491	-0.7234	-0.8536	-0.6063	-0.7579	0.1929	0.349	-0.374	-1.228	-2.592
G15	55.86	1.6526	0.4847	-0.2305	1.5800	-0.1859	-1.3338	1.653	2.137	1.907	3.301
G16	53.19	2.2951	0.8285	0.5168	-0.1115	0.8442	0.3540	2.295	3.124	3.640	4.373
G17	49.89	1.2242	-1.4376	1.3444	-1.1676	-0.2037	1.4230	1.224	-0.213	1.131	-0.240
G18	46.38	-0.1057	0.9280	1.0437	1.7158	1.4756	0.9544	-0.106	0.822	1.866	5.057
G19	41.61	0.4760	-1.1842	-1.3504	-1.7756	-1.4101	0.5046	0.476	-0.708	-2.059	-5.244
G20	57.53	2.1680	1.3261	0.1683	0.0872	-1.9012	-0.1929	2.168	3.494	3.662	1.848
G21	41.33	-1.3984	-2.3117	-0.6640	1.2770	0.0366	-0.0490	-1.398	-3.710	-4.374	-3.061
G22	53.86	2.1056	-1.7843	-0.1680	0.3158	-0.4959	-0.5734	2.106	0.321	0.153	-0.027
G23	48.25	-1.5462	0.5668	1.3107	0.0342	-1.7251	0.4092	-1.546	-0.979	0.331	-1.360
G24	51.16	0.0807	1.9532	-2.2746	0.5162	0.0949	-0.5213	0.081	2.034	-0.241	0.370
G25	50.90	-1.6004	1.5738	-0.6087	-0.7805	1.0368	0.3277	-1.600	-0.027	-0.635	-0.379

IPCA, principal component of interaction; ASV: AMMI stability value; MASV: Modified AMMI stability value

values simultaneously and favoured the G25, G17 and G22 genotypes for the considered locations. However, all the five measures IPCA1 to IPCA5 had been utilized by measure SIPC5 and final values of this measure pointed out for G22, G17 and G2 feed barley genotypes.

In recent studies, agronomic concept of stability would be more preferred instead of static concept of stability (Karimizadeh, et al., 2016). Using first two IPCAs in stability analysis could benefits dynamic concept of stability in identification of the stable high yielder genotypes. Measure ASV based on 59.8% had favoured the G11, G14 and G18 whereas MASV measures had exploited the total of variation of the GxE interactions up to extent of 97% had identified G06, G14 and G13 feed barley genotypes. ASV1 recommended (G11, G18, G14) as of stable performance and unsuitable were G07, G08 (Table 6). The two IPCAs

have different values and meanings and the ASV parameter using the Pythagoras theorem and to get estimated values between IPCA1 and IPCA2 scores to produce a balanced measure between the two IPCA scores (Purchase, 1997). Also, MASV1 measure of this investigation used advantages of cross validation due to computation from first two IPCAs. Results put forward by ASV measure have many similarities with the other AMMI stability parameters which calculated from the first two IPCAs scores (Kumar et al., 2021). MASV1 recommended (G14, G06, G13) as of stable performance and unsuitable were G2, G08.

3.3. Performance of feed barley genotypes as per AMMI-based measures

AMMI-derived measures based on the use of significant IPCAs were calculated as EV1, ASTAB1, SIPC1, D1 measures (only first significant IPCA), while ASV, EV2,

Table 6: Estimates of GxE interaction based on AMMI analysis for feed barley genotypes

	ASV	MASV	EV1	EV2	EV3	EV5	D1	D2	D3	D5	ASV1	MASV1
G1	2.45	4.612	0.001	0.052	0.034	0.038	2.47	18.43	18.46	21.02	2.48	4.826
G2	3.04	5.325	0.048	0.037	0.055	0.040	17.74	19.91	25.33	26.15	4.13	6.943
G3	3.05	5.182	0.016	0.067	0.058	0.042	10.33	22.09	24.52	25.37	3.46	6.057
G4	2.06	3.498	0.026	0.013	0.009	0.024	12.95	13.12	13.17	16.91	2.90	4.115
G5	0.95	5.041	0.003	0.005	0.049	0.031	4.52	6.55	20.23	20.56	1.19	6.573
G6	1.29	2.244	0.010	0.006	0.008	0.007	7.90	8.30	9.93	10.63	1.79	2.841
G7	4.40	4.882	0.114	0.065	0.043	0.035	27.32	28.21	28.25	29.19	6.16	6.556
G8	3.78	5.265	0.080	0.052	0.044	0.044	22.91	24.49	26.01	27.93	5.24	6.709
G9	1.37	3.856	0.006	0.010	0.021	0.027	6.45	9.45	14.24	16.86	1.70	4.647
G10	1.53	4.659	0.014	0.007	0.023	0.025	9.69	9.75	15.65	17.78	2.17	5.600
G11	0.64	3.388	0.002	0.002	0.008	0.024	3.78	4.16	8.76	13.58	0.87	3.862
G12	2.62	3.190	0.042	0.021	0.019	0.014	16.63	16.63	17.71	18.14	3.71	4.342
G13	2.01	3.058	0.024	0.013	0.009	0.007	12.63	12.86	13.05	13.41	2.84	3.690
G14	0.88	2.386	0.002	0.005	0.008	0.010	3.14	6.31	8.81	10.48	1.01	2.817
G15	2.39	3.652	0.034	0.019	0.013	0.022	14.87	15.31	15.40	18.08	3.35	4.405
G16	3.35	3.814	0.065	0.039	0.027	0.021	20.65	21.58	21.89	22.44	4.68	5.104
G17	2.25	4.274	0.019	0.027	0.030	0.026	11.01	15.47	18.25	19.57	2.85	5.139
G18	0.94	4.125	0.000	0.008	0.012	0.037	0.95	7.08	10.32	16.85	0.95	4.526
G19	1.36	4.511	0.003	0.014	0.021	0.042	4.28	9.92	13.89	19.27	1.52	5.118
G20	3.34	4.574	0.058	0.044	0.030	0.040	19.50	21.93	21.96	24.56	4.55	5.584
G21	3.04	4.540	0.024	0.059	0.042	0.034	12.58	21.53	22.06	23.33	3.64	5.221
G22	3.48	4.133	0.055	0.055	0.037	0.024	18.94	23.25	23.28	23.54	4.59	5.192
G23	2.26	4.148	0.030	0.018	0.023	0.031	13.91	14.55	17.35	20.01	3.15	5.146
G24	1.96	5.054	0.000	0.033	0.056	0.035	0.73	14.78	22.06	22.28	1.96	6.256
G25	2.76	3.925	0.032	0.037	0.027	0.026	14.40	18.68	19.18	20.63	3.58	4.720

SIPC: Sum of the value of the IPC scores; D: Parameter of annicchiarico

ASTAB2, SIPC2, D2 considered IPCA1 and IPCA2 both, measures EV3, ASTAB3, SIPC3 and D3 used three IPCAs, EV5, ASTAB5, SIPC5 and D5 (based on five IPCAs), whereas measures EV7, ASTAB7, SIPC7 and D7 utilized all significant IPCAs.

Explained variation of G×E interaction accounted by each of IPCA exploited by defined measures, as type-1 measures benefited 39.9%, type-2 measures utilized 59.8%, type 3 measures used up to 76.2%, type 5 measures benefited up to 90.6% as observed from table (Table 7). This justified the use of AMMI-derived measures based on the larger numbers of IPCAs resulted in the most usage of G×E interaction variations. Minimum and maximum values of EV1 observed for (G24, G18, G1) and (G7, G8) while corresponding to D1 were (G24, G18, G01) and (G7, G8) while the absolute values of ASTAB1 for (G24, G18,

G01) and (G07, G08) and for I1 were (G10, G21, G01) and (G20, G15), genotypes (Tables 4 and 5). Genotypes (G11, G5, G14) pointed by EV2 as desirable and at the same time undesirable genotypes (G7, G) the values of D2 had favoured genotypes (G11, G14, G5) and (G7, G8), and of ASTAB2 were (G14, G17, G19) and (G20, G21) (Tables 5 and 6). I2 were (G10, G21, G02) and (G20, G15) (Tables 5 and 6). Minimum values EV3 preferred G06, G14, G11 as well of unstable performance of G3, G24 while D3 pointed towards G11, G14, G06 and G07, G08 whereas the value of ASTAB3 measure had considered the suitability of G24, G11, G23 and G3, G21 (Table 5). Least values of I3 expressed by G10, G21 and G01 genotypes. G06, G13 and G14 preferred by least values EV5 and maximum values found for G08, G19, measure SIPC5 identified G22, G17, G02 whereas D5 considered G14, G06, G13 as suitable

Table 7: Further AMMI analysis-based estimates for G×E interaction for feed barley genotypes

	ASTAB1	ASTAB2	ASTAB3	ASTAB5	I1	I2	I3	I4
G1	-22.23	-160.31	-153.88	-155.23	0.8504	0.8503	0.8502	0.8501
G2	-159.56	-227.95	-115.14	-91.50	0.9492	0.9492	0.9492	0.9492
G3	92.93	240.50	317.13	312.40	1.0204	1.0204	1.0204	1.0204
G4	-116.51	-132.16	-140.44	-103.09	0.9487	0.9487	0.9487	0.9487
G5	40.66	76.49	-61.32	-88.07	1.0823	1.0833	1.0849	1.0846
G6	71.10	51.92	91.14	114.52	1.1428	1.1427	1.1427	1.1427
G7	-245.74	-192.43	-203.12	-228.41	1.0419	1.0419	1.0419	1.0419
G8	-206.05	-140.52	-77.48	-159.33	1.0727	1.0727	1.0727	1.0727
G9	-57.98	-110.25	-186.97	-140.11	0.9538	0.9538	0.9537	0.9537
G10	-87.17	-78.88	-167.04	-121.80	0.8019	0.8018	0.8018	0.8018
G11	-34.00	-47.15	8.35	26.14	1.0289	1.0280	1.0243	1.0270
G12	149.61	151.65	195.53	227.94	0.9252	0.9252	0.9252	0.9252
G13	113.62	95.17	110.91	92.28	1.0057	1.0056	1.0056	1.0056
G14	28.25	-13.08	-57.35	-104.16	0.9127	0.9131	0.9142	0.9135
G15	133.74	161.44	149.49	199.35	1.1441	1.1440	1.1440	1.1440
G16	185.73	233.07	259.87	284.10	1.0892	1.0892	1.0892	1.0892
G17	99.07	16.94	86.66	38.42	1.0219	1.0219	1.0218	1.0218
G18	-8.55	44.47	98.60	208.74	0.9485	0.9490	0.9499	0.9495
G19	38.52	-29.14	-99.17	-209.26	0.8518	0.8519	0.8523	0.8521
G20	175.45	251.22	259.94	199.57	1.1782	1.1781	1.1781	1.1781
G21	-113.17	-245.25	-279.69	-233.15	0.8465	0.8465	0.8465	0.8465
G22	170.40	68.45	59.74	54.39	1.1032	1.1031	1.1032	1.1031
G23	-125.13	-92.75	-24.77	-81.15	0.9882	0.9882	0.9883	0.9881
G24	6.53	118.13	0.17	21.65	1.0520	1.0505	1.1095	1.0488
G25	-129.52	-39.59	-71.16	-64.25	1.0425	1.0425	1.0425	1.0424

and G7, G8 as unsuitable ones; ASTAB5 selected G24, G11, G17 as suitable and G3, G16 as unsuitable genotypes.

ASTAB had considered a statistical measure used in multi-location trials to assess the stability of genotypes across different environments, according to a study on multi-location trials. It helped researchers identify genotypes that performed consistently well across various locations, years, or other environmental factors. By analyzing the genotype-by-environment interaction (GEI), ASTAB could help breeders to select genotypes that were not only high-yielding but also stable and adaptable to a range of conditions. A genotype with a lower ASTAB value was considered more stable because it exhibited consistent performance regardless of the environment. Conversely, a genotype with a higher ASTAB value was less stable, meaning its performance varies significantly across different environments. In genotype stability analysis, negative ASTAB values

generally indicated greater stability, while positive values might suggest less stable genotypes. Absolute values of stability measures were often used to rank genotypes based on their overall stability across different environments, with lower absolute values indicating greater stability. ASTAB1 had highlighted the suitability of G24, G18 and G1 whereas the lower values of ASTAB2 had expressed by G14, G19 and G17 while the ASTAB3 had favoured G24, G11 and G5, and lastly the values of ASTAB5 had pointed out G24, G11 and G17 feed barley genotypes.

The stability index was a measure that assessed the consistency and reliability of a genotype's performance across different environments. This index helped to identify genotypes that exhibited stable and consistent yields or other traits across various locations, years, or other environmental condition. This index was a specific type of stability statistic that measures the deviation of a genotype's performance

from its mean performance across all environments. A lower value generally indicated greater stability, as the genotype's performance was more consistent across the different environments. The index was often used in conjunction with other stability measures and performance metrics to provided a comprehensive assessment of a genotype's suitability for a range of condition The least values of I1, I2, I3, I4 had been expressed the feed barley genotypes as

of G10, G21 and G01 only in this study (Table 7).

3.4. Clustering pattern of measures and genotypes by biplot analysis

First two significant principal components had accounted for 63.3% of variation among the evaluated genotypes and studied measures for the current study with 33.4% and 29.9% respective share Kumar et al., 2021 (Table 8).

Table 8: Loadings of AMMI-based measures as per principal components

Measure	Principal component 1	Principal component 2	Genotype	Principal component 1	Principal component 2
Mean	0.261	-0.048	G1	-0.266	-0.033
IPC1	0.215	0.154	G2	-0.154	-0.285
IPC2	0.164	-0.057	G3	0.282	-0.129
IPC3	0.089	-0.051	G4	-0.160	0.064
IPC4	0.005	0.051	G5	0.018	0.035
IPC5	-0.018	0.079	G6	0.172	0.296
IPC6	-0.057	0.053	G7	-0.080	-0.483
ASV1	0.100	-0.271	G8	-0.006	-0.417
MASV1	-0.005	-0.270	G9	-0.199	0.118
ASV	0.091	-0.283	G10	-0.306	0.084
MASV	-0.040	-0.248	G11	-0.034	0.254
SIPC1	0.215	0.154	G 12	0.130	0.124
SIPC2	0.270	0.081	G 13	0.087	0.216
SIPC3	0.277	0.042	G 14	-0.157	0.327
SIPC5	0.233	0.084	G 15	0.281	0.097
D1	0.105	-0.228	G 16	0.346	-0.033
D2	0.083	-0.285	G 17	0.057	0.035
D3	0.059	-0.307	G 18	-0.004	0.233
D5	0.034	-0.314	G 19	-0.251	0.095
ASTAB1	0.215	0.154	G 20	0.397	-0.130
ASTAB2	0.269	0.103	G 21	-0.330	-0.171
ASTAB3	0.282	0.074	G 22	0.195	-0.125
ASTAB5	0.267	0.097	G 23	-0.076	-0.049
I1	0.261	-0.048	G 24	0.071	-0.039
I2	0.261	-0.048	G 25	-0.012	-0.082
I3	0.259	-0.049			
I4	0.261	-0.048			
EV1	0.093	-0.248			
EV2	0.054	-0.272			
EV3	0.011	-0.251			
EV5	-0.057	-0.215			
% share of measures (Total=63.32%)	33.38%	29.95%			

Measures ASTAB3, SIPC3, SIPC2, ASTAB5 along with G20, G16, G21 genotypes had contributed more in first principal component whereas D5, D3, D2, ASV were of major share in second component. In terms of evaluated genotypes share of G 8, G7, G14 was significant as reflected by Khalid et al., 2023.

Biplot analysis based on first two significant principal components helped to visualize the relationships among yield of feed barley and measures (Mohan et al, 2021). In total, PC1 and PC2 accounted for more than 63.3% total

variation among measures (Figure 1). Measures MASV1, MASV had clubbed with EV5 values in first smaller cluster while next cluster consisted of D1, D2, D3, D5, EV1, EV2, EV3, EV5, ASV and ASV1 measures placed near with the cluster of IPC2, IPC3, Mean, I1, I2, I3 and I4 values. Large cluster had joined ASTAB1, ASTAB2, ASTAB3, ASTAB5 IPC1, SIPC1, SIPC2, SIPC3 SIPC4, SIPC5 along with IPCA1 measures. The fifth, smaller cluster had placed only IPC4, IPC5 and IPC6 measures.

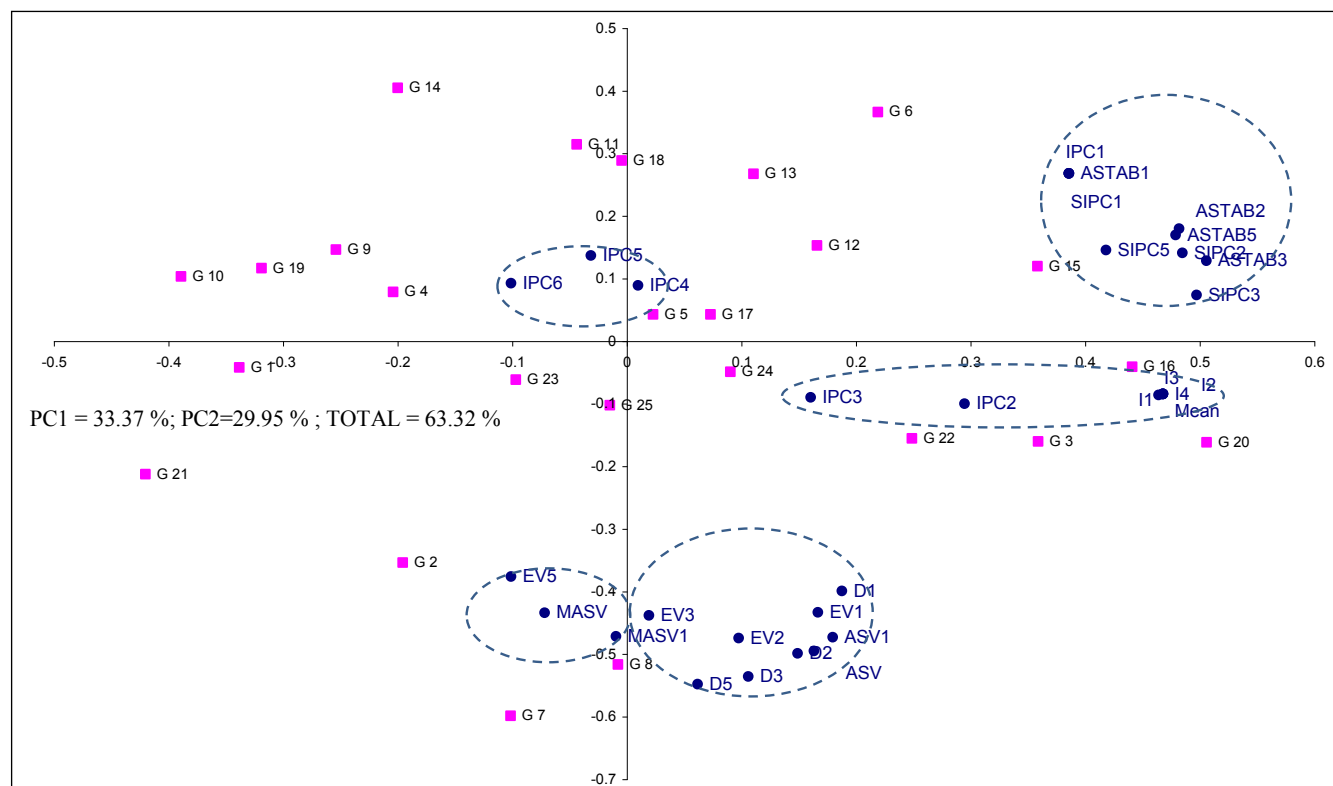


Figure 1: Clustering pattern of adaptability measures and feed barley genotypes

4. CONCLUSION

AMMI analysis had showed a significant difference E, G, and GEI for during field evaluation of twenty five feed barley genotypes across the eight test environments in the country. The significant interaction effects were further divided into six IPCAs, which in turn suggested that tested genotype responded differently under environmental conditions. At the same time, first four components of the interaction (IPCA) had been accounted for much of the variation in grain yield, they would be sufficient to identify the better genotypes.

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6. REFERENCE

- Aditi, Rani, S., Khandelwal, V., Devvart, Vaish, A., 2023. Proposed new stability indices using the AMMI model and GGE biplot approach to assess G×E interaction. International Journal Statistics Applied Mathematics 8(3), 111–117. Available from: <https://api.semanticscholar.org/CorpusID:260798220>.
- Ahakupaz, F., Abdi, H., Neyestani, E., Hesami, A., Mohammadi, B., Nader, Mahmoudi, K., Abedi-Asl, G., Jazayeri, Noshabadi, M.R., Ahakupaz, F., Alipour, H., 2021. Genotype-by-environment interaction analysis for grain yield of barley genotypes under dry land conditions and the role of monthly rainfall.

- Agricultural Water Management 245, 10665. DOI: <https://doi.org/10.1016/j.heliyon.2024.e38131>.
- Akbarzai, D.K., Akbari, G.R., Mohammadi, L., Saif, M.N., Farhang, A., 2022. AMMI analysis of yield stability and adaptability in barley: A case study of Afghanistan. *Journal of Environmental and Agricultural Sciences* 24(1and2), 18–25. DOI: <https://doi.org/10.13140/RG.2.2.36655.41123>.
- Assefa, A., Girmay, G., Alemayehu, T., Lakew, A., 2021. Performance evaluation and stability analysis of malt barley (*Hordeum vulgare* L.) varieties for yield and quality traits in Eastern Amhara, Ethiopia. *CABI Agriculture Biosciences* 2, 31. DOI: <https://doi.org/10.1186/s43170-021-00051-w>.
- Bocianowski, J., Tratwal, A., Nowosad, K., 2021. Genotype by environment interaction for main winter triticale varieties characteristics at two levels of technology using the additive main effects and multiplicative interaction model. *Euphytica* 217, 26. DOI: <https://doi.org/10.1007/s10681-020-02756-x>.
- Dinsa, G.F., Tadesse, E., Sebsibe, H., Tadesse, K., 2022. Selection index and stability analysis for malting barley variety release in Ethiopia. *Journal Crop Science Biotechnology* 25, 243–252. DOI: <https://doi.org/10.1007/s12892-021-00127-z>.
- Gerrano, A.S., Rensburg, W.S.J.V., Mathew, I., Shayanowako, A.I.T., Bairu, M.W., Venter, S.L., Swart, W., Mofokeng, A., Mellem, J., Labuschagne, M., 2020. Genotype and genotype×environment interaction effects on the grain yield performance of cowpea genotypes in a dry land farming system in South Africa. *Euphytica* 216, 80. DOI: <https://doi.org/10.1007/s10681-020-02611-z>.
- Islam, S.S., Anothai, J., Nualsri, C., Soonsuwon, W., 2020. Analysis of genotype-environment interaction and yield stability of Thai upland rice (*Oryza sativa* L.) genotypes using AMMI model. *Australian Journal Crop Science* 14, 362–370. DOI: <https://doi.org/10.21475/ajcs.20.14.02.p1847>.
- Jedzura, S., Bocianowski, J., Matysik, P., 2023. The AMMI model application to analyze the genotype–environmental interaction of spring wheat grain yield for breeding program purposes. *Cereal Research Communications* 51, 197–205. DOI: <https://doi.org/10.1007/s42976-022-00296-9>.
- Karimizadeh, R., Ali, A., Chinipardaz, R., Sofalian, O., Ghaffari, A., 2016. Determining yield stability and model selection by the AMMI method in rain-fed durum wheat genotypes Turkish. *Journal Field Crops* 21(2), 174–183. DOI: <https://doi.org/10.17557/tjfc.17390>.
- Karimizadeh, R., Pezeshkpour, P., Mirzaee, A., Barzali, M., Sharifi, P., Safari, Motlagh, M.R., 2023. Stability analysis for seed yield of chickpea (*Cicer arietinum* L.) genotypes by experimental and biological approaches. *Vavilovskii Zhurnal Genetiki i Seleksii*=Vavilov Journal of Genetics and Breeding 27(2), 135–145. DOI: 10.18699/VJGB-23-19.
- Khalid, A., Hameed, A., Tahir, M.F., 2023. Estimation of genetic divergence in wheat genotypes based on agro-morphological traits through agglomerative hierarchical clustering and principal component analysis. *Cereal Research Communications* 51, 217–224. DOI: <https://doi.org/10.1007/s42976-022-00287-w>.
- Kilic, H., 2014. Additive main effect and multiplicative interactions (AMMI) analysis of grain yield in barley genotypes across environments. *Journal Agricultural Science* 20, 337–344. DOI: https://doi.org/10.1501/Tarimbil_0000001292.
- Krishna, S.K., Chaudhary, K.R., Kumar, M., 2022. Stability analysis for assessment of yield performance and adaptability of selected mango (*Mangifera indica* L.) genotypes under multi location trials in India. *International Journal of Bio-resource and Stress Management* 13(5), 454–462. DOI: <https://doi.org/10.23910/1.2022.2870>.
- Kumar, M.N., Ramya, V., Kumar, C.S., Raju, T., Kumar, N.S., Seshu, G., Sathish, G., Bhadr, D., Ramana, M.V., 2021. Identification of pigeonpea genotypes with wider adaptability to rainfed environments through AMMI and GGE biplot analyses. *Indian Journal of Genetics and Plant Breeding* 81(1), 63–73. DOI: <https://doi.org/10.31742/IJGPB.81.1.7>.
- Lee, S.Y., Lee, H.S., Lee, C.M., Ha, S.K., Park, H.M., Lee, S.M., Kwon, Y., Jeung, J.U., Mo, Y., 2023. Multi-environment trials and stability analysis for yield-related traits of commercial rice cultivars. *Agriculture* 13, 256. DOI: <https://doi.org/10.3390/agriculture13020256>.
- Mehraban, R.A., Hossein-Pour, T., Koohkan, E., Ghasemi, S., Moradkhani, H., Siddique, K.H., 2019. Integrating different stability models to investigate genotype×environment interactions and identify stable and high-yielding barley genotypes. *Euphytica* 215, 63. DOI: https://doi.org/10.1007/s10681-019-2386-5?urlappend=%3Futm_source%3Dresearchgate.net%26utm_medium%3Darticle.
- Mohan, Y.C., Krishna, L., Sreedhar, S., Chandra, B.S., Madhukar, P., Sridhar, V., Kylash, K.S., Singh, T.V.J., Sudhishna, E., Kumar, E.S., Reddy, P.R.R., 2025. Delineation of genotype×environment interaction for identification of stable rice hybrids for Telangana State, India. *Plant Archives* 25(1), 261–268. DOI: <https://doi.org/10.51470/plantarchives.2025.v25.no.1.040>.

- Mohan, Y.C., Krishna, L., Sreedhar, S., Chandra, B.S., Raju, C.D., Madhukar, P., Ramana, M.V., 2021. Stability analysis of rice hybrids for grain yield in Telangana through AMMI and GGE Bi-plot model. International Journal. Bio-resource Stress Management 12(6), 687–695. DOI: <https://doi.org/10.23910/1.2021.2575>.
- PourAboughadareh, A., Ali, B.K.S., Mehdi, J., Akbar, M., Ahmad, G., Kamal, S.H., Hassan, Z., Poodineh, Omid, Masoome, K., 2022. Dissection of genotypebyenvironment interaction and yield stability analysis in barley using AMMI model and stability statistics. Bulletin of the National Research Centre 46, 19. DOI: <https://doi.org/10.1186/s42269-022-00703-5>.
- Rao, P.J.M., Kishore, N.S., Sandeep, S., Neelima, G., Rao, P.M., Das, D.M., Saritha, A., 2020. Evaluation of performance and yield stability analysis based on AMMI and GGE biplot in promising pigeonpea [*Cajanus cajan* (L.) millspaugh genotypes. Legume Research 1–7. DOI: 10.18805/LR-4299.
- Roy, D.G., Pandey, A., Barman, I.D., Ahmed, M., Bulbul, 2024. Designing an index for multi-location yield stability analysis involving univariate and multivariate methods in rice (*Oryza sativa* L.). Brazilian Archives Biology Technology, 67. DOI: <https://doi.org/10.1590/1678-4324-2024230303>.
- Rahmati, S., Azizi-Nezhad, R., Pour-Aboughadareh, A., Etminan, A., Shooshtari, L., 2024. Analysis of genotype-by-environment interaction effect in barley genotypes using AMMI and GGE biplot methods. Heliyon 10(18), e38131, ISSN 2405-8440. DOI: <https://doi.org/10.1016/j.Heliyon.2024.e38131>.
- Zali, H., Farshadfar, E., Sabaghpour, S.H., Karimizadeh, R., 2012. Evaluation of genotype×environment interaction in chickpea using measures of stability from AMMI Model. Annals Biological Research 3(7), 3126–3136. Available from: https://www.researchgate.net/publication/259391764_Evaluation_of_genotype_environment_interaction_in_chickpea_using_measures_of_stability_from_AMMI_model.