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ADAPTABILITY INDICES BASED ON AMMI ANALYSIS OF BARLEY GENOTYPES EVALUATED UNDER MULTI LOCATION TRIALS

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ABSTRACT

AMMI analysis had observed the highly significant effects due environments, genotypes and genotypes $\times$ environments interactions effects during field evaluation of eighteen genotypes at thirteen locations during 2024-25 cropping season. The share augmented by environment and G $\times$ E interactions effects were to the tune of 44.7% and 21.9% respectively, while genotypes had contributed only 7.9% of the total variance. The first principal component of interaction effects made up of 36 % followed by the 21.5%, 11% and 9.8% of second, third and fourth components towards the interaction effects. Simultaneous consideration of yield and adaptability measures in YSI, genotypes of choice were G4, G18, G15 while G8, G1, G3 whereas G18, G3, G4 by ASTAB, ASV and MASV measures. Genotypes G15, G03, G01 would be suitable as per least values of WAAS while AVAMGE measure had selected G03, G15, G18 while lower values of DA had expressed by G3, G18, G15 and genotypes favoured by EV measure were G04, G06, G18. AMMI1 plot had observed genotypes G1, G15, G11, G5 exhibit greater stability with minimal interaction effects as located near the centre region of the IPCA1 axis. Which won where pattern of genotypes verses environments plot had found the short arrow for E12, E7 whereas long arrows were expressed of E4, E8, E13, E6 in the study.

Key words: ASTAB, ASV, MASV, AVAMGE, WAAS, SI, SIPC, ZA,D

Introduction

Good number of statistical techniques have been planned recently to take advantage of the positive G $\times$ E interaction to assist the breeding program's choices of cultivars and recommendations for the set of target environments (Pereira *et al.*, 2025). To maximize yield performance and control phenotypic expression, plant breeders must choose certain genotypes that are stable in or adaptable to a given environment (Lopez *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). AMMI allocates the majority of G $\times$ E interactions patterns in the first interaction principal

component axis (IPCA), and most of the random errors are preserved in the final IPCAs (Ashwini *et al.*, 2021). AMMI analysis has been observed as useful for exploring complex G $\times$ E interaction, improving selections and increasing experimental efficiency (Agahi, *et al.*, 2020, Verma *et al.*, 2021). For choosing an adaptable genotype with high yields, number of selection indices was created such as selection index, parametric and non-parametric genotype selection index, and others (Koundinya *et al.*, 2021). The relative performance of genetic values (RPVG), harmonic mean of the relative performance of genetic values (HMRPGC), and harmonic mean of genetic values (HMGV) predicted values, which have been used to interpret the genotypic stability and adaptability of perennial plants as alternatives to the simulation of selection by yield, stability, and adaptability (Nataraj *et al.*, 2021; Pour-Aboughadareh *et al.*, 2022).

These indices direct the simultaneous choice of both stability and high yield using information from yield and stability parameters (Daba *et al.*, 2023). It is possible to argue that selection techniques that use yield as the only criterion are preferable to those that combine stability and adaptability into a single statistic (Salim *et al.*, 2024).

Method and Materials

The adaptability of the genotypes for several places or a specific genotype for different environmental circumstances might be determined with the help of estimation and proper utilization the $G \times E$ in METs (Singh *et al.*, 2025). In changing environmental vagaries, the selection of locations plays a crucial role in genotypes' environment interaction that influences crop production. In assessing the adaptability of genotypes ASI, ASV, ASTAB, AVAMGE, DA, DZ, EV, FA, MASI, MASV, SIPC, Za, HMGV, RPGV, and HMRPG, were computed by Metan software (Olivoto *et al.*, 2020) and further the use of AMMI plots derived from additive main effects and multiplicative interaction and the genotype plus genotype–environment interaction was studied to compare their efficiency for identification of genotypes. The details of genotypes along with locations for the present study (Table 1) and several adaptability measures based on AMMI analysis were mentioned below for completeness.

Sums of the averages of squared eigenvector values (EV), Zobel (1994).

$$EV = \sum_{n=1}^{N'} \frac{\gamma_{in}^2}{N'}$$

Annicchiarico D parameter values (Da), Annicchiarico (1997).

$$D_a = \sqrt{\sum_{n=1}^{N'} (\lambda_n \gamma_{in})^2}$$

Sums of the absolute value of the IPC scores (SIPC), Sneller *et al.*, (1997).

$$SIPC = \sum_{n=1}^{N'} |\lambda_n^{0.5} \gamma_{in}|$$

Zhang's parameter (Dz), Zhang's *et al.*, (1998).

$$D_z = \sqrt{\sum_{n=1}^{N'} \gamma_{in}^2}$$

AMMI stability value(ASV), Purchase *et al.*, (2000).

$$ASV_i = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1)^2 + (IPCA2)^2}$$

Stability measure based on fitted AMMI model (FA), Raju (2002).

$$FA = \sum_{n=1}^{N'} \lambda_n^2 \gamma_{in}^2$$

AMMI based stability parameter (ASTAB), Rao and Prabhakaran (2005).

$$ASTAB = \sum_{n=1}^{N'} \lambda_n \gamma_{in}^2$$

Harmonic mean of genotypic values (HMGV), Resende (2007).

$$HMGV_i = \frac{E}{\sum_{j=1}^E \frac{1}{Gv_{ij}}}$$

Table 1: Parentage and locations details of the study.

Genotype	Code	Parentage	Location	Latitude	Longitude	Mean Sea Level
DWRB-2311	AVT-MB-1	DWRB101/DWRB123	Bawal	28° 10' N	76° 50' E	266
DWRB-182	AVT-MB-2	DWRUB52/DWRB78	Bathinda	30° 09' N	74° 55' E	211
DWRB-2307	AVT-MB-3	DWRB101/DWRUB52	Bulandshahr	28° 40' N	77° 84' E	195
DWRB-238	AVT-MB-4	DWRB101/DWR28	Durgapura	26° 51' N	75° 47' E	390
RD-2849	AVT-MB-5	DWRUB52/PL705	Hissar	29° 10' N	75° 46' E	229
DWRB-235	AVT-MB-6	DWR47/RD2035	Karnal	29° 43' N	70° 58' E	245
RD-3086	AVT-MB-7	DWRUB 52 X BH 946	Ludhiana	30° 54' N	75° 48' E	247
DWRB137	AVT-MB-8	DWR28/DWRUB64	Meerut			
DWRB-219	AVT-MB-9	BETZS/DWRB88	Nagina	29° 28' N	78° 32' E	245
PL-958	AVT-MB-10	ATAHUALPA/PL807//PL807	Navgaon	26° 35' N	74° 61' E	508
DWRUB 52	AVT-MB-11	DWR17/K551	Pantnagar	29° 02' N	79° 48' E	243.8
PL-959	AVT-MB-12	ATAHUALPA/PL807//PL807	SG Nagar	29° 66' N	75° 53' E	175.6
RD-3087	AVT-MB-13	DWRUB 64 X BH 946	Tabijji	26° 35' N	74° 61' E	508
RD-3105	AVT-MB-14	RD 2849 x RD 2668				
DWRB-2309	AVT-MB-15	DWRB101/BH976				
RD-3084	AVT-MB-16	RD 2849 X DWRUB 64				
RD-3064	AVT-MB-17	NBPGR 92 X RD 2668 X RD 2894				
DWRB-2312	AVT-MB-18	DWRUB52/DWR81				

Table 2: AMMI analysis of eighteen genotypes evaluated at thirteen locations of the zone.

SV	DF	MSS	SI	RP	AC
ENV	12	3844.23	***	44.72	
REP(ENV)	26	16.48	***		
GEN	17	478.78	***	7.89	
GEN:ENV	204	110.61	***	21.87	
PC1	28	290.44	***	36.00	36.00
PC2	26	186.56	***	21.50	57.50
PC3	24	103.02	***	11.00	68.50
PC4	22	100.48	***	9.80	78.30
PC5	20	78.93	***	7.00	85.30
PC6	18	61.35	***	4.90	90.20
PC7	16	54.86	***	3.90	94.10
PC8	14	47.29	***	2.90	97.00
PC9	12	25.10	***	1.30	98.30
PC10	10	22.51	***	1.00	99.30
PC11	8	11.28	***	0.40	99.70
PC12	6	9.92	***	0.30	100.00
Residuals	442	7.53			
Total	905	113.99			

SV: Source of variation; DF: Degree of freedom; MSS: Mean Sum of Squares; SI: Significance; RP: Respective Proportion in total; AC: Accumulated share by components

Relative performance of genotypic values (RPGV), Resende (2007).

$$RPGV_i = \frac{1}{E} \sum_{j=1}^E Gv_{ij} / \mu_j$$

Harmonic mean of relative performance of genotypic values (HMRPGV), Resende (2007).

$$HMRPGV_i = \frac{E}{\sum_{j=1}^E \frac{1}{Gv_{ij} / \mu_j}}$$

Yield stability index (YSI), Farshadfar (2011).

YSI = RASV + RY RASV is the rank of AMMI stability value and RY is the rank of mean grain yield of genotypes (RY) across environments

Absolute value of the relative contribution of IPCs to the interaction (Za), Zali *et al.*, (2012).

$$Za = \sum_{i=1}^{N'} |\theta_n \gamma_{in}|$$

Sum across environments of absolute values of GEI modelled by AMMI(AV(AMGE)), Zali *et al.*, (2012).

$$AV_{(AMGE)} = \sum_{j=1}^E \sum_{n=1}^{N'} |\lambda_n \gamma_{in} \delta_{jn}|$$

AMMI stability index (ASI), Jambhulkar *et al.*, (2017).

$$ASI = \sqrt{[PC_1^2 \times \theta_1^2] + [PC_2^2 \times \theta_2^2]}$$

Modified AMMI stability index (MASI), Ajay *et al.*, (2018).

$$MASI = \sqrt{\sum_{n=1}^{N'} PC_n^2 \times \theta_n^2}$$

Weighted average of absolute scores (WAAS), Olivoto *et al.*, (2019).

$$WAAS_i = \frac{\sum_{k=1}^p |IPCA_{ik}| \times EP_k}{\sum_{k=1}^p EP_k}$$

Modified AMMI stability value (MASV), Ajay *et al.*, (2019).

$$MASV = \sqrt{\sum_{n=1}^{N'-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}} \right) \times (PC_n)^2 + (PC_{N'})^2}$$

Weighted average of absolute scores of BLUP's (WAASB), Olivoto *et al.*, (2019).

$$WAASB_i = \frac{\sum_{k=1}^p |IPCA_{ik}| \times EP_k}{\sum_{k=1}^p EP_k}$$

Results and Discussion

AMMI analysis of variance revealed that environments were the largest contributor to the overall variation in yield followed by genotypes $\times$ environments interaction and genotypes (Table 2). The yield exhibited significant differences between environments, genotypes, and G $\times$ E interactions, according to mean squares from the combined ANOVA as mentioned by Daba *et al.*, 2023. Accordingly factors due to the environment and G $\times$ E interactions have contributed about 44.7% and 21.9%

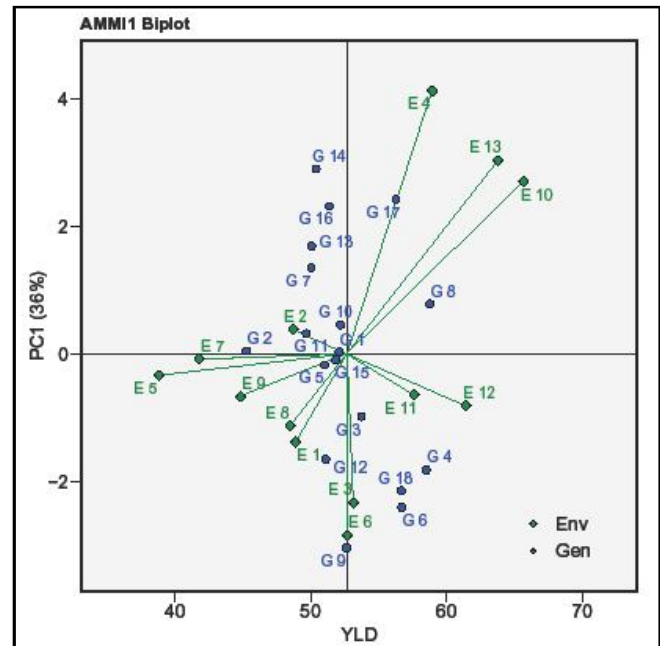


Fig. 1: AMMI 1 biplot based on PC1 and yield of barley genotypes.

Table 3: Performance of genotypes as per adaptability measures.

GT	Y	CV	AS TAB	ASI	ASV	AVA MGE	DA	DZ	EV	FA	MA SI	MA SV	SI PC	ZA	WA AS	WA ASB	HM GV	RP GV	HMR PGV
G 1	52.1	19.2	14.2	0.010	0.047	52.5	17.8	0.841	0.071	317.7	0.294	5.3	8.7	0.112	0.547	0.543	50.4	0.989	0.980
G 2	45.3	22.2	15.9	0.475	2.209	60.3	21.7	0.778	0.061	471.6	0.567	5.9	9.2	0.181	1.017	1.071	43.6	0.862	0.847
G 3	53.7	17.6	12.3	0.398	1.854	48.7	17.4	0.749	0.056	301.6	0.451	4.9	9.1	0.176	1.009	0.963	52.1	1.020	1.013
G 4	58.5	14.4	10.8	0.811	3.773	66.2	20.8	0.547	0.030	433.6	0.822	5.8	7.4	0.215	1.382	1.374	57.2	1.117	1.106
G 5	51.0	15.2	11.5	0.064	0.298	48.9	16.0	0.755	0.057	254.6	0.267	5.1	7.9	0.106	0.533	0.474	49.8	0.973	0.966
G 6	56.7	14.2	13.2	0.980	4.561	75.4	23.2	0.630	0.040	539.1	0.986	6.5	8.3	0.236	1.543	1.495	55.5	1.084	1.071
G 7	50.1	21.4	9.8	0.493	2.296	52.8	16.3	0.702	0.049	264.7	0.538	4.4	8.5	0.165	0.981	0.933	48.2	0.947	0.939
G 8	58.8	20.9	18.7	0.562	2.613	67.2	23.7	0.850	0.072	561.5	0.656	6.4	11.0	0.228	1.339	1.276	56.2	1.110	1.097
G 9	52.7	18.8	16.3	1.121	5.219	68.3	25.2	0.754	0.057	635.4	1.129	6.8	9.9	0.251	1.627	1.564	50.9	1.002	0.987
G 10	52.2	21.2	18.1	0.711	3.306	66.4	24.4	0.802	0.064	595.1	0.745	7.5	10.2	0.216	1.269	1.254	50.1	0.990	0.976
G 11	49.7	18.5	15.3	0.266	1.237	55.6	19.0	0.861	0.074	360.3	0.379	5.5	10.0	0.166	0.905	0.894	48.3	0.946	0.937
G 12	51.1	16.5	10.2	0.598	2.784	55.6	17.5	0.642	0.041	305.9	0.627	4.6	7.9	0.167	1.011	0.990	49.8	0.973	0.966
G 13	50.1	23.0	14.3	0.715	3.330	65.7	20.7	0.792	0.063	429.0	0.733	5.9	10.2	0.219	1.340	1.267	47.8	0.947	0.933
G 14	50.4	25.3	14.3	1.085	5.053	67.7	24.7	0.634	0.040	609.2	1.100	6.1	9.1	0.257	1.677	1.598	48.0	0.951	0.938
G 15	51.9	18.1	9.7	0.083	0.385	36.9	13.1	0.762	0.058	170.6	0.161	5.7	7.1	0.090	0.444	0.421	50.2	0.983	0.978
G 16	51.4	24.7	10.9	0.864	4.022	60.1	20.0	0.640	0.041	401.9	0.872	5.8	8.1	0.202	1.301	1.253	48.8	0.966	0.957
G 17	56.3	23.3	14.5	0.893	4.161	70.9	21.8	0.835	0.070	475.9	0.912	5.7	10.0	0.227	1.435	1.405	53.7	1.059	1.051
G 18	56.7	14.1	10.8	0.783	3.645	57.1	18.5	0.750	0.056	343.6	0.794	4.8	8.6	0.185	1.170	1.113	55.6	1.081	1.074

GT: Genotype; Y: Genotype average yield; ASV: AMMI Stability Value; AMGE: Sum across environments of GEI modeled by AMMI; ASI: AMMI Stability Index; ASTAB: AMMI-based stability parameter; AVAMGE: Sum across environments of the absolute value of genotype $\times$ environment interaction model by AMMI; DA: Annicchiarico's D parameter; DZ: Zhang's D parameter or AMMI statistic coefficient; FA: Stability measure based on fitted AMMI model; MASI: Modified AMMI Stability Index and MASV: Modified AMMI Stability Value; SIPC: Sums of the absolute value of the IPC scores; Za: Absolute value of the relative contribution of IPCs to the interaction

respectively, whereas genotypes had augmented only 7.9% of the total variance. The first PC among them made up 36 % of the total $G \times E$, which was followed by the second, third and fourth PCs at 21.5%, 11% and 9.8%, respectively. The total of about 78.3 % accumulated by four whereas the proportion of first two was 57.5% as proportion of first two was more than fifty per cent (Rahmati *et al.*, 2024)

Performance of genotypes as per indices based on AMMI

Genotype G17 followed by G14, G15 and G10 were able to achieve the comparative more yield as compared to remaining genotypes while environment E10 had exceeded as trailed by E13, E12 were more adaptable locations for the evaluated genotypes (Table 3). G08, G04, G18 and G17 genotypes were able to express the more yield and consistent yield were achieved by G18, G06, G04 as evident by lower values of CV measure. AMMI based stability measure (ASV) had pointed towards the G15, G07, G12 genotypes whereas AMMI stability index (ASI) had identified G1, G5, G15 genotypes while genotypes G1, G5, G15 had been selected by AMMI stability value based on first two significant interaction principal components (Azam *et al.*, 2020). Measure

based on Sum across environments of the absolute value of genotype $\times$ environment interaction model by AMMI (AVAMGE) had favoured G15, G3 and G5 whereas Annicchiarico's D parameter measure (DA) had advocated for G15, G5 and G7 genotypes. Zhang's D parameter or AMMI statistic coefficient (DZ) had expressed the least values by G4, G6, G14, Genotypes G4, G6, G14 whereas G15, G5, G7 and G15, G5, G1 as well as G7, G12, G18 by EV, FA, MASI and MASV measures respectively for the current study. SIPC measure had achieved the desirable least values by G15, G4, G12 while ZA found suitability of G15, G5, G1 further the measures Weighted Average of Absolute Scores (WAAS) along with WAASB was hopeful for G15, G5, G1 (Olivoto *et al.*, 2019). Lastly adaptability measure based on Harmonic mean of genotypic values had selected G4, G8, G18 which was supported by RPGV and HMRPV measures (Ashwini *et al.*, 2021).

Genotypes behaviour as per Simultaneous Selection Index

The Simultaneous Selection Index (SI), which considered into account both yield and stability per se as quantified by ASV in a single criterion (Farshadfar, 2011) was estimated as $SI = RASV + RY$ where, RASV is

Table 4: Ranking of genotypes based on adaptability measures and yield performance.

Geno type	Y	AST AB	ASV	MA SV	WA AS	AVA MGE	DA	EV	FA	SI PC	ZA	DZ	MA SI	WAA SB	HM GV	RP GV	HMR PGV
G1	9	19	10	15	12	13	15	25	15	18	12	25	12	12	17	18	17
G2	18	33	24	31	26	28	30	30	30	30	26	30	25	22	32	35	34
G3	6	14	11	10	12	8	10	13	10	17	13	13	11	13	18	17	17
G4	2	7	15	12	16	14	13	3	13	4	13	3	15	14	19	17	19
G5	13	20	15	18	15	16	15	23	15	17	15	23	15	31	29	27	28
G6	3	12	19	19	19	21	17	5	17	9	19	5	19	4	12	13	12
G7	16	18	23	17	21	21	19	22	19	23	20	22	22	26	29	29	29
G8	1	19	9	16	13	15	16	18	16	19	16	18	10	16	6	6	6
G9	7	23	25	24	24	23	25	16	25	20	24	16	25	16	10	11	10
G10	8	25	18	26	18	21	24	22	24	25	20	22	19	16	26	26	26
G11	17	31	21	24	21	24	25	35	25	31	22	35	21	23	23	23	23
G12	12	15	21	14	19	18	17	17	17	15	18	17	20	26	13	13	13
G13	15	27	26	27	28	26	25	28	25	31	28	28	25	17	26	27	27
G14	14	25	31	28	32	29	31	17	31	24	32	17	31	30	18	17	18
G15	10	11	13	18	11	11	11	21	11	11	11	21	11	15	25	26	24
G16	11	17	25	22	22	20	20	15	20	16	21	15	25	24	13	13	13
G17	5	18	20	14	20	22	18	20	18	20	19	20	20	22	12	12	12
G18	4	8	16	7	13	12	11	12	11	12	13	12	16	15	14	12	14

rank of the genotypes based on ASV and RY is the rank of genotype based on grain yield across dates of sowing. The genotypes with lower ASV and higher yield were assigned lower rank and those with higher ASV and lower yield were assigned higher ranks. The simultaneous selection index was also computed by summation of the ranks of the adaptability measures and mean performance of the genotypes under multi locational trials (Vaezi *et al.*, 2019). Simultaneous consideration of yield and adaptability measures, genotypes were of choice G4,

G18, G15 while G8, G1, G3 whereas G18, G3, G4 by ASTAB, ASV and MASV measures (Table 4) (Kumar *et al.*, 2024). Genotypes G15, G03, G01 would be suitable as per least values of WAAS while AVAMGE had selected G03, G15, G18 and lower values of DA had expressed by G3, G18, G15 and genotypes favoured by EV measure were G04, G06, G18 (Kebede *et al.*, 2024). Next in series, the values of FA had pointed out for G03, G18, G15 and by SPIC were G04, G06, G15 while ZA was optimistic for G15, G01, G03 whereas ZA had

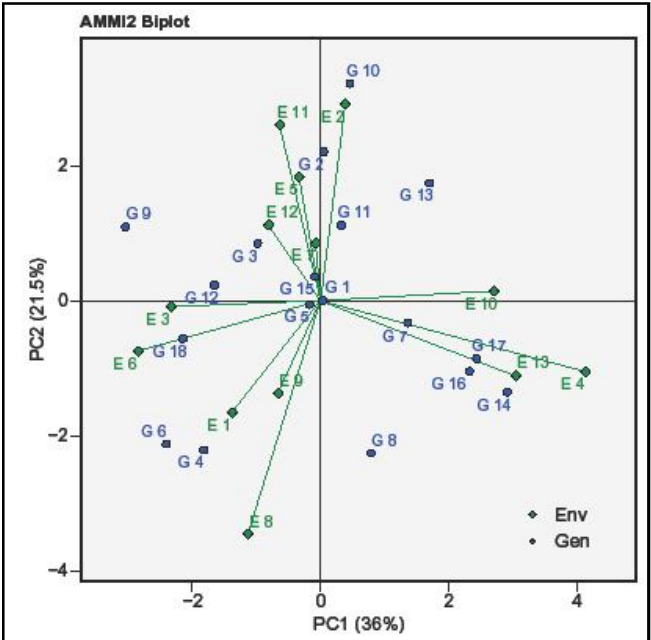


Fig. 2: Performance of genotypes and locations based on first two principal components.

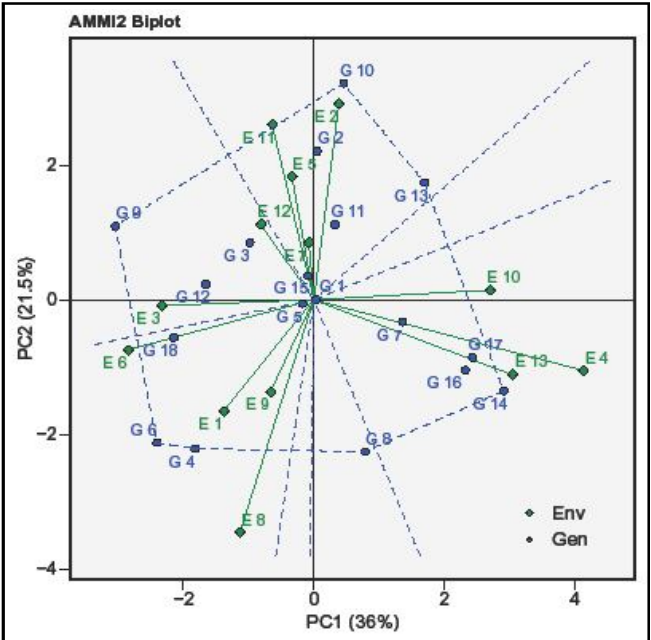


Fig. 3: Which won where pattern of genotypes vs environments.

identified G15, G01, G03 and values of DZ had identified G04, G06, G18 genotypes. The lower values of MASI had isolated G08, G15, G3 form others and WAASB had selected G06, G01, G03 (Nataraj *et al.*, 2021) and last three measures had maintained consensus for G08, G09, G17 genotypes for the current study (Giang *et al.*, 2024).

AMMI 1 plot (PC1 and yield of genotypes)

In the context of the AMMI1 investigation, it has been observed that genotypes G1, G15, G11, G5 located near the centre region of the IPCA1 axis exhibited greater stability with minimal interaction effects as compared to G9, G14, G6 similarly the suitability of environmental locations E2, E11, E8 vis-à-vis E5, E4, E13, E10 (Fig. 1) (Pour *et al.*, 2022). As a result, these genotypes demonstrated a wide range of adaptation to various environmental situations. In contrast, the detection of a positive interaction occurred when there was congruent polarity between the genotype and environment on the IPCA axis. Genotypes G4 G18 G6 for E11, E12 environments would achieve yield with unstable performance due to G×E interactions effects whereas G8, G17 had maximum yield at E10, E13, E4 environments only. Conversely, a deleterious interaction arises when there was a discrepancy in polarity between the genotype and the environment. The outcomes derived from the present research were consistent with the findings documented.

AMMI 2 plot (genotypes vis-a-vis locations based on first two principal components)

The first two IPCAs were responsible for the 57.5% of the (G×E interaction) variance. The AMMI2 biplot used the distances from the biplot origin to provide insights into the degree of interaction exhibited by genotypes across environments, or conversely. Genotypes G1, G11, G10, G13 with E2, E10 whereas G16, G17, G14 at E4, E13 moreover G15, G3, G2 at E12, E5, E7 and G5, G18, G12 at E1, E9, E6 (Fig. 2). The methods for analyzing genotype

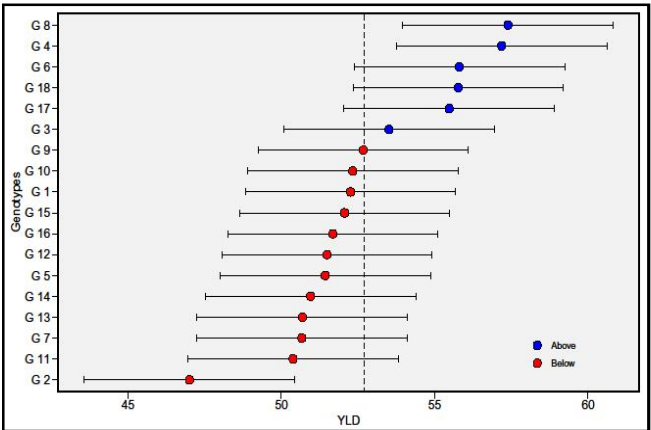


Fig. 4: Predicted yield of genotypes.

stability derived from additive main effects and multiplicative interaction and the genotype plus genotype–environment interaction. Environments with low IPCA1 and IPCA2 scores, located near the origin, had a notable influence on genotype stability was reported. Moreover, the E07, E9, E5 and E12 exhibit a constrained impact on genotype-by-environment interaction, implying a broad adaptability to diverse developmental circumstances. The findings derived from the AMMI 2 analysis have yielded support for the significance of including IPCA2 scores in conjunction with IPCA1 scores to enhance our understanding of genotype-environment interactions (Verma *et al.*, 2021). The outcomes of the present study consistent with the findings, who noted that the initial two primary components adequately serve as a basis for projecting the AMMI model (Pour *et al.*, 2022).

Polygon view of promising genotypes with favourable locations

The environments and genotypes close to the biplot’s origin had the least impact on G×E interaction, whereas environments and genotypes that were far from the biplot’s origin had the most influence on G×E interaction. As a result, in comparison to other genotypes, those closest to the origin were thought to be stable (Rahmati *et al.*, 2024). The genotypes G1, G15, and G5 expressed either favourably or negatively high interactive behaviours in the current study, or they contributed more to the observed G×E interaction (Fig. 3). When compared to the E5, E7, E11 and E12 environments, the G15 genotype performed the best. G1 and G11 genotypes were adapted to E02 and E10, respectively. Since G10, G06 and G14 are less affected by the G×E interaction, they would perform well in various environments. Through lateral

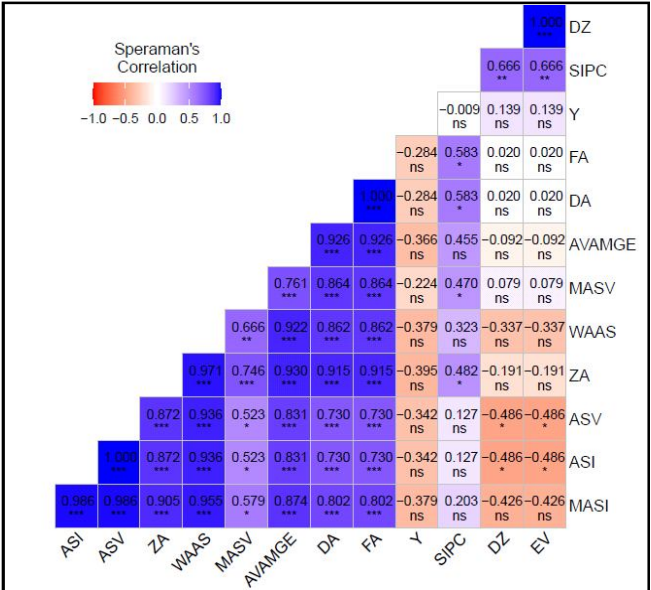


Fig. 5: Correlation hat map among AMMI based indices.

lines, the environmental scores are linked to their point of origin. Short arrow sites do not impose a lot of interaction forces E12, E7 while long arrows of E4, E8, E13, E6 expressed in the strong interaction. The genotypes near the ordinates reflected a more adaptation to the surroundings, whilst the following genotypes expressed a more specific adaptation to the environment G10, G13, G11 for E2 and G14, G17, G16, G7 for E13 & E14 while G6, G4, G18 for E1, E6, E9 lastly G8, G3, G12 for E3 & E12. The nature of $G \times E$ is governed by the angle between the genotype and the environmental vectors: it is positive for acute angles *i.e.* E13 with E4 and of E9 with E1 and of E5 with E11 & E12, insignificant for straight angles of E3 with E10 and E2 with E8 expressed straight line angles, and negative for obtuse angles of E1 with E4, E6 with E13, E12 with E13 in the present study.

Predicted yield and association among adaptability measures

The predicted yield of the evaluate genotypes had been expressed in figure to point out the genotypes G08, G04, G06, G18, G17, G03 would be able to maintain their yield over the average yield of genotypes which were evaluated in the current study (Fig. 4) as mentioned by Olivoto *et al.*, 2019. In an attempt to reveal the relationship between each pair of AMMI adaptability measures, Pearson rank correlations revealed a strong association among the estimated AMMI-based indices except AMGE and AVGE (Fig. 5). Strong positive of ASI with ASV, ZA, WAAS, AVAMGE, DA, FA had found from association analysis. Negative association of yield had been observed with MASI, ASI, ASV, WAAS, ZA, AMGE, DA, FA and indirect relation of DZ and EV had expressed with MASI, ASI, ASV, WAAS, ZA measures. Significance of Spearman's rank correlation among adaptability measures expressed by *, **, and *** at 0.05, 0.01, and 0.001 probability levels, respectively.

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