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Analysis of the Phenotypic Adaptability and Stability of Wheat Genotypes through the Biplot Approach

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ABSTRACT

The present study was conducted during the cropping season during October to April in the year 2022–23. Highly significant effects of environments, genotypes×environments interactions and genotypes had been observed as per the AMMI analysis of twelve wheat genotypes evaluated under advanced varietal trials at eleven major locations and Environments effects had augmented about 49% of the total sum of squares. ASV measure had utilized the 51.7% of the interaction effects had pointed for DBW296, HI1654, PBW899 while MASV measure had exploited nearly 98% of total interaction effects had selected the DBW296, WH1311, UP3111 genotypes as Superiority index measure also the suitability of same genotypes. The simultaneous selection index based on yield and ASV had pointed towards the HI1653, HI1654, HD3369 and genotypes HI1653, DBW397, WH1311 were identified by ssi MASV and genotypes HI1654, HD3369, HI1653 genotypes settled by ssi WAASB measure. Non parametric S_i^1 had pointed for DBW296, HD3369, NIAW3170 and the values of S_i^2 and S_i^3 had pointed towards DBW296, WH1311, HD3369. Composite non parametric measures First measure $NP_i^{(1)}$ had favoured the DBW296, HI1653, HD3369 while as per $NP_i^{(2)}$ values the DBW296, NIAW3170, PBW899 would be suitable genotypes. Out of the five clusters in the biplot analysis the ASV & WAASB had clustered with $NP_i^{(1)}$, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7 non parametric measures as placed in the first quadrant.

KEYWORDS: AMMI, biplots, BLUP, composite non parametric, ward's clustering, selection index

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1. INTRODUCTION

The identification and recommendations of compatible genotypes for a diverse array of environmental conditions have been always dominated in the breeding programs (Jedzura et al., 2023). The more awareness about the genotype by environment interaction (G×E) had assisted the breeders to evaluate the performance of genotypes more precisely and put forward the specially promising genotypes (Saremirad and Taleghani, 2022). Developing broadly adapted genotypes with a high level of phenotypic stability and yield potential is a tool to overcome the genotype by environment interaction (Shojaei et al., 2021). The cross over interactions between the genotypes and the environments affect the selection of the superior genotypes as leads to inconsistent responses of the genotypes in the multi-location trials evaluation (Mohammadi et al., 2020a; Bocianowski and Prazak, 2022). This differential response of the genotypes to different environmental conditions decreases the correlation between the phenotype and genotype values, hampering the identification and recommendation of promising genotypes for large area cultivation (Jedzura et al., 2023). G×E interaction may be simple when the classification of the genotypes is constant in the variable environments, and the significant interaction is due to differences in the magnitude of the answer; or complex, as the classification of the genotype is different in each environment, displaying higher relevance in the breeding of the plants (Karimizadeh et al., 2023). As the breeding program detects a interaction, it is crucial to infer its magnitude through a study of phenotypic adaptability and stability (Shojaei et al., 2021; Saremirad and Taleghani, 2022). 2016). The phenotypic adaptability and stability analysis allows the identification of the genotypes with predictable performance, in respond to the variable environmental conditions for specific or general breeding advantages (Pour-Aboughadareh et al., 2019; Sharif et al., 2021; Karimizadeh et al., 2023). Several different and recent analytic methods were observed in literature to explain the main effects of (Genotypes and environments) and their interactions more precisely (Taleghani et al., 2023). Parametric methods defined the stability indices considered the interaction effects and the normal distribution of errors, thought their robust assurance might not be applicable for situations when these assumptions are not fulfilled (Pour-Aboughadareh et al., 2019; Shojaei et al., 2021). Apart from the BLUP based analytic measures good number of non-parametric methods considered the ranks of genotypes as per their performance in each environment had been proposed to interpret and describe the responses of genotypes to various environmental conditions (Sharif et al., 2021). Among the multivariate methods apart from AMMI analysis, a new superiority index WAASB has been added to the indices based on the AMMI model (Olivoto et al., 2019). The plant breeders usually employ both parametric and non-parametric approaches to assess the stability and adaptability of genotypes to fully comprehend the interactions pattern among test genotypes across the locations of the target area (Olivoto et al., 2019; Mohammadi et al., 2023). The present study has considered to find any type of relationships among the recent measures as per various analytic approaches mostly cited in latest literature.

2. MATERIALS AND METHODS

Twelve promising wheat genotypes were evaluated under field trials at thirteen major locations of the north western plains zone of the country during October to April months of 2022–23 cropping seasons. Randomised block design with four replications were employed with plot size of 6×2.4 m^2 to accommodate the 12 rows of plants and sowing were completed during October 25 to 05 of November 2022. The recommended dose of fertilizers in the ration 150:60:40 (N:P:K) were applied to ensure good harvest of the healthy crop. The plots were irrigated with pre-sowing and one irrigation at 45–50 DAS of the crop as experiment was conducted for rain fed conditions. The details of AMMI analysis, BLUP and Non parametric based measures mentioned in the literature were tabulated below for ready reference as (Zali et al., 2012; Vineeth, 2022; Saeidnia et al., 2023):

AMMI Stability Value	$ASV=[(\frac{SSIPC\ 1}{SSIPC\ 2}PCI)^2+(PC2)^2]^{1/2}$
Modified AMMI stability Value	$MASV=\sqrt{\sum_{n-1}^{N-1}\frac{SSIPC_n}{SSIPC_{n+1}}PC_n)^2+(PC_{n+1})^2}$
Harmonic Mean Genotypic Value	$HMGV=\text{No. of environments}/\sum_{j=1}^{k}\frac{1}{GV_{ij}}$ GV_{ij} genetic value of ith genotype in jth environments
Relative performance of genotypic values across environments	$RPGVij=\sum_{j}^{k}GV_{ij}/\sum_{j}^{k}GV_{j}$
Harmonic mean of relative performance of genotypic values	$HMRPGV_{i}=\text{No. of environments}/\sum_{j=1}^{k}\frac{1}{RPGV_{ij}}$
Geometric adaptability index	$GAI=\sqrt[n]{\prod_{k=1}^{n}\bar{X}_k}$
Simultaneous selection index	SSI=R(AMMI stability indices)+RY

Weighted average of absolute scores $WAASB=\sum_{k=1}^{p}|IPCA_{ik}\times EP_k|/\sum_{k=1}^{p}EP_k$

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

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

$$S_i^{(2)}=\frac{\sum_{j=1}^{n}(r_{ij}-r_{j'})^2}{(n-1)}$$

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

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

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

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

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

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

$$NP_i^{(1)}=\frac{1}{n}\sum_{j=1}^{n}|r^*_{ij}-M^*_{di}|$$

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

$$NP_i^{(3)}=\frac{\sqrt{\sum(r_{ij}-\bar{r}_i)^{2/n}}}{\bar{r}_i}$$

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

The recent analysis software's viz. Meta-R, AMMIsoft and SAS were used to analyse the research data generated under multi location evaluation of wheat genotypes (Table 1).

3. RESULTS AND DISCUSSION

Highly significant effects of environments, genotypes×environments interactions and genotypes had been observed as per the AMMI analysis of twelve wheat genotypes evaluated under advanced varietal trials at eleven major locations of the north western plains zone of the country. Environments effects had augmented about 49% of the total sum of squares in ANOVA table (Mohammadi et al., 2020b). Interactions effects about 30.5% and 10.8% had been accounted by the genotypes in the current study. Further analysis of interaction effects had expressed significant seven components and first two components had totalled of 51.7% while 97.9% had contributed by seven components and very less left for residual effects in the analysis (Table 2).

3.1. Performance of genotypes based on simultaneous selection index

HI1653, DBW397, HD3369 were top ranked three genotypes in terms of their average yield across the locations. First interaction principal component IPC1 had expressed lower values for the HI1654, PBW899, DBW296 genotypes while as per IPC2 values the desirable genotypes would be DBW296, WH1402, HD3369 and the genotypes DBW296, HI1654, WH1311 had identified by IPC3 measure. The minimum values of IPC4 had expressed by DBW397, DBW398, NIAW3170 genotypes whereas the lower values of IPC5 had maintained by HI1653, PBW644, DBW296 wheat genotypes and the last measure with total of 2.9% of interaction share had settled for HD3369, PBW644, DBW398 genotypes. ASV measure had utilized the 51.7% of first two interaction components had pointed for DBW296, HI1654, PBW899 genotypes for their stable performance while the measure MASV had exploited nearly 98% of total interaction effects had selected the DBW296, WH1311, UP3111 genotypes and Superiority index measure based on AMMI analysis of twelve genotypes at eleven major locations of the zone had found the suitability of DBW296, HI1654, WH1311 genotypes (Olivoto et al., 2019). The simultaneous consideration of yield and stable performance of the genotypes would be more suitable in a single measure to observe the high yield on sustainable basis at the locations of the zone (Jedzura et al., 2023). The simultaneous selection index based on yield and ASV i.e. ssiASV had pointed towards the HI1653, HI1654, HD3369 and genotypes HI1653, DBW397, WH1311 were identified by ssiMASV whereas ssiWAASB measure had settled for HI1654, HD3369, HI1653 wheat genotypes (Table 3).

3.2. Behaviour of genotypes as per BLUP and non parametric measures

More values of average yield of the genotypes as per their BLUP values across the locations of the zone had been observed for DBW397 HI1653 HD3369 and the consistent yield performance had been exhibited NIAW3170 DBW296 PBW899 genotypes. Larger values of geometric adaptability index (GAI) had expressed by DBW397, HI1653, HD3369 genotypes and the lowest yield value by NIAW3170 wheat genotype (Hossain et al., 2023). HMGV measure had found more values for DBW397, HD3369, HI1653 genotypes as compared to other genotypes evaluated at numb of locations of the north western planes zone of the country. RPGV and RPGV* Mean had observed the large values of DBW397, HI1653,

Table 1: Information of wheat genotypes and locations used in the study

Code	Genotype	Parentage	Location	Latitude	Longitude	Altitude
NWRI301	UP3111	BECARD#1/4/KIRITATI/ 3/2* SERI.1B*2//KAUZ*3/BOW/ BAVI5/2*FRANCOLIN#1	Delhi	28 o4'N	77 o13 ’E	228
NWRI302	DBW296	SOKOLL/3/PASTOR// HXL7573/2*BAU/4/MASSIV/ PPR47.89C(23SAWYT321)	Jammu	32 o 40' N	74 o 54’E	356
NWRI303	WH1311	QUAIU/FRNCLN	Ludhiana	30 o 54' N	75 o 48 ’E	247
NWRI304	DBW397	ROLF07/YANAC//TACUPETOF2001/ BRAMBLING/4/WBLL1/KUKUNA// TACUPETOF2001/3/BAJ	Gurdaspur	30o 02' N	75 o 24 ’E	265
NWRI305	WH1402	SHORTENEDSR26TRANSLOCATION//2*WBLL1*2/KKTS/3/BECARDQUAIU/FRNCLN	Hisar	29 o 10' N	75 o 46’E	229
NWRI306	HI1654	TOR/3/BERKUT	Karnal	29 o 43' N	70 o 58’E	245
NWRI307	HD3369	HD3070/HD3078	Modipuram	29 o05' N	77 o70’E	226
NWRI308	PBW644	PBW175/HD2643	Nagina	29 o 28' N	78 o 32’E	245
NWRI309	PBW899	PULSAR/2*PBW683	Bulandshahr	28 o 40'N	77 o 84’E	195
NWRI310	DBW398	23rdSAWYT326(SOKOLL/3/PASTOR// HXL7573/2*BAU/4/GLADIUS)	Durgapura	26 o51'N	75 o 47’E	390
NWRI311	HI1653	NADI/COPIO//NADI	Pantnagar	29 o 02'N	79 o 48’E	243.8
NWRI312	NIAW3170	SKOLL/ROLF07				

Table 2: AMMI analysis of variance for wheat genotypes in locations

Source	Degree of freedom	Sum of squares	Mean sum of squares	Level of significance	Share of factors	Contribution of IPCA’s	Cumulative sum of IPCA’s
Treatments	131	29189.77	222.82	***	90.24		
Genotypes (G)	11	3481.16	316.47	***	10.76		
Environments (E)	10	15851.79	1585.18	***	49.01		
GxE interactions	110	9856.82	89.61	***	30.47		
IPC1	20	2774.43	138.72	***		28.15	28.15
IPC2	18	2320.49	128.92	***		23.54	51.69
IPC3	16	1391.91	86.99	***		14.12	65.81
IPC4	14	1192.80	85.20	***		12.10	77.91
IPC5	12	1001.01	83.42	***		10.16	88.07
IPC6	10	689.37	68.94	***		6.99	95.06
IPC7	8	281.99	35.25	***		2.86	97.92
Residual	12	204.83	17.07	**			
Error	396	3156.01	7.97				
Total	527	32345.79	61.38				

HD3369 genotypes and last two measures HMRPGV and HMRPGV* Mean had identified the DBW397, HI1653, HD3369for their more values. Non parametric measures had considered the ranks of the genotypes based on their yield performance across the locations of the zone. Minimum values of S_i^1 had showed byDBW296, HD3369,

Table 3: Simultaneous selection index and AMMI analysis based measures

	Mean	rMean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	ASV
UP3111	41.74	12	-3.45	0.54	-0.17	-0.67	0.63	0.81	-1.16	3.81
DBW296	47.76	9	0.46	0.09	-0.08	1.88	-0.11	-0.03	-0.66	0.51
WH1311	48.54	5	1.25	0.85	0.12	-1.92	-0.20	0.47	-0.61	1.61
DBW397	51.24	2	2.17	-1.75	0.76	-0.29	1.01	0.49	-1.15	2.94
WH1402	47.77	8	0.99	0.45	0.78	-1.54	-1.08	-1.69	0.74	1.17
HI1654	48.69	4	-0.03	-0.92	0.09	1.70	-1.18	1.40	1.13	0.92
HD3369	50.27	3	1.31	0.48	0.94	1.04	1.82	0.02	0.29	1.51
PBW644	45.60	10	-1.46	-3.79	-0.31	-0.61	-0.11	-0.88	0.37	4.11
PBW899	48.38	6	0.12	0.94	-1.21	1.23	-1.84	-1.35	-1.12	0.95
DBW398	48.36	7	-1.12	1.21	2.50	-0.30	-0.99	0.85	0.51	1.72
HI1653	51.28	1	0.84	0.61	-2.90	-0.98	0.04	1.34	0.79	1.11
NIAW3170	45.41	11	-1.07	1.28	-0.53	0.46	2.02	-1.44	0.87	1.74

Table: 3: Continue...

	rASV	ssiASV	MASV	rMASV	ssiMASV	WAASB	rWAASB	ssiWAASB	Meanb	CV
UP3111	11	23	4.87	3	15	1.23	10	22	42.07	17.27
DBW296	1	10	2.93	1	10	0.44	1	10	47.83	12.00
WH1311	7	12	3.67	2	7	0.84	3	8	48.55	17.14
DBW397	10	12	5.27	4	6	1.24	11	13	51.10	15.87
WH1402	5	13	5.52	6	14	1.00	5	13	47.85	13.71
HI1654	2	6	5.57	7	11	0.82	2	6	48.65	14.80
HD3369	6	9	6.40	9	12	0.92	4	7	50.12	13.52
PBW644	12	22	6.69	10	20	1.36	12	22	45.76	15.58
PBW899	3	9	7.14	11	17	1.01	6	12	48.42	12.19
DBW398	8	15	5.65	8	15	1.14	9	16	48.28	14.86
HI1653	4	5	5.39	5	6	1.04	7	8	50.91	18.31
NIAW3170	9	20	7.51	12	23	1.11	8	19	45.50	11.07

Meanb: 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

NIAW3170 for stable performance whereas the values of S_i^2 had pointed towards DBW296, WH1311, HD3369 while as per S_i^3 values the desirable genotypes would be DBW296, WH1311, HD3369 and magnitude of S_i^4 for DBW296, HD3369, WH1311 genotypes. Next measure S_i^5 had settled for DBW296, HI1653, HD3369 and values of S_i^6 had pointed by DBW296, WH1311, HD3369 moreover wheat genotypes DBW296, HD3369, WH1311had identified by last non parametric measure S_i^7. The standardised values of S_i^1 and S_i^2 non parametric measures had been computed as Z1 and Z2 for individuals genotypes as sum of Z1 and Z2 would provide a tool to test the significant differences among the genotypes based on their ranks corresponding to yield performance across the locations of the zone. No significant differences had been showed by sums of Z1 and Z2 values in the current study. Composite non parametric measures had exploited the ranks of the genotypes as per their yield and corrected yield at locations of the zone and minimum values of these measures provide a sight for the stable performance. First measures $NP_i^{(1)}$ had favoured the DBW296, HI1653, HD3369 while as per $NP_i^{(2)}$ values the suitable genotypes would be DBW296, NIAW3170, PBW899 and as per values of $NP_i^{(3)}$ measures the desirable genotypes would be DBW296, NIAW3170, PBW644 and the last measure $NP_i^{(4)}$ had settled for DBW296, NIAW3170, UP3111 wheat genotypes (Taleghani et al., 2023) (Table 4).

Table 4: Performance of wheat genotypes as per BLUP based analytic and non parametric measures

	GAI	HMGV	RPGV	RPGV×Mean	HMRPGV	HMRPGV×Mean	Si^{1}	Si^{2}	Si^{3}
UP3111	41.50	40.95	0.88	42.10	0.87	41.48	4.152	4.739	3.633
DBW296	47.50	47.16	1.00	47.90	1.00	47.76	1.924	2.861	0.826
WH1311	47.88	47.19	1.01	48.32	1.00	48.11	3.227	3.409	1.415
DBW397	50.46	49.78	1.06	51.00	1.06	50.63	3.712	4.235	2.057
WH1402	47.46	47.09	1.00	47.89	1.00	47.69	3.379	4.006	1.936
HI1654	48.15	47.66	1.01	48.59	1.01	48.38	3.515	3.918	2.203
HD3369	49.71	49.31	1.05	50.17	1.04	49.93	2.848	3.459	1.530
PBW644	45.28	44.82	0.96	45.89	0.95	45.30	3.500	4.261	2.136
PBW899	48.08	47.73	1.01	48.55	1.01	48.28	3.667	4.106	1.960
DBW398	47.82	47.37	1.01	48.34	1.00	47.94	3.636	4.010	2.606
HI1653	50.00	48.94	1.06	50.59	1.04	50.08	3.167	4.140	1.854
NIAW3170	45.22	44.91	0.95	45.70	0.95	45.36	2.970	3.741	1.937

Table 4: Continue...

	Si^{4}	Si^{5}	Si^{6}	Si^{7}	Z1	Z2	NPi$^{(1)}$	NPi$^{(2)}$	NPi$^{(3)}$	NPi$^{(4)}$
UP3111	4.669	4.182	7.667	21.800	0.449	0.779	4.18	0.35	0.47	0.42
DBW296	2.292	1.669	2.886	5.255	5.130	0.525	1.64	0.23	0.34	0.29
WH1311	3.188	2.711	4.152	10.164	1.866	0.138	2.64	0.38	0.50	0.51
DBW397	3.795	3.091	4.857	14.400	0.652	0.196	3.00	0.75	0.76	0.74
WH1402	3.560	2.876	4.833	12.673	1.486	0.060	2.64	0.38	0.54	0.51
HI1654	3.717	3.207	5.623	13.818	1.145	0.150	3.09	0.62	0.64	0.60
HD3369	3.142	2.595	4.423	9.873	2.815	0.161	2.55	0.51	0.60	0.54
PBW644	3.816	3.107	5.013	14.564	1.183	0.209	3.09	0.39	0.46	0.42
PBW899	3.656	2.959	4.773	13.364	0.765	0.114	2.82	0.35	0.57	0.58
DBW398	3.894	3.438	6.500	15.164	0.841	0.256	3.27	0.55	0.69	0.65
HI1653	3.360	2.479	4.478	11.291	2.018	0.049	2.45	0.61	0.88	0.83
NIAW3170	3.585	3.124	5.178	12.855	2.511	0.074	3.00	0.30	0.45	0.37
		χ^2=	21.03	28.30		$\sum$=	20.86	2.71		

HMGV: Harmonic mean of genotypes to investigate the mean yield and genotypic adaptability; RPGV: Relative performance of genotypes values; HMRPGV: Harmonic mean of RPGV

3.3. *Hierarchical clustering of genotypes and measures*

Ward's method of clustering had found three groups of genotypes as high yielders were placed in third and DBW296 with minimum values of non-parametric measures was in second group as moderate yielder and pointed by non-parametric measures were in first group (Khalid et al., 2023). The seventh Interaction principal component under the AMMI analysis i.e. IPC7 had bifurcated the various measures in two categories at the first node of division (Figure 1). MASV, ASV, WAASB, $NP_i^{(1)}$, S_i^3, S_i^4, S_i^5, S_i^6 were placed in smaller group whereas larger group consisted of composite no parametric measures, BLUP based analytic measures, IPC1, IPC6, IPC2, IPC3, IPC5, IPC4 values. Further at the second node this group was further divided into thirteen smaller sub groups with various measures more over the first group had partitioned only in five sub groups.

3.4. *Biplot analysis of genotypes and measures*

The biplot analysis of the evaluated wheat genotypes and the various measures AMMI, BLUP and Non parametric based had found the total of 69% of the variations had been accounted by first two principal components with respective share of 43.9% and 25.1% in the study (Table 5). Major share had been accounted by HMRPGV, HMRPGV×Mean,

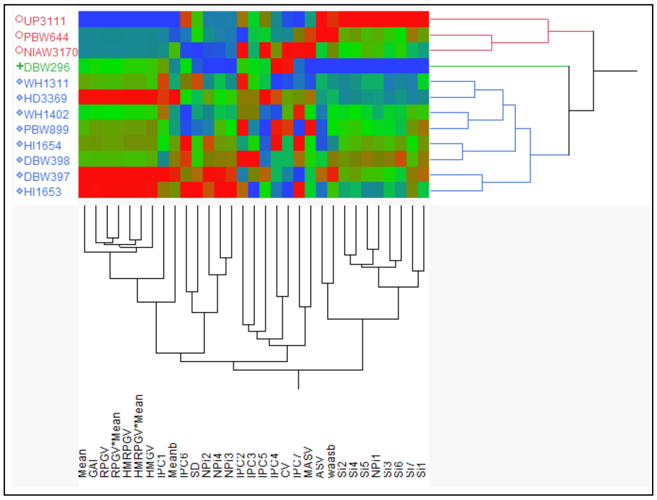

Figure 1: Hierarchical clustering of measures as well as evaluated wheat genotypes

HMGV, GAI, RPGV×Mean, RPGV measures in the first component whereas NP$_i^{(4)}$, NP$_i^{(2)}$, NP$_i^{(3)}$, SD ,CV were measures augmented more in the second principal components. In terms of the evaluated genotypes the larger contributions were of UP3111, DBW296, HD3369 and DBW296, DBW397, HI1653 had exhibited in the respective principal components. Non parametric measure S$_i^4$ had expressed direct association with WAASB, S$_i^7$, S$_i^1$ on one side and with ASV, NP$_i^{(1)}$, NP$_i^{(2)}$, NP$_i^{(3)}$, S$_i^3$, S$_i^4$, S$_i^5$, S$_i^6$ in the first quadrant (Figure 2). Tight relation had observed of NP$_i^{(4)}$, NP$_i^{(2)}$, NP$_i^{(3)}$ with SD and IPC6 values and strong direct bondage had showed by BLUP based analytic measures HMRPGV, HMRPGV×Mean, HMGV, GAI, RPGV×Mean, RPGV of the study in the biplot analysis (Karimizadeh et al., 2023). Direct relation of IPC2 with IPC4 and CV values was also found. Ninety degree angles had expressed by ASV with SD measure, S$_i^5$ with NP$_i^{(3)}$, S$_i^4$ with NP$_i^{(4)}$, S$_i^1$ with Meanb, IPC1 with CV values and straight line angles of IP2, IPC4 with S$_i^7$, WAASB measures (Azam et al., 2023).

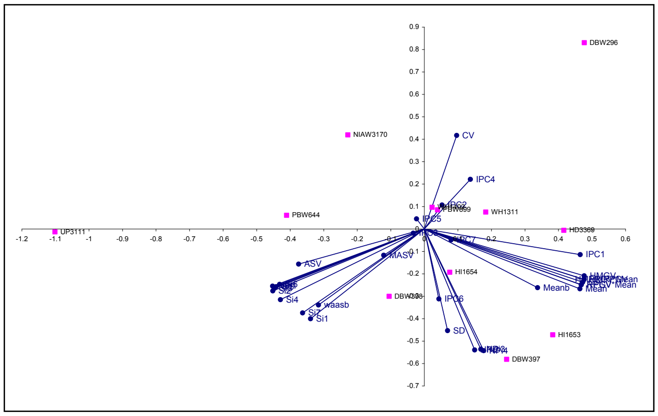

Figure 2: Association among measures and evaluated wheat genotypes based on biplot analysis

Table 5: Loadings of measures and evaluated wheat genotypes as per principal components

Measure	PC1	PC2	Measure	PC1	PC2	Genotype	PC1	PC2
Mean	0.241	-0.160	RPGV	0.244	-0.149	UP3111	-0.761	-0.011
IPC1	0.242	-0.069	RPGV×Mean	0.244	-0.149	DBW296	0.330	0.661
IPC2	0.028	0.064	HMRPGV	0.248	-0.135	WH1311	0.127	0.060
IPC3	-0.017	-0.011	HMRPGV×Mean	0.248	-0.135	DBW397	0.170	-0.463
IPC4	0.072	0.132	S$_i^1$	-0.176	-0.240	WH1402	0.016	0.077
IPC5	-0.012	0.027	S$_i^2$	-0.235	-0.166	HI1654	0.053	-0.154
IPC6	0.023	-0.187	S$_i^3$	-0.232	-0.159	HD3369	0.288	-0.005
IPC7	0.042	-0.029	S$_i^4$	-0.223	-0.189	PBW644	-0.284	0.048
ASV	-0.195	-0.094	S$_i^5$	-0.230	-0.155	PBW899	0.027	0.067
MASV	-0.063	-0.070	S$_i^6$	-0.224	-0.148	DBW398	-0.072	-0.239
WAASB	-0.164	-0.203	S$_i^7$	-0.189	-0.224	HI1653	0.265	-0.376
Meanb	0.176	-0.157	NP$_i^{(1)}$	-0.235	-0.153	NIAW3170	-0.158	0.334
SD	0.036	-0.272	NP$_i^{(2)}$	0.078	-0.323			
CV	0.050	0.250	NP$_i^{(3)}$	0.088	-0.321			
GAI	0.246	-0.142	NP$_i^{(4)}$	0.092	-0.325			
HMGV	0.248	-0.125	% share of measures (69.02%)	43.97%	25.05%			

In total five clusters had been observed for their association pattern of the measures to decipher their association among themselves (Figure 3). AMMI analysis based measures ASV & WAASB had clustered with $NP_i^{(1)}$, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7 non parametric measures as observed in the first quadrant of the biplot analysis of the various measures of the current study. Moreover MASV measure had joined with PC3 values in the same quadrant. First cluster of the second quadrant had consisted of IPC6, SD, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ measures whereas the BLUP based analytic measures Mean, HMRPGV, HMRPGV×Mean, HMGV, GAI, RPGV×Mean, RPGV had grouped together with IPC1 and occupied a place near to former cluster of the same quadrant. Last cluster of IPC2, IPC4, CV measures had found in the third quadrant.

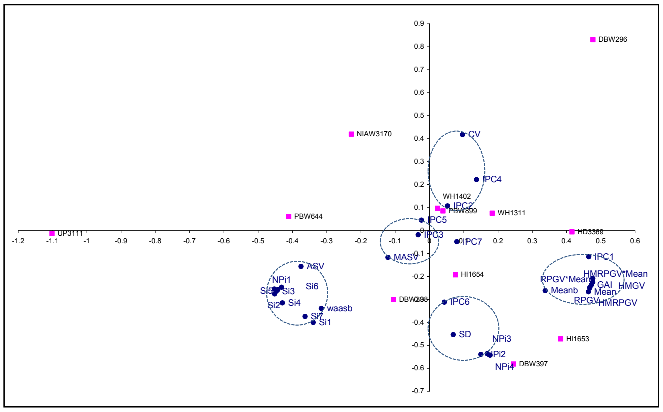

Figure 3: Grouping of AMMI, BLUP and non-parametric measures based on principal components

4. CONCLUSION

ASV measure had pointed for DBW296, HI1654, PBW899 while MASV measure had selected the DBW296, WH1311, UP3111 genotypes as per tha Superiority index measure also. The simultaneous selection index based on yield and ASV had pointed towards the HI1653, HI1654, HD3369 and genotypes HI1653, DBW397, WH1311 were identified by ssiMASV and genotypes HI1654, HD3369, HI1653 genotypes settled by ssiWAASB measure. Out of the five clusters in the biplot analysis the ASV and WAASB had clustered with $NP_i^{(1)}$, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7 non parametric measures as placed in the first quadrant.

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