GXE INTERACTIONS OF FEED BARLEY GENOTYPES EVALUATED IN COORDINATED TRIALS BY AMMI, BLUP AND NON PARAMETRIC MEASURES

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ABSTRACT

AMMI analysis observed highly significant variations due to environments 52.8%, GxE interactions18.9%, and genotypes 1.9% AMMI1 explained a total variation of 48.6%, followed by 19.5% for AMMI2, 12.4% for AMMI3, AMMI4 accounted for 8.9% and followed by 5.8%, 1.8 & & 1.3% respectively. First two AMMI components in total showed 68.2% of the total variation and ASV1 and ASV selected G3, G2 genotypes. 98.6% of GxE interactions sum of squares utilized by MASV and MASV1 measures to select G5, G4 as desirable genotypes. BLUP-based measures G9, G3 would be desirable genotypes. Non parametric composite measures settled for G5, G7 genotypes.). Measures S_i^1, S_i^2, S_i^3, S_i^4, S_i^5,S_i^6 ,S_i^7,$NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, MASV, MASV1 accounted more in first principal component whereas Mean, Average, HMPRVG, PRVG, IPC5, GM, HM were major contributors for second principal component in biplot analysis. Out of total six clusters Large group consisted of IPC2, $NP_i^{(1)}$ S_i^1 , S_i^4 S_i^7 S_i^2 ,S_i^5 ,S_i^6 measures.

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

Introduction

Stable yield performance of the genotypes had been evaluated under Multi-environment trials before their wide scale cultivation recommendations across various environments (Ahakpaz *et al.,* 2021). Barley is a crop that is cultivated in both highly productive agricultural systems but also in marginal and subsistence environments. Barley's ability to adapt to multiple biotic and abiotic stresses would be very substantial to mitigate the ill effects of environmental change to ensure food security. As cultivar performance in different environments has been affected by significant crossover genotype × environment interaction effects (Anuradha *et al.,* 2022). More advanced analytic approaches relied on accumulation of main effects of genotypes, environments with their multiplicative interactions in recent studies (Pour-Aboughadareh *et al.,* 2022). The consideration of accumulation of main effects of genotypes, environments with their multiplicative interactions have been advocated (Pour-Aboughadareh *et al.,* 2019). Good number of AMMI based measures (AMMI stability value (ASV), ASV1, Modified AMMI stability value (MASV) & MASV1) has been mentioned in literature (Sousa *et al.,* 2020). 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 exploited for the stability and adaptability of genotypes (Gonçalves *et al.,* 2020). 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 in GxE interaction studies (Pour-Aboughadareh *et al.,* 2019). Galaxy of analytic measures have been compared to decipher the GxE interactions effects for feed barey genotypes evaluated in north eastern and north western zones of the country.

Materials and Methods

Ten promising genotypes were evaluated in research field trials at 14 centers of All India Coordinated Research Project on Wheat & Barley across the country during 2020-21 cropping season in field trials. More emphasis had been placed to increase the feed baley production 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.

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

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

$$S_i^{(2)} = \frac{\sum_{j=1}^{n}(r_{ij} - \bar{r}_{i\prime})^2}{(n-1)} \qquad \bar{r}_{i} = \frac{1}{n}\sum_{j=1}^{n}r_{ij\cdot}$$

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.

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

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

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

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

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

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

$HMGV_i$

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

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

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

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, GxE interactions, and genotypes were observed by AMMI analysis (Table 2). This analysis also revealed about 52.8% of the total sum square of variation for yield was due to environments followed by 18.9% of GxE interactions, whereas genotypes accounted marginally 1.9%. Diversity of the testing sites were approved by AMMI analysis (Mehraban *et al.,* 2019). Interaction effects further portioned into seven Interaction principal components totalled for more than 98.6% interactions sum of square variations. AMMI1 explained a total variation of 48.6%, followed by 19.5% for AMMI2, 12.4% for AMMI3, AMMI4 accounted for 8.9% and followed by 5.8%, 1.8 & & 1.3% respectively. The first two AMMI components in total showed 68.2% 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 61.4% and 38.6% of total G×E respectively. Early IPCs selectively capture signal, and late ones noise. Note that the sum of squares for GxE-signal is 6.01 times that for genotypes main effects. Hence, narrow adaptations are important for this dataset (Vaezi *et al.,* 2018). Even just IPC1 alone is 4.76 times the genotypes main effects. Also note that GxE-noise is 3.78 times the genotypes effects. Discarding noise improves accuracy, increases repeatability, simplifies conclusions, and accelerates progress.

Ranking of genotypes as per AMMI based 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, G8 with lowest yield of G6 (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 G3, G6 as per IPCA-2, G10, G5 genotypes would be of choice. Values of IPCA-3 favored G8, G4 genotypes. As per IPCA-4, G4, G1 genotypes would be of stable performance. First two IPCAs in ASV & ASV1 measures utilized 68.2% 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 (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 (G3, G2) and ASV pointed towards (G3, G2) as of stable performance. Adaptability

measures MASV and MASV1considered all seven significant IPCAs of the AMMI analysis using 98.6% of GxE interactions sum of squares (Gerrano *et al.,* 2020). Values of MASV1 identified G5, G4 genotypes would express stable yield whereas genotypes G5, G4 be of stable yield performance by MASV measure respectively.

Ranking of genotypes based on BLUP and Non parametric measures

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 G3, G8 as high yielders. Consistent yield of G 9, G2 as per least values of standard deviation more over the values of CV identified G9, G2 genotypes for the consistent yield performance for northern hills zone of the country. More over the values of BLGM favored G3, G8. The BLUP-based simultaneous selections, such as HMGV identified G9, G3 while values of RPGV favored G9, G3 and HMRPGV settled for G9, G3 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. Non parametric measures ranked the genotypes as per their corrected yield across environments S_i^1 values pointed for G5, G4 while S_i^2 selected G5, G4 and

values of S_i^3 favoured G5, G1 as desirable genotypes (Table 4). G5, G1 selected by values of S_i^4 , S_i^5 ,S_i^6 and lastly S_i^7 for G5, G4 (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 G5, G1 whereas as per $NP_i^{(2)}$, genotypes G5, G1 would be of choice while $NP_i^{(3)}$ identified G5, G7. Last composite measure $NP_i^{(4)}$ found G5, G7 as genotypes of choice.

Biplot analysis

The first two significant PC's has explained about 62.4% of the total variation in the AMMI, BLUP and non parametric measures considered for this study in biplot analysis (Table 5) with respective contributions of 37.6% & 24.7% by first and second principal components respectively (Ahakpaz *et al.,* 2021). Measures S_i^1, S_i^2, S_i^3, S_i^4, S_i^5,S_i^6 ,S_i^7,$NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, MASV, MASV1 accounted more of share in first principal component whereas Mean, Average, HMPRVG, PRVG, IPC5, GM, HM were major contributors 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 for IPC7 with MASV, MASV1, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. AMMI based measure IPC2 expressed close relation with $NP_i^{(1)}$ S_i^1, S_i^4 S_i^7 S_i^2, S_i^5, S_i^6 measures. Stdev showed tight linkage with ASV & ASV1. IPC6 tightly associated with CV values. BLUP based measures exhibited strong association among them. IPC5 expressed straight line with Mean and Average yield of genotypes. Stdev also expressed similar nature with IPC2. Moreover right angles of BLUP based measures (GM, HM, PRVG, HMPRVG) observed with AMMI based measures ($NP_i^{(1)}$ S_i^1, S_i^4 S_i^7 S_i^2, S_i^5, S_i^6). In total six clusters were maintained by considered measures in biplot analysis. Smaller group consisted of CV with IPC6 in one quadrant. Large cluster consisted of IPC2, $NP_i^{(1)}$ S_i^1, S_i^4 S_i^7 S_i^2, S_i^5, S_i^6 measures in other quadrant. Two clusters viz IPC7 with MASV & MASV1 and $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ were observed in adjacent quadrant. Last cluster of Stdev with ASV & ASV1 measure observed in last quadrant. The considered measures have clustered evenly in all quadrats of biplot analysis(Fig. 2).

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Conflict of Interests

No conflict of interests reported by the authors

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Table 1: Parentage vis-a-vis location details of genotypes

Code	Genotype	Parentage	Locations	Latitude	Longitude	Altitude
G 1	PL911	DWR83/RD2798	CAU, Pusa	25°98' N	25°67 E	52
G 2	BH902	BH495/RD2552	Kanpur	26° 26' N	80° 19' E	126
G 3	DWRB137	DWR28/DWRUB64	Ranchi	23° 20'N	85° 18'E	644
G 4	BH946	BHMS22A/BH549//RD2552	Varanasi	25° 19' N	82° 59' E	81
G 5	HUB272	BH 550 / IBON-39-1	Sabour	25°23' N	87°04' E	46
G 6	K1822	K 996/K 508	Bathinda	30° 09' N	74° 55 'E	211
G 7	BH1029	RD 2833 / RD 2870	Hisar	29° 10' N	75° 46'E	229
G 8	HUB113	KARAN280/C138	Durgapura	26°51'N	75° 47'E	390
G 9	PL917	STANDER-BAR/CABUYA/6/ROBUR-BAR/142-B// ASTRIX/SUTTER334.3/3/ SUMBARD400/5/ CI10622/CI5824//PAICO/3/GLORIA-BAR/COPAL/4/BBSC(IBON-2013-14-E83)	Karnal	29° 43' N	70° 58'E	245
G 10	RD3012	RD 2660 / NDB1173	Ludhiana	30° 54' N	75° 48 'E	247
			Modipuram	29°05' N	77 °70'E	226
			Pantnagar	29° 02'N	79° 48'E	243.8
			SG Nagar	29° 66'N	75° 53'E	175.6
			Tabiji	26° 35'N	74° 61'E	508

Table 2: AMMI analysis of feed barley genotypes evaluated under coordinated trials

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	139	726.7081	***	73.72		
Genotype (G)	9	295.1847	***	1.94		
Environment (E)	13	5567.002	***	52.82		
GxE interactions	117	222.0919	***	18.96		
IPC1	21	601.7818	***		48.63	48.63
IPC2	19	267.8659	***		19.59	68.22
IPC3	17	190.6099			12.47	80.69
IPC4	15	155.3691			8.97	89.66
IPC5	13	116.764			5.84	95.50
IPC6	11	42.60379			1.80	97.30
IPC7	9	38.29791			1.33	98.63
Residual	12	29.64306				
Error	378	84.95824				
Total	559	245.111				

Table 3: AMMI based measures of genotypes

Genotype	Mean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	ASV1	ASV	MASV1	MASV	Average	Stdev	CV
G 1	47.48	6.5465	-1.9629	-0.3362	0.1343	0.0438	0.2351	0.1249	16.37	10.50	16.679	10.807	43.96	12.47	28.37
G 2	42.74	-0.8471	1.4342	-3.2563	0.5166	0.4022	-0.1132	-0.8415	2.55	1.96	6.794	5.875	42.72	10.88	25.47
G 3	46.59	0.0453	1.5165	4.0164	0.8297	0.1124	-0.7099	-0.0986	1.52	1.52	7.694	6.890	46.44	13.77	29.65
G 4	44.55	-0.8295	1.9011	0.0750	-0.1031	-0.5495	2.0099	0.8186	2.80	2.31	5.698	4.746	44.53	10.37	23.28
G 5	43.02	-1.2124	-1.3843	0.2848	0.7074	-0.2443	-0.6233	-2.0867	3.31	2.36	4.875	3.945	43.26	14.55	33.64
G 6	40.78	0.6139	2.0704	-0.1056	-2.3764	2.7529	-0.5481	0.0471	2.57	2.29	11.141	7.690	40.97	11.20	27.32
G 7	41.75	-1.7733	-2.3396	0.7245	0.3741	0.9085	1.8920	-0.3360	4.99	3.64	7.757	5.962	42.09	15.60	37.07
G 8	46.58	-1.8591	-2.2445	-0.0449	-3.1917	-1.6758	-0.7287	0.6437	5.13	3.69	10.353	7.806	46.39	16.15	34.81
G 9	46.31	0.9349	2.3243	-0.4950	0.5936	-2.6356	-0.2521	-0.0024	3.29	2.75	10.297	6.865	45.91	8.64	18.83
G 10	44.48	-1.6193	-1.3152	-0.8627	2.5154	0.8853	-1.1618	1.7308	4.23	2.87	7.838	6.187	44.44	13.89	31.25

Table 4: BLUP based and Non parametric measures of genotypes

	Genotype	GM	HM	PRVG	HMPRVG	S_i^1	S_i^2	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
PL911	G 1	42.29	40.61	0.9961	0.9873	3.02	6.58	1.20	2.56	2.07	5.27	15.55	2.07	0.3580	0.2716	0.5223
BH902	G 2	41.43	40.15	0.9782	0.9651	3.65	9.54	1.91	3.09	2.71	7.60	24.80	2.71	0.4691	0.2630	0.6306
DWRB137	G 3	44.56	42.75	1.0520	1.0383	3.65	9.67	1.65	3.11	2.57	6.15	21.46	2.57	0.5625	0.3698	0.7981
BH946	G 4	43.37	42.18	1.0198	1.0144	2.69	5.87	1.13	2.42	2.18	5.86	14.64	2.07	0.4143	0.2716	0.5385
HUB272	G 5	41.16	39.23	0.9676	0.9630	2.47	4.84	0.82	2.20	1.67	3.95	10.61	1.64	0.2473	0.1900	0.3722
K1822	G 6	39.54	38.09	0.9366	0.9173	3.89	11.34	2.48	3.37	2.86	8.75	32.25	2.86	0.4444	0.2924	0.6051
BH1029	G 7	39.74	37.64	0.9375	0.9264	3.37	8.58	1.32	2.93	2.64	5.69	17.15	2.64	0.3700	0.2109	0.4723
HUB113	G 8	44.17	42.23	1.0417	1.0299	3.26	7.96	1.45	2.82	2.21	5.64	18.82	2.21	0.5254	0.3861	0.7744
PL917	G 9	45.13	44.35	1.0656	1.0514	3.99	11.81	2.15	3.44	3.07	7.82	27.91	3.07	0.7288	0.4547	0.9465
RD3012	G 10	42.58	40.91	1.0049	0.9916	3.60	9.96	1.83	3.16	2.69	6.95	23.84	2.43	0.4857	0.4043	0.7209

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

Measure	Principal Component 1	Principal Component 2	Measure	Principal Component 1	Principal Component 2
Mean	0.0824	0.3371	GM	0.1617	0.2996
IPC1	0.0040	0.0914	HM	0.1848	0.2730
IPC2	0.1845	-0.0841	PRVG	0.1723	0.2913
IPC3	-0.0063	0.1131	HMPRVG	0.1503	0.3074
IPC4	-0.0035	0.0283	S_i^1	0.2539	-0.1473
IPC5	-0.0767	-0.2860	S_i^2	0.2575	-0.1577
IPC6	-0.1046	-0.0246	S_i^3	0.2433	-0.1946
IPC7	0.1317	0.0654	S_i^4	0.2562	-0.1550
MASV1	0.0556	0.0612	S_i^5	0.2463	-0.1716
MASV	0.0685	0.0711	S_i^6	0.2338	-0.2089
ASV1	-0.0935	0.1269	S_i^7	0.2433	-0.1946
ASV	-0.0855	0.1256	$NP_i^{(1)}$	0.2408	-0.1718
Average	0.1209	0.3188	$NP_i^{(2)}$	0.2856	0.0718
Stdev	-0.1603	0.0453	$NP_i^{(3)}$	0.2575	0.1327
CV	-0.1858	-0.0253	$NP_i^{(4)}$	0.2787	0.1016
62.40	37.68	24.72			

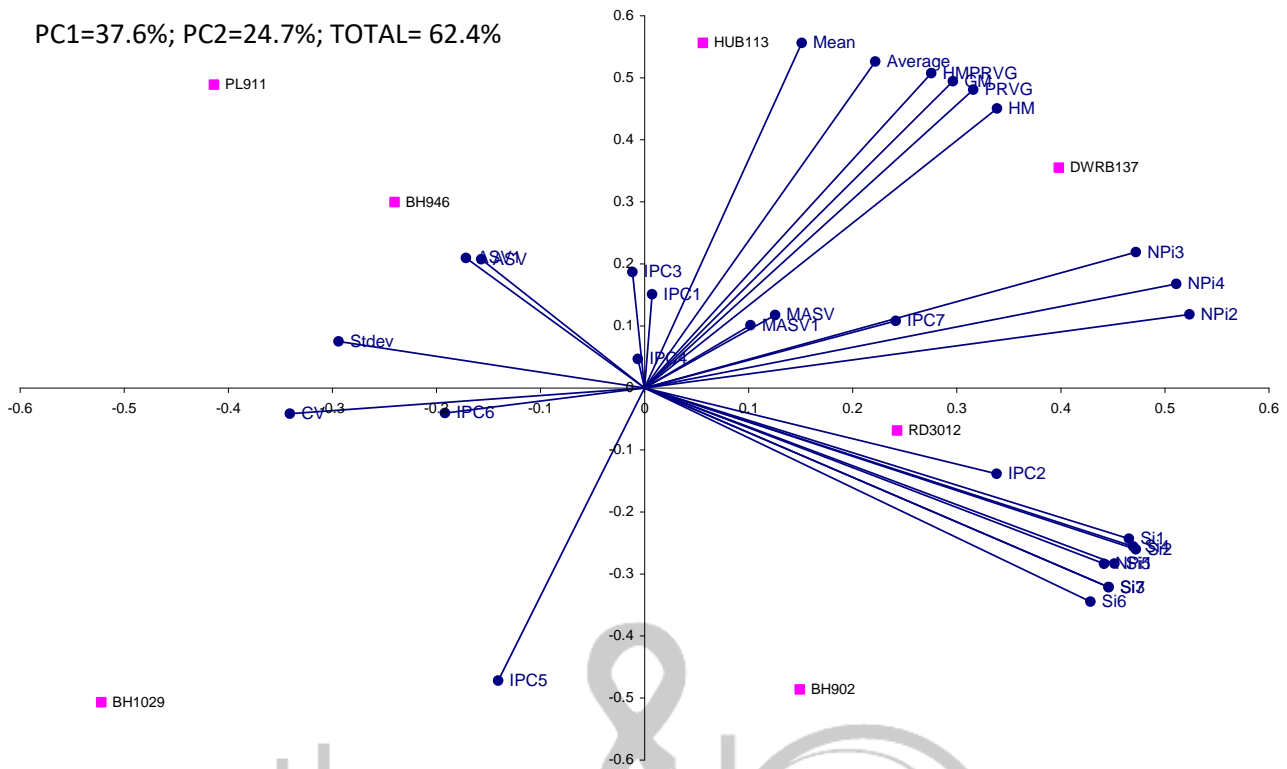PC1=37.6%; PC2=24.7%; TOTAL= 62.4%

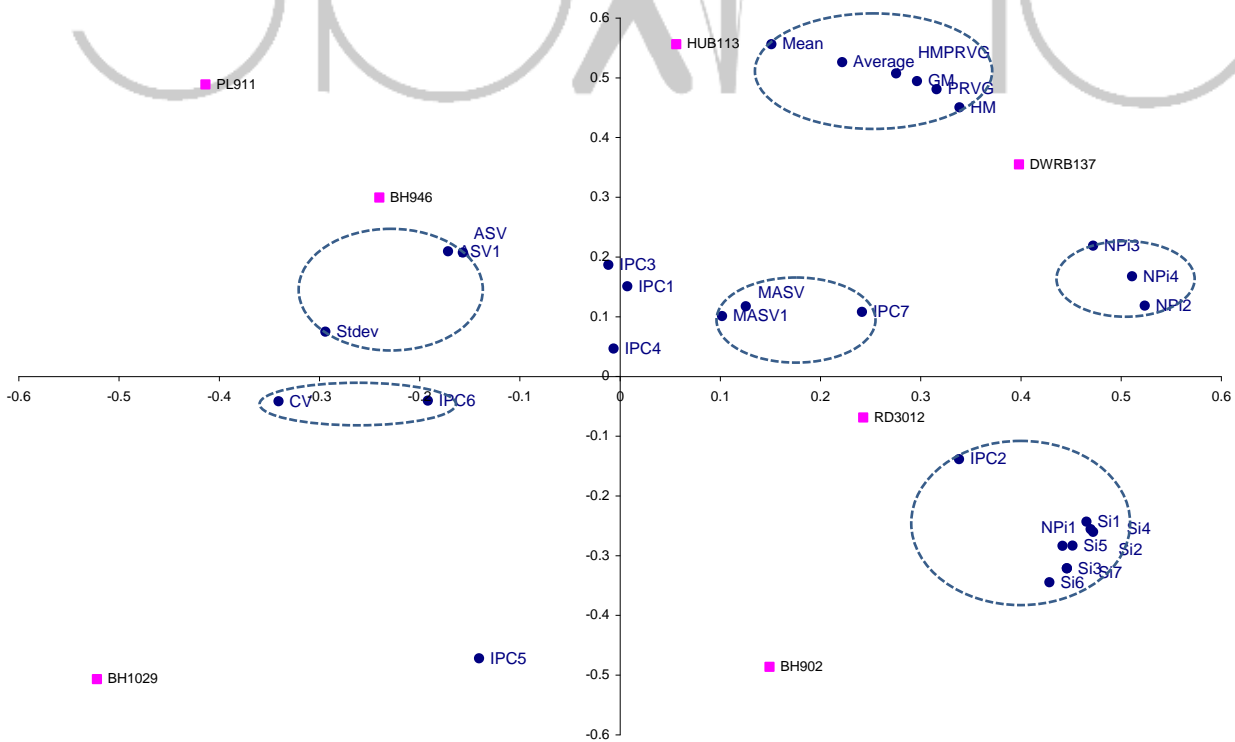Figure 1: Biplot analysis of AMMI, BLUP and Non parametric measures

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