



Barley Genotypes Evaluated under Salinity Conditions by AMMI, BLUP and Non Parametric Measures

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Abstract

Highly significant variations due to environments, GxE interactions, and genotypes were observed by AMMI analysis. About 22.3% of the total sum square of variation for yield was due to environments followed by 35% of GxE interactions, whereas genotypes accounted 34.2%. AMMI1 explained a total variation of 54.9%, AMMI2 augmented about 23.7%, 11.8% for AMMI3. First two AMMI components totalled 78.7% of the total variation. Using first two IPCAs in stability analysis could benefit in identification of the stable high yielder genotypes. Dynamic concept of stability explained by ASV1 and ASV measures as both recommended (G6, G5, G12) wheat genotypes. MASV and MASV1 considered all significant IPCAs of the AMMI analysis identified same genotypes G6, G5, G12. BLUP based measures BLUP-based simultaneous selections, such as HM identified G3, G4, G1 while values of PRVG favored G4, G3, G1 and HMPRVG settled for G4, G3, G1 genotypes. Non parametric composite measures $NP_i^{(1)}$ to $NP_i^{(4)}$ found G3, G4, G5 as genotypes of choice for salinity conditions. Biplot analysis observed ASV, ASV1, MASV, MASV1 $S_i^1, S_i^2, S_i^3, S_i^4, S_i^7$, accounted more of in first principal component whereas Mean, Average, GM, HM PRVG, HMPRVG, $NP_i^{(2)}, NP_i^{(3)}, NP_i^{(4)}$ were major contributors in PC2. Non parametric measures $NP_i^{(2)}, NP_i^{(3)}, NP_i^{(4)}$ formed one cluster whereas BLUP based measures Mean, GM, HM, PRVG, HMPRVG grouped with average yield of genotypes.

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

Introduction

The selection of better performers possessing stable yield across wider environmental conditions advocated after Multi-environment trials (Ahakpaz. *et al.*, 2021). Genotype \times environment interaction effects have been estimated to have an idea about cultivar performance in different environments (Anuradha. *et al.*, 2022). Recent studies have been reported the use of latest analytic approaches in the genotype \times environment estimation (Pour-Aboughadareh. *et al.*, 2022). Accumulation of main effects of genotypes, environments with their multiplicative interactions have been used in Additive main effect and multiplicative interaction (AMMI) model (Pour-Aboughadareh. *et al.*, 2019). AMMI based measures (AMMI stability value (ASV), ASV1, Modified AMMI stability value

(MASV) & MASV1) have also gained visibility (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 also mentioned in the stability and adaptability of genotypes (Gonçalves. *et al.*, 2020). Nonparametric measures $S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7, NP_i^{(1)}, NP_i^{(2)}, NP_i^{(3)}, NP_i^{(4)}$ have been also utilized for genotypes \times environmental interaction effects (Pour-Aboughadareh. *et al.*, 2019). The analytic measures have been compared to decipher the GxE interactions effects for wheat genotypes evaluated in the country under salinity conditions.

Materials and Methods

Fifteen promising wheat genotypes were evaluated in research field trials at 05 centers of All India Coordinated Research Project on Wheat during 2020-21 cropping season in field trials for salinity conditions. More emphasis had been placed to increase the wheat production of from problem soils 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 $i=1,2, \dots,k, j =, 1,2, \dots,n$ 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 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.

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

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

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

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

ASV

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

ASV1

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

Modified AMMI stability Value

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

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 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

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

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 22.3% of the total sum square of variation for yield was due to environments followed by 35% of G×E interactions, whereas genotypes accounted 34.2%. Diversity of the testing sites were approved by AMMI analysis (Mehraban. *et al.*, 2019). Interaction effects further portioned into three significant Interaction principal components totalled for more than 90.5% interactions sum of square variations. AMMI1 explained a total variation of 54.9%, followed by 23.7% for AMMI2, 11.8% for AMMI3 respectively. The first two AMMI components in total showed 78.7% 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 94.3% and 5.6% of total G×E respectively. Early IPCs selectively capture signal, and late ones noise. Note that the sum of squares for G×E-signal is 0.96 times that for genotypes main effects. Hence, narrow adaptations are important for this dataset (Vaezi. *et al.*, 2018). Even just IPC1 alone is 0.56 times the genotypes main effects. Also note that G×E-noise is 0.06 times the genotypes effects. Discarding noise improves accuracy, increases repeatability, simplifies conclusions, and accelerates progress.

Ranking of Genotypes as per AMMI Based Measures

Average yield of genotypes was considered as an important measure to assess the yield potential as yield expressed highly significant variations among genotypes. Mean yield of genotypes selected G4, G8, G3 with very low yield of G15 (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 G6, G11, G5 while as per IPCA-2 values, G12, G13, G10 genotypes would be of choice. Values of IPCA-3 favored G7, G4, G10 genotypes would be of stable performance. First two IPCAs in ASV & ASV1 measures utilized 78.7% 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 (G6, G5, G12) and ASV pointed towards (G6, G5, G12) as of stable performance. Adaptability measures MASV and MASV1 considered all significant IPCAs of the AMMI analysis using 90.5% of G×E interactions sum of squares (Gerrano. *et al.*,

2020). Values of MASV1 identified G6, G5, G12 genotypes would express stable yield whereas genotypes G12, G6, 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 G4, G8, G3 as high yielders. Consistent yield of G 1, G6, G10 as per least values of standard deviation more over the values of CV identified G1, G3, G6 genotypes for the consistent yield performance under salinity conditions.

Based on BLUP & Non Parametric Measures

More over the values of GM favored G4, G3, G1. The BLUP-based simultaneous selections, such as HM identified G3, G4, G1 while values of PRVG favored G4, G3, G1 and HMPRVG settled for G4, G3, 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.*, 2022. Non parametric measures ranked the genotypes as per their corrected yield across environments S_i^1 values pointed for G3, G8, G11 while S_i^2 selected G3, G8, G10 and values of S_i^3 favoured G9, G3, G11 as desirable genotypes (Table 4). G3, G8, G10 selected by values of S_i^4 , G3, G8, G11 as per S_i^5 , G3, G9, G11 by S_i^6 and lastly S_i^7 for G9, G3, G8 (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 G3, G8, G10 whereas as

per $NP_i^{(2)}$, genotypes G3, G4, G5 would be of choice while $NP_i^{(3)}$ identified G3, G4, G5. Last composite measure $NP_i^{(4)}$ found G3, G4, G5 as genotypes of choice for salinity conditions.

Biplot Analysis

The first two significant PC's has explained about 75.1% 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 43.5% & 31.5% by first and second principal components respectively (Ahakpaz. *et al.*, 2021). Measures ASV, ASV1, MASV, MASV1 S_i^1 , S_i^2 , S_i^3 , S_i^4 , S_i^7 , accounted more of share in first principal component whereas Mean, Average, GM, HM PRVG, HMPRVG, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ 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 ASV with ASV1 & CV, while MSV with MASV1, S_i^7 · SDev showed IPC3, IPC1, $NP_i^{(1)}$, S_i^2 , S_i^3 S_i^5 , S_i^6 . Tight relation of $NP_i^{(2)}$ with $NP_i^{(3)}$, $NP_i^{(4)}$ BLUP based measures observed in separate quadrant along with average yield. This group expressed right angles with group of measures $NP_i^{(1)}$, S_i^2 , S_i^3 S_i^5 , S_i^6 . While right angles of $NP_i^{(2)}$ · $NP_i^{(3)}$, $NP_i^{(4)}$ with CV, ASV and ASV1 measures. In total six clusters of small and large sizes were observed for the studied measures. Smaller cluster consisted on C with ASV, ASV1 in separate quadrant. Three clusters were placed in adjacent quadrant. IPC1, IPC3 with Stdev in one, while nearby second consisted of $NP_i^{(1)}$, S_i^2 S_i^4 , S_i^5 , S_i^6 S_i^3 while third of S_i^7 with MASV, MASV1. Two more clusters observed in adjacent quadrant. Non parametric measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ formed one cluster. BLUP based measures Mean, GM, HM, PRVG, HMPRVG grouped with average yield of genotypes (Fig. 2).

Table 1: Parentage vis-a-vis location details of genotypes Salinity 2020-21

Code	Genotype	Parentage	Code	Genotype	Parentage	Locations
G1	RD3040		G9	NDB1757	EIBGN (18-19) -55 (RD 2715)	Ayodhya
G2	NDB1173	BYTLRA 3-(1994-95)/NDB217	G10	KB1911	BH 920/AZAD	Dalipnagar
G3	RD2794	RD2035/RD2683	G11	RD3016	RD 2715 / RD 2552	CSSRI, Karnal
G4	DWRB224	CDC MANLEY/RD2592	G12	RD3041		CCSHAU, Hisar
G5	BH1039	RD 2784 / BHS 415	G13	KB1822	K 996/K 508	Bhilwara
G6	RD2907	RD103/RD2518//RD2592	G14	RD3042		
G7	HUB280	14th HBSN-05-146 x RD 2508-1	G15	KB1909	K 1155/RD 2811	
G8	RD3039					

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	74	402.57019	.0000000 ***	91.61		
Genotype (G)	14	796.08244	.0000000 ***	34.27		
Environment (E)	4	1812.88015	.0000000 ***	22.30		
GxE interactions	56	203.4557	.0000000 ***	35.04		
IPC1	17	368.18711	.0000000 ***		54.94	54.94
IPC2	15	180.69376	.0000000 ***		23.79	78.73
IPC3	13	103.21303	.0000000 ***		11.78	90.50
Residual	11	98.37843	.0000000 ***			
Error	225	12.11895				
Blocks/Env	15	21.257	.0294817 *			
Pure Error	210	11.46623				
Total	299	108.75237				

Table 3: AMMI and BLUP based measures of genotypes

Genotype	Mean	IPCA1	IPCA2	IPCA3	ASV1	ASV	MASV1	MASV	Average	Stdev	CV
G1	28.50	-0.4347	1.6140	1.2750	1.90	1.74	3.983	3.151	28.50	3.26	11.43
G2	25.84	-0.7090	-1.1955	-0.4494	2.03	1.61	3.185	2.383	25.84	6.94	26.87
G3	29.57	-1.4722	0.9169	1.1299	3.52	2.42	4.136	2.970	29.57	5.43	18.38
G4	30.71	0.2580	-1.6210	-0.1789	1.73	1.67	3.706	2.850	30.71	8.77	28.57
G5	28.23	-0.2530	0.5316	-0.9976	0.79	0.66	1.665	1.413	28.23	7.90	27.98
G6	27.03	0.1511	0.5510	-0.2597	0.65	0.60	1.316	1.018	27.03	5.03	18.61
G7	20.45	1.5878	1.9678	0.1032	4.16	3.11	5.756	4.186	20.44	9.05	44.28
G8	30.11	2.2947	-2.8719	1.4974	6.03	4.52	8.499	6.270	30.11	15.35	51.00
G9	24.71	2.9116	0.9734	1.3713	6.79	4.53	7.204	4.931	24.71	13.58	54.94
G10	14.54	-2.5276	0.1932	0.2295	5.84	3.85	5.858	3.863	14.54	5.24	36.03
G11	25.93	0.2233	-1.8289	-1.4787	1.90	1.86	4.410	3.522	25.93	10.06	38.82
G12	27.85	0.4727	0.0489	0.4085	1.09	0.72	1.171	0.831	27.85	7.20	25.85

Genotype	Mean	IPCA1	IPCA2	IPCA3	ASV1	ASV	MASV1	MASV	Average	Stdev	CV
G13	14.48	-2.0414	0.0507	-0.6559	4.71	3.10	4.761	3.172	14.48	5.92	40.87
G14	21.45	1.9310	1.1298	-2.6031	4.60	3.14	5.757	4.387	21.45	12.52	58.38
G15	10.77	-2.3922	-0.4600	0.6084	5.54	3.66	5.654	3.772	10.77	6.16	57.17

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⁾
G1	28.34	28.17	1.2477	1.1751	5.40	20.70	2.52	4.55	3.36	2.05	4.93	3.00	0.4286	0.6691	0.7941
G2	24.98	24.02	1.0756	1.0538	4.00	11.00	1.38	3.32	2.80	1.75	3.14	2.60	0.2889	0.4364	0.5263
G3	29.16	28.75	1.2692	1.2144	7.00	32.80	4.32	5.73	4.72	3.11	5.56	4.20	1.4000	1.1932	1.4583
G4	29.67	28.61	1.2706	1.2578	5.40	18.70	2.13	4.32	3.36	1.91	4.45	3.20	1.0667	1.1380	1.4211
G5	27.25	26.19	1.1722	1.1492	5.60	20.80	2.74	4.56	3.68	2.42	4.52	3.60	0.9000	0.8446	1.0370
G6	26.67	26.32	1.1486	1.1251	4.40	13.20	1.69	3.63	2.56	1.64	4.13	2.40	0.3000	0.5505	0.6667
G7	17.97	14.66	0.8564	0.6474	5.60	21.20	2.94	4.60	3.36	2.33	5.05	3.20	0.3200	0.4604	0.5600
G8	26.94	23.95	1.1969	1.1026	7.00	32.20	3.66	5.67	4.64	2.64	5.55	4.20	0.6000	0.8106	1.0000
G9	19.76	13.58	0.9954	0.6197	6.00	27.70	4.47	5.26	3.84	3.10	5.77	3.40	0.8500	0.8224	0.9375
G10	13.92	13.43	0.6338	0.5614	6.60	28.80	3.35	5.37	4.48	2.60	5.14	4.20	0.3231	0.4548	0.5593
G11	24.27	22.63	1.0585	1.0079	6.80	30.70	3.74	5.54	4.64	2.83	5.29	4.20	0.7000	0.7915	0.9714
G12	27.03	26.15	1.1544	1.1484	4.00	10.70	1.49	3.27	2.64	1.83	3.24	2.40	0.4800	0.5640	0.6897
G13	13.39	12.20	0.6090	0.5392	4.80	15.70	1.78	3.96	2.64	1.50	4.76	2.60	0.2000	0.3145	0.3810
G14	18.79	16.61	0.8561	0.7476	6.00	26.20	2.85	5.12	3.44	1.87	6.09	3.40	0.3091	0.5445	0.6383
G15	9.21	7.59	0.4557	0.3452	6.60	28.70	3.68	5.36	4.16	2.67	5.52	3.80	0.2533	0.3773	0.4648

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	-0.1552	-0.2798	PRVG	-0.1675	-0.2757
IPCA1	0.0212	-0.1244	HMPRVG	-0.2028	-0.2438
IPCA2	-0.0172	0.0884	S _i ¹	0.2460	-0.1594
IPCA3	0.0488	-0.1004	S _i ²	0.2524	-0.1602
ASV1	0.2672	0.0602	S _i ³	0.2447	-0.1625
ASV	0.2710	0.0321	S _i ⁴	0.2540	-0.1555
MASV1	0.2642	-0.0204	S _i ⁵	0.2168	-0.1918
MASV	0.2535	-0.0485	S _i ⁶	0.2020	-0.1886
Average	-0.1552	-0.2798	S _i ⁷	0.2545	-0.0793
Stdev	0.1367	-0.1116	NP _i ⁽¹⁾	0.2211	-0.1745
CV	0.2309	0.0947	NP _i ⁽²⁾	-0.0017	-0.3048
GM	-0.1864	-0.2641	NP _i ⁽³⁾	-0.0146	-0.3293
HM	-0.2079	-0.2377	NP _i ⁽⁴⁾	-0.0191	-0.3279
75.12	43.56	31.56			

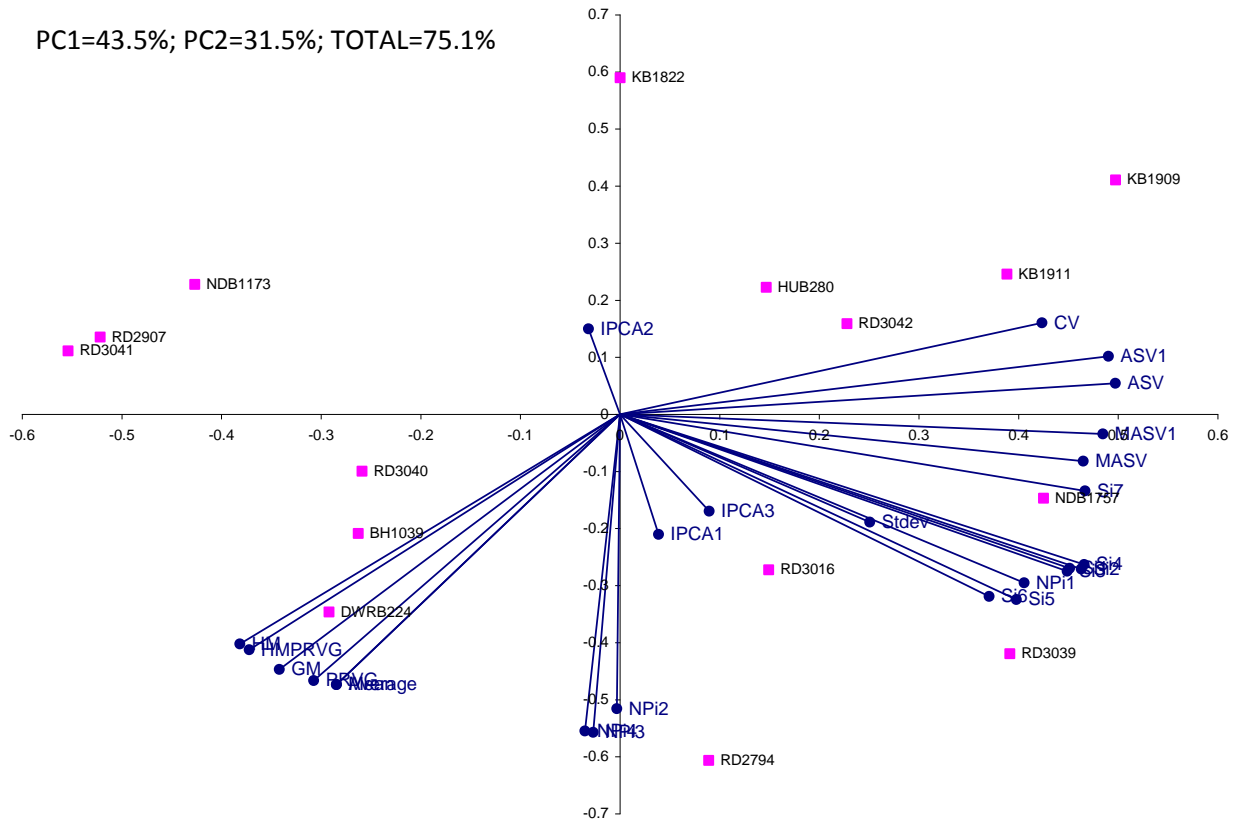


Figure 1: Biplot analysis of AMMI, BLUP and Non parametric measures

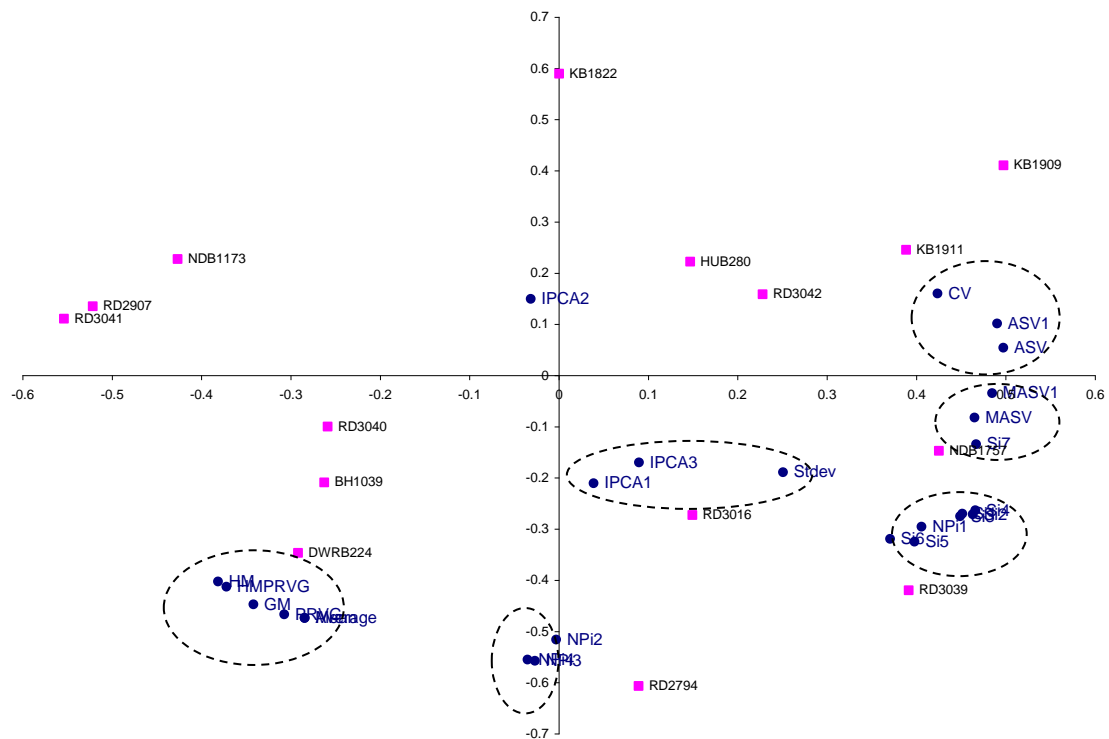


Figure 2: Clustering pattern of AMMI, BLUP and Non parametric measures

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