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RESEARCH PAPER

Emulations of AMMI, BLUP and non-parametric measures to decipher GXE interaction of wheat genotypes evaluated in CZ

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Abstract : AMMI analysis observed highly significant variations due to environments, GxE interactions, and genotypes with, respective 63.2% 18.3% 5.5% towards the total sum square of variations. Absolute IPCA-1 scores pointed for G 2, G4, G7 as per IPCA-2, genotypes G8, G2 G7 would be of choice. ASV and ASV1 measures utilized 54.5% of interaction sum of squares recommended (G2, G7, G3). 96.9% of interaction effects utilized by MASV and MASV1 settled for G7, G2, G13 genotypes. BLUP-based HMGV RPGV HMRPGV measures pointed for G3, G13, G8 genotypes. Non parametric measures $NP_i^{(1)}$ observed suitability of G13, G9 whereas $NP_i^{(2)}$, $NP_i^{(3)}$ $NP_i^{(4)}$ identified G7, G10 wheat genotypes. First two significant principal components accounted for 68.5% of the total variation in the AMMI, BLUP and non-parametric measures in biplot analysis. Measures BLHM, MHPRVG, BLGM, PRVG, HM, Average, BLAvg accounted more of share in first component whereas $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ S_i^1 ,S_i^2 BLStdev S_i^4 were major contributors for second component. Clustering analysis observed the group of average, GAI, HM and BLAvg, BLHM, BLGM, PRVG, MHPRVG measures along with second cluster of CV, BLCV, Stdev, BLStdev , IPC1 placed in one quadrant. AMMI based measures ASV, ASV1, MASV, MASV1 clustered with non-parametric measures $NP_i^{(1)}$, S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7 in bigger cluster.

Key Words : AMMI, BLUP, $S_i^{(s)}$, $NP_i^{(s)}$, Spearman rank co-efficient, Biplot analysis

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INTRODUCTION

Genotype × environment interaction effects masks the association between phenotypic and genotypic expression of genotypes and hinders in the identification of superior genotypes across environments (Ahakpaz *et al.,* 2012). More over this genotype × environment interaction provides valuable information for genotypes performance in various environments as performance assisted for spegific and general adaptations of genotypes (Gerrano *et al.,* 2020). Modeling the GxE in METs assists in defining the phenotypic stability of the genotypes for a range of locations or a particular genotype for varied environmental conditions (George and Lundy, 2019 and Anuradha *et al.,* 2022). Additive main effects and multiplicative interaction (AMMI) has gained very significant usage as multivariate approach as compared to joint regression analysis in many crop

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improvement studies (Bocianowski *et al.,* 2021). Number of measures AMMI stability value (ASV), ASV1, Modified AMMI stability value (MASV) and MASV1 marked their presence in recent literature (Vaezi *et al.,* 2018). Best linear unbiased prediction (BLUP) estimates have the potential to improve the predictive accuracy of random effects of genotypes under multi-environment trials. Harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV) and harmonic mean of relative performance of genotypic values (HMRPGV), were mentioned for the stability and adaptability of genotypes (Gonçalves *et al.,* 2020). Non-parametric measures for stability assessment *viz.,* S_i^1 S_i^2 S_i^3 S_i^4 S_i^5 S_i^6 S_i^7 along with $NP_i^{(1)}$, $NP_i^{(2)}$, $NP^{(3)}$, $NP_i^{(4)}$ have been suggested (Pour-Aboughadareh *et al.,* 2019).

MATERIAL AND METHODS

Thirteen promising wheat genotypes were evaluated in research fields of Central Zone at 14 centers of All India Co-ordinated Research Project on wheat during 2020-21 cropping seasons. 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} de-notes the phenotypic value of ith genotype in jth environ-ment 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 geno-type. 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.

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

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

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

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

$NP_i^{(1)} = \frac{1}{n}\sum_{j=1}^{n} \lvert r^*_{ij} - M^*_{di} \rvert$	$NP_i^{(3)} = \frac{\sqrt{\Sigma(r^*_{ij} - \bar{r}^*_{i.})^2/n}}{\bar{r}_{i}.}$
$NP_i^{(2)} = \frac{1}{n}\left(\frac{\sum_{j=1}^{n} \lvert r^*_{ij} - M^*_{di} \rvert}{M_{di}}\right)$	$NP_i^{(4)} = \frac{2}{n(n-1)}\left[\sum_{j=1}^{n-1}\sum_{j'=j+1}^{m} \frac{\lvert r^*_{ij} - r^*_{ij'} \rvert}{\bar{r}_{i}.}\right]$
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	$\mathrm{MASV1} = \sqrt{\sum_{n=1}^{N-1} (\frac{SSIPC_n}{SSIPC_{n+1}}PC_n)^2 + (PC_{n+1})^2}$
$HMGV_i$	= 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	$RPGV_{ij} = \sum GV_{ij} / \sum GV_j$
Harmonic mean of relative performance of genotypic values	$HMRPGV_{i.}$ = Number of environments / $\sum_{j=1}^{k} \frac{1}{RPGV_{ij}}$
Geometric adaptability index	GAI = $\sqrt[n]{\prod_{k=1}^{n} \bar{X}_k}$

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

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

RESULTS AND DISCUSSION

The results obtained from the present investigation as well as relevant discussion have been summarized under following heads :

AMMI analysis :

Highly significant variations due to environments, GxE interactions and genotypes were observed by AMMI analysis (Table 3). This analysis also revealed about 63.2% of the total sum square of variation for yield was due to environments followed by 18.3% by environment whereas due to genotypes was only 5.5%.

Table 1 : Parentage *vis-a-vis* location details for evaluated wheat genotypes

Genotype	Code	Parentage	Code	Locations	Latitude	Longitude	Altitude
HI8833	G 1	HI8498+sr36+sr2	E 1	Vijapur	23°33' N	72°45' E	129.4
GW322	G 2	PBW173/GW196	E 2	SK Nagar	21°18' N	72°85 E	11
MP3535	G 3	BABAX/LR42//BABAX/3/ER2000/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA(224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92	E 3	Anand	22° 33' N	72° 56' E	39
GW523	G 4	23ESWYT-19PED.CHEN/AQ.SE(TAUS)//BUC/ KAUZ/ PEWTI-1	E 4	Amreli	21° 36' N	71° 13' E	126
GW513	G 5	PBW559/WR1873	E 5	Junagadh	21° 30' N	70° 27' E	90
HI1636	G 6	DL788-2/HW4032	E 6	Gwalior	26° 13' N	78° 10' E	211
HI8832	G 7	HI8498+sr36+sr2	E 7	Jabalpur	23° 10' N	79° 55' E	403
MACS6768	G 8	MACS6221*2/Raj4037	E 8	Powarkheda	22° 70 N	77° 73 E	308
HI1544	G 9	HINDI62/BOBWHITE/CPAN2099	E 9	Indore	22° 43' N	75° 51' E	550
HI1667	G 10	HI1544/HD2987	E 10	Sagar			
HI8498	G 11	RAJ6070/RAJ911	E 11	Raipur	21° 15' N	81° 37' E	289
HI8713	G 12	HD4672/PDW233	E 12	Kota	25°12' N	75°51' E	271
HI1650	G 13	Giant3/HI1395	E 13	Udaipur	24° 34' N	73° 41' E	600
			E 14	Mandor	27.64' N	77.13' E	

Table 2: AMMI analysis of wheat genotypes evaluated under central zone of the country

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	194	78180.35	***	86.92		
Genotype (G)	12	4902.74	***	5.45		
Environment (E)	14	56830.90	***	63.19		
GxE interaction	168	16446.71	***	18.29		
IPC1	25	5903.51	***		35.89	35.89
IPC2	23	3064.71	***		18.63	54.53
IPC3	21	2318.62	***		14.10	68.63
IPC4	19	1792.35	***		10.90	79.52
IPC5	17	978.57	***		5.95	85.47
IPC6	15	852.76	***		5.18	90.66
IPC7	13	542.05	**		3.30	93.96
Residual	35	994.14	0.0608067			
Error	585	11762.81				
Total	779	89943.17				

Diversity of the evaluation sites was very supported by AMMI results (Mehraban *et al.,* 2019). Bifurcation of interactions effects into seven significant Interaction principal components account more than 93.9% variation. AMMI I explained a total variation of 35.9%, followed by 18.6% for AMMI 2, 14.1% by AMMI3 for, 10.9% AMMI 4, AMMI 5 contributed 5.9% followed by 5.2% and 3.3% by AMMI 6 and AMMI 7, respectively. The first two AMMI components in total showed 54.5% of the total variation indicating the two AMMI components well fit and confirm the use of AMMI model. Estimated sums of squares for G×E signal and noise were 79.46% and 20.54% of total G×E. Early IPCs selectively capture signal, and late ones noise. Accordingly, this much signal suggests AMMI6 or maybe AMMI7. Note that the sum of squares for GxE-signal is 2.67 times that for genotypes main effects. Hence, narrow adaptations are important for this dataset. Even just IPC1 alone is 1.20 times the genotypes main effects. Also note that GxE-noise is 0.69 times the genotypes effects. Discarding noise improves accuracy, increases repeatability, simplifies conclusions, and accelerates progress (PourAboughadareh *et al.,* 2022).

Ranking of genotypes as per measures :

Since the genotypes yield expressed highly significant variations, mean yield was considered as an important measure to assess the yield potential of genotypes. Mean yield of genotypes selected G3, G13,

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

Genotype	Average	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	MASV1	MASV	ASV1	ASV	BLAvg	BLStdev	BLCV	BLGM
G 1	49.19	3.060	-1.141	1.062	-0.704	-1.562	-1.357	-1.400	7.48	6.03	6.00	4.40	49.30	10.64	21.58	48.23
G 2	53.40	0.188	0.365	-1.005	1.374	0.256	1.338	-0.395	3.49	3.24	0.51	0.45	53.32	9.66	18.11	52.47
G 3	56.62	0.365	0.776	-0.723	-1.780	1.810	0.197	-0.023	3.92	3.86	1.05	0.93	56.07	10.16	18.12	55.17
G 4	53.43	-0.227	-1.278	-2.429	2.002	-0.717	-0.172	-0.866	5.26	5.06	1.35	1.32	53.40	8.55	16.01	52.79
G 5	52.99	-1.136	-1.879	-1.726	-0.167	0.137	-1.554	1.691	5.81	5.16	2.88	2.45	52.97	9.05	17.08	52.24
G 6	50.31	-2.863	1.103	1.752	-0.019	-1.783	-0.188	0.376	7.04	5.72	5.62	4.12	50.50	9.05	17.92	49.70
G 7	47.83	-0.282	-0.608	1.351	0.986	0.342	-0.163	1.178	3.03	2.90	0.82	0.72	48.40	8.37	17.29	47.70
G 8	54.81	-1.013	0.296	-1.024	-2.667	0.262	-0.507	-0.734	4.20	4.11	1.97	1.44	54.50	9.40	17.25	53.74
G 9	52.82	-1.545	2.215	0.544	0.401	-0.030	-0.816	-0.260	5.07	4.32	3.71	3.08	52.72	8.50	16.12	52.05
G 10	48.37	-0.975	-2.531	2.356	0.474	1.845	0.521	-0.891	6.77	6.21	3.15	2.87	48.94	7.90	16.15	48.26
G 11	50.66	1.714	-0.889	0.164	-1.317	-1.287	2.213	1.318	6.16	5.30	3.42	2.54	50.88	10.67	20.96	49.80
G 12	53.40	3.392	2.187	0.416	1.138	0.928	-0.809	0.794	7.93	6.31	6.89	5.19	53.13	12.00	22.59	51.81
G 13	55.28	-0.677	1.385	-0.737	0.279	-0.201	1.296	-0.787	3.88	3.42	1.90	1.67	54.97	9.50	17.28	54.18

Table 4 : Non-parametric measures of yield for wheat genotypes

Genotype	BLHM	PRVG	MHPRVG	S_i^1	$S_i^{2,}$	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
G 1	47.18	0.940	0.932	5.12	19.05	2.78	4.37	3.51	7.17	5.04	3.57	0.340	0.474	0.556
G 2	51.59	1.020	1.017	4.26	13.14	1.80	3.63	2.78	5.33	4.40	3.00	0.429	0.577	0.678
G 3	54.24	1.072	1.069	4.13	12.26	1.62	3.50	2.76	5.09	4.13	2.86	0.816	0.875	1.033
G 4	52.21	1.027	1.022	4.46	14.77	2.11	3.84	3.14	6.29	4.36	3.29	0.548	0.618	0.718
G 5	51.52	1.017	1.011	5.51	22.49	3.31	4.74	3.76	7.76	5.55	4.07	0.543	0.714	0.829
G 6	48.86	0.967	0.962	4.36	14.09	2.12	3.75	3.19	6.72	4.10	3.07	0.361	0.473	0.550
G 7	46.98	0.927	0.924	3.82	10.99	1.75	3.31	2.88	6.41	3.55	3.00	0.273	0.316	0.364
G 8	52.98	1.045	1.041	4.45	14.03	1.94	3.75	2.98	5.79	4.36	3.21	0.714	0.760	0.903
G 9	51.35	1.011	1.009	4.07	11.96	1.86	3.46	2.68	5.84	4.14	2.71	0.494	0.563	0.662
G 10	47.49	0.942	0.931	4.87	17.30	2.50	4.16	2.92	5.91	5.50	3.21	0.280	0.413	0.483
G 11	48.71	0.968	0.964	4.14	12.27	1.64	3.50	2.75	5.13	4.14	3.07	0.341	0.419	0.496
G 12	50.43	1.012	0.998	5.52	22.88	3.02	4.78	3.69	6.83	5.75	4.00	0.727	0.752	0.868
G 13	53.36	1.052	1.050	3.44	8.53	1.23	2.92	2.22	4.48	3.57	2.21	0.492	0.682	0.803

G8 with lowest yield of G7 (Table 4). 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 G 2, G4, G7 as per IPCA-2, genotypes G8, G2 G7 would be of choice (Table 4). Values of IPCA-3 favored G11, G12, G9 genotypes. As per IPCA-4, G6, G5, G13 genotypes would be of stable performance. Genotypes G9, G5, G13 selected as per IPCA5 while values of IPCA6 pointed for G7, G4, G6 and finally IPCA7 observed suitability of G3, G9, G6. First two IPCAs in ASV and ASV1 measures utilized 54.5% 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 (G2, G7, G3) and ASV pointed towards (G2 G7, G3) as of stable performance. Adaptability measures MASV and MASV1considered all seven significant IPCAs of the AMMI analysis and utilized about 96.9% of interaction effects. Values of MASV1 identified G7, G2, G13 genotypes would express stable yield whereas genotypes G7, G2, G 13 be of stable yield performance by MASV measure, respectively. The chief advantage of BLUP based measures is to consider the randomness of the genotypic effects and to allow ranking genotypes in relation to their performance based on the genetic effects (Sousa *et al.,* 2020). Average yield of genotypes pointed towards G3, G13 G8 as high yielders. More over the values of GAI favored G3, G13, G8. Least values of standard deviation observed for the consistent yield of G10, G9, G4 more over the values of CV identified G4, G9, G10 genotypes for CZ zone of the country. The BLUP-based simultaneous selections, such as HMGV identified G3, G13, G8, values of RPGV favored G3, G13, G8 and HMRPGV estimates selected G3, G13, G8 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.,*

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

Measure	Principal component 1	Principal component 2	Measure	Principal component 1	Principal component 2
Average	0.221	0.183	BLStdev	-0.036	0.215
Stdev	-0.036	0.213	BLCV	-0.124	0.150
CV	-0.123	0.148	BLGM	0.232	0.161
GAI	0.229	0.167	BLHM	0.237	0.145
HM	0.235	0.151	PRVG	0.227	0.169
IPC1	-0.092	0.143	MHPRVG	0.236	0.152
IPC2	0.110	0.076	S_i^1	-0.173	0.221
IPC3	-0.166	-0.137	S_i^2	-0.173	0.223
IPC4	-0.049	-0.062	S_i^3	-0.187	0.188
IPC5	0.074	0.057	S_i^4	-0.176	0.218
IPC6	0.094	-0.147	S_i^5	-0.180	0.199
IPC7	-0.052	0.027	S_i^6	-0.192	0.110
MASV1	-0.206	0.132	S_i^7	-0.157	0.205
MASV	-0.197	0.131	$NP_i^{(1)}$	-0.172	0.205
ASV1	-0.187	0.132	$NP_i^{(2)}$	0.148	0.250
ASV	-0.188	0.129	$NP_i^{(3)}$	0.160	0.254
BLAvg	0.225	0.176	$NP_i^{(4)}$	0.164	0.250
			68.54	40.48	28.06

2022.

Non-parametric measures :

Measure based on ranks as per corrected yield S_i^1 selected G13, G9, while S_i^2 favored G13, G7 as per values of S_i^3 desirable genotypes would be G13 , G3. Values of measure S_i^4 identified G13, G7 and measure S_i^5 pointed towards G13, G9 while S_i^6 observed suitability of G13, G11 and lastly S_i^7 values identified G7, G13 genotypes (Table 3). The mentioned strategy determines the stability of genotype over environment if its rank is similar over other environments (biological concept). Non-parametric measures of phenotypic stability were associated with the biological concept of stability (Vaezi *et al.,* 2018). Non-parametric measures $NP_i^{(1)}$ to $NP_i^{(4)}$, consider the ranks of genotypes as per yield and corrected yield simultaneously, values of $NP_i^{(1)}$ measure observed suitability of G13, G9 whereas as per $NP_i^{(2)}$, genotypes G7, G10 would be of choice while $NP_i^{(3)}$ identified G7, G10. Last composite measure $NP_i^{(4)}$ found G7, G10 as genotypes of choice for this zone.

Biplot analysis :

The first two significant PC's has explained about 68.5% of the total variation in the AMMI, BLUP and non parametric measures (Table 5) with respective contributions of 40.5% and 28.1% by PC1 and PC2. Measures BLHM, MHPRVG, BLGM, PRVG, HM, Average, BLAvg accounted more of share in PC1 whereas $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ S_i^1 ,S_i^2 BLStdev S_i^4 contributed more in PC2. The association analysis among measures had been explored with the biplot analysis. In the biplot vectors of measures expressed acute angles would be positively correlated whereas those achieved obtuse or straight line angles would be negatively correlated. Independent type of relationships had expressed by right angles between vectors. Very tight positive relationships observed among MASV and MASV1, ASV, ASV1, S_i^6, IPC4, IPC7. While $NP_i^{(1)}$ expressed high degree of positive relationship with S_i^1, S_i^2 ,S_i^3 ,S_i^4 ,S_i^5 ,S_i^7 and CV, BLCV, IPC1 measures. Standard deviation and BLStdev expressed no relationship with IPC3, IPC4 measures. $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ values showed positive association. Average yield, GAI, HM maintained strong direct relationship with BLUP based measures BLAvg, BLGM, BLHM, RPGV, MHPRVG, IPC2, IPC5 measures. Measure IPC6 expressed no relation with BLUP based measures. Opposite or indirect

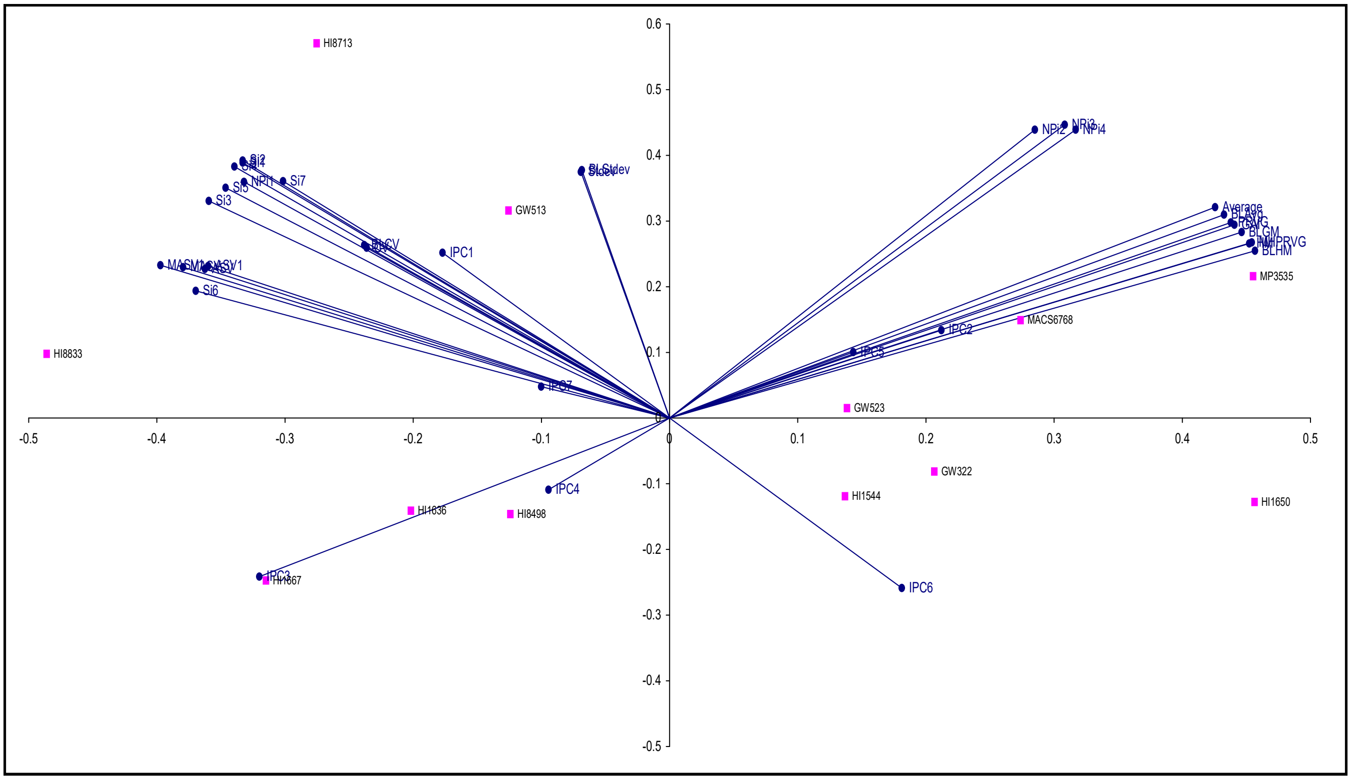

Fig. 1: Biplot analysis of AMMI, BLUP and non- parametric measures

relationship portrayed with S_i^1 to S_i^7 and CV, BLCV, IPC1 Similar type of relationship expressed by IPC3 with BLUP based measures. IPC4 exhibited negative relationship with $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ measures. (Fig. 1). In total six clusters of studied measures had been observed in biplot analysis. Smallest clusters comprises of IPC4, IPC7 and IPC5, IPC5 measures. Next smaller comprised of $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. Adjacent cluster consists of average, GAI, HM and BLAvg, BLHM, BLGM, PRVG, MHPRVG measures and placed in one quadrant together. CV, BLCV, Stdev, BLStdev joined hands with IPC1. AMMI based measures ASV, ASV1, MASV, MASV1 clustered with $NP_i^{(1)}$, S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7 in bigger group of measures (Fig. 2).

Association analysis:

Average yield had expressed direct and indirect relationships with other measures (Table 6). Highly significant positive with GM, HM, IPC3, BLMean, BLGM, BLHM, PRVG, MHPRVG and strong negative with $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. Also expressed moderate to weak direct and indirect with other measures. AMMI based measures ASV and ASV1 showed only moderate direct correlations while weak negative with $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ (Anuradha *et al.* 2022). Both MASV and MASV1 measures exhibited moderate to strong positive correlation values along with weak nature of indirect relationship with $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. BLUP based measures maintained strong to moderate positive with other measures along with strong negative values with non parametric measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. 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 portrayed moderate positive with other measures while negative of weak nature with IPC1, IPC2, IPC3, IPC4, IPC5, IPC6, IPC7 values. Non-parametric composite measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ maintained strong negative relationships with mostly measures in contrast to expression of $NP_i^{(1)}$ (Pour Aboughadareh *et al.,* 2022).

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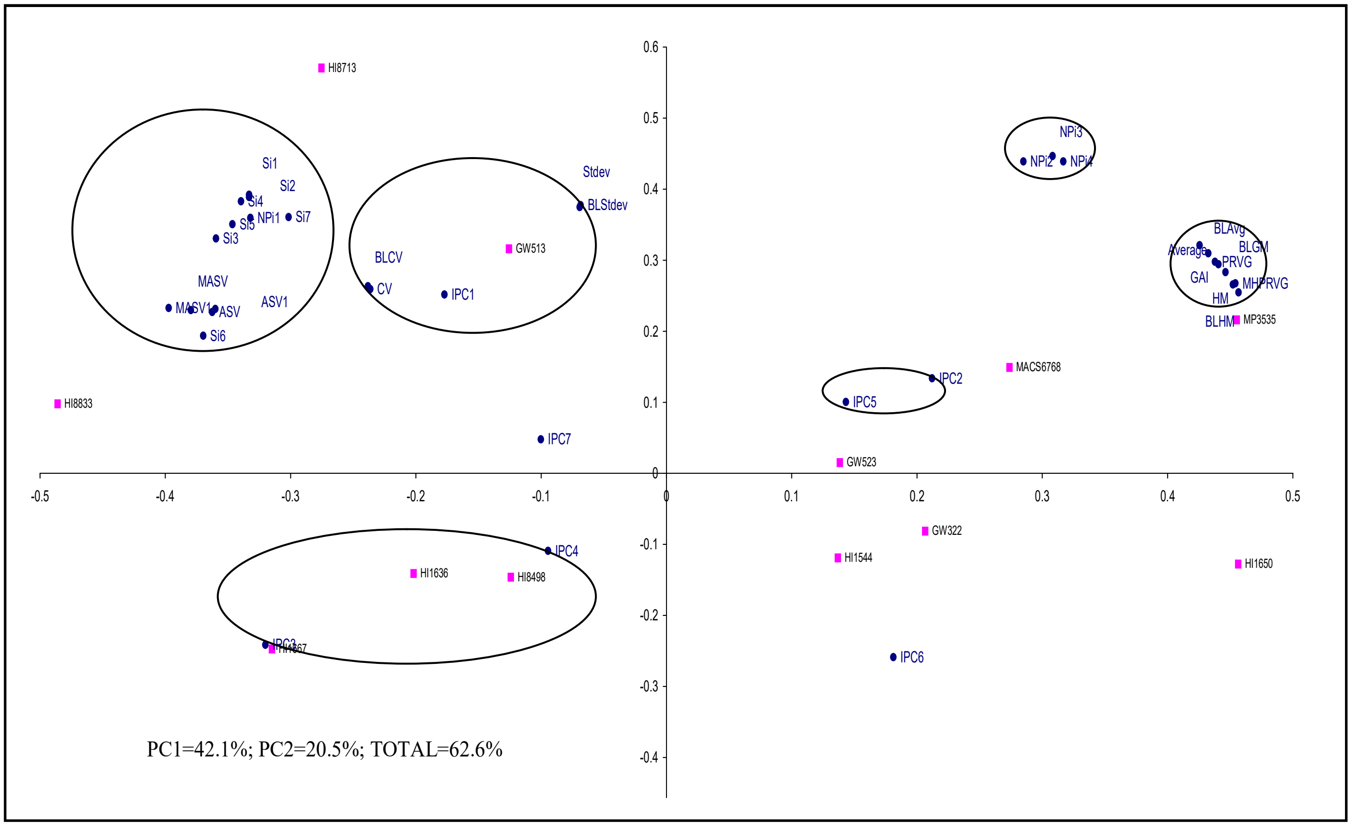

Fig. 2: Clustering pattern of AMMI, BLUP and non-parametric measures

Table 6 : Spearman rank correlation analysis among AMMI, BLUP and non-parametric measures

	Stdev	CV	GM	HM	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	MASV1	MASV	ASV1	ASV	BLAvg	BLStdev	BLCV	BLGM	BLHM	PRVG	MHPRVG	S_i^1	$S_i^{2,}$	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
Average	-0.374	-0.044	0.967	0.962	-0.126	-0.374	0.736	0.159	-0.148	-0.093	0.082	0.291	0.308	0.302	0.313	0.995	-0.379	0.027	0.962	0.956	0.978	0.967	0.110	0.148	0.324	0.148	0.198	0.505	0.027	0.217	-0.868	-0.901	-0.901
Stdev		0.890	-0.253	-0.220	0.709	0.286	-0.198	-0.346	-0.159	0.066	0.143	0.302	0.220	0.291	0.225	-0.352	0.995	0.846	-0.198	-0.165	-0.253	-0.253	0.214	0.203	-0.049	0.203	0.099	-0.126	0.258	0.168	0.352	0.423	0.423
CV			0.093	0.110	0.720	0.187	0.143	-0.297	-0.044	0.093	0.192	0.324	0.247	0.280	0.225	-0.022	0.879	0.978	0.143	0.159	0.077	0.093	0.225	0.231	0.016	0.231	0.214	0.044	0.192	0.212	0.060	0.148	0.148
GAI				0.995	0.011	-0.302	0.786	0.203	-0.082	-0.115	0.104	0.418	0.434	0.418	0.429	0.984	-0.258	0.159	0.995	0.989	0.989	1.000	0.209	0.247	0.390	0.247	0.286	0.560	0.099	0.305	-0.797	-0.846	-0.846
HM					0.066	-0.330	0.758	0.187	-0.071	-0.077	0.121	0.407	0.429	0.407	0.412	0.978	-0.225	0.176	0.989	0.995	0.984	0.995	0.198	0.231	0.357	0.231	0.247	0.522	0.115	0.305	-0.802	-0.852	-0.852
IPC1						-0.049	-0.066	0.093	0.121	0.236	-0.066	0.170	0.154	0.033	0.011	-0.104	0.720	0.714	0.049	0.104	-0.011	0.011	0.198	0.181	-0.082	0.181	0.049	-0.066	0.275	0.195	0.077	0.115	0.115
IPC2							0.104	0.033	-0.027	-0.016	0.165	-0.148	-0.214	0.165	0.165	-0.352	0.308	0.258	-0.286	-0.313	-0.280	-0.302	-0.434	-0.418	-0.352	-0.418	-0.379	-0.313	-0.374	-0.558	0.374	0.308	0.308
IPC3								0.022	0.060	0.022	-0.049	0.341	0.363	0.445	0.489	0.758	-0.187	0.242	0.769	0.742	0.775	0.786	-0.082	-0.033	0.099	-0.033	-0.038	0.209	-0.170	-0.118	-0.637	-0.681	-0.681
IPC4									0.126	0.132	-0.132	-0.088	-0.044	-0.192	-0.126	0.154	-0.313	-0.242	0.176	0.159	0.159	0.203	0.071	0.099	0.148	0.099	0.066	0.192	0.110	0.036	-0.143	-0.264	-0.264
IPC5										0.126	0.055	-0.264	-0.137	-0.330	-0.297	-0.132	-0.181	-0.049	-0.143	-0.132	-0.170	-0.082	0.060	0.016	-0.022	0.016	-0.049	-0.148	0.242	-0.014	0.236	0.253	0.253
IPC6											-0.049	-0.423	-0.357	-0.511	-0.495	-0.137	0.099	0.121	-0.159	-0.121	-0.165	-0.115	-0.533	-0.527	-0.720	-0.527	-0.665	-0.764	-0.379	-0.503	-0.269	-0.264	-0.264
IPC7												-0.049	-0.082	0.016	-0.044	0.104	0.137	0.242	0.099	0.115	0.082	0.104	-0.082	-0.060	-0.027	-0.060	0.088	0.154	-0.104	0.058	0.110	0.016	0.016
MASV1													0.984	0.896	0.890	0.352	0.291	0.286	0.429	0.418	0.390	0.418	0.747	0.780	0.731	0.780	0.615	0.582	0.577	0.673	-0.016	-0.093	-0.093
MASV														0.857	0.863	0.368	0.209	0.209	0.429	0.423	0.390	0.434	0.758	0.786	0.731	0.786	0.577	0.538	0.626	0.673	-0.038	-0.121	-0.121
ASV1															0.989	0.368	0.286	0.286	0.440	0.429	0.423	0.418	0.500	0.527	0.582	0.527	0.401	0.489	0.385	0.426	-0.038	-0.110	-0.110
ASV																0.379	0.231	0.247	0.445	0.429	0.429	0.429	0.489	0.522	0.588	0.522	0.385	0.489	0.379	0.393	-0.071	-0.132	-0.132
BLAvg																	-0.357	0.049	0.978	0.973	0.989	0.984	0.148	0.187	0.363	0.187	0.236	0.544	0.049	0.255	-0.835	-0.879	-0.879
BLStdev																		0.852	-0.203	-0.170	-0.258	-0.258	0.176	0.170	-0.082	0.170	0.060	-0.148	0.225	0.124	0.330	0.407	0.407
BLCV																			0.209	0.225	0.148	0.159	0.121	0.137	-0.044	0.137	0.126	0.033	0.110	0.102	-0.027	0.060	0.060
BLGM																				0.995	0.995	0.995	0.214	0.253	0.396	0.253	0.308	0.588	0.093	0.316	-0.791	-0.830	-0.830
BLHM																					0.989	0.989	0.203	0.236	0.363	0.236	0.269	0.549	0.110	0.316	-0.797	-0.835	-0.835
PRVG																						0.989	0.159	0.198	0.363	0.198	0.253	0.560	0.049	0.261	-0.813	-0.857	-0.857
MHPRVG																							0.209	0.247	0.390	0.247	0.286	0.560	0.099	0.305	-0.797	-0.846	-0.846
S_i^1																								0.995	0.918	0.995	0.885	0.714	0.896	0.942	0.187	0.192	0.192
$S_i^{2,}$																									0.929	1.000	0.896	0.742	0.868	0.931	0.154	0.148	0.148
S_i^3																										0.929	0.901	0.885	0.775	0.871	0.033	0.016	0.016
S_i^4																											0.896	0.742	0.868	0.931	0.154	0.148	0.148
S_i^5																												0.885	0.637	0.909	0.121	0.137	0.137
S_i^6																													0.484	0.766	-0.148	-0.170	-0.170
S_i^1																														0.788	0.203	0.242	0.242
$NP_i^{(1)}$																															0.080	0.085	0.085
$NP_i^{(2)}$																																0.940	0.940
$NP_i^{(3)}$																																	0.990

Conflict of interests :

Authors declare no known conflict of interests for the work reported in this paper.

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