

## Decipher GXE Interaction of Wheat Genotypes by Multivariate, BLUP and Non Parametric Measures Evaluated in NEPZ

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**ABSTRACT:** Quite numbers of studies have compared with AMMI with BLUP or AMMI with non parametric measures, the present study made comparative analysis considering all type of analytic measures. AMMI analysis observed highly significant variations due to environments, GxE interactions, and genotypes with respective percent share 63.3% 20.7% 2.8% towards total sum square of variation for yield. Absolute IPCA-1 scores pointed for G1, G3 as per IPCA-2, genotypes G8, G7 would be of choice First two IPCAs in ASV & ASV1 measures utilized 50.1% of G×E interaction sum of squares. Set of genotypes (G1, G7) and (G7, G6) recommended ASV1 and ASV. All seven significant IPCAs considered by MASV and MASV1 measures pointed towards G4, G2 genotypes. BLUP-based simultaneous selections, such as HMGV identified G8, G4, values of RPGV favored G8, G1 and HMRPGV estimates selected G8, G4 genotypes. Non parametric composite measure  $NP_i^{(1)}$  observed suitability of G6, G2 while  $NP_i^{(2)}$  selected G6, G9 whereas  $NP_i^{(3)}$  identified G9, G6 and lastly  $NP_i^{(4)}$  found G9, G6 as genotypes of choice. Biplot analysis of AMMI, BLUP and non parametric measures observed 62.6% of the total variation accounted by significant PC1 & PC2. Very tight positive relationships observed between with MASV & MASV1 ASV, ASV1, IPC4, IPC7 measures. AMMI based measure comprised in one cluster adjacent to other cluster of non parametric measures  $S_i^1$  to  $S_i^7$  with  $NP_i^{(1)}$ ,  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$  as six clusters of studied measures had been visualized graphically. BLUP based measures maintained strong to moderate negative correlation with non parametric measures while achieved strong positive type relationships among themselves. Composite non parametric measures  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$  expressed only indirect with non parametric measures  $S_i^1$  to  $S_i^7$  at the same time moderate positive with standard deviation and CV of BLUP estimates.

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

### INTRODUCTION

Grain yield is a complex trait and is genetically governed by many quantitative genes with small additive effects (Ahakpaz *et al.*, 2012). Hence, the expression of this is generally affected by genotype, environment, and genotype × environment interaction (GxE) (Gerrano *et al.*, 2020). Modeling the GxE in METs assists in defining the phenotypic stability of the genotypes for a range of locations or a particular genotype for varied environmental conditions (George and Lundy 2019). Additive main effects and multiplicative interaction (AMMI) has gained very significant usage as multivariate approach as compared to joint regression analysis in many crop improvement studies (Bocianowski *et al.*, 2021). Another approach called the AMMI stability value (ASV), which is based on the first and second interaction principal component axis (IPCA) scores of the AMMI model for each genotype, has also been developed. More recently ASV and ASV1 measures defined as the distance from the

genotype coordinate point to the origin in a two-dimensional scatter diagram of IPCA2 against IPCA1 scores (Vaezi *et al.*, 2018). Genotypes with the lowest ASV & ASV1 values have been recommended for the stable yield performance. Other AMMI based measures while exploiting all significant IPCA's were MASV & MASV1 were also compared with other stability measures. Best linear unbiased prediction (BLUP)-based simultaneous selections, such as harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV), and harmonic mean of relative performance of genotypic values (HMRPGV), were mentioned for the stability and adaptability of genotypes to adverse environmental conditions (Gonçalves *et al.*, 2020). Several nonparametric methods have been proposed to interpret the response of genotypes to environmental variation. Distribution-free nonparametric and composite measures for stability assessment viz  $S_i^1$ ,  $S_i^2$ ,  $S_i^3$ ,  $S_i^4$ ,  $S_i^5$ ,  $S_i^6$ ,  $S_i^7$  along with  $NP_i^{(1)}$ ,  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$  have been suggested (Pour-Aboughadareh *et al.*, 2019).

**MATERIALS AND METHODS**

Nine promising wheat genotypes were evaluated in research field trials at 14 centers of All India Coordinated Research Project on Wheat across this zone of the country during 2020-21 cropping season in field trials. Field trials were laid out in Randomized block designs with four replications. Recommended practices of packages had followed in total to harvest the good yield. Parentage details and environmental conditions were reflected in Table 1 for ready reference. Pour-Aboughadareh *et al.*, (2019) recommended various non parametric and parametric measures for assessing GxE interaction and stability analysis. For a two-way dataset with k genotypes and n environments  $X_{ij}$  denotes the phenotypic value of  $i^{th}$

genotype in  $j^{th}$  environment where  $i=1,2, \dots,k, j = 1,2, \dots,n$  and  $r_{ij}$  as the rank of the  $i^{th}$  genotype in the  $j^{th}$  environment, and  $\bar{r}_i$  as the mean rank across all environments for the  $i^{th}$  genotype. The correction for yield of  $i^{th}$  genotype in  $j^{th}$  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  $i^{th}$  genotype in all environments and  $\bar{X}_.$  was the grand mean.

Non parametric composite measures  $NP_i^{(1)}, NP_i^{(2)}, NP_i^{(3)}$  and  $NP_i^{(4)}$  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.

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

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

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

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

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

ASV  $ASV = [(\frac{SSIPC1}{SSIPC2} PCI)^2 + (PC2)^2]^{1/2}$

ASV1  $ASV1 = [\frac{SSIPC1}{SSIPC2} (PCI)^2 + (PC2)^2]^{1/2}$

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

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

HMGV<sub>i</sub> = 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 environments  $RPGV_{ij} = GV_{ij} / GV_j$

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

AMMISOFT version 1.0 software 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	HD2733	ATTILA/3/TUI/CARC//CHEN/CHTO/4/ATTILA	E 1	Kanpur	26° 26' N	80° 19' E	126
G 2	HD3249	PBW343*2/KUKUNA//SRTU/3/PBW343*2/KHVAKI	E 2	Prayagraj			
G 3	DBW187	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU	E 3	Ghaghrahat	26° 54' N	81° 56' E	100
G 4	HD3406	HD2967*3/Trinakriya(LrTrk/YrTrk)	E 4	Ayodhya			
G 5	HD3411	C306/2*HD2733	E 5	Gorakhpur	26° 45' N	83° 21' E	84
G 6	DBW39	ATTILA/HUI	E 6	Sabour	25°23' N	87°04' E	46
G 7	HD2967	ALD/CUC//URES/HD2160M/HD2278	E 7	RPCAUC- Pusa	25°98' N	25°67' E	52
G 8	PBW826	WBLL1*2/KKTS//PASTOR/KUKUNA/3/KINGBIRD#1//INQALAB91*2/ TU KURU/5/KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/SAUAL	E 8	Coochbehar	26° 8' N	91° 43' E	86
G 9	HD3086	DBW14/HD2733//HUW468	E 9	Kalyani	22° 58' N	88° 26' E	11
			E 10	Burdwan	23° 13' N	87° 51' E	30
			E 11	Manikchak			
			E 12	Ranchi	23° 20' N	85° 18' E	644
			E 13	Chianki	23°45' N	85°30' E	215
			E 14	Dumka	24°27' N	87°26' E	137

**Table 2: AMMI analysis of yield for wheat genotypes evaluated in fourteen.**

Source	Degree of freedom	Mean Sum of Squares	Significance level	Proportional contribution of factors	GxE interaction Sum of Squares (%)	Cumulative Sum of Squares (%) by IPCA's
Treatments	134	251.57	***	86.80		
Genotype (G)	8	135.68	***	2.79		
Environment ( E )	14	1755.58	***	63.29		
GxE interaction	112	71.84	***	20.72		
IPC1	21	118.79	***		31.00	31.00
IPC2	19	80.84	***		19.09	50.09
IPC3	17	82.01	***		17.33	67.42
IPC4	15	77.79	***		14.50	81.92
IPC5	13	65.74	***		10.62	92.54
IPC6	11	37.36	**		5.11	97.65
IPC7	9	17.47			1.95	99.61
Residual	7	4.52				
Error	405	12.66				
Total	539	72.05				

## RESULTS AND DISCUSSION

### A. AMMI analysis

Highly significant variations due to environments, GxE interactions, and genotypes were observed by AMMI analysis (Table 2, 3). This analysis also revealed about 63.3% of the total sum square of variation for yield was due to environments followed by 20.7% by environment whereas due to genotypes was only 2.8%. Diversity of the testing sites were approved by AMMI analysis followed by GxE interactions in grain yield (Mehraban *et al.*, 2019). Further bifurcation of interactions sum of square into seven significant Interaction principal components account more than 99% variation Since the AMMI model revealed the significance of the G×E interaction and AMMI 1 explained a total variation of 31%, followed by 19.1% for AMMI 2, 17.3% for AMMI 3, 14.5 for AMMI 4, AMMI 5 contributed 10.6% followed by 5.1% and 1.9% by AMMI 6 AMMI 7 respectively. The first two AMMI components in total showed 50.1% of the total variation indicating the two AMMI components well fit and confirm the use of AMMI model. Estimated sums of squares for G×E signal and noise were 84.8% and 15.1% of total G×E. Early IPCs selectively capture signal, and late ones noise. Accordingly, this much signal suggests AMMI6 or maybe AMMI7.

Note that the sum of squares for GE-signal is 6.29 times that for genotypes main effects. Hence, narrow adaptations are important for this dataset. Even just IPC1 alone is 2.3 times the genotypes main effects. Also note that GE-noise is 1.12 times the genotypes effects. Discarding noise improves accuracy, increases repeatability, simplifies conclusions, and accelerates progress (Pour-Aboughadareh *et al.*, 2019).

**Ranking of genotypes as per measures.** Since the genotypes yield expressed highly significant variations, mean yield was considered as an important measure to assess the yield potential of genotypes. Mean yield of genotypes selected G8, G4, G1 with lowest yield of G9 (Table 4). This measure is simple, but not fully exploiting all information contained in the dataset. Values of IPCA's in the AMMI analysis indicate stability or adaptability of genotypes. 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. Absolute IPCA-1 scores pointed for G1, G3 as per IPCA-2, genotypes G8, G7 would be of choice (Table 4). Values of IPCA-3 favored G4, G2, genotypes. As per IPCA-4, G7, G3 genotypes would be of stable performance.

**Table 3: AMMI along with BLUP based measures of yield for wheat genotypes.**

	Mean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	MASV1	MASV	ASV1	ASV	BLAvg	BLStdev	BLCV	BLGM	HMGV
G 1	46.74	0.478	1.619	-2.398	-1.760	0.415	-1.295	0.701	6.30	5.56	1.80	1.73	46.75	9.19	19.66	45.99	45.29
G 2	46.58	-1.250	-1.331	-0.369	-1.460	0.585	1.253	-0.072	5.08	4.12	2.43	2.08	45.85	7.29	15.91	45.33	44.84
G 3	45.57	-0.821	2.591	0.687	0.408	-0.594	1.893	0.647	6.96	5.57	2.91	2.79	46.05	7.94	17.24	45.43	44.83
G 4	46.83	1.614	1.538	-0.276	1.703	0.555	-0.270	-1.501	4.61	4.23	3.04	2.57	46.76	8.05	17.21	46.15	45.57
G 5	46.70	2.410	-1.731	-0.776	-0.907	-0.867	0.999	-0.640	6.08	4.98	4.28	3.53	46.05	8.27	17.95	45.42	44.84
G 6	44.64	1.151	-0.862	0.743	1.167	-2.202	-0.824	1.095	6.40	5.09	2.06	1.70	44.98	7.08	15.74	44.50	44.04
G 7	46.49	1.183	-0.513	2.436	-0.236	2.419	-0.437	0.604	7.19	5.92	1.99	1.59	45.77	9.14	19.96	44.98	44.24
G 8	47.36	-2.472	0.141	1.580	-1.183	-1.141	-1.157	-1.042	6.55	5.27	4.02	3.15	46.91	7.73	16.48	46.34	45.80
G 9	42.55	-2.293	-1.450	-1.628	2.268	0.831	-0.161	0.209	6.07	5.47	4.00	3.26	43.25	6.46	14.94	42.82	42.39

**Table 4: Non parametric measures of yield for wheat genotypes.**

2031	S <sub>i</sub> <sup>1</sup>	S <sub>i</sub> <sup>2</sup>	S <sub>i</sub> <sup>3</sup>	S <sub>i</sub> <sup>4</sup>	S <sub>i</sub> <sup>5</sup>	S <sub>i</sub> <sup>6</sup>	S <sub>i</sub> <sup>7</sup>	NP <sub>i</sub> <sup>(1)</sup>	NP <sub>i</sub> <sup>(2)</sup>	NP <sub>i</sub> <sup>(3)</sup>	NP <sub>i</sub> <sup>(4)</sup>	RPGV	HMRPGV
G 1	3.132	7.016	1.511	2.649	2.265	6.831	2.876	2.214	0.492	0.562	0.664	1.017	1.012
G 2	2.945	6.681	1.264	2.585	2.204	5.838	2.815	2.000	0.333	0.540	0.615	1.001	0.999
G 3	3.154	7.324	1.367	2.706	2.357	6.160	2.885	2.357	0.429	0.519	0.605	1.004	1.000
G 4	3.011	6.527	1.385	2.555	2.143	6.364	2.829	2.143	0.714	0.650	0.766	1.020	1.017
G 5	3.396	8.379	1.700	2.895	2.357	6.696	3.301	2.357	0.524	0.623	0.731	1.005	0.999
G 6	2.791	5.692	1.138	2.386	1.857	5.200	2.846	1.857	0.265	0.402	0.471	0.984	0.980
G 7	3.198	7.874	1.510	2.806	2.418	6.493	3.023	2.357	0.524	0.569	0.649	0.995	0.990
G 8	3.275	7.692	1.538	2.774	2.286	6.400	3.125	2.286	0.571	0.669	0.790	1.026	1.020
G 9	3.077	6.901	1.421	2.627	2.184	6.294	2.935	2.143	0.268	0.395	0.463	0.948	0.941

Genotypes G1, G4 selected as per IPCA5 while values of IPCA6 pointed for G9, G4 and finally IPCA7 observed suitability of G2, G9. First two IPCAs in ASV & ASV1 measures utilized 50.1% of G×E interaction sum of squares. The two IPCAs have different values and meanings and the ASV and ASV1 parameters using the Pythagoras theorem and to get estimated values between IPCA1 and IPCA2 scores to produce a balanced measure between the two IPCA scores. Also, ASV parameter of this investigation used advantages of cross validation due to computation from first two IPCAs (Silva *et al.*, 2019). Using first two IPCAs in stability analysis could benefit dynamic concept of stability in identification of the stable high yielding genotypes. ASV1 measures recommended (G1, G7) and ASV pointed towards (G7, G6) as of stable performance. Adaptability measures MASV and MASV1 considered all seven significant IPCAs of the AMMI analysis. Values of MASV1 identified G4, G2, genotypes would express stable yield whereas genotypes G2, G4, be of stable yield performance by MASV measure respectively. The chief advantage of BLUP based measures is to consider the randomness of the genotypic effects and to allow ranking genotypes in relation to their performance based on the genetic effects (Sousa *et al.*, 2020). Average yield of genotypes pointed towards, G8, G4 as high yielders. More over the values of GAI favored G8, G4. Least values of standard deviation observed for the consistent yield of G9, G6 more over the values of CV identified G9, G6 genotypes for NEPZ zone of the country. The BLUP-based simultaneous selections, such as HMGV identified G8, G4, values of RPGV favored G8, G1 and HMRPGV estimates selected G8, G4 genotypes.

The evaluation of adaptability and stability of wheat genotypes through these BLUP-based indices was reported by Pour-Aboughadareh *et al.*, (2019). The estimates of HMGV, RPGV, and HMRPGV had the same genotype ranking that was reported Anuradha *et al.*, (2022).

**B. Non parametric measures**

Measure based on ranks as per corrected yield S<sub>i</sub><sup>1</sup> selected G6, G2, while S<sub>i</sub><sup>2</sup> favored G6, G4 as per values of S<sub>i</sub><sup>3</sup> desirable genotypes would be G6, G2. Values of measure S<sub>i</sub><sup>4</sup> identified G6, G2 & measure S<sub>i</sub><sup>5</sup> pointed towards G6, G4 while S<sub>i</sub><sup>6</sup> observed suitability of G6, G2 and lastly S<sub>i</sub><sup>7</sup> values identified G2, G4 genotypes (Table 3). The mentioned strategy determines the stability of genotype over environment if its rank is similar over other environments (biological concept). Nonparametric measures of phenotypic stability were associated with the biological concept of stability (Vaezi *et al.*, 2018). Non parametric measures NP<sub>i</sub><sup>(1)</sup> to NP<sub>i</sub><sup>(4)</sup>, consider the ranks of genotypes as per yield and corrected yield simultaneously, values of NP<sub>i</sub><sup>(1)</sup> measure observed suitability of G6, G2 whereas as per NP<sub>i</sub><sup>(2)</sup>, genotypes G6, G9 would be of choice while NP<sub>i</sub><sup>(3)</sup> identified G9, G6. Last composite measure NP<sub>i</sub><sup>(4)</sup> found G9, G6 as genotypes of choice for this zone.

**C. Biplot analysis**

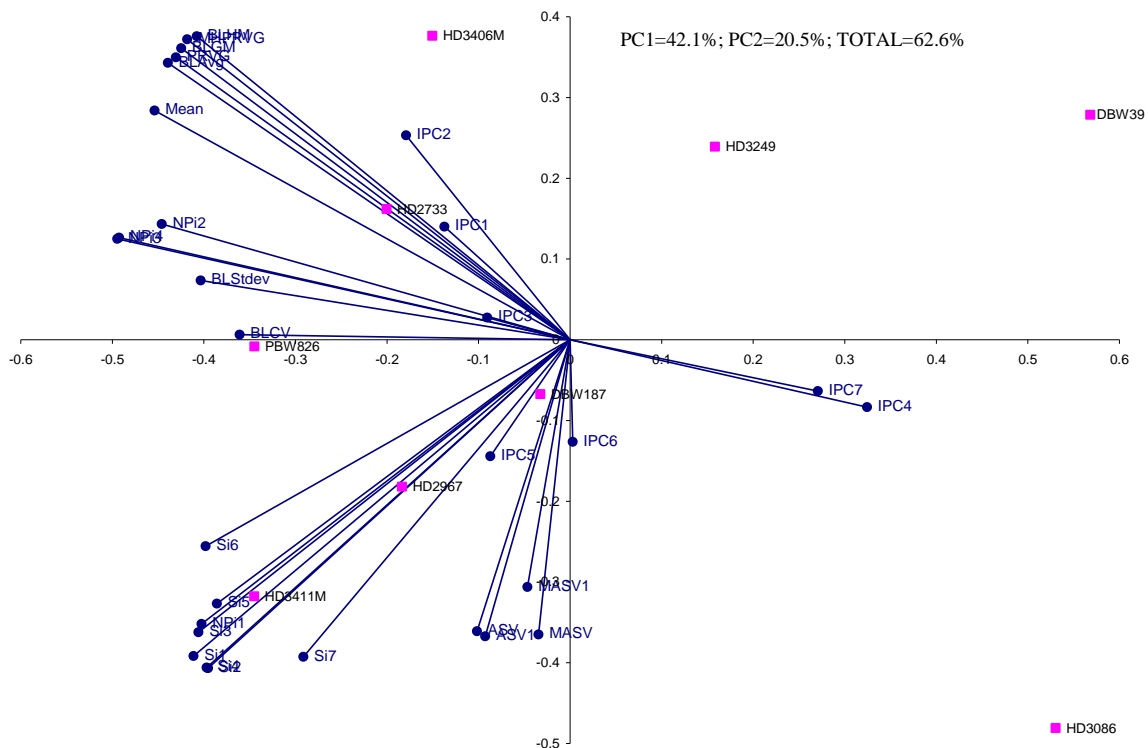
The first two significant PC's has explained about 62.6% of the total variation in the AMMI, BLUP and non parametric measures (Table 5) with respective contributions of 42.1 & 20.5 by PC1 & PC2. Measures NP<sub>i</sub><sup>(3)</sup>, NP<sub>i</sub><sup>(4)</sup>, NP<sub>i</sub><sup>(2)</sup>, mean, RPGV, BLGM, HMGV, HMRPGV accounted more of share in PC1 whereas S<sub>i</sub><sup>2</sup>, S<sub>i</sub><sup>4</sup>, S<sub>i</sub><sup>7</sup>, S<sub>i</sub><sup>1</sup>, S<sub>i</sub><sup>5</sup>, NP<sub>i</sub><sup>(1)</sup> 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. Very tight positive relationships observed between with MASV & MASV1 ASV, ASV1, IPC4, IPC7. Measure  $NP_i^{(1)}$  expressed high degree of positive relationship with  $S_i^1$  to  $S_i^7$ . Standard deviation and CV values showed positive association with  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$ . Average yield maintained strong direct relationship with BLUP based

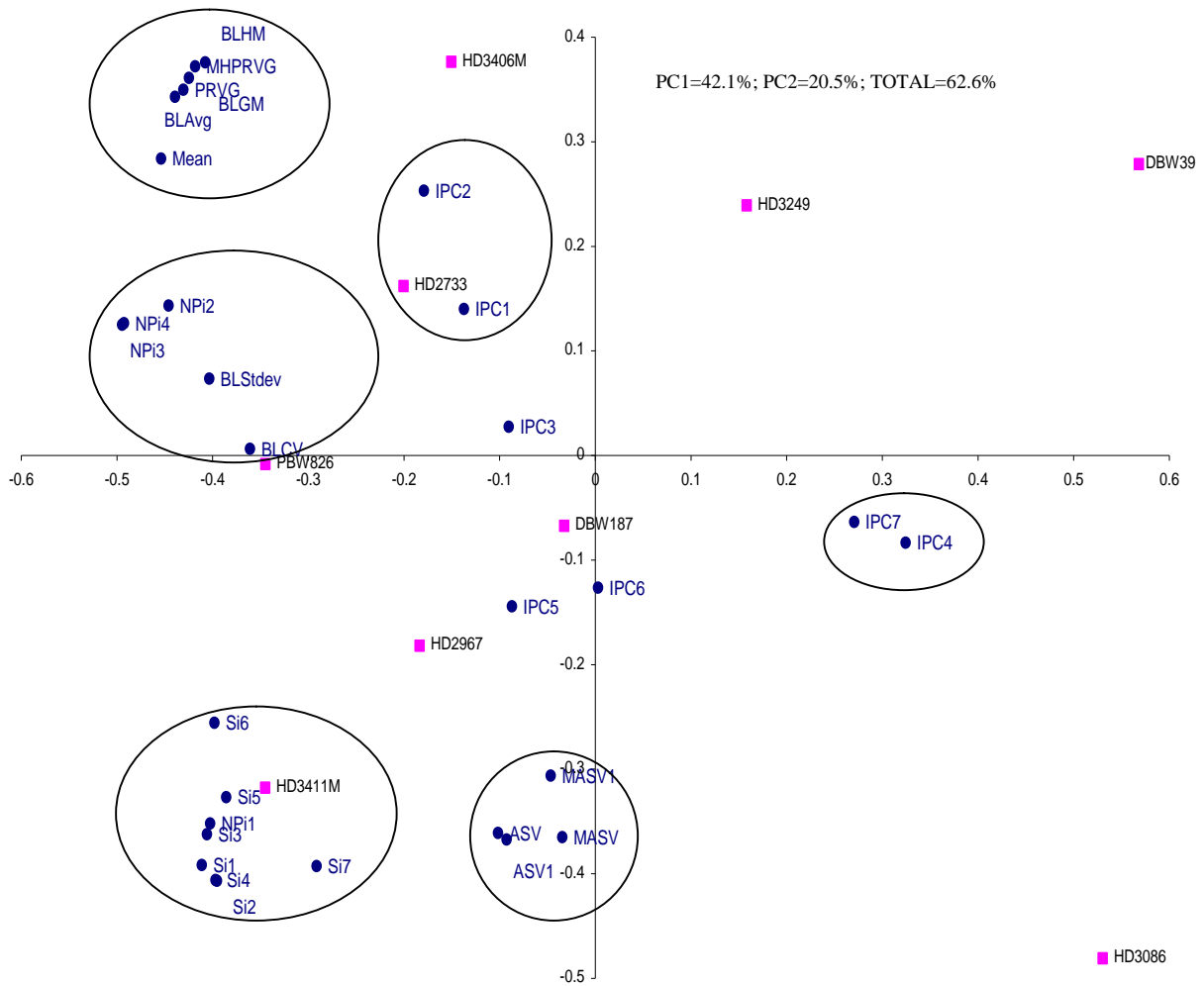
measures. While IPC4, IPC7 expressed no relation with measures of this group. Similar type of relationship expressed with  $S_i^1$  to  $S_i^7$  along  $NP_i^{(1)}$  measure. MASV & MASV1 exhibited no relation with BLUP based measures (Fig. 1). In total six clusters of studied measures had been observed in biplot analysis. Smallest cluster comprises of IPC4 & IPC7 measures and second small comprised of IPC1 to IPC3. AMMI based measure comprised in one cluster adjacent to other cluster of Non parametric measures  $S_i^1$  to  $S_i^7$  with  $NP_i^{(1)}$ ,  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$  clustered with standard deviation and CV measures. Mean along with BLUP based measures formed a separate cluster (Fig. 2).

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

Measure	Component PC1	Component PC2	Measure	Component PC1	Component PC2
Mean	-0.241	0.180	BLGM	-0.225	0.229
IPC1	-0.073	0.089	HMGV	-0.216	0.239
IPC2	-0.095	0.161	RPGV	-0.228	0.222
IPC3	-0.048	0.017	HMRPGV	-0.222	0.236
IPC4	0.172	-0.053	$NP_i^{(1)}$	-0.213	-0.224
IPC5	-0.046	-0.092	$NP_i^{(2)}$	-0.237	0.091
IPC6	0.002	-0.080	$NP_i^{(3)}$	-0.262	0.079
IPC7	0.144	-0.040	$NP_i^{(4)}$	-0.261	0.080
MASV1	-0.025	-0.194	$S_i^1$	-0.218	-0.249
MASV	-0.018	-0.232	$S_i^2$	-0.210	-0.258
ASV1	-0.049	-0.233	$S_i^3$	-0.215	-0.230
ASV	-0.054	-0.229	$S_i^4$	-0.211	-0.258
BLAvg	-0.233	0.218	$S_i^5$	-0.205	-0.208
BLStdev	-0.214	0.047	$S_i^6$	-0.211	-0.162
BLCV	-0.191	0.004	$S_i^7$	-0.154	-0.249
			62.56	42.10	20.46



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



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

#### D. Association analysis

Average yield had expressed direct and indirect relationships with other measures (Table 6). Highly significant positive relationships were noted with BLAvg, BLGM, HMGV, RPGV, HMRPGV, IPC4, IPC2 and strong negative with  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$  while moderate to weak with  $S_i^1$  to  $S_i^7$ . AMMI based measures ASV & ASV1 showed only weak to moderate direct and moderate indirect with measures ( $S_i^1$  to  $S_i^7$ ) (Anuradha *et al.* 2022).

Measures considered all significant IPC's showed moderate 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 for ASV & ASV1. BLUP based measures maintained

strong to moderate negative correlation with non parametric measures with strong positive type relationships among themselves. Composite non parametric measures  $NP_i^{(5)}, S_i^4, NP_i^{(3)}, NP_i^{(4)}$  expressed only indirect with non parametric measures  $S_i^1$  to  $S_i^7$  at the same time moderate positive with BLStdev, BLCV values.  $S_i^1$  to  $S_i^7$  exhibited weak to moderate negative correlation values with other measures whereas strong positive with  $NP_i^{(2)}, NP_i^{(3)}, NP_i^{(4)}$  and among themselves (Pour-Aboughadareh *et al.*, 2019). Lastly IPCs non parametric measures expressed weak to moderate negative values with other measures mean, while few positive values of moderate nature also observed.

**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	NP <sub>i</sub> <sup>(1)</sup>	NP <sub>i</sub> <sup>(2)</sup>	NP <sub>i</sub> <sup>(3)</sup>	NP <sub>i</sub> <sup>(4)</sup>	S <sub>i</sub> <sup>1</sup>	S <sub>i</sub> <sup>2</sup>	S <sub>i</sub> <sup>3</sup>	S <sub>i</sub> <sup>4</sup>	S <sub>i</sub> <sup>5</sup>	S <sub>i</sub> <sup>6</sup>	S <sub>i</sub> <sup>7</sup>		
Mean	-0.100	-0.317	-0.033	0.533	0.217	0.383	0.617	0.167	0.300	-0.200	-0.117	0.950	-0.517	-0.383	0.900	0.983	0.950	0.900	-0.283	-0.858	-0.917	-0.967	-0.367	-0.233	-0.533	-0.233	-0.167	-0.550	-0.083		
IPC1		-0.100	0.000	0.133	-0.017	0.050	-0.033	-0.100	-0.133	-0.083	-0.183	-0.067	0.567	0.533	0.017	-0.050	-0.067	0.017	0.167	0.342	0.267	0.233	0.100	0.117	0.117	0.117	0.150	0.317	0.033		
IPC2			0.200	-0.133	-0.100	-0.233	0.200	0.350	0.433	-0.417	-0.333	-0.483	0.400	0.383	-0.617	-0.383	-0.483	-0.617	0.067	0.242	0.183	0.233	0.000	-0.083	-0.117	-0.083	0.050	0.100	-0.250		
IPC3				0.133	-0.150	-0.117	-0.033	0.633	0.233	-0.067	-0.383	-0.017	-0.050	0.100	-0.067	0.017	-0.017	-0.067	0.083	0.225	0.283	0.150	0.133	0.133	-0.167	0.133	0.233	-0.250	0.167		
IPC4					0.133	0.250	-0.050	-0.150	0.033	0.267	0.167	0.450	-0.483	-0.450	0.417	0.517	0.450	0.417	-0.267	-0.208	-0.367	-0.433	-0.300	-0.367	-0.367	-0.367	-0.417	-0.433	-0.050		
IPC5						0.233	-0.117	-0.183	0.217	-0.267	-0.200	0.350	0.133	0.167	0.333	0.300	0.350	0.333	-0.017	0.025	-0.150	-0.217	-0.083	0.050	-0.033	0.050	0.167	0.133	-0.150		
IPC6							-0.183	-0.217	-0.217	0.350	0.400	0.283	-0.267	-0.150	0.250	0.300	0.283	0.250	0.117	-0.225	-0.300	-0.350	-0.017	0.067	-0.317	0.067	0.167	-0.417	-0.100		
IPC7								0.483	0.533	-0.717	-0.550	0.550	0.000	0.067	0.483	0.600	0.550	0.483	-0.267	-0.742	-0.700	-0.667	-0.300	-0.183	-0.383	-0.183	-0.067	-0.200	-0.167		
MASV1									0.800	-0.283	-0.317	0.083	0.250	0.433	0.017	0.183	0.083	0.017	0.483	-0.008	0.000	-0.067	0.467	0.517	0.150	0.517	0.600	0.133	0.500		
MASV										-0.383	-0.250	0.200	0.333	0.467	0.117	0.317	0.200	0.117	0.500	-0.058	-0.200	-0.233	0.400	0.450	0.217	0.450	0.517	0.317	0.433		
ASV1											0.917	-0.267	-0.317	-0.317	-0.200	-0.250	-0.267	-0.200	0.117	0.292	0.317	0.300	0.433	0.300	0.400	0.300	0.083	0.033	0.500		
ASV												-0.233	-0.250	-0.267	-0.183	-0.200	-0.233	-0.183	0.167	0.142	0.133	0.167	0.450	0.333	0.450	0.333	0.117	0.133	0.483		
BLAvg													-0.500	-0.383	0.983	0.983	1.000	0.983	-0.400	-0.825	-0.850	-0.917	-0.417	-0.250	-0.500	-0.250	-0.183	-0.500	-0.117		
BLStdev														0.967	-0.467	-0.467	-0.500	-0.467	0.533	0.625	0.550	0.567	0.517	0.533	0.550	0.533	0.600	0.817	0.233		
BLCV															-0.367	-0.333	-0.383	-0.367	0.683	0.575	0.483	0.467	0.600	0.650	0.517	0.650	0.750	0.750	0.333		
BLGM																0.950	0.983	1.000	-0.400	-0.775	-0.783	-0.850	-0.367	-0.200	-0.400	-0.200	-0.167	-0.417	-0.050		
HMGV																				0.983	0.950	-0.283	-0.808	-0.867	-0.933	-0.350	-0.200	-0.483	-0.200	-0.483	
RPGV																					0.983	-0.400	-0.825	-0.850	-0.917	-0.417	-0.250	-0.500	-0.250	-0.183	-0.500
HMRPGV																						-0.400	-0.775	-0.783	-0.850	-0.367	-0.200	-0.400	-0.200	-0.417	
NP <sub>i</sub> <sup>(1)</sup>																															
NP <sub>i</sub> <sup>(2)</sup>																					0.442	0.267	0.200	0.850	0.867	0.550	0.867	0.883	0.517	0.683	
NP <sub>i</sub> <sup>(3)</sup>																						0.942	0.908	0.592	0.475	0.625	0.475	0.425	0.642	0.342	
NP <sub>i</sub> <sup>(4)</sup>																							0.983	0.550	0.433	0.617	0.433	0.367	0.583	0.317	
S <sub>i</sub> <sup>1</sup>																								0.517	0.383	0.633	0.383	0.300	0.617	0.267	
S <sub>i</sub> <sup>2</sup>																									0.967	0.867	0.967	0.867	0.717	0.900	
S <sub>i</sub> <sup>3</sup>																											0.800	1.000	0.950	0.683	0.867
S <sub>i</sub> <sup>4</sup>																												0.800	0.617	0.900	0.800
S <sub>i</sub> <sup>5</sup>																												0.950	0.683	0.867	
S <sub>i</sub> <sup>6</sup>																													0.583	0.700	
S <sub>i</sub> <sup>7</sup>																														0.567	

## CONCLUSIONS

Environment and G x E interaction effects contributed were the most important with 63.3% and 20.7% of the variation, respectively. The results of the biplot and correlation analysis indicated weak and strong both types of relationships among the measures. However the nonparametric measures can be used to assess the stable behavior of genotypes over various environments.

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