

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 MASV1 and 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 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

The goal of wheat breeders is to develop genotypes with good adaptation to diverse environmental conditions. Preferred genotypes possessed stable performance accompanied by 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 in pointing out unexplained variability by individual genotypes and environmental effects. A stable genotype across diverse environments contributes little to G x E interaction. There are numerous numerical and graphical measures to estimate the nature and extent of G x E interaction. There is number of approaches to model G x E interaction effects efficiently (Gonçalves et al. 2020). The main effects of genotypes and environments with multiplicative interactions have been exploited in the 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, the harmonic mean of genotypic values (HMGV), the relative performance of genotypic values (RPGV), and the 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 non-parametric measures $S_i^1 S_i^2 S_i^3 S_i^4 S_i^5 S_i^6 S_i^7$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ have been also utilized to interpret the response of genotypes. All current analytic measures have been compared to decipher the effects GxE interactions for wheat genotypes evaluated in northern hills zone of the country under rain-fed irrigated conditions.

Materials and Methods

Sixteen promising wheat genotypes were evaluated in research field trials at 08 centers of the All India Coordinated Research Project on Wheat across this zone during the 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 a two-way dataset with k genotypes and n environments X_{ij} denotes the phenotypic value of ith genotype in jth environment where $i=1,2, \dots, k$, $j = 1,2, \dots, n$ 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 the 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.

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

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

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

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

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

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

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

$$\bar{r}_i = \frac{1}{n} \sum_{j=1}^n r_{ij}$$

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 $\bar{r}_i$ 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.

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

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

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

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

ASV

$$ASV = [(\frac{SSIPC_1}{SSIPC_2} PCI)^2 + (PC2)^2]^{1/2}$$

ASV1

$$ASV1 = [(\frac{SSIPC_1}{SSIPC_2} (PCI)^2 + (PC2)^2]^{1/2}$$

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

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

HMGV_i

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

GV_{ij} genetic value of i th genotype in j th environments

Relative performance of genotypic values across environments

$$RPGV_{ij} = \sum_j^k GV_{ij} / \sum_j^k GV_j$$

Harmonic mean of Relative performance of genotypic values

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

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

Results and Discussion

AMMI analysis

Highly significant variations due to environments, G×E 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 G×E 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 G×E-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 G×E-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 genotype's yield expressed highly significant variations, mean yield was considered as an important measure to assess the yield potential of genotypes. The mean yield of genotypes selected G10, G9, G15 with the lowest yield of G3 (Table 3). This measure is simple, but does 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 and G15 as per IPCA-2, G14, G10, G7 genotypes would be of choice. Values of IPCA-3 favored G4, G10 and G2 genotypes. As per IPCA-4, G3, G1 and G 7 genotypes would be of stable performance. Genotypes G12, G15 and G5 were selected as per IPCA5 while values of IPCA6 pointed for G2, G4 and G8. Measures ASV & ASV1 considered the 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 used 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 the computation from first two IPCAs (Silva *et al.*, 2019). Using the first two IPCAs in stability analysis could benefits the dynamic concept of stability in the 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 MASV1 considered six significant IPCAs of the AMMI analysis utilized 97.4% of G×E 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 in climatic conditions. At the same time allow the ranking genotypes in relation to their performance based on the genetic effects (Sousa *et al.* 2020). The average yield of genotypes pointed towards, G10, G9, G15 as high yielders. The 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 by 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 to 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. The last composite measure $NP_i^{(4)}$ found G1, G4, and 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, HMPRGV, 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, MHPRGV 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 AMMI 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 neighboring quadrant. Measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ formed a cluster with BLUP based measures Mean, BLAvg, BLGM, PRVG, MHPRGV. 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

The 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 with the exception of IPC4 and IPC2 with PRVG, MHPRGV 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^7 expressed both type of relationships while weak negative with IPC5, 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, HMRPGV whereas for others showed positive values. (Pour-Aboughadareh et al. 2022).

Conclusions

Measures based on first two interaction principal components as well based on all significant principal components expressed indirect relationships with BLUP-based measures. Non parametric measures exhibited negative association with higher order principal components and BLUP-based measures. Non parametric would be utilized for studies as computationally easy and express robust behavior even with the presence of outliers in research data sets.

References

- Ahakpaz F., Abdi H., Neyestani E., Hesami A., Mohammadi B., Nader Mahmoudi K., Abedi-Asl G., Jazayeri Noshabadi M.R., Ahakpaz F., Alipour H .(2021). Genotype-by-environment interaction analysis for grain yield of barley genotypes under dry land conditions and the role of monthly rainfall. *Agric Water Manag* 245:10665
- Alizadeh, B., Rezaizad, A., Hamedani, M.Y., Shiresmaeili G., Nasserghadim F., Khademhamzeh H. R., Gholizadeh A.(2021). Genotype $\times$ Environment Interactions and Simultaneous Selection for High Seed Yield and Stability in Winter Rapeseed (*Brassica napus*) Multi-Environment Trials. *Agric Res* (2021). <https://doi.org/10.1007/s40003-021-00565-9>
- Anuradha N., Patro T.S.S.K., Singamsetti A., Sandhya Rani Y., Triveni U., Nirmala Kumari A., Govanakoppa N., Lakshmi Pathy T. and Tonapi V.A .(2022). Comparative Study of AMMI- and BLUP-Based Simultaneous Selection for Grain Yield and Stability of Finger Millet [*Eleusine coracana* (L.) Gaertn.] Genotypes. *Front. Plant Sci.* 12:786839. doi: 10.3389/fpls.2021.786839
- Bocianowski J., Tratwal A., Nowosad K .(2021). Genotype by environment interaction for main winter triticale varieties characteristics at two levels of technology using additive main effects and multiplicative interaction model. *Euphytica* 217:26
- George N., Lundy M .(2019). Quantifying genotype $\times$ Environment effects in long-term common wheat yield trials from an agroecologically diverse production region. *Crop Science* 59:1960–1972
- Gerrano A.S., Rensburg W.S.J.V., Mathew I., Shayanowako A.I.T., Bairu M.W., Venter S.L., Swart W., Mofokeng A., Mellem J., Labuschagne M.(2020). Genotype and genotype $\times$ environment interaction effects on the grain yield performance of cowpea genotypes in dry land farming system in South Africa. *Euphytica* 216:80
- Gonçalves G. de M. C. , Gomes R. L. F., Lopes Â. C. de A. and Vieira P. Fe. de M. J. (2020). Adaptability and yield stability of soybean genotypes by REML/BLUP and GGE Biplot. *Crop Breeding and Applied Biotechnology*, 20(2): e282920217.
- Mehraban R. A., Hossein-Pour T., Koohkan E., Ghasemi S., Moradkhani H., Siddique K.H .(2019). Integrating different stability models to investigate genotype $\times$ environment interactions and identify stable and high-yielding barley genotypes. *Euphytica* 215:63
- Pour-Aboughadareh, A. , Ali B., Ali K. S., Mehdi J., Akbar M., Ahmad G., Kamal S.H., Hassan Z., Poodineh Omid and Masoome, K. (2022). Dissection

of genotype-by-environment interaction and yield stability analysis in barley using AMMI model and stability statistics. *Bulletin of the National Research Centre* 46:19

- Pour-Aboughadareh, A., Yousefian M., Moradkhani H., Pocza P., and Siddique K.H. (2019). STABILITYSOFT: A new online program to calculate parametric and non-parametric stability statistics for crop traits. *Applications in Plant Sciences* 7(1): e1211
- Silva E. M. da, Nunes E. W. L. P., Costa J. M. da, Ricarte A. de O., Nunes G. H. de S. and Aragão Fernando Antonio Souza de .(2019). Genotype x environment interaction, adaptability and stability of 'Piel de Sapo' melon hybrids through mixed models *Crop Breeding and Applied Biotechnology*, 19(4): 402-411.
- Sousa, A.M.C.B., Silva V.B., Lopes A.C.A., Ferreira-Gomes R.L. and Carvalho L.C.B .(2020). Prediction of grain yield, adaptability, and stability in landrace varieties of lima bean (*Phaseolus lunatus* L.) *Crop Breeding and Applied Biotechnology*, 20: e295120115
- Vaezi, B., A. Pour-Aboughadareh, A. Mehraban, T. Hossein-Pour, Mohammadi R. Armion, M. and Dorri, M. (2018). The use of parametric and non- parametric measures for selecting stable and adapted barley lines. *Archives of Agronomy and Soil Science*, 64: 597-611

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

UNDER PEER REVIEW

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

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

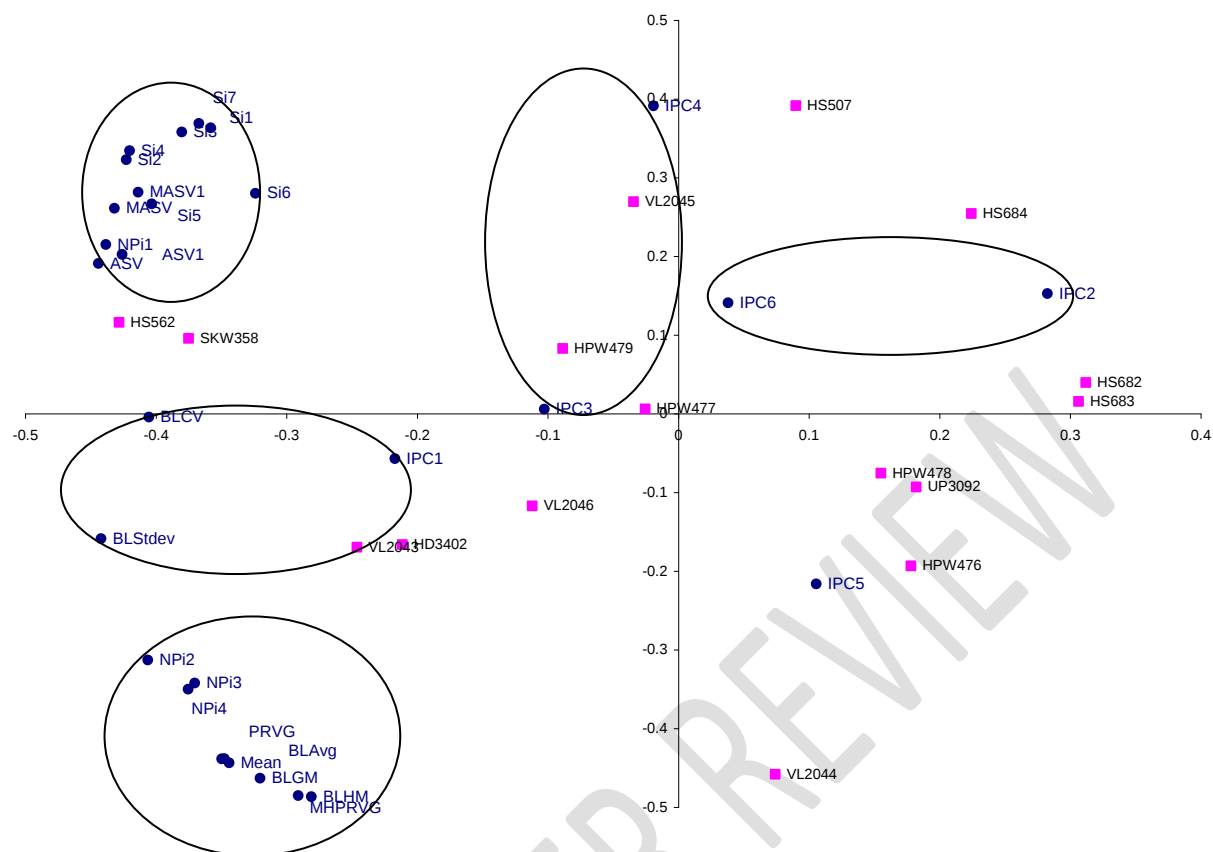


Figure 2: Clustering pattern of AMMI, BLUP and non-parametric measures

[illegible]