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Research Article

Parametric and Non Parametric measures to compare Fixed and random effects of malt barley genotypes

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Abstract
AMMI analysis of 21 malt barley genotypes evaluated at nine locations of north western plains zone revealed highly significant variation due to environments (61.8%), G x E interactions (19.5%) and genotypes (8.2%). Further, interaction effects were partitioned into seven interactions principal components. AMMI stability Value measures (ASV1 and ASV) had considered first two interaction principal components and based on 54.1% of total interaction variations had recommended (PL926, PL931, RD2849) and (BH1036, PL931, RD2849) malt barley genotypes respectively. Modified AMMI Stability Values measures (MASV1 and MASV) had exploited nearly 97.6% of total interaction variations, based on which BH1036, DWRB219, RD2849 and BH1036, DWRB219, PL926 malt barley genotypes were identified for stable yield performance. Geometric Mean (GM) based on BLUP effects of genotypes yield was in favour of DWRB219, BH1036 and DWRB221 while corresponding to Harmonic Mean of yield values, DWRB219, BH1036, DWRB221 genotypes would be of choice. Relative Performance of Genotypic Values (RPGV) favored DWRB219, BH1036 , DWRB221 barley genotypes and Harmonic Mean of Relative Performance of Genotypic Value (HMRPGV) measure favoured DWRB219, BH1036, DWRB220 malt genotypes. Non parametric composite measure, $NP_i^{(1)}$, suggested that UPB1097, RD3029, DWRB218 were suitable, whereas DWRB219, RD3029, G4 genotypes would be preferable as per values $NP_i^{(2)}$ while $NP_i^{(3)}$ identified DWRB219, BH1036, DWRB160. The composite measure $NP_i^{(4)}$ found DWRB219, BH1036, DWRB160 as genotypes of choice for this zone. Measures MASV, MASV1, S_i^1, S_i^3, S_i^4, S_i^5,S_i^6 ,S_i^7, S_i^2, $NP_i^{(1)}$, ASV and ASV1 accounted more in first principal component, whereas $NP_i^{(2),}$ $NP_i^{(3)}$, $NP_i^{(4),}$ Average, GM, HM, Mean, PRVG, HMPRVG were major contributors for second principal component. Small cluster of standard deviation (Stdev) with CV, IPC4 and IPC7 were placed in second quadrant. Smallest cluster of IPC1 and IPC6 was also observed in this quadrant. Large cluster comprised of $NP_i^{(1)}$, S_i^2 ,S_i^5 S_i^2 ,S_i^5 ,S_i^6 with ASV and ASV1. Measures GM, HM, PRVG and HMPRVG considered random effects of genotypes grouped with average and placed in last quadrant while adjacent cluster of $NP_i^{(2)}$, $NP_i^{(3)}$, and $NP_i^{(4)}$ observed in same quadrant. Close association among the AMMI analysis based measures had been observed with adaptability measures based on BLUP effects of malt barley genotypes in the present study based on the Biplot analysis while considering first two principal components.

Keywords: Barley, Multivariate parametric, Random, Fixed, Non parametric composite measures

INTRODUCTION

The importance of barley has been appreciated owing to its human health benefits and as a good source of beta glucans (Assefa *et al.,* 2021). It has wider adaptability to varying environment conditions as compared to other cereal crops. Besides the nutritional properties, the value-added products of the crop, *i.e.* malt, has been traded in large volumes at the global level (Dinsa *et al*., 2022). Although a small proportion of malt is used in a number of food applications, major chunk of malt have been used in distillery for manufacturing of alcoholic beverages. Information about the stable performance of cultivars in different environments is obtained by studying the genotype × environment (G x E) interaction effects of the genotypes in multi-environment trials (Anuradha *et al.,* 2022; Ahakpaz *et al.,* 2021). Good number of analytic approaches for the precise estimation of GxE interaction effects has been reflected in recent publications (Pour-Aboughadareh *et al.,* 2019). Many multivariate analysis based measures like Additive Main effects and Multiplicative Interaction (AMMI) stability value like ASV, ASV1, Modified AMMI stability value like MASV and MASV1 have been advocated (Sousa *et al.,* 2020). The random effects of genotypic performance under Best Linear Unbiased Prediction (BLUP) based measures were also exploited for the stability and adaptability of genotypes *via* harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV) and harmonic mean of relative performance of genotypic values (HMRPGV) (Gonçalves *et al.,* 2020; Pour-Aboughadareh *et al.,* 2022). Nonparametric measures like 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 also been utilized to interpret the response of genotypes to environmental conditions (Pour-Aboughadareh *et al.,* 2019). In the present study, analytic parametric and non-parametric measures have been compared to decipher the G x E interactions effects for malt barley genotypes evaluated in north western plains zone of India.

MATERIALS AND METHODS

Twenty one malt barley genotypes were evaluated in field trials at nine centers of All India Coordinated Research Project across north western plains zone of the country during 2020-21 cropping season from November to April months. Randomized block designs with four replications was adopted for field evaluation of genotypes. Details about parentage and the environmental conditions are furnished in **Table 1**. Pour-Aboughadareh *et al,* (2019) recommended various non-parametric and parametric measures for assessing GxE interaction and stability analysis as follows:

$$S_i^{(1)} = \frac{2\Sigma_j^{n-1}\Sigma_{j'=j+1}^{n}\left|r_{ij} - r_{ij'}\right|}{[n(n-1)]} \qquad S_i^{(7)} = \frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{\Sigma_{j=1}^{n}|r_{ij} - \bar{r}_i|}$$

$$S_i^{(3)} = \frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{\bar{r}_{i.}} \qquad S_i^{(4)} = \sqrt{\frac{\Sigma_{j=1}^{n}(r_{ij} - \bar{r}_i)^2}{n}}$$

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

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

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 were calculated as follows:

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

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

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

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

ASV	ASV = $[(\frac{SSIPC1}{SSIPC2}PCI)^2 + (PC2)^2]^{1/2}$
ASV1	ASV1 = $[\frac{SSIPC1}{SSIPC2}(PCI)^2 + (PC2)^2]^{1/2}$
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 = $\sqrt[n]{\prod_{k=1}^{n}\bar{X}_k}$

Data analysis was carried out using SAS version 9.3 and AMMISOFT software.

RESULTS AND DISCUSSION

AMMI analysis: AMMI analysis revealed that about 61.8% of the total sum square for yield was due to environments followed by 19.5% of G x E interactions, whereas genotypes had accounted for 8.2% (**Table 2**). The significant interaction effects were further portioned into seven interaction principal components that totalled for more than 97.6% of interactions sum of squares. AMMI1 was observed to explain about 28.9 % of variation followed by 25.1% for AMMI 2, 18.2% for AMMI 3. The

Table 1. Parentage vis-a-vis location details of malt barley genotypes

Code	Genotype	Parentage	Locations	Latitude	Longitude	Altitude
G1	RD3030	IBYT-LRA-8/IBYT -LRA-19	Bathinda	30° 09’ N	74° 55 ’E	211
G2	PL930	PL807/*Hordeum Spontaneum* Acc.361	Bawal	28° 10’N	76° 50’E	266
G3	DWRB182	DWRUB52/DWRB78	Durgapura	26°51’N	75° 47’E	390
G4	DWRB160	DWRB62/DWRB73	Hisar	29° 10’ N	75° 46’E	229
G5	UPB1097	6th GSBYT Plot 4 2018-19	Karnal	29° 43’ N	70° 58’E	245
G6	PL926	BK9816/DWRUB52	Ludhiana	30° 54’ N	75° 48 ’E	247
G7	RD3028	NBGSN-11/RD 2668	Modipuram	29°05’ N	77°70’E	226
G8	BH1034	HBL 712/BH 885	Pantnagar	29° 02’N	79° 48’E	243.8
G9	RD3029	NBGSN-20/RD 2668	SG Nagar	29° 66’N	75° 53’E	175.6
G10	DWRB218	DWRUB52/DWRB68				
G11	PL931	PL807/*Hordeum Spontaneum* Acc.361				
G12	BH946	BHMS22A/BH549//RD2552				
G13	BH1036	VLB 130/BH 902				
G14	BH1035	BH 976/BH946				
G15	RD3027	DWR 73 /IBYT-LRA-5				
G16	DWRB221	DWRUB52/RD2508				
G17	DWRUB52	DWR17/K551				
G18	DWRB219	BETZS/DWRB88				
G19	DWRB220	DWRB73/BK1127				
G20	RD2849	DWRUB52/PL705				
G21	UPB1098	UPB1021/DWRB107				

Table 2. AMMI analysis of malt barley genotypes evaluated under coordinated trials

Source	Degree of freedom	Mean Sum of Squares	Significance level	Proportional contribution of factors	G x E interaction Sum of Squares (%)	Cumulative Sum of Squares (%) by IPCA’s
Treatments	188	748.02	***	89.68		
Genotype (G)	20	647.04	***	8.25		
Environment (E)	8	12125.43	***	61.86		
GxE interactions	160	191.77	***	19.57		
IPC1	27	329.46	***		28.99	28.99
IPC2	25	308.11	***		25.10	54.09
IPC3	23	243.21	***		18.23	72.32
IPC4	21	131.59	***		9.01	81.33
IPC5	19	111.46	***		6.90	88.23
IPC6	17	89.007	***		4.93	93.16
IPC7	15	91.68	***		4.48	97.65
Residual	13	55.57	*			
Error	567	28.54				
Total	755	207.69				

first two AMMI components accounted for 54.1% of the total variations. The sums of squares for G × E signal and noise were 85.1% and 14.8% of total interaction effects. The sum of squares for G x E was 2.02 times of genotypes main effects (Vaezi *et al.*, 2018) and the first interaction component had accounted 0.69 times of the genotypes main effects.

Ranking of genotypes as per on AMMI analysis based measures: Significant variation among the genotypes was observed for mean yield. The genotypes BH1034, BH1036, DWRB221 exhibited highest yield, while it was lowest in PL930 and RD3027 (**Table 3**). Values of IPCA's in AMMI analysis give an indication about the stability or adaptability of the evaluated genotypes. The specific adaptation of genotype to certain locations is reflected by the larger IPCA scores and general adaptation of the genotype is indicated by least values. The barley genotypes RD3030, DWRB182, PL926 had expressed the least values of IPCA-1 measure, whereas UPB1098, BH946, DWRB220 genotypes had showed the smaller values of IPCA-2 measure. ASV and ASV1 measures accounted for 54.1% of G × E interaction sum of squares. ASV measures are used for cross validation of computations from first two IPCAs (Silva *et al.,* 2019). Values of ASV1 indicated that PL926, PL931, RD2849 and ASV measure indicated BH1036, PL931, RD2849 are stable genotypes. Adaptability measures MASV and MASV1 takes in to consideration all seven significant IPCAs of the AMMI analysis and it was found to account for 97.6% of G x E interactions sum of squares (Gerrano *et al.,* 2020). In the present study, based on MASV 1, BH1036, DWRB219, RD2849 were identified as stable yielders, while based on MASV , BH1036, DWRB219 and PL926 were found to be stable.

Ranking of genotypes on the basis of BLUP and Non parametric measures: The random nature of the genotypic performances in changing climatic conditions had been accommodated by BLUP based measures (Sousa *et al.,* 2020). Genotypes DWRB219, BH1036, DWRB221 were of high yield values. Least values of standard deviation had been expressed by DWRB160, UPB1098, PL930 genotypes, while values of Coefficient of Variation (CV) measure had identified DWRB160, UPB1098, BH946 malt genotypes for the consistent yield performance across locations of the study of malt barley genotypes for north western plains zone of the country. Genotypes DWRB219, BH1036, DWRB221 were favored by the values of Geometric Mean (GM) measure and values of Harmonic Mean (HM) measure had identified DWRB219, BH1036, DWRB221 malt genotypes, while the values of RPGV measure had favored DWRB219, BH1036, DWRB221 malt genotypes and values of HMRPGV measure had been selected DWRB219, BH1036, DWRB220 malt genotypes. Adaptability and stability of wheat genotypes by BLUP-based measures was reported by Pour-Aboughadareh *et al.,* (2019). The same ranking of genotypes performance had been observed by HM, RPGV, and HMRPGV measures as reported by Anuradha *et al.,* (2022).

Table 3. AMMI based measures of malt barley genotypes

Genotype	Mean	IPC1	IPC2	IPC3	IPC4	IPC5	IPC6	IPC7	ASV1	ASV	MASV1	MASV	Average	Stdev	CV
G1	48.68	-0.0943	-1.5862	1.5120	-0.5993	0.1594	0.2176	-1.7290	1.59	1.59	4.805	4.109	48.68	15.17	31.16
G2	41.80	-1.6670	2.1113	-0.8819	0.6901	-0.0663	-2.1842	-0.2257	2.86	2.77	5.699	5.228	41.80	9.65	23.10
G3	52.87	0.1937	0.8636	0.9785	1.5773	0.7606	-0.4979	1.3152	0.89	0.89	4.220	3.753	52.87	13.79	26.09
G4	51.21	-2.5524	1.0388	-1.9012	-1.1860	-0.8785	0.5647	0.7332	3.13	2.93	6.129	5.227	51.21	5.69	11.10
G5	45.28	3.0327	1.0970	-1.9272	-0.4954	1.2739	0.1752	-0.4572	3.67	3.44	6.358	5.426	45.28	18.08	39.94
G6	49.30	0.3030	-0.3786	0.7786	-0.5657	1.5063	-0.0775	0.2749	0.52	0.50	3.361	2.924	49.30	14.26	28.92
G7	47.33	1.0308	1.3969	2.6345	-0.6815	-1.3926	-0.2646	0.5802	1.84	1.78	7.066	5.750	47.34	17.49	36.95
G8	42.25	-1.2059	-2.0929	0.8543	0.2980	-1.8753	-0.8584	0.1746	2.51	2.46	5.536	4.952	42.25	12.92	30.57
G9	48.42	1.9211	-3.8145	-0.6520	-1.0138	-0.5937	-0.0981	0.6443	4.41	4.34	7.314	6.617	48.42	19.08	39.40
G10	53.03	-0.5345	-0.4255	-0.7980	-1.9169	1.5219	1.0454	0.3677	0.75	0.71	4.846	4.375	53.03	11.75	22.16
G11	49.23	-0.3686	-0.3205	2.0885	1.6763	1.9618	0.2738	-0.6554	0.53	0.51	6.503	5.467	49.23	14.98	30.43
G12	49.51	-2.9031	-0.2021	1.8513	-0.2444	0.1476	1.0728	-0.5161	3.36	3.13	5.645	4.803	49.51	10.91	22.03
G13	55.02	0.3345	-0.3015	-0.6767	0.7880	0.3505	0.2329	-0.5436	0.49	0.47	2.281	1.966	55.02	12.28	22.32
G14	50.24	2.5481	0.3458	0.2050	1.8483	-1.7331	1.5676	0.8799	2.96	2.76	5.792	5.378	50.24	17.60	35.04
G15	43.90	-0.5175	-2.4344	-1.7663	1.6535	0.6410	-0.9351	0.2903	2.51	2.50	6.637	5.748	43.90	12.37	28.19
G16	54.13	0.8048	1.0574	-1.0328	0.8500	-0.8239	-0.5402	-1.9192	1.41	1.37	4.222	3.771	54.13	13.46	24.87
G17	52.81	0.6626	2.0373	0.4869	-0.3553	0.2270	1.1667	0.6489	2.18	2.16	4.212	3.845	52.81	14.33	27.14
G18	58.55	0.9692	0.9832	-0.3544	-0.8025	-0.3823	-0.5833	-1.2202	1.49	1.43	3.018	2.793	58.55	14.26	24.36
G19	53.62	0.4882	0.2767	0.6124	-1.9431	-0.6417	-0.9539	-0.4107	0.63	0.59	4.007	3.655	53.62	14.71	27.43
G20	51.96	-0.4023	0.2781	-0.1481	-0.3950	0.5912	-1.1407	2.0793	0.54	0.51	3.034	2.948	51.96	11.92	22.94
G21	49.08	-2.0430	0.0701	-1.8634	0.8175	-0.7538	1.8173	-0.3114	2.36	2.20	5.845	5.027	49.08	5.77	11.76

Nonparametric measures of phenotypic stability were associated with the biological concept of stability (Vaezi *et al.,* 2018). Non parametric measures ranked the genotypes as per their corrected yield values across environments, and as per values of measure S_i^1 barley genotypes RD3029, UPB1097, DWRB218 would be of stable performance while the S_i^2 measure values had pointed for RD3029, DWRB160, UPB1097 genotypes and values of S_i^3 had favoured RD3029, DWRB160, UPB1097 as desirable malt barley genotypes (**Table 4**). Genotypes RD3029, DWRB160, UPB1097 were selected by values of S_i^4 measure while values of S_i^5 measure had identified UPB1097, RD3029 DWRB218 and as per the values of S_i^6 measure the desirable genotypes would be RD3029, DWRB160, UPB1097 and lastly the vales of S_i^7 measure had settled for RD3029, UPB1097, DWRB160 (**Table 4**). Non Parametric Composite measures $NP_i^{(1)}$ to $NP_i^{(4)}$, had been defined based on the ranks of genotypes as per their yield and corrected yield values across the study locations simultaneously. First non-parametric measure $NP_i^{(1)}$ had observed suitability of UPB1097, RD3029, DWRB218genotypes whereas as per $NP_i^{(2)}$ values, DWRB219, DWRB160, RD3029 genotypes would be of choice while $NP_i^{(3)}$ had identified DWRB219, BH1036, DWRB160 genotypes. The last composite measure $NP_i^{(4)}$ had found DWRB219, BH1036, DWRB160 as genotypes of choice for this zone.

Multivariate clustering of genotypes as per Ward's method: Group of five genotypes DWRB160, BH946, UPB1098, DWRB218 and DWRB221 had occupied a central place out of three groups (**Fig. 1).** As the lower group consisted of DWRB182, RD2849, DWRUB52, PL926, DWRB220, BH1036 and DWRB219 genotypes and had maintained a good distance from genotypes of first group. Three clusters were formed by the considered measures as per multivariate hierarchical clustering based on Ward's method. Non parametric measures $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ had been observed with BLUP based measures as per Average, HM, GM, PRVG, HMPRVG values, whereas AMMI based measures had been clubbed with nonparametric composite measure $NP_i^{(1)}$ (**Fig. 2**).

Biplot Graphical Analysis: The first two significant principal components in the biplot analysis had accounted about 65.7% of the total variations (**Table 5**) with 45.5% and 20.2% of respective shares(Ahakpaz *et al.,* 2021). Measures MASV, MASV1, S_i^1, S_i^3, S_i^4, S_i^5,S_i^6 ,S_i^7, S_i^2, $NP_i^{(1)}$, ASV, ASV1 accounted more of share in first principal component, whereas $NP_i^{(2),}$ $NP_i^{(3)}$, $NP_i^{(4),}$ Average, GM,

Table 4. BLUP based and Non parametric measures of malt barley genotypes

Genotype	GM	HM	RPGV	HMRPGV	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	47.03	45.73	0.9685	0.9546	7.056	6.677	3.569	5.874	4.593	4.276	34.500	4.556	0.304	0.481	0.577
G2	40.82	39.86	0.8425	0.8272	7.611	6.950	3.694	6.502	5.407	4.252	42.278	5.000	0.294	0.401	0.469
G3	51.49	50.30	1.0576	1.0482	6.278	6.207	2.707	5.318	4.049	3.489	28.278	4.000	0.571	0.647	0.764
G4	50.93	50.66	1.0505	1.0319	8.611	7.814	5.421	7.322	6.099	5.551	53.611	5.889	0.736	0.834	0.981
G5	42.16	38.90	0.8891	0.8305	9.167	7.715	5.119	7.801	7.012	5.308	60.861	6.556	0.386	0.512	0.602
G6	47.80	46.56	0.9800	0.9747	6.167	5.483	2.430	5.118	4.247	3.546	26.194	4.222	0.302	0.397	0.478
G7	45.06	43.25	0.9331	0.9088	7.944	7.274	4.031	6.591	5.309	4.433	43.444	5.222	0.348	0.482	0.581
G8	40.80	39.60	0.8469	0.8213	7.500	6.650	3.745	6.287	5.284	4.505	39.528	5.111	0.284	0.382	0.456
G9	45.87	43.90	0.9588	0.9145	9.444	8.580	6.298	8.110	6.815	5.872	65.778	6.444	0.644	0.695	0.810
G10	51.98	51.03	1.0684	1.0573	8.667	7.335	4.713	7.236	6.346	5.140	52.361	6.111	1.019	0.794	0.951
G11	47.30	45.40	0.9796	0.9523	7.167	7.065	3.776	6.042	4.593	4.276	36.500	4.556	0.350	0.513	0.608
G12	48.38	47.16	1.0039	0.9738	8.333	7.713	4.862	7.126	5.852	5.043	50.778	5.444	0.544	0.682	0.798
G13	54.02	53.20	1.1066	1.1028	5.889	5.434	2.118	4.899	3.926	3.118	24.000	3.889	0.648	0.848	1.019
G14	48.16	46.58	0.9970	0.9711	8.056	7.200	4.091	6.708	5.556	4.545	45.000	5.444	0.454	0.598	0.718
G15	42.52	41.29	0.8828	0.8549	8.444	7.194	4.533	7.026	6.099	5.041	49.361	5.889	0.346	0.462	0.555
G16	52.83	51.70	1.0861	1.0748	7.722	7.333	3.667	6.633	5.333	4.000	44.000	4.889	0.543	0.796	0.927
G17	51.37	50.19	1.0558	1.0458	5.889	7.020	2.194	5.408	3.704	2.500	29.250	3.667	0.333	0.579	0.631
G18	57.23	56.08	1.1733	1.1673	6.500	5.913	2.799	5.659	4.815	3.786	32.028	4.222	1.407	1.415	1.625
G19	52.14	50.92	1.0703	1.0619	5.778	5.444	2.227	4.950	4.000	3.273	24.500	4.000	0.571	0.627	0.732
G20	50.92	50.02	1.0442	1.0384	5.889	6.875	2.292	5.244	3.556	2.667	27.500	3.556	0.395	0.542	0.609
G21	48.81	48.57	1.0050	0.9910	7.556	6.493	3.661	6.314	5.457	4.510	39.861	5.333	0.410	0.536	0.642

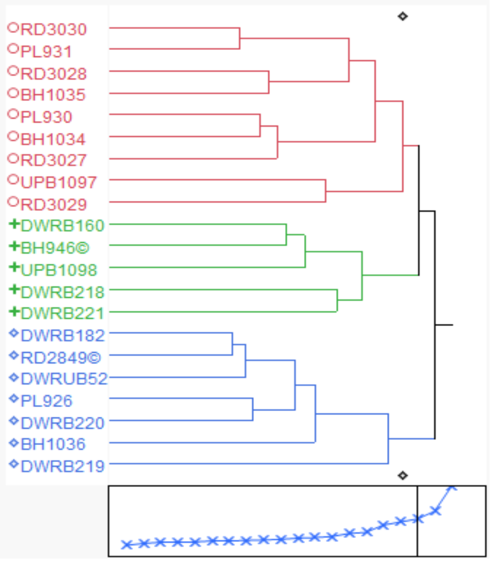

Fig.1. Multivariate clustering of malt barley genotypes as per Ward's method

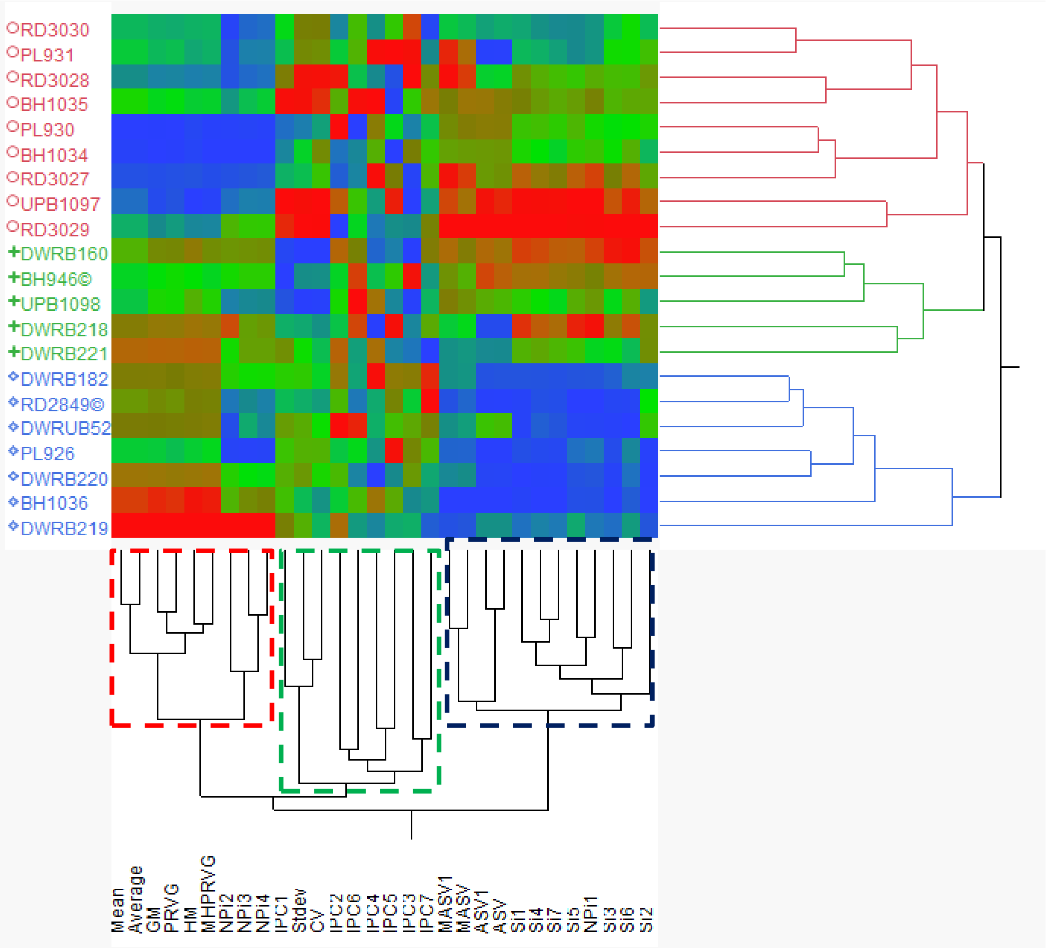

Fig. 2. Two way multivariate hierarchical clustering of malt barley genotypes vis-à-vis measures

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	-0.2202	0.2111	GM	-0.2263	0.2096
IPC1	0.0027	0.0121	HM	-0.2279	0.2029
IPC2	-0.0989	-0.0016	RPGV	-0.2198	0.2225
IPC3	-0.0475	-0.1758	MHPRVG	-0.2325	0.1953
IPC4	0.0246	-0.1400	S_i^1	0.2357	0.1842
IPC5	-0.0450	-0.0530	S_i^2	0.2056	0.1506
IPC6	0.0076	0.1594	S_i^3	0.2299	0.1960
IPC7	0.0220	-0.0715	S_i^4	0.2322	0.1975
MASV1	0.2447	0.0233	S_i^5	0.2242	0.2043
MASV	0.2478	0.0279	S_i^6	0.2232	0.1890
ASV1	0.2169	0.1188	S_i^7	0.2302	0.2018
ASV	0.2180	0.1132	$NP_i^{(1)}$	0.2319	0.1803
Average	-0.2202	0.2110	$NP_i^{(2)}$	-0.1020	0.3322
Stdev	0.0387	-0.0580	$NP_i^{(3)}$	-0.1279	0.3261
CV	0.1055	-0.1124	$NP_i^{(4)}$	-0.1248	0.3295
Per cent contribution (65.74%)				45.52%	20.22%

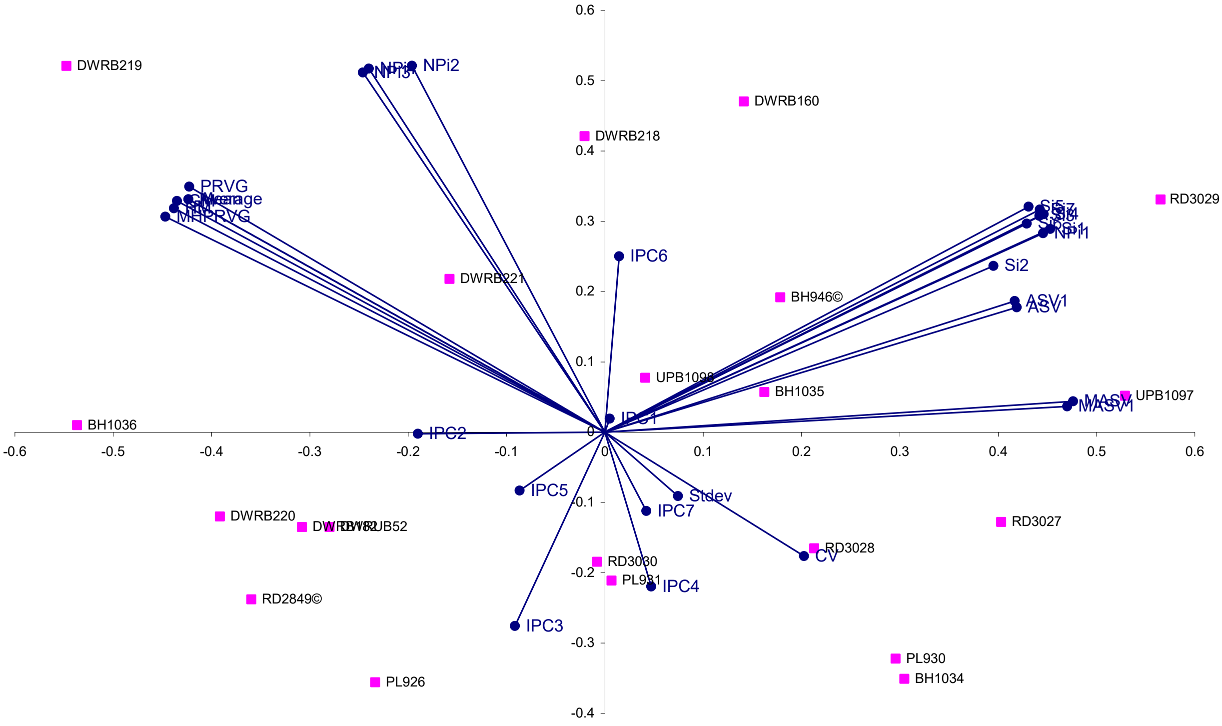

Fig. 3. Biplot analysis of AMMI, BLUP and Non parametric measures

HM, Mean, , PRVG HMPRVG were major contributors in PC2. The association analysis among genotypes and measures had been studied by the biplot analysis based on principal components of the considered measures of the present study. In the biplot, vectors of measures expressed in acute angles would be positively correlated, whereas those with obtuse or straight line angles would be negatively correlated. Independent type of relationships was indicated by right angles between vectors.

Very tight positive relationships was observed for $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ measures, whereas BLUP based measures GM, HM, RPGV, HMRPGV and average also expressed tight relationship among themselves in same quadrant. Values of standard deviation measure was associated with IPC7, IPC4 and CV values in separate quadrant of biplot analysis. All AMMI based measures were closely associated though ASV & ASV1 were placed between them as MASV, MASV1 were on one side, while other measures observed on other side. BLUP based measures expressed right angles with CV, IPC7, standard deviation (Stdev) value. Right angle of measure IPC3 was observed with S_i^2, S_i^3 S_i^5, S_i^6, $NP_i^{(1)}$ and IPC4 maintained ninety degree angles with $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ values. Right angles were also exhibited by S_i^2, S_i^3 S_i^5, S_i^6 values with $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ measures (**Fig 3**).

Seven clusters of small and moderate sizes were observed in biplot analysis. AMMI analysis based measures IPC2, IPC3 and IPC5 formed first cluster , placed in first quadrant. Small cluster of standard deviation (Stdev) with CV, IPC4 & IPC7 placed in second quadrant. Three clusters were observed in next quadrant. Smallest cluster of IPC1 & IPC6 observed in this quadrant. Largest cluster comprised of $NP_i^{(1)}$, S_i^2 ,S_i^5, S_i^2 ,S_i^5 ,S_i^6 with ASV, ASV1 though small cluster MASV and MASV1 placed adjacent. BLUP based measures GM, HM, PRVG and HMPRVG were grouped with average and placed in last quadrant while adjacent cluster of $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ observed in same quadrant (**Fig. 4**).

The presence of significant genotype by environment interaction complicates the process of malt barley genotypes selection for their wider or specific adaptability. This situation would provide the more meaningful interpretations by the usage of recently advocated analytic measures.

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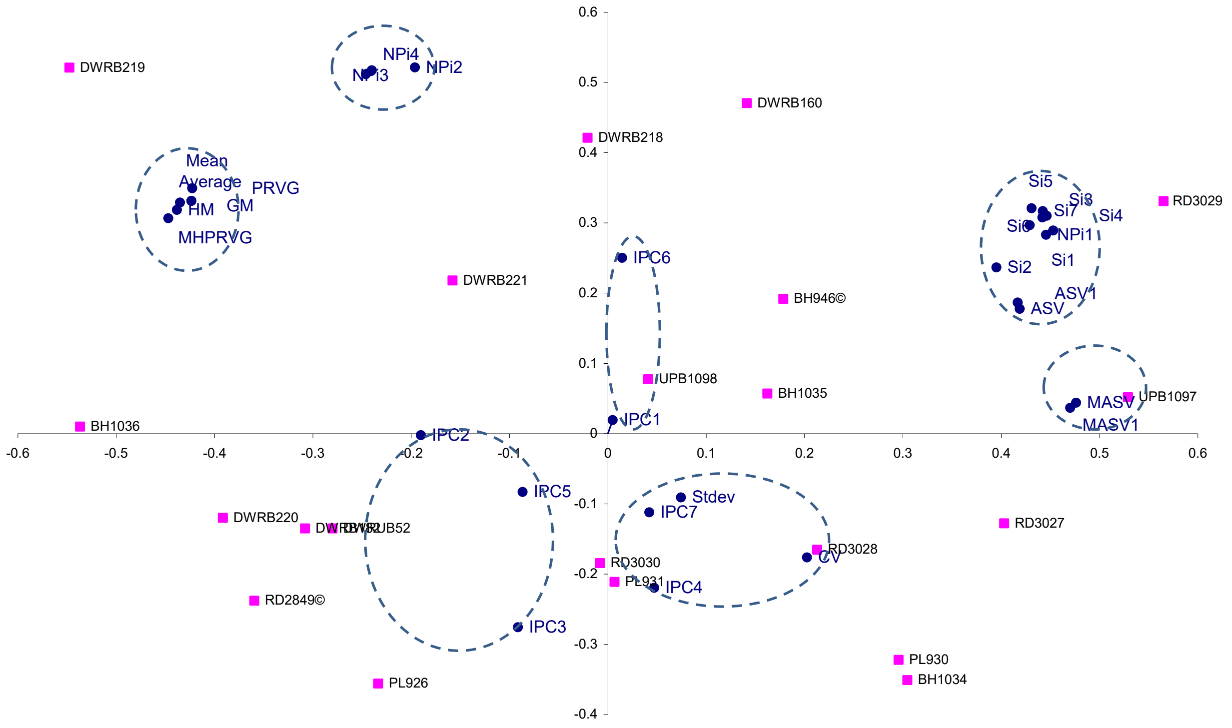

Fig. 4. Clustering pattern of AMMI, BLUP and Non parametric measures

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