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GENETICS & PLANT BREEDING

G×E Effects Elucidated by AMMI, BLUP and Non-parametric Measures of Wheat Genotypes Evaluated in NEPZ

Ajay Verma* and Gyanendra Pratap Singh

ICAR-Indian Institute of Wheat & Barley Research, Post Bag # 158 Agrasain Marg, Karnal, Haryana, India

*Corresponding author: verma.dwr@gmail.com (**ORCID ID:** 0000-0001-9255-6134)

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ABSTRACT

Highly significant variations due to G×E interactions, environments and genotypes had been observed AMMI analysis. Values of IPCA's in the AMMI analysis indicate stability or adaptability of genotypes. G11, G1 selected by IPCA-1 and G1, G2 as per IPCA-2. Utilizing 60.6% of G×E interactions ASV identified G1, G7 and ASV1 settled for (G1, G7) genotypes. Nearly 97.8% of variations exploited by MASV1 pointed for G9, G2 whereas MASV judged G9, G8 genotypes. BLUP based HMGV RPGV HMRPGV measures identified G11 & G3. Consistent yield of G2, G3 wheat genotypes supported by the least values of standard deviation and CV measures. Biplot analysis of studied measures observed that two significant PC's has accounted for 65.8% of the total variation with respective percent share of 40.4% & 25.5% respectively. S_i^2, S_i^4, S_i^1, S_i^3, $NP_i^{(3)}$, IPC5 contributed more in PC1 whereas for PC2 contributors were BLGM, RPGV, HMGV, HMRPGV $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. High degree of positive relationship expressed by $NP_i^{(2)}$ $NP_i^{(3)}$, $NP_i^{(4)}$ with MASV, MASV1. Measures S_i^1 to S_i^7 clubbed with standard deviation, CV along with $NP_i^{(1)}$. No association of ASV & ASV1 observed with $NP_i^{(2)}$ $NP_i^{(3)}$, $NP_i^{(4)}$. Clustering pattern seen BLUP based measures in separate cluster while $NP_i^{(2)}$ seen with S_i^1 to S_i^7 along with standard deviation and CV measures.

HIGHLIGHTS

- Negative correlation of composite non parametric measures with BLUP based measures as well as with AMMI based measures for the present study of wheat genotypes evaluated under late sown conditions. Non parametric measures have been observed less computationally intensive and robust against the outliers.

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

Wheat breeder focused more on the development of stable high-yielding varieties particularly to a target environment over the years instead of across environments owing to different varieties in varying climatic conditions (George & Lundy 2019; Bocianowski *et al.* 2021). Recommendation or identification of high yield stability or adaptability is more appropriate for north eastern plains zone of India, where the adoption ratio for improved technologies is somewhat at lower side. Large number of approaches has been advocated in literature to analyze the stable performance of promising genotypes (Pour-Aboughadareh *et al.* 2022). Analytic approach additive main effects and multiplicative interaction (AMMI) has gained popularity in recent studies as compared to joint regression analysis (Pour-Aboughadareh *et al.* 2019). Good number of AMMI based measures AMMI stability value (ASV, ASV1), based on the first two interaction principal component axes along with MASV & MASV1 measures exploiting all significant IPCA's (Sousa *et al.* 2020). Best linear unbiased prediction (BLUP) based measures,

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harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV), and harmonic mean of relative performance of genotypic values (HMRPGV), were also highlighted for the stability and adaptability of genotypes (Gonçalves *et al.* 2020). Besides that number of nonparametric measures S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7 along with $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ have been also utilized to interpret the response of genotypes to environmental conditions (Pour-Aboughadareh *et al.* 2019). Available measures have been compared to illuminate the G×E interactions for wheat genotypes evaluated in north eastern plains zone of the country under late sown conditions.

MATERIALS AND METHODS

Twelve promising wheat genotypes were evaluated in research field trials at 11 centers of All India Coordinated Research Project on Wheat across this zone of the country during 2020-21 cropping season in field trials. More emphasis had been placed to increase the wheat production of this zone 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 G×E interaction and stability analysis. For a two-way dataset with k genotypes and n environments X_{ij} denotes the phenotypic value of i^{th} genotype in j^{th} environment where i = 1,2, ...k, ,j =, 1,2 ,...,n and r_{ij} as the rank of the i^{th} genotype in the j^{th} environment, and $\bar{r}_l$ as the mean rank across all environments for the i^{th} genotype. The correction for yield of i^{th} genotype in j^{th} environment as ($X^*_{ij} = X_{ij} - \bar{x}_{l\cdot} + \bar{x}_{\cdot\cdot}$) as X^*_{ij}, was the corrected phenotypic value; $\bar{X}_l$. was the mean of i^{th} 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 $\bar{r}_l$ and M_{di} were the mean and median ranks for original (unadjusted) grain yield, where $\bar{r}_l^*$ and M^*_{di} were the same parameters computed from the corrected (adjusted) data.

$$NP_i^{(1)} = \frac{1}{n}\sum_{j=1}^{n}|r^*_{ij} - M^*_{di}| \qquad NP_i^{(3)} = \frac{\sqrt{\sum(r^*_{ij} - \bar{r}^*_{i.})^2/n}}{\bar{r}_{i.}}$$

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

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

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

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

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

$HMGV_i$ $\quad$ = 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 $\quad RPGV_{ij} = \sum GV_{ij} / \sum GV_j$

Harmonic mean of Relative performance of genotypic values $\quad HMRPGV_{i.}$ = Number of environments / $\sum_{j=1}^{k}\frac{1}{RPGV_{ij}}$

Geometric Adaptability Index $\quad GAI = \sqrt[n]{\prod_{k=1}^{n}\bar{X}_k}$

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 G×E interactions, environments and genotypes were observed by AMMI analysis (Table 2). This analysis also revealed about 15.4% of the total sum square of variation for yield was due to G×E interactions, followed by 7.7% by environments whereas due to genotypes was only 4.7%. Diversity of the testing sites were approved by AMMI analysis (Mehraban *et al.* 2019). Seven Interaction principal components accounted for more than 97.8% interactions sum of square variations. AMMI 1 explained a total variation of

Table 1: Parentage and location details under multi environmental trials of wheat genotypes

Genotype	Code	Parentage	Code	Locations	Latitude	Longitude	Altitude
DBW317	G 1	K307/NEPAL05	E 1	Kanpur	26° 26′ N	80° 19′ E	126
DBW318	G 2	DBW42/DBW90	E 2	Prayagraj			
PBW835	G 3	BWL2760/BWL1879//BWL2752/BWL1797	E 3	Ghaghraghat	26° 54′ N	81° 56′E	100
HI1563	G 4	MACS2496*2/MC10	E 4	Ayodhya			
DBW107	G 5	TUKURU/INQLAB 91	E 5	Gorakhpur	26° 45′N	83° 22′E	84
PBW834	G 6	GLADIUS/5/2*W15.92/4/PASTOR// HXL7573/2*BAU/3/WBLL1	E 6	Sabour	25°23′ N	87°04′ E	46
UP3060	G 7	D67.2/PARANA66.270// AE.SQUARROSA(320)/3/ CUNNINGHAM/4/P ASTOR/SLVS/5/ SUNCO/2*PASTOR//E/CALIBUR/6/ MTRWA92.161/ PRINIA/5/SERI*3//RL6010/4*Yr/3/	E 7	Kalyani	22° 58′ N	88° 26′E	11
HD3118	G 8	ATTILA*2/PBW65//WBLL1*2/TUKURU	E 8	Burdwan	23° 13′ N	87° 51′ E	30
HI1621	G 9	W15.92/4/PASTOR//HXL7573/2*BAU/3/ WBLL1	E 9	Manikchak			
DBW316	G 10	DBW18/DBW66	E 10	Ranchi	23°20′N	85°18′E	651
PBW833	G 11	BWL0762/PBW621//HD3086	E 11	Chianki	23°45′N	85°30′E	215
HD3360	G 12	HD3086/HI1500					

Table 2: AMMI analysis of yield for wheat genotypes evaluated in fourteen

Source	Degree of freedom	Mean Sum of Squares	Proportional contribution of factors	G×E interaction Sum of Squares (%)	Cumulative Sum of Squares (%) by IPCA's
Treatments	143	53.60	27.79		
Genotype (G)	11	117.85	4.70		
Environment (E)	11	194.06	7.74		
G×E interaction	121	34.99	15.35		
IPC1	21	74.31		36.86	36.86
IPC2	19	52.95		23.76	60.62
IPC3	17	48.63		19.53	80.15
IPC4	15	19.11		6.77	86.92
IPC5	13	16.99		5.22	92.14
IPC6	11	14.41		3.75	95.88
IPC7	9	9.15		1.94	97.83
Residual	16	5.75			
Error	432	46.11			
Total	**575**	**47.97**			

36.9%, followed by 23.7% for AMMI 2, 19.5% for AMMI 3, 6.7% for AMMI 4, AMMI 5 contributed 5.2% followed by 3.8% and 1.9% by AMMI 6, AMMI 7 respectively. The first two AMMI components in total showed 60.6% of the total variation indicating the two AMMI components well fit and confirm the use of AMMI model (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, G5, G2 with lowest yield of G11 (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

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

Code	Mean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	MASV1	MASV	ASV1	ASV	BLAvg	BLSt dev	BLCV	BLGM	HMGV
G 1	36.02	-0.193	0.102	-2.299	0.704	-0.205	-0.848	0.096	7.33	4.87	0.32	0.26	37.50	5.42	14.46	37.15	36.82
G 2	36.13	-1.679	-0.354	-0.136	-1.561	1.047	-0.276	-0.504	3.87	3.48	2.63	2.12	37.04	5.25	14.17	36.70	36.37
G 3	36.51	2.734	0.634	0.221	-0.244	1.473	-0.260	-0.007	5.12	4.26	4.29	3.46	39.18	5.31	13.57	38.84	38.50
G 4	35.16	-0.739	-1.056	0.458	1.451	0.379	1.220	0.236	4.11	3.55	1.56	1.40	37.81	5.45	14.42	37.46	37.12
G 5	36.17	-1.051	1.022	1.225	0.517	-0.675	-0.176	-0.102	4.60	3.39	1.92	1.66	38.48	7.44	19.32	37.80	37.12
G 6	34.64	1.637	-0.751	1.794	0.623	-0.385	-0.785	-0.408	6.48	4.57	2.65	2.17	38.10	8.14	21.36	37.27	36.40
G 7	35.09	-0.295	0.895	1.191	-1.344	-1.001	0.313	0.428	4.68	3.67	1.01	0.97	34.23	6.54	19.11	33.66	33.08
G 8	34.38	0.343	-0.566	-1.024	-0.118	-1.094	0.002	-1.340	4.02	3.11	0.78	0.71	35.78	7.05	19.69	35.17	34.57
G 9	35.62	-0.640	-1.071	0.074	-0.078	0.696	0.937	-0.382	3.10	2.66	1.46	1.34	37.64	6.36	16.91	37.11	36.56
G 10	34.24	1.517	1.143	-1.250	-0.359	-0.516	1.196	0.513	5.60	4.22	2.62	2.21	38.61	6.05	15.66	38.18	37.76
G 11	31.37	-0.171	-2.123	-0.242	-0.376	-0.299	-0.754	1.270	4.07	3.74	2.14	2.13	39.83	7.10	17.82	39.24	38.64
G 12	32.39	-1.464	2.125	-0.013	0.785	0.582	-0.570	0.199	4.46	4.03	3.11	2.80	37.81	5.52	14.60	37.41	36.99

general adaptations of the genotype. Absolute IPCA-1 scores pointed for G11, G1 as per IPCA-2, genotypes G1, G2 would be of choice (Table 3). Values of IPCA-3 favored G12, G9 genotypes. As per IPCA-4, G9, G8 genotypes would be of stable performance. Genotypes G1, G11 selected as per IPCA5 while values of IPCA6 pointed for G8, G5 and finally IPCA7 observed suitability of G3, G1. First two IPCAs in ASV & ASV1 measures utilized 60.6% of G×E interaction sum of squares. The two IPCAs have different values and meanings and the ASV and ASV1 parameters using the Pythagoras theorem and to get estimated values between IPCA1 and IPCA2 scores to produce a balanced measure between the two IPCA scores. Also, ASV parameter of this investigation used advantages of cross validation due to computation from first two IPCAs (Silva *et al.* 2019). Using first two IPCAs in stability analysis could benefits dynamic concept of stability in identification of the stable high yielder genotypes. ASV1 measures recommended (G1, G7) and ASV pointed towards (G1, G8) as of stable performance. Adaptability measures MASV and MASV1considered all seven significant IPCAs of the AMMI analysis using 97.8% of GxE interactions sum of squares (Gerrano *et al.* 2020). Values of MASV1 identified G9, G2, genotypes would express stable yield whereas genotypes G9, G8 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, G11, G3 as high yielders. More over the values of GAI favored G11, G3. Least values of standard deviation observed for the consistent yield of G2, G3 more over the values of CV identified G3, G2 genotypes for the consistent yield performance for NEPZ zone of the country. The BLUP-based simultaneous selections, such as HMGV identified G11, G3, values of RPGV favored G11, G3 and HMRPGV estimates selected G11, 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

Measure based on ranks as per corrected yield of genotypes S_i^1 values pointed for G3, G2, while S_i^2 selected G3, G2 and values of S_i^3 favoured G3, G9 as desirable genotypes (Table 4). G3, G2 selected by values of S_i^4 & measure S_i^5 pointed towards G3, G2 while S_i^6 observed suitability of G3, G4 and lastly S_i^7 values identified G3, G5 genotypes (Table 4). The mentioned strategy determines the stability of genotype over environment if its rank is similar over other environments (biological concept). Nonparametric measures of phenotypic stability were associated with the biological concept of stability (Vaezi *et al.* 2018). Non parametric measures $NP_i^{(1)}$ to $NP_i^{(4)}$, consider the ranks of genotypes as per yield and corrected yield simultaneously. $NP_i^{(1)}$ measure observed suitability of G3, G4 whereas as per $NP_i^{(2)}$, genotypes G7, G2 would be of choice

Table 4: Non parametric measures of yield for wheat genotypes

Code	S_i^1	S_i^2	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	RPGV	HMRPGV
G 1	4.636	15.242	2.472	3.904	3.333	6.486	4.192	3.636	0.485	0.601	0.713	0.999	0.992
G 2	3.591	9.477	1.516	3.079	2.458	4.720	3.534	2.636	0.377	0.410	0.479	0.986	0.982
G 3	2.364	4.364	0.727	2.089	1.500	3.000	2.667	1.636	0.409	0.464	0.525	1.042	1.040
G 4	3.803	10.568	1.566	3.251	2.458	4.370	3.941	2.636	0.377	0.500	0.585	1.007	1.001
G 5	3.818	10.515	1.539	3.243	2.833	4.976	3.402	3.091	0.515	0.533	0.628	1.015	1.011
G 6	5.030	18.242	2.736	4.271	3.500	6.300	4.778	3.818	0.636	0.712	0.838	1.005	0.993
G 7	4.530	16.386	2.260	4.048	3.208	5.310	4.682	3.364	0.280	0.442	0.494	0.909	0.896
G 8	4.985	18.629	3.149	4.316	3.903	7.915	4.375	3.909	0.460	0.557	0.643	0.949	0.936
G 9	3.697	9.727	1.497	3.119	2.583	4.769	3.452	2.727	0.341	0.462	0.548	0.999	0.990
G 10	4.606	15.000	2.308	3.873	3.333	6.154	4.125	3.636	0.606	0.645	0.768	1.026	1.021
G 11	4.591	14.992	2.277	3.872	3.319	6.051	4.140	3.545	0.788	0.860	1.020	1.054	1.049
G 12	3.955	11.174	1.697	3.343	2.847	5.190	3.598	3.000	0.462	0.514	0.608	1.007	0.998

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

Measure	Component PC1	Component PC2	Measure	Component PC1	Component PC2
Mean	0.092	0.196	BLHM	0.174	-0.276
IPC1	0.020	-0.132	PRVG	0.155	-0.295
IPC2	0.053	0.088	MHPRVG	0.164	-0.286
IPC3	0.027	0.051	S_i^1	-0.277	-0.073
IPC4	0.009	-0.123	$S_i^{2,}$	-0.282	-0.050
IPC5	0.256	0.011	S_i^3	-0.276	-0.054
IPC6	0.036	0.132	S_i^4	-0.282	-0.046
IPC7	0.041	-0.183	S_i^5	-0.277	-0.063
MASV1	-0.071	-0.134	S_i^6	-0.260	-0.065
MASV	-0.009	-0.180	S_i^7	0.265	-0.019
ASV1	0.200	-0.122	$NP_i^{(1)}$	-0.272	-0.089
ASV	0.194	-0.139	$NP_i^{(2)}$	-0.077	-0.339
BLAvg	0.143	-0.303	$NP_i^{(3)}$	-0.123	-0.320
BLStdev	-0.174	-0.100	$NP_i^{(4)}$	-0.120	-0.323
BLCV	-0.206	-0.014	% contribution	40.39	25.46
BLGM	0.160	-0.291			

while $NP_i^{(3)}$ identified G2, G7. Last composite measure $NP_i^{(4)}$ found G2, G7 as genotypes of choice for this zone.

Biplot analysis

The first two significant PC's has explained about 65.8% of the total variation in the AMMI, BLUP and non parametric measures considered for this study (Table 5) with respective contributions of 40.4% & 25.5% by first and second principal components respectively (Ahakpaz *et al.* 2021). Measures S_i^2, S_i^4, S_i^1, S_i^3, $NP_i^{(3)}$, IPC5 accounted more of share in PC1 whereas BLGM, RPGV, HMGV, HMRPGV, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ 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. Very tight positive relationships observed between with ASV & ASV1 with BLUP based measures RPGV, HMGV, and HMRPGV. Measure $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ expressed high degree of positive relationship with MASV, MASV1 measures. Measures S_i^1 to S_i^7 clubbed with standard deviation, CV along with $NP_i^{(1)}$. Mean yield expressed positive association IPC2, IPC3, IPC6. ASV & ASV1 maintained no association with $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. Set of measures S_i^1 maintained no relationship with BLUP based measures (Fig. 1). In total seven clusters of studied measures had been observed in biplot analysis. Smaller clusters comprise of IPC1, IPC4, IPC7 while measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ clustered and ASV with ASV1 while MASV joined hands with MASV1.

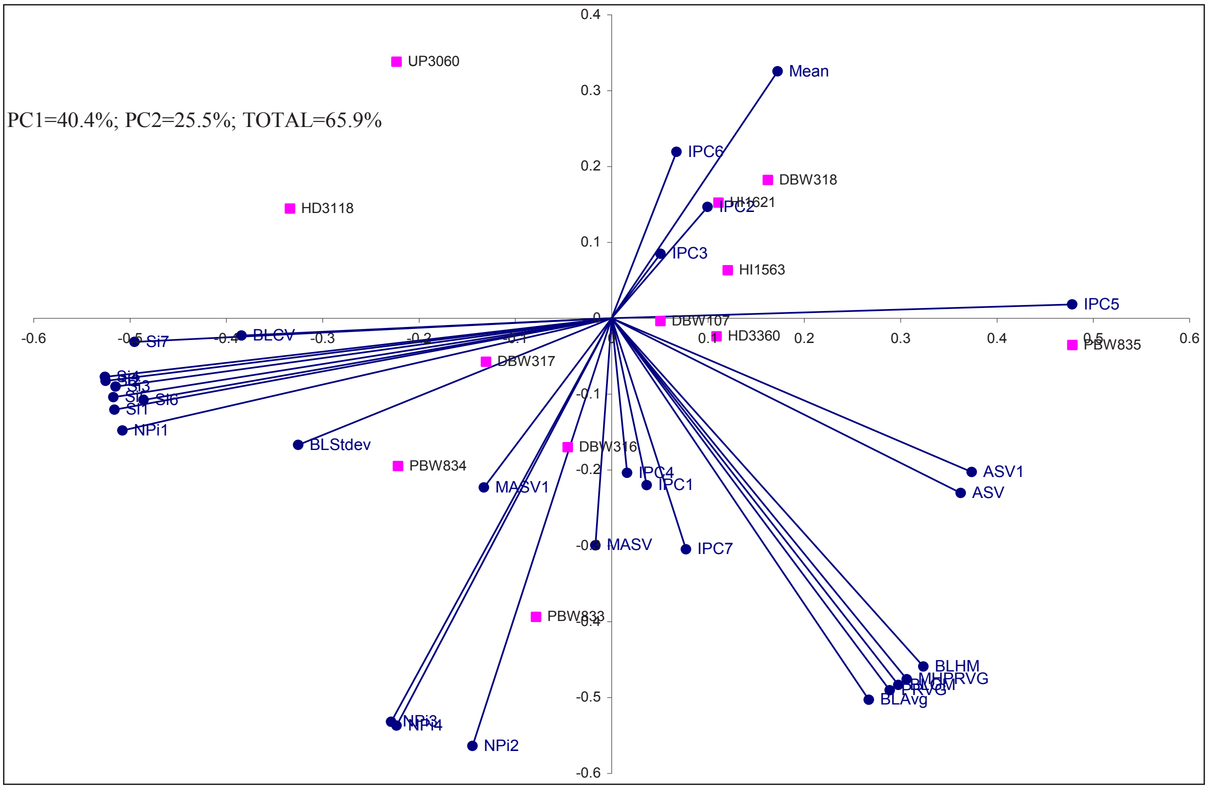

Fig. 1: Biplot analysis of AMMI, BLUP and non parametric measures

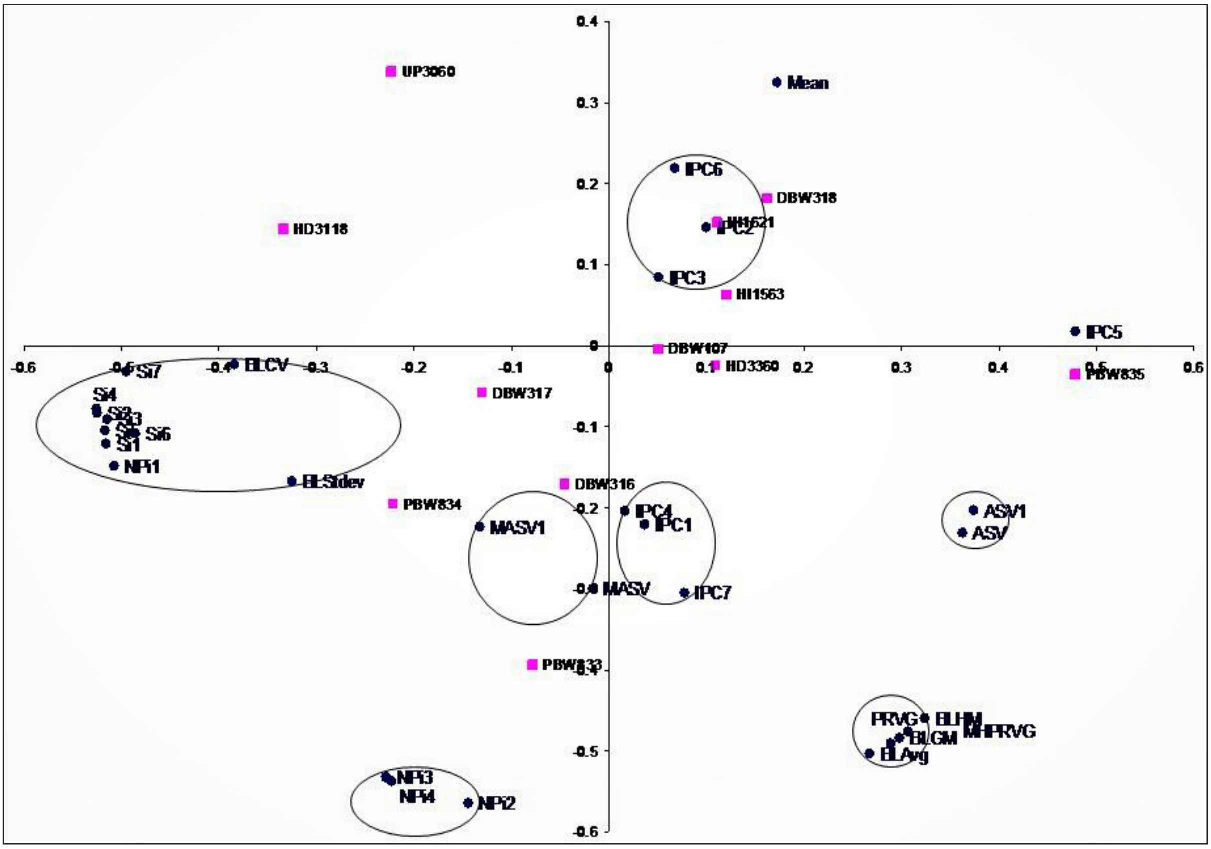

Fig. 2: Clustering pattern of AMMI, BLUP and non parametric measures

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

	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	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	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
Mean	0.098	-0.119	-0.336	-0.035	-0.434	-0.077	0.392	-0.112	0.056	-0.028	0.098	-0.091	0.371	0.364	-0.091	-0.042	-0.098	-0.091	0.552	0.552	0.573	0.552	0.549	0.503	0.524	0.483	0.374	0.510	0.538
IPC1		-0.133	-0.084	-0.126	-0.210	-0.098	0.077	0.510	0.503	0.105	0.210	-0.434	0.238	0.217	-0.336	-0.266	-0.322	-0.336	0.434	0.378	0.399	0.378	0.416	0.378	0.343	0.427	0.374	0.517	0.469
IPC2			-0.028	0.014	-0.147	0.035	0.161	0.455	0.266	0.259	0.308	0.007	-0.189	-0.126	-0.077	-0.084	-0.042	-0.077	-0.028	-0.014	-0.042	-0.014	-0.003	0.014	-0.182	-0.007	0.031	-0.133	-0.175
IPC3				0.175	-0.035	0.126	-0.147	0.063	-0.126	0.280	0.182	-0.133	0.392	0.294	-0.028	0.084	-0.070	-0.028	-0.238	-0.154	-0.329	-0.154	-0.297	-0.420	-0.091	-0.315	-0.164	-0.266	-0.273
IPC4					0.084	-0.077	-0.056	0.238	0.182	-0.070	-0.070	-0.112	0.042	0.000	-0.168	-0.161	-0.147	-0.168	0.161	0.091	0.126	0.091	0.094	0.035	-0.014	0.035	0.157	0.238	0.252
IPC5						-0.154	-0.091	-0.210	0.133	0.503	0.413	-0.245	-0.713	-0.804	-0.273	-0.322	-0.294	-0.273	-0.720	-0.790	-0.706	-0.790	-0.675	-0.699	-0.636	-0.755	-0.234	-0.427	-0.441
IPC6							0.154	-0.336	-0.559	-0.217	-0.126	0.056	-0.056	-0.056	0.035	-0.014	-0.028	0.035	-0.322	-0.161	-0.280	-0.161	-0.276	-0.350	-0.224	-0.245	-0.479	-0.392	-0.364
IPC7								0.287	0.357	0.021	0.210	-0.455	-0.014	-0.175	-0.552	-0.587	-0.531	-0.552	0.042	0.056	0.042	0.056	-0.010	-0.028	0.105	-0.021	0.220	0.259	0.245
MASV1									0.860	0.112	0.175	-0.287	0.042	0.035	-0.287	-0.224	-0.210	-0.287	0.441	0.357	0.378	0.357	0.353	0.343	0.329	0.364	0.423	0.427	0.371
MASV										0.343	0.385	-0.392	-0.175	-0.217	-0.406	-0.343	-0.329	-0.406	0.350	0.231	0.322	0.231	0.269	0.259	0.301	0.231	0.486	0.455	0.392
ASV1											0.965	-0.615	-0.154	-0.294	-0.566	-0.462	-0.587	-0.566	-0.336	-0.448	-0.364	-0.448	-0.353	-0.434	-0.392	-0.399	0.290	0.000	-0.056
ASV												-0.741	-0.098	-0.266	-0.706	-0.615	-0.727	-0.706	-0.266	-0.392	-0.301	-0.392	-0.290	-0.364	-0.378	-0.322	0.381	0.133	0.077
BLAvg													-0.210	0.063	0.972	0.923	0.979	0.972	0.063	0.280	0.133	0.280	0.164	0.175	0.308	0.091	-0.668	-0.566	-0.524
BLSt dev														0.951	-0.077	0.021	-0.105	-0.077	0.573	0.538	0.462	0.538	0.563	0.490	0.434	0.580	0.458	0.538	0.573
BLCV															0.196	0.287	0.175	0.196	0.678	0.685	0.587	0.685	0.696	0.636	0.566	0.706	0.339	0.455	0.497
BLGM																0.979	0.993	1.000	0.112	0.315	0.154	0.315	0.213	0.210	0.357	0.147	-0.633	-0.531	-0.483
BLHM																	0.972	0.979	0.189	0.385	0.224	0.385	0.269	0.245	0.441	0.203	-0.549	-0.462	-0.420
PRVG																		0.993	0.161	0.357	0.210	0.357	0.255	0.259	0.399	0.189	-0.591	-0.490	-0.448
MHP-RVG																			0.112	0.315	0.154	0.315	0.213	0.210	0.357	0.147	-0.633	-0.531	-0.483
S_i^1																				0.944	0.979	0.944	0.983	0.958	0.860	0.972	0.577	0.762	0.776
S_i^2																					0.951	1.000	0.934	0.902	0.937	0.909	0.318	0.552	0.566
S_i^3																						0.951	0.969	0.944	0.881	0.951	0.521	0.713	0.720
S_i^4																							0.934	0.902	0.937	0.909	0.318	0.552	0.566
S_i^5																								0.990	0.836	0.990	0.538	0.717	0.738
S_i^6																									0.790	0.979	0.507	0.685	0.706
S_i^7																										0.797	0.241	0.455	0.469
$NP_i^{(1)}$																											0.556	0.727	0.748
$NP_i^{(2)}$																												0.920	0.899
$NP_i^{(3)}$																													0.993

Another cluster consisted of IPC2, IPC3 and IPC6. BLUP based measures placed together in separate cluster. Composite measure $NP_i^{(2)}$ seen with S_i^1 to S_i^7 along with standard deviation and CV measures (Fig. 2).

Association analysis

Average yield had expressed direct and indirect relationships with other measures (Table 6). Highly positive noted with $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6, S_i^7, IPC7 (Anuradha *et al.* 2022). Negative correlation of high nature expressed by IPC1 to IPC7 measures with most of the measures along with positive of IPC1 to IPC4 with MASV as well as MASV1 measures. AMMI analysis based measures exhibited both type of correlation with other measures. Need to point out significant negative with BLUP based measures. Negative values were observed for BLUP based measures with composite non parametric measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$. Set of non parametric measures S_i^1, to S_i^7 expressed dual nature of correlation as negative with IPC5, IPC6, ASV, ASV1 values and positive with remaining measures. Negative correlation of composite $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ non parametric measures with BLUP based measures needed to be pointed out. $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ expressed negative values for their relations and particularly $NP_i^{(1)}$ expressed indirect with IPC5 along with ASV & ASV1 (PourAboughadareh *et al.* 2022).

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