

## Research Article

# Non parametric measures to investigate genotype x environment interaction for feed barley genotypes evaluated under multi environment trials

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(Received: 03 May 2017; Revised: 20 Aug 2017; Accepted: 27 Aug 2017)

### Abstract

In the present investigation g x e interaction of twenty seven feed barley genotypes were evaluated at fifteen locations by non parametric measures. Results based on nonparametric measures do not require distributional assumptions for testing of effects. JB322 was high yielder followed by PL890 & HUB250 among studied genotypes. CMR and CSD measures pointed towards HUB113, NDB1634 and UPB1054, JB322 as desirable genotypes by respective measures.  $S_i^1$  and  $S_i^2$  measures identified JB322 and UPB1054 along with UPB1054 & HUB 113 as of stable yield performance. Values of the sum of  $Z_i^1$  and  $Z_i^2$  denoted significant differences among feed barley genotypes across 15 studied environments. Genotypes UPB1054, HUB113, BH1005 based on  $S_i^3$  and  $S_i^6$  were identified as the stable genotypes whereas KB1436 & RD2552 were unstable. First two NPs were very similar for unstable performance of RD2552 and last two NP<sup>8</sup> for similar behaviour of HUB250. Biplot analysis observed highly significant negative rank correlation of yield with corrected mean yield, SD and no significant correlation with MR.

### Key words

Non-parametric measures, Spearman rank correlation, Ward's hierarchical clustering, biplot analysis

### Introduction

Genotype × environment interaction reflects the change in response of cultivars across the environments (Rasoli *et al.*, 2015). Recently GxE interaction has been considered a prerequisite to point out cultivars' recommendation for general or specific adaptation (Farshadfar *et al.*, 2014). Interpretation of GxE interaction as well as yield stability was feasible in different crops using nonparametric strategy as several nonparametric measures had observed in literature (Nassar and Hühn, 1987). These measures are mainly based on the ranks,  $r^{ij}$ , or adjusted ranks,  $r^{*ij}$ , as per genotypes responses in each environment. One of the major concerns is to categorize stable genotypes based on similar rankings across environments. Some measures consider only stability of genotypes like  $S_i^3$  and  $S_i^4$  while others like  $S_i^1$ ,  $S_i^2$  combine both yield and stability to propose an ideal genotype. Four non-parametric stability measures,  $NP_i^{(1)}$ ,  $NP_i^{(2)}$ ,  $NP_i^{(3)}$  &  $NP_i^{(4)}$  based on ranks calculated from adjusted yield proposed by Thenarasu, 1995. Association among non parametric measures helped breeder to choose most informative measure for reliable prediction of cultivar behaviors (Mahtabi *et al.*, 2013). The objectives of this study were to (i) identify feed barley genotypes by nonparametric measures possessing high yield along with stable performance across different test environments (ii) study the relationships among different nonparametric stability statistics.

### Materials and methods

Twenty seven feed barley genotypes were used as plant material for this study. Cultivars were grown in 15 environments. The field experimental layout was of randomized complete block design with four replications in each environment. All agronomical practices were followed as per zone wise recommendations for considered locations. Grain yield of each cultivar was recorded on a plot basis. For a two-way classification of k genotypes into 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  $\bar{r}_i$  was the average rank of the ith genotype across considered environments. Nonparametric measures based on corrected yield to remove the effect of genotype from phenotypic value 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 (Mortazavian and Azizinia, 2014). The genotype with the lowest adjusted yield was given highest rank and vice versa for highest adjusted yielder (Rasoli *et al.*, 2015). Stable genotypes would show similar ranks over environments; i.e. maximum stability occurs with equal ranks over environments.

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

$$S_i^{(3)} = \frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{\bar{r}_i}$$

$$S_i^{(4)} = \sqrt{\frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{n}}$$

$$S_i^{(5)} = \frac{\sum_{j=1}^n |r_{ij} - \bar{r}_i|}{n}$$

$$S_i^{(6)} = \frac{\sum_{j=1}^n |r_{ij} - \bar{r}_i|}{\bar{r}_i}$$

Thenarasu (1995) proposed the nonparametric stability measures  $NP_i^{(1)}$ ,  $NP_i^{(2)}$ ,  $NP_i^{(3)}$  and  $NP_i^{(4)}$ , based on ranks of adjusted means of genotypes, as those whose position in relation to the others remained unaltered in the set of environments. In the above formulas,  $r_{ij}^*$  was the rank of  $X_{ij}^*$ , and  $\bar{r}_i$  and  $M_{di}$  were the mean and median ranks for original yield, where  $\bar{r}_i^*$  and  $M_{di}^*$  were the same parameters computed from the corrected yield values.

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

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

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

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

All nonparametric stability statistics calculated using SAS-based program, and Microsoft Excel (Hussein *et al.*, 2000). To understand relationships among stability methods, principal component analysis (PCA) based on rank correlation matrices and to group different parameters into clusters, hierarchical cluster analysis were performed. Spearman's coefficient of rank correlation was employed to statistically compare the non parametric measures used in this study.

### Results and discussion

According to mean yield, genotype JB322 (41.9 q/ha) followed by PL890 & HUB250 while large variation observed in yield values among genotypes. As per the mean of ranks, KB1436 and PB891 showed higher values over environments while SD pointed towards JB322 and UPB1054 and regarding to CMR and CSD the desirable genotypes would be HUB113, NDB1634 & UPB1054, JB322 respectively. The effect of correction and removing the genotype effect from phenotypic data is in agreement with Karimizadeh *et al.* (2012). According to CV & corrected CV nonparametric measures contain mean and standard deviation of ranks, genotypes KB1436 &

KB1434 UPB1054, JB322 identified as the stable genotypes respectively whereas HUB250, BH946 & DWRB156, BH946 as unstable (Mortazavian and Azizinia, 2014). Genotypes JB322 and UPB1054 along with UPB1054 & HUB 113 with minimum two nonparametric  $S_i^1$  and  $S_i^2$  measures where.  $S_i^1$  estimate considered all possible pairwise rank differences, while  $S_i^2$  was based on variances of ranks for each genotype across environments. These statistics ranked genotypes similarly for stability. Genotype RD2552 was most unstable by both measures. Further significance tests of  $S_i^1$  and  $S_i^2$  developed by Nassar and Huehn (1987). For each feed barley genotype,  $Z_i^1$  and  $Z_i^2$  values were calculated as per ranks of adjusted yield and summed over genotypes to obtain total Z values. Since sum of  $Z_i^1 = 41.49$  and  $Z_i^2 = 92.51$  were more than the critical value of  $\chi^2 = 27.58$ , there were significant differences among 27 feed barley genotypes across 15 studied environments (Rasoli *et al.*, 2015). Inspecting the individual Z values, it was found that some genotypes were significantly unstable relative to others, because large Z values were observed as compared to the critical value of  $\chi^2$  at 5% level of significance i.e. 3.84.

Non-parametric statistics of  $S_i^3$  and  $S_i^6$  combine yield and stability based on yield ranks of genotypes in each environment. Genotypes UPB1054, HUB113, BH1005 based on  $S_i^3$  and  $S_i^6$  statistics were identified as the stable genotypes at the same time KB1436 and RD2552 were unstable by both measures. The numerical value of  $S_i^3$  is determined by both yield and stability. Among these stable genotypes, PL890 had relatively high yield.

Nonparametric measures  $S_i^1$ ,  $S_i^2$ ,  $S_i^3$ ,  $S_i^4$ ,  $S_i^5$  and  $S_i^6$  identified UPB1054, HUB113 & BH1005 as the stable genotypes at the same times KB1436 & RD2552 as unstable genotypes (Karimizadeh *et al.*, 2012). Nonparametric stability indices judged different genotypes i.e.  $NP_i^{(1)}$  pointed towards JB322 and UPB1054 as stable in comparison to others and RD2552 along BH946 unstable while, genotype PB891 showed lowest value  $NP_i^{(2)}$  followed by KB1434 and because of high value stabilities of BH946 & RD2552 were low,  $NP_i^{(3)}$  unlike  $NP_i^{(2)}$  identified BH1005 as the most stable followed by BH949. The unstable genotypes based on  $NP_i^{(3)}$  were JB322 & HUB250. Stability parameters  $NP_i^{(4)}$  like  $NP_i^{(2)}$  identified PB891 & KB1434 and BH946 but like  $NP_i^{(3)}$  pointed towards unstable performance of HUB250 (Khalili and Aboughadareh, 2016). The results of first two  $NP^s$  were very similar for unstable performance of RD2552 and last two  $NP^s$  towards HUB250 as unstable genotypes (Table 2).

*Cluster Analysis:* To better reveal associations among evaluated genotypes, the two-way data of

genotypes' mean yield and ranks based on different nonparametric stability measures, was performed further using a clustering procedure. The dissimilarity between two clusters is shown by the "loss of information" from joining the two clusters with this loss of information measured by the increase in error sum of squares. First cluster consisted of high yielding genotypes JB322, PL890, BH 902 and JB325. Second cluster consisted of genotypes DWR156, RD2552 and BH946 were of unstable performance. Third cluster consisted of moderate to high yielder with moderate stable genotypes HUB250, BH946 and DWRB156. Rest of remaining genotypes clustered in last group.

**Biplot analysis:** Principal component analysis based on rank correlation matrices was performed to understand the relationship among the nonparametric measures. For better visualization, the first two principal components (PC1 and PC2) were plotted against each other (Figure 2). Table 3 shows the loading of the first two PCA of ranks of non parametric measures as two first PCs (PC1 and PC2) explained 83.8% (52.4 and 31.4 % by PC1 and PC2, respectively) of the total variance. Biplot classified the stability measures in 3 groups. The lines that connect the stability estimates to the biplot origin are called stability vectors. An acute angle between the vectors of two stability indices approximates the positive correlation between them while an obtuse angle reveals independence or very weak correlation between these stability measures. Yield shows a highly significant negative rank correlation with corrected mean yield, SD whereas no correlation with MR. This result was also shown by Karimzadeh et al (2012). In this plot, CV showed high correlation with  $NP_i^{(2)}$ ,  $NP_i^{(3)}$  and  $NP_i^{(4)}$ , corrected mean of rank (CMR). Sabaghnia *et al.* (2012) reported  $NP_i^{(2)}$  was similar in concept to GE interaction measures as it defines stability in the sense of biological concept. Also there is significant positive correlation of SD with CV,  $S_i^1$ ,  $S_i^2$ ,  $S_i^3$ ,  $S_i^4$ ,  $S_i^5$  &  $S_i^6$  while yield expressed negative correlation with these measures. However, Mahtabi *et al.* (2013) found significantly and negatively correlated between mean yield and  $S_i^3$ ,  $S_i^6$ ,  $NP_i^{(2)}$  and  $NP_i^{(4)}$  measures that is in contradiction with our result. They referred the high correlation between mean yield and stability statistics to higher values of these statistics for high yielding genotypes. Meanwhile, also showed  $S_i^6$  has more strongly correlated with mean yield. Karimzadeh *et al.*, (2012) reported that the parameters  $S_i^1$  and  $S_i^2$  were nearly perfectly associated for grain yield in winter wheat.

**Relationship among nonparametric statistics:** Spearman's rank correlations calculated among ranks generated by genotype ranking as per different non parametric measures. Highly

significant ( $p < 0.01$ ) positive rank correlation of yield observed with CV with  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$  whereas negative with MR (Mahtabi *et al.*, 2013). Significant positive correlation of MR seen with CSD, CCV, CV,  $S_i^1$ ,  $S_i^2$ ,  $S_i^3$ ,  $S_i^4$ ,  $S_i^5$ ,  $S_i^6$ ,  $NP_i^{(1)}$  and negative with CV as well as with  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$ . SD expressed positive correlation of moderate to higher order with all considered measures. CV maintained significant positive correlation with  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$  and surprisingly very low correlation with  $S_i^2$ ,  $S_i^3$ ,  $S_i^4$ ,  $S_i^6$ . Also CSD had a highly significant positive association with  $S_i^1$ ,  $S_i^2$ ,  $S_i^3$ ,  $S_i^4$ ,  $S_i^5$ ,  $S_i^6$  (Khalili and Aboughadareh, 2016). Similar behavior had shown by CCV. Highly significant positive correlation expressed by  $S_i^8$  among themselves. Very low correlation observed among  $NP_i^{(6)}$  except of  $NP_i^{(4)}$ . Measures  $NP_i^{(1)}$  and  $NP_i^{(4)}$  showed significant correlation with other measures. CD and CCV were observed good measures as both had significantly high ( $p < 0.01$ ) positive rank correlation with  $S_i^8$ .

#### Acknowledgement

The multi-environment trials of barley genotypes were performed within the AICW&BIP project at centers across the country. Authors are grateful to all the staff of testing centers for their hard work to carry out the field evaluation and data recording.

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**Table 1. Environmental conditions and parentage details of barley genotypes**

Code	Genotype	Parentage	Locations	Latitude	Longitude	Altitude (m)
IVTIRFB-1	KB1436	LAKHAN/JB137	Durgapura	26° 51 ' N	75° 47 ' E	390
IVTIRFB-2	BH959	BH393/BH331	Hisar	29° 10 ' N	75° 46 ' E	215.2
IVTIRFB-3	RD2922	RD2809/RD2743	Ludhiana	30° 54 ' N	75° 52 ' E	247
IVTIRFB-4	HUB250	RD2618/RD2660	Tabiji	26° 35' N	74° 61' E	456.1
IVTIRFB-5	BH1004	33rd IBON200/BH902	Pant nagar	29° 02 ' N	79° 48 ' E	237
IVTIRFB-6	UPB1054	IBYT-LRA-M-12(Sr.No.27 of EIBGN 2013-14)	Karnal	29 ° 43 ' N	76° 58 ' E	252
IVTIRFB-7	PL890	DWRUB52/DWRUB62	Varanasi	25° 20 ' N	83° 03 ' E	75.5
IVTIRFB-8	JB325	RD2615/DL88	Rewa	24° 31 ' N	81° 15 ' E	365.7
IVTIRFB-9	BH1006	15th HBSN-4/BH902	Faizabad	26° 47 ' N	82° 12 ' E	113
IVTIRFB-10	HUB113	KARAN280/C138	Kanpur	26° 29 ' N	80° 18 ' E	125.9
IVTIRFB-11	KB1434	GLORIA- BAR/COPAL//PM5/BEN/3/SEN/4/PETUNIA1/5/ BBSC/CONGONA// BLLU/3/CIRU	Sabour	25° 24 ' N	87° 04 ' E	41
IVTIRFB-12	RD2786	RD2634/NDB1020//K425	SK Nagar	24° 19 ' N	72 ° 19 ' E	154.5
IVTIRFB-13	BH902	BH495/RD2552	Sagar	23° 83 ' N	78° 73 ' E	523
IVTIRFB-14	JB322	JB101/BH331	Morena	26° 56 ' N	78° 80 ' E	152
IVTIRFB-15	UPB1053	IBYT-MRA-12(Sr.No.35 of EIBGN 2013-14)	Udaipur	24° 34 ' N	70° 42 ' E	582
IVTIRFB-16	PB891	IBON 343/12th HSBN-176				
IVTIRFB-17	BH1005	BHMS24A/WG127				
IVTIRFB-18	HUB249	RD2618/RD2660				
IVTIRFB-19	NDB1634	IBON-HI-40 (2009-10)				
IVTIRFB-20	BH946	BHMS22A/BH549//RD2552				
IVTIRFB-21	RD2923	RD2552/RD2786				
IVTIRFB-22	KB1425	K508/NDB1295				
IVTIRFB-23	DWRB157	ALANDA02/4/ARIZONA5908/ATHS//ASSE/3/F 208.74/5/ALANDA/3/CI08887/CI05761//LIGNEE 640-34				
IVTIRFB-24	RD2921	RD2508/RD2743				
IVTIRFB-25	JB319	LAKHAN/BH353				
IVTIRFB-26	RD2552	RD2035/DL472				
IVTIRFB-27	DWRB156	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/ 5/PETUNIA 1/6/M9846//CCXX14.ARZ3/PA				

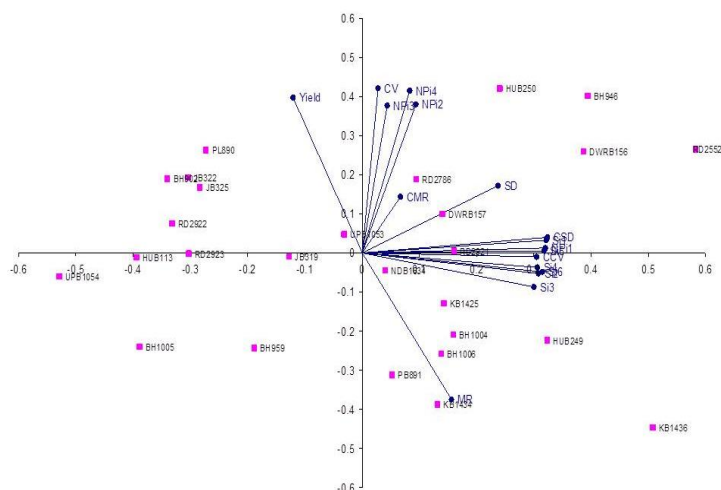


**Table 2. Descriptive statistics and non parametric measures for grain yield**

Genotype	Yield (q/ha)	MR	SD	CV	CMR	CSD	CCV	S <sub>i</sub> <sup>1</sup>	S <sub>i</sub> <sup>2</sup>	S <sub>i</sub> <sup>3</sup>	S <sub>i</sub> <sup>4</sup>	S <sub>i</sub> <sup>5</sup>	S <sub>i</sub> <sup>6</sup>	NP <sub>i</sub> (1)	NP <sub>i</sub> (2)	NP <sub>i</sub> (3)	NP <sub>i</sub> (4)	Z <sub>1</sub>	Z <sub>2</sub>	
KB1436	32.52	20.87	6.13	0.29	13.33	8.99	0.67	10.53	141.61	148.70	10.53	9.49	10.68	7.667	0.333	0.551	0.505	1.73	<b>28.42</b>	
BH959	36.74	16.67	6.43	0.39	14.07	7.19	0.51	8.44	58.88	58.60	7.33	6.51	6.94	6.267	0.348	0.445	0.506	0.22	0.01	
RD2922	39.68	11.00	6.60	0.60	13.13	6.75	0.51	7.85	50.43	53.76	6.86	5.33	6.09	5.333	0.533	0.624	0.713	0.94	0.45	
HUB250	41.30	10.53	8.35	0.79	14.60	8.87	0.61	10.44	96.40	92.44	8.48	8.16	8.38	7.333	0.815	0.901	0.991	1.52	<b>5.54</b>	
BH1004	35.55	16.87	7.14	0.42	13.60	8.61	0.63	10.21	85.55	88.06	8.48	7.64	8.43	7.333	0.386	0.530	0.605	1.08	2.69	
UPB1054	39.91	11.53	5.30	0.46	14.33	5.77	0.40	6.80	41.64	40.67	6.20	5.42	5.67	4.733	0.364	0.541	0.590	3.46	1.57	
PL890	41.45	10.07	6.80	0.68	14.00	6.81	0.49	7.89	63.00	63.00	6.47	5.98	6.40	5.267	0.752	0.762	0.783	0.88	0.02	
JB325	40.76	9.87	6.28	0.64	13.87	6.65	0.48	7.71	61.41	62.00	7.50	6.21	6.72	4.933	0.493	0.767	0.782	1.17	0.00	
BH1006	35.52	18.40	6.66	0.36	14.80	8.64	0.58	9.96	88.49	83.70	9.05	7.63	7.73	7.533	0.377	0.494	0.541	0.69	3.36	
HUB113	39.51	11.60	6.56	0.57	12.40	6.54	0.53	7.56	43.51	49.13	6.22	5.09	6.16	5.067	0.461	0.549	0.652	1.47	1.28	
KB1434	33.79	19.40	6.32	0.33	13.40	7.94	0.59	9.28	101.69	106.24	9.55	7.39	8.27	6.467	0.323	0.502	0.478	0.06	<b>7.30</b>	
RD2786	40.52	11.93	7.89	0.66	14.13	8.58	0.61	10.15	78.74	78.00	8.48	7.22	7.67	6.933	0.533	0.718	0.851	0.98	1.42	
BH902	40.99	10.13	6.59	0.65	13.87	6.61	0.48	7.43	58.63	59.19	7.38	5.19	5.62	5.067	0.633	0.730	0.733	1.76	0.02	
JB322	41.85	8.87	4.79	0.54	14.80	5.99	0.40	6.78	73.60	69.63	7.95	7.36	7.46	4.600	0.511	0.935	0.765	3.52	0.73	
UPB1053	38.97	13.00	7.73	0.59	13.33	8.16	0.61	9.64	66.64	69.98	7.25	6.60	7.43	6.467	0.497	0.607	0.741	0.31	0.15	
PB891	33.77	19.60	8.19	0.42	14.87	7.90	0.53	9.24	86.41	81.38	8.98	7.03	7.09	6.467	0.269	0.458	0.471	0.05	2.88	
BH1005	37.35	15.67	6.07	0.39	13.53	6.53	0.48	7.62	47.57	49.21	6.07	5.47	6.06	5.333	0.356	0.425	0.486	1.36	0.74	
HUB249	34.93	18.00	7.65	0.43	13.67	8.98	0.66	10.57	100.79	103.24	9.00	8.60	9.44	7.733	0.430	0.539	0.587	1.81	<b>6.98</b>	
NDB1634	37.52	14.27	7.56	0.53	13.07	8.18	0.63	9.66	68.47	73.36	7.74	7.08	8.13	6.933	0.533	0.560	0.677	0.32	0.26	
BH946	41.24	11.80	8.82	0.75	15.00	9.58	0.64	11.22	102.83	95.97	9.79	8.48	8.48	8.400	0.933	0.830	0.951	3.60	<b>7.71</b>	
RD2923	39.59	12.73	6.86	0.54	14.33	7.02	0.49	8.25	51.98	50.77	6.27	5.88	6.16	5.733	0.410	0.547	0.648	0.40	0.33	
KB1425	36.77	15.73	7.52	0.48	13.33	8.70	0.65	10.21	81.84	85.93	7.99	7.45	8.38	7.333	0.407	0.555	0.649	1.08	1.94	
DWRB157	39.57	13.93	8.17	0.59	15.87	8.81	0.56	10.15	81.70	72.09	8.59	8.15	7.70	7.400	0.493	0.627	0.729	0.98	1.92	
RD2921	38.33	14.73	8.28	0.56	13.73	8.72	0.64	10.34	77.14	78.64	8.48	7.52	8.21	7.467	0.533	0.576	0.702	1.33	1.18	
JB319	38.72	13.53	7.42	0.55	14.00	7.76	0.55	9.20	60.38	60.38	7.00	6.43	6.89	6.400	0.427	0.555	0.680	0.03	0.00	
RD2552	39.01	13.27	9.71	0.73	13.80	10.29	0.75	12.00	106.19	107.73	9.94	9.22	10.02	9.067	0.824	0.750	0.905	<b>6.57</b>	<b>8.99</b>	
DWRB156	40.54	13.00	9.51	0.73	15.13	9.74	0.64	11.39	99.71	92.25	9.30	8.80	8.72	8.200	0.586	0.742	0.876	<b>4.18</b>	<b>6.61</b>	
ES <sup>1</sup>	8.99	ES <sup>2</sup>	60.67	VS <sup>1</sup>	1.38	VS <sup>2</sup>	230.53											Sum	41.49	92.51

**Table 3. Loadings of ranks derived from measures**

83.79	Component PC1	Component PC2
Yield	-0.121	0.397
MR	0.156	-0.374
SD	0.238	0.172
CV	0.028	0.421
CMR	0.067	0.144
CSD	0.324	0.040
CCV	0.305	-0.010
Si1	0.322	0.033
Si2	0.308	-0.053
Si3	0.300	-0.087
Si4	0.306	-0.037
Si5	0.318	0.006
Si6	0.315	-0.049
NPi1	0.320	0.013
NPi2	0.094	0.380
NPi3	0.044	0.377
NPi4	0.083	0.415
% Variance	52.38	31.41

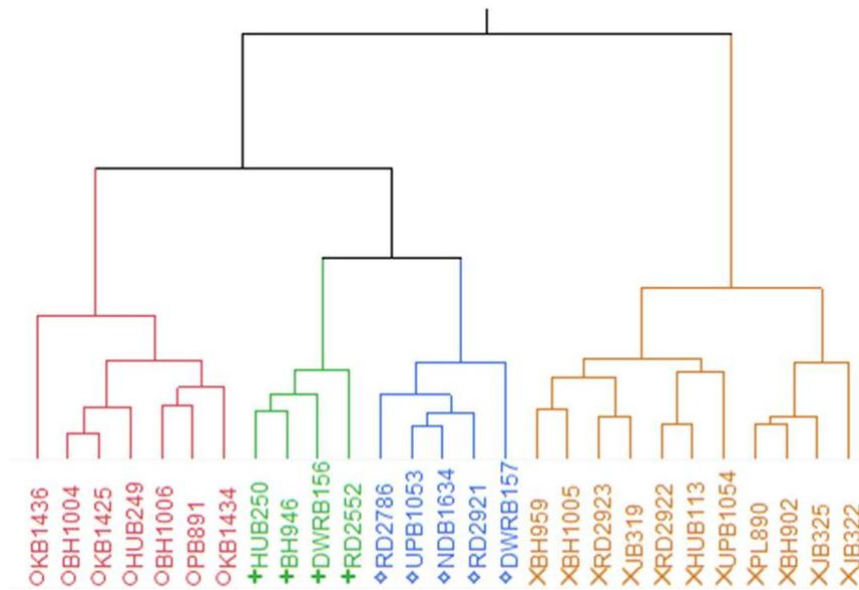


**Fig.1: Biplot of PC1 versus PC2 for non parametric measures**

**Table 4. Spearman rank correlation among measures for feed barley genotypes**

	Yield	MR	SD	CV	CMR	CSD	CCV	S <sub>i</sub> <sup>1</sup>	S <sub>i</sub> <sup>2</sup>	S <sub>i</sub> <sup>3</sup>	S <sub>i</sub> <sup>4</sup>	S <sub>i</sub> <sup>5</sup>	S <sub>i</sub> <sup>6</sup>	NP <sub>i</sub> <sup>(1)</sup>	NP <sub>i</sub> <sup>(2)</sup>	NP <sub>i</sub> <sup>(3)</sup>
MR	-0.950															
SD	0.070	0.105														
CV	0.817	-0.729	0.553													
CMR	0.392	-0.172	0.281	0.283												
CSD	-0.239	0.433	0.756	0.193	0.155											
CCV	-0.353	0.496	0.672	0.097	-0.172	0.916										
S <sub>i</sub> <sup>1</sup>	-0.270	0.447	0.757	0.171	0.097	0.988	0.939									
S <sub>i</sub> <sup>2</sup>	-0.287	0.464	0.515	0.009	0.202	0.857	0.772	0.838								
S <sub>i</sub> <sup>3</sup>	-0.319	0.474	0.514	0.000	0.070	0.860	0.824	0.855	0.985							
S <sub>i</sub> <sup>4</sup>	-0.299	0.455	0.495	-0.003	0.244	0.832	0.730	0.800	0.960	0.934						
S <sub>i</sub> <sup>5</sup>	-0.237	0.436	0.543	0.033	0.251	0.910	0.805	0.896	0.929	0.912	0.897					
S <sub>i</sub> <sup>6</sup>	-0.308	0.469	0.535	0.004	0.038	0.904	0.894	0.910	0.922	0.938	0.869	0.959				
NP <sub>i</sub> <sup>(1)</sup>	-0.357	0.552	0.729	0.074	0.117	0.975	0.917	0.972	0.835	0.838	0.819	0.882	0.878			
NP <sub>i</sub> <sup>(2)</sup>	0.733	-0.692	0.518	0.900	0.106	0.247	0.203	0.224	0.063	0.083	0.060	0.110	0.105	0.154		
NP <sub>i</sub> <sup>(3)</sup>	0.824	-0.745	0.323	0.853	0.263	0.178	0.086	0.132	0.153	0.143	0.133	0.181	0.143	0.023	0.849	
NP <sub>i</sub> <sup>(4)</sup>	0.827	-0.730	0.488	0.949	0.286	0.247	0.153	0.223	0.109	0.103	0.089	0.170	0.136	0.115	0.915	0.936

Critical values of Spearman correlation at 5% and 1% level of significance (df 25) are 0.398 & 0.510 respectively



**Fig. 2: Hierarchical clustering of Feed barley genotypes by Ward's method**