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## INTEGRATING DIFFERENT ADAPTABILITY MEASURES TO INVESTIGATE GENOTYPE × ENVIRONMENT INTERACTIONS TO IDENTIFY STABLE HIGH-YIELDING WHEAT GENOTYPES

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### ABSTRACT

AMMI analysis had expressed the major share of variations in yield had been accounted by environments effects 37.5% followed by genotypes of 18.5% in a study of 12 wheat genotypes were evaluated at nine major locations of the peninsular zone during last cropping season. ASV had considered the first two interaction principal components and selected the DBW359, HI1605, NIDW1149, while MASV measure had exploited the contribution of significant interaction principal components had pointed for the DBW359, NIDW1149, UAS478 genotypes. The superiority index values had been identified the DBW359, NIDW1149, HI 1605 as of suitable genotypes for the zone. BLUP based analytic measures RPGV and RPGV\*Meanb had favoured the DBW359, NIAW4028, NIAW3170 and HMRPGV & HMRPGV\*Meanb had settled for DBW359, NIAW3170, HI 1665 wheat genotypes. Biplot analysis based on two principal components had observed  $NP_1^{(3)}$  had maintained the direct association with  $NP_1^{(4)}$ , IPC7 on one side and with  $S_1^6$ ,  $NP_1^{(2)}$ , IPC1 measures on other side. Direct association of WAASB had observed with rASV, rMASV, ASV, MASV on right hand side and with W2, W3, W4, W5, rWAASB on the left side. Composite non parametric measures  $NP_1^{(2)}$ ,  $NP_1^{(3)}$ ,  $NP_1^{(4)}$  had clustered with IPC1,  $S_1^6$  values and placed besides the cluster of W2, W3, W4, W5, WAASB, ASV, MASV, rASV, rMASV, rWAASB in the second quadrant.

**Key words :** AMMI analysis, Biplot graphical presentation, BLUP based analytic measures.

### Introduction

The weather vagaries would be more challenging in the scenario of changing climatic conditions as more emphasis had been placed on the cultivation of stable and resilient varieties with efficient water management and natural resources (Hossain *et al.*, 2023). For this purpose, breeders have the necessary statistical tools for the more correct interpretation regarding the performance of the genotypes under multi locations trials (Karimizadeh *et al.*, 2023). The wheat crop had been looked for sustaining yield potential and stable performance are largely taken into account in the major strategies to ensure the feeding the burgeoning population (Jêdzura *et al.*, 2023). The growth and development in the yield potential of cultivated genotypes had been influenced by the

number of abiotic and biotic factors, as well as the cultivation and fertilization activities (Saremirad and Taleghani, 2022). These aspects, apart from the difference in genetic makeup of genotypes, affect the degree and direction of the genotype × environment interaction. The sustainability in the response to a complex set of factors, combined with the ability to maintain a relatively high mean for yield, is a prerequisite for broad genotype adaptation as genotypes with higher adaptability are preferred in the recent agricultural practices (Taleghani *et al.*, 2023). The grain yield is a complex trait that has been governed by genotype (G), environment (E) and their interaction (G×E) effects (Azam *et al.*, 2023). This interaction effect reflects the yield variation unexplained by individual G and E effects. In other words, the significant cross over G×E interaction effect reduces

the relationship between phenotypic and genotypic values, so it hampers the selection of genuine genotypes (Olivoto *et al.*, 2019)). The meaningful Interpretation of the G×E interaction effect in multi-environment trials (METs) helps in the selection of stable varieties for different environments and even specific varieties for specific environmental conditions (Mohammadi *et al.*, 2023). Several numerical and graphical analyses approaches have been reflected in recent literature to estimate and better understanding the G×E interactions to recommend better performing and higher yielding genotypes across different environments (Saeidnia *et al.*, 2023). There are two main types of numerical analyses for interpreting GEI effects: parametric and non-parametric methods (Pour-Aboughadareh *et al.*, 2019). Non-parametric methods are a feasible alternative to existing parametric measurements because their performance is based on ranks of data and no assumptions are needed about the distribution of model residuals and homogeneity of variances (Shojaei *et al.*, 2021). Each analytic process has its strengths and weaknesses for the selection of

desirable varieties and specific ways for addressing GEI effects; therefore, most breeding programs incorporate parameters from both parametric and non parametric methods.

## Materials and Methods

Twelve wheat genotypes at nine locations of the peninsular plains zone were evaluated under field trials during the cropping season 2022-23 as mentioned in Table 1 for ready reference. Balanced random block design with four replications were used as the genotypes were evaluated at third and final stage before their recommendation for large area cultivation in the zone (Table 1). The plot size at each location was 6 × 2.40 m<sup>2</sup> and the inner 12 rows of each genotype were considered for data recording to overcome the effect of border rows. The recommended fertilizer dose (kg/ha) 90:60:40 (N:P:K) was thoroughly mixed with soil and sowing was completed during October 25 to 5 November 2022 with 00 kg per acre as seed rate. One pre sowing irrigation was applied and latter one during 40-45 days after sowing of

**Table 1 :** Locations and parentage details of wheat genotypes evaluated under rain fed irrigation.

Code	Genotype	Parentage	Location	Latitude	Longitude	Altitude
PZRI301	NIAW3170	SKOLL/ROLF07	Pune	18° 31' N	73° 51' E	562
PZRI302	NIAW4028	WHEAR/SOKOLL/3/TRCH/SRTU//KACHU	Niphad	20° 4' N	74° 6' E	551
PZRI303	DBW397Q	ROLF07/YANAC//TACUPETOF2001/ BRAMBLING/4/WBLL1/KUKUNA// TACUPETOF2001/3/BAJ	Nashik	19° 59 ' N	73° 47' E	583
PZRI304	UAS481	AMRUTH/(MINIMUS/COMBUCK-2//CHAM-3 /3/CANELO-9/USDA595/3/D67.3/RABI//CRA /4/ALO/5/HUI/YAV-1/6/ARDENTE/7/ HUI/ YAV79/8/POD-9/10/TARRO-1/2*YUAN-1// AJAIA-13/YAZI/3/SOMAT-4/INTER-8/4/ ARMENT//SRN-3/NIGRIS-4/3/CANELO-9.1)	Parbhani	19° 15' N	76° 46' E	413
PZRI305	UAS478	AMRUTH/(MINIMUS/COMBUCK-2//CHAM-3/ 3/CANELO-9/9/USDA595/3/D67.3/RABI//CRA/ 4/ALO/5/HUI/YAV-1/6/ARDENTE/7/HUI/YAV79/ 8/POD-9/10/TARRO-1/2*YUAN-1//AJAIA-13 /YAZI/	Dharwad	15° 27' N	75° 0' E	724
PZRI306	DBW359	DBW17/NI5439//43rdIBWSN1137	Nippani	16° 23 ' N	74° 22' E	606
PZRI307	HI1665	HI1531/HI1544	Bagalkot			
PZRI308	DDW61	HI8498/PDW233//PDW291	Ugar-Khurd	16° 39 ' N	74° 49' E	548
PZRI309	NIDW1149	NIDW295/NIDW15	Kalloli	16° 26 ' N	74° 86' E	625
PZRI310	HI1605	BOW/VEE/5/ND/VG9144//KAL//BB/3/YACO/4/ CHIL/6/CASKOR/3/CROC-1/A.SQUARROSA (224)//OPATA/7/				
PZRI311	UAS446	DWR185/DWR2006//UAS419				
PZRI312	HI8840	HI8681/HI8627				

genotypes. The details of AMMI analysis, BLUP and Non parametric based measures mentioned in the literature were reflected below for completeness as: (Zali *et al.*, 2012; Vineeth, 2022):

AMMI Stability Value :

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

Modified AMMI stability Value

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

Harmonic Mean Genotypic Value

$$HMGV = \text{Number of environments} / \sum_{j=1}^k \frac{1}{GV_{ij}}$$

$GV_{ij}$  genetic value of  $i$ th genotype in  $j$ th environments  
Relative performance of genotypic values across

$$\text{environments } RPGV_{ij} = \sum_{j=1}^k \frac{GV_{ij}}{\sum_{j=1}^k GV_j}$$

Harmonic mean of Relative performance of genotypic values

$$HMRPGV_i = \text{Number of environments} / \sum_{j=1}^k \frac{1}{RPGV_{ij}}$$

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

Simultaneous selection index

$$SSI = R \text{ (AMMI stability indices)} + RY$$

Weighted Average of Absolute Scores

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

$$\text{Superiority index : } SI = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(\theta_Y + \theta_S)}$$

Non parametric measures based on the ranks

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

$$S_i^{(3)} = \frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{\bar{r}_i}$$

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

$$S_i^{(5)} = \frac{\sum_{j=1}^n |r_{ij} - \bar{r}|}{n}$$

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

$$S_i^{(7)} = \frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{\sum_{j=1}^n |r_{ij} - \bar{r}_i|}$$

Measures based ranks of corrected means of genotypes with average of ranks and median

$$NP_i^{(1)} = \frac{1}{n} \sum_{j=1}^n |r_{ij}^* - M_{di}^*|$$

$$NP_i^{(2)} = \frac{1}{n} \left( \frac{\sum_{j=1}^n |r_{ij}^* - M_{di}^*|}{M_{di}^*} \right)$$

$$NP_i^{(3)} = \sqrt{\frac{\sum (r_{ij}^* - \bar{r}_i^*) / n}{\bar{r}_i}}$$

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

The recent and well known software's *viz.* Meta-R, AMMI soft and SAS were used to analyse the research data generated under multi location evaluation of wheat genotypes

## Results and Discussion

The highly significant effects of environments, genotypes and genotype × environments interactions were observed by AMMI analysis of 12 wheat genotypes evaluated at nine major locations of the peninsular zone during 2022-23 cropping season. Major share of variation accounted by environments effects 37.5% followed by genotypes of 18.5% whereas the G×E interactions accounted for 17.3% only (Table 2) as reflected by Mohammadi *et al.* 2020a. Interaction effects had been

**Table 2 :** Additive and multiplicative effects analysis of variance of AMMI model.

Source	Degree of freedom	Sum of squares	Mean sum of squares	Level of significance	Share of factors (%)	IPC's share (%)	Cumulative share of IPC's (%)
Treatments	107	9492.19	88.71	***	74.35		
Genotype (G)	11	2487.74	226.16	***	19.49		
Environment (E)	8	4790.86	598.86	***	37.53		
G × E interaction	88	2213.59	25.15	***	17.34		
IPC1	18	993.96	55.22	***		<b>44.90</b>	44.90
IPC2	16	653.47	40.84	***		<b>29.52</b>	74.42
IPC3	14	304.30	21.74			<b>13.75</b>	88.17
IPC4	12	131.67	10.97			<b>5.95</b>	94.12
IPC5	10	59.61	5.96				
IPC6	8	34.77	4.35				
IPC7	6	19.83	3.30				
Residual	4	15.99	4.00				
Error	324	3274.51	10.11				
Blocks/Env	27	632.73	23.43				
Pure Error	297	2641.78	8.89				
Total	431	12766.70	29.62				

further partitioned into seven interactions effects whereas only first four were of the significant types more over the respective contributions were 44.9%, 29.5%, 13.8%, 5.9%, respectively (Mohammadi *et al.*, 2020b). A total of 74.4% of interaction effects had been augmented by first two significant interaction components whereas the total of significant interaction components was of 94.1% in the current study as observed by Bocianowski and Prażak (2022).

#### Performance of genotypes as per simultaneous selection indices

Table 3 had showed that DBW359, NIAW3170, HI1665 genotypes had expressed the higher yield values as compared to the others as least values of IPC1 had observed for HI8840, DBW359, DDW 61 wheat genotypes, while the genotypes UAS481, UAS446, DBW397 had exhibited the least values of IPC3 measure. DBW397, DBW359, DDW61 genotypes had pointed out by IPC4 measure whereas by IPC5 values the desirable genotypes would be NIAW4028, UAS478, HI1665 as IPC7 measure had favoured to HI1665, NIAW4028, DBW397 and last measure had settled for HI1665, NIDW1149, UAS478 wheat genotypes. Measure ASV had selected the DBW359, HI1605, NIDW1149 as top ranked among the evaluated genotypes and MASV values had ranked the DBW359, NIDW1149, UAS 478 as first three genotypes. The minimum values of W2 measure had expressed by DBW359, HI1605, NIDW 1149 and values of W3 had exhibited by DBW359, NIDW1149, HI1605 genotypes. The superiority index

values had been identified the DBW359, NIDW1149, HI 1605 as suitable genotypes for the zone as per their performance among the major locations of the zone.

#### Behaviour of genotypes assessed by Non parametric measures

Average of BLUP values of the genotypes across the locations had achieved by DBW359, NIAW3170, HI1665 wheat genotypes, whereas the consistent performance had observed for DBW397, NIAW4028, DBW359 genotypes by SD and values of CV measure had expressed by DBW397, DBW359, NIAW4028 genotypes (Table 4). More values of Genotypic Adaptability Index had exhibited by DBW359, NIAW3170, HI1665 genotypes while the more values for HMGV measure showed by DBW359, HI1665, NIAW4028 genotypes. The more values of next two adaptability measures RPGV and RPGV\*Meanb expressed by DBW359, NIAW4028, NIAW3170 whereas the last measures HMRPGV & HMRPGV\*Meanb had settled for DBW359, NIAW3170, HI1665 wheat genotypes in the present study. The lower values of non parametric measures had expressed the stable behaviour of the genotypes and calculated as per the ranks of the genotypes over the locations of the zone. First measure  $S_1^1$  found the suitability of NIDW1149, HI1605, UAS478, while the values of  $S_1^2$  had favoured the NIDW1149, DBW359, HI1605 and next measure  $S_1^3$  had pointed towards the NIDW1149 DBW359, HI1605. The least values of  $S_1^4$  had expressed by NIDW1149, DBW359, HI1605 and minimum values of  $S_1^5$  had

**Table 3 :** Simultaneous selection index and AMMI analysis based indexes.

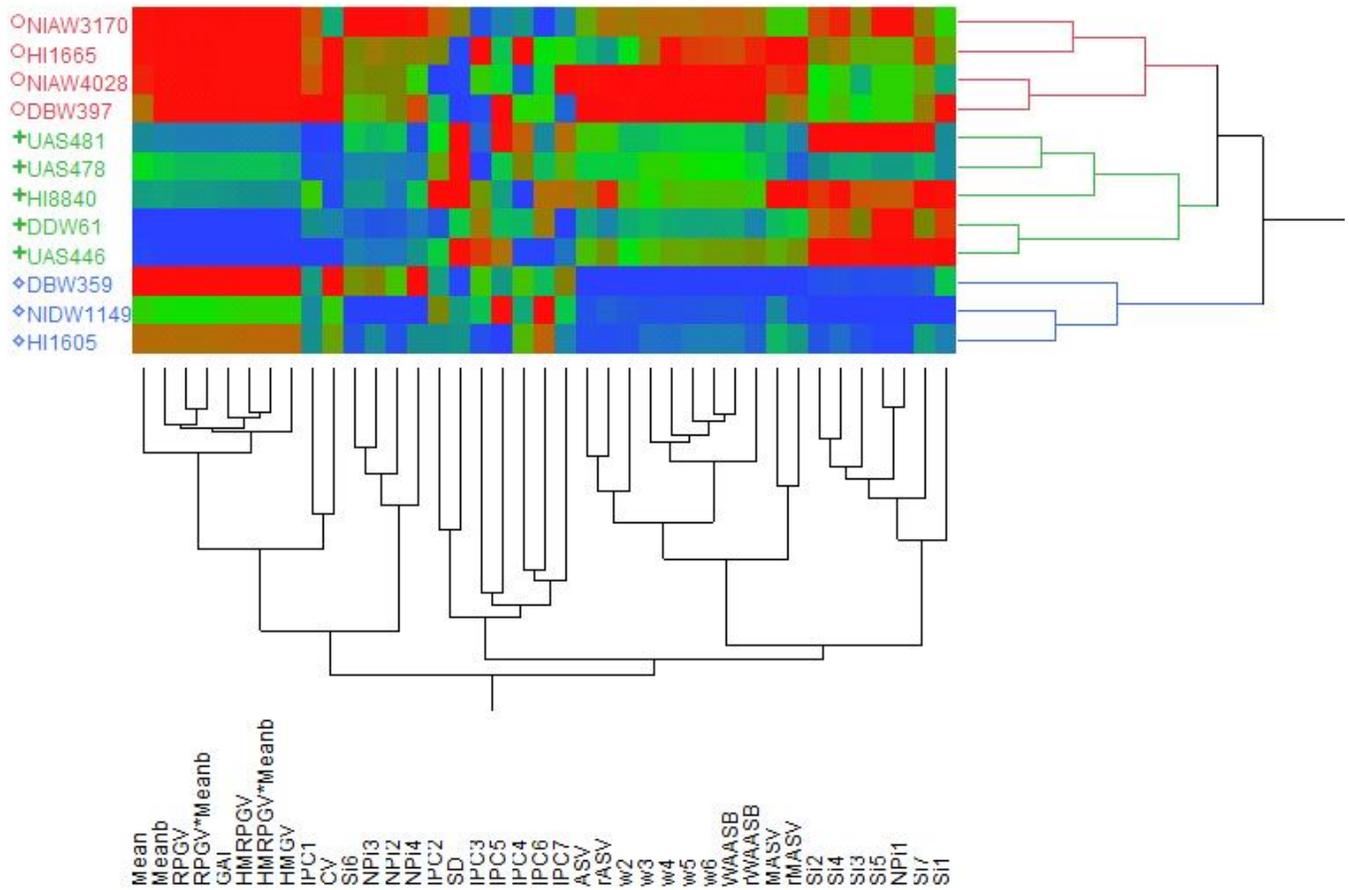
Genotype	Mean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	ASV	rASV	MAS V	rMA SV	W2	W3	W4	W5	W6	WAA SB	rWA ASB
NIAW3170	32.34	1.217	1.103	-0.770	-0.309	-0.537	-0.842	-0.325	1.863	9	3.345	7	1.169	1.095	1.028	1.006	1.001	0.985	9
NIAW4028	32.13	1.220	-1.924	0.155	-0.677	-0.063	-0.055	0.870	2.442	11	4.030	10	1.519	1.267	1.217	1.166	1.131	1.125	11
DBW397	31.62	2.253	-0.305	-0.889	0.080	0.909	0.058	-0.429	2.795	12	3.618	9	1.424	1.326	1.220	1.206	1.170	1.153	12
UAS481	28.46	-1.423	-0.060	-0.661	0.788	0.659	-0.343	0.414	1.756	7	2.864	4	0.843	0.810	0.808	0.801	0.787	0.778	5
UAS478	30.02	-1.207	0.436	-1.072	0.529	-0.125	-0.127	0.153	1.551	6	2.762	3	0.879	0.915	0.882	0.848	0.826	0.810	6
DBW359	33.18	-0.388	-0.488	0.187	0.172	-0.321	-0.126	0.307	0.683	1	1.267	1	0.430	0.386	0.367	0.365	0.358	0.357	1
HII665	32.32	1.089	0.656	1.768	1.511	-0.135	-0.018	0.048	1.495	5	4.570	12	0.905	1.064	1.102	1.060	1.027	1.004	10
DDW61	25.55	-0.468	-1.290	0.738	-0.176	-0.172	0.387	-0.688	1.414	4	2.906	6	0.818	0.803	0.750	0.724	0.713	0.713	4
NIDW1149	30.44	-0.575	0.621	-0.144	-0.227	0.782	0.936	-0.076	0.943	3	2.456	2	0.595	0.512	0.487	0.500	0.514	0.504	2
HII605	31.65	-0.469	-0.666	-0.819	0.219	-1.126	0.482	-0.306	0.882	2	2.878	5	0.552	0.602	0.569	0.594	0.590	0.584	3
UAS446	26.05	-1.447	-0.177	1.067	-0.894	0.421	-0.794	-0.381	1.793	8	3.461	8	0.907	0.937	0.933	0.910	0.907	0.894	8
HI8840	28.98	0.198	2.093	0.440	-1.016	-0.291	0.442	0.414	2.108	10	4.330	11	1.004	0.900	0.910	0.882	0.868	0.858	7

SD: Standard deviation; GAI: Geometric Adaptability Index; HMGV: Harmonic mean of Genotypic values; HMGV: Relative performance of genotypic values; HMRPGV: Harmonic mean of relative performance and BLUP based analytic indexes.

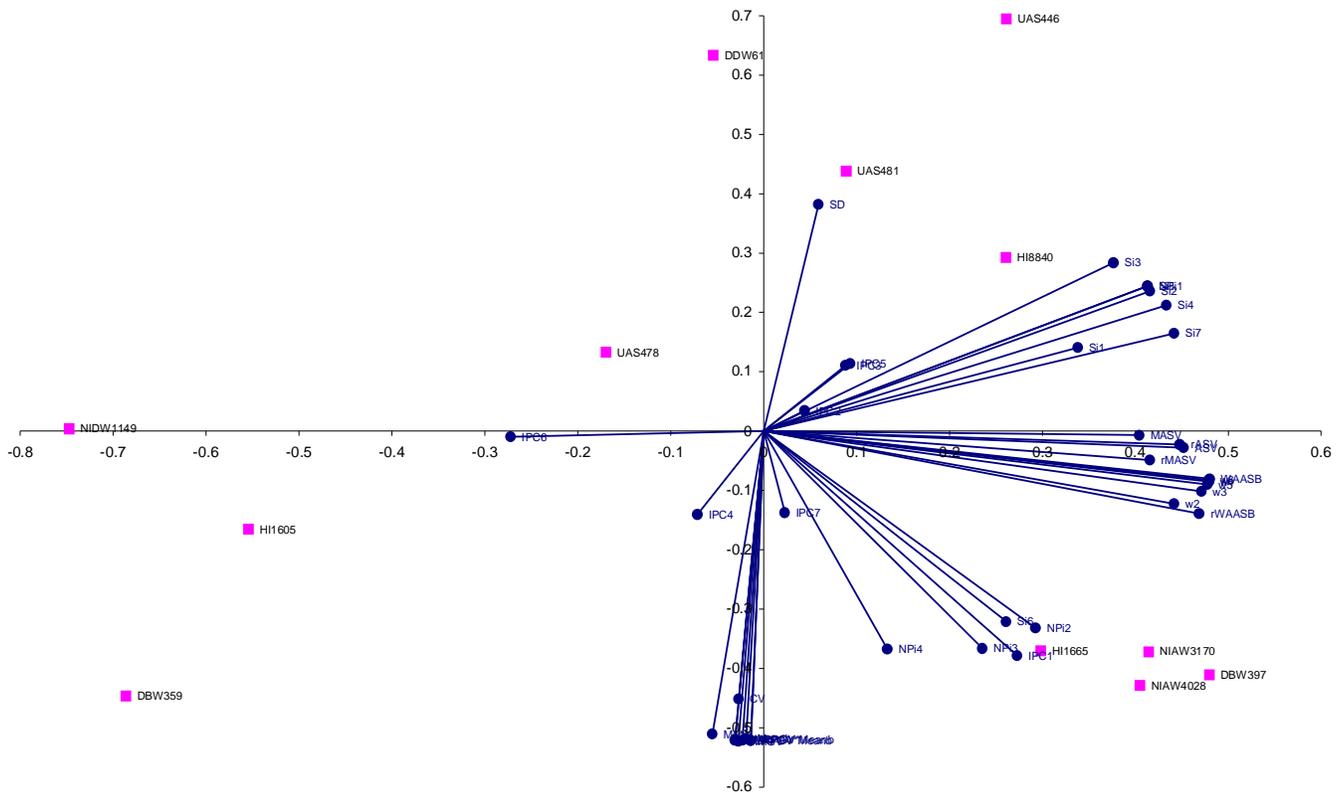
**Table 4 :** Non parametric and BLUP based analytic indexes.

Genotype	S <sub>1</sub> <sup>1</sup>	S <sub>1</sub> <sup>2</sup>	S <sub>1</sub> <sup>3</sup>	S <sub>1</sub> <sup>4</sup>	S <sub>1</sub> <sup>5</sup>	S <sub>1</sub> <sup>6</sup>	S <sub>1</sub> <sup>7</sup>	NP <sub>1</sub> <sup>(1)</sup>	NP <sub>1</sub> <sup>(2)</sup>	NP <sub>1</sub> <sup>(3)</sup>	NP <sub>1</sub> <sup>(4)</sup>	Meamb	SD	CV	GAI	HM GV	RP GV	RPGV *Mean b	HMR PGV *Mea nb	
NIAW3170	22.000	15.506	2.288	3.938	0.395	0.970	4.078	3.556	1.185	1.139	6.000	32.05	4.38	13.67	31.76	31.43	1.060	32.04	1.055	31.90
NIAW4028	18.500	11.580	1.533	3.403	0.321	0.619	3.941	2.889	0.722	0.773	3.964	31.88	3.21	10.07	31.72	31.55	1.062	32.10	1.052	31.79
DBW397	28.833	11.951	1.763	3.457	0.321	0.553	4.102	2.889	0.722	0.702	5.521	31.81	3.12	9.82	31.68	31.54	1.058	31.98	1.052	31.80
UAS481	16.667	18.321	3.111	4.280	0.420	0.453	4.470	3.778	0.472	0.545	2.000	28.61	5.03	17.58	28.17	27.69	0.941	28.44	0.935	28.27
UAS478	16.333	8.667	1.529	2.944	0.272	0.361	3.441	2.444	0.349	0.461	2.410	29.84	4.91	16.45	29.43	28.96	0.982	29.69	0.978	29.56
DBW359	19.833	4.691	0.716	2.166	0.198	0.615	2.568	1.778	0.593	0.795	6.865	32.30	3.23	9.99	32.15	31.99	1.071	32.39	1.070	32.35
HII665	23.500	13.951	2.058	3.735	0.333	0.628	4.280	3.000	0.750	0.829	4.919	31.90	3.25	10.19	31.74	31.57	1.059	32.02	1.055	31.89
DDW61	27.167	14.889	2.233	3.859	0.395	0.317	4.020	3.556	0.296	0.365	2.421	26.71	3.94	14.75	26.44	26.16	0.883	26.70	0.878	26.53
NIDW1149	8.833	2.765	0.453	1.663	0.160	0.217	1.898	1.444	0.181	0.265	1.325	30.30	3.78	12.49	30.06	29.78	1.002	30.28	1.000	30.24
HII605	15.167	5.506	0.812	2.347	0.173	0.298	3.279	1.556	0.259	0.477	2.904	31.22	3.75	12.02	31.02	30.80	1.034	31.25	1.032	31.20
UAS446	31.000	16.617	2.671	4.076	0.407	0.355	4.428	3.667	0.333	0.418	3.000	26.77	4.81	17.98	26.36	25.92	0.881	26.64	0.875	26.44
HI8840	28.167	15.728	2.528	3.966	0.370	0.405	4.616	3.333	0.333	0.512	3.426	29.35	4.98	16.95	28.86	28.22	0.966	29.21	0.955	28.88

Meamb : Average of BLUP ; rASV, rMASV and rWAASB: Rank of genotypes for ASV, MASV and WAASB values; ssiASV, ssiMASV and ssiWAASB : Simultaneous selection index based on ranks of yield and of ASV, MASV and WAASB simultaneous.



**Fig. 1 :** Two ways clustering of genotypes and measures as per Ward's method.



**Fig. 2 :** Biplot analysis for the genotypes and measures for evaluated wheat genotypes.

**Table 5 :** Loadings of measures and genotypes based on significant principal components.

Measures	Contribution in PC1	Contribution in PC2	Measures	Contribution in PC1	Contribution in PC2	Genotype	Contribution in PC1	Contribution in PC2
Mean	-0.028	-0.268	SD	0.030	0.201	NIAW3170	0.282	-0.261
IPC1	0.139	-0.199	CV	-0.014	-0.237	NIAW4028	0.275	-0.301
IPC2	0.023	0.018	GAI	-0.011	-0.274	DBW397	0.326	-0.288
IPC3	0.045	0.058	HMGV	-0.014	-0.275	UAS481	0.061	0.307
IPC4	-0.036	-0.074	RPGV	-0.007	-0.274	UAS478	-0.115	0.093
IPC5	0.048	0.060	RPGV* Meanb	-0.007	-0.274	DBW359	-0.466	-0.313
IPC6	-0.138	-0.005	HMRPGV	-0.016	-0.274	HI1665	0.203	-0.260
IPC7	0.012	-0.072	HMRPGV *Meanb	-0.016	-0.274	DDW61	-0.037	0.444
ASV	0.230	-0.015	S <sub>i</sub> <sup>1</sup>	0.172	0.074	NIDW1149	-0.507	0.003
rASV	0.228	-0.012	S <sub>i</sub> <sup>2</sup>	0.225	0.086	HI1605	-0.376	-0.116
MASV	0.206	-0.004	S <sub>i</sub> <sup>3</sup>	0.192	0.149	UAS446	0.178	0.487
rMASV	0.212	-0.026	S <sub>i</sub> <sup>4</sup>	0.220	0.111	HI8840	0.177	0.205
W2	0.225	-0.064	S <sub>i</sub> <sup>5</sup>	0.210	0.128			
W3	0.240	-0.053	S <sub>i</sub> <sup>6</sup>	0.133	-0.169			
W4	0.244	-0.045	S <sub>i</sub> <sup>7</sup>	0.212	0.124			
W5	0.243	-0.047	NP <sub>i</sub> <sup>(1)</sup>	0.210	0.128			
W6	0.244	-0.043	NP <sub>i</sub> <sup>(2)</sup>	0.149	-0.174			
WAASB	0.244	-0.042	NP <sub>i</sub> <sup>(3)</sup>	0.120	-0.193			
rWAASB	0.239	-0.073	NP <sub>i</sub> <sup>(4)</sup>	0.068	-0.193			
Meanb	-0.010	-0.272	% share of factors (71.98%)	38.26%	33.71%			

expressed by NIDW1149, HI1605, DBW359 genotypes. Wheat genotypes NIDW1149, HI1605, DDW61 had selected by S<sub>i</sub><sup>6</sup> measure whereas the last measure S<sub>i</sub><sup>7</sup> had settled for NIDW1149, DBW359, HI1605. The composite non parametric measures had considered the ranks of genotypes performance based on original and corrected yield of genotypes across the locations of the zone as minimum values of NP<sub>i</sub><sup>(1)</sup> had expressed by NIDW1149, HI1605, DBW359, while NIDW1149, HI1605, DDW61 genotypes had maintained the lower values of NP<sub>i</sub><sup>(2)</sup> and the measure NP<sub>i</sub><sup>(3)</sup> had pointed towards the NIDW1149, DDW61, UAS478 genotypes while the last composite non parametric measure had found the suitability of NIDW1149, UAS481, UAS478 genotypes as compared to the others in the study.

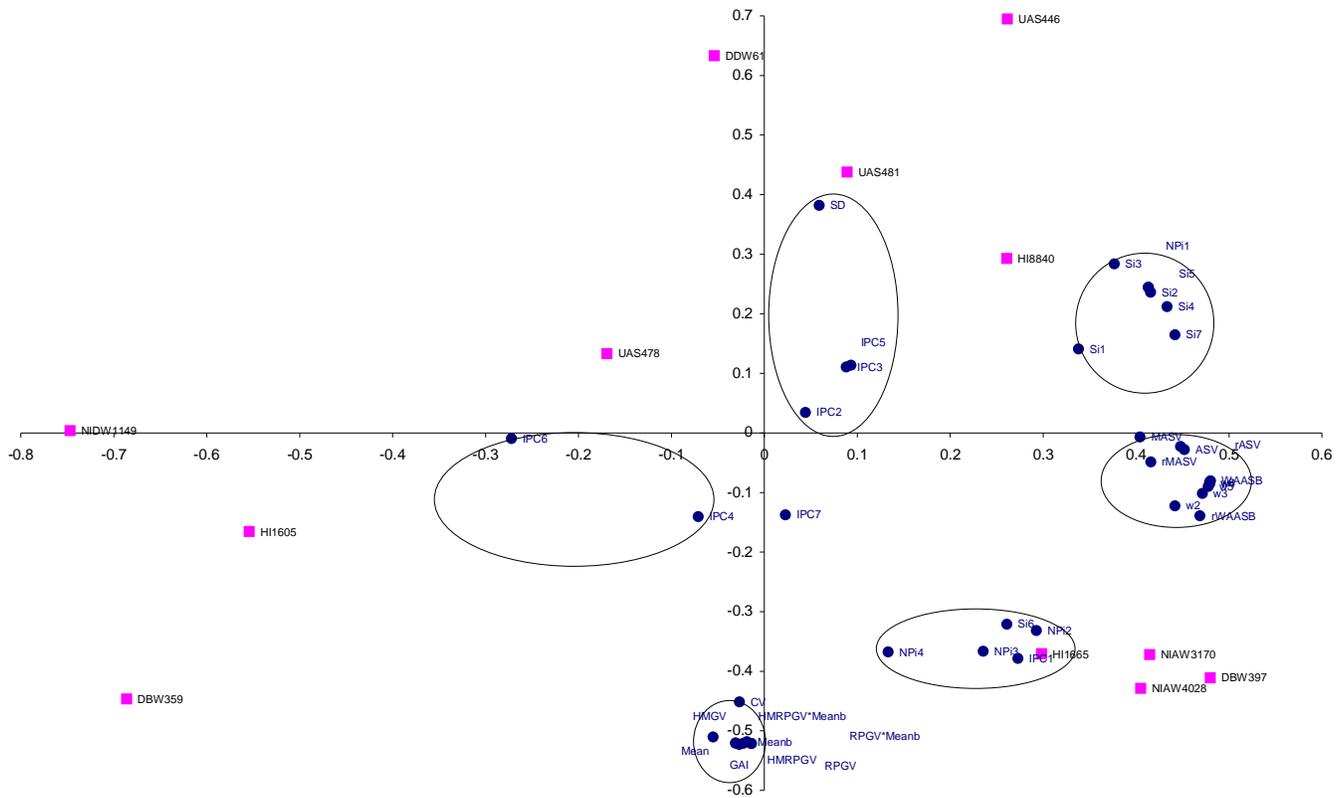
#### Ward's method of clustering for genotypes and measures

Broadly three groups of genotypes had been observed

by the Ward's method of clustering (Khalid *et al.*, 2023) in the present study with respective five, four and three in groups (Fig. 1). Measure IPC5 had divided the studied measures as AMMI based measures with non parametric measures in one side and BLUP based analytic measures with composite non parametric measures on the other side at the first node of bifurcation. Further division of AMMI based measures at the second node had expressed in two groups consisted of six and ten measures while large numbers of further smaller groups found for BLUP based analytic measures.

#### Biplot analysis of genotypes and measures

Total of 71.9% of variation among the evaluated wheat genotypes and various measures calculated in the study had accounted by first two principal components with respective share of 38.3% and 33.7% (Table 5) as observed by Saeidnia *et al.* (2023). More share of the measures W4, W6, WAASB, W5, W3, rWAASB



**Fig. 3 :** Association analysis among the measures based on two principal components.

contributed in first principal component whereas the HMGV, HMRPGV\*Meanb, HMRPGV, RPGV\* Meanb, RPGV, Mean had accounted more in second principal component. In terms of the contributions of genotypes more of NIDW1149 HI1605 DBW397 in first component while for second components UAS446, DDW61, DBW359 of wheat genotypes. Genotypes NIDW1149, DBW359, UAS446, NIAW4028 were placed at far from the origin as compared to UAS478 & HI8840 wheat genotypes (Fig. 2). Very tight relationship had observed among the BLUP based analytic measures and direct association with IPC4 values in the first quadrant. Measure  $NP_i^{(3)}$  had maintained the direct association with  $NP_i^{(4)}$ ,  $IPC7$  on one side and with  $S_i^6$ ,  $NP_i^{(2)}$ ,  $IPC1$  measures on other side. Direct association of WAASB had observed with rASV, rMASV, ASV, MASV on right hand side and with W2, W3, W4, W5, rWAASB on the left side. Next quadrant had exhibited the strong relation of  $S_i^2$  with SD,  $S_i^1$  Ninety degree angles observed for BLUP based analytic measures with AMMI analysis based WAASB, of  $S_i^3$  with  $NP_i^{(4)}$ ,  $IPC4$  with  $NP_i^{(2)}$ ,  $NP_i^{(3)}$  with  $S_i^3$ , SD with rASV,  $S_i^4$  with  $NP_i^{(3)}$  etc. Moreover, the straight line angle of  $IPC6$  with MASV values.

Total of six clusters had observed in the biplot graphical analysis of evaluated genotypes and estimated values of various measures of the current study (Fig. 3).

CV measure had observed with BLUP based analytic measures along with another group of  $IPC6$  &  $IPC4$  in the first quadrant of the biplot analysis as per first two principal components. Composite non parametric measures  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$  had clustered with  $IPC1$ ,  $S_i^6$  values and placed besides the cluster of W2, W3, W4, W5, WAASB, ASV, MASV, rASV, rMASV, rWAASB in the second quadrant. Non parametric measure had joined hands with  $NP_i^{(1)}$  in cluster of third quadrant moreover the cluster of  $IPC2$ ,  $IPC3$ ,  $IPC5$  with SD values was placed in the same quadrant.

### Conclusion

AMMI analysis had expressed the major share of variations in yield had been accounted by environments followed by genotypes. ASV measure had considered the first two interaction principal components and selected the DBW359, HI1605, NIDW1149, while MASV measures had exploited the contribution of significant interaction principal components had pointed for the DBW359, NIDW1149, UAS478 genotypes. The superiority index values had been identified the DBW359, NIDW1149, HI 1605 as suitable genotypes for the zone. BLUP based analytic measures RPGV and  $RPGV*Meanb$  had favoured the DBW359, NIAW4028, NIAW3170 and HMRPGV &  $HMRPGV*Meanb$  had settled for DBW359, NIAW3170, HI1665 wheat

genotypes. Biplot analysis had observed that  $NP_i^{(3)}$  had maintained the direct association with  $NP_i^{(4)}$ , IPC7 on one side and with  $S_i^6$ ,  $NP_i^{(2)}$ , IPC1 values on other side. Direct association of WAASB had observed with rASV, rMASV, ASV, MASV on right hand side and with W2, W3, W4, W5, rWAASB on the left side. Composite non parametric measures  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$  had clustered with IPC1,  $S_i^6$  values and placed besides the cluster of W2, W3, W4, W5, WAASB, ASV, MASV, rASV, rMASV, rWAASB in the second quadrant.

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### Conflict of interest

The authors declared no conflict of interests to report this work in the paper.

### Authors' statement

Authors read, reviewed, agreed and approved the final manuscript. The manuscript has not been submitted to any other journal for publication.

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