



Comparative analysis of genotype x environment interaction for wheat genotypes by AMMI and BLUP for Peninsular zone

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ABSTRACT

Genotype x environment interaction of wheat genotypes had been deciphered by AMMI, BLUP and Non parametric measures. Analysis revealed the highly significance of the GxE interaction which further bifurcated in seven interaction principal components accounted for 78.7% of total interaction variation. Measures (ASV and ASV) based on first two IPCAs recommended G1, G12, G9 and G12, G1, G14 genotypes respectively. MASV and MASV measures had been utilized seven significant IPCAs recommended G14, G1, G11 and G14, G11, G7 wheat genotypes for this zone respectively. BLUP-based measure, HMGV settled for G3, G8, G12 while RPGV measure favoured G3, G8, G4 and HMRPGV selected G3, G8, G4 genotypes. Non parametric composite measures $NP_i^{(1)}$ observed suitability of G11, G1, G3 whereas $NP_i^{(2)}$ selected G11, G1, G9 while $NP_i^{(3)}$ identified G11, G1, G9 genotypes. Genotypes G11, G1, G9 were of choice by $NP_i^{(4)}$. The biplot analysis of considered measures observed seven clusters. ASV joined hands with ASV, IPC1, IPC3, IPC5 along with $NP_i^{(2)}$ in one cluster. Mean yield formed cluster with HMGV, RPGV, HMRPGV i.e. BLUP based measures.

Keywords : AMMI, BLUP, Biplot analysis, $NP_i^{(s)}$, $S_i^{(s)}$, Spearman rank Coefficient

Stable and high-yielding varieties of cereal and other crops had been identified by researchers to aspiring farmers to sustain the higher yield of the country (Anuradha *et al.*, 2022). In general, wheat breeders put forward widely adaptable suitable genotypes especially in changing climatic conditions (George and Lundy, 2019). Complexity of yield, expressed by many quantitative genes, mechanism to decipher the genotype x environment interaction (GxE) under multi-environment trials (METs) have much significance for breeders (Ahakpaz *et al.*, 2021). Several approaches have been recommended over the years to analyze genotype x environment interaction, including additive main effects and multiplicative interaction (AMMI) biplots (Bocianowski *et al.*, 2021). AMMI Stability Index (ASI) and AMMI stability value (ASV) using two PCs and Modified AMMI stability value (MASV), using all the significant principal components were also advocated to demonstrate the stability (Gerrano *et al.*, 2020). Best linear unbiased prediction (BLUP)- measures viz. harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV), and harmonic mean of relative performance of genotypic values (HMRPGV), were utilized (Gonçalves *et al.*, 2020). Several distribution-free nonparametric measures $S_1^1 S_1^2 S_1^3 S_1^4 S_1^5 S_1^6 S_1^7$ and composite measures $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ have been already suggested in the literature. Comparative assessment of all the measures suggested

for GxE interactions studies was lacking in literature and present study was planned to look after any type of significance in association among the multivariate. Best linear unbiased predictors and non parametric measures for the wheat genotypes evaluated in Peninsular zone of the country.

MATERIALS AND METHODS

Field trials were conducted in research center of All India Coordinated Research Project for promising fourteen wheat genotypes during 2020-21 cropping season. Randomized block design with four replications laid out for field evaluations. Experimental details of locations and parentage of genotypes had been elaborated in Table 1 for ready reference. The recommended agronomical practices for zone were followed in total to ensure good harvest of the yield. Various non parametric and parametric measures for assessing GxE interaction and stability analysis had been mentioned by Pour-Aboughadareh *et al.*, 2019 and mentioned below for completeness:

Non parametric composite measures $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ were based on the ranks of genotypes as per yield and corrected yield of genotypes. In the formulas, r_{ij}^* was the rank of X_{ij}^* and M_{di} were the mean and median ranks for original (unadjusted) grain yield, where * and M_{di}^* were the same parameters computed from the corrected (adjusted) data.

Comparative analysis of genotype x environments interaction

The correction for yield of ith genotype in jth environment as $(X_{ij}^* = X_{ij} - \bar{x}_{i*} + \bar{x}_{**})$ as X_{ij}^* , was the corrected phenotypic value; \bar{X}_{i*} was the mean of ith genotype in all environments and \bar{X}_{**} was the grand mean.

$$S_i^{(1)} = \frac{2 \sum_j^{n-1} \sum_{j=j+1}^n |r_{ij} - r_{ij'}|}{[n(n-1)]} \quad S_i^{(7)} = \frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{\sum_{j=1}^n |r_{ij} - \bar{r}_i|} \quad S_i^{(3)} = \frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{\bar{r}_i}$$

$$S_i^{(4)} = \sqrt{\frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{n}} \quad S_i^{(5)} = \frac{\sum_{j=1}^n |r_{ij} - \bar{r}_i|}{n} \quad S_i^{(6)} = \frac{\sum_{j=1}^n |r_{ij} - \bar{r}_i|}{\bar{r}_i}$$

$$S_i^{(2)} = \frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{(n-1)} \quad \bar{r}_i = \frac{1}{n} \sum_{j=1}^n r_{ij}.$$

Non parametric composite measures $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ were based on the ranks of genotypes as per yield and corrected yield of genotypes. In the formulas, r_{ij}^* was the rank of X_{ij}^* , and \bar{r}_i and M_{di} were the mean and median ranks for original (unadjusted) grain yield, where \bar{r}_i^* and M_{di}^* were the same parameters computed from the corrected (adjusted) data.

$$NP_i^{(1)} = \frac{1}{n} \sum_{j=1}^n |r_{ij}^* - M_{di}^*| \quad NP_i^{(3)} = \sqrt{\frac{\sum (r_{ij}^* - \bar{r}_i^*)^2 / n}{\bar{r}_i^*}}$$

$$NP_i^{(2)} = \frac{1}{n} \left(\frac{\sum_{j=1}^n |r_{ij}^* - M_{di}^*|}{M_{di}^*} \right) \quad NP_i^{(4)} = \frac{2}{n(n-1)} \left[\sum_{j=1}^{n-1} \sum_{j=j+1}^n \left| \frac{r_{ij}^* - r_{ij'}^*}{\bar{r}_i^*} \right| \right]$$

ASV $ASV = \left[\left(\frac{SSIPC\ 1}{SSIPC\ 2} PCI \right)^2 + (PC2)^2 \right]^{1/2}$

ASV1 $ASV1 = \left[\frac{SSIPC\ 1}{SSIPC\ 2} (PCI)^2 + (PC2)^2 \right]^{1/2}$

Modified AMMI stability Value $MASV = \sqrt{\sum_{n=1}^{N-1} \frac{SSIPC_n}{SSIPC_{n+1}} (PC_n)^2 + (PC_{n+1})^2}$

$MASV1 = \sqrt{\sum_{n=1}^{N-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}} PC_n \right)^2 + (PC_{n+1})^2}$

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 $RPGV_{ij} = \Sigma GV_{ij} / \Sigma GV_j$

Harmonic mean of Relative Performance of genotypic values $HMRPGV_i = \text{Number of environments} / \sum_{j=1}^k \frac{1}{RPGV_{ij}}$

Geometric Adaptability Index $GAI = GAI = \sqrt[n]{\prod_{k=1}^n \bar{X}_k}$

AMMISOFT version 1.0 software was utilized for AMMI analysis of data sets and SAS software version 9.3 for further analysis.

Table 1: Parentage and location details under multi environmental trials of wheat genotypes

Code	Genotype	Parentage	Code	Locations	Latitude	Longitude	Altitude
G 1	WHD965	GUAYACAN/N/A/2*SNITAN/3/ SOMAT_3/GREEN_22	E 1	Niphad	20° 4' N	74° 6' E	551
G 2	UAS428	GREEN-14/YAN-10/AUK/JUAS402	E 2	Pune	18° 31' N	73° 51' E	562
G 3	HI8826	HI8713/HI8663	E 3	Akola	20° 42' N	77° 0' E	292
G 4	MACS4100	CBC509CHILE/6/ECO/CMH76A.722//BIT/3/ ALTAR84/4/AJAJA_2/5/KJ OVE_17/1 AJAJA_12/F3LOCAL(SEL.ETHIO.135.85)// PLATA_13/8/SO O TY_9/RASCON_37// WODUCK/CHAM_3	E 4	Parbhani	19° 15' N	76° 46' E	413
G 5	MACS3949	STOT//ALTAR84/ALD/3/THB/CEP7780//2*MUSK_4	E 5	Karad	17° 17' N	74° 10' E	577
G 6	DDW53	HI8737/HI8498	E 6	Dharwad	15° 27' N	75° 0' E	724
G 7	NIDW1345	DDW06/AKDW4021	E 7	Ugar-Khurd	16° 39' N	74° 49' E	548
G 8	MACS6222	HD2189*2/MACS2496	E 8	Kalloli	16° 26' N	74° 86' E	625
G 9	MACS4106	MACS2846/DDDW01//HI8662	E 9	Mudhol	16° 19' N	75° 17' E	546
G 10	NIDW1348	NIDW295/DDDW06	E 10	Nippani	16° 23' N	74° 22' E	606
G 11	HI8828	HI8682/WH896	E 11	Pravaranagar			
G 12	GW322	PBW173/GW196	E 12	Arbhavi	15° 84' N	74° 51' E	625
G 13	HI8827	HI8627/HI8691	E 13	Mandya			
G 14	DDW48	HI8498/PDW233//PDW291	E 14	Nasik	19° 59' N	73° 47' E	583

Table 2: GxE analysis of evaluated wheat genotypes

Source	Degree of freedom	Mean Sum of Squares	Significance level	Contribution of factors (%)	GxE interaction Sum of Squares (%)	Cumulative Sum of Squares(%) by IPCA's
Treatments	195	329.53	***	24.90		
Genotype (G)	13	279.05	***	1.66		
Environment (E)	13	3668.49	***	1.66		
GxE interaction	169	76.57	***	21.58		
IPC1	25	205.82	***		14.79	14.79
IPC2	23	98.25	***		13.61	28.40
IPC3	21	77.62	***		12.43	40.83
IPC4	19	69.19	***		11.24	52.07
IPC5	17	48.98	***		10.06	62.13
IPC6	15	38.70	***		8.88	71.01
IPC7	13	40.30	*		7.69	78.70
Residual	36	18.12				
Error 588	18.73					
Total 783	96.13					

RESULTS AND DISCUSSION

AMMI analysis

Highly significant effects of GxE interactions (21.6%), both environments and genotypes with 1.7% variation for yield (Table 2). This revealed that the testing sites were more diverse for the variation in grain yield observed by the genotype (PourAboughadareh *et al.*, 2022). Since the AMMI model revealed the significance of the GxE interaction and first seven Interaction principal components showed 78.7% significant variation at $P < 0.01$ and AMMI 1 explained a total variation of 14.8%, followed by 13.6% for AMMI 2, 12.4% for AMMI 3, 11.2% for AMMI 4, AMMI 5 contributed 10.1% followed by 8.9% and 7.7% by AMMI 6 and AMMI 7, respectively. The first two AMMI components in total showed 28.4% of the total variation indicating the two AMMI components well fit and confirmed the use of AMMI model. GxE signal and GxE noise sums of squares were 79.2% and 20.8% of total interactions, respectively. Early IPCs selectively capture signal, and late ones noise. Accordingly, this much signal suggests AMMI 6 or maybe AMMI 7. Narrow adaptations for genotype effects were governed by the fact that GxE-signal sum of squares was 2.82 times and GxE-noise accounted only 0.74 times the genotypes (Vaezi *et al.*, 2018). More over the first interaction principal component was only 1.42 times the genotypes main effects.

Ranking of genotypes as per measures

Since the genotypes yield expressed highly significant variations, and G3, G4, G8 were higher while lowest was by G9 (Table 3). The stability or adaptability

of genotypes were also assessed by values of IPCAs. The, greater the IPCA scores reflect the specific adaptation of genotype to certain locations. While, the values approximate to zero were recommended for in general adaptations of the genotype (Sousa *et al.*, 2020). Absolute IPCA-1 scores pointed for G1, G9, G12. While for IPCA-2, G12, G14, G1 would be genotypes of choice (Table 4). Values of IPCA-3 favoured G4, G3, G7 genotypes. As per IPCA-4, G1, G5, G4 genotypes would be of stable performance. Genotypes G13, G14, G5 were selected as per IPCA5 while values of IPCA 6 pointed for G13, G6, G3 and finally IPCA 7 observed suitability of G14, G9, G12. First two IPCAs in ASV & ASV1 measures utilized 28.4% of GxE interaction sum of squares. ASV1 measures settled for G1, G12, G9 and ASV pointed G12, G1, G14 genotypes for stable performance. Adaptability measures MASV and MASV1 considered all seven significant IPCAs of the AMMI analysis. Values of MASV1 identified G14, G1, G11 genotypes express stable yield whereas genotypes G14, G11, G7 be of stable yield performance by MASV measure respectively. BLUP based measures consider the randomness of the genotypic effects (Silva *et al.*, 2019). Average yield of genotypes pointed towards G3, G8, G4 as high yielders. More over the values of corrected GAI favored G3, G8, G4. Least values of standard deviation were observed for the consistent yield of G13, G12, G2 more over the values of CV identified G7, G8, G12 genotypes for Peninsular zone of the country. The HMGV identified G3, G8, G12 while values of RPGV favoured G3, G8, G4 and HMRPGV estimates selected G3, G8, G4 genotypes. HMGV, RPGV, and

Table 3: AMMI and BLUP based measures of yield

Genotype	Mean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	MASV1	MASV	ASV1	ASV	BLAvg	BLStdv	BLCV	BLGM	HMGV
G1	37.08	0.0135	0.4152	2.1393	0.2390	-0.4663	-0.9733	-1.4098	4.12	3.91	0.42	0.42	37.08	8.56	23.10	35.94	34.57
G2	36.89	1.0882	-1.7318	-0.9546	1.5766	-1.5523	0.2622	1.1382	5.43	4.82	3.02	2.39	37.16	8.43	22.68	35.94	34.31
G3	40.68	-2.0571	-1.0541	0.1663	0.5663	1.2793	-0.2244	-0.7444	5.60	4.19	4.80	3.28	39.90	9.53	23.89	38.60	37.06
G4	39.86	2.0646	-1.8710	0.0110	0.5326	-0.6400	-0.9660	-0.6339	6.04	4.68	5.06	3.63	39.44	9.51	24.12	37.90	35.78
G5	37.54	-2.0897	-0.5223	-1.3528	0.4091	-0.4385	0.9543	-1.7206	5.82	4.51	4.79	3.20	37.24	9.36	25.13	35.91	34.36
G6	35.48	-2.7126	-0.5652	0.3858	-0.5436	1.0674	0.0384	1.2145	6.70	4.75	6.20	4.13	35.85	9.56	26.66	34.45	32.84
G7	36.98	0.8403	1.2297	0.1855	1.4612	1.4369	0.5311	0.7448	4.32	3.87	2.27	1.77	37.20	6.97	18.74	36.44	35.50
G8	39.70	2.7593	-0.7893	-0.7694	-0.8920	1.5211	1.6120	-0.4035	7.55	5.72	6.33	4.24	39.47	8.46	21.42	38.36	36.91
G9	32.80	0.1828	2.0646	-2.2835	-1.4366	-0.8267	-0.6079	0.1669	5.63	5.27	2.11	2.08	33.47	9.39	28.07	31.74	29.25
G10	38.37	1.2692	-0.4813	0.5697	-0.9117	0.9217	-1.7066	0.6938	4.54	3.87	2.93	1.97	38.27	9.22	24.09	36.82	34.82
G11	33.58	-1.4356	0.6604	0.4884	1.3349	-0.8302	0.2685	1.0679	4.30	3.49	3.33	2.26	34.30	8.61	25.12	33.07	31.63
G12	38.46	0.1965	0.0300	2.2569	-1.9698	-1.3355	1.5421	0.3106	5.42	5.22	0.45	0.30	38.21	8.27	21.64	37.15	35.79
G13	36.65	1.0337	2.8740	0.2269	1.0342	0.0535	-0.0081	-0.5414	5.62	4.93	3.71	3.27	36.57	8.22	22.49	35.54	34.33
G14	36.57	-1.1531	-0.2588	-1.0695	-1.4003	-0.1904	-0.7225	0.1171	3.75	3.19	2.64	1.76	36.49	9.21	25.25	35.10	33.34

Table 4: Non parametric composite measures of yield

Genotype	S _i ¹	S _i ²	S _i ³	S _i ⁴	S _i ⁵	S _i ⁶	S _i ⁷	NP _i ⁽¹⁾	NP _i ⁽²⁾	NP _i ⁽³⁾	NP _i ⁽⁴⁾	HMRPGV	RPGV
G1	3.473	8.593	1.203	2.931	2.429	4.760	3.286	2.429	0.347	0.395	0.467	0.992	0.999
G2	4.736	15.962	2.128	3.995	3.357	6.267	4.415	3.357	0.353	0.455	0.539	0.991	1.000
G3	3.769	11.302	1.400	3.362	2.500	4.336	4.198	2.500	1.667	0.941	1.055	1.065	1.073
G4	4.692	15.764	1.953	3.970	3.357	5.823	4.360	3.357	0.610	0.695	0.821	1.043	1.056
G5	5.110	18.951	2.434	4.353	3.786	6.807	4.648	3.786	0.631	0.677	0.795	0.989	1.000
G6	5.560	22.901	3.340	4.786	4.306	8.792	4.938	4.143	0.518	0.578	0.671	0.945	0.962
G7	5.604	22.725	3.001	4.767	4.143	7.660	5.094	4.143	0.518	0.618	0.726	1.006	1.012
G8	4.626	18.731	3.406	4.328	3.357	8.545	5.181	3.071	0.512	0.689	0.736	1.056	1.070
G9	5.198	19.478	2.254	4.413	3.643	5.901	4.965	3.643	0.347	0.409	0.482	0.870	0.887
G10	4.000	11.912	1.635	3.451	2.612	5.020	4.234	2.571	0.396	0.520	0.602	1.017	1.023
G11	3.396	10.027	1.088	3.167	2.214	3.364	4.205	2.214	0.185	0.290	0.311	0.911	0.920
G12	5.868	25.231	3.604	5.023	4.429	8.857	5.290	4.286	0.612	0.725	0.847	1.024	1.034
G13	4.099	12.225	2.014	3.496	2.796	6.447	4.060	2.786	0.398	0.453	0.531	0.978	0.990
G14	4.516	15.016	1.965	3.875	3.357	6.150	4.153	3.357	0.448	0.502	0.585	0.970	0.974

Table 5: Loadings of AMMI, BLUP and non parametric measures

Measure	Principal Component 1	Principal Component 2	Measure	Principal Component 1	Principal Component 2
Mean	0.227	-0.238	BLGM	0.232	-0.229
IPC1	0.073	-0.043	HMGV	0.229	-0.222
IPC2	-0.134	0.129	RPGV	0.237	-0.225
IPC3	0.019	-0.114	HMRPGV	0.227	-0.233
IPC4	-0.060	-0.119	S _i ¹	0.184	0.268
IPC5	0.123	-0.086	S _i ²	0.199	0.268
IPC6	0.176	0.127	S _i ³	0.233	0.223
IPC7	-0.043	0.161	S _i ⁴	0.201	0.267
MASV1	0.199	0.061	S _i ⁵	0.187	0.264
MASV	0.169	0.124	S _i ⁶	0.229	0.206
ASV1	0.125	-0.039	S _i ⁷	0.199	0.239
ASV	0.107	-0.024	NP _i ⁽¹⁾	0.170	0.264
BLAvg	0.230	-0.234	NP _i ⁽²⁾	0.154	-0.174
BLStdev	-0.035	-0.049	NP _i ⁽³⁾	0.265	-0.109
BLCV	-0.149	0.089	NP _i ⁽⁴⁾	0.264	-0.100
			% contribution	33.76	26.27

Table 6: Spearman rank Correlation analysis among measures of wheat genotypes

IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	MASV1	MASV	ASV1	ASV	BLAvg	BLStdev	BLCV	BLGM	HMGV	RPGV	HMRPGV	S _i ¹	S _i ²	S _i ³	S _i ⁴	S _i ⁵	S _i ⁶	S _i ⁷	NP _i ⁽¹⁾	NP _i ⁽²⁾	NP _i ⁽³⁾	NP _i ⁽⁴⁾								
Mean	-0.363	0.587	-0.152	0.024	-0.279	-0.200	0.978	-0.051	0.486	0.956	0.952	0.960	0.965	0.604	0.064	0.086	-0.029	0.086	0.046	-0.011	0.046	-0.011	0.046	-0.011	0.046	-0.011	0.046	-0.011	0.046	-0.011	0.046					
IPC1		-0.138	0.007	0.033	0.020	-0.051	0.037	0.147	0.345	0.024	0.200	-0.420	-0.451	-0.565	-0.490	-0.389	-0.473	0.020	-0.007	0.116	-0.007	0.015	0.090	0.191	-0.099	-0.169	-0.103	0.059	-0.613	-0.798						
IPC2			0.218	-0.103	-0.055	0.002	0.073	-0.424	-0.103	-0.600	-0.530	0.609	-0.459	-0.042	0.574	0.411	0.591	0.538	-0.011	-0.024	-0.024	-0.073	-0.002	-0.108	-0.090	-0.420	-0.578	-0.578	-0.569	0.103						
IPC3				-0.033	0.015	-0.086	0.209	-0.354	-0.182	-0.257	-0.327	-0.077	-0.253	-0.363	-0.169	-0.240	-0.121	-0.209	-0.213	-0.178	-0.213	-0.235	-0.051	-0.143	-0.284	-0.077	-0.046	-0.046	-0.059	0.051						
IPC4					0.015	0.143	0.108	-0.068	-0.262	0.253	0.284	-0.029	-0.257	-0.319	-0.059	0.007	-0.064	-0.029	-0.231	-0.314	-0.297	-0.284	-0.240	-0.270	-0.284	-0.055	-0.152	-0.152	-0.138	0.051						
IPC5						0.055	0.138	0.244	-0.103	0.437	0.393	-0.363	0.081	-0.231	-0.323	-0.407	-0.327	-0.345	-0.059	-0.169	-0.169	0.015	0.191	0.042	-0.095	-0.385	-0.385	-0.358	-0.327	0.051						
IPC6							0.305	0.244	0.367	0.235	0.187	-0.116	-0.411	-0.411	-0.108	-0.169	-0.152	-0.077	0.468	0.560	0.679	0.560	0.648	0.670	0.376	0.323	0.314	0.305	0.314	0.305	0.314					
IPC7								-0.121	-0.042	-0.068	-0.077	0.407	-0.152	0.024	0.310	0.420	0.314	0.358	0.310	0.345	0.235	0.345	0.292	0.363	0.262	-0.314	-0.248	-0.270	-0.270	-0.270	-0.270					
MASV1								0.732	0.741	0.833	-0.270	0.380	0.095	-0.187	-0.160	-0.226	-0.165	0.367	0.451	0.503	0.451	0.420	0.424	0.464	0.270	0.415	0.437	0.424	0.424	0.424	0.424					
MASV									0.226	0.393	-0.125	-0.068	-0.187	-0.147	-0.130	-0.156	-0.125	0.437	0.495	0.613	0.495	0.464	0.516	0.521	0.275	0.125	0.222	0.191	0.191	0.191	0.191					
ASV1										0.956	-0.345	0.424	0.095	-0.248	-0.191	-0.288	-0.222	-0.086	0.024	0.112	0.024	0.011	0.125	0.077	-0.103	0.393	0.407	0.389	0.389	0.389	0.389					
ASV											-0.262	0.424	0.099	-0.187	-0.121	-0.218	-0.160	-0.051	0.046	0.125	0.046	0.020	0.103	0.095	-0.112	0.292	0.305	0.284	0.284	0.284	0.284					
BLAvg												-0.015	0.521	0.969	0.943	0.982	0.965	0.033	-0.073	-0.240	-0.073	-0.095	-0.323	-0.116	-0.077	-0.604	-0.811	-0.793	0.196	0.218						
BLStdev													0.789	0.095	0.143	0.077	0.086	-0.108	-0.064	-0.037	-0.248	-0.037	-0.301	-0.200	0.007	-0.130	-0.284	-0.244	0.196	0.218						
BLCV														0.635	0.666	0.613	0.631	-0.064	-0.037	-0.248	-0.037	-0.059	-0.301	-0.200	0.007	-0.130	-0.284	-0.244	0.196	0.218						
BLGM														0.965	0.966	0.966	0.996	0.015	0.037	-0.090	0.037	0.007	-0.064	-0.182	0.033	-0.538	-0.776	-0.745	0.196	0.218						
HMGV															0.960	0.978	0.978	0.987	-0.007	-0.138	0.007	0.020	-0.125	-0.187	0.011	-0.609	-0.793	-0.767	0.196	0.218						
RPGV																0.987	0.987	0.987	-0.020	-0.125	-0.002	-0.033	-0.095	-0.218	-0.007	-0.582	-0.811	-0.785	0.196	0.218						
HMRPGV																	0.960	0.987	0.987	0.046	0.068	0.068	0.037	-0.042	-0.152	0.064	-0.534	-0.763	-0.732	0.196	0.218					
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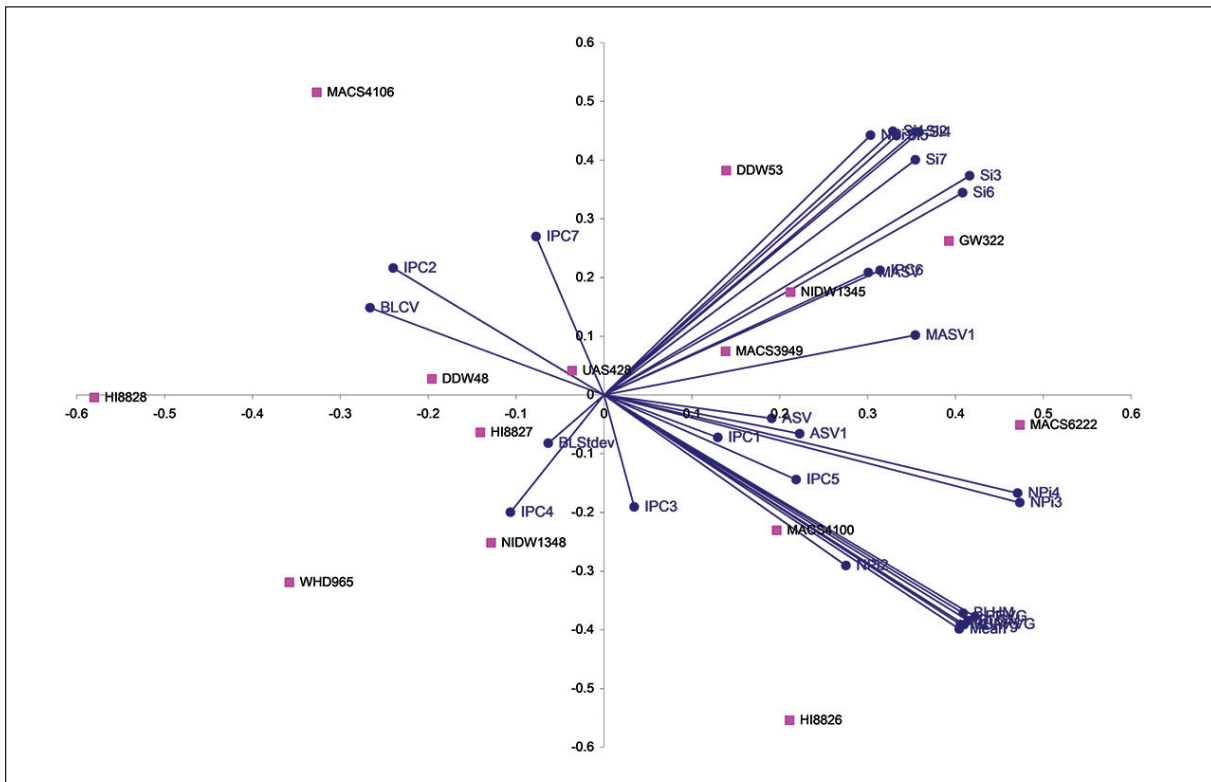


Fig. 1: Biplot analysis of AMMI, BLUP and non parametric measures

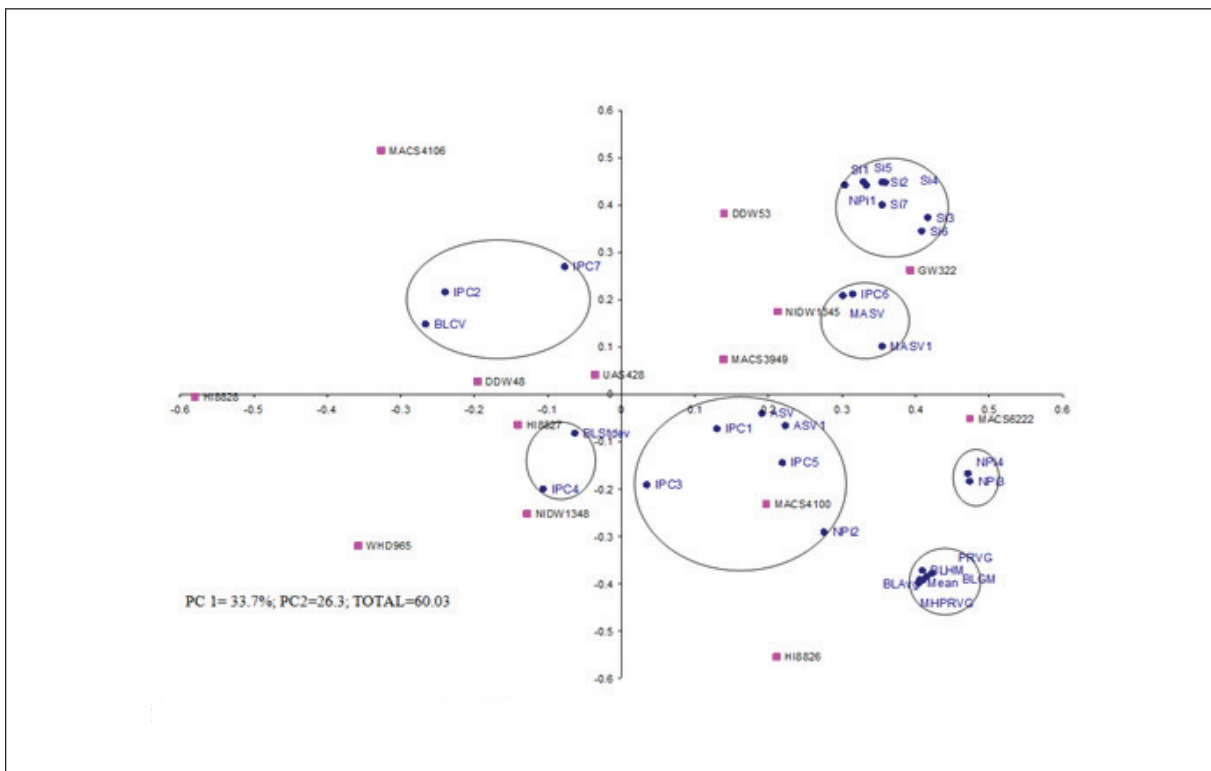


Fig. 2: Clustering pattern of AMMI, BLUP and non parametric measures

Comparative analysis of genotype x environments interaction

HMRPGV measures had the same genotypes as per ranking that was reported by Gonçalves *et al.* (2020); Anuradha *et al.* (2022).

Non parametric composite measures

Measure S_i^1 selected G11, G1, G3 while S_i^2 favoured G1, G11, G3 as per values of S_i^3 desirable genotypes would be G11, G1, G3. Values of measure S_i^4 identified G1, G11, G3 and measure S_i^5 pointed towards G11, G1, G3 while S_i^6 observed suitability of G11, G3, G1 genotypes and lastly S_i^7 values identified G1, G13, G14 genotypes (Table 4). These measures determine the stability of genotype in biological concept over environment (Mehraban *et al.*, 2019). Non parametric $NP_i^{(1)}$ measure observed suitability of G11, G1, G3 whereas as per $NP_i^{(2)}$, genotypes G11, G1, G9 would be of choice while $NP_i^{(3)}$ identified G11, G1, G9. Last composite measure $NP_i^{(4)}$ found G11, G1, G9 as genotypes of choice for this zone

Biplot analysis of measures

The first two significant PCs have explained about 60% of the total variation in the AMMI, BLUP and non parametric measures (Table 5) with respective contributions of 33.7 and 26.3 by PC1 and PC2. Measures $NP_i^{(3)}$, $NP_i^{(4)}$, RPGV, BLGM, HMGV accounted more of share in PC1 whereas S_i^6 , S_i^1 , S_i^2 , S_i^4 , S_i^5 , $NP_i^{(1)}$ contributed more in PC2. The association analysis among measures had been explored with the biplot analysis. In the biplot vectors of measures expressed acute angles would be positively correlated whereas those achieved obtuse or straight line angles would be negatively correlated. Independent type of relationships had expressed by right angles between vectors. $NP_i^{(3)}$, $NP_i^{(4)}$ showed very tight positive relationships with ASV, ASV1, IPC1, IPC5. Average yield maintained strong direct relationship with BLUP based measures and $NP_i^{(2)}$. MASV and MASV1 exhibited direct relation with IPC6. Non parametric measure $NP_i^{(1)}$ achieved strong relation with other non parametric measures, S_i^1 , S_i^2 , S_i^3 , S_i^4 , S_i^5 , S_i^6 , S_i^7 . This group of measures had no relationship with BLUP based measures as evident with right angles among vectors of respective measures. IPC2 and IPC7 expressed no relation with MASV and MASV1 measures (Fig. 1). In total seven clusters of studied measures had been observed in biplot analysis (Fig. 2). Smallest cluster comprises of $NP_i^{(3)}$ & $NP_i^{(4)}$ measures and second comprised of IPC4 with BLStdev. Two clusters consisted on three measures MASV, MASV1, IPC6; IPC2, IPC7, BLCV measures.

ASV joined hands with ASV1, IPC1, IPC3, IPC5 along with $NP_i^{(2)}$ in large sized cluster, besides with cluster of mean yield with BLUP based measures. Further cluster comprises of S_i^1 , S_i^2 , S_i^3 , S_i^4 , S_i^5 , S_i^6 , S_i^7 with $NP_i^{(1)}$.

Spearman rank correlation analysis

Average yield had expressed direct and indirect relationships with measures (Table 6). It was notably positive with IPC2, IPC7, BLAVg, BLGM, HMGV, RPGV, HMRPGV and negative with $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. AMMI based measures ASV and ASV1 showed only weak to moderate direct and indirect with measures (Anuradha *et al.*, 2022). Measures considered all significant IPC's showed moderate to strong positive correlation values (S_i^1 , S_i^2 , S_i^3 , S_i^4 , $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$) along with weak negative values. BLUP based measures maintained weak relation with other measures and strong to moderate negative correlation with non parametric measures. S_i^8 exhibited weak to moderate correlation negative values with other measures whereas it was strong and positive with $NP_i^{(6)}$, S_i^4 , $NP_i^{(3)}$, $NP_i^{(4)}$ (Pour Aboughadareh *et al.*, 2022). Lastly composite non parametric measures expressed strong negative values with mean IPC2 while positive with IPC5, IPC6, IPC7 measures. Strong negative with BLUP based measures were also evident from correlation table. Highly positive relation was observed with S_i^8 as well as among themselves.

CONCLUSION

Modeling of genotype x environment interaction under multi environment trials needs merit to assess the phenotypic stability of the promising genotypes for a range of environmental conditions. Quite number of measures started from multivariate approach AMMI as compared to joint regression analysis to BLUP based and computationally easy non parametric had been compared in current study. Association analysis among measures as per ranking of genotypes to corresponding measures observed measures considered all significant interaction principal components showed moderate to strong positive correlation values with non parametric measures. Besides BLUP based measures maintained strong to moderate negative correlation with non parametric measures

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