GxE Interactions Elucidated by AMMI, BLUP and Non Parametric Measures of Wheat Genotypes by Evaluated in North Eastern Plains Zone

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Highly significant effects of environments, GxE interactions and genotypes showed by AMMI analysis with respective contributions 53.2%, 24.9%, 3.5% towards total sum of squares. Interaction Principal Components axes (IPCA) values recommended the general adaptations of the genotype. IPCA-1 scores pointed for G4, G2, G7 while IPCA-2 selected G10, G3, G9 genotypes. Both ASV & ASV1 utilized 46.2% of interaction sum of squares recommended G4, G1, G12 wheat genotypes. Based on 97.8% of interactions sum of squares MASV1 measures identified G7, G3, G5   whereas MASV measure settled for G7, G3, G9. BLUP-based measures HMGV, RPGV and HMRPGV identified G2, G8, G1 genotypes. Non parametric composite measures viz $NP_i^{(1)}$ observed suitability of G2, G5, G7   whereas $NP_i^{(2)}$,   for G10, G7, G9   while $NP_i^{(3)}$ identified G10, G9,G7 genotypes of choice. $NP_i^{(4)}$ found suitability of G10, G7, G9 genotypes. Biplot analysis of considered measures had seen about 65.4% of the total variation explained by first two significant Principal Components. $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ formed a cluster adjacent to cluster of ASV, ASV1, MASV, MASV1, S_i^7 BLStd, BLCV measures. Small cluster of IPC4, IPC3 placed near to cluster of BLUP based measures. ASV and ASV1 showed moderate to strong positive correlations values while MASV and MASV1 showed moderate strong positive correlation values with $S_i^{1,}$ $S_i^{2,}$ S_i^3 $S_i^{4,}$ $S_i^{5,}$ $S_i^{6,}$ S_i^7 $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ measures. Non parametric measures would be useful to explain the GxE interaction while augmented with other measures.

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1. INTRODUCTION

The bad effects of climate change on wheat production can be mitigated by varieties adapted to vagaries of weather fluctuations complemented by appropriate farming practices [1]. The recommendation of wheat genotypes possessing high yield with stable performance posed a great concern to breeder especially for north eastern plains zone of India where the usage of natural resources and improved technologies has been reported on lower side. Wheat breeder focused more on the development of stable high-yielding varieties particularly to a target environment over the years instead of across environments owing to different varieties in varying climatic conditions [2,3]. Multi location trials have been conducted to have an estimate of variance due to the genotype-by-environment (GxE interaction) effect, as this component assist significantly in the identification of stable genotypes. Literature has been advocated to use of recent approaches in analyzing the stable performance of promising genotypes [4]. Additive main effects and multiplicative interaction (AMMI) has gained much popularity in latest studies as compared to joint regression analysis [5]. Number of AMMI based measures AMMI stability value (ASV, ASV1, MASV & MASV1) has also gained visibility i measures exploiting all significant IPCA's [6]. Best linear unbiased prediction (BLUP) based measures, harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV), and harmonic mean of relative performance of genotypic values (HMRPGV), were also highlighted for the stability and adaptability of genotypes [7]. Besides that number of nonparametric measures S_i^1 S_i^2 S_i^3 S_i^4 S_i^5 S_i^6 S_i^7 along with $NP_i^{(1)}$, $NP_i^{(2)}$, $NP^{(3)}$, $NP_i^{(4)}$ have been also utilized to interpret the response of genotypes to environmental conditions [7]. Recent analytic measures have been compared to decipher the GxE interactions effects for wheat genotypes evaluated in north eastern plains zone

of the country under restricted irrigation sown conditions. All measures would augment for efficient interaction estimation and meaningful explanations.

2. MATERIALS AND METHODS

Fourteen 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 for restricted irrigation conditions. More emphasis had been placed to increase the wheat production of this zone to augment the total cereal production of the country. 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 ith genotype in jth environment where i=1,2, ...k, ,j =, 1,2 ,...,n and r_{ij} as the rank of the ith genotype in the jth environment, and $\bar{r}_i$ as the mean rank across all environments for the ith genotype. 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.

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.

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

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

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

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

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

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

$$S_i^{(2)} = \frac{\Sigma_{j=1}^n (r_{ij} - \bar{r}_{i'})^2}{(n-1)}$$

$$\bar{r}_{i=} \frac{1}{n}\Sigma_{j=1}^n r_{ij.}$$

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

$$NP_i^{(3)} = \frac{\sqrt{\Sigma(r_{ij}^* - \bar{r}_{i.}^*)^2/n}}{\bar{r}_{i.}}$$

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

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

AMMI Stability Value

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

Corrected AMMI Stability Value

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

Modified AMMI stability
Value

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

Modified corrected AMMI stability
Value

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

Harmonic mean of genotypic
values (HMGV$_i$)

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

GV_{ij} genetic value of ith genotype in jth environments

Relative performance of
genotypic values across
environments

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

Harmonic mean of Relative
performance of genotypic values
Geometric Adaptability Index

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

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

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

3. RESULTS AND DISCUSSION

3.1 AMMI Analysis

Highly significant variations due to environments, GxE interactions, and genotypes were observed by AMMI analysis (Table 2). This analysis also revealed about 53.2% of the total sum square of variation for yield was due to environments followed by GxE interactions, 24.9% whereas genotypes accounted only 3.5%. Diversity of the testing sites were approved by AMMI analysis [8]. Seven Interaction principal components accounted for more than 92.9% interactions sum of square variations. AMMI1 explained a total variation of 27.3%, followed by 18.9% for AMMI2, 15.3% for AMMI3, 10.4% for AMMI4, AMMI5 contributed 10.1% followed by 7.2% and 3.7% by AMMI6, AMMI7 respectively. The first two AMMI components in total showed 46.2% of the total variation indicating the two AMMI components well fit and confirm the use of AMMI model [6]. Estimated sums of squares for G×E signal and noise were 83.46% and 16.54% 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 5.97 times that for genotypes main effects. Hence, narrow adaptations are important for this dataset [9]. Even just IPC1 alone is 1.95 times the genotypes main effects. Also note that GE-noise is 1.18 times the genotypes effects. Discarding noise improves accuracy, increases repeatability, simplifies conclusions, and accelerates progress.

3.2 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 G3, G2, G1 with lowest yield of G10 (Table 3). 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 G4, G2, G7 as per IPCA-2, G10, G3, G9 genotypes would be of choice. Values of IPCA-3 favored G7, G11, G2 genotypes. As per IPCA-4, G1, G5, G3 genotypes would be of stable performance. Genotypes G2, G14, G5 selected as per IPCA5 while values of IPCA6 pointed for G7, G9, G1 and finally IPCA7 observed suitability of G3, G8, G12. First two IPCAs in ASV & ASV1 measures utilized 46.2% 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 [10]. Using first two IPCAs in stability analysis could benefits dynamic concept of stability in identification of the stable high yielder genotypes. ASV1 measures recommended (G4, G1, G12) and ASV pointed towards (G4, G1, G12) as of stable performance. Adaptability measures MASV and MASV1considered all seven significant IPCAs of the AMMI analysis using 97.8% of GxE interactions sum of squares [11]. Values of MASV1 identified G7, G3, G5 genotypes would express stable yield whereas genotypes G7, G3, G9 be of stable yield performance by MASV measure respectively. Major advantages of BLUP based measures are to account for the random nature of the genotype behaviour in changes climatic conditions. At the same time allow ranking genotypes in relation to their performance based on the genetic effects [12]. Average yield of genotypes pointed towards, G3, G2, G1 as high yielders. More over the values of BLGM favored G3, G2, G1. Consistent yield of G7, G1, G10 as per least values of standard deviation more over the values of CV identified G7, G1, G10, genotypes for the consistent yield performance for NEPZ zone of the country. The BLUP-based simultaneous selections, such as HMGV identified G2, G1, G8, while values of RPGV favored G2, G8, G1 and HMRPGV settled for G2, G8, G1 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. [13].

3.3 Non Parametric Measures

These measures consider the ranks of genotypes as per their corrected yield across environments S_i^1 values pointed for G7, G2, G5 while S_i^2 selected G7, G2, G4 and values of S_i^3 favoured G7, G4, G6 as desirable genotypes (Table 4). G7, G2, G6 selected by values of S_i^4 & measure S_i^5 pointed towards G 2, G7, G8while S_i^6 observed suitability of G5, G7, G4 and lastly S_i^7 values identified G7, G6, G4 genotypes (Table 4). 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 [9]. Non parametric composite measures $NP_i^{(1)}$ to $NP_i^{(4)}$, consider the ranks of genotypes as per their yield and corrected yield across environments simultaneously. $NP_i^{(1)}$ measure observed suitability of G2, G5, G7 whereas as per $NP_i^{(2)}$, genotypes G10, G7, G9 would be of choice while $NP_i^{(3)}$ identified G10, G9,G7. Last composite measure $NP_i^{(4)}$ found G10, G7, G9 as genotypes of choice for this zone.

3.4 Biplot Analysis

The first two significant PC's has explained about 65.4% of the total variation in the AMMI, BLUP and non parametric measures considered for this study (Table 5) with respective contributions of 35.4% & 29.9% by first and second principal components respectively [11]. Measures S_i^1, S_i^2, S_i^4, S_i^3, $NP_i^{(1)}$, S_i^6, ASV, ASV1, IPC7 accounted more of share in PC1 whereas RPGV HMRPGV, HMGV, BLAvg, BLGM, $NP_i^{(4)}$ 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 ASV, ASV1, MASV, MASV1, S_i^7, BLStd, BLCV. Measure $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ expressed moderate degree of positive relationship with IPC1, and mean yield Measures and maintained positive relationship with IPC5, IPC2, IPC6. BLUP based measures RPGV, HMGV and HMRPGV expressed positive association IPC4, IPC3. Set of measures S_i^1 to S_i^7 clubbed with $NP_i^{(1)}$ expressed no relationship with BLUP based measures (Fig. 1). Measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ formed a cluster adjacent to

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

Genotype	Code	Parentage	Code	Locations	Latitude	Longitude	Altitude
HI1653	G 1	NADI/COPIO//NADI	E 1	Kanpur	26° 26' N	80° 19' E	126
DBW322	G 2	CIMMYT165/PBW585	E 2	Prayagraj			
HI1612	G 3	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES	E 3	Araul	26° 54'N	80° 01'E	139
DBW252	G 4	PFAU/MILAN/5/CHEN/AE.SQ(TAUS)//BCN/3/VEE#7/BOW/4/PASTOR	E 4	Ghaghraghat	26° 54' N	81° 56'E	100
DBW321	G 5	DBW39/DL7882	E 5	Ayodhya	26° 47' N	82°12' E	113
HD3368	G 6	HD2932/HD3086	E 6	Varanasi	25° 19' N	82° 59' E	81
HI1654	G 7	NADI/COPIO//NADI	E 7	Sabour	25°23' N	87°04' E	46
HD3293	G 8	HD2967/DBW46	E 8	RPCAU-Pusa	25°98' N	25°67 E	52
WH1281	G 9	TACUPETOF2001/BRAMLING/5/NAC/TH.AC//3*PVN/3/MIRLO	E 9	Kalyani	22° 58' N	88° 26'E	11
PBW848	G 10	CROC_1AE.SQ(224)//OPATA/3/PASTOR/4/2*SOKOLL/3/ PASTOR//HXL7573/2*BAU	E 10	Burdwan	23° 13' N	87° 51' E	30
HD3171	G 11	PBW343/HD2879	E 11	Manikchak			
HD3369	G 12	HD3070/HD3078	E 12	Ranchi	23° 20'N	85° 18'E	644
K1317	G 13	K0307/K9162	E 13	Chianki	24° 01' N	84° 10'E	241
UP3062	G 14	QLD28/PBW621	E 14	Shillongani	26° 8' N	91° 43' E	86

Table 2. AMMI analysis of wheat genotypes evaluated in fourteen environments

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	169.80471	***	81.64		
Genotype (G)	13	108.59454	***	3.48		
Environment (E)	13	1661.11543	***	53.24		
GxE interaction	169	59.79698	***	24.92		
IPC1	25	110.20486	***		27.26	27.26
IPC2	23	83.20295	***		18.94	46.20
IPC3	21	73.48065	***		15.27	61.47
IPC4	19	55.33978	***		10.40	71.87
IPC5	17	60.41301	***		10.16	82.04
IPC6	15	48.3638	***		7.18	89.22
IPC7	13	28.95611	***		3.72	92.94
Residual	36	19.81786	***			
Error	588	12.66188				
Total	783	51.79707				

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

Code	Mean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	MASV1	MASV	ASV1	ASV	BLAvg	BLStdev	BLCV	BLGM	BLHM
G 1	35.69	0.691	-2.628	1.825	-0.046	0.228	0.307	-0.349	5.45	5.01	2.81	2.76	35.59	5.38	15.12	35.21	34.83
G 2	36.01	0.051	-0.859	0.066	-0.375	-0.040	-2.053	0.275	4.70	4.68	0.86	0.86	35.87	5.65	15.87	35.42	34.93
G 3	36.19	1.630	0.530	0.795	-0.105	-0.626	-0.644	-0.020	3.37	2.99	2.41	2.03	35.96	7.04	19.79	35.28	34.55
G 4	35.59	0.016	0.765	-0.830	2.510	0.408	0.572	1.525	4.51	4.44	0.77	0.77	35.34	6.67	18.75	34.72	34.08
G 5	35.22	1.674	-0.156	-1.811	0.084	-0.213	-0.399	0.611	4.18	3.66	2.42	2.01	35.29	6.73	18.92	34.69	34.09
G 6	35.33	-1.023	0.856	1.439	0.684	-0.962	1.878	-0.262	5.56	5.30	1.70	1.50	35.08	6.48	18.21	34.49	33.87
G 7	34.21	0.061	-1.554	0.015	0.571	0.868	0.024	0.443	3.04	2.84	1.56	1.56	34.36	4.29	12.04	34.10	33.83
G 8	35.68	0.824	-1.138	-1.138	-0.691	-2.427	0.809	-0.086	5.52	5.03	1.64	1.51	35.71	5.69	16.00	35.28	34.83
G 9	32.74	-1.316	0.579	-0.872	-1.498	1.548	-0.032	0.409	4.31	3.94	1.98	1.68	33.01	5.59	15.71	32.53	32.01
G 10	31.37	-0.930	0.004	0.153	-2.098	0.768	1.268	0.828	4.53	4.44	1.34	1.12	31.88	5.51	15.49	31.42	30.96
G 11	33.97	-0.594	2.328	0.064	-0.709	-1.430	-0.854	-0.171	5.01	4.70	2.48	2.43	34.00	7.88	22.15	33.06	32.06
G 12	34.35	-0.542	0.884	2.269	0.549	0.313	-1.070	0.143	5.01	4.60	1.18	1.10	34.21	6.85	19.24	33.54	32.85
G 13	35.66	2.484	1.263	-0.512	0.115	1.631	0.634	-1.789	5.55	4.96	3.79	3.24	35.44	7.56	21.25	34.58	33.61
G 14	33.65	-3.026	-0.874	-1.463	1.010	-0.065	-0.439	-1.558	5.75	5.05	4.44	3.73	33.94	5.88	16.53	33.48	33.05

Table 4. Non parametric measures of yield for wheat genotypes

Code	S_i^1	S_i^2	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	PRVG	MHPRVG
G 1	5.341	21.143	2.902	4.598	3.898	7.490	5.037	4.000	0.644	1.022	0.859	1.033	1.022
G 2	4.264	13.670	1.914	3.697	2.898	5.680	4.380	3.077	0.538	0.739	0.746	1.036	1.031
G 3	4.714	16.374	1.976	4.046	3.388	5.724	4.488	3.538	0.576	0.736	0.767	1.032	1.027
G 4	4.527	14.995	1.891	3.872	3.214	5.676	4.332	3.462	0.510	0.596	0.667	1.016	1.011
G 5	4.516	17.302	2.144	4.160	3.194	5.540	5.030	3.154	0.417	0.489	0.597	1.015	1.010
G 6	4.462	14.995	1.891	3.872	3.224	5.694	4.318	3.308	0.482	0.553	0.651	1.009	1.003
G 7	4.176	13.192	1.759	3.632	3.000	5.600	4.083	3.154	0.374	0.404	0.495	0.997	0.993
G 8	4.714	17.478	2.376	4.181	3.163	6.019	5.131	3.308	0.520	0.597	0.742	1.035	1.024
G 9	4.725	16.264	2.148	4.033	3.286	6.075	4.596	3.538	0.390	0.403	0.521	0.953	0.945
G 10	4.835	18.225	2.630	4.269	3.776	7.629	4.482	3.769	0.354	0.371	0.454	0.921	0.913
G 11	5.000	19.451	2.670	4.410	3.796	7.294	4.758	4.000	0.505	0.519	0.631	0.971	0.958
G 12	4.626	16.132	2.353	4.016	3.306	6.750	4.531	3.538	0.472	0.446	0.617	0.982	0.975
G 13	5.396	21.962	2.928	4.686	4.143	7.733	4.922	4.231	0.604	0.852	0.771	1.017	1.001
G 14	5.319	21.324	2.898	4.618	4.071	7.748	4.863	4.385	0.520	0.543	0.631	0.983	0.971

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

Measure	PC1	PC2	Measure	PC1	PC2
Mean	0.001	-0.330	BLHM	0.039	-0.321
IPC1	-0.005	-0.203	PRVG	0.004	-0.332
IPC2	-0.022	0.089	MHPRVG	0.035	-0.330
IPC3	0.009	-0.036	S_i^1	-0.299	0.029
IPC4	0.023	-0.154	$S_i^{2,}$	-0.299	0.032
IPC5	-0.004	0.121	S_i^3	-0.286	0.073
IPC6	-0.032	0.060	S_i^4	-0.297	0.035
IPC7	0.243	0.048	S_i^5	-0.285	0.087
MASV1	-0.212	-0.028	S_i^6	-0.261	0.132
MASV	-0.174	-0.021	S_i^7	-0.217	-0.067
ASV1	-0.254	-0.002	$NP_i^{(1)}$	-0.280	0.088
ASV	-0.259	-0.013	$NP_i^{(2)}$	-0.181	-0.245
BLAvg	0.000	-0.332	$NP_i^{(3)}$	-0.153	-0.245
BLStdev	-0.125	-0.053	$NP_i^{(4)}$	-0.134	-0.284
BLCV	-0.125	-0.053			
BLGM	0.019	-0.331	Total contribution (65.36 %)	35.48 %	29.87 %

Fig. 1. Biplot analysis of AMMI, BLUP and non parametric measures
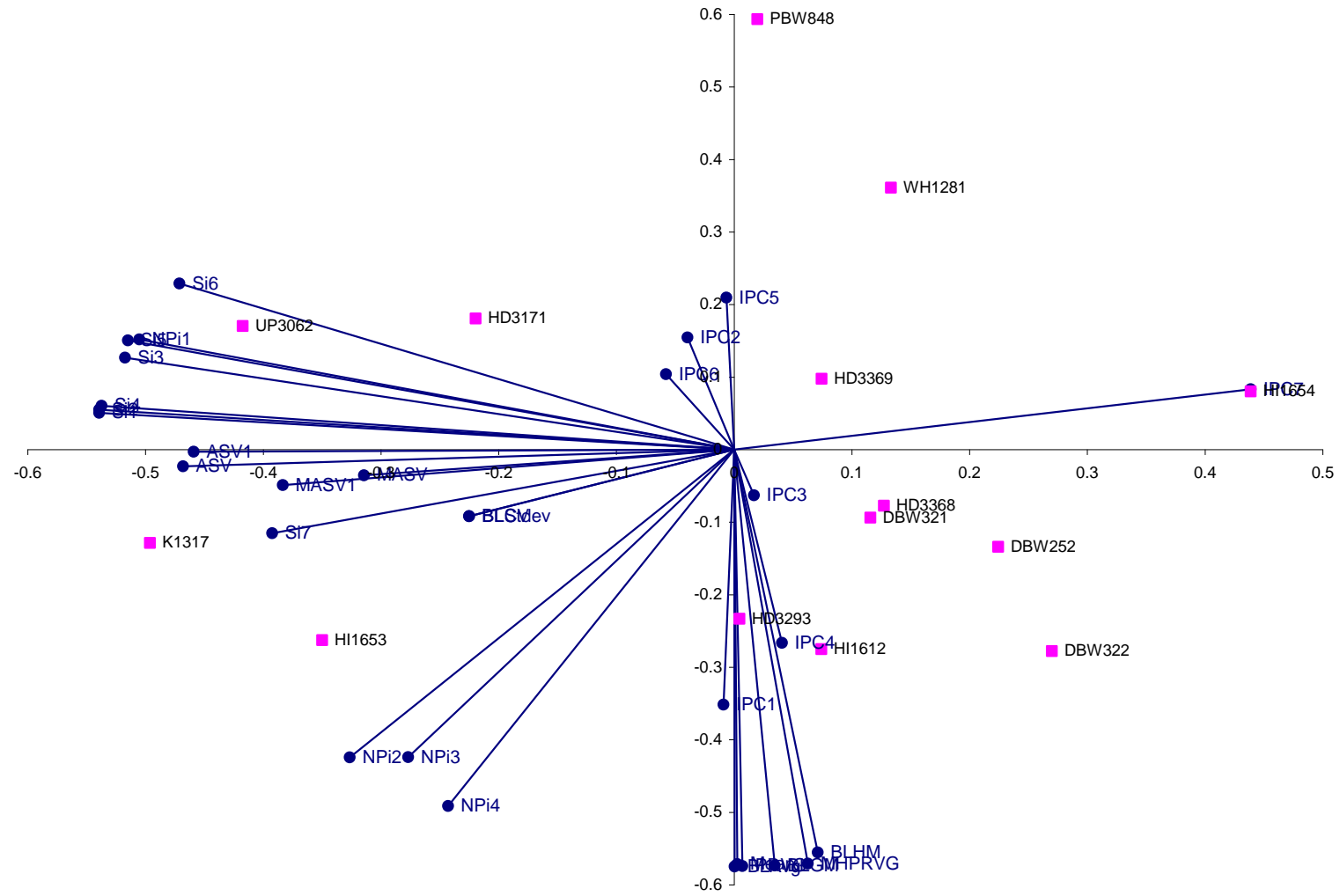
Fig. 2. Clustering pattern of AMMI, BLUP and non parametric measures

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	BLHM	PRVG	MHPRVG	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	-0.240	0.459	-0.022	-0.088	0.554	0.268	0.503	0.075	-0.077	0.200	0.196	0.987	0.022	0.022	0.971	0.930	0.952	0.974	0.297	0.303	0.323	0.303	0.380	0.433	-0.042	0.433	-0.637	-0.681	-0.668
IPC1		-0.134	0.075	0.360	0.035	0.075	0.332	0.132	0.099	0.490	0.538	-0.301	0.316	0.316	-0.347	-0.363	-0.319	-0.327	0.253	0.435	0.323	0.435	0.187	0.086	0.547	0.160	0.602	0.611	0.567
IPC2			0.299	0.224	0.070	-0.062	0.240	0.352	0.253	0.204	0.134	0.516	0.791	0.791	0.523	0.613	0.600	0.508	0.284	0.268	0.248	0.268	0.495	0.380	-0.081	0.503	-0.040	-0.101	-0.031
IPC3				0.231	0.182	0.007	-0.092	0.473	0.369	0.185	0.185	0.101	0.143	0.143	0.121	0.167	0.136	0.101	0.325	0.240	0.347	0.240	0.576	0.567	-0.149	0.541	0.345	0.314	0.367
IPC4					0.235	0.222	0.268	0.253	0.202	0.035	0.018	-0.062	0.253	0.253	-0.138	-0.141	-0.092	-0.158	-0.215	-0.121	-0.193	-0.121	0.035	-0.171	-0.255	-0.022	0.191	0.301	0.275
IPC5						0.152	0.664	-0.099	-0.246	0.004	0.079	0.563	-0.305	-0.305	0.495	0.510	0.497	0.514	0.189	0.059	0.145	0.059	0.264	0.303	-0.189	0.308	-0.213	-0.231	-0.222
IPC6							0.220	0.433	0.418	0.180	0.119	0.264	-0.270	-0.270	0.222	0.119	0.145	0.193	0.251	0.341	0.202	0.341	0.224	0.268	0.040	0.215	-0.068	0.024	0.015
IPC7								-0.189	-0.292	-0.095	-0.055	0.442	0.092	0.092	0.343	0.367	0.415	0.358	0.011	0.066	0.011	0.066	0.029	0.020	-0.099	0.077	-0.224	-0.189	-0.220
MASV1									0.976	0.374	0.264	0.149	0.270	0.270	0.130	0.066	0.031	0.105	0.475	0.538	0.607	0.538	0.475	0.624	0.404	0.448	0.481	0.495	0.512
MASV										0.345	0.226	-0.007	0.198	0.198	-0.031	-0.112	-0.143	-0.059	0.407	0.479	0.525	0.479	0.371	0.512	0.363	0.349	0.523	0.558	0.563
ASV1											0.978	0.204	0.365	0.365	0.237	0.182	0.200	0.240	0.701	0.791	0.684	0.791	0.705	0.530	0.675	0.653	0.431	0.365	0.378
ASV												0.187	0.312	0.312	0.229	0.187	0.196	0.240	0.701	0.760	0.662	0.760	0.692	0.525	0.640	0.662	0.431	0.347	0.360
BLAvg													0.040	0.040	0.989	0.956	0.969	0.987	0.336	0.316	0.358	0.316	0.455	0.499	-0.064	0.499	-0.598	-0.646	-0.620
BLStdev														1.000	0.051	0.149	0.154	0.048	0.264	0.371	0.268	0.371	0.413	0.202	0.211	0.387	0.279	0.209	0.257
BLCV															0.051	0.149	0.154	0.048	0.264	0.371	0.268	0.371	0.413	0.202	0.211	0.387	0.279	0.209	0.257
BLGM																0.976	0.980	0.998	0.374	0.336	0.374	0.336	0.501	0.536	-0.079	0.549	-0.613	-0.684	-0.644
BLHM																	0.987	0.978	0.389	0.312	0.349	0.312	0.543	0.552	-0.143	0.596	-0.585	-0.681	-0.620
PRVG																		0.978	0.319	0.281	0.297	0.281	0.490	0.468	-0.147	0.534	-0.637	-0.712	-0.664
MHPRVG																			0.393	0.352	0.393	0.352	0.508	0.547	-0.055	0.560	-0.607	-0.686	-0.646
S_i^1																				0.932	0.934	0.932	0.899	0.899	0.684	0.930	0.440	0.299	0.369
$S_i^{2,}$																					0.945	1.000	0.840	0.809	0.804	0.822	0.442	0.345	0.376
S_i^3																						0.945	0.824	0.899	0.793	0.837	0.426	0.308	0.347
S_i^4																							0.840	0.809	0.804	0.822	0.442	0.345	0.376
S_i^5																								0.877	0.437	0.969	0.356	0.237	0.312
S_i^6																									0.477	0.899	0.321	0.193	0.264
S_i^7																										0.468	0.435	0.338	0.356
$NP_i^{(1)}$																											0.334	0.193	0.281
$NP_i^{(2)}$																												0.974	0.987
$NP_i^{(3)}$																													0.987

cluster of ASV, ASV1, MASV, MASV1, S_i^7 BLStd, BLCV measures as observed in same quadrant of biplot analysis. Small cluster of IPC4, IPC3 placed near to cluster of BLUP based measures. These two were placed in separate quadrant. Measures S_i^1 to S_i^6 clustered along with $NP_i^{(1)}$ exhibited close proximity with last cluster of IPC5, IPC2, IPC6 measures(Fig. 2).

3.5 Association Analysis

Average yield had expressed direct and indirect relationships with measures as explained by positive and negative values of correlation coefficients (Table 6). Notably positive with IPC2, IPC5, IPC7, BLAvg, BLGM, HMGV, RPGV, HMRPGV , $NP_i^{(1)}$ and negative with $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. AMMI based measures ASV & ASV1 showed moderate to strong positive correlations with measures [12]. Measures considered all significant IPC's showed moderate strong positive correlation values (S_i^1, S_i^2, S_i^3 S_i^4, S_i^5, S_i^6, S_i^7 $NP_i^{(1)}$ $NP_i^{(2)}$ $NP_i^{(3)}$, $NP_i^{(4)}$) along with few very weak negative values also. BLUP based measures expressed weak relation with other measures whereas strong to moderate negative correlations with non parametric measures ($NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$). S_i^s exhibited only moderate to strong positive values with other measures with only weak negative values with IPC4 [13]. Lastly composite non parametric measures expressed both type of relationships with other measures. Mostly positive values expressed by $NP_i^{(1)}$ contrasting to few of negative values by $NP_i^{(2)}$ $NP_i^{(3)}$, $NP_i^{(4)}$

4. CONCLUSIONS

AMMI analysis observed highly significant environments, GxE interactions and genotypes effects. Genotypes G4, G1, G12 identified by ASV & ASV1 while as per MASV1 G7, G3, G9 would be of better performance. BLUP-based measures HMGV, RPGV and HMRPGV identified G2, G8, G1 genotypes. Non parametric composite measures settled for G10, G7, G9. Biplot analysis found cluster of $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ adjacent to cluster of ASV, ASV1, MASV, MASV1, S_i^7, BLStd, BLCV measures. Non parametric measures should be augmented with other measures.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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