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RANK BASED STABILITY MEASURES TO SELECT STABLE AND ADAPTED DUAL PURPOSE BARLEY (*Hordeum vulgare* L) GENOTYPES

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KEYWORDS

GxE interaction

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ABSTRACT

Seventeen promising dual purpose barley genotypes were evaluated at eleven major barley producing locations of the country by distribution free nonparametric measures. Average forage yield identified higher yielder genotypes as RD2928, RD2927 and JB325 while descriptive statistics pointed out towards KB1420, RD2927 and KB1401 & JB322. Nonparametric measures showed highly significant positive correlation among these measures. More over S_i^6 expressed no correlation with measures based on corrected yield values. Ward's method of clustering based on 21 nonparametric measures along with average forage yield, clustered the with higher to moderate yielding genotypes into group comprised of RD29276, AZAD, UPB1053, RD2552, BH1010 and KB1401 genotypes. Descriptive statistics based on grain yield MR pointed towards RD2925, BH1008 and SD for KB1401, UPB1054 whereas CV for JB322, RD2925 as stable genotypes at the same time AZAD, NDB1650 based on MR, UPB1053, RD2715 based on SD and AZAD, RD2035 based on CV were most unstable. Spearman's rank correlation established highly significant positive correlation of mean yield with SD, S_i^1 , S_i^2 , S_i^5 , S_i^7 whereas negative association was observed for MR, Med. $NP_i^{(2)}$ expressed negative correlation with CV, S_i^6 , MR and Med. $NP_i^{(3)}$ showed negative correlation of low magnitude with other considered measures.

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1 Introduction

Traditionally barley considered as a poor man's crop owing to low inputs requirement (Kharub et al., 2013). Barley provides green fodder at vegetative stage to supplement nutrition of animals and grains can be harvested from the regenerated plants additionally. Farm economics favors the cultivation of dual purpose instead of barley crop for grain only. Now the cultivation of dual purpose barley proved to be a boon to meet out forage as well as food requirements of the farmers for sustaining livelihood.

Genotype x environment interaction complicates the selection of genotypes for improved yield (Adugna & Labuschagne, 2003). Researchers have highlighted the importance of changes in cultivars rank in multi environments trials as evident from literature (Dorostkara et al., 2015). Non parametric measures were based on ranks and stable genotypes possess relatively constant rank across environments (Asghar et al., 2008; Delić et al, 2009). Large number of nonparametric procedures namely Huehn (1979), Huehn & Leon (1995), Thennarasu (1995) and Farshadfar et al., (2014) had developed to interpret the GxE interaction in multi-environmental trials (MET). Also, Khalili & Aboughadareh (2016) have proposed some procedures to test the GxE interaction apart from methods based on analysis of variance. Among these nonparametric procedures, stable performance of genotypes

evaluated under in MET were determined by Huehns' statistics (Balalić et al., 2011; Lima et al., 2013; Farshadfar et al., 2014). The objectives of this study were to apply nonparametric measures to estimate GxE interaction in coordinated trials to identify stable dual purpose barley genotypes possess high forage and grain yield. The relationships among nonparametric measures for evaluating stable yield performance of genotypes were also examined.

2 Materials and Methods

Seventeen dual purpose barley genotypes were evaluated at 11 locations during 2015-2016 cropping season by randomized block designs with three replications. Parentage details and environmental conditions had reflected in table 1 for ready reference. Zone wise agronomical recommendations were followed to harvest good forage yield. The forage and grain yield of these genotypes were further analyzed statistically to calculate non parametric measures. Huehn (1979) and Huehn (1990) proposed seven nonparametric methods for assessing GxE interaction and stability analysis. The rank of i^{th} genotype in j^{th} environment was denoted as r_{ij} calculated from X_{ij} where $i = 1, 2, \dots, k$ with $j = 1, 2, \dots, n$ and mean rank for i -th genotype over all environments was $\bar{r}_i$. Commonly used non parametric measures based on ranks were explained below:

Table 1 Parentage details of dual purpose genotypes along with environmental conditions

Code	Genotype	Parentage	Code	Environments	Latitude	Longitude	Altitude (m)
IVTIRTS DP-2	RD2715	RD387/BH602/RD2035					
IVTIRTS DP-3	UPB1054	IBYT-LRA-M-12					
IVTIRTS DP-4	KB1420	EIBGN(13)-7					
IVTIRTS DP-5	BH1008	EIBGN-9/BH902(2009)	E1	Durgapura	26° 51 'N	75° 47 'E	390
IVTIRTS DP-6	RD2927	RD2624/RD2696	E2	Bikaner	28° 02' N	73° 31' E	225.3
IVTIRTS DP-7	RD2035	RD103/PL101	E3	Ludhiana	30° 54' N	75° 52 'E	247
IVTIRTS DP-8	BH1010	BHMS22A/WG81	E4	Hisar	29° 10' N	75° 46 'E	215.2
IVTIRTS DP-9	JB325	RD2615/DL88	E5	Varanasi	25° 20 'N	83° 03 'E	75.5
IVTIRTS DP-10	RD2925	RD2606/RD2719/RD2660	E6	Kanpur	26° 29 'N	80° 18 'E	125.9
IVTIRTS DP-11	AZAD	K12/K19	E7	Faizabad	26° 47 'N	82° 12 'E	113
IVTIRTS DP-12	RD2552	RD2035/DL472	E8	Rewa	24° 31 'N	81° 15 'E	365.7
IVTIRTS DP-13	KB1401	IBYT-HI (13)-14	E9	Kota	25° 21' N	75° 86 'E	259.7
IVTIRTS DP-14	UPB1053	IBYT-MRA-12	E10	Udaipur	24° 34 'N	70° 42 'E	582
IVTIRTS DP-15	JB319	LAKHAN/BH353	E11	Jabalpur	23 ° 90' N	79° 58 'E	394
IVTIRTS DP-16	RD2928	RD2552/BH902					
IVTIRTS DP-17	JB322	JB101/BH331					
IVTIRTS DP-18	NDB1650	38th IBON-9030 (2006-07)/NB3					

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

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

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

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

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

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

$$S_i^{(7)} = \frac{\sum_{j=1}^n (r_{ij} - \bar{r}_i)^2}{(n-1)}$$

Further, Huehn (1990) proposed the correction for the trait value of i^{th} genotype in j^{th} environment as X_{ij}^* ($X_{ij}^* = X_{ij} - \bar{X}_i + \bar{X}_.$), was the corrected phenotypic value; $\bar{X}_i$ was the mean i^{th} genotype in all environments and $\bar{X}_.$ was the grand mean. These measures were also calculated based on corrected phenotypic data points (Sabaghnia et al., 2012).

Non parametric stability measures of Thennarasu (1995) based on the ranks as per adjusted means were also studied for completeness. 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 (unadjusted) traits, where $\bar{r}_i^*$ and M_{di}^* were the same parameters computed from the corrected (adjusted) trait values.

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

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

$$NP_i^{(3)} = \frac{\sqrt{\sum_{j=1}^m (r_{ij}^* - \bar{r}_i^*)^2 / m}}{\bar{r}_i^*}$$

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

SAS-based computer program of SASGESTAB (Hussein et al., 2000) exploited to calculate nonparametric measures. SAS version 9.3 and Microsoft Excel, were used to calculate different uncorrected and corrected nonparametric stability statistics. Spearman's rank correlation coefficient calculates the correlation among each possible pairs as follows :

$$\bar{r}_s = 1 - \frac{6 \sum_{i=1}^n d_i^2}{n(n^2-1)}$$

d_i = difference between two ranks of considered traits; n = number of correlated pairs.

3 Results and Discussion

Nonparametric statistical analysis based on forage yield of barley genotypes presented in Table 2. According to average forage

Table 2 Descriptive statistics and non parametric measures based on forage yield values

Forage yield	Genotype	Yield (q/ha)	MR	SD	CV	Med	S_i^1	S_i^2	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
IVTIRTS DP-2	RD2715	169.01	9.64	5.01	0.52	10.00	5.25	5.32	26.00	4.77	4.28	4.89	25.05	5.720	0.817	0.682	0.751
IVTIRTS DP-3	UPB1054	127.05	7.64	6.87	0.90	5.00	6.95	6.99	61.88	6.55	6.15	8.86	47.25	2.175	0.155	0.622	0.659
IVTIRTS DP-4	KB1420	115.82	7.82	6.31	0.81	4.00	6.33	6.23	50.86	6.01	5.80	8.16	39.76	1.984	0.124	0.441	0.464
IVTIRTS DP-5	BH1008	151.93	8.64	5.05	0.58	8.00	5.16	5.67	29.47	4.81	4.08	5.20	25.45	3.982	0.664	0.569	0.611
IVTIRTS DP-6	RD2927	178.84	10.64	4.70	0.44	13.00	4.64	5.12	20.74	4.48	3.92	4.05	22.05	9.084	1.817	0.880	0.911
IVTIRTS DP-7	RD2035	160.86	8.27	5.18	0.63	7.00	5.45	5.44	32.42	4.94	4.48	5.96	26.82	2.835	0.709	0.705	0.779
IVTIRTS DP-8	BH1010	147.51	9.09	2.77	0.31	9.00	2.78	3.07	8.46	2.64	2.28	2.76	7.69	6.719	0.560	0.240	0.253
IVTIRTS DP-9	JB325	175.66	9.45	5.48	0.58	9.00	5.91	6.08	31.81	5.23	4.50	5.23	30.07	4.505	1.126	0.871	0.985
IVTIRTS DP-10	RD2925	155.80	8.64	4.43	0.51	9.00	4.47	5.81	22.76	4.23	3.07	3.91	19.65	5.927	0.659	0.505	0.535
IVTIRTS DP-11	AZAD	151.50	9.45	4.76	0.50	11.00	4.53	5.56	23.98	4.54	3.70	4.31	22.67	7.295	0.730	0.446	0.445
IVTIRTS DP-12	RD2552	157.45	9.64	2.66	0.28	8.00	2.76	2.83	7.32	2.53	2.27	2.59	7.05	5.735	0.717	0.320	0.349
IVTIRTS DP-13	KB1401	140.89	8.09	3.78	0.47	6.00	3.60	4.27	17.66	3.60	3.04	4.13	14.29	3.125	0.284	0.336	0.336
IVTIRTS DP-14	UPB1053	144.57	8.82	4.53	0.51	8.00	4.76	5.44	23.32	4.32	3.44	4.29	20.56	4.595	0.459	0.432	0.476
IVTIRTS DP-15	JB319	155.61	8.91	5.19	0.58	9.00	5.35	5.96	30.18	4.94	4.10	5.06	26.89	4.901	0.613	0.625	0.676
IVTIRTS DP-16	RD2928	182.84	11.64	5.95	0.51	15.00	6.00	6.52	30.47	5.68	4.94	4.67	35.45	10.058	2.515	0.991	1.048
IVTIRTS DP-17	JB322	129.50	8.18	5.46	0.67	7.00	5.85	5.89	36.38	5.20	4.59	6.18	29.76	2.736	0.195	0.430	0.484
IVTIRTS DP-18	NDB1650	141.41	8.45	5.47	0.65	6.00	5.80	5.59	35.33	5.21	4.86	6.32	29.87	1.786	0.162	0.507	0.565

yield, genotype RD2928 (182.8 q/ ha) was the highest yielder followed by RD2927 and JB325, although remarkable differences (127 to 182) were observed for forage yield of dual purpose barley genotypes. Three descriptive statistics; mean of ranks (MR), standard deviation of ranks (SD) and coefficient of variation of ranks (CV) based on corrected forage yield were calculated. As per values of these statistics, genotypes RD2928, RD2927, BH1010 RD2552 were the stable, while UPB1054, KB1420 based on MR, SD and CV, were identified as the unstable genotypes. These simple descriptive statistics based on ranks able to discriminate genotypes (Karimizadeh et al., 2012). Nonparametric measures ($S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6$ and S_i^7) suggested BH1010 and RD2552 were the stable genotypes, however most of the these measures isolated UPB1054, KB1420 as the most unstable genotypes (Table 2). Nonparametric stability indices i.e. $NP_i^{(1)}$ pointed towards NDB1650 and RD2928 as stable and unstable while, $NP_i^{(2)}$ showed the KB1420 and RD2928 as stable and unstable, $NP_i^{(3)}$ found out BH1010 and RD2927 and $NP_i^{(4)}$ identified BH1010 & JB325 as the stable genotypes and overall by most of measures RD2927 & RD2928 were unstable genotypes (Parmar et al., 2012).

As per average grain yield of dual purpose barley genotypes, RD2552 was the highest yielding genotype with 32.9q/ha

followed by RD2035, although not large differences (23 to 32) were evident among the studied genotypes (Table 3). The three descriptive statistics MR, SD and CV were calculated based on corrected yield. MR pointed towards KB1401 & BH1010 and SD for RD2552 & JB322 whereas CV for NDB1650 & JB322 as stable genotypes, while KB1401 & BH1010 based on MR, UPB1053 & RD2715 based on SD and RD2715 & RD2927 based on CV, were of unstable nature. These descriptive statistics were able to discriminate genotype comparative performance (Sabaghnia et al., 2012). Seven nonparametric measures based on grain yield of genotypes ($S_i^1, S_i^2, S_i^3, S_i^4, S_i^5, S_i^6$ and S_i^7) indicated that UPB1054 & JB322 by S_i^1 , JB322 & RD2552 by S_i^2 , while S_i^3 & S_i^4 pointed towards JB322, NDB1650 and RD2552 & NDB1650 by S_i^5, S_i^6 RD2552 and JB322 by S_i^7 as stable genotypes, however UPB1053, RD2715 & RD2927 were unstable genotypes by these measures (Khalili & Aboughadareh, 2016).

Nonparametric stability indices i.e. $NP_i^{(1)}$ pointed towards RD2927 and RD2928 as stable while, $NP_i^{(2)}$ showed the RD2928 and RD2715 as stable, $NP_i^{(3)}$ found out JB322 and RD2925 and $NP_i^{(4)}$ identified RD2925 & JB322 as the stable genotypes while UPB1034, Azad & RD2035 were of unstable performance by stability measures.

Table 3 Descriptive statistics and non parametric measures based on grain yield

Grain yield	Genotype	Yield (q/ha)	MR	SD	CV	Med	S_i^1	S_i^2	S_i^3	S_i^4	S_i^5	S_i^6	S_i^7	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
IVTIRTSDP-2	RD2715	23.64	7.55	6.31	0.84	6.00	6.44	6.59	52.84	6.02	5.50	8.02	39.87	2.050	0.158	0.538	0.576
IVTIRTSDP-3	UPB1054	30.32	9.73	4.27	0.44	11.00	3.91	4.64	18.73	4.07	3.57	4.04	18.22	7.430	1.238	0.589	0.566
IVTIRTSDP-4	KB1420	28.05	10.09	5.24	0.52	11.00	5.11	5.88	27.24	5.00	4.25	4.63	27.49	6.752	0.675	0.495	0.506
IVTIRTSDP-5	BH1008	24.57	8.55	5.05	0.59	8.00	5.22	5.99	29.81	4.81	3.87	4.98	25.47	4.214	0.351	0.427	0.463
IVTIRTSDP-6	RD2927	26.59	7.73	5.82	0.75	5.00	5.58	5.96	43.76	5.54	5.16	7.34	33.82	1.577	0.175	0.629	0.633
IVTIRTSDP-7	RD2035	32.76	9.45	5.99	0.63	8.00	6.40	6.24	37.94	5.71	5.22	6.08	35.87	2.859	0.477	0.872	0.978
IVTIRTSDP-8	BH1010	28.06	10.36	4.86	0.47	10.00	4.98	5.10	22.82	4.64	4.21	4.47	23.65	5.785	0.643	0.440	0.472
IVTIRTSDP-9	JB325	27.37	7.82	4.26	0.55	8.00	4.53	5.02	23.23	4.06	3.29	4.63	18.16	4.711	0.471	0.447	0.498
IVTIRTSDP-10	RD2925	23.34	7.64	5.32	0.70	6.00	5.22	5.55	37.00	5.07	4.63	6.67	28.25	1.865	0.133	0.401	0.413
IVTIRTSDP-11	AZAD	31.96	9.09	4.95	0.54	10.00	5.36	5.71	26.94	4.72	3.90	4.72	24.49	6.099	2.033	0.837	0.952
IVTIRTSDP-12	RD2552	32.88	9.45	3.62	0.38	9.00	3.84	4.16	13.83	3.45	2.86	3.33	13.07	6.141	1.228	0.593	0.659
IVTIRTSDP-13	KB1401	29.06	10.64	5.10	0.48	13.00	5.20	5.53	24.50	4.87	4.28	4.43	26.05	8.720	0.969	0.500	0.535
IVTIRTSDP-14	UPB1053	29.43	9.36	6.17	0.66	8.00	6.76	6.30	40.64	5.88	5.49	6.45	38.05	2.578	0.430	0.703	0.809
IVTIRTSDP-15	JB319	27.29	8.64	4.15	0.48	9.00	4.36	4.75	19.98	3.96	3.31	4.21	17.25	5.695	0.518	0.431	0.475
IVTIRTSDP-16	RD2928	24.55	8.18	5.69	0.70	6.00	5.75	5.76	39.56	5.42	5.11	6.87	32.36	1.736	0.158	0.523	0.554
IVTIRTSDP-17	JB322	26.14	9.00	3.74	0.42	7.00	4.07	4.12	15.56	3.57	3.09	3.78	14.00	3.909	0.355	0.335	0.383
IVTIRTSDP-18	NDB1650	32.64	9.73	3.98	0.41	10.00	4.11	5.40	16.26	3.79	2.66	3.01	15.82	7.339	1.223	0.695	0.753

3.1 Clustering of genotypes by Ward method

Hierarchical cluster analysis of dual purpose barley genotypes by Ward's method (Ward, 1963) based on nonparametric measures along with average forage yield, classified the genotypes into major groups (Figure 1). Two major clusters were observed by using the squared Euclidean distance as dissimilarity measure. Group 1 included the high yielding genotypes RD2927, BH1010, RD2552 and JB325. These genotypes were identified stable genotypes by rank measures. Most of the unstable genotypes, clustered as separate group with UPB1054 & KB1420.

The cluster analysis based on grain yield and nonparametric measures revealed two distinct clusters among seventeen genotypes: cluster A consisted of higher to good yielder genotypes RD2552, NDB1650, UPB1054 and AZAD and cluster B consisted of unstable JB319, JB325, JB322 genotypes. Low yielder and unstable genotypes put together in separate cluster as reported by Karimizadeh et al. (2012).

3.2 Association among nonparametric measurements

Highly significant ($p < 0.01$) positive rank correlation of forage yield observed with mean rank, median, as well as with corrected median (Table 3). Yield showed highly significant negative correlation with rank mean, median, $NP_1^{(1)}$, $NP_1^{(2)}$, $NP_1^{(3)}$ and $NP_1^{(4)}$ whereas negative correlation of moderate magnitude with CV, Si^3 , Si^6 as reflected by Scapim et al. (2010). Rank mean showed highly significant positive correlation ($p < 0.01$) with Median, $NP_1^{(1)}$, and $NP_1^{(2)}$ at the same time moderate to significant negative relation with Si^2 , Si^3 , Si^4 , Si^5 and CV & Si^6 . SD indicated

significant positive association with CV, Si^1 , Si^2 , Si^3 , Si^4 , Si^5 , Si^6 and moderate with $NP_1^{(3)}$, $NP_1^{(4)}$. Significant positive correlation seen among Si^1 , Si^2 , Si^3 , Si^4 , Si^5 , Si^6 measures. Similar trend of positive relationship expressed by $NP_1^{(1)}$, $NP_1^{(2)}$, $NP_1^{(3)}$ and $NP_1^{(4)}$. Forage yield expressed low negative correlation with Si^1 , Si^2 , Si^3 , Si^4 , Si^5 and Si^6 (Table 3). Correlation analysis of grain yield exhibited highly significant positive SD, CV, Si^1 , Si^2 , Si^3 , Si^4 , Si^5 , Si^6 while negative with MR & CV (Scapim et al., 2010). Whereas low magnitude of negative and positive values of coefficient with $NP_1^{(1)}$, $NP_1^{(2)}$, $NP_1^{(3)}$ and $NP_1^{(4)}$. MR expressed highly significant negative to moderate correlation with CV, Median $NP_1^{(1)}$ & moderate negative with $NP_1^{(2)}$, Si^1 , Si^2 , Si^3 , Si^4 , Si^5 , Si^6 (Mahtabi et al., 2013). Highly significant ($p < 0.01$) positive rank correlation maintained by SD with CV, Si^1 , Si^2 , Si^3 , Si^4 , Si^5 , Si^6 , Median. SD showed highly significant positive rank correlation with Si^1 , Si^2 , Si^3 , Si^5 , SD, CV, Si^1 , Si^2 , Si^3 , Si^4 , Si^5 , Si^6 and Si^7 . Highly significant positive correlation of CV with Si^1 , Si^2 , Si^3 , Si^4 , Si^5 , Si^6 except negative with Median. Significant positive relationship observed among Si^8 . Similar pattern of positive nature was also revealed in $NP_1^{(5)}$. More or less $NP_1^{(5)}$ had negative correlation of low magnitude with other measures (Rasoli et al., 2015). Grain yield had low values of correlation with $NP_1^{(5)}$ as observed by Karimizadeh et al. (2012).

Nonparametric measures, being distribution free, proved to be useful alternative to parametric statistics (Farshadfar et al., 2014; Rasoli et al., 2015). Average yield and stability considered simultaneously to quantify GxE interactions and to make precise selection of promising genotype. RD2927 and RD2552 may be recommended as favorable genotype in terms of forage and grain

Figure 1 Hierarchical cluster analysis of dual purpose barley genotypes based on forages and grain yield by Ward's method

Table 4 Correlation analysis among non parametric measures based on forage yield

	Yield	MR	SD	CV	Med	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⁾
MR	0.825														
SD	-0.157	-0.337													
CV	-0.397	-0.656	0.850												
Med	0.781	0.887	-0.317	-0.565											
C Si1	-0.152	-0.357	0.983	0.863	-0.347										
C Si2	-0.151	-0.319	0.879	0.778	-0.169	0.854									
C Si3	-0.328	-0.548	0.944	0.949	-0.506	0.946	0.808								
C Si4	-0.151	-0.350	0.999	0.857	-0.328	0.984	0.870	0.950							
C Si5	-0.162	-0.352	0.978	0.846	-0.357	0.980	0.805	0.949	0.979						
C Si6	-0.404	-0.616	0.895	0.949	-0.602	0.890	0.705	0.971	0.901	0.900					
C Si7	-0.157	-0.337	1.000	0.850	-0.317	0.983	0.879	0.944	0.999	0.978	0.895				
NP _i ¹	0.681	0.844	-0.488	-0.765	0.906	-0.512	-0.303	-0.674	-0.501	-0.512	-0.779	-0.488			
NP _i ²	0.946	0.879	-0.199	-0.490	0.835	-0.213	-0.188	-0.382	-0.197	-0.216	-0.446	-0.199	0.765		
NP _i ³	0.659	0.335	0.532	0.292	0.381	0.522	0.440	0.370	0.540	0.527	0.314	0.532	0.174	0.576	
NP _i ⁴	0.652	0.308	0.556	0.360	0.339	0.574	0.469	0.419	0.565	0.559	0.350	0.556	0.105	0.537	0.971

Critical values of Spearman correlation at 5% and 1% level of significance (df 15) are 0.521 & 0.604 respectively

Table 5 Correlation analysis among non parametric measures based on grain yield

	Yield	MR	SD	CV	Med	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⁾
MR	-0.616														
SD	0.895	-0.337													
CV	0.949	-0.656	0.850												
Med	-0.602	0.887	-0.317	-0.565											
C Si1	0.890	-0.357	0.983	0.863	-0.347										
C Si2	0.705	-0.319	0.879	0.778	-0.169	0.854									
C Si3	0.971	-0.548	0.944	0.949	-0.506	0.946	0.808								
C Si4	0.901	-0.350	0.999	0.857	-0.328	0.984	0.870	0.950							
C Si5	0.900	-0.352	0.978	0.846	-0.357	0.980	0.805	0.949	0.979						
C Si6	1.000	-0.616	0.895	0.949	-0.602	0.890	0.705	0.971	0.901	0.900					
C Si7	0.895	-0.337	1.000	0.850	-0.317	0.983	0.879	0.944	0.999	0.978	0.895				
NP _i ¹	0.282	-0.580	0.100	0.154	-0.688	0.027	0.004	0.159	0.089	0.049	0.282	0.100			
NP _i ²	0.195	-0.343	0.055	0.023	-0.483	-0.021	-0.074	0.107	0.051	0.009	0.195	0.055	0.891		
NP _i ³	-0.010	0.141	-0.061	-0.181	-0.060	-0.049	-0.298	-0.044	-0.045	0.002	-0.010	-0.061	0.061	0.406	
NP _i ⁴	-0.017	0.170	-0.074	-0.181	-0.048	-0.061	-0.308	-0.054	-0.058	-0.012	-0.017	-0.074	0.059	0.398	0.993

Critical values of Spearman correlation at 5% and 1% level of significance (df 15) are 0.521 & 0.604 respectively

yield (Table 4). This genotype was the most stable genotype based on corrected (static concept). Both genotypes could be regarded as good candidates for other environments of the country. Nonparametric tests for interactions provided more specific information about the nature of GE interactions (Rasoli et al., 2015; Mohammadi et al., 2016). The main purpose of barley improvement programs is to sustain higher yield with stability.

Genotypes RD2927 and RD2552 were identified as stable barley genotypes as far as considered non parametric measures. Highly significant positive rank correlation of forage yield observed with mean rank, median, corrected median whereas grain yield exhibited highly significant positive correlation with non parametric measures S_i¹, S_i², S_i³, S_i⁴, S_i⁵ and S_i⁶ (Table 5).

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