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Yield Stability Analysis in Hulless Barley (*Hordeum vulgare* L.)

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Abstract: In order to evaluate the stability, the adaptation and the highest yield, 20 hulless barley genotypes were tested in a thrice replicated randomized complete block design at six locations for two seasons, 2002-2004 in Iran. Simple and Compound analyses of variances indicated significant differences among genotypes. Determining the stability of genotypes, various analyses was RUN: environmental coefficient of variation, Eberhart and Russell's, Finlay and Wilkinson's and Perkins and Jinks's regression methods, equivalence of Wrink, stability variance of Shukla, Lin and Binn's years within location mean squares method, the years within location environmental coefficient of variation, the average and deviation from rank and yield index ratio. Based on the results, ICN93-328 and Aleli/4/mola2 were stable genotypes and Gloria was for lower yielding areas.

Key words: Genotype, Hulless barley, interaction, stability, yield

INTRODUCTION

In plant breeding programme, many potential genotypes are usually evaluated in different environments (locations and years) before selecting certain desirable genotypes. For quantitative traits such as seed yield, the relative performance of different genotype often varies from one environment to another i.e., genotype-environment ($G \times E$) interaction exists. Such as $G \times E$ interaction results in change the relative rank of genotypes or change in the magnitudes of differences between genotypes from one environment to another. Changes in ranking make it difficult to the plant breeders to decide which genotypes should be selected. A number of statistics have been proposed to measure the genotypic stability; however, no single method can adequately explain cultivars performance across environment.

Lin *et al.* (1986) has established three major concepts of stability. Type 1 stability (genotype mean square = S^2 and genotypic coefficient of variation = CV_i) measure the variation within a genotype across environment. This stability parameter is related to homeostasis and has been associated with low yield (Rashid *et al.*, 2002). Type 2 stability (ecovalance = W^2 and shukla's stability variance = δ^2) which basically measure the deviation of the individual genotypes from the location means of all genotypes in test. Type 3 (regression slope = b_i) stability

is calculated by the residual mean square from the regression of individual cultivar yield on an environmental index (Rashid *et al.*, 2002).

However, Eberhart and Russell's model is one of the best techniques used to rank the genotypes for stability. They defined a stable variety as having unit regression over the environments ($b = 1.00$) and minimum deviation from the regression ($Sd_i^2 = 0$). Therefore, a variety with a high mean yield over the environments, unit regression coefficient ($b = 1$) and deviation from regression as small as possible ($Sd_i^2 = 0$) will be a better choice as a stable variety.

The $G \times E$ interaction has been reported in maize (Aslam *et al.*, 1988), rice (Qayyum *et al.*, 2002), mash (Zubair *et al.*, 2002) and mungbean (Zubair and Ghafoor, 2002), but very little information is available on stability of hulless barley genotypes. Thus, this study was undertaken to evaluate 20 hulless barley genotypes for their yield stability in Iran.

MATERIALS AND METHODS

Twenty Hulless Barley genotypes (Table 1) were used of advanced lines from the Hulless Barley breeding programme of Iran, ICARDA/CIMMYT for two seasons, 2002-2004. These trials were conducted at six research locations of Iran. The locations were in Birjand, Esfahan, Karaj, Neyshabour, Yazd and Zarghan. The experiments were laid according to randomized complete block design with three replications.

Table 1: Genotype and Origin of hulless barley genotypes

Genotype	Origin	Genotype	Origin
EHBYTM80-1	Iran	ICNBF 8-582	ICARDA/CIMMYT
ALELI/4/MOLA/2...	ICARDA/CIMMYT	ICNB 93-328	ICARDA/CIMMYT
ALELI/4/MOLA/3...	ICARDA/CIMMYT	SB91925(13)	ICARDA/CIMMYT
CONDOR-BAR/4/...	ICARDA/CIMMYT	BF 891M-592	ICARDA/CIMMYT
BF 891M-609	ICARDA/CIMMYT	Gloria	ICARDA/CIMMYT
SB 91488	ICARDA/CIMMYT	ICNBF 8-617	ICARDA/CIMMYT
SB 91915	ICARDA/CIMMYT	ICNBF 8-653	ICARDA/CIMMYT
ICNBF 8-611	ICARDA/CIMMYT	SB 91925(18)	ICARDA/CIMMYT
CENTENO/CAM/...	ICARDA/CIMMYT	ICNB 93-369	ICARDA/CIMMYT
LINO (CMB92.392-A-...)	ICARDA/CIMMYT	EHBYTM 80-20	Iran

Also, varieties were considered as a fixed factor in the test. Each plot had a length of 5 m and a width of 1.20×0.5 m was deleted from both sides of each plot.

Statistics analysis: Crop was harvested at physiological maturity and data on seed yield recorded. The analysis of variance combine over locations and years was carried out to direct the differences among genotypes, locations and genotype-environment interaction using the statistical packages SAS and GEST. Here, used some parameters to determine stable genotypes such as environmental variance, environmental coefficient of variation, Eberhart and Russell's, Finlay and Wilkinson's and Perkins and Jinks's regression methods, equivalence of Wruck, stability variance of Shukla, Lin and Bim's years within location mean squares method, the years within location environmental coefficient of variation, the average and deviation from rank and yield index ratio. The genotype having had the lowest amount of environmental coefficient of variation, equivalence of Wruck and stability variance of Shukla, could be identified as a stable genotype. Also, if one genotype had the lowest average rank of yield that will be obtained with the average and deviation from rank method, it could be recognized for the unpropitious weak areas. Yield index ratio was one of the distribution free methods that we could use to offer stable genotypes the same as the mentioned earlier.

RESULTS AND DISCUSSION

In order to do compound varieties analysis of yield (Table 2) the difference between genotypes and the interaction of genotype, year and place were signified, that indicated the difference between genotypes in different environments. Also, Shahmohammadi (2003) indicated the significant interactions of year, genotype and place for barley genotypes and the best variety has been specified for each place and also for the whole areas. Kang *et al.* (1991) studies on 5 corn genotypes indicated the interaction of genotype and environment was significant in all tests. They also indicated that selecting just based on yield is not sufficient when the

Table 2: Combined analysis of variance for yield of 20 Hulless Barley genotype in six locations and two years

SOV	df	MS
Location (L)	5	81.099 ^{ns}
Year (Y)	1	0.455 ^{ns}
Y×L	5	27.538**
Error (a)	24	0.554
Genotype (G)	19	3.547*
L×G	95	1.097 ^{ns}
Y×G	19	1.329 ^{ns}
Y×L×G	95	0.89**
Error (b)	456	0.377
Total	719	
CV (%)	13.78	

ns: non significant, *: Significant, **: Highly significant

interaction of genotype and environment is significant due to testing in different environments. One of the basic problems in evaluation of genotypes in tests with specified year and place is that the effect of place can be remarkably variable from year to year and this will be made known by means of signifying the effect of place and year in variance analysis table.

Mean genotype yield ranged from 3.904-5.034 t ha⁻¹. The highest yield genotypes were ALELI/4/MOLA/3, ALELI/4/MOLA/2, SB 91915 and ICNB 93-328 (Table 4). Since the interaction of genotype, year and place had been signified ($p < 0.01$), the application of compound variance analysis and attendances mean comparison based on calculated error was not sufficient. Therefore, in order to specify varieties adaptation degree and classifying them, different methods of stability analysis were used.

Bernardo (2002) reported that the extent of such performance testing depended on the magnitude of genotype×environment interaction, which occurs when, genotypes differ in their relative performance across environments. Following the genotype×environment interaction, Eberhart and Russell's stability analysis were performed and the results were shown in Table 3. The effects of genotypes and environments have been signified that means they have very significant difference. The genotype×environment interaction has been signified that means varieties react differently in responding to environmental conditions.

Also, the ideal genotype as proposed by Eberhart and Russell (1966) would have a high mean performance over a range of environments, a regression coefficient of one and deviation mean square from regression of zero. Genotypes with regression coefficient greater than 1.0 would be adapted to more favourable environment, while those with coefficient less than would be relatively better adapted to less favourable growing conditions (Table 4) (Rashid *et al.*, 2002; Unay *et al.*, 2004).

Therefore, relationship between the regression coefficients and mean yield for 20 Hulless Barley genotypes are shown graphically in Fig. 1. The regression coefficients of ICNBF 8-582, LINO, CONDOR-BAR/4 and ICNB 93-328 genotypes were magnitude due to close to 1. ALELI/4/MOLA/2 and ICNB 93-328 had the highest yield at confidence limits for yield and their regression coefficients were close to 1 at confidence limits for regression. These two genotypes, therefore, were the group of the best adaptation to all environments. Also, the other stability parameters for ALELI/4/MOLA/2 and ICNB 93-328 genotypes were parallel to results of graphic. When the other genotypes were shown in Fig. 1,

EHBYTM80-1, CONDOR-BAR/4, BF891M-609, SB91488, ICNBF 8-611, CENTENO/CAM, LINO, ICNBF 8-582, BF 891M-592, ICNB 93-369 and EHBYTM 80-20 were defined as mid-adaptation to all environments while GLORIA and ICNBF 8-617 had bad adaptation. Other genotypes were found to be outside of confidence limits.

CV_i is the variance of genotypes across environments, weighted by the cultivar mean and it reflects homeostasis or buffering ability of cultivar. The low CV_i values indicated that SB91925 (13) and ALELI/4/MOLA/3 had the most consistent yield, therefore had relatively better buffering ability. The high CV_i value indicated that SB 91925 (18) and EHBYTM80-1 had least consistent yields. Lin *et al.* (1986) and Rashid *et al.* (2002) have argued that well-buffered cultivars are generally low yielding. Based on environmental variance method, SB91925 (13) and ALELI/4/MOLA/3 had high stability (Table 4).

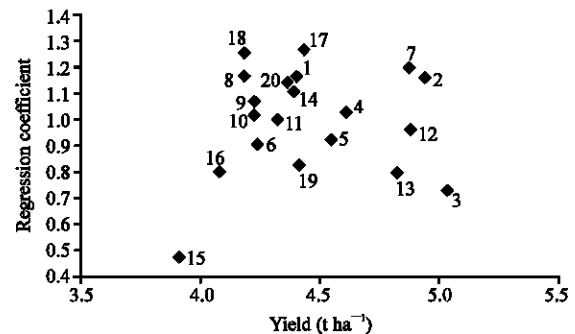


Fig. 1: The diagram of hulless barley genotypes diffusion in terms of yield and regression coefficient

Table 3: Yield stability analysis of hulless barley genotypes in different environments

SOV	DF	SS	MS
(E×G)+E	220	272.609	1.239**
Genotype(G)	19	22.450	1.18**
Environment(E)	11	181.190	16.47**
E×G	209	71.340	0.34**
Linear environment	1	181.190	181.19**
Genotype in linear environment	19	6.950	0.37 ^{ns}
Deviation of regression	200	64.000	0.32
Pooled error	456	172.017	0.377

**p<0.01, ns: non significant

Table 4: Different stability parameters in Hulless Barley genotypes

Genotype	Yield (t ha ⁻¹)	Eberhart and Russell's regression coefficient (b _i)	Deviation of regression line (S _d ²)	R-square (R _i ²)	Environmental variance	Environmental coefficient of variation	Variance of Shukla	Equivalence of Wruck	Finlay and Wilkinson's regression	Perkins and Jinks's regression
1	4.403	1.159 ^{ns}	0.482	66.7	1.66	29.26	0.618	6.307	0.159	0.159
2	4.945	1.159 ^{ns}	0.049	87.4	1.27	22.76	0.181	1.976	0.159	0.159
3	5.034	0.732 ^{ns}	0.165	62.5	0.74	17.17	0.240	3.557	0.732	-0.268
4	4.608	1.023 ^{ns}	0.371	65.7	1.38	24.83	0.487	5.007	0.023	0.023
5	4.547	0.923 ^{ns}	0.315	63.7	1.10	23.10	0.433	4.475	0.923	-0.077
6	4.239	0.906 ^{ns}	0.333	61.8	1.09	24.69	0.454	4.680	0.906	-0.094
7	4.881	1.193 ^{ns}	0.110	84.5	1.39	24.13	0.253	2.689	0.193	0.193
8	4.184	1.171 ^{ns}	0.015	89.8	1.26	26.81	0.151	1.682	0.171	0.171
9	4.223	1.063 ^{ns}	-0.059	93.8	0.992	23.59	0.053	0.710	1.063	0.063
10	4.230	1.025 ^{ns}	0.195	74.7	1.16	25.44	0.306	3.215	1.025	0.025
11	4.321	1.002 ^{ns}	0.257	70.5	1.17	25.08	0.367	3.826	1.002	0.002
12	4.875	0.965 ^{ns}	0.355	63.6	1.20	22.47	0.468	4.819	0.965	-0.035
13	4.821	0.793 ^{ns}	0.046	770	0.67	17.03	0.193	2.103	0.793	-0.207
14	4.391	1.112 ^{ns}	0.164	79.3	1.28	25.78	0.286	3.017	1.112	0.112
15	3.904	0.476 ^{ns}	0.548	23.4	0.80	22.90	0.913	9.224	0.476	-0.524
16	4.082	0.799 ^{ns}	0.121	70.0	0.75	21.22	0.268	2.842	0.799	-0.201
17	4.438	1.271 ^{ns}	0.078	87.7	1.51	27.74	0.254	2.706	1.271	0.271
18	4.185	1.253 ^{ns}	0.170	82.9	1.56	29.86	0.338	3.538	1.253	0.253
19	4.420	1.832 ^{ns}	0.080	75.4	0.70	18.98	0.215	2.312	0.832	-0.160
20	4.378	1.141 ^{ns}	0.125	82.5	1.30	26.02	0.252	2.682	1.140	0.140

ns: non-significant

Table 5: Stability analysis in hulless barley genotypes by non-parametric methods

Genotype	Average of rank ($\bar{R}_i$)	Deviation from rank (STD-R)	Yield index ratio (YIR)	Years within location mean squares	Years within location environmental coefficient of variation
1	11.25	6.57	98.83	19.55	0.741
2	5.17	4.26	111.00	10.91	0.291
3	5.67	3.65	113.00	13.72	0.477
4	8.83	6.04	103.43	12.14	0.313
5	10.25	6.06	102.06	19.72	0.804
6	12.08	5.25	95.15	16.02	0.461
7	6.75	4.29	109.56	14.59	0.507
8	13.17	4.65	93.00	19.54	0.669
9	14.08	3.34	92.00	18.05	0.581
10	12.50	5.45	94.95	21.00	0.789
11	12.58	6.23	96.99	22.54	0.949
12	6.50	6.01	109.43	21.45	1.094
13	6.67	4.18	108.21	16.05	0.599
14	10.92	5.91	98.56	24.09	1.058
15	13.83	6.82	87.63	21.06	0.676
16	14.08	3.60	91.63	16.27	0.441
17	10.83	4.57	99.62	21.08	0.875
18	13.83	4.95	93.33	23.31	0.952
19	10.08	5.77	99.21	17.07	0.569
20	10.92	4.54	98.27	21.77	0.904

The low ecovalence of wricke (W^2_i) and stability variance of Shukla (δ^2_i) values are characteristics for stable variety. When the lowest values were considered, ecovalence value of wricke (W^2_i) and stability variance parameter of Shukla (δ^2_i) showed similar values and trends (Unay *et al.*, 2004). According to these two parameters, ALELI/4/MOLA/2, SB91925 (13), ICNBF 8-611 and CENTENO/CAM would be considered as the most stable genotypes. ICNB 93-32812 and CONDOR-BAR/4 had the highest stability and yield if we checked them with Perkins and Jinks's regression method, also in this method GLORIA was recognized as an unstable one (Table 4).

Based on Finlay and Wilkinson's regression method, ICNB 93-328 and after that CONDOR-BAR/4 and BF 891M-609 was identified as stable genotypes. ALELI/4/MOLA/2 had the lowest amount of average and standard deviation, so that we determined it as a stable genotype with this method, after ALELI/4/MOLA/2, there were some genotypes, such as ALELI/4/MOLA/3, ICNB 93-328, SB91925 (13) and SB 919157 that were distinguished as stable ones. This method was recognized ICNBF 8-617 and GLORIA as unstable ones (Table 4).

Examining genotypes with average of rank and deviation from rank of Non-parametric methods showed that ALELI/4/MOLA/2, ALELI/4/MOLA/3, ICNB 93-328 and SB91925 (13) had high stability and ICNBF 8-617 and GLORIA had low stability among the other genotypes (Table 5). Also, Examining genotypes with yield index ratio revealed ALELI/4/MOLA/3, ALELI/4/MOLA/2, SB 91915, ICNB 93-328 and SB91925 (13) had most stability among the other genotypes. GLORIA with this method was introduced as an unstable one (Table 5).

In breeding programs the breeders is interested in a particular set of genotypes and in how they perform over a range of years. From the selections under test, he is interested in those which have a high yield and which are relatively stable over the years tested. For this purpose, he should look for a high mean yield a relatively low the years within location mean squares and the years within location environmental coefficient of variation (Lin and Binn, 1988; Shahmohammadi, 2003). The results (Table 5) indicated that genotypes ALELI/4/MOLA/2, ALELI/4/MOLA/3 and CONDOR-BAR/4 had most stability among the other genotypes.

CONCLUSION

The result of this investigation demonstrated that production response index (regression coefficient) and other stability parameters are suitable means of selecting cultivars that are stable high yielding and responsive. It is further illustrated that the regression coefficient is the most useful stability statistics which can be applied for the selection of hulless barley genotypes adapted to wide range of environments or adapted to restricted environments.

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REFERENCES

- Aslam, M., I.H. Javaid, N.H. Malik and H. Rehman, 1988. Genotype×environment interaction and stability of performance among different varieties maize in Pakistan. Pak. J. Agric. Res., 9: 52-55.
- Bernardo, R., 2002. Breeding For Quantitative Traits in Plants. Stemma Press, USA, ISBN 0-9720724-0-3, pp: 369.
- Eberhart, S.A. and W.A. Russell, 1966. Stability parameters for comparing varieties. Crop Sci., 6: 36-40.
- Kang, M.S., P.D. Gorman and N.H. Pham, 1991. Application of stability statistic to international maize yield trials. TAG, 81: 162-165.
- Lin, C.S., M.R. Binns and L.P. Lefkovich, 1986. Stability analysis: Where do we stand? Crop Sci., 26: 894-900.
- Lin, C.S. and M.R. Binns, 1988. A method of analyzing cultivar×location×year experiments: A new stability parameter. TAG, 76: 425-430.

- Qayyum, A., M.U. Mufti and S.A. Rabbani, 2002. Evaluation of different rice genotypes for stability in yield performance. *Pak. J. Sci. Ind. Res.*, 43: 188-190.
- Rashid, A., G.R. Hazara, N. Javed, M.S. Nawaz and G.M. Ali, 2002. Genotype×environment interaction and stability analysis in mustard. *Asian J. Plant. Sci.*, 5: 591-592.
- Unay, A., H. Basal, A. Erkul and Z. Yuksekkaya, 2004. Stability analysis of upland cotton genotypes to the Aegean region in Turkey. *Asian J. Plant. Sci.*, 3: 36-38.
- Zubair, M. and A. Ghafoor, 2002. Genotype environment interaction in mungbean. *Pak. J. Bot.*, 33: 187-190.
- Zubair, M., M. Anwar, A.M. Haqqani and M.A. Zhid, 2002. Genotype-environment interaction for grain yield in mash (*Vigna mungo* L. Hepper). *Asian J. Plant. Sci.*, 1: 128-129.