Parametric vis-a-vis non parametric measures describing G x E interactions for salt salinity tolerant barley genotypes in multi-environment trials

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Abstract
GxE interaction to know adaptability of 19 salt salinity tolerant barley genotypes was studied by parametric and non-parametric measures. Genotypes KB1516, RD2907 and RD2794 showed minimum environmental variance over different environments. Superiority index identified genotypes RD2907 and NDB1445 with lowest value accompanied with higher. Wricke's measure exhibited lower values of DWRB168, DWRB165 and NDB1445. Higher values of GAI showed consistent performance of RD2907, NDB1445 and RD2552. Non-parametric measures $S_i^{(1)}$, $S_i^{(3)}$ and $S_i^{(6)}$ the considered DWRB165 and DWRB168 as desirable genotypes. Thennarasu's first measure $NP_i^{(1)}$ found DWRB168 and NDB1445 as desirable adaptable and KB1546, RD2907 and NDB1173 were unstable genotypes. Wricke's parameter was positively correlated with $NP_i^{(1)}$, $NP_i^{(3)}$ and Kang. GAI had significant positive with P_i and Kang while negative with $S_{i(6)}$, $NP_{i(2)}$ & $NP_{i(4)}$. Worth to mention the negative association of P_i with $S_{i(6)}$, $NP_i^{(2)}$, $NP_i^{(4)}$. Non parametric measures $S_i^{(3)}$ $S_i^{(6)}$ $NP_i^{(2)}$ & $NP_i^{(4)}$ clubbed together while Kang, W_i^2, s^2_i, $S_i^{(1)}$, $S_i^{(2)}$, $NP_i^{(1)}$ & $NP_i^{(3)}$ joined in another cluster. Left over parametric measures were grouped in two separate clusters i.e. (b_i, S^2_{xi}, CV_i), (Yield, GAI P_i) respectively. Biplot analysis based on first two principal components showed three groups among the measures.

Keywords: Adaptability G x E interaction, Parametric and nonparametric measures, Salinity tolerant barley

INTRODUCTION

Genotype x environment interactions had been exploited for better adaptation of genotypes in a broad range of environments (Baxevanos *et al.,* 2008). Genotypes with stable trait expression across environments contribute little to GxE interaction and performance would be predictable from the main effects of genotypes and environments (Henryk *et al.,* 2014). Statistical methods have been proposed for the adaptability analysis, with the prime aim to explain the GxE interaction (Dehghani *et al.,* 2016). Mostly two approaches had been highlighted in literature for the G x E interaction to determine the adaptation of genotypes (Elahe *et al.,* 2015). First one is parametric which relies on distributional assumptions about the genotypes, environments and G x E effects. The second approach is known as non-parametric independent of assumptions about the distribution of the model residuals and homogeneity of variances. Moreover these methods would supplement and complement each other to interpret genotype by environment interaction. Each method has its own merits and weaknesses, and each method represents a specific way of looking at the

phenomenon of genotype by environment interaction (Van Eeuwijk *et al.*, 2001). Now a days breeding programs are incorporating elements of both parametric and nonparametric measures (Mohammadi and Amri, 2008, Sisay and Sharma, 2016).

Prime objectives of the study were to (1) analyze GxE interactions on yield of 19 barley genotypes under salt salinity trials (2) identify barley genotypes that have high yield and stable performance across different environments (3) study the relationship among parametric and non parametric measures.

MATERIALS AND METHODS

Parametric measures i.e. Regression coefficient (Finlay and Wilkinson, 1963), Environmental variance (Becker and Leon, 1988), Shukla variance (1972), Ecovalence (Wricke's, 1962), Coefficient of variation (Francis and Kanenberg 1978), Superiority index (Lin and Binns, 1988), Geometric adaptability index (Mohammadi and Amri, 2008), Kang's rank sum (1988) ; were studied to estimate g x e interaction for nineteen salt salinity tolerant barley genotypes evaluated at 06 locations. Treatments were laid in field trials by Randomized block design with four replications. Recommended agronomical practices were utilized to harvest the good crop and yield was considered for further analysis. Non parametric measures of Hühn and Nassar (1989) were considered to study adaptability behavior proposed based on ranks of genotypes and use the idea of homeostasis as measure of the stability. Additionally four non parametric measures of Thennarasu's (1995) based on adjusted ranks of genotypes within each test environments. Spearman's rank correlation analysis (Piepho & Lotito, 1992) estimates the correlation among ranks as follows :

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

(i)

where d_i denotes difference between ranks for i-th genotype and n is total number of pairs.

Stable genotype would be with regression coefficient b_i equals to one. GxE interaction effect for i-th genotype, squared and summed across environments to obtain Wricke's Ecovalence measure. Low ecovalence value indicates high relative stability, greatest stability is when W_i^2 =0. Environmental variance is a measure for static concept of stability and a genotype with minimum S_{x2}^i under different environments is considered to be stable. The stability was also measured through combining mean yield and coefficient of variation, genotypes with low CV_i and high mean yield were considered as most desirable. Superiority measure P_i is the mean square of distance between i th-genotype and the genotype with maximum yield within each environment. A low value of P_i indicates high relative stability. Geometric mean can be use as a measure of adaptability of genotype

which called as geometric adaptability index (GAI). Genotypes will high GAI will be desirable.

Spearman's rank correlation was calculated to measure the relationship among the statistical measures using SAS software and principal component analysis (PCA) were performed by JMP (2007) Software to comprehend the relationships among the statistics. For hierarchical clustering the Euclidean distance was used as a dissimilarity measure required in Ward's (Ward, 1963) clustering method. SAS-based computer program SASGESTAB (Hussein *et al.,* 2000) employed to calcu-late nonparametric measures.

RESULTS AND DISCUSSION

Main effects of environment (E), genotype (G) and G x E interaction were highly significant P<0.01 as per analysis of variance. The mean yield of genotypes over environments was ranged from 40.9 to 30.7 along with grand mean yield of 35.76 q/ha. Ten genotypes out of nineteen with yield more than grand mean yield. Since the GxE interaction was significant, the average yield of the genotypes was subjected to further adaptability analysis (Truberg and Hühn, 2000). According to Finlay and Wilkinson (1963) all the genotypes had b_i near 1.0, indicating average stability over environments. As per environmental variance (S_{xi}^2) the KB1516, RD2907 and RD2794 with minimum variance over different environments were considered to be stable while RD2958 and RD2956 considered being unstable genotypes (Sisay and Sharma, 2016).

By using Francis and Kannenberg's (1978) stability parameter (CV_i) the genotypes KB1546, RD2907 and RD2794 considered to be stable with different average yields other hand, RD2958, NDB1173 and RD2794 with high CVi considered to be unstable genotypes. Superiority index (P_i) identified genotypes RD2907 and NDB1445 with the highest yield considered to be stable while RD2958 and KB1546 with the highest P_i value were the unstable genotypes along with the lower yield (Tables 3 and 4) (Dehghani *et al*., 2016). According to Wricke's (1962) stability parameter (W_i^2) the genotypes DWRB168, DWRB165 and NDB1445 with lower ecovalence were considered to be stable and RDB2958, KB1546, and RD2552 with high ecovalance were unstable genotypes. On the basis of GAI RD2907, NDB1445 and RD2552 ranked as three stable genotypes and RD2958 and DWRB165 as unstable genotypes (Mohammadi and Amri, 2008).

Significance of $S_i^{(1)}$ and $S_i^{(2)}$ were tested as per Hühn and Nassar (1989). For each genotype, Z_1 and Z_2 values were calculated based on the ranks of adjusted data and then summed: Z_1 sum = 24.17 and Z_2 sum = 17.30 (Table 5). Both these statistics are distributed as c^2 and were less than the critical value of x^2 (0.01, 19) = 30.6. This indi-

Table 1. Parentage details and environmental conditions.

Code	Genotype	Parentage	Code	Environments	Latitude	Longitude	Altitude (m)
G 1	KB1507	RD 2742/K 877	E 1	Hisar	29°10'N	75° 46'E	215.2
G 2	KB1523	K 508/ RD 2676	E 2	Faizabad-I	26°47' N	82°12' E	113
G 3	KB1546	IBYT-HI-08 (2013-14)	E 3	Faizabad-II	26°47 ' N	82°12 ' E	113
G 4	NDB1655	EIBGN-66 (2008-09)	E 4	Dalipnagar	26.59 ' N	79.18 ' E	145
G 5	NDB1665	1st GSBSN-32 (2013-14)	E 5	Banasthali	26.40 ' N	75.87 ' E	287.27
G 6	NDB1673	1st GSBSN-106 (2013-14)	E 6	DWR Hisar	29° 10' N	75° 48' E	215
G 7	HUB258	EMBSN-27/RD2503					
G 8	DWRB165	PETUNIA.1/LAMOLIN95					
G 9	DWRB168	EXCEL-BAR/4/GLORIA-BAR/ COME//LIGNEE640/3/SPB					
G 10	BH1017	NBGSN-13 (2009)/DWRB73					
G 11	RD2907	RD103/RD2518//RD2592					
G 12	RD2955	RD2666/DWR46					
G 13	RD2956	DL472/BL2//RD2508					
G 14	RD2957	RD2552/RD2786					
G 15	RD2958	RD2552/RD2786					
G 16	RD2552	RD2035/DL472					
G 17	NDB1173	BYTLRA 3-(1994-95)/NDB217					
G 18	NDB1445	NDB940/Ratna					
G 19	RD2794	RD2035/RD2683					

Table 2. Parametric measures of GxE interactions.

Genotype	Yield	b_i	S^2_{xi}	CV_i	W_i^2	s^2_i	GAI	P_i
KB1507	38.47	0.9980	142.90	31.07	134.12	28.71	37.03	32.38
KB1523	34.59	0.9983	127.94	32.70	43.20	8.39	33.10	64.60
KB1546	31.92	0.9864	24.30	15.45	267.01	58.41	31.60	114.58
NDB1655	37.20	1.00	217.00	39.60	87.72	18.34	34.84	47.21
NDB1665	37.72	1.00	231.04	40.29	64.00	13.04	35.29	37.56
NDB1673	36.92	1.00	219.44	40.12	87.32	18.25	34.25	46.81
HUB258	34.63	1.00	205.93	41.43	80.62	16.75	31.96	67.69
DWRB165	30.71	0.9959	98.30	32.28	40.20	7.72	29.53	113.67
DWRB168	34.06	1.000	152.64	36.27	20.74	3.37	32.16	70.43
BH1017	31.89	0.9950	105.94	32.27	139.81	29.98	30.29	106.74
RD2907	40.92	0.9914	59.50	18.85	131.59	28.14	40.33	19.68
RD2955	34.61	1.00	229.01	43.72	120.40	25.64	31.67	74.93
RD2956	37.11	1.00	236.30	41.42	131.48	28.12	35.04	45.40
RD2957	36.58	0.9978	127.62	30.88	68.24	13.98	35.41	44.28
RD2958	31.28	1.00	269.39	52.47	371.25	81.72	28.25	125.01
RD2552	39.81	0.9999	169.13	32.66	144.34	30.99	38.09	26.03
NDB1173	32.97	1.00	233.90	46.39	131.00	28.01	30.06	97.67
NDB1445	40.85	1.00	167.09	31.64	40.83	7.86	39.08	20.53
RD2794	37.16	0.9956	97.74	26.60	60.45	12.24	36.16	44.41

Table 3. Non - parametric measures of GxE interactions.

	Yield	$S_i^{(1)}$	Z_1	$S_i^{(2)}$	Z_2	$S_i^{(3)}$	$S_i^{(6)}$	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	Kang
KB1507	7.33	4.27	1.75	13.07	2.18	8.91	2.18	4.67	0.5833	5.72	1.05	19
KB1523	12.00	5.73	0.14	26.00	0.12	10.83	2.17	3.67	0.2529	5.19	0.52	17
KB1546	12.50	7.67	0.76	40.30	0.81	16.12	2.64	5.83	0.4321	6.34	0.60	34
NDB1655	8.50	7.40	0.49	37.10	0.38	21.82	3.65	5.17	0.6078	5.77	0.89	16
NDB1665	7.17	4.73	1.05	14.97	1.72	10.44	2.42	4.17	0.6410	4.82	0.84	11
NDB1673	8.67	7.07	0.24	34.67	0.17	20.00	3.23	4.67	0.6667	5.83	0.83	18
HUB258	11.83	6.33	0.00	27.37	0.05	11.56	1.97	5.00	0.4167	5.62	0.61	19
DWRB165	15.83	3.27	3.88	9.37	3.24	2.96	0.84	3.33	0.1961	3.65	0.34	21
DWRB168	12.33	3.87	2.50	10.27	2.96	4.16	1.30	2.50	0.2174	2.87	0.31	15
BH1017	13.33	7.07	0.24	34.67	0.17	13.00	2.10	5.50	0.3667	6.18	0.64	33
RD2907	5.83	5.53	0.26	23.37	0.33	20.03	3.94	5.83	1.2963	6.21	1.28	15
RD2955	11.33	6.80	0.10	30.27	0.00	13.35	2.29	5.50	0.4783	6.15	0.71	23
RD2956	8.67	6.27	0.00	27.07	0.07	15.62	3.00	4.50	0.5000	5.55	0.92	21
RD2957	9.33	5.60	0.21	21.87	0.50	11.71	2.57	5.33	0.5079	5.56	0.70	17
RD2958	12.17	7.13	0.28	34.17	0.13	14.04	2.22	4.67	0.3457	5.99	0.60	37
RD2552	5.67	6.27	0.00	31.47	0.02	27.76	4.47	4.50	1.2857	5.25	1.07	20
NDB1173	13.00	5.07	0.65	19.60	0.82	7.54	1.69	5.83	0.5303	7.15	0.66	27
NDB1445	3.83	3.53	3.23	8.97	3.37	11.70	3.39	2.83	0.8095	3.94	1.04	5
RD2794	8.67	10.80	8.39	24.27	0.25	14.00	2.62	4.17	0.4386	5.43	1.64	12
		Sum =	24.17		17.30				x^2 (0.05,1)	3.84	x^2 (0.01,1)	6.63
$E(s^1)$	6.3158	$E(s^2)$	30.0	$V(s^1)$	2.3956	$V(s^2)$	131.40		x^2 (0.05,19)	30.1	x^2 (0.01,19)	36.2

Table 4. Ranking of genotypes by parametric vis-à-vis non parametric measures.

	Yield	b_i	S^2_{xi}	CV_i	W_i^2	s^2_i	GAI	Pi	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	Kang	SRT
KB1507	4	12	8	5	15	15	4	4	4	4	4	7	11	13	11	16	11	148
KB1523	13	5	7	10	4	4	11	11	9	10	6	6	4	3	5	3	8	119
KB1546	16	1	1	1	18	18	15	18	18	19	15	13	19	7	18	5	18	**220**
NDB1655	6	16	13	12	10	10	9	10	17	18	18	17	13	14	12	13	6	214
NDB1665	5	17	16	14	6	6	7	5	5	5	5	10	6	15	4	12	2	140
NDB1673	9	13	14	13	9	9	10	9	15	17	16	15	11	16	13	11	9	209
HUB258	11	10	12	16	8	8	13	12	12	12	7	4	12	6	10	6	11	170
DWRB165	19	4	4	8	2	2	18	17	1	2	1	1	3	1	2	2	14	101
DWRB168	14	7	9	11	1	1	12	13	3	3	2	2	1	2	1	1	5	88
BH1017	17	2	5	7	16	16	16	16	15	16	10	5	16	5	16	7	17	202
RD2907	1	3	2	2	14	14	1	1	7	8	17	18	19	19	17	18	5	166
RD2955	12	14	15	17	11	11	14	14	13	13	11	9	16	9	15	10	15	**219**
RD2956	8	19	18	15	13	13	8	8	11	11	14	14	8	10	8	14	14	206
RD2957	10	11	6	4	7	7	6	6	8	7	9	11	14	11	9	9	8	143
RD2958	18	18	19	19	19	19	19	19	16	15	13	8	11	4	14	4	19	**254**
RD2552	3	9	11	9	17	17	3	3	11	14	19	19	8	18	6	17	12	196
NDB1173	15	15	17	18	12	12	17	15	6	6	3	3	19	12	19	8	16	213
NDB1445	2	8	10	6	3	3	2	2	1	8	16	2	2	17	3	15	1	101
RD2794	7	6	3	3	5	5	5	7	19	9	12	12	6	8	7	19	3	136

Table 5. Loading of parametric and non parametric measures.

Measure	PCA 1	PCA 2
Yield	0.3827	-0.1156
Bi	0.0081	0.0757
S^2_{xi}	0.0744	0.0519
CV_i	0.1842	-0.0153
$W_i 2$	0.1237	0.3621
s^2_i	0.1237	0.3621
GAI	0.3968	-0.0686
Pi	0.3960	-0.0464
$S_i^{(1)}$	0.1293	0.2869
$S_i^{(2)}$	0.1642	0.3199
$S_i^{(3)}$	-0.0808	0.3646
$S_i^{(6)}$	-0.2589	0.2837
$NP_i^{(1)}$	0.1324	0.3090
$NP_i^{(2)}$	-0.2976	0.2216
$NP_i^{(3)}$	0.1696	0.3180
$NP_i^{(4)}$	-0.3175	0.2095
Kang	0.3410	0.1452
% variance	34.89	32.25

cated the non-significant differences among genotypes as per ranks of $S_i^{(1)}$ and $S_i^{(2)}$ measures (Elahe and Ebadi, 2015). More over the individual Z values showed RD2794 & DWRB165 were significantly unstable relative to others, with $Z_{i\,(1)}$ values more than the critical value of x^2 (0.05, 1) = 3.84.

Results of non-parametric stability statistics showed that considering to $S_i^{(1)}$, $S_i^{(3)}$ and $S_i^{(6)}$ the genotypes DWRB165 and DWRB168 were the stable genotypes but had the low mean yield. Based on $S_i^{(3)}$, $S_i^{(6)}$ the genotypes NDB1173 apart from DWRB168 were of stable performance but had the lower yield (Tables 3 and 4). All of these non-parametric statistics were identified NDB1665 and RD2552 as unstable genotypes. According to Thennarasu's (1995) nonparametric measures, which considered ranks of adjusted yield, genotypes with minimum low values are considered more stable. Based on the first measure $NP_i^{(1)}$ DWRB168 and NDB1445 were stable and KB1546, RD2907 and NDB1173 were unstable genotypes. According to the other three methods ($NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$) genotypes DWRB168 and DWRB165 were stable and the genotypes RD2907 and RD2552 were unstable (Baxevanos *et al.*, 2008). Most of cases these measures selected genotypes with low average yield as stable genotypes.
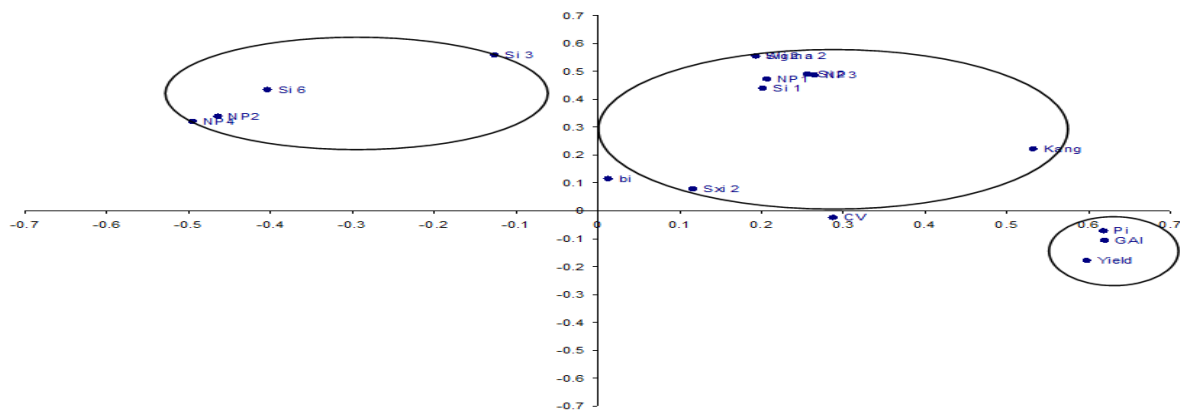

Fig. 1. *Biplot analysis of parametric and non parametric measures of G x E .*

Table 6. Association analysis among measures.

	Yield	bi	Sxi 2	CVi	Wi 2	s2 i	GAI	Pi	Si(1)	Si(2)	Si(3)	Si(6)	NPi(1)	NPi(2)	NPi(3)	NPi(4)
bi	-0.2158															
S 2 xi	-0.2298	0.9930														
CVi	0.0877	0.9193	0.9140													
Wi 2	0.1333	0.1246	0.1596	0.1368												
s2 i	0.1333	0.1246	0.1596	0.1368	1.0000											
GAI	0.9509	0.0281	0.0140	0.3351	0.2281	0.2281										
Pi	0.9719	-0.2053	-0.2316	0.0789	0.1561	0.1561	0.9421									
Si (1)	0.2246	0.0351	-0.0193	-0.0298	0.3316	0.3316	0.1947	0.2947								
Si (2)	0.2474	0.0561	-0.0035	0.0193	0.4474	0.4474	0.2772	0.3474	0.8930							
Si (3)	-0.3351	0.0667	0.0070	-0.1491	0.3140	0.3140	-0.3070	-0.2193	0.6912	0.7456						
Si (6)	-0.7053	0.1035	0.0614	-0.2228	0.0667	0.0667	-0.6842	-0.5912	0.3246	0.3544	0.8491					
NPi (1)	0.1105	0.1263	0.1298	0.1684	0.6368	0.6368	0.2053	0.1719	0.3175	0.4158	0.2140	-0.0263				
NPi (2)	-0.8105	0.2877	0.2807	0.0000	0.0526	0.0526	-0.7298	-0.7158	-0.0421	0.0456	0.5281	0.7877	0.1386			
NPi (3)	0.1158	0.2070	0.2333	0.1982	0.6825	0.6825	0.1965	0.1456	0.3982	0.4421	0.2456	0.0263	0.8070	0.1895		
NPi (4)	-0.8158	0.1649	0.1754	-0.1456	0.0579	0.0579	-0.8193	-0.7754	0.0982	-0.0281	0.4965	0.7368	0.0526	0.8421	0.2035	
Kang	0.7149	0.0535	0.0728	0.2816	0.7465	0.7465	0.7798	0.6991	0.2377	0.3851	-0.0711	-0.4202	0.5430	-0.4009	0.5588	-0.4781

Critical values of correlation at 5% and 1% level of significance are 0.4853 and 0.6152 respectively.
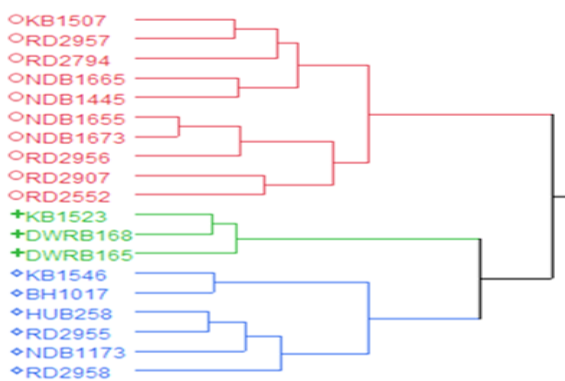

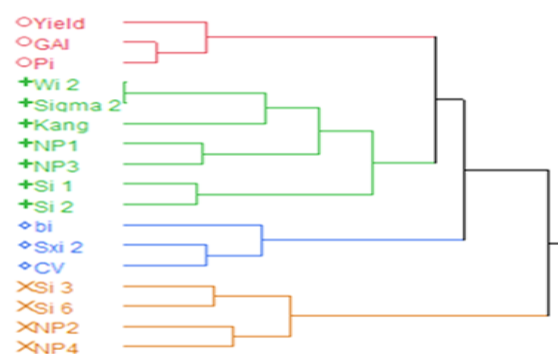**Fig. 2.** *Dendogram of salt salinity tolerant barley genotypes.*

Fig. 3. *Clustering of parametric and non parametric measures.*

Interrelationship among parametric and non-parametric measures: Spearman's rank correlation (Table 5) among measures exhibited high positive correlation of yield with two parametric measures (P_i, GAI) and Kang measure that is expected as the low values of P_i and high values of GAI were related to high yielder genotypes (Sisay and Sharma, 2016). Negative significant correlation of yield with most of nonparametric measures except $NP_i^{(1)}$ $NP_i^{(3)}$ suggested that selection of stable genotypes based on these statistics should be considered seriously with genotype yield. The regression coefficient (b_i) was positively and strongly correlated with S_{xi}^2 and CV_i. Environmental variance (S_{xi}^2) was significantly and positively correlated with CV_i. Wricke's parameter (W_i^2) was positively correlated with $NP_i^{(1)}$, $NP_i^{(3)}$ and Kang. s_i^2 maintained high linear relation with $NP_i^{(1)}$, $NP_i^{(3)}$ and Kang and moderate with $S_i^{(1)}$, $S_i^{(2)}$. GAI had significant positive with P_i and Kang while negative with $S_i^{(6)}$, $NP_i^{(2)}$ & $NP_i^{(4)}$. Worth to mention the negative association of P_i with $S_i^{(6)}$, $NP_i^{(2)}$, $NP_i^{(4)}$

Similar results reported by Mohammadi and Amri (2008). Nassar and Hühn (1987) reported that S_{xi}^2, $S_i^{(1)}$ and $S_i^{(2)}$ are associated with the static or biological concept of stability. Flores et al. (1998) categorized S^{2xi}, $S_i^{(1)}$ and $S_i^{(2)}$ in same group and de-

fined them in the sense of homeostasis. Piepho and Lotito (1992) reported high rank correlation among parametric and non-parametric measures. Truberg and Huehn (2000) suggested an alternative use of non-parametric measures, such as stability variance whenever assumptions, such as normal distribution, independence, homogeneity of error variances, absence of outliers, etc. are violated.

Non-parametric measures $S_i^{(s)}$ were positively and significantly correlated among themselves and with Thennarasu's $NP_i^{(s)}$ measures also mentioned by Hühn and Nassar (1989). $NP_i^{(s)}$ also showed strong positive correlation among themselves. The positive correlation of Kang with parametric and non-parametric measures except $S_i^{(1)}$ $NP_i^{(2)}$ $NP_i^{(4)}$ indicated similar aspects of stability by these measures. Therefore, it is possible to Kang only as one of the measure of adaptability.

Hierarchical clustering of genotypes and measures: Clustering of barley genotypes as per ranks of yields and GxE measures was performed. Output of analysis in form of dendrogram separated the genotypes into three clusters (Figure 2). The cluster of desirable genotypes DWRB165, DWRB 168, KB1523 identified by non parametric measures. Separate cluster of RD2958, RD2955, NDB 1173, KB 1546, BH1017, HUB258 were pointed out by para-

metric measures. Large cluster of higher and moderate yielders genotypes mentioned by parametric and non parametric measures.

Attempt was made to find pattern if any among the measures of GxE interaction for considered salt salinity tolerant barley genotypes. Clustering mentioned four groups of studied measures. Non parametric measures $S_i^{(3)}$ $S_i^{(6)}$ $NP_i^{(2)}$ & $NP_i^{(4)}$ clubbed together while Kang, W_i^2, s^2_i $S_i^{(1)}$, $S_i^{(2)}$ $NP_i^{(1)}$ & $NP_i^{(3)}$ joined in another cluster. Remaining parametric measures were grouped in two separate clusters i.e. (b_i, S^2_{xi}, CV_i) (Yield, GAI Pi). This showed the clear difference of parametric measures from non parametric measures.

Biplot analysis of parametric and non parametric measures: Graphical display of the relationships among measures is displayed in a biplot of first two principal components (PC1 and PC2) as these PC's accounts for more than 67% of total variation. Major three groups to be distinguished as below:

Group I: GAI, P_i , Yield

Group II: $S_{i(3)}$, $S_{i(6)}$, $NP_{i(2)}$, $NP_{i(4)}$

GroupIII:S^2_{xi}, Kang, $NP_{i(1)}$, $NP_{i(3)}$, $S_{i(1)}$, $S_{i(2)}$, W_i^2 s^2_i

Yield is included in group I, suggesting group I comprised those methods where yield had an important influence on the ranking across environments. According to this group genotypes RD2907, NDB1445, RD2552, and KB1507 introduced as stable genotypes that were the first five high yielding genotypes (Tables 3 and 4). There were strong positive rank correlation between these two measures and yield. Therefore, yield would be good measure for selection (Table 5). Superiority measure (P_i) and GAI as measures of genotypic performance attempt to integrate both yield and stability. Selection based on these stability parameters is related to the dynamic or agronomic concept of stability.

Non-parametric measures $S_i^{(3)}$,$S_i^{(6)}$,$NP_i^{(2)}$ and $NP_i^{(4)}$ were included in group II. These measures selected DWRB165 & DWRB168 as stable genotypes that were the low yielding genotypes. The measures of this group were negatively correlated with mean yield. High yielder genotypes would be unstable as per these non parametric measures. This need further study in other crops also (Table 5).

Measures of Group III S^2_{xi}, Kang, $NP_i^{(1)}$, $NP_i^{(3)}$, $S_i^{(1)}$, $S_i^{(2)}$, W_i^2, s^2_i identified NDB1655, BH1017, RD2958 were as undesirable genotypes for yield and specific adaptable behavior.

Conclusion

Parametric and nonparametric measures have been studied to quantify GxE interaction of 19 barley genotypes. Both yield and stable performance considered simultaneously to exploit the useful effect of GxE interaction in order to select promising genotypes. For salt affected area of the country, the availability of salinity tolerant genotypes with high yield is very much needed to insure good farmer income.

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