QUANTIFICATION OF $G \times E$ INTERACTION FOR FEED BARLEY GENOTYPES BY PARAMETRIC AND NON-PARAMETRIC MEASURES

AJAY VERMA*, V KUMAR, AS KHARAB AND GP SINGH

Statistics and Computer Center, ICAR-Indian Institute of Wheat and Barley Research, Karnal 132001, Haryana, India

Keywords: Parametric, Non-parametric measures, Rank correlation, Biplot analysis, Hierarchical clustering

Abstract

Genotype × environment (G × E) interaction of 28 feed barley genotypes in 12 environments was quantified by the parametric and non-parametric measures. Significant differences among G × E, environments and genotypes were observed as 42.3% of the total variance accounted for interaction effect. Interaction Principal Component Axes (IPCA1, IPCA2, IPCA3 and IPCA4) contributed 32.2, 20.3, 15.6 and 10.5% of the interaction sum of squares. Crossover interaction among genotypes and environments was confirmed by positive and negative values IPCAs. RD2786 followed by RD2876 had large negative IPCA1 score along with positive IPCA3 and IPCA4 values. Desirable genotypes were arranged in ascending order by D values as G23 (1.32) < G2 (1.42) < G20 (1.47) < G21 (1.63). The least AMMI Stability Value (ASV) score was observed for KB1367 followed by JB290 for yield performance. Smallest Pi was satisfied by BH 946, HUB 113 and RD2552. Environmental variance and CV identified non-stable performance of RD2874 and NDB1578 along with RD2876. Wricke's ecovalence showed UPB1040 and UPB1042 as promising genotypes, however, S₁⁵, S₁⁶ selected UPB1040 and UPB1042 as of stable yield. More or less similar results were observed by parametric as well as non-parametric measures.

Introduction

Barley (Hordeum vulgare L. ssp. vulgare) has been cultivated as the world's fourth important cereal crop owing to broader environmental adaptation as compared to other cereals. Multifarious uses of barley as a feed, food and malt for brewing industries have been well known in world wide. Barley is popularly grown as feed in many parts of the world including Indian subcontinent. Feed barley genotypes are evaluated in multi-environment trials (MET) to select the promising genotypes for specific environments. $G \times E$ interaction in MET helps to evaluate stable performance of genotypes (Sisay and Sharma 2016). Large numbers of stability measures were been observed (Mohammadi et al. 2016). Crop improvement programs incorporate both parametric and non-parametric approaches (Mohammadi and Ahmed 2008). Several parametric methods including univariate and multivariate are the environmental variance (S^2_{vi}) (Lin *et al.* 1986), Wricke's ecovalence (W_i^2) (Wricke 1962) and the coefficient of variability (CV_i) (Francis and Kanenberg 1978), AMMI stability value (ASV) (Purchase et al. (2000). Ranks of genotypes as per their yield performance across environments used to calculate non-parametric measures as suggested by Huehn (1990), Nassar and Huehn (1987), Kang and Pham (1991) and Thennarasu (1995). The genotypes with similar ranking across environments were considered as of stable yield performance (Farshadfar et al. 2014).

Hence, this study was conducted to quantify the magnitude of genotype \times environment interaction by parametric and non parametric measures for feed barley genotypes evaluated under multi-location trials. The prime objectives of this study were to (i) interpret genotype-environment interaction by latest analysis procedures and (ii) association analysis among different measures as per the various statistics.

^{*}Author for correspondence: <verma.dwr@gmail.com>.

Materials and Methods

Twelve barley growing locations across the India were identified for evaluating 28 feed barley genotypes in field trials during cropping season 2013 - 2014. The randomized block design with four replications was laid out with recommended agronomical practices to ensure good harvest. The feed yield of genotypes were further analysed by statistical methods. The pedigrees of genotypes along with environmental conditions were given in Table 1 to highlight the variations in the considered locations. These promising genotypes are developed and contributed by various research centers under All India Wheat & Barley Improvement programme of the country.

Environmental variance (S_{yi}^2) : Lin *et al.* (1986) calculated environmental variance as stability measures for each genotype across test environments as: $S_{yi}^2 = \frac{\sum (Y_{ij} - Y_{ij})^2}{(E-1)}$

Superiority index (P_i): Genotypes with the largest yield difference as compared to highest yielder would have the highest P_i-value (Lin and Binns 1988) and calculated as $P_i = \frac{\sum_{j=i}^{n} (V_{ij} - M_j)^2}{2E}$

where Y_{ij} is the yield of i-th genotype in environment j, M_j is the maximum yield of the genotype at environment j and E is the number of environments.

Wricke's ecovalence (W_i^2) denotes the contribution of each genotype to the G × E interaction sum of squares and calculated as: $W_i^2 = \sum (Y_{ij} - \overline{Y}i - \overline{Y}.j + \overline{Y}..)^2$

where Y_{ij} observed yield of ith genotype for jth environment, $\overline{\mathbf{Y}}_{i}$ average yield ith genotype across environments; $\overline{\mathbf{Y}}_{ij}$ average for j-th environment; $\overline{\mathbf{Y}}_{..}$ was the grand mean. Greatest stability associated with $W_{i}^{2} = 0$.

Coefficient of variation (CV_i): Stability was also measured by CV_i and genotypes with low CVs for yield were regarded as most desirable (Francis and Kannenberg 1978). $CV_i = (S_{Yi} / \overline{Y}_i) x$ 100.

Mohammadi and Amri (2008) defined geometric adaptability index (GAI) to evaluate the adaptability of genotypes and calculated as: $GAI = \sqrt[n]{\prod_{k=1}^{n} \overline{Y}_{k}}$

in which $\overline{\mathbf{Y}}_1, \mathbf{Y}_2, \overline{\mathbf{Y}}_3, \dots \overline{\mathbf{Y}}_m$ are the mean yields of the first, second and m-th genotype across environments and n is number of environments. Genotypes with high GAI will be desirable.

AMMI Stability Value (ASV) is the distance from the coordinate point to the origin in a twodimensional scatter graph of IPCA1 scores against IPCA2 scores (Purchase *et al.* 2000). AMMI

Stability Value (ASV) =
$$\sqrt{\left[\frac{\text{SSIPCA1}}{\text{SSIPCA2}} * \text{IPCA1 score}\right]^2 + \text{IPCA2 score}^2}$$

where SSIPCA1 and SSIPCA2 are sum of squares by the IPCA1, IPCA2, respectively.

AMMI distance statistic coefficient (D) (Zang et al. 1998) was calculated as the distance of

the interaction principal component (IPC) from the origin equals to $\sum_{i=1}^{n} \gamma_{is}^2$ (i = 1, 2, 3,...n).

Non-parametric measures: Let Y_{ij} denotes the phenotypic value of i-th genotype in j-th environment, where i = 1, 2, ..., k, j = 1, 2, ..., n. Rank of the i-th genotype in the jth environment denoted by r_{ij} and the average rank of the i-th genotype across environments by $\overline{r_i}$. Karimzadeh

et al. (2012) used the corrected yield of i-th genotype in j-th environment as $(Y^*_{ij} = Y_{ij} - \overline{Y}_{e} + \overline{Y}_{a})$ as Y^*_{ij} , was the corrected phenotypic value; \overline{Y}_{e} . was the mean of ith genotype in all environments and \overline{Y}_{a} was the grand mean. The ranks obtained from these adjusted values Y^*_{ij} , depend only on GxE interaction and error effects. The ranks obtained from these adjusted values Y^*_{ij} , depend only on G × E interaction and error effects. The genotype with the highest adjusted yield was given a rank of 1 and *vice versa* for lowest adjusted yielder. Nonparametric measures were calculated based on the ranks assigned by corrected values of yield to genotypes as:

$$S_{i}^{(1)} = \frac{2\sum_{j=1}^{m-1}\sum_{j=j+1}^{m} |r_{ij} - r_{ij'}|}{[m(m-1)]} \qquad S_{i}^{(2)} = \frac{\sum_{j=1}^{m} (r_{ij} - \bar{r}_{i})^{-2}}{(m-1)} \qquad S_{i}^{(3)} = \frac{\sum_{j=1}^{m} (r_{ij} - \bar{r}_{i})^{2}}{\bar{r}_{i}}$$
$$S_{i}^{(4)} = \sqrt{\frac{\sum_{j=1}^{m} (r_{ij} - \bar{r}_{i})^{2}}{m}} \qquad S_{i}^{(5)} = \frac{\sum_{j=1}^{m} |r_{ij} - \bar{r}_{i}|}{m}}{S_{i}^{(6)} = \frac{\sum_{j=1}^{m} |r_{ij} - \bar{r}_{i}|}{\bar{r}_{i}}}$$

Non-parametric measures of Thennarasu's (1995) considered r_{ij}^* was the rank of Y_{ij}^* , and $\overline{r_i}$ and M_{di} were the mean and median ranks for original, where $\overline{r_i}^*$ and M_{di}^* were the same parameters computed from the corrected yield values. SAS-based computer program SASGESTAB (Hussein *et al.* 2000) was employed to calculate non-parametric measures.

Results and Discussion

AMMI analysis of variance yielded highly significant (p < 0.01) differences among environments, genotypes and interaction effects (Table 2). The highly significant G × E interaction confirmed the differential response of genotypes in various environments and about 42.3% of the total variance accounted by interaction effect. Of the total variance, a larger portion was described by the environmental effects (36.4%) while the genotypes accounted merely 6.9% of total variation. Significant interaction effects were further partitioned into four IPCAs which explained 32.2, 20.3, 15.6 and 10.5% of the interaction sum of squares, respectively. First two components accounted for more than 50% of the interaction sum of squares.

Genotype G20(BH946) observed as highest yielder was followed by G19(RD2552) and G21(HUB113) (Table 3) whereas G10(RD2876), G9(RD2877) and G12(UPB1042) were lower yielders.

G22 (RD 2786) followed by G10 (2876) had large negative IPCA1 score as well as positive IPCA3 and IPCA4 value, respectively (Table 3). This is referred to as crossover $G \times E$ interaction response. G26 (RD 2854) and G4 (BH 981) genotypes showed negative and positive IPCA1 values, respectively. G26 (RD 2874) and G4 (BH 981) yielded more than overall mean and lower absolute IPCA1 scores had a combination of high yield and stable performance.

AMMI stability index (D) incorporates the scores of significant IPCA towards the interaction SS and the lower D values indicate high stability across the tested environments and *vice versa*

(Zang *et al.* 1988). G23 (1.32) < G2 (1.42) < G20 (1.47) < G21 (1.63) i.e. genotypes were arranged in as per D values. G10 (RD 2876) and G24 (RD2877) expressed lowest yield along with larger D values of 3.19 and 3.49, respectively.

Table 1. Details of feed barley genotypes, parentage and environmental conditions.

Code	Genotype	Parentage		Locations	Altitude (m)	Latitude	Longitude
G1	HUB 236	DL88/22nd 1BYT15	E1	Durgapura	390	26°51 ' N	75°47 ' E
G2	KB 1353	K508/RD2676	E2	Navgaon	8.5	18°70 ' N	7286' E
G3	NDB 1580	NB3/HUB114	E3	Hisar	215.2	29°10 ' N	75°46 ' E
G4	BH 981	RD2660/RD2683	E4	Ludhiana	247	30°56 ' N	75°52 ' E
G5	KB 1369	Jaqriti/K169	E5	Varanasi	75.5	25°20 ' N	83°03 ' E
G6	HUB 237	EIBGNOT-18/RD250B	E6	Rewa	365.7	24°31 ' N	81°15 ' E
G7	BH 982	'13" EMBSN-14/RD2683	E7	Faizabad	113	26°47 'N	82°12 'E
G8	BH 980	NBD1276/8H393	E8	Kanpur	125.9	26°29 ' N	80°18 ' E
G9	RD 2875	RD2552/PL419//RD2508	E9	Vijapur	41.1	$23^{\rm o}35$ 'N	72°55 ' E
G10	RD 2876	RD2660/PENCO/CHEVRON-BAR	E10	Udaipur	582	24°34 ' N	70°42 ' E
G11	UPB 1040	IBON-LRA-M-31 (EIBGN 2010-11-30)	E11	SK Nagar	154.52	24°19 ' N	72°19 ' E
G12	UPB 1042	INBYT-LRA-M-17 (EIBGN 2010-11)	E12	Banswara	216.44	23° 55 ' N	74°45' E
G13	JB 291	DL88/K633					
G14	PL 880	PL426/BC473					
G15	BH 902	BH495/RD2552					
G16	PL 881	PL426/K537					
G17	JYOTI	K 12/C 251					
G18	PL 751	K226/PL226					
G19	RD 2552	RD2035/DL472					
G20	BH 946	BHMS22A/BH549 //RD2552					
G21	HUB 113	KARAN2BO/C138					
G22	RD 2786	RD2634/NDB1020//K425					
G23	JB 290	JB58/RD25OB					
G24	RD 2877	RD2052/DWR64//RD2660					
G25	UPB 1041	IBON-HI-33 (EIBGN 2012-13-45)					
G26	RD 2874	NDB 1173 /BH902// RD27I5					
G27	NDB 1578	BCB128/NDB940					
G28	KB 1367	PFCBO23/MSEL					

Least AMMI Stability Value (ASV) score observed for G26 (KB1367), followed by G23 (JB 290), G11 (UPB1040) and G12 (UPB1042) were the stable one, while G22 (RD2786) and G9 (RD2875) were of unstable yield performance (Table 3).

Genotype's variance across environments and coefficient of variation were listed in Table 3. Genotypes G26 (RD 2874) and G27 (NDB 1578) were observed as of desirable performance as per these criteria and also non-stable performance of G10 (RD 2876) followed by G6 (HUB 237) and G24 (RD 2877).

36

The least superiority index (P_i) was considered for desirable genotype. The condition satisfied by G20 (BH 946), G21(HUB 113) was followed by G19 (RD 2552), G14 (PL 880).

Stable genotypes according to Wricke's ecovalence were G11 (UPB 1040) and G12 (UPB 1042). Higher values for unstable yield were observed for G16 (PL 881) and G9(RD 2875) genotypes.

Source of	Degree of	Mean Sum of	Variance	% TSS	%
variation	freedom	squares	ratio		$\boldsymbol{G}\times\boldsymbol{E}$
Treatments	335	437.4	18.17	85.63	
Genotypes	27	439.4	18.26	6.93	
Environments	11	5669.1	169.23	36.44	
Block	36	33.5	1.39		
Interactions	297	243.4	10.12	42.25	
IPCA 1	37	628.2	26.10		32.15
IPCA 2	35	418.3	17.38		20.25
IPCA 3	33	341.6	14.20		15.59
IPCA 4	31	245.0	10.18		10.51
Residuals	161	96.5	4.01		
Error	972	24.1			
Total	1343	127.4			

% TSS, percentage of total sum of squares, % G \times E, percentage of G \times E total sum of squares

***denotes significant at 0.001 level of significance.

Non-parametric descriptive statistics based on original ranks, mean of ranks (MR), standard deviation of ranks (SD) and coefficient of variation of ranks (CV) identified G11(UPB1040) and G25(UPB1041) of stable performance, while unstable nature of G10(RD2876) and G24(RD2877) by MR, G16(PL881) and G9(RD2875) by SD and G19(RD2552) and G14(PL880) by CV, were also noticed. Simple descriptive statistics based on ranks discriminated among genotype performance (Karimzadeh *et al.* 2012). Genotype G25(UPB1041), G16(PL881) followed by G19(RD2552) were the unstable as well as G19(RD2552), G11(UPB1040) and G12(UPB1042) were of stable performance based on a corrected dataset that produced a mean of corrected ranks (CCW). First four nonparametric measures $(S_i^{-1}, S_i^{-2} S_i^{-3}, S_i^{-4})$ observed G11(UPB1040) and G16(PL881) as stable and unstable genotypes, respectively (Mortazavian and Azizinia 2014), however, last two measures selected G11(UPB1040) and G12(UPB1042) as of stable performance whereas G16(PL 881) and G24(RD 2877) by S_i^{-5} and G9(RD 2875) and G15(BH 902) by S_i^{-6} for unstable performance. All measures were selected G11 (UPB1040) as desirable genotype for stable and G16(PL881) for unstable behavior for the considered set of feed barley genotypes.

Significant tests for S_i^1 and S_i^2 were developed by Nassar and Huehn (1987). Since sum of $Z_i^1 = 33.19$ and $Z_i^2 = 44.16$ were more than critical value of $\chi^2 = 31.41$, there were significant differences among the genotypes grown in the 12 environments (Sisay and Sharma 2016). Unstable performance of a few genotypes judged by large Z values as compared to the critical value of χ^2 at 5% level of significance for one degree of freedom is i.e. 3.84.

Code	Genotype	Gm	R_{Gm}	GAI	R _{GAI}	Wi	R _{Wi}	Pi	R _{Pi}	\mathbf{S}_{y2}	R sy2	CV	R _{CV}	IPCA1	IPCA2	IPCA3	IPCA4	ASV]	RASV	D	R _D
G1	HUB 236	40.68	18	39.93	17	513.30	11	165.93	17	72.58	10	20.94	12	1.44	1.28	-1.05	0.39	2.61	15	2.22	12
G2	KB 1353	43.51	8	42.61	8	259.41	3	121.02	7	86.12	12	21.33	14	0.48	0.33	-1.02	-0.80	0.83	5	1.42	2
G	NDB 1580	43.64	7	43.06	7	357.49	8	121.50	8	57.61	5	17.39	ŝ	1.68	-0.02	0.72	0.44	2.66	16	1.88	7
G4	BH 981	42.78	13	42.02	12	649.89	16	122.23	6	69.75	8	19.52	r~	0.17	1.66	1.44	-2.57	1.69	13	3.39	21
G5	KB 1369	41.84	15	41.01	14	620.26	15	161.28	15	70.16	6	20.02	6	-0.16	0.82	1.10	2.38	0.86	9	2.75	15
G6	HUB 237	42.30	14	40.44	15	1013.67	25	133.93	11	206.19	27	33.95	25	-2.50	2.23	-1.19	0.93	4.56	24	3.68	25
G7	BH 982	41.33	17	40.04	16	662.98	18	170.81	19	115.62	19	26.02	21	0.32	-3.11	0.13	-0.38	3.16	19	3.16	17
G8	BH 980	43.33	6	41.99	13	948.47	24	171.53	20	106.38	17	23.81	17	2.95	-1.54	-0.54	1.13	4.93	25	3.56	24
69	RD 2875	38.70	25	35.83	26	1424.98	27	220.64	26	280.31	28	43.27	28	-3.52	-0.64	-2.33	1.79	5.62	27	4.62	27
G10	RD 2876	36.34	28	34.39	27	658.01	17	259.91	27	166.66	23	35.52	26	-1.38	-2.49	-1.03	1.02	3.32	21	3.19	18
G11	UPB 1040	38.92	24	38.22	24	194.30	1	175.42	22	62.02	9	20.23	11	0.16	-0.72	0.45	-1.55	0.77	3	1.77	5
G12	UPB 1042	38.29	26	37.31	25	229.23	2	193.15	24	88.76	15	24.61	19	0.11	-0.76	-0.90	-1.38	0.78	4	1.81	9
G13	JB 291	40.16	20	39.67	18	272.43	4	169.97	18	45.76	3	16.84	4	0.12	0.96	0.58	1.68	0.98	8	2.02	6
G14	PL 880	44.97	5	43.69	5	532.53	12	96.75	4	122.52	20	24.61	20	0.81	1.09	-1.80	-1.67	1.68	12	2.81	16
G15	BH 902	45.08	4	44.36	4	760.79	21	108.16	5	75.49	11	19.27	9	-0.69	-1.04	3.10	-0.74	1.51	10	3.42	22
G16	PL 881	40.51	19	38.72	22	1563.26	28	178.32	23	170.21	25	32.21	23	-2.73	2.69	2.77	-0.36	5.10	26	4.74	28
G17	ITOYL	43.13	10	42.08	11	868.50	23	140.21	12	104.81	16	23.73	16	2.21	1.87	-0.47	1.58	3.98	23	3.33	20
G18	PL 751	42.90	11	42.37	10	584.72	14	153.66	13	51.47	4	16.72	б	1.91	-1.21	1.42	-0.64	3.27	20	2.75	14
G19	RD 2552	47.78	7	46.89	2	728.84	20	71.33	б	87.80	13	19.61	×	1.20	0.31	0.82	1.38	1.93	14	2.03	10
G20	BH 946	47.98	1	46.90	1	354.09	7	45.80	1	113.03	18	22.16	15	-0.68	0.38	-0.28	-1.22	1.14	6	1.47	3
G21	HUB 113	46.95	Э	45.79	3	540.56	13	65.86	7	127.24	21	24.03	18	0.33	0.80	-1.26	-0.57	0.95	2	1.63	4
G22	RD 2786	41.69	16	39.47	19	1363.96	26	165.80	16	197.15	26	33.68	24	-3.83	-1.23	1.45	-0.47	6.20	28	4.30	26
G23	JB 290	44.18	9	43.30	9	350.52	9	111.51	9	88.63	14	21.31	13	-0.34	0.16	-1.10	-0.63	0.57	5	1.32	1
G24	RD 2877	36.51	27	34.26	28	837.69	22	261.20	28	169.12	24	35.62	27	-0.78	-3.38	-0.29	0.27	3.60	22	3.49	23
G25	UPB 1041	40.01	21	38.40	23	665.30	19	158.25	14	160.54	22	31.67	22	-0.85	1.00	-2.67	-1.24	1.67	11	3.22	19
G26	RD 2874	42.85	12	42.60	6	281.99	5	125.17	10	24.14	1	11.47	1	-0.05	0.21	1.31	1.43	0.22	-	1.95	8
G27	NDB 1578	39.35	23	38.85	21	422.63	10	197.89	25	39.89	2	16.05	7	1.680	0.494	0.560	0.979	2.71	17	2.08	11
G28	KB 1367	39.78	22	39.05	20	373.63	6	173.05	21	64.31	7	20.16	10	1.907	-0.129	0.068	-1.185	3.03	18	2.25	13
Gm -	Genotype mea	ın yield,	ASV	- AMM	I stabi	lity value,	D-A	MMI Dis	tance												

Table 3. AMMI estimates vis-a-vis genotypes ranking.

VERMA et al.



Fig.1. Biplot analysis of feed barley genotypes.

Yield values showed highly significant (p < 0.01) positive rank correlation with R_{GAL} , R_{Pi} , MR, CMR and highly significant negative association with CV, CCV, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ (Scapim *et al.* 2010). Yield also expressed direct low correlation with R_{CV} , S_i^3 , S_i^4 and $NP_i^{(1)}$. MR had low positive relation with $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ whereas significant positive relationship with S_i^1 , S_i^2 , S_i^3 , S_i^4 , S_i^5 and S_i^6 (Mortazavian and Azizinia 2014). S_i^1 , S_i^2 , S_i^3 , S_i^4 , S_i^5 and S_i^6 showed only direct relation with all measures and significant positive association among themselves (Zali *et al.* 2011).

Principal component (PC) analysis based on the rank correlation matrix was performed and presented in Fig. 1. Group I included the MR, R_{Gm} , R_{GAI} and R_{Pi} . Yield has been placed in first quadrant and showed right angle with the measures clustered in group 1. Measures in quadrant 2 split into two sub groups with NPi⁸ separated themselves from Si⁸ as well as with R_{Wi} , R_{Sx2} and CCV. Sub groups of NPi², NPi³ and NPi⁴ showed acute angle with yield values. However, yield maintained right angle with measures of subgroups comprises of Si⁸.

Hierarchical clustering of genotypes by Ward's method performing the cluster analysis revealed four distinct clusters among 28 genotypes: cluster I consisted of stable and low yielders genotypes G11(UPB1040), G12(UPB1042), G13(JB291), G1(HUB236), G27(NDP1578), G28(KB1367) and next cluster of seven genotypes consisted of higher yielder genotypes G20(BH946), G23(JB 290), G21(HUB113), G15(BH902), G18(PL 751), G26(RD2874), G3(NDB1580). Third cluster of nine genotypes comprised of unstable genotypes as per NPi^s with high yielder G19(RD2552). Finally, fourth cluster grouped highly unstable genotypes as per parametric, AMMI based along with non-parametric measures.

Code	Genotype	MR	CMR	SD	CSD	CV	CCV	Si^1	\mathbf{Z}^{1}	Si^2	\mathbf{Z}^2	Si^3	Si^4	Si^{5}	Si^{6}	$NP_i^{(1)}$	$\mathrm{NP_i}^{(2)}$	$\mathrm{NP_i}^{(3)}$	$NP_i^{(4)}$
G1	HUB 236	16.42	14.73	7.27	8.71	0.44	0.59	9.61	0.041	70.19	0.070	88.67	8.02	7.20	9.93	6.750	0.397	0.489	0.585
G2	KB 1353	12.33	15.91	5.91	6.95	0.48	0.44	8.09	0.768	48.24	0.833	76.36	6.65	6.17	10.65	6.167	0.536	0.539	0.656
G3	NDB 1580	12.17	13.82	6.37	6.95	0.52	0.50	8.77	0.153	57.46	0.175	90.88	7.26	6.03	10.41	6.000	0.414	0.596	0.721
G4	BH 981	14.50	14.64	8.27	9.85	0.57	0.67	11.30	1.991	96.20	2.759	107.42	9.39	8.48	10.33	8.250	0.516	0.648	0.780
G5	KB 1369	12.83	12.64	8.61	8.95	0.67	0.71	10.26	0.444	76.46	0.362	94.00	8.37	7.50	10.06	7.500	0.682	0.652	0.799
G6	HUB 237	14.58	16.45	8.98	7.72	0.62	0.47	10.03	0.255	73.24	0.184	104.30	8.19	7.08	11.00	7.083	0.443	0.562	0.688
G7	BH 982	14.50	13.55	8.51	9.15	0.59	0.68	10.67	0.918	84.19	1.033	101.24	8.79	7.58	9.94	7.500	0.484	0.606	0.736
G8	BH 980	12.08	13.09	7.84	8.34	0.65	0.64	9.91	0.175	76.07	0.337	100.37	8.35	6.58	9.48	6.583	0.693	0.691	0.820
$\mathbf{G}0$	RD 2875	17.58	16.82	10.22	10.37	0.58	0.62	12.12	3.975	120.53	8.801	127.84	10.51	9.70	11.22	9.667	0.411	0.598	0.689
G10	RD 2876	19.58	15.64	8.49	9.35	0.43	0.60	10.76	1.046	86.28	1.274	101.49	8.89	7.98	10.24	7.750	0.323	0.454	0.549
G11	UPB 1040	18.42	13.82	4.60	6.03	0.25	0.44	6.62	3.697	34.65	2.697	63.20	5.64	4.33	8.62	4.333	0.228	0.306	0.360
G12	UPB 1042	19.25	15.27	5.53	6.72	0.29	0.44	7.65	1.414	43.63	1.345	71.38	6.32	5.21	9.30	5.167	0.265	0.329	0.397
G13	JB 291	15.25	13.64	7.55	7.78	0.49	0.57	8.62	0.249	55.47	0.276	78.47	7.13	6.56	10.13	6.333	0.396	0.468	0.565
G14	PL 880	12.08	15.73	8.82	8.88	0.73	0.56	10.38	0.567	82.11	0.819	101.74	8.68	7.45	10.08	7.167	0.623	0.718	0.859
G15	BH 902	10.92	13.45	7.49	6.12	0.69	0.45	8.09	0.768	53.30	0.411	95.78	6.99	6.02	11.79	5.333	0.464	0.640	0.741
G16	PL 881	15.25	15.36	11.00	12.05	0.72	0.78	13.23	7.735	132.06	12.854	120.53	11.00	10.33	10.29	10.333	0.590	0.721	0.867
G17	ITOYL	13.67	14.45	8.13	8.78	0.59	0.61	9.79	0.110	70.26	0.072	88.03	8.03	6.76	9.24	6.667	0.460	0.587	0.716
G18	PL 751	12.75	12.55	7.00	5.65	0.55	0.45	7.70	1.338	47.97	0.860	93.46	6.63	5.25	11.16	5.250	0.457	0.520	0.604
G19	RD 2552	9.42	9.64	7.89	8.36	0.84	0.87	9.06	0.034	64.01	0.004	84.25	7.66	6.33	9.09	6.333	0.792	0.813	0.962
G20	BH 946	8.58	16.55	6.20	6.93	0.72	0.42	8.24	0.590	50.34	0.640	79.87	6.79	6.00	10.38	6.000	1.091	0.791	0.960
G21	HUB 113	10.25	17.09	7.17	7.85	0.70	0.46	9.82	0.125	71.66	0.118	100.36	8.10	7.17	10.95	7.167	0.896	0.791	0.958
G22	RD 2786	13.92	14.18	8.47	9.79	0.61	0.69	10.83	1.159	87.06	1.370	97.86	8.93	8.03	9.85	8.000	0.727	0.642	0.778
G23	JB 290	11.75	15.09	6.90	6.86	0.59	0.45	8.30	0.526	50.32	0.642	80.67	6.79	6.18	10.81	6.000	0.500	0.578	0.707
G24	RD 2877	19.33	14.00	8.57	10.51	0.44	0.75	11.68	2.825	101.18	3.718	105.93	9.63	8.92	10.18	8.417	0.366	0.498	0.604
G25	UPB 1041	17.25	16.64	8.06	8.18	0.47	0.49	10.12	0.324	77.68	0.445	104.51	8.44	7.50	11.01	7.500	0.417	0.489	0.587
G26	RD 2874	12.83	13.64	6.56	6.50	0.51	0.48	7.68	1.363	43.34	1.382	73.35	6.30	5.25	9.69	5.250	0.375	0.491	0.599
G27	NDB 1578	17.33	12.73	7.77	8.11	0.45	0.64	9.56	0.029	67.65	0.017	91.73	7.87	6.67	9.86	6.667	0.333	0.454	0.552
G28	KB 1367	18.50	14.91	6.04	7.25	0.33	0.49	8.26	0.574	50.08	0.663	76.03	6.78	5.85	9.69	5.667	0.283	0.366	0.446
			$E(S^1)$	= 9.321	$E(S^2)=$	65.25			33.192		44.162			$V(S^1) =$	1.972	$V(S^2) =$	347.26		

Table 4. Descriptive statistics and non-parametric measures.



Fig. 2. Ward's clustering of genotypes.

Non-parametric (Thennarasu 1995) indices expressed the consistent performance of G11 (UPB1040), G12 (UPB1042) for stable yield as compared to G20 (BH 946), G21 (HUB113) along G19 (RD2552) as unstable genotypes (Table 4). The selection of $NP_i^{(1)}$ was different from rest three NP^s towards G16(PL881) as unstable genotype (Truberg and Hühn (2000).

Parametric methods may not perform well if certain assumptions are violated. Non-parametric measures provide a useful alternative. These considerations supported the use of different parametric and non-parametric methods. Biplot analysis revealed strong to moderate association among parametric / non-parametric measures. Results favour the genotypes G20(BH946), G19(RD2552) and G21(HUB113) for further inclusion in the breeding program.

Acknowledgements

The multi-environment trials of feed barley genotypes were performed at AICW&BIP centers across the country. Authors sincerely acknowledge the hard work of the staffs at these centers to carry out the field layout and data recording.

References

Annicchiarico P, Bellah F and Chiari T 2005. Defining sub regions and estimating benefits for a specificadaptation strategy by breeding programs. Crop Sci. 45: 1741-1749.

- Farshadfar E, Mahmudi N and Sheibanirad A 2014. Non-parametric methods for interpreting genotype×environment interaction in bread wheat genotypes. J. Biol. & Env. Sci. 4: 55-62.
- Francis TR and Kannenberg LW 1978. Yield stability studies in the short season maize. I. A descriptive method for grouping genotypes. Can. J. Pl. Sci. **58**: 1029-1034.

- Huehn M 1990. Non-parametric measures of phenotypic stability: Part 2. Application. Euphytica 47: 195-201.
- Hussein MA, Bjornstad A and Aastveit AH 2000. SASG × ESTAB: A SAS program for computing genotype × environment stability statistics. Agron. J. 92: 454-459.
- Kang MS and Pham HN 1991. Simultaneous selection for high yielding and stable crop genotypes. Agron. J. **83**:161-165.
- Karimizadeh R, Mohammadi M, Sabaghnia N and Shefazadeh MK 2012. Using Huehn's nonparametric stability statistics to investigate genotype × environment interaction. Not. Bot. Horti. Agrobo. 40: 195-200.
- Lin CS and Binns MR. 1988. A superiority measure of cultivar performance for cultivar \times location data. Can. J. Pl. Sci. 68: 193-198.
- Lin CS, Binns MR and Lefkovitch LP 1986. Stability analysis: where do we stand? Crop Sci. 26: 894-900.
- Mohammadi R and Ahmed A 2008. Comparison of parametric and non-parametric methods for selecting stable and adapted durum wheat genotypes in variable environments. Euphytica 159: 419-432.
- Mohammadi R, Farshadfar E and Amri A 2016. Comparison of rank-based stability statistics for grain yield in rainfed durum wheat. New Zealand J. Crop & Hort. Sci. 44(1): 25-40.
- Mohammadi R and Amri A 2008. Analysis of genotype \times environment interaction for grain yield in durum wheat. Crop Sci. 49: 1177-1186.
- Mortazavian SMM and Azizinia S 2014. Non-parametric stability analysis in multi-environment trial of canola. Tur. J. Field Crops. 19(1): 108-117.
- Nassar R and Huehn M 1987. Studies on estimation of phenotypic stability: Tests of significance for nonparametric measures of phenotypic stability. Biometrics 43: 45-53.
- Purchase JL, Hatting H and Van Deventer CS 2000. Genotype × environment interaction of winter wheat in south Africa: II. Stability analysis of yield performance. S Afr. J. Plant Soil. 17(3): 101-107.
- Scapim CA, Pacheco CAP, do Amaral ATJúnior, Vieira RA, Pinto RJB and Conrado TV 2010. Correlations between the stability and adaptability statistics of popcorn cultivars. Euphytica **174**: 209-218.
- Sisay A and Sharma M 2016. Parametric and non-parametric methods to describe genotype by environment interaction and grain yield stability of bread wheat. Stat. & App. 14(1&2): 9-29.
- Suadric A, Simic D and Vrataric M 2006. Characterization of genotype by environment interactions in soybean breeding programmes of southeast Europe. Pl. Breed. 125: 191-194.
- Thennarasu K 1995. On certain non-parametric procedures for studying genotype \times environment interactions and yield stability. Ph.D. Thesis. P.J. School, IARI, New Delhi, India.
- Truberg B and Hühn M 2000. Contributions to the analysis of genotype × environments interactions: Comparison of different parametric and non-parametric tests for interactions with emphasis on crossover interaction. J. Agron. Crop Sci. 185: 267-274.
- Ward JH 1963. Hierarchical grouping to optimize an objective function. J. Amer. Stat. Assoc. 58: 236-224.
- Wricke G 1962. Über eine Methode zur Erfassung der ökologischen Streubreite in Feldversuchen. Z. Pflanzenzüchtg 47: 92-96.
- Zali H, Farshadfar E and Sabaghpour H 2011. Non-parametric analysis of phenotypic stability in chickpea (Cicer arietinum L.) genotypes in Iran. Crop Breed. J. 1: 85-96.
- Zhang Z, Lu C and Xiang ZH 1998. Analysis of variety stability based on AMMI model. Acta Agron. Sin. **24**: 304-309.

(Manuscript received on 17 June, 2017; revised on 12 September, 2018)