



Research Paper

Interpreting genotype x environment by non-parametric methods for malt barley evaluated under north western plains zone

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ABSTRACT : The present study was carried out to identify malt barley genotypes with high yield and stability across eight different environments, using non-parametric statistical measures. Descriptive statistics MR, SD and CV identified DWRB147, DWRB150 and RD2943 stable genotypes. BH902 and PL890 were identified as unstable genotypes by CMR CSD and CCV. Non-parametric measures selected DWRB147 and DWRB150 as the stable genotypes and BH902 and PL890 unstable genotypes. Significant tests for S_i^1 and S_i^2 were based on sum of Z_i^1 and Z_i^2 measures and sum of Z_i^1 was greater than critical value confirmed significant differences among the twenty genotypes. Results of the NP_i^2 , NP_i^3 and NP_i^4 were similar for unstable performance of BH902, DWRB150 and DWRB147. Biplot analysis of PCA1 and PCA2 accounting for 70.08 per cent showed three distinguish groups among non-parametric measures. Clustering by Ward's hierarchical method expressed four clusters by using the squared Euclidean distance as dissimilarity measure.

KEY WORDS: Non-parametric measurements, Rank correlation, Biplot analysis, Hierarchical clustering

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INTRODUCTION :

Barley crop is cultivated since ancient time for food, feed, medicinal purposes and malt of alcoholic beverages. Today, barley has recognized as a crop of industrial importance as cater the increased demand of malt for brewing, distillation, baby foods and medicinal syrups in domestic as well as international market (Verma *et al.*, 2011). Nearly 20-25 per cent of the total barley production of the country is utilized by the malting industries. The demand for malt barley is directly associated with the expansion of the brewery industry (Kumar *et al.*, 2014).

The quality characteristics as well as grain yield of malt barley influenced to large extent by environmental conditions (Kadi *et al.*, 2010). G×E interaction possess a major challenge to crop improvement programmes (Farshadfar *et al.*, 2014). Genotype is assumed to be stable if it has high mean yield but a low degree of yield variability over diverse environments (Karimizadeh *et al.*, 2012). For an initial look, the non-parametric methods, based on the order of merit of the genotypes, constitute a valid and useful tool (Sabaghnia *et al.*, 2012). Several non-parametric methods have been used for the interpretation of G x E interaction (Delic *et al.*, 2009;

Sabaghnia *et al.*, 2014 and Mahtabi *et al.*, 2013). Recently literature had witnessed increased number of non-parametric measures to evaluate genotypes grown in different environments. The objectives of this study were to evaluate the stable yield performance of twenty malt barley genotypes at eight experimental locations by non-parametric measures and cluster analysis of these different non-parametric measures for their cohesiveness.

MATERIALS AND METHODS :

Twenty malt barley genotypes, including checks of six row feed and two row malt, were evaluated at eight major experimental locations of North Western plains zone under irrigated conditions during 2015-2016 cropping seasons. The Randomized Block Designs with three replications adopted for field trials and recommended cultural practices were followed to harvest the good yield. The grain yield of genotypes were further analysed statistically to calculate non parametric measures. Huehn (1996) and Nassar and Huehn (1987) proposed non-parametric measures that combine mean yield and stability. Let X_{ij} denotes the phenotypic value of i th genotype in j th environment where $i = 1, 2, \dots, k$, $j = 1, 2, \dots, n$ for a two-way dataset and r_{ij} as the rank of the i th genotype in the j th environment and \bar{r}_i was the average rank of the i th genotype across all environments. Corrected yield of i th genotype in j th environment calculated as $(X_{ij}^* = X_{ij} - \bar{X}_i + \bar{X}_.)$ as X_{ij}^* , was the corrected phenotypic value; \bar{X}_i was the mean i th genotype in all environments and $\bar{X}_.$ was the grand mean. The ranks obtained from these adjusted values depend only on G x E interaction and error effects. The genotype with the highest adjusted yield was given a rank of 1 and that with the lowest adjusted yield was assigned a rank of 20. Four parameters based on yield ranks of genotypes in each environment are derived as follows:

$$S_i^{(1)} = \frac{2}{n} \sum_{j=1}^{n-1} \sum_{j+1}^n |r_{ij} - r_{ij+1}| / \ln(n > 1)$$

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

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

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

Thenarasu (1995) proposed non-parametric stability measures $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ based on the ranks for values. In the above formulas, r_{ij}^* was the rank of X_{ij}^* , and \bar{r} and M_{di} were the mean and median ranks for original (unadjusted) traits, where \bar{r}^* and M_{di}^* were the same parameters computed from the corrected (adjusted) trait values.

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

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

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

$$NP_i^{(4)} = \frac{2}{m(m > 1)} \sum_{j=1}^{m-1} \sum_{j+1}^m \frac{|r_{ij}^* - r_{ij+1}^*|}{\bar{r}_i}$$

SAS computer programme SASTESTAB (Hussein *et al.*, 2000) calculated non-parametric measures. Hierarchical clustering of genotypes based on yield along with non parametric measures by Ward’s method (Ward, 1963) was performed to understand the relationships among the non-parametric methods.

RESULTS AND DATA ANALYSIS :

Non-parametric statistical analysis was presented in Table 2. Genotype KB1426 (27.5 q/ha) was the highest yielder followed by BH1012 and BH1013 as remarkable differences (16.7 to 27.5) were observed. Three descriptive statistics; mean of ranks (MR), standard deviation of ranks (SD) and co-efficient of variation of ranks (CV) based on original yield were calculated (Sabaghnia *et al.*, 2006). These statistics pointed towards DWRB147, DWRB150 and RD2943 were the stable genotypes, while DWRB150 and DWRUB53 based on MR, PL890 and BH1012 based on SD and BH902 and RD2849 based on CV, were unstable ones. These simple descriptive statistics based on ranks able to discriminate genotypes (Parmar *et al.*, 2012). Non-parametric measures based on original yield suggested DWRUB52 and DWRB147 as genotypes of stable performance, however, most of the measures isolated PL890 as the most unstable genotype.

Genotypes evaluation as per descriptive statistics based on corrected yield presented in Table 3. Mean of ranks of (CMR) pointed towards RD2940 followed by

Table 1: Environmental conditions and parentage details of barley genotypes

Code	Genotype	Parentage	Code	Environments	Latitude	Longitude	Altitude (m)
IVT-MB-TS-1	KB1426	IBYT-HI(11)-12	E1	Bawal	28° 10 ' N	76°59 ' E	263
IVT-MB-TS-2	DWRB101	DWR28/BH581	E2	Durgapura	26° 51 ' N	75° 47 ' E	390
IVT-MB-TS-3	KB1405	IBYT-HI (13-14)-16	E3	Hisar	29° 10 ' N	75° 46 ' E	215.2
IVT-MB-TS-4	RD2943	DWRUB52/RD2618	E4	Ludhiana	30°54 ' N	75° 52' E	247
IVT-MB-TS-5	DWRB148	DWRB78/DWRB77	E5	Bathinda	30°21 ' N	74° 95' E	208
IVT-MB-TS-6	RD2849	ISEBON-128 (08-09)/PL705	E6	Karnal	29° 43 ' N	76° 58 ' E	252
IVT-MB-TS-7	BH902	BH495/RD2552	E7	Modipuram	29°07 ' N	77° 71' E	232
IVT-MB-TS-8	BH1011	EIBGN-17/BH919(2007)	E8	Pantnagar	29°02 ' N	79° 48' E	237
IVT-MB-TS-9	DWRB149	DWRB78/DWRB77					
IVT-MB-TS-10	PL890	DWRUB52/DWRUB62					
IVT-MB-TS-11	BH1013	28 th IBYT-23/DWRUB52					
IVT-MB-TS-12	DWRB150	DWRB54/XANADU					
IVT-MB-TS-13	RD2941	DWRUB49/RD2615					
IVT-MB-TS-14	RD2939	RD2668/IBON-HI 2010-11					
IVT-MB-TS-15	DWRB92	DWR28/DWR45					
IVT-MB-TS-16	DWRUB52	DWR17/K551					
IVT-MB-TS-17	BH1012	33 rd IBON71/DWRUB52					
IVT-MB-TS-18	DWRB147	DWRB78/DWRB73					
IVT-MB-TS-19	RD2940	RD2668/PL426					
IVT-MB-TS-20	KWS Amadora	Conchita/ Quench//KWS Bambina					

Table 2: Descriptive statistics and non-parametric measures for grain yield (Original)

		Yield	MR	SD	CV	Med	S _i ¹	S _i ²	S _i ³	S _i ⁶
IVT-MB-TS-1	KB1426	27.52	12.63	6.00	0.48	12.0	8.09	35.98	19.95	3.03
IVT-MB-TS-2	DWRB101	23.07	9.38	4.47	0.48	8.5	5.96	19.98	14.92	2.75
IVT-MB-TS-3	KB1405	21.98	13.38	5.76	0.43	15.0	6.22	33.13	17.34	2.50
IVT-MB-TS-4	RD2943	17.95	13.00	4.28	0.33	13.5	5.39	18.29	9.85	2.15
IVT-MB-TS-5	DWRB148	24.91	14.38	5.63	0.39	16.0	6.96	31.70	15.43	2.38
IVT-MB-TS-6	RD2849	21.60	7.38	5.58	0.76	6.0	6.70	31.13	29.54	3.86
IVT-MB-TS-7	BH902	22.26	5.00	4.87	0.97	3.5	5.04	23.71	33.20	6.00
IVT-MB-TS-8	BH1011	26.51	11.50	5.37	0.47	13.0	6.39	28.86	17.57	2.87
IVT-MB-TS-9	DWRB149	26.35	10.25	6.25	0.61	11.0	8.17	39.07	26.68	3.90
IVT-MB-TS-10	PL890	19.41	8.88	6.62	0.75	7.5	8.61	43.84	34.58	5.07
IVT-MB-TS-11	BH1013	27.02	9.50	3.55	0.37	10.5	4.70	12.57	9.26	2.42
IVT-MB-TS-12	DWRB150	24.39	4.38	3.34	0.76	3.0	4.22	11.13	17.80	4.69
IVT-MB-TS-13	RD2941	19.46	15.13	5.25	0.35	18.0	6.83	27.55	12.75	2.43
IVT-MB-TS-14	RD2939	20.39	10.38	6.39	0.62	12.0	7.78	40.84	27.55	4.07
IVT-MB-TS-15	DWRB92	16.70	9.25	4.98	0.54	11.0	6.39	24.79	18.76	3.62
IVT-MB-TS-16	DWRUB52	18.56	6.00	3.12	0.52	6.5	3.87	9.71	11.33	3.33
IVT-MB-TS-17	BH1012	27.35	10.63	6.41	0.60	9.5	8.35	41.13	27.09	4.05
IVT-MB-TS-18	DWRB147	18.71	15.25	4.23	0.28	17.5	4.83	17.93	8.23	1.77
IVT-MB-TS-19	RD2940	25.44	10.63	5.58	0.53	12.5	7.70	31.13	20.51	3.36
IVT-MB-TS-20	KWS Amadora	24.05	12.25	4.71	0.38	13.0	6.17	22.21	12.69	2.24

RD2939 genotype. CSD and CCV measures identified DWRB150 along with DWRB147 as the stable genotypes. More over BH902 and PL890 were identified as the genotypes with unstable performance. Non-parametric measures based on corrected values identified DWRB147 and DWRB150 as the stable genotypes at the same times BH902 and PL890 unstable genotypes.

The significant tests for S_i^1 and S_i^2 were developed by Nassar and Huehn (1987). For each genotype Z_i^1 and Z_i^2 values were calculated based on the ranks of adjusted data and summed over genotypes to obtain Z values. As sum of $Z_i^1 = 59.77$ was greater than critical value of $\chi^2 = 31.41$, therefore significant differences were found in rank stability among the twenty genotypes grown in the eight environments and sum of $Z_i^2 = 18.75$ less than the critical value of χ^2 thus, indicating non-significant differences in rank stability among the twenty genotypes grown in the eight environments (Mortazavian and Azizinia, 2014). Few genotypes were significantly unstable as compared to the other genotypes as observed large Z values compared with the critical χ^2 at 5 per cent level of significance for one degree of freedom *i.e.* 3.84.

The S_i^1 and S_i^2 statistics are based on ranks of genotypes across environments and assign equal weight to all environments. Genotypes with fewer changes in ranking are considered to be more stable (Karimizadeh *et al.*, 2012). Accordingly RD2849, RD2943 DWRB150 and DWRB147 had the smallest changes in rank and regarded as the stable genotypes unlike to BH902 and PL890. Two other non-parametric statistics S_i^3 and S_i^6 combining yield and stability based on yield ranks of genotypes in each environment (Mortazavian and Azizinia, 2014). These parameters measure stability in units of the mean rank of each genotype. As for S_i^1 and S_i^2 , DWRB150 followed by DWRB147 were the most stable according to the S_i^3 and S_i^6 measures.

Results of Thennarasu (1995) non-parametric stability statistics, calculated from the ranks of adjusted yield, depicted in Table 3. According to the NP_i^1 , DWRB101 and RD2849 were considered stable as compared to other genotypes. RD2943 and DWRB148 had the lowest value of NP_i^2 and were stable genotypes followed by DWR147 and KWS Amadora. Measure, like NP_i^2 identified DWRB150 as the stable genotype, though

Table 3: Descriptive statistics and non-parametric measures for grain yield (corrected)

	CMR	CSD	CCV	Cmed	C S_i^1	Z^1	C S_i^3	C S_i^6	C S_i^2	Z^2	NP_i^1	NP_i^2	NP_i^3	NP_i^4
IVT-MB-TS-1	11.0	5.63	0.51	9.5	7.61	1.062	20.18	3.27	31.71	0.016	8.313	0.693	5.268	0.603
IVT-MB-TS-2	9.8	5.52	0.57	8.5	7.57	0.968	21.90	3.69	30.50	0.051	7.625	0.897	5.166	0.807
IVT-MB-TS-3	10.5	5.90	0.56	12.0	7.65	1.161	23.24	3.71	34.86	0.017	10.500	0.700	5.523	0.572
IVT-MB-TS-4	9.6	4.93	0.51	10.0	5.87	0.704	17.65	3.43	24.27	0.541	8.750	0.648	4.608	0.452
IVT-MB-TS-5	10.3	6.50	0.63	10.5	8.17	2.684	28.83	3.90	42.21	0.539	9.188	0.574	6.078	0.569
IVT-MB-TS-6	9.1	4.97	0.54	8.0	5.70	1.053	18.95	2.79	24.70	0.490	7.719	1.286	4.649	0.772
IVT-MB-TS-7	9.8	7.67	0.79	10.0	9.39	8.685	42.21	5.54	58.79	4.370	8.813	2.518	7.172	1.878
IVT-MB-TS-8	10.6	6.35	0.60	12.0	7.83	1.599	26.53	3.93	40.27	0.330	10.500	0.808	5.936	0.681
IVT-MB-TS-9	11.1	6.85	0.62	11.5	9.13	7.110	29.56	3.87	46.98	1.264	10.063	0.915	6.412	0.891
IVT-MB-TS-10	10.1	7.40	0.73	7.5	9.22	7.618	37.81	5.06	54.70	3.083	7.750	1.033	6.918	1.039
IVT-MB-TS-11	10.0	5.01	0.50	10.0	6.39	0.077	17.60	2.80	25.14	0.440	8.750	0.833	4.690	0.673
IVT-MB-TS-12	10.8	4.06	0.38	10.5	5.48	1.587	10.74	2.42	16.50	1.880	9.188	3.063	3.800	1.252
IVT-MB-TS-13	10.0	6.05	0.60	10.0	8.35	3.331	25.60	4.00	36.57	0.074	8.750	0.486	5.657	0.552
IVT-MB-TS-14	12.0	6.82	0.57	12.5	8.17	2.684	27.17	3.83	46.57	1.189	10.938	0.911	6.384	0.788
IVT-MB-TS-15	11.4	6.00	0.53	13.5	7.74	1.371	22.14	3.36	35.98	0.050	11.813	1.074	5.611	0.837
IVT-MB-TS-16	10.4	5.58	0.54	11.0	6.78	0.020	21.00	3.57	31.13	0.030	9.625	1.481	5.219	1.130
IVT-MB-TS-17	10.1	7.18	0.71	9.0	9.04	6.621	35.64	4.84	51.55	2.245	8.094	0.852	6.716	0.851
IVT-MB-TS-18	11.1	4.79	0.43	12.0	6.43	0.054	14.46	2.79	22.98	0.707	10.500	0.600	4.484	0.422
IVT-MB-TS-19	12.9	6.71	0.52	16.0	8.87	5.693	24.46	3.51	44.98	0.922	14.000	1.120	6.274	0.835
IVT-MB-TS-20	9.5	6.48	0.68	8.5	8.87	5.693	30.95	4.63	42.00	0.513	7.938	0.611	6.062	0.724
$E(S_i^1) = 6.65$	$Var(S_i^1) =$	0.8659	$E(S_i^2) =$	33.25		59.77	$Var(S_i^3) =$	149.21		18.75	$\chi^2 =$	3.84	$\chi^2 =$	31.14

with lower yield (Zali *et al.*, 2011). Most unstable genotype based on NP_i^3 was BH902 followed by PL890 and BH1012, which had the higher mean yield. The NP_i^3 showed a negative relationship with yield (Mut *et al.*, 2009). Stability parameter NP_i^4 selected DWRB147 as a stable genotype, followed by RD2943, RD2941 and DWRB148. The results of the three parameters (NP_i^2 , NP_i^3 and NP_i^4) were similar as identified BH902, DWRB150 and DWRB147 as unstable, although had lowest minimum yield performances (Kilic *et al.*, 2010).

Biplot analysis :

To better understand the relationships among non-parametric measures and to assess their relationships with the concepts of stability, principal component (PC) analysis based on the rank correlation matrix was performed. Table 4 showed the loadings of the first two PCA of ranks of various measures accounting for 70.08 per cent of the variance of original variables. The

relationships among the different stability statistics are graphically displayed in a biplot of PCA1 and PCA2 (Fig. 1) allowing three groups to be distinguished: Group I included CMR, SD, S_i^1 , S_i^2 , CV, CCV, CS_i^1 , CS_i^2 and mean yield. Mean yield was included in the group I suggesting that the genotypes BH1012, DWRB149, BH1011 and RD2940 comprised those methods where yield mean had the main influence on the ranking across environments. Fig. 1 shows that these measures are strongly related to grain yield. Based on these parameters, selection based on grain yield is favoured and is related to the dynamic concept of stability. According to Sabaghnia *et al.* (2014), it was not a requirement that the genotypic response to environmental conditions should be equal for all genotypes. Therefore, these parameters can be used to recommend genotypes adapted to favorable conditions in western Iran. Group II included measures S_i^3 , S_i^6 , NP_i^2 , NP_i^4 and CV. These provide a measure of stability in the static sense. All these

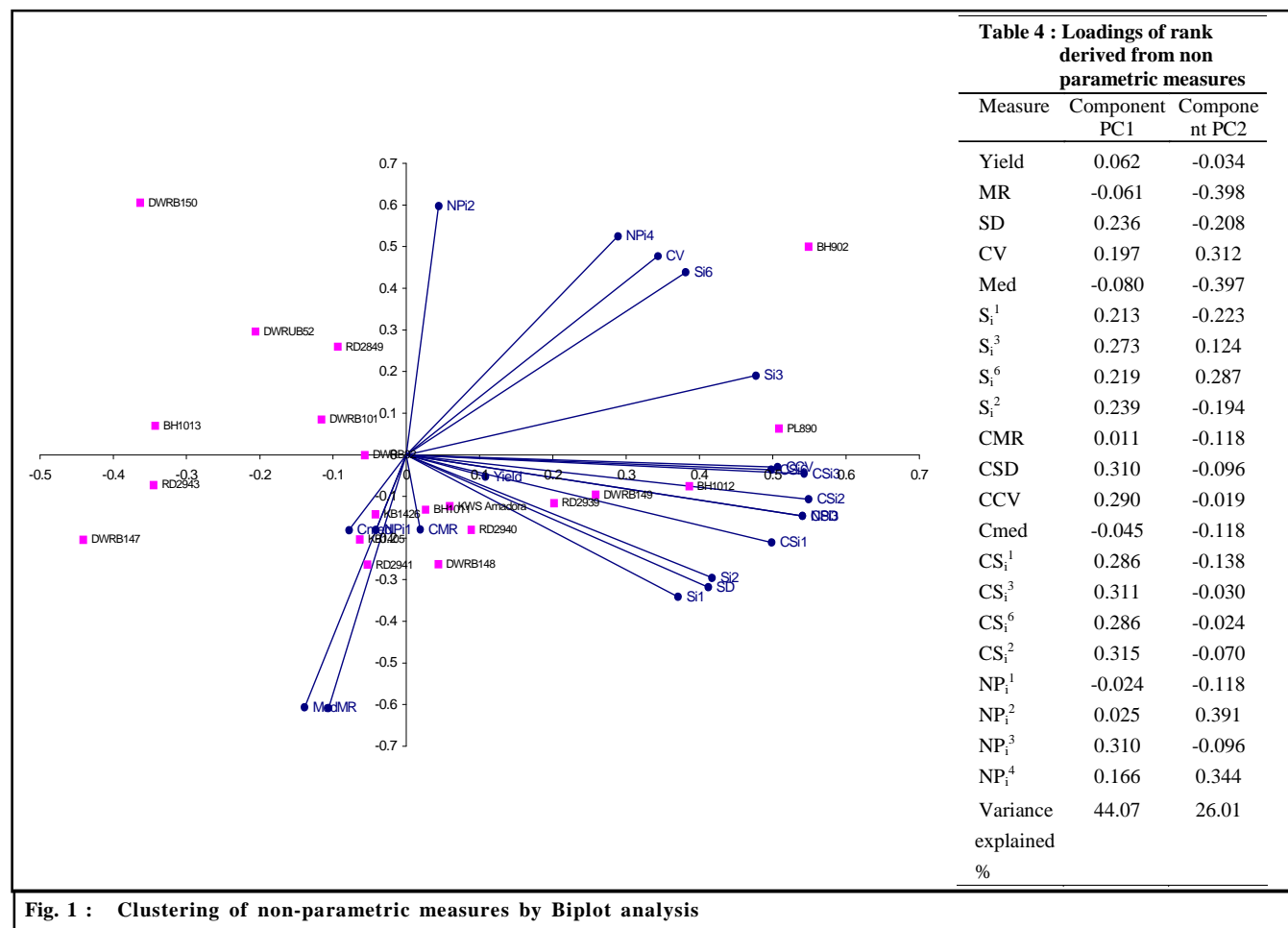


Fig. 1 : Clustering of non-parametric measures by Biplot analysis

parameters were significantly correlated with mean yield. Therefore, these parameters allow the identification of genotypes adapted to environments with unfavourable growing conditions (Kaya and Taner, 2003). Group III consists of parameters that were influenced simultaneously by both grain yield and stability. It was noted that genotypes identified according to these methods showed an average stability, however, these genotypes may not be as good as the responsive ones under favourable conditions. This group included the measures of NP_i^1 , MR, Median and C Median which were negatively associated with the mean grain yield.

Vector view of the biplot showed the degree of the relationships among the indicators. The lines that connect the stability estimates to the biplot origin are called stability vectors. The cosine of the angle between the vectors of two stability indices approximates the correlation between them (Mortazavian and Azizinia, 2014). For example, measures of G2 expressed positive correlation (an acute angle), the same conclusion was obtained for the G3 stability estimates, while G1 was negatively correlated with G3 indices (an obtuse angle) and independence or very weak correlation (almost right angle) between G1 and G2 stability measures.

Cluster analysis :

Hierarchical cluster analysis of malt barley genotypes by Ward's method (Ward, 1963) based on descriptive and non-parametric stability measures along with average yield, was used to classify the genotypes into major groups (Fig. 2) (Akcura *et al.*, 2009). Four major clusters were observed by using the squared Euclidean distance as dissimilarity measure. Group III included the high yielding genotypes BH1012 with BH902 and PL890. These genotypes were identified as unstable genotypes by mean rank measures. Most of the genotypes with moderate to low yields clustered in Group I included genotypes RD2941, BH1011, DWRB148 and KWS Amadora. The other genotypes, which had higher yields clustered in Group II included DWRB149, RD2939 and RD2940 genotypes. Largest group IV consisted of stable genotypes as per measures based on original and corrected grain yield.

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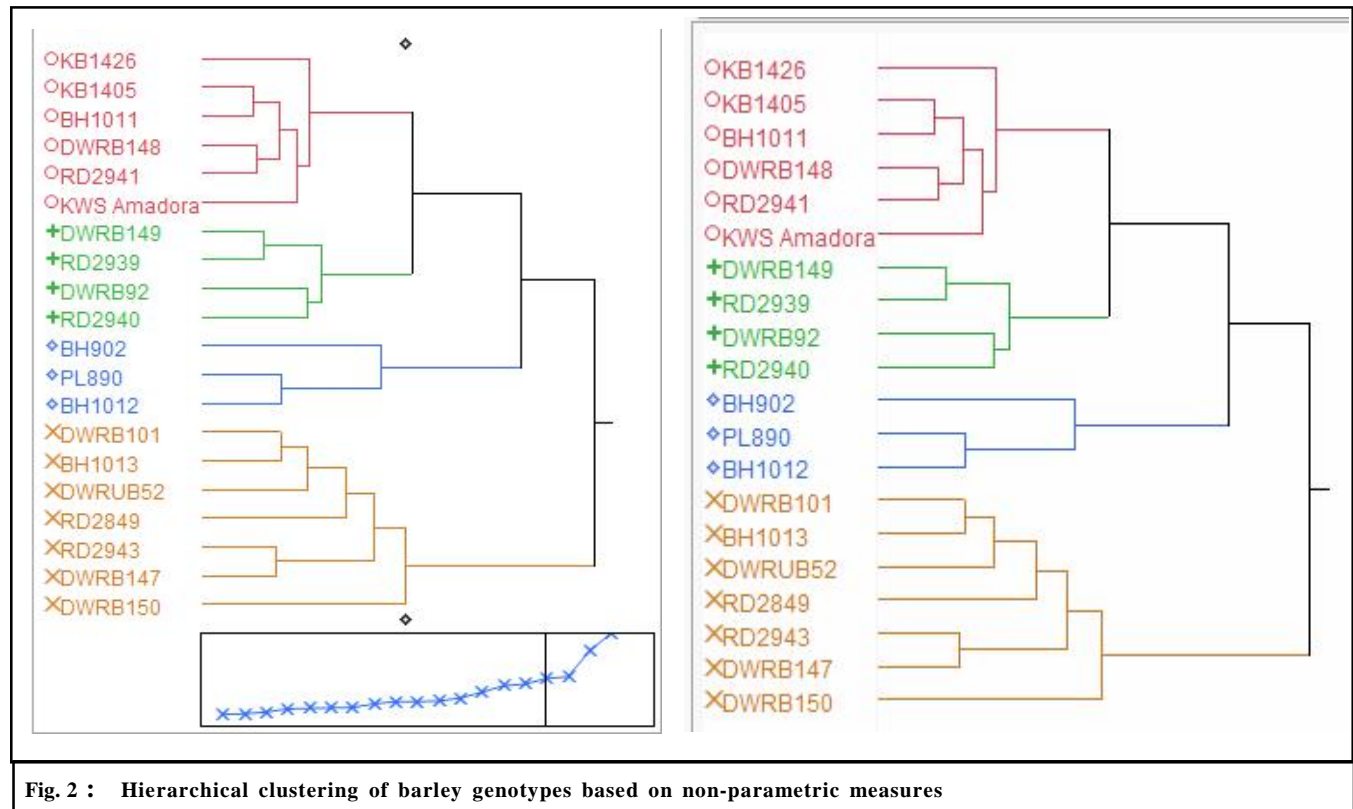


Fig. 2 : Hierarchical clustering of barley genotypes based on non-parametric measures

out the field evaluation and data recording.

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