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Interpretation of Genotype by Environment Interaction for Barley Genotypes Via Simultaneous Selection for Yield and Stability

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Genotype × environment (GE) interaction was investigated for grain yield of barley (*Hordeum vulgare* L.). Data included were 18 genotypes and 15 environments (five locations and three years). Interaction effect was modeled by four types of stability parameters and studied parameters were plotted against mean yield performance for graphic analysis of stability and simultaneous selection for yield and stability. About 60% of the total variance was explained by environment differences, about 24% by GE differences and 15% by genotype differences. G8, G10 and G18 according to S_i^2 and G2, G6 and G10 considering CV_i were stable while G2, G6 and G10 were identified as the most stable genotypes based on θ_i, $\theta_{(i)}$, W_i^2 and σ_i^2 parameters. Genotypes with b_i and β_i (coefficients of linear regression) values greater than 1 (such as G3, G7, G15 and G17) indicated higher yield in more favorable environments. Overall based on Type IV stability, G8, G10, G11 and G18 were identified as the most stable genotypes for each of the five locations. According to graphic analysis of S_i^2 and CV_i parameters, G2, G5, G6, G10 and G12 were the most stable genotypes while based on θ_i, $\theta_{(i)}$, W_i^2 and σ_i^2 parameters, G1, G2, G4, G5, G6, G10, G12 and G15 were identified as the most favorable genotypes. Based on graphic analysis, G1, G4, G6, G10 and G15 were common with the high-yielding genotypes. Finally, G1 (2325.2 kg ha^{-1}) and G15 (2348.6 kg ha^{-1}) were the most favorable genotypes for barley grain yield and are therefore recommended for commercial release.

Key Words: barley, graphic analysis, yield stability

Abbreviations: GE – genotype x environment, S_i^2 – variance of a genotype across environments, CV_{GI} – coefficient of variability, θ_i – mean variance component for pairwise GE interaction, $\theta_{(i)}$ – variance component for GE interaction, W_i^2 – ecovalence, σ_i^2 – stability variance, b_i – regression coefficient, β_i – regression coefficient, δ_i^2 – deviation parameter from regression, $\delta_{(i)}^2$ – residual mean square of deviation from the regression

INTRODUCTION

Barley (*Hordeum vulgare* L.) as a major cereal grain crop, is one of the oldest cultivated grains and is now one of the most widespread cereals in world. In Iran barley is the second important crop and it has been estimated that its production in Iran exceeded 2.9 million tons from an area of 1.6 million ha land (FAOSTAT. 2016). In Iran barley is used almost exclusively as animal feed and it is produced almost on dry-farmed lands, located on mountain slopes, thus yield stability is an important issue in breeding programs as well as high grain yield.

New genetically improved genotypes generally require to be tested at many sites and for several years before they are recommended as a formal variety for a target area. To achieve this purpose, multi-environment trials (MET) were performed as varietal testing programs in many countries which have to face the recurring problem of genotype by environment (GE) interactions (Kang et al. 2006). Indeed, differential genotypic responses to environmental changes or the GE interaction phenomena, especially when associated with changes in genotypic ranking, limit the identification of most superior genotypes, stable as well as high yielding. Identification of causal factors of the GE interaction and quantification of unexplained observed variation are of prime importance in selecting for stability performance or in recommending specific genotypes for each environmental condition (Gauch et al. 2008). In the recent

decades, new developments have been achieved in biometry and some integrated approaches have been used for GE interaction evaluation and likewise many statistical models have been used for detecting and characterizing the GE interaction and stability analysis (Hristov et al. 2010; Sabaghnia et al. 2012).

Breeders need a practical method that would exploit GE interaction, but in spite of the availability of several statistical methods and comparisons among them as well as the designing of some methods to combine yield and stability into a single selection criterion (Kang. 1993), practical integration of stability with yield has not been achieved. When a crossover GE interaction occurs, mean yield of genotypes selected via a statistical method that combines both yield and stability would usually be lower than that of genotypes selected on the basis of yield alone (Bachireddy et al. 1992). The fact that stability is of economic importance for the cultivation of a certain genotype was already recognized by Roemer (1917 cited in Becker and Leon. 1988) who used the variance across environments, which is classified as Type I stability, meaning that it is a relative index dependent on changes of genotypes across the test environments (Lin et al. 1986). Stability concept based on Shukla's (1972) stability variance is classified as Group B and Type I stability, meaning that it is a relative measure dependent on genotypes included in the test (Lin et al. 1986).

Eberhart and Russell (1966) proposed the estimated variance of genotype deviations from linear regression model as a further stability measure for consideration while Lin et al. (1986) ascribed this index to a Type III stability concept and interpreted it as an indicator of the goodness of fit of the regression model for explaining stability. Lin and Binns' (1988) Type IV stability concept relates to stability only in time, averaged across test sites and its stability index can be derived from an ANOVA that can be performed on yield values averaged across experiment replicates, including just location and year within locations. These stability indices follow a static concept meaning that a stable genotype is defined as one having an unchanged yield performance regardless of any variation in the environmental conditions (Becker and Leon. 1988). However, the yield performance of a genotype usually responds to favorable or unfavorable environmental conditions and, hence, varies in its performance and a genotype is therefore considered to be economically stable if its contribution to the GE interaction variance is low. Advantages and disadvantages of such statistical methods for stability analysis as well as the relationships between them have been reviewed by several authors (Flores et al. 1998; Adugna 2008; Sabaghnia et al. 2014).

Until now, there have been few attempts to analyze the GE interactions for the newly improved genotypes of barley via simultaneous selection of yield and stability. The aim of this research was to evaluate GE interaction for barley grain yield in warm regions of the semi-arid areas of Iran. The efficiency and ability of our method to use the biological concept of stability for interpretation of the GE interaction and selecting high yield genotypes through a graphic tool will be discussed subsequently.

MATERIALS AND METHODS

Experimental Data

Data used for this study were collected within the barley trial network of DARI (Dryland Agricultural Research Institute, Iran) from 2014 to 2016. Each year, the trials were conducted in five chosen locations (Gachsaran, Moghan, Gorgan, Lorestan and Ilam). The trial locations were selected to sample climatic and edaphic conditions likely to be encountered in barley growing throughout Iran and to vary in latitude, rainfall, soil types, temperature and other agro-climatic factors; their characteristics are given in Table 1. Within each location in a given year, genotypes were planted following a randomized complete block design with three replicates. Entries of the trials consisted of checks (two reference varieties including Khorrm and Mahour), and 16 new improved genotypes. Their name and the origin of the barley genotypes are given in Table 2. The check cultivars were the most famous cultivars which are cultivated commercially in Iran. This study focused on grain yield at 150 g kg 21% of moisture. The total data set considered included 18 entries and 15 trials. Each experimental unit consisted of a 7.35 m^2 plot (six rows 7 m long with 17.5 cm between rows). Seed density was about 230 seeds m^{-2} according to the standard practices and about 70 kg ha^{-1} of N fertilizer was applied according to standard agronomic practices. Appropriate pesticides were used to control insects, weeds and diseases, and appropriate fertilizers were applied at recommended rates usual for the environment.

Stability Statistic

The nine stability statistics most frequently cited are used and a brief description of each follows. The variance of a genotype across environments (S_i^2) can be a measure of

Table 1. Geographical properties of four test locatios.

Location	Altitude (m)	Rainfall§ (mm)	Longitude Latitude	Soil Texture	Soil Type¶
Gachsaran	710	460.8	50°50'E 30°20'N	Silty clay loam	Regosols
Moghan	1100	271.2	48°03'E 39°01'N	Sandy-loam	Cambisols
Gorgan	45	367.5	55°12'E 37°16'N	Silty clay loam	Regosols
Lorestan	1148	433.1	23°26'E 48°17'N	Silt-loam	Regosols
Ilam	975	350.0	46°36'E 33°47'N	Clay-loam	Cambisolas

§ Annual rainfall in trial year.
¶ Based on the FAO soil classification system (FAO 1990).

stability (Roemer 1917; cited in Becker 1981) and coefficient of variability (CV_i) is used as the conventional CV% of each genotype as a stability measure (Francis and Kannenberg 1978). Plaisted and Peterson's (1959) mean variance component for pairwise GE interaction (θ_i) and Plaisted's (1960) variance component for GE interaction ($\theta_{(i)}$) were computed. Wricke's (1962) ecovalence (W_i^2), which is the sum of squared GE interaction of a genotype across all environments, and Shukla's (1972) stability variance (σ_i^2) were calculated. Finlay and Wilkinson's (1963) regression coefficient (b_i) and

Table 2. Origin of the 18 barley genotypes, studied in 15 environments in Iran.

Line No.	Pedigree Information
1	Mahor as check
2	Khorram as check
3	Soufara-02/3/RM1508/Por//Wi2269/4/Hml-02-ArabiAbiad//ER/Apm ICB92-0926-0AP-18AP-0AP-3TR-0AP(7-RBYTA1-2010-11)
4	Soufara02/3/RM1508/Por//Wi2269/4/Hml02ArabiAbiad//ER/Apm ICB92-0926-0AP-18AP-0AP-17TR-0AP(16-PRBYT2009-10)(9-RBYTA1-2010-11)
5	Lignee527/Arar ICB92-0755-22AP-0AP-6AP-0AP-0AP-1AP-0AP(2-RBYTA1-2010-11)
6	Moroc9-75//WI2291/CI01387/3/WI2291*2/WI2269 ICB00-0070-0AP-16AP-0AP(10-RBYTA1-2010-11)
7	ALELI/GOB//E.QUEBRACHO/3/MSEL CBSS00Y00227T-K-0Y-OM-2Y-1M-0M(18-RBYTA1-2010-11)
8	TOCTE/5/ABETO//GLORIA-BAR/COME/3/SEN/4/… CBSS00Y00485T-S-0Y-0M-2Y-0M(17-RBYTA1-2010-11)
9	Rt013/4/Rhn03//Lignee527/NK1272/3/Lignee527/Chn-01//Losaika ICB98-0888-0AP-8AP-0AP-5TR-0AP(14-RBYTA2-2010-11)
10	Hml/Galleon ICB93-1096-0AP-12AP-25TR-3TR-0AP(13-RBYTA2-2010-11)
11	AwBlack/Aths//Rhn-08/3/Malouh(5-RBYTA2-2010-11)
12	ESCOBA/MORADILLA/3/ZHEDAR#2/ND B112//MORA/4/…CBSS00Y00241T-E-OY-0M-2Y-0M(3-RBYTA2-2010-11)
13	Avt/Attiki//M-Att-73-337-1/3/Aths/Lignee686/4/M-Att-73-337-1/3/Mari/Aths*2//Avt/Attik(8-RBYTA2-2010-11)
14	Alanda/Hamra//Alanda-01(10-RBYTA2-2010-11)
15	Eldorado//Alanda/Hamra-01 ICB94-0189-0AP-18AP-0AP(12-RBYTA2-2010-11)
16	GOB/HUMAI10/3/MPYT169(15-RBYTA2-2010-11)
17	Courlis/Rhn-03 ICB93-0923-0AP-2AP-0AP(11-RBYTA2-2010-11)
18	MONA//MZQ/DL71/3/5.(7-RBYTA2-2010-11)

Table 3. Yearly analysis of variance and contribution of each site (S), genotype (g) and their interaction (GS) due to S+G+GS,

		2014		2015		2016	
SOV	DF†	MS‡	%GS	MS	%GS	MS	%GS
Site (S)	4	307336803.9**	70.4	113338631.8**	36.4	774613662.3**	74.1
R/S	15	77125838.6		184363501.0		258434352.4	
Genotype (G)	17	253010888.9**	13.6	333420561.8**	25.2	328859119.0**	7.4
G x S	68	1183985521.4*	16.0	2032843614.6**	38.4	3280614568.7**	18.5
Error	255	5196764390.9		14008912478.5		14070610606.8	
CV§		14.1		20.1		22.7	

** Significant F test at the 0.01 level.
†DF, degrees of freedom
‡MS, Mean Squares
§CV, coefficient of variation

its deviation parameter or δ_i^2 (Eberhart and Russell 1966) via regression of observed values on environmental indices were computed. Perkins and Jinks' (1968) regression coefficient (β_i), similar to b_i except that the observed values are adjusted for site effects before the regression and the residual mean square of deviation from the regression defined in $\delta_{(i)}^2$, is the measure of stability for each genotype (Perkins and Jinks 1968). All analyses were carried out using the SAS program of Hussein et al. (2000) and via a program that was written in QuickBasic to take the stability measurements (Dehghani 1994). These statistical methods have been described in detail by Lin et al. (1986) and Hussein et al. (2000).

Table 4. Combined analysis of variance and contribution of each site (S), year (Y), genotype (g) and their interaction (YS, GY, GS, GYS) due to E + G + GE (environment, genotype and GE).

SOV	DF†	MS‡	% E+G+GE	Sum
Year (Y)	2	9749594.3**	4.2	68.1
Site (S)	4	14721214.3**	12.6	
Y x S	8	29992177.2**	51.3	
R / Y xS	45	770257.3		
Genotype (G)	17	2534604.4**	9.2	9.2
G x Y	34	316245.5**	2.3	22.7
G x S	68	608691.8**	8.8	
G x Y x S	136	398232.3**	11.6	
Error	765	170582.0		
CV§		19.5		

** Significant F test at the 0.01 level.
†DF, degrees of freedom
‡MS, Mean Squares
§CV, coefficient of variation

RESULTS AND DISCUSSION

Analysis of Variance

Considering single year data sets, the components of variance due to genotypes, sites, and their interaction were highly significant (Table 3). The magnitude variance components of estimates of genotype main effect and genotype × site (GS) interaction were relatively equal. The environmental variance represents, on the average, 70% of the phenotypic variance in the first and third years. The analyses showed on average comparable results with a tendency toward a higher relative magnitude of GS effect (16%, 38% and 19% in the first, second and third years, respectively). Overall, for these data sets, about 60% of the total variance was explained by environment differences, about 24% by GE differences and 15% by genotype differences (Table 4). May and Kozub (1995) and Sabaghnia et al. (2013) found somewhat different results for a data set of barley genotypes while Van Eeuwijk et al. (1995) studied maize dry matter with 18 selected cultivars at four locations and found that GE interaction was small in comparison to the genotype main effect. Similarly, Sabaghnia et al. (2012) used additive main effect and multiplicative interaction (AMMI) model for durum wheat multi-environmental trials and found that genotype main effect was small in comparison to the GE interaction. Besides differences in species, traits, and regions, the difference between our results and previous results from the literature may be partly described by the structure of the data sets that were regarded and the selection of the genotypes.

Table 5. Mean yield and parametric stability parameters classified according to three types (Lin et al. 1986) for grain yield of 18 barley genotypes evaluated in 15 environments.

No.	Mean Yield	Type I						Type II		Type III	
		S_i^2	CV_i	W_i^2	θ_i	$\Theta_{(i)}$	σ_i^2	bi	βi	δ_i^2	$\delta_{(i)}^2$
G1	2325.3 A§	45.32	28.95	90.18	8.99	11.44	6.55	1.12	0.12	48.35	6.48
G2	2256.4 AB	34.18	25.91	47.08	7.36	11.64	3.09	0.99	-0.01	36.80	3.62
G3	2391.4 A	59.45	32.24	158.93	11.59	11.11	12.07	1.26	0.26	61.70	9.90
G4	2256.5 AB	46.39	30.19	80.11	8.61	11.49	5.74	1.14	0.14	49.26	5.46
G5	2124.6 BC	35.29	27.96	86.22	8.84	11.46	6.23	0.96	-0.04	37.95	6.58
G6	2293.4 A	31.00	24.28	51.94	7.55	11.62	3.48	0.93	-0.07	33.23	3.84
G7	2018.0 CDE	84.66	45.60	311.74	17.37	10.39	24.35	1.49	0.49	83.08	15.89
G8	1719.0 F	25.20	29.20	329.30	18.04	10.31	25.76	0.53	-0.47	19.52	17.71
G9	2051.4 CDE	51.27	34.90	158.16	11.56	11.12	12.01	1.13	0.13	54.61	11.57
G10	2226.9 AB	27.90	23.72	37.73	7.01	11.69	2.33	0.90	-0.10	29.70	2.56
G11	1964.9 CDE	30.84	28.26	206.55	13.39	10.89	15.90	0.75	-0.25	31.17	13.84
G12	2127.5 BC	30.50	25.96	125.95	10.35	11.27	9.42	0.84	-0.16	31.98	8.82
G13	2096.2 BCD	45.98	32.35	139.23	10.85	10.8311.21	10.49	1.07	0.07	49.34	10.54
G14	1945.0 DE	34.94	30.39	118.08	10.05	11.31	8.79	0.92	-0.08	37.41	8.86
G15	2348.6 A	56.61	32.04	99.58	9.35	11.39	7.30	1.28	0.28	58.23	4.92
G16	1927.1 E	28.59	27.75	216.37	13.77	10.84	16.69	0.71	-0.29	27.89	13.74
G17	2389.8 A	65.53	33.88	181.54	12.45	11.01	13.89	1.33	0.33	66.82	10.21
G18	1759.0 F	24.60	28.20	218.88	13.86	10.83	16.89	0.64	-0.36	22.13	12.48

§ Means of genotypes were compared via Duncan's test.

Stability Analysis

Roemer's (1917 cited in Becker and Leon, 1988) stability index, S_i^2, which describes biological stability or Type I, quantitatively reflects the yield of a genotype in all tested environments. Therefore, genotypes such as G3, G7 and G17 have low biological stability while genotypes such as G8, G10 and G18 have high biological stability (Table 5). The S_i^2 ranged from 24.60 to 84.66 (Table 5). Similarly, Francis and Kannenberg's (1978) coefficient of variability, CV_i, which explains static stability or Type I, quantitatively reflects the yield of a genotype in all tested environments. Thus, genotypes such as G7, G9 and G17 have low static stability while genotypes such as G2, G6 and G10 have high biological static (Table 5).

The CV_i ranged from 23.72 to 45.60 (Table 5). Although Type I is statistically sound theoretically, plant breeders do not use it frequently as they would like to select genotypes with high yield performances besides having biologic (static) or Type I stability. Type I stability is associated with relatively poor yield in environments which are high yielding for other cultivars (Lin et al. 1986).

According to the θ_i parameter of Plaisted and Peterson

Table 6. Variance within location across years (Lin and Binns 1988) and ranks as type IV stability for all five tested locations.

No.	Gachsaran		Moghan		Gorgan		Lorestan		Ilam		Total Rank
	Value	Rank	Value	Rank	Value	Rank	Value	Rank	Value	Rank	
G1	13.7	11	118.8	12	10.3	2	1.0	3	120.7	16	10
G2	12.8	10	127.8	13	19.5	10	0.7	2	38.5	7	9
G3	34.0	18	93.2	5	9.6	1	12.4	11	167.3	17	12
G4	29.3	17	105.9	10	20.4	11	9.5	10	109.7	14	15
G5	20.8	16	74.9	4	14.6	6	13.5	14	74.0	11	11
G6	12.5	9	102.9	9	16.8	8	3.4	6	42.1	9	8
G7	16.3	15	111.1	11	40.9	13	47.3	18	174.4	18	18
G8	2.9	2	30.9	1	18.8	9	8.6	9	41.3	8	2
G9	16.3	14	133.8	15	29.6	12	2.6	5	82.0	12	14
G10	8.4	7	95.5	6	15.0	7	3.6	7	36.8	6	3.5
G11	5.2	4	150.1	16	10.6	3	4.1	8	15.0	2	3.5
G12	3.5	3	99.2	7	43.2	15	13.0	12	19.2	3	7
G13	6.2	5	168.2	18	13.8	5	19.6	17	46.4	10	13
G14	14.2	12	101.3	8	11.7	4	13.3	13	13.8	1	6
G15	15.5	13	129.0	14	44.0	16	16.4	15	89.7	13	17
G16	9.5	8	33.5	2	76.7	18	2.5	4	32.3	5	5
G17	7.2	6	155.5	17	42.9	14	17.9	16	113.3	15	16
G18	2.4	1	56.0	3	64.9	17	0.0	1	26.9	4	1

(1959) which is used in estimating the variance component of GE interaction for each of the possible pairs of genotypes, G2, G6 and G10 genotypes have low magnitudes of θ_i as the average of the estimate for all combinations with a common genotype (Table 5). Based on Plaisted's (1960) $\theta_{(i)}$ which is the modified form of θi parameter, genotypes G2, G6 and G10 have high amounts of $\theta_{(i)}$ and were the most stable genotypes. Ecovalence (W_i^2) of Wricke (1962) was a relative measure based on the genotypes included because the mean of all genotypes was used as standard response in each environment, however, drawing an inference from this type of stability needs caution and so genotypes such as G7, G8 and G18 had relatively higher values, indicating lower stability while G2, G6 and G10 were the most stable genotypes (Table 5). Stability concept being based on Shukla's (1972) stability variance, Lin et al. (1986) classified σ_i^2 as Group B, meaning that it was a relative measure dependent on genotypes included in the test, thus genotypes such as G2, G6 and G10 had relatively lower values, indicating higher stability while G7, G8 and G18 were the least stable genotypes (Table 5).

Linear regression coefficient of Finlay and Wilkinson (1963) represents Type II stability concept, that is, a genotype is stable when its response approaches the average response of all tested genotypes ($b_i = 1$) and genotypes have different bi values, suggests that they

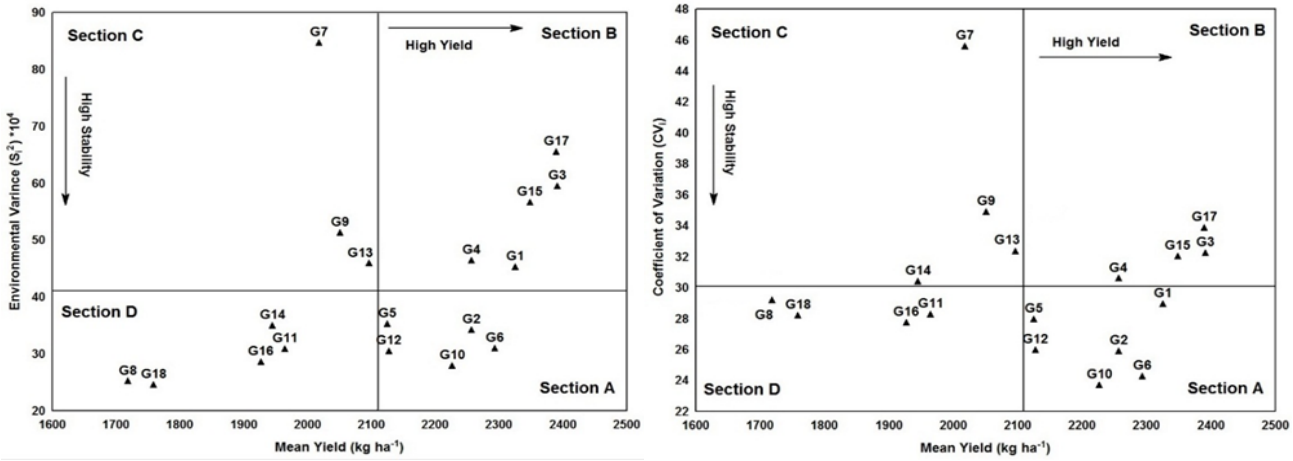

Fig. 1. Group A of stability parameters: (left) environmental variance (Si^2) and (right) coefficient of variation (CV_i).

responded differently to different environments. Genotypes with bi values greater than 1 (such as G3, G7, G15 and G17) indicated higher yield in more favorable environments whereas some genotypes such as G8, G11, G16 and G18, with values less than 1 were adapted to marginal environments while other genotypes such as G2, G5 and G13, with values closer to 1 were more stable (Table 5). Out of the genotypes, eight genotypes (G1, G3, G4, G7, G9, G13, G15 and G17) had the regression value significantly more than zero ($\beta_i > 0$) in the Perkins and Jinks' (1968) regression model, hence, these genotypes were found to be suitable for the favorable environments and there is yield reduction in the unfavorable environments (Table 5). The genotypes G8, G10, G11, G12, G16 and G18 had the negative regression value (below zero, $\beta_i < 0$) and were found to be suited for unfavorable or poor environments while in this method a genotype is stable when its response approaches the average response of all tested genotypes ($\beta_i = 0$) such as genotypes G2, G5, G6 and G14. Similar results were observed by Sabaghnia et al. (2013).

According to Eberhart and Russell (1966), regression coefficient (bi) approximating 1.0 coupled with deviation from regression (δ_i^2) of zero indicates average stability and genotypes have general adaptability when associated with high mean yield while genotypes are poorly adapted to environments when associated with low mean yield. Genotypes G8, G16 and G18 had lower deviation from regression (δ_i^2) values and could be considered as the most stable genotypes while genotypes G3, G7 and G17 had higher δ_i^2 values and could be considered as the most unstable genotypes (Table 5). It is interesting that according to both b_i and δ_i^2 parameters, genotypes G8, G16 and G18 could be regarded as the most stable genotypes. Similar to δ_i^2, Perkins and Jinks (1968) proposed parameter as $\delta_{(i)}^2$ which is indicates deviation from their linear regression model. According to $\delta_{(i)}^2$ parameter, genotypes G2, G6 and G10 were the most stable genotypes while based on both β_i and $\delta_{(i)}^2$ parameters of the Perkins and Jinks (1968) regression model, only genotype G10 could be regarded as the most stable genotype.

Lin and Binns (1988) defined that a Type IV concept of stability relates to consistency of yield exclusively across years within locations. In Gachsaran, genotypes G8, G12 and G18 and in Moghan, genotypes G8, G16 and G18 were identified as the most stable genotypes while in Gorgan, genotypes G1, G2 and G18 and in Lorestan, genotypes G11, G12 and G14 were identified as the most stable genotypes (Table 6). In Ilam location, genotypes G8, G16 and G18 were identified as the most stable genotypes and overall genotypes G8, G10, G11 and G18 were identified as the most stable genotypes based on Type IV stability concept (Table 6).

Graphic Analysis

Due to the complexity of simultaneous selection for both yield performance and stability, most of the suggested methods currently in use do not include graphical facilities, thus, the mean yield is plotted versus each stability parameter. Therefore, to identify the most favorable genotypes (high mean yield and high stability), two dimensional plots were drawn and the X-Y plane is divided into four sections and marked as section A to section D where section A is the best section containing the most favorable genotypes which have high mean yield as well as high stability. According to Fig. 1, genotypes G2, G5, G6, G10 and G12 were identified in the Si^2 parameter while genotypes G1, G2, G5, G6, G10 and G12 were identified in the CV_i parameter. Although only genotype G10 was similar with the previous analysis (in terms of only the stability parameter) based

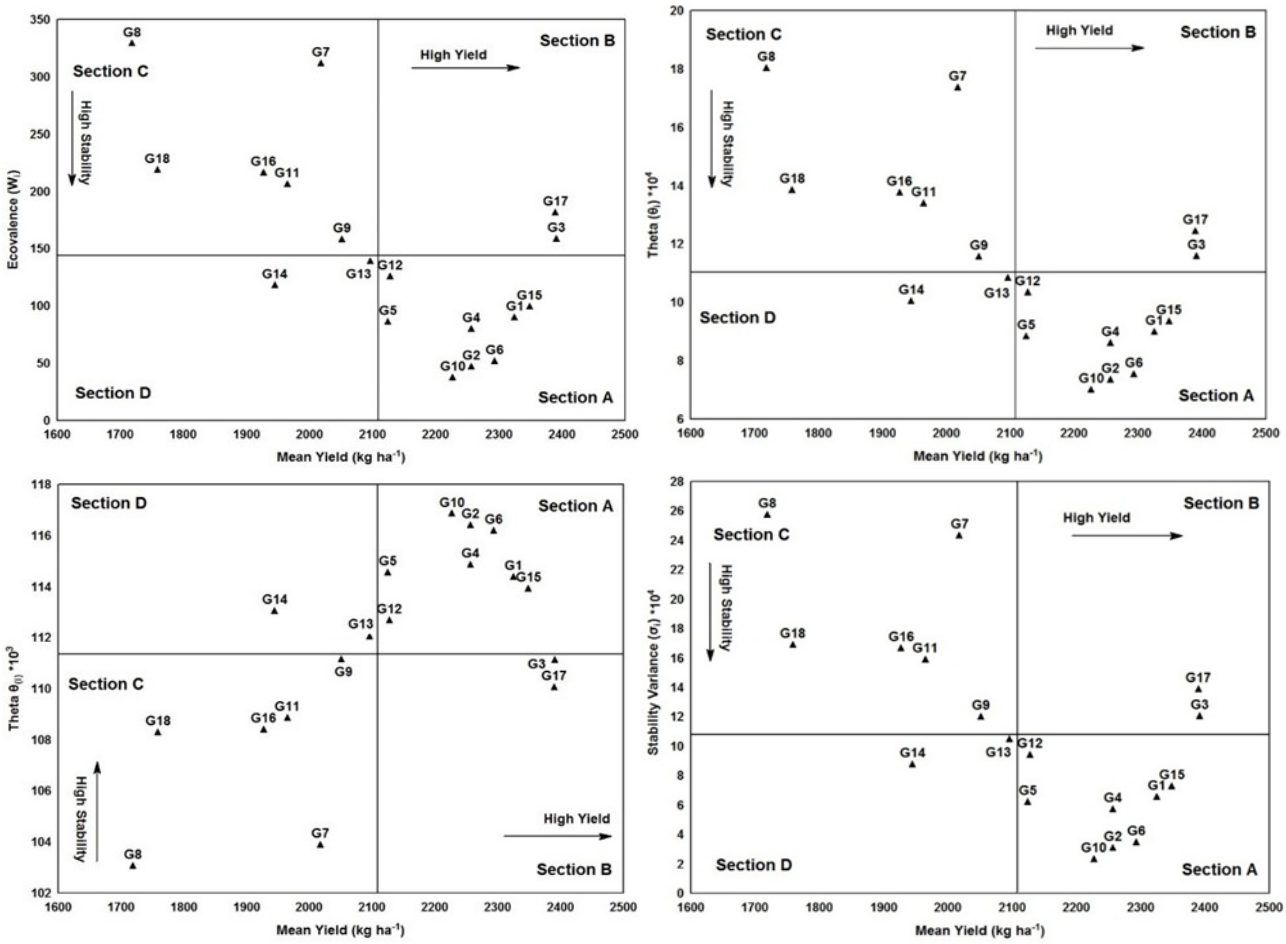

Fig. 2. Group B of stability parameters: (up-left) Ecovalence (W_i^2), (up-right) Theta (θ_i), (down-left) Theta ($\theta_{(i)}$) and (down-right) stability variance (σ_i^2).

on S_i^2, the genotypes G2, G6 and G10 were similar with the pervious analysis based on CV_i parameter. These two mentioned parameters (S_i^2 and CV_i) were classified as Group A through Lin et al. (1986) which represents Type I stability concept.

According to Fig. 2, regarding ecovalence (W_i^2) and mean yield, genotypes G1, G2, G4, G5, G6, G10, G12 and G15 were identified as the most favorable genotypes and similarly, based on theta (θ_i) of Plaisted and Peterson's (1959) model and yield performance, genotypes G1, G2, G4, G5, G6, G10, G12 and G15 were the most favorable genotypes. Genotypes G1, G2, G4, G5, G6, G10, G12 and G15 were identified as the most favorable genotypes based on theta ($\theta_{(i)}$) of Plaisted (1960) and mean yield (section A in this case) while genotypes G1, G2, G4, G5, G6, G10, G12 and G15 were the most favorable genotypes based on Shukla's (1972) stability variance (σ_i^2) (Fig. 2). Group B of stability parameters including Ecovalence (W_i^2), Theta (θ_i), Theta ($\theta_{(i)}$) and stability variance (σ_i^2) according to Lin et al. (1986) which have SS (sums of squares) identified the same genotypes as the most favorable genotypes. These parameters represent Type I stability concept similar to Group A, and therefore have biological concept of stability. Considering high coefficient of linear regression (bi) and high mean yield simultaneously, genotypes G1, G2, G3, G4, G5, G6 , G10, G15 and G17 were located in section A and were identified as the favorable genotypes (Fig. 3). Similar results were obtained for β_i of Perkins and Jinks' (1968) model, thus, both regression coefficients (b_i and β_i) having Type II stability concept determined same genotypes that some of them were identified as the most stable genotypes previously but most of them were the high mean yielding genotypes. According to Fig. 4, regarding deviation mean squares from liner regression (δ_i^2) of Eberhart and Russell (1966) and mean yield performance, genotypes G2, G5, G6, G10 and G12 were identified as the most favorable genotypes while based

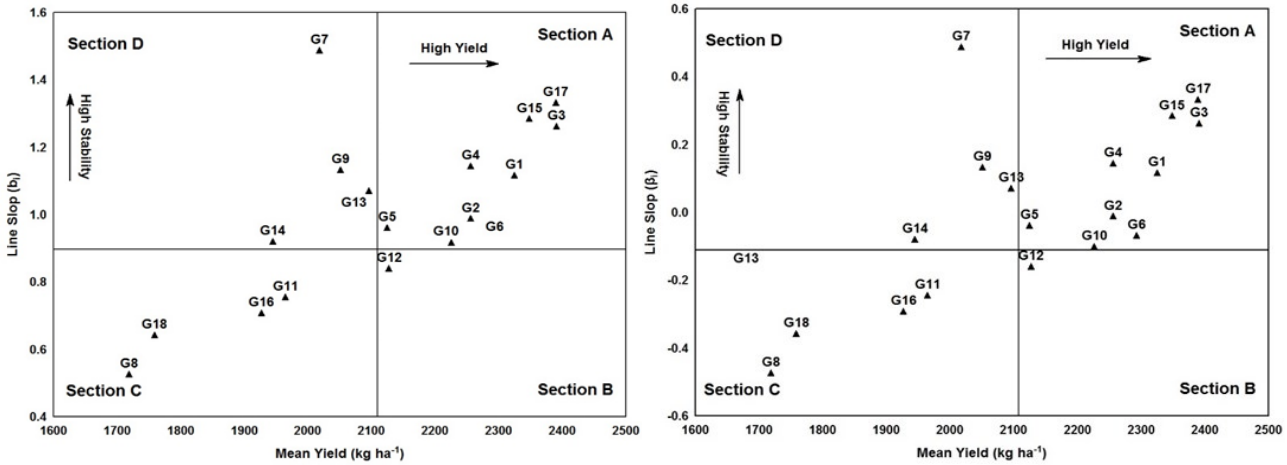

Fig. 3. Group C of stability parameters: (left) linear regression coefficient (b_i) and (right) line slope (β_i).

on $\delta_{(i)}^2$ of Perkins and Jinks (1968) and yield genotypes, G1, G2, G4, G5, G6, G10, G12 and G15 were located in section A as the most favorable genotypes. Both of the above mentioned parameters illustrated Type III stability concept. According to plot of mean yield versus variance across years within locations (as the index of Type IV stability concept), the most favorable genotypes at Gachsaran were G10, G12 and G17, at Moghan were G3, G10 and G13, at Gorgan were G1, G2, G3, G4, G6 and G10, at Lorestan were G1, G2, G4, G6 and G10, and at Ilam were G2, G6, G10 and G12 (results are not shown).

Final Decision

The simultaneous selection for yield and stability need to compare genotypes across the yield and stability issues and such comparisons would identify genotypes that had good performance in poor environments as well as those that act good in favorable environments. Usually, the most stable genotypes are expected to perform highly in low yield environments while the high-yielding genotypes, particularly those that respond favorably when growing conditions are more ideal, are likely to be suitable for high-yielding environments (Kang and Phan 1991). All of the four stability types (Type I to Type IV) tend to be somewhat higher for measures that relate to the static concept of stability. Most crop geneticists have used the Stability to characterize a genotype which has a relatively constant yield performance, independent of environmental condition changes and so they have looked for genotypes with minimum variation of yield over environments, thus this stability definition may be considered as a Biological or Static concept of stability (Becker and Leon 1988).

However, it is clear that all of the stability types of Lin et al. (1986) and static stability concept of Becker (1981) are preferable for most farmers but these stability tools

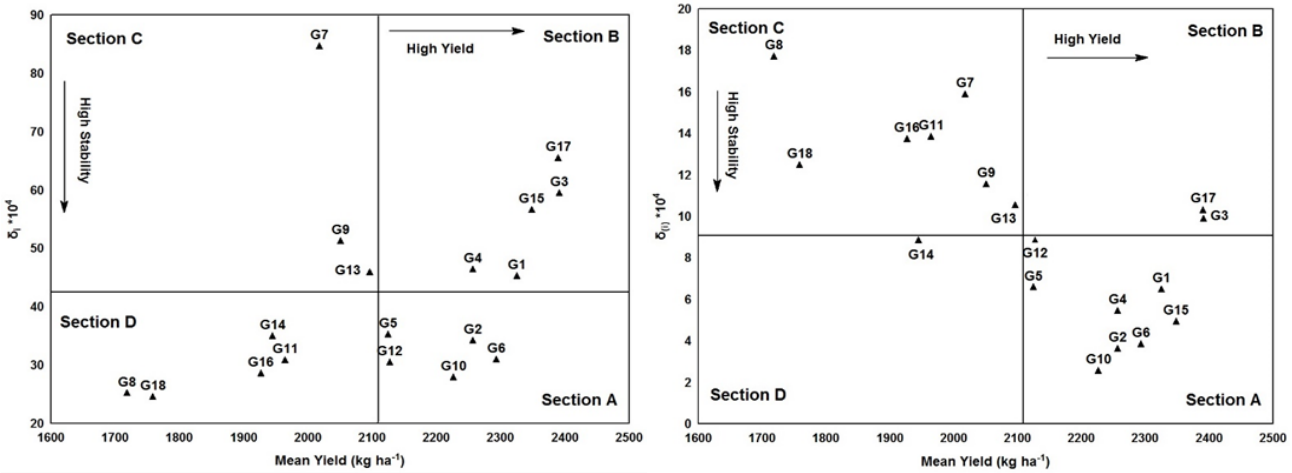

Fig. 4. Group D of stability parameters: (left) deviation mean squares (MS) from linear regression (δ_i^2) and (right) deviation MS from linear regression ($\delta_{(i)}^2$).

usually introduce low or moderate yielding genotypes as the most stable ones. To overcome this problem, simultaneous selection for both yield and stability is suggested (Kang 1993). Plots of graphic analysis can be used effectively to distinguish the high-yielding genotypes with stable performance, two-dimensional plots (yield versus stability) are presented to separate the genotypes of section A (high-yielding and stable genotypes) from the other sections (B, C and D), and to illustrate the advantage of stability indices as selection criterion for identifying high-yielding and the most stable genotypes. We found that according to Types I, II and III of stability, genotypes G2, G5, G6, G10 and G12 were determined as the most stable genotypes and based on Type IV of stability, genotypes G8, G10, G11, G16 and G18 were identified as the most stable genotypes while genotypes G1, G3, G4, G6, G10, G15 and G17 were identified as the high-yielding genotypes. Only genotypes G6 and G10 were common between stability indices and mean yield performance and other stable genotypes did not have high yield performance. Regarding graphic analysis, genotypes G1, G2, G4, G5, G6, G10, G12 and G15 were selected as the most favorable genotypes whereas genotypes G1, G4, G6, G10 and G15 were common with the high-yielding genotypes. Therefore, it could be concluded that graphic analysis of stability could determine high mean yielding genotypes with real stability concept (static or biologic concept).

CONCLUSION

Finally, the following major findings can be summarized from this research: (1) graphic analysis of stability (plotting mean yield versus stability parameter) is useful for identification of the most favorable genotypes and could help to simultaneously select for both high yielding and high stable genotypes, (2) Genotypes G1 (2325.2 kg ha^{-1}), G2 (2256.4 kg ha^{-1}), G6 (2293.4 kg ha^{-1}), G10 (2226.9 kg ha^{-1}) and G15 (2348.6 kg ha^{-1}) were the most favorable genotypes for barley grain yield, and are thus recommended for commercial release in Iran, (3) Whenever new cultivars are proposed for commercial release, information on GE interactions and stability, clearly indicating their specific and/or general adaptations, needs to be available to the farmers.

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