Genotype x environment effects elucidation of wheat genotypes evaluated in Northern Hills Zone by AMMI, BLUP and Non Parametric measures

Abstract

AMMI analysis of sixteen wheat genotypes evaluated at eight locations of northern hills zone revealed that significant environments, GxE interactions and genotypes contributed 44.8%, 30.9% & 8.9% respectively. Signal component of interactions accounted 87.91% of total interactions sum of squares. Values of IPCA1 pointed for G8, G2, G15 while G14, G10, G7 would be of choice as per IPCA-2. ASV1 measure while utilizing 58.5% of interactions recommended (G1, G8, G5) whereas (G1, G14, G5) pointed by ASV. Measures MASV1and MASV as per 97.4% of interactions settled for G10, G4, G5. BLUP based measures i.e. HMGV identified G10, G9, G16, while RPGV favored G9, G15, G6 and HMRPGV identified G9, G15, G6 wheat genotypes for this zone of the country. Suitability of G1, G10, G4 observed by $NP_i^{(1)}$ measure whereas $NP_i^{(2)}$ selected G4, G12, G1 while $NP_i^{(3)}$ identified G4, G1, G12 and $NP_i^{(4)}$ pointed for G1, G4, G12. Biplot analysis of measures found total 75.4% of accounted by first two principal components with with 43.2% & 29.2% contributions . BLStdev ASV MASV ASV1 MASV1 BLCV S_i^4 $S_i^{2,}$ $NP_i^{(1)}$ $NP_i^{(2)}$ accounted for more share in first component while BLHM MHPRVG BLGM PRVG Mean BLAvg BLGM S_i^7 $NP_i^{(4)}$ were major contributors in second one. Measures ASV, ASV1, MASV, MASV1, $NP_i^{(1)}$, S_i^1 ,S_i^2 , S_i^3 ,S_i^4 ,S_i^5 ,S_i^6 , S_i^7 clustered in biplot graphical analysis. Measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ formed a cluster with BLUP based measures Mean, BLAvg, BLGM, PRVG, MHPRVG.

Keywords: AMMI, BLUP, Biplot analysis, Non parametric composite measures

Introduction

Goal of wheat breeders is to develop genotypes with good adaptation for diverse environmental conditions. Preferred genotypes possessed stable performance accompanied with high yield for that sets of different genotypes evaluated in different locations under multi environmental trials (Alizadeh et al 2021). The yield performance for each genotype has been always affected by genotypes, environment and G x E interaction (Bocianowski et al 2021). Breeders conceptualized the importance G x E interaction effect to pointing out unexplained variability by individual genotypes and environment effects. A stable genotype across diverse environments contributes little to G x E interaction. There are a numerous numerical and graphical measures to estimate the nature and extent of G x E interaction. There are number of approaches to model G x E interaction effects efficiently (Gonçalves et al. 2020). Main effects of genotypes, environments with multiplicative interactions have been exploited in Additive main effect and multiplicative interaction (AMMI) model in recent studies as compared to joint regression analysis (Pour-Aboughadareh et al. 2019). Apart from AMMI based measures, Best linear unbiased prediction (BLUP) measures proved their potential to improve the predictive accuracy of random effects, 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 (Anuradha et al. 2022). Besides that nonparametric measures S_i^1 S_i^2 S_i^3 S_i^4 S_i^5 S_i^6 S_i^7 , $NP_i^{(1)}$, $NP_i^{(2)}$, $NP^{(3)}$, $NP_i^{(4)}$ have been also utilized to interpret the response of genotypes All current analytic measures have been compared to decipher the GxE interactions effects for wheat genotypes evaluated in northern hills zone of the country under rainfed irrigated conditions.

Materials and Methods

Sixteen promising wheat genotypes were evaluated in research field trials at 08 centers of All India Coordinated Research Project on Wheat across this zone during 2020-21 cropping season for rain fed conditions. Recommended agronomical practices had followed to harvest the good yield in field trials laid out in Randomized block designs with four replications. Parentage details and environmental conditions were reflected in table 1 for ready reference. Quite large number of parametric and non parametric measures had been recommended for assessing GxE interaction analysis (Pour-Aboughadareh et al. 2019). For a multi locations trials 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 $\overline{r_i}$ 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; $\overline{X}_{i.}$was the mean of ith genotype in all environments and $\overline{X}_{..}$was the grand mean.

$$S_i^{(1)} = \frac{2\Sigma_j^{n-1}\Sigma_{j'=j+1}^{n}\left|r_{ij} - r_{ij'}\right|}{[n(n-1)]} \qquad S_i^{(7)} = \frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{\Sigma_{j=1}^{n}|r_{ij} - \bar{r}_i|} \qquad S_i^{(3)} = \frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{\bar{r}_{i.}}$$

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

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

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 $\overline{r_i}$ and M_{di} were the mean and median ranks for original (unadjusted) grain yield, where $\overline{r_i}^*$ and M^*_{di} were the same parameters computed from the corrected (adjusted) data.

$$NP_i^{(1)} = \frac{1}{n}\Sigma_{j=1}^{n}\left|\,r_{ij}^* - M_{di}^*\right| \qquad NP_i^{(3)} = \frac{\sqrt{\Sigma(r_{ij}^* - \bar{r}_{i.}^*)^2/n}}{\bar{r}_i.}$$

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

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

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

Modified AMMI stability Value

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

MASV1	$\mathrm{MASV1} = \sqrt{\sum_{n=1}^{N-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}} PC_n\right)^2 + (PC_{n+1})^2}$
HMGV_i	= Number of environments / $\sum_{j=1}^{k} \frac{1}{GV_{ij}}$ GV_{ij} genetic value of ith genotype in jth environments
Relative performance of genotypic values across environments	$\mathrm{RPGV}_{ij} = \sum_j^k GV_{ij} / \sum_j^k GV_j$
Harmonic mean of Relative performance of genotypic values	$\mathrm{HMRPGV}_{i.}$ = Number of environments / $\sum_{j=1}^{k} \frac{1}{RPGV_{ij}}$
Geometric Adaptability Index	$\mathrm{GAI} = \sqrt[n]{\prod_{k=1}^{n} \bar{X}_k}$

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

Results and Discussion

AMMI analysis

Highly significant variations due to environments, GxE interactions, and genotypes were observed by AMMI analysis (Table 2). This analysis also revealed about 44.8% of the total sum square of variation for yield was due to environments followed by GxE interactions, 30.9% whereas genotypes accounted only 8.9%. Diversity of the testing sites were approved by AMMI analysis (Mehraban et al. 2019). Six Interaction principal components accounted for more than 97.4% interactions sum of square variations. AMMI1 explained a total variation of 36.7%, followed by 21.8% for AMMI2, 17.6% for AMMI3, 9.3% for AMMI4, AMMI5 contributed 7.7% followed by 4.4% by AMMI6 respectively. The first two AMMI components in total showed 58.5% of the total variation indicating the two AMMI components well fit and confirm the use of AMMI model (Pour-Aboughadareh et al. 2022). Estimated sums of squares for G×E signal and noise were 87.91% and 12.09 % of total G×E respectively. Early IPCs selectively capture signal, and late ones noise. Accordingly, this much signal suggests AMMI6. Note that the sum of squares for GxE-signal is 3.05times that for genotypes main effects. Hence, narrow adaptations are important for this dataset (Vaezi et al. 2018). Even just IPC1 alone is 1.28times the genotypes main effects. Also note that GxE-noise is 0 .42 times the genotypes effects. Discarding noise improves accuracy, increases repeatability, simplifies conclusions, and accelerates progress.

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 G10, G9, G15 with lowest yield of G3 (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 G8, G2, G15 as per IPCA-2, G14, G10, G7 genotypes would be of choice. Values of IPCA-3 favored G4, G10, G2 genotypes. As per IPCA-4, G3, G1, G 7 genotypes would be of stable performance. Genotypes G12, G15 G5 selected as per IPCA5 while values of IPCA6 pointed for G2, G4, G8. Measures ASV & ASV1 considered first two IPCAs had utilized 58.5% 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 benefits dynamic concept of stability in identification of the stable high yielder genotypes. ASV1 measures recommended (G1, G8, G5) and ASV pointed towards (G1, G14, G5) as of stable performance. Adaptability measures MASV and MASV1considered six significant IPCAs of the AMMI analysis utilized 97.4% of GxE interactions sum of squares (Gerrano et al. 2020). Values of MASV1 identified G10, G4, G5 genotypes would express stable yield whereas genotypes G4, G10, G5 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 behavior in changes climatic conditions. At the same time allow ranking genotypes in relation to their performance based on the genetic effects (Sousa et al. 2020). Average yield of genotypes pointed towards, G10, G9, G15 as high yielders. Consistent yield of G12, G4, G1 as per least values of standard deviation more over the values of CV identified G10, G8, G4, genotypes for the consistent yield performance for northern hills zone of the country. More over the values of BLGM favored G10, G9, G15. The BLUP-based simultaneous selections, such as HMGV identified G10, G9, G16, while values of RPGV favored G9, G15, G6 and HMRPGV settled for G9, G15, G6 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 G9, G15, G6 genotypes ranking that was reported Anuradha et al. 2022.

Non parametric measures

These measures consider the ranks of genotypes as per their corrected yield across environments S_i^1 values pointed for G10, G14, G1 while S_i^2 selected G10, G5, G1 and values of S_i^3 favoured G4, G10, G1 as desirable genotypes (Table 4). G5 , G1, G4 selected by values of S_i^4 & measure S_i^5 pointed towards G10, G4, G9 while S_i^6 observed suitability of G4, G5, G9 and lastly S_i^7 values identified G10, G1, G5 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 (Vaezi *et al.* 2018). 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

G1, G10, G4 whereas as per $NP_i^{(2)}$, genotypes G4, G12, G1 would be of choice while $NP_i^{(3)}$ identified G4, G1, G12. Last composite measure $NP_i^{(4)}$ found G1, G4, G12 as genotypes of choice for this zone.

Biplot analysis

The first two significant principal components has explained about 75.4% of the total variation in the AMMI, BLUP and non parametric measures considered for this study (Table 5) with 43.2% & 29.2% respective contributions of first and second principal components (Ahakpaz et al. 2021). Measures BLStdev ASV MASV ASV1 MASV1 BLCV S_i^4 $S_i^{2,}$ $NP_i^{(1)}$ $NP_i^{(2)}$ accounted more of share in PC1 whereas BLHM MHPRVG BLGM PRVG Mean BLAvg BLGM S_i^7 $NP_i^{(4)}$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. Strong positive relationships of $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ observed with BLUP based measures BLGM, BLHM, PRVG, MHPRVG on one side as well as with IPC1, BLStdev, BLCV on other side. IPC6 showed positive bondage with IPC2, IPC4. Measure S_i^1 to S_i^7 exhibited very tight positive association among themselves along with positive relationships with AAMI based measures ASV, ASV1, MASV, MASV1, $NP_i^{(1)}$ only in separate quadrant. Measure IPC2 expressed no bondage with IPC4 and IPC5 while opposite with IPC1 & BLStdev as observed in figure. BLUP based measures expressed no relationship with non parametric measures S_i^1 to S_i^7 . Similarly IPC4 had no affinity with non parametric composite measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ (Fig. 1). Measures IPC3, IPC4 observed far away from cluster of ASV, ASV1, MASV, MASV1, $NP_i^{(1)}$, S_i^1 ,S_i^2 , S_i^3 ,S_i^4 ,S_i^5 ,S_i^6 , S_i^7 in same quadrant of biplot graphical analysis. Cluster of IPC2, IPC6 only seen neighbouring quadrant. Measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ formed a cluster with BLUP based measures Mean, BLAvg, BLGM, PRVG, MHPRVG. Moreover small cluster of IPC7 with BLStdev, BLCV placed in same quadrant. Five clusters grouped the measures except of IPC5 values (Fig. 2).

Association analysis

Average yield had expressed direct and indirect relationships with measures (Table 6). Notably positive values for BLAvg, BLGM, HMGV, RPGV, HMRPGV and negative values for with $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$,BLStdev (Anuradha et al. 2022). . IPC1 to IPC6 showed negative values for most of the measures wth exception of IPC4 and IPC2 with PRVG, MHPRVG measures. Based on two significant IPC’s, ASV & ASV1 showed moderate positive correlations with measures except with BLUP based measures similar nature of MASV & MASV1 were also observed with other studied measures for this study. Set of non parametric measures $S_i^{1,}$ $S_i^{2,}$ S_i^3 $S_i^{4,}$ $S_i^{5,}$ S_i^{6} ’ S_i^7expressed both type of relationships while weak negative withIPC5, BlAvg, PRVG values. Non parametric composite measures $NP_i^{(1)}$’$NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ exhibited negative association with IPC5.IPC6, BlAvg, BLGM, PRVG, MHPRVG whereas for others showed positive values. (Pour-Aboughadareh et al. 2022).

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Table 1: Parentage and location details for wheat genotypes evaluated under rain fed timely sown conditions

Genotype	Code	Parentage	Code	Locations	Latitude	Longitude	Altitude
HS683	G 1	HS461/PBW507	E 1	Malan	32°08 ' N	76°35'E	846
HPW479	G 2	HPW236/HS507	E 2	Shimla	31°10 ' N	77°17'E	2276
HS507	G 3	KAUZ/MYNA/VUL//BUC/FLK/4/MILAN	E 3	Bajaura	31°50'N	77°9'E	1103.85
HS682	G 4	HS461/HD2894	E 4	Dhaulakuan	28°59 N	77°16 E	468
HPW476	G 5	HPW155/HW4024-P12	E 5	Almora	29° 35 ' N	79° 39 'E	1610
HS562	G 6	OASIS/SKUAZ//4*BCN/3/2*PASTOR	E 6	Khudwani	33° 70' N	75°10' E	1590
HPW477	G 7	AC8528/WBLL1-2	E 7	Wadura	21° 18' N	77° 41' E	508
HPW478	G 8	VL829/HPW349	E 8	Imphal	24°81° N	93°93 E	786
HD3402	G 9	HD2967/PBW550//HD2967+Yr10					
VL2044	G 10	EIGSN43((MUNAL#1/FRANCOLIN#1/4/KZA//WH542/2*PASTOR/3/B ACEU#1/5/MUNAL*2//WAXWING*2/TUKURU)					
SKW358	G 11	Secondary selection from HS634					
HS684	G 12	HS461/PBW507					
VL2045	G 13	BUC/PVN//MILAN/3/TX96V2427/VL892					
UP3092	G 14	WBLL1/4/BOW/NKT//CBRD/3/CBRD/5/WBLL1#2/TUKURU/6/					
VL2043	G 15	38thESWYT145(MUNAL#1/FRANCOLIN#1/4/KZA//WH542/2*PAST OR/3/BACEU#1/5/MUNAL*2//WAXWING*2/TUKURU)					
VL2046	G 16	VL907/VL616//VL907					

Table 2: AMMI analysis of wheat genotypes evaluated rain fed timely sown conditions

Source	Degree of freedom	Mean Sum of Squares	Significance level	% share of factors	GxE interaction Sum of Squares (%)	Cumulative Sum of Squares (%) by IPCA's
Treatments	127	176.75	***	84.63		
Genotype (G)	15	157.42	***	8.90		
Environment (E)	7	1697.39	***	44.80		
GxE interaction	105	78.14	***	30.93		
IPC1	21	143.54	***		36.74	36.74
IPC2	19	93.98	***		21.76	58.51
IPC3	17	84.78	***		17.57	76.07
IPC4	15	50.85	***		9.30	85.37
IPC5	13	48.42	***		7.67	93.04
IPC6	11	32.78	***		4.39	97.44
Residual	9	23.37	**			
Error	384	10.62				
Total	511	51.91				

Table 3: AMMI and BLUP based measures of wheat genotypes

Code	Mean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	MASV1	MASV	ASV1	ASV	BLAvg	BLStdev	BLCV	BLGM	BLHM
G 1	23.92	-0.332	0.581	-1.217	0.310	1.042	0.221	3.54	2.90	0.81	0.72	24.09	5.90	24.51	23.44	22.79
G 2	25.98	-2.326	-1.476	-0.455	0.486	-1.140	-0.078	5.25	4.31	4.19	3.36	25.99	7.28	28.02	25.18	24.45
G 3	21.94	-1.505	0.474	1.840	0.569	-1.174	1.724	5.62	4.63	2.58	2.01	22.46	4.82	21.47	22.03	21.62
G 4	23.67	0.968	0.814	0.098	-0.149	-0.758	-0.118	2.60	2.17	1.83	1.50	23.95	4.73	19.75	23.51	23.04
G 5	26.49	0.410	0.723	1.175	-0.621	0.397	-0.361	3.09	2.59	1.00	0.90	26.43	5.79	21.92	25.89	25.36
G 6	28.02	2.394	1.170	1.618	0.645	-0.670	-0.409	5.87	4.74	4.21	3.32	27.85	7.46	26.79	26.97	26.12
G 7	25.99	-1.127	-0.320	0.687	-0.445	1.796	0.514	4.44	3.64	1.93	1.50	25.95	6.67	25.69	25.28	24.69
G 8	26.04	-0.168	0.933	-1.712	-0.493	0.384	0.172	4.09	3.37	0.97	0.96	25.96	5.12	19.74	25.50	25.02
G 9	28.69	0.616	-2.180	-1.026	-0.598	-1.213	-0.143	4.95	4.36	2.42	2.32	28.45	8.05	28.30	27.45	26.45
G 10	29.04	-0.801	0.270	0.106	-1.033	0.778	0.517	2.56	2.27	1.38	1.07	28.66	5.65	19.71	28.23	27.85
G 11	27.56	2.475	-1.881	-0.592	1.562	0.774	0.578	5.91	5.07	4.58	3.73	27.43	8.14	29.66	26.29	25.06
G 12	22.52	0.184	1.004	-0.980	1.376	0.113	0.660	3.27	3.00	1.05	1.03	22.88	4.70	20.54	22.42	21.93
G 13	24.07	-1.316	1.325	-1.135	0.530	-0.775	-1.219	4.43	3.77	2.59	2.16	24.22	5.48	22.63	23.57	22.82
G 14	25.78	-0.620	0.046	0.833	0.690	0.678	-1.656	3.11	2.74	1.05	0.81	25.77	6.41	24.89	25.03	24.28
G 15	28.50	-0.314	-1.889	1.343	-0.590	0.358	-0.700	4.38	3.85	1.96	1.93	28.26	8.05	28.48	27.27	26.30
G 16	27.47	1.462	0.408	-0.582	-2.241	-0.589	0.297	4.24	3.89	2.50	1.94	27.32	6.61	24.18	26.58	25.81

Table 4: Non parametric measures of 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	5.571	17.143	2.017	4.140	3.375	3.176	4.444	3.000	0.261	0.356	0.479	0.925	0.911
G 2	6.821	24.500	2.800	4.950	3.688	3.371	5.814	3.500	0.368	0.535	0.737	1.001	0.970
G 3	7.393	26.268	3.562	5.125	3.813	4.136	6.029	3.625	0.269	0.406	0.586	0.879	0.846
G 4	6.250	17.839	1.955	4.224	3.156	2.767	4.946	3.125	0.231	0.338	0.500	0.924	0.918
G 5	5.964	16.839	2.011	4.104	3.281	3.134	4.490	3.125	0.446	0.538	0.782	1.018	1.010
G 6	7.786	38.268	4.082	6.186	5.281	4.507	6.340	4.875	0.650	0.811	1.021	1.073	1.041
G 7	6.500	24.696	3.136	4.970	4.125	4.190	5.239	4.125	0.485	0.576	0.754	0.997	0.983
G 8	5.750	21.411	2.284	4.627	3.781	3.227	4.955	3.375	0.321	0.561	0.697	1.005	0.993

G 9	7.536	24.000	2.526	4.899	3.750	3.158	5.600	3.750	0.750	0.676	1.039	1.084	1.066
G 10	5.179	15.357	1.982	3.919	3.063	3.161	4.388	3.000	0.750	0.950	1.255	1.109	1.102
G 11	7.750	32.125	3.521	5.668	4.656	4.082	6.037	4.625	0.771	0.687	0.939	1.050	1.009
G 12	7.321	23.982	2.781	4.897	4.219	3.913	4.974	3.875	0.250	0.359	0.537	0.884	0.872
G 13	7.429	30.786	3.732	5.548	4.688	4.545	5.747	4.500	0.375	0.562	0.752	0.936	0.911
G 14	5.429	18.268	2.396	4.274	3.281	3.443	4.871	3.125	0.368	0.482	0.612	0.986	0.975
G 15	7.000	25.357	3.074	5.036	4.500	4.364	4.931	4.500	1.000	0.746	1.037	1.076	1.060
G 16	6.500	24.125	2.969	4.912	4.125	4.062	5.117	4.125	0.635	0.714	0.945	1.052	1.029

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

Measure	Principal Component 1	Principal Component 2	Measure	Principal Component 1	Principal Component 2
	-0.183	-0.260	BLHM	-0.149	-0.285
IPC1	-0.115	-0.033	PRVG	-0.185	-0.257
IPC2	0.150	0.090	MHPRVG	-0.155	-0.285
IPC3	-0.055	0.003	S_i^1	-0.190	0.213
IPC4	-0.010	0.229	$S_i^{2,}$	-0.225	0.189
IPC5	0.056	-0.127	S_i^3	-0.202	0.210
IPC6	0.020	0.083	S_i^4	-0.223	0.196
MASV1	-0.220	0.165	S_i^5	-0.214	0.156
MASV	-0.230	0.153	S_i^6	-0.172	0.164
ASV1	-0.226	0.119	S_i^7	-0.195	0.216
ASV	-0.236	0.112	$NP_i^{(1)}$	-0.233	0.126
BLAvg	-0.186	-0.257	$NP_i^{(2)}$	-0.216	-0.183
BLStdev	-0.235	-0.093	$NP_i^{(3)}$	-0.197	-0.201
BLCV	-0.216	-0.002	$NP_i^{(4)}$	-0.200	-0.205
BLGM	-0.170	-0.272	72.42	43.22	29.20

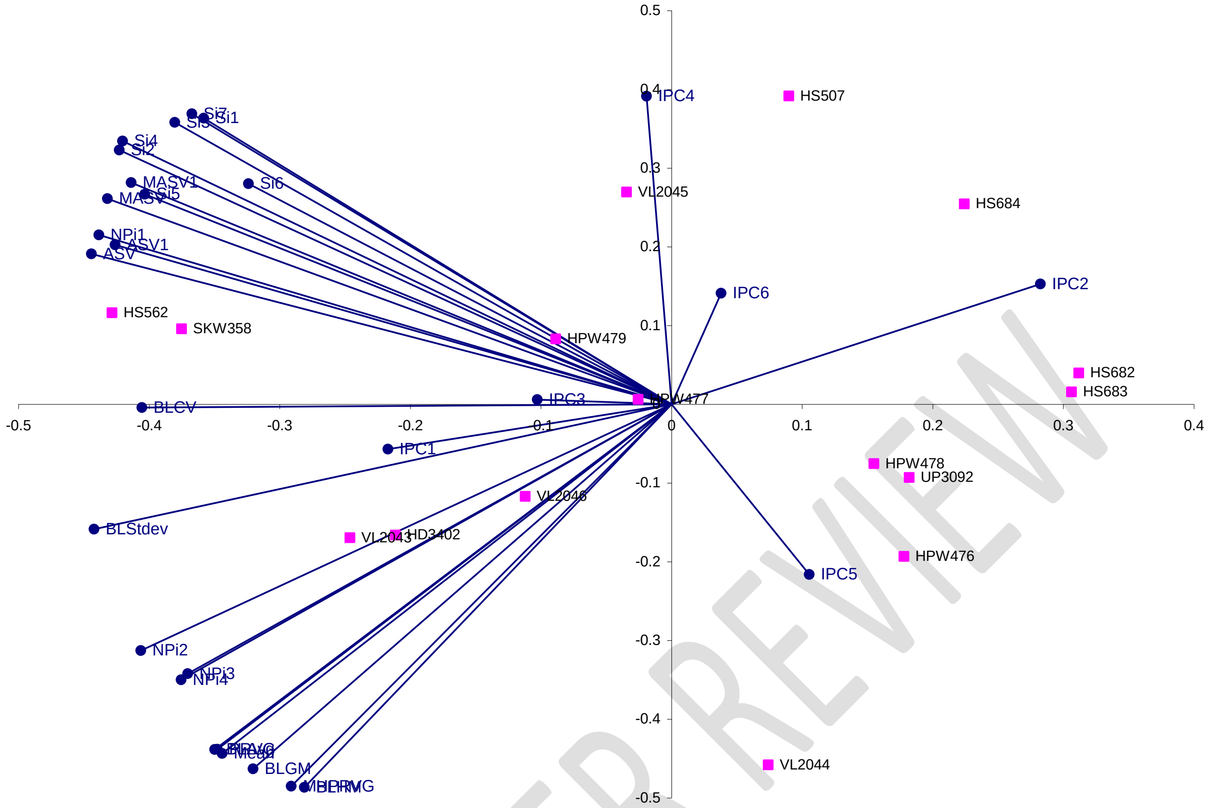

Figure 1: Biplot analysis of AMMI, BLUP and non parametric measures

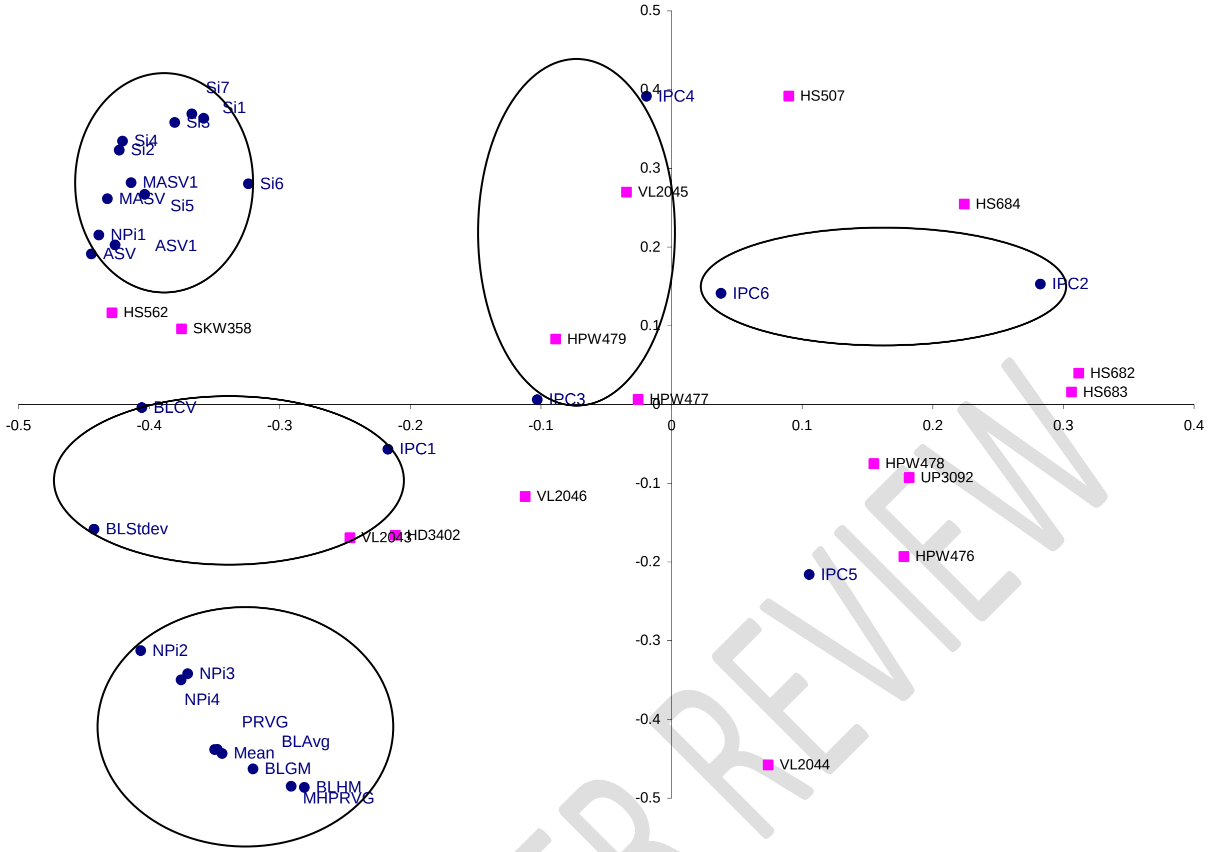

Figure 2: Clustering pattern of AMMI, BLUP and non parametric measures

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

	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	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	-0.374	0.465	-0.103	0.503	-0.159	0.203	-0.121	-0.229	-0.206	-0.288	0.991	-0.682	-0.371	0.994	0.982	0.994	0.976	-0.090	-0.053	-0.009	-0.053	-0.071	0.018	0.041	-0.188	-0.937	-0.891	-0.938
IPC1		0.065	-0.085	-0.029	0.029	-0.029	0.032	0.153	0.097	0.124	-0.341	0.274	0.174	-0.385	-0.400	-0.359	-0.426	0.287	0.053	-0.062	0.053	0.221	-0.159	0.106	0.335	0.246	0.247	0.256
IPC2			-0.147	0.215	-0.103	-0.068	-0.256	-0.282	-0.194	-0.274	0.494	-0.697	-0.632	0.444	0.432	0.453	0.444	-0.019	-0.053	0.018	-0.053	0.159	0.100	0.003	0.012	-0.590	-0.297	-0.429
IPC3				0.024	-0.038	-0.109	0.097	0.094	0.229	0.103	-0.115	0.126	0.126	-0.126	-0.165	-0.097	-0.174	0.081	0.197	0.235	0.197	0.015	0.247	0.079	0.174	0.207	0.200	0.232
IPC4					-0.059	0.082	0.397	0.309	0.303	0.212	0.482	-0.050	0.224	0.550	0.597	0.538	0.591	0.413	0.465	0.444	0.465	0.397	0.406	0.485	0.318	-0.343	-0.362	-0.476
IPC5						0.176	-0.356	-0.421	-0.497	-0.547	-0.100	0.076	-0.047	-0.112	-0.109	-0.103	-0.168	-0.546	-0.356	-0.282	-0.356	-0.153	-0.062	-0.535	-0.182	0.107	0.118	-0.006
IPC6							0.115	0.135	0.032	0.059	0.218	-0.250	-0.279	0.221	0.232	0.224	0.229	0.034	-0.018	0.012	-0.018	-0.003	-0.059	0.138	-0.065	-0.169	-0.103	-0.165
MASV1								0.962	0.800	0.824	-0.144	0.582	0.676	-0.085	-0.024	-0.103	0.015	0.819	0.891	0.841	0.891	0.697	0.618	0.903	0.709	0.346	0.291	0.224
MASV									0.812	0.835	-0.256	0.600	0.656	-0.203	-0.141	-0.226	-0.106	0.834	0.865	0.821	0.865	0.712	0.594	0.871	0.729	0.434	0.394	0.338
ASV1										0.968	-0.259	0.488	0.535	-0.209	-0.153	-0.209	-0.088	0.807	0.844	0.771	0.844	0.606	0.576	0.862	0.738	0.443	0.429	0.391
ASV											-0.341	0.535	0.556	-0.288	-0.235	-0.291	-0.165	0.825	0.797	0.691	0.797	0.559	0.456	0.865	0.697	0.478	0.441	0.441
BLAvg												-0.709	-0.409	0.985	0.974	0.994	0.962	-0.107	-0.062	-0.012	-0.062	-0.050	0.032	0.015	-0.176	-0.934	-0.874	-0.935
BLStdev													0.915	-0.647	-0.612	-0.668	-0.612	0.393	0.435	0.368	0.435	0.329	0.247	0.329	0.488	0.781	0.600	0.632
BLCV														-0.329	-0.288	-0.353	-0.285	0.537	0.576	0.506	0.576	0.459	0.382	0.444	0.579	0.563	0.329	0.362
BLGM															0.994	0.994	0.985	-0.078	-0.038	0.009	-0.038	-0.053	0.032	0.047	-0.188	-0.919	-0.891	-0.944
BLHM																0.985	0.994	-0.028	0.029	0.079	0.029	0.015	0.103	0.100	-0.132	-0.881	-0.853	-0.924
PRVG																	0.976	-0.072	-0.032	0.009	-0.032	-0.047	0.038	0.050	-0.165	-0.916	-0.882	-0.935
MHPRVG																		0.022	0.076	0.121	0.076	0.050	0.132	0.156	-0.091	-0.863	-0.829	-0.897
S_i^1																			0.860	0.796	0.860	0.793	0.578	0.872	0.837	0.315	0.269	0.266
$S_i^{2,}$																				0.962	1.000	0.879	0.853	0.879	0.897	0.334	0.350	0.221
S_i^3																					0.962	0.891	0.924	0.818	0.865	0.310	0.359	0.215
S_i^4																						0.879	0.853	0.879	0.897	0.334	0.350	0.221
S_i^5																							0.874	0.688	0.941	0.319	0.391	0.226
S_i^6																								0.574	0.815	0.272	0.376	0.168
S_i^7																									0.726	0.151	0.179	0.115
$NP_i^{(1)}$																										0.493	0.515	0.409
$NP_i^{(2)}$																											0.916	0.946
$NP_i^{(3)}$																												0.941