Iranian Journal of Genetics and Plant Breeding, 10(1): 11-30, (2021)

IMAM KHOMEINI INTERNATIONAL UNIVERSITY
IJGPB
Iranian Journal of Genetics and Plant Breeding
Print ISSN : 2251-9610
Online ISSN : 2676-346X

Appraising of barley promising lines relying on high grain yield and desirable agronomy traits in rainfed conditions using SIIG and ASIIG techniques

Ibrahim Hemadesh[1], Jafar Ahmadi[1*], Sedigheh Fabriki-Ourang[1], Behrouz Vaezi[2]

[1]Department of Genetics and Plant Breeding, Imam Khomeini International University, Qazvin, Iran.
[2]Kohgiluyeh-Boyerahmad Agricultural and Natural Resources Research and Education Center, Agricultural Research, Education and Extension Organization (AREEO), Yasuj, Iran.
[*]Corresponding author, 0000-0002-2709-9392. Email: j.ahmadi@eng.ikiu.ac.ir. Tel: +98-28-33901227.

ABSTRACT INFO

Research Paper

Received: 24 Apr 2022

Accepted: 20 Jul 2022

ABSTRACT

This study aimed to investigate the genetic diversity of 140 barley advanced lines, using Selection Index of Ideal Genotype (SIIG) and Adjusted Selection Index of Ideal Genotype (ASIIG) indicators for introduction and cultivation of suitable lines in rainfed conditions. The highest coefficient of variation was related to the type of spike, flag leaf area, seeds per spike, peduncle length, flag leaf width, and early growth vigor. The stepwise regression showed that the early growth vigor, 1000-seeds weight, spike type, days to heading, plant height, number of seeds per spike, and flag leaf length were the most critical components, which affect the grain yield under the rainfed conditions. The results of SIIG showed that lines 4, 43, 47, 40, 70, 96, 137, 3, 57, and 45 were the best lines with the highest SIIG values. The SIIG index divided all lines into seven groups; the average grain yield of lines in groups I and II were higher than the average grain yield of control cultivars and the other groups. According to ASIIG plots, lines 47, 3, 43, 45, 137, 96, and 40 were placed in the ideal quarter. Finally, the SIIG and ASIIG were compatible in selecting the best lines. ASIIG was more suitable for separating the ideal lines, because it participated all traits commensurate with their importance in the end product quantity and quality.

Key words: Drought stress, Genetic diversity, PCV, Stepwise regression, TOPSIS model.

How to cite this article:
Hemadesh I., Ahmadi J., Fabriki-Ourang S., and Vaezi B. (2021). Appraising of barley promising lines relying on high grain yield and desirable agronomy traits in rainfed conditions using SIIG and ASIIG techniques. *Iranian Journal of Genetics and Plant Breeding,* 10(1): 11-30.
DOI: 10.30479/IJGPB.2022.17153.1315

INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of the most important cereal crops with an area of approximately 50 million hectares and a production of 145 million tons worldwide (Faostat, 2015). Barley is widely cultivated in arid and semi-arid Mediterranean regions for forage, and as a grain crop (Al-Karaki, 2001), has a relatively high drought tolerance, where it can grow with less soil moisture (Mishra *et al.,* 2000). Drought increases the demand for irrigation, which currently accounts for 70% of global water consumption and it is expected to increase to 10% by 2050 due to climate change alone (Wada *et al.,* 2013). Therefore, fighting against drought will not be possible by improving the irrigation infrastructure. Barley is a critical crop in semi-arid areas due to its drought tolerance compared to other essential grains, especially in the Middle East, North Africa, Southern and Eastern Europe (Newman and Newman, 2006). Due to desertification and soil salinity in many regions of the world, it is necessary to identify compatible accessions with higher resistance to abiotic stresses (Sebi *et al.,* 2012). For understanding the plants adaptation to different stresses, a study on genetic diversity and stress resistance mechanisms must be carried out under stressful conditions (Bracki *et al.,* 2015; Kerwin *et al.,* 2015). Examination of drought tolerance in arid regions should be considered with regard to several agronomic and physiological characteristics (Jabbari *et al.,* 2019).

Researchers have performed many studies to evaluate the traits and their relationships with grain yield using factor analysis and other multivariate methods (Drikvand *et al.,* 2011; Mohtashami, 2015; Zeng, 2015). Most of these studies only dealt with the topic of discussing the relationship between the traits and performance, and did not address the topic of selecting the best genotype. Therefore, there is a need for methods that can select the desired genotypes according to the studied traits; the selection index of ideal genotype (SIIG) is one of these methods. This technique, SIIG, was first used to integrate stability analysis methods (Zali *et al.,* 2015) and different drought tolerance indices (Zali *et al.,* 2015) to increase the selection efficiency of ideal genotypes. This technique was derived from TOPSIS model (the technique for order of preference by similarity to an ideal solution), where Wang and Yoon (1981) introduced this technique for the first time as a multi-criteria decision method. Since each genotype may be superior in terms of index or attribute and by increasing the number of characteristics or indices, it may be difficult for the researcher to select the appropriate genotype; with the help of the SIIG method, all indices and characteristics become one index, and therefore, ranking and determining superior genotypes become more straightforward (Zali *et al.,* 2019). The basic concept of this method is to select the best genotype, which must be at the shortest distance from the favorable ideal genotype and the maximum distance from the unfavorable ideal genotype. Simultaneous selection for grain yield and stability can be made by this method to evaluate the final ranking of stable cultivars (Zali *et al.,* 2015). The SIIG method can rank and compare different genotypes, select the best genotypes, determine the distances between genotypes, and their grouping. While this method has many advantages, it does not consider the appropriate weight for critical traits based on the researcher's goal. Therefore, it is necessary to somehow adjust this index with the proper weight for essential traits. Adjusted Selection Index of Ideal Selection (ASIIG) method, in addition to modifying the SIIG method based on trait weighting, facilitates decisions about the nature of genotype performance (Taghizadeh *et al.,* 2020).

Regarding the important role of genetic diversity in the breeding program, there is no doubt that studying new barley lines with the desirable morphological characteristics is one of the most appropriate methods to improve breeding and introduce commercial cultivars, which ultimately leads to increased barley production. Therefore, this study aimed to investigate the genetic diversity of barley advanced lines in terms of grain yield and several morphological traits and integrate several critical morphological traits to evaluate genotypes better, using SIIG and ASIIG indicators for introduction and cultivation of suitable lines in rainfed conditions.

MATERIALS AND METHODS

In order to investigate the genetic diversity and the selection of barley germplasm under rainfed conditions, a field experiment was carried out using 140 barley advanced lines obtained from ICARDA, International Center for Agricultural Research in the Dry Areas, (Supplementary Table 1) along with two local cultivars Khorram and Fardan as controls. The characteristics of the two control cultivars include early maturity, high grain yield, and tolerance to abiotic stresses. For this purpose, an experiment was performed in Gachsaran Agriculture Research Station of Kohgiluyeh and Boyer-Ahmad Province, Iran, located in Nazlu region, with a latitude of 30° and 18′ and a longitude of 50° and 59′ and an altitude of 668 meters above the sea level in silty-clay loam soil with organic matter of 0.5 to 0.75%. This experiment was carried out using a systematic preliminary performance comparison in the field condition. The lines were planted before adequate rainfall with a grain density of 200 seeds per square meter using a winter stiger planting machine. Different traits were measured during the growing season and after harvesting, including early growth vigor, flag leaf length, flag leaf width, flag leaf area, days to maturity, days to heading, days to flag leaf senescence, plant height, peduncle length, spike length, awn length, fertile tiller, 1000-seed weight, grain yield, agricultural score (scored from one to five), number of seeds per spike, number of spikes per square meter, canopy temperature and chlorophyll content.

First of all, the range of traits, mean, variance, standard deviation, and coefficients of variation for agronomic traits were calculated. Then, stepwise regression was used to identify the traits playing the most crucial role in justifying grain yield changes. Traits that entered the regression model were used to investigate genetic diversity, and their integration was done by the SIIG method. The method of calculating SIIG and ASIIG are as follows:

1. Formation of decision matrix: According to the number of genotypes and different studied traits, the data matrix was formed as follows: $D = \begin{bmatrix} X11 & X12 & \ldots & X1m \\ Xn1 & Xn2 & \ldots & Xnm \end{bmatrix}$, where **xij**: the value of **i** attribute (i=1, 2,… n) is concerning **j** genotype (j=1, 2,… m).

2. Converting the data matrix to a normal matrix (R matrix): The equation $\mathrm{rij} = \frac{\mathrm{xij}}{\sqrt{\sum_{i=1}^{n} \mathrm{xij}^{2}}}$ was formed to normalize data: The R matrix is defined as follows: $R = \begin{bmatrix} r11 & r12 & \ldots & r1m \\ rn1 & rn2 & \ldots & rnm \end{bmatrix}$

3. Determining the favorable ideal and unfavorable ideal genotypes: The favorable genotype is obtained from the sum of the ideal values of each of the studied traits. In contrast, the unfavorable genotype was obtainted from the sum of the weak values of each of the desired. For example, in grain yield, the maximum grain yield of a genotype is considered favorable, and the low grain yield is considered unfavorable. Also, regarding the number of days to flowering, if the early maturity of the genotypes is essential, the positive value is similar to the minimum number of days to flowering for genotypes, and the negative value is equal to the maximum number of days to flowering for genotypes.

4. Identifying the weight of the traits: Only the traits entered in multiple regression were used in SIIG calculation with equal weights. In calculating ASIIG, due to creating a balance between traits and observing the weight of each trait according to the researcher's vision, the purpose of the research and the motivation for selection are needed. The optimal weight of each trait in this research was identified based on regression coeficients.

5. Calculating the distance from favorable and unfavorable ideal genotypes: For each trait, the distance from the favorable ideal genotype (di^{+}) and unfavorable ideal genotype (di^{-}) was calculated using

$$di^{+} = \sqrt{\sum_{j=1}^{m} (rij - rj^{+})^{2}} \text{ and } di^{-} = \sqrt{\sum_{j=1}^{m} (rij - rj^{-})^{2}},$$

rij: the normalized value of the trait of **i** (i=1, 2,… n) concerning the genotype of **j** (j=1, 2,… m). **ri+** and **ri-**: the normalized value of the favorable ideal genotype and the unfavorable ideal genotype for each trait, respectively. **di**$^{+}$: distance from favorable ideal genotype; **di-**: distance from unfavorable ideal genotype.

6. Calculation of SIIG and ASIIG indicators: $ASIIG/SIIG = \frac{di^{-}}{di^{+} + di^{-}}$; The SIIG/ASIIG value varies from 0 to 1, the best genotype was the one that had the shortest distance from the favorable ideal and was the farthest from unfavorable genotypes, the closer the option is to the ideal genotype, the closer its SIIG value is to 1 (Zali *et al.,* 2015; Zali *et al.,* 2016).

In this study, we used JMP software in order to calculate the descriptive statistics of traits and stepwise regression for grain yield, also Excel ver. 2016 and R ver 3.4.4 softwares were used to calculate SIIG and ASIIG values.

RESULTS AND DISCUSSION

Trait variation and genetic diversity

In this research, the descriptive statistics for all studied traits are presented in Table 1. The higher range of variations emphasized the existence of significant diversity in most traits. Maximum ranges were attributed to grain yield (1703-5545 kg/ha) with a mean of 3805.12 kg/ha, the number of seeds per spike (18-64) with a mean of 35.91, plant height (67.66-107.66 cm)

Table 1. Descriptive statistics for all studied traits in 140 barley advanced lines.

Traits	Mean	Standard deviation	Minimum	Maximum	Coefficient of variation (%)
R/T	3.72	1.81	2	6	53.44
E.G.V	6.60	2.20	1	9	33.28
DHE	92.26	2.63	85	98	2.85
DMA	133.28	2.48	126	139	1.86
F.L.L	9.04	1.83	5	15	20.29
F.L.W	1.08	0.83	0.5	2.16	35.1
L.A	7.74	3.86	2	20.5	49.85
PED.L	6.16	2.51	2	13.33	40.78
Sp.L	6.92	1.30	4	11.33	18.8
AWN.L	10.45	1.37	7	20	13.03
PLH	87.63	7.79	67.66	107.66	8.89
Can.t	22.79	1.34	19.83	26.77	5.9
Chl. C	48.24	4.91	31.1	57.8	10.19
DFLS	129.46	3.7	124	161	2.86
F.T	3.87	0.9	1.9	6.65	23.71
Ag.S	4.36	0.85	2	5	19.54
G/S	35.91	15.99	18	64	44.54
TKW	37.52	1.78	34.4	43.4	4.76
GY	3805.12	834.33	1703	5545	21.92

R/T: Spike type, E.G.V: Early growth vigor, DHE: Days to heading (days), DMA: Days to maturity (days), F.L.L: Flag leaf length (cm), F.L.W: Flag leaf width (cm), L.A: Flag leaf area (cm^2), PED.L: Pedal length (cm), Sp.L: Spike length (cm), AWN.L: Awn length (cm), PLH: Plant height (cm), Can.t: Canopy temperature, Chl. C: Chlorophyll content (mg/gfw), DFLS: Days to flag leaf senescence (days), F.T: Fertile Tillers, Ag.S: agricultural score, G/S: Number of seeds per spike, TKW: Weight of a thousand seeds (g), GY: Grain yield (kg/ha).

with a mean of 87.63 cm, flag leaf area (2-20.5 cm^2) with a mean of 7.74 cm^2, days to heading (85-98) with a mean of 92.26 days, peduncle length (2-13.33 cm) with a mean of 6.16 cm and 1000-seed weight (34.4-43.4 g) with a mean of 37.52 g. The highest coefficient of variation was related to the type of spike (53%), flag leaf area (49.85%), seed per spike (44.54%), peduncle length (40.78%), flag leaf width (35.1%), early growth vigor (33.28%), fertile tillers (23.71%), grain yield (21.92%), and flag leaf length (20.29%). The lowest coefficient of variation was related to days to maturity (1.86%), days to heading (2.85%), days to flag leaf senescence (2.86%), 1000-seed weight (4.76%), and canopy temperature (5.9%), as shown in Table 1.

Phenotypic coefficient of variation (PCV) values of more than 20% are considered to be high, and values less than 10% are considered low. Values in between are known as medium (Yacoubi *et al.,* 2020). In our study we showed that the highest coefficient of variation was related to the type of spike, flag leaf area, seeds per spike, and peduncle length and the lowest coefficient was related to days to maturity, days to heading, and days to flag leaf senescence. In a study by Derbew *et al.* (2013) on 225 genotypes, they concluded that flag leaf width, spikelets per spike, days to heading, head length, 1000-seed weight, plant height, and grain yield per plant displayed moderate values of PCV, whereas days to maturity had the lowest PCV value. In another study, in drought stress conditions, the highest coefficient of variation was recorded for plant height, a number of effective tillers per plant, spike length, biological yield per plant, relative water content, and seed yield per plant. Moderate PCV was observed for a number of spikelets per spike and harvest index. Low PCVs were observed for days to 50% flowering, days to maturity, membrane stability index, and chlorophyll content, which indicated that selection might not be effective for these characteristics (Shrimali *et al.,* 2017). In a study conducted by Addisu and Shumet (2015), variability, heritability, and genetic advance of grain yield were assessed based on morphological traits of 36 barley accessions. The number of tillers per plant (46.1%), grain yield (37.6%), the number of spikelets per spike (29.1%), and the number of grains per spike (26.4%) had high PCVs. Also, Jalata *et al.* (2011), in a study concluded that PCV was relatively higher for grain yield per plot (23.27%), the number of kernels per spike (20.70%) and spike weight (15.20%). In the study of Shakhatreh *et al.* (2010), results showed a high variability among *Hordeum vulgare* ssp.spontaneum C. Koch accessions for most of the traits. In our study, the high PCVs obtained for spike type, early growth vigor, flag leaf area, flag leaf width, peduncle length, seed per spike, number of fertile tillers, and grain yield per hectare indicated that these traits play a decisive role in creating diversity. The PCV of the studied traits showed a great diversity among the studied lines, and thus breeders can select with high efficiency among these genetic materials.

In a study carried out by Abdul Ghani *et al.* (2015), in order to screen a diverse collection of 233 spring barleys, a substantial level of phenotypic and genetic variation was observed. A wide variation among genotypes of North African barley was reported for morphological traits (Naceur *et al.,* 2012). Haseneyer *et al.* (2010) studied 224 genotypes of spring barley and reported a significant variation in characteristics of flowering time, plant height, 1000-grain weight, crude protein content, and starch content. Ebrahim *et al.* (2014) reported the highest range (2258 to 6202 kg/ha) for grain yield followed by plant height (82.9 to 118.1 cm) and days to maturity (110.3 to 137) in barley genotypes. Derbew *et al.* (2013) reported that grain yield showed the most comprehensive range (436 to 3752 kg/ha) followed by plant height (44.95 to 94.1 cm), days to maturity (92 to 131), and days to heading (57 to 94). According to the grain yield range in the current study, we observed a great variation compared to the varieties used by Ebrahim *et al.* (2014) and Derbew *et al.* (2013). However, the range of variation in plant height showed no difference with other studies except for Derbew *et al.* (2013) study. Also, the number of days to heading and weight of 1000-seeds in barley lines used in this study showed a small range of variability compared to the cultivars used by Alemayehu and Parlevliet (1997), which ranged from 62 to 97 days and 21.22 to 52.7 g, respectively.

Stepwise regression

The regression model eliminated the ineffective traits and examined the traits that justify a significant amount of grain yield changes. In this study, the stepwise regression model was used to determine the effective components in the grain yield of 140 barley advanced lines based on the 19 traits considered under rainfed conditions. A total of seven traits entered the model; the early growth vigor, which was the first trait entering the model, explained 58% of the grain yield changes. The following entered traits in the model were as follows: 1000-seed weight, spike type, plant height, days to heading, number of seeds per spike, and flag leaf length, which explained a total of 69% of grain yield changes. The contribution of other traits in justifying grain yield changes was minimal.

Selection Index of Ideal Genotype (SIIG) and Adjusted SIIG (ASIIG)

The seven traits entered in the regression model, along with grain yield, were used to investigate genetic diversity and their integration to select the best lines in terms of grain yield and the other traits using the SIIG method. The results of SIIG index showed that lines 4, 43, 47, 40, 70, 96, 137, 3, 57, 45 with the highest SIIG values (0.819, 0.816, 0.808, 0.800, 0.753, 0.749, 0.748, 0.747, 0.733 and 0.709, respectively) were the best lines. The grain yield of these selected lines (except line 70) was higher than other lines, and both control cultivars. On the other hand, according to the study, lines 166, 56, 106, 167, 124, 10, 136, and 107 with the lowest SIIG values (0.163, 0.179, 0.199, 0.232, 0.240, 0.266, 0.275, and 0.286, respectively) were the weakest lines in terms of grain yield and other grain yield -related traits (Table 2 and Figure 1). These lines had a lower grain yield compared to other studied lines and control cultivars.

By evaluating the efficiency of the SIIG index on selecting the best lines in terms of grain yield, 1000-seed weight, spike type, early growth vigor, day to heading, plant height, number of seeds per spike, and flag leaf length simultaneously, the studied lines were segregated into seven groups. It is also worth noting that since the SIIG index in this study was less than 0.9, the first group consisted of lines whose SIIG values were greater than 0.8 and less than 0.9. Lines whose index was greater than 0.7 and less than 0.8 were in the second group, and other lines were also grouped accordingly (Table 3 and Figure 1). The results of lines grouping based on SIIG index (Table 3) showed that in group I, there were four lines with an average grain yield of 5015.42 kg/ha, an average number of seeds per spike of 60.5, 1000-seed weight of 38.6 g, flag leaf length of 12.17 cm, and early growth vigor of 8.25. These traits in the first group were higher than the average performance of all other groups and control cultivars. On the other hand, no significant differences were observed for days to heading and plant height in any of the groups (except groups 6 and 7) with the control cultivars (Tables 2 and 3). In group II, there were seven lines whose average grain yield, number of seeds per spike, flag leaf length, and growth vigor were 4376.85 kg/ha, 57.11, 10.22 cm, and 8.22, respectively. In group II, lines in terms of grain yield, number of seeds per spike, flag leaf length, and early growth vigor had higher values compared to all other groups and control cultivars except for group I. But the 1000-seed weight obtained for this group had no significant difference from other groups and control cultivars.

Table 2. Amounts of SIIG and ASIIG indices for 140 barley advanced lines under rainfed conditions.

SIIG index					Line no.	ASIIG index			
Group	Rank	SIIG	d-	d+		Rank	ASIIG	d-	d+
6	114	0.393	0.095	0.146	Con.k	81	0.530	0.018	0.020
5	106	0.403	0.099	0.147	Con.F	72	0.553	0.017	0.021
2	**8**	**0.748**	**0.173**	**0.058**	**3**	**2**	**0.856**	**0.005**	**0.031**
1	**1**	**0.819**	**0.178**	**0.039**	**4**	**3**	**0.852**	**0.005**	**0.030**
3	17	0.683	0.149	0.069	5	42	0.628	0.013	0.022
2	**13**	**0.697**	**0.163**	**0.071**	**6**	**13**	**0.729**	**0.010**	**0.026**
4	48	0.572	0.138	0.103	7	92	0.511	0.018	0.019
3	32	0.644	0.146	0.081	8	55	0.605	0.014	0.022
5	94	0.431	0.101	0.134	9	109	0.461	0.019	0.017
7	137	0.266	0.060	0.165	10	129	0.352	0.023	0.012
6	126	0.344	0.079	0.151	11	123	0.373	0.022	0.013
4	51	0.555	0.126	0.101	12	103	0.477	0.019	0.017
3	34	0.642	0.147	0.082	15	18	0.672	0.012	0.024
5	98	0.415	0.100	0.141	16	89	0.518	0.018	0.0198
4	46	0.583	0.129	0.092	17	70	0.557	0.016	0.020
5	63	0.484	0.125	0.134	18	40	0.629	0.015	0.026
5	68	0.475	0.128	0.141	19	30	0.648	0.015	0.028
5	95	0.430	0.106	0.140	20	98	0.489	0.019	0.018
3	14	0.695	0.165	0.072	**21**	**6**	**0.840**	**0.006**	**0.030**
5	67	0.475	0.117	0.130	22	60	0.595	0.016	0.023
4	49	0.572	0.130	0.097	23	105	0.473	0.019	0.017
6	115	0.392	0.093	0.143	24	101	0.480	0.019	0.018
5	70	0.472	0.118	0.132	27	130	0.346	0.026	0.014
5	104	0.405	0.097	0.142	28	77	0.538	0.017	0.020
3	33	0.644	0.143	0.079	29	21	0.664	0.012	0.023
3	20	0.669	0.160	0.079	30	35	0.638	0.013	0.024
5	89	0.437	0.105	0.135	31	96	0.4922	0.019	0.018
4	50	0.561	0.129	0.101	32	75	0.543	0.017	0.020
3	38	0.619	0.147	0.09	33	17	0.680	0.011	0.024
3	28	0.649	0.155	0.084	34	54	0.606	0.015	0.023
5	64	0.483	0.124	0.133	35	37	0.632	0.015	0.026
5	83	0.445	0.120	0.149	36	41	0.629	0.015	0.026
6	130	0.336	0.078	0.154	39	134	0.313	0.024	0.011
1	**4**	**0.801**	**0.176**	**0.044**	**40**	**9**	**0.756**	**0.008**	**0.026**
5	112	0.397	0.095	0.144	41	110	0.458	0.020	0.017
5	100	0.412	0.097	0.138	42	83	0.527	0.017	0.019
1	**2**	**0.816**	**0.181**	**0.041**	**43**	**4**	**0.849**	**0.005**	**0.031**
3	29	0.646	0.143	0.078	44	26	0.651	0.012	0.023
2	**10**	**0.709**	**0.169**	**0.069**	**45**	5	0.847	0.005	0.030
5	71	0.470	0.123	0.138	46	34	0.640	0.015	0.026
1	**3**	**0.808**	**0.184**	**0.044**	**47**	**1**	**0.907**	**0.003**	**0.031**
3	36	0.625	0.138	0.083	48	59	0.598	0.014	0.021
5	113	0.395	0.097	0.148	51	106	0.469	0.020	0.018
5	86	0.442	0.109	0.138	52	61	0.591	0.016	0.023
3	**19**	**0.669**	**0.146**	**0.072**	**53**	53	0.608	0.014	0.022
3	18	0.672	0.153	0.075	**54**	**10**	**0.732**	**0.009**	**0.026**
6	133	0.300	0.067	0.155	55	135	0.274	0.025	0.010
7	141	0.179	0.039	0.181	56	139	0.156	0.029	0.005
2	**9**	**0.733**	**0.158**	**0.058**	**57**	11	0.732	0.009	0.025
5	105	0.404	0.097	0.143	58	111	0.451	0.020	0.0169
5	102	0.411	0.102	0.146	59	79	0.535	0.018	0.021
5	99	0.414	0.099	0.140	60	76	0.541	0.017	0.020

SIIG: Selection index of ideal genotype, ASIIG: Adjusted selection index of ideal genotype, di$^+$: Favorable ideal genotype, di$^-$: Unfavorable ideal genotype.

Table 2 (Continued). Amounts of SIIG and ASIIG indices for 140 barley advanced lines under rainfed conditions.

SIIG index					Line no.	ASIIG index			
Group	Rank	SIIG	d-	d+		Rank	ASIIG	d-	d+
5	111	0.397	0.098	0.149	63	91	0.515	0.018	0.019
5	74	0.466	0.128	0.146	64	25	0.653	0.015	0.028
4	56	0.515	0.133	0.126	65	31	0.647	0.015	0.027
6	134	0.296	0.067	0.159	66	126	0.363	0.023	0.013
5	84	0.444	0.108	0.136	67	51	0.614	0.015	0.024
3	37	0.622	0.142	0.086	68	94	0.504	0.018	0.018
4	53	0.548	0.150	0.124	69	38	0.631	0.015	0.026
2	**5**	**0.753**	**0.172**	**0.056**	**70**	15	0.706	0.011	0.026
5	93	0.431	0.105	0.139	71	112	0.450	0.020	0.017
6	120	0.358	0.082	0.148	72	117	0.412	0.021	0.015
3	31	0.645	0.148	0.081	75	48	0.618	0.014	0.023
5	61	0.493	0.130	0.134	76	23	0.660	0.014	0.028
4	52	0.553	0.128	0.103	77	88	0.521	0.017	0.019
4	47	0.574	0.131	0.097	78	69	0.568	0.015	0.020
4	60	0.501	0.130	0.129	79	27	0.650	0.014	0.027
5	80	0.450	0.110	0.134	80	90	0.516	0.018	0.019
3	30	0.645	0.144	0.079	81	33	0.643	0.013	0.023
3	11	0.610	0.157	0.068	82	47	0.619	0.014	0.022
4	58	0.508	0.132	0.127	83	28	0.650	0.014	0.027
4	57	0.513	0.137	0.130	84	46	0.620	0.016	0.025
5	85	0.442	0.112	0.142	87	49	0.616	0.015	0.025
6	124	0.350	0.079	0.146	88	122	0.377	0.022	0.013
5	107	0.402	0.095	0.141	89	93	0.505	0.018	0.019
6	121	0.355	0.081	0.148	90	121	0.378	0.022	0.013
5	65	0.478	0.120	0.131	91	64	0.579	0.016	0.023
5	108	0.401	0.094	0.140	92	104	0.476	0.019	0.018
5	91	0.435	0.105	0.136	93	66	0.575	0.016	0.022
5	81	0.450	0.110	0.135	94	78	0.537	0.017	0.020
3	42	0.602	0.135	0.089	95	63	0.585	0.015	0.021
2	**6**	**0.749**	**0.167**	**0.056**	**96**	**7**	**0.800**	**0.007**	**0.028**
3	12	0.698	0.157	0.068	99	24	0.654	0.012	0.023
3	25	0.655	0.154	0.081	100	14	0.710	0.010	0.025
3	21	0.668	0.160	0.079	101	45	0.625	0.014	0.023
5	88	0.439	0.110	0.140	102	58	0.599	0.016	0.024
5	101	0.411	0.099	0.141	103	97	0.491	0.019	0.018
6	131	0.333	0.075	0.151	104	115	0.422	0.020	0.015
6	129	0.338	0.077	0.150	105	124	0.370	0.022	0.013
7	140	0.199	0.047	0.187	106	142	0.069	0.033	0.002
7	135	0.287	0.066	0.164	107	119	0.380	0.023	0.014
6	119	0.365	0.084	0.147	108	116	0.412	0.021	0.015
6	117	0.382	0.091	0.147	111	107	0.467	0.020	0.017
5	62	0.487	0.131	0.138	112	22	0.662	0.015	0.029
6	110	0.398	0.096	0.146	113	86	0.527	0.018	0.020
5	109	0.399	0.103	0.155	114	71	0.554	0.017	0.022
6	127	0.344	0.078	0.149	115	118	0.382	0.022	0.014
6	116	0.390	0.089	0.140	116	100	0.481	0.019	0.017
6	128	0.339	0.079	0.154	117	113	0.429	0.021	0.016
5	79	0.453	0.108	0.131	118	85	0.527	0.018	0.019
5	87	0.440	0.108	0.137	119	84	0.527	0.018	0.020
6	122	0.354	0.083	0.151	120	132	0.323	0.025	0.012
5	96	0.421	0.108	0.149	123	56	0.600	0.016	0.024
7	138	0.240	0.052	0.166	124	138	0.220	0.027	0.008

SIIG: Selection index of ideal genotype, ASIIG: Adjusted selection index of ideal genotype, d_i^+: Favorable ideal genotype, d_i^-: Unfavorable ideal genotype.

Table 2 (Continued). Amounts of SIIG and ASIIG indices for 140 barley advanced lines under rainfed conditions.

SIIG index					Line no.	ASIIG index			
Group	Rank	SIIG	d-	d+		Rank	ASIIG	d-	d+
3	23	0.656	0.143	0.075	125	52	0.614	0.013	0.021
6	132	0.303	0.068	0.156	126	137	0.262	0.025	0.009
5	90	0.437	0.105	0.135	127	67	0.572	0.016	0.022
3	26	0.651	0.148	0.079	128	73	0.549	0.0169	0.021
5	66	0.476	0.130	0.143	129	20	0.668	0.015	0.029
3	16	0.684	0.156	0.072	130	16	0.691	0.011	0.024
3	41	0.610	0.144	0.092	131	68	0.570	0.016	0.022
5	73	0.467	0.124	0.142	132	32	0.645	0.015	0.027
5	103	0.409	0.099	0.145	135	95	0.504	0.019	0.019
7	136	0.275	0.061	0.161	136	136	0.272	0.026	0.010
2	**7**	**0.748**	**0.173**	**0.058**	**137**	**8**	**0.790**	**0.008**	**0.028**
3	15	0.689	0.1660	0.075	138	36	0.632	0.014	0.025
6	123	0.352	0.086	0.159	139	99	0.485	0.019	0.018
5	92	0.434	0.111	0.145	140	50	0.616	0.015	0.025
5	69	0.473	0.124	0.137	141	44	0.627	0.015	0.026
5	78	0.457	0.117	0.139	142	65	0.575	0.017	0.023
3	40	0.610	0.143	0.092	143	108	0.466	0.021	0.018
3	24	0.655	0.150	0.079	144	74	0.546	0.017	0.020
3	27	0.649	0.154	0.083	147	29	0.648	0.013	0.025
4	45	0.587	0.133	0.094	148	57	0.599	0.014	0.021
3	35	0.627	0.142	0.085	149	43	0.627	0.014	0.023
3	22	0.664	0.157	0.079	150	12	0.729	0.010	0.027
5	76	0.463	0.110	0.128	151	120	0.379	0.023	0.014
5	72	0.469	0.120	0.136	152	125	0.368	0.025	0.015
5	82	0.447	0.114	0.141	153	133	0.318	0.028	0.013
4	59	0.504	0.121	0.119	154	127	0.355	0.025	0.014
5	97	0.419	0.108	0.149	1551	131	0.336	0.027	0.013
5	75	0.463	0.119	0.138	1552	128	0.353	0.026	0.014
3	39	0.617	0.147	0.091	158	19	0.671	0.012	0.024
4	54	0.548	0.135	0.111	159	62	0.585	0.015	0.021
3	44	0.596	0.135	0.091	160	87	0.527	0.017	0.019
4	55	0.541	0.129	0.109	161	82	0.529	0.017	0.019
3	43	0.602	0.135	0.089	162	80	0.532	0.017	0.019
6	125	0.348	0.080	0.150	163	114	0.426	0.021	0.015
6	118	0.371	0.090	0.154	164	102	0.479	0.019	0.018
5	77	0.460	0.121	0.142	165	39	0.631	0.015	0.026
7	142	0.163	0.037	0.188	166	141	0.075	0.032	0.003
7	139	0.232	0.054	0.178	167	140	0.097	0.031	0.003

SIIG: Selection index of ideal genotype, ASIIG: Adjusted selection index of ideal genotype, di^{+}: Favorable ideal genotype, di^{-}: Unfavorable ideal genotype.

Table 3. Grouping of 140 barley advanced lines based on SIIG index and mean of different traits in each group.

Average of groups							No. Lines	R/T	Groups	SIIG
E.G.V	DHE	F.L.L(cm)	PLH(cm)	G/S	GY(kg/ha)	TKW(gr)				
8.25	94	12.17	88.33	60.5	5015.42	38.6	4	6	1	0.8<SIIG<0.9
8.22	92.89	10.22	88.26	57.11	4376.85	37.71	7	6	2	0.7<SIIG<0.8
7.29	92.68	9.22	87.18	53.20	3617.04	37.25	34	6	3	0.6<SIIG<0.7
6.25	92.56	9.48	91.31	42.29	3772.08	37.61	16	2&6	4	0.5<SIIG<0.6
7.04	92.06	8.65	89.51	26.05	4102.27	37.77	51	2&6	5	0.4<SIIG<0.5
5.36	91.86	8.91	83.134	22.18	3393.17	37.04	22	2	6	0.3<SIIG<0.4
2.5	91.25	7.79	80.54	22	2482.5	37.42	8	2	7	0<SIIG<0.3

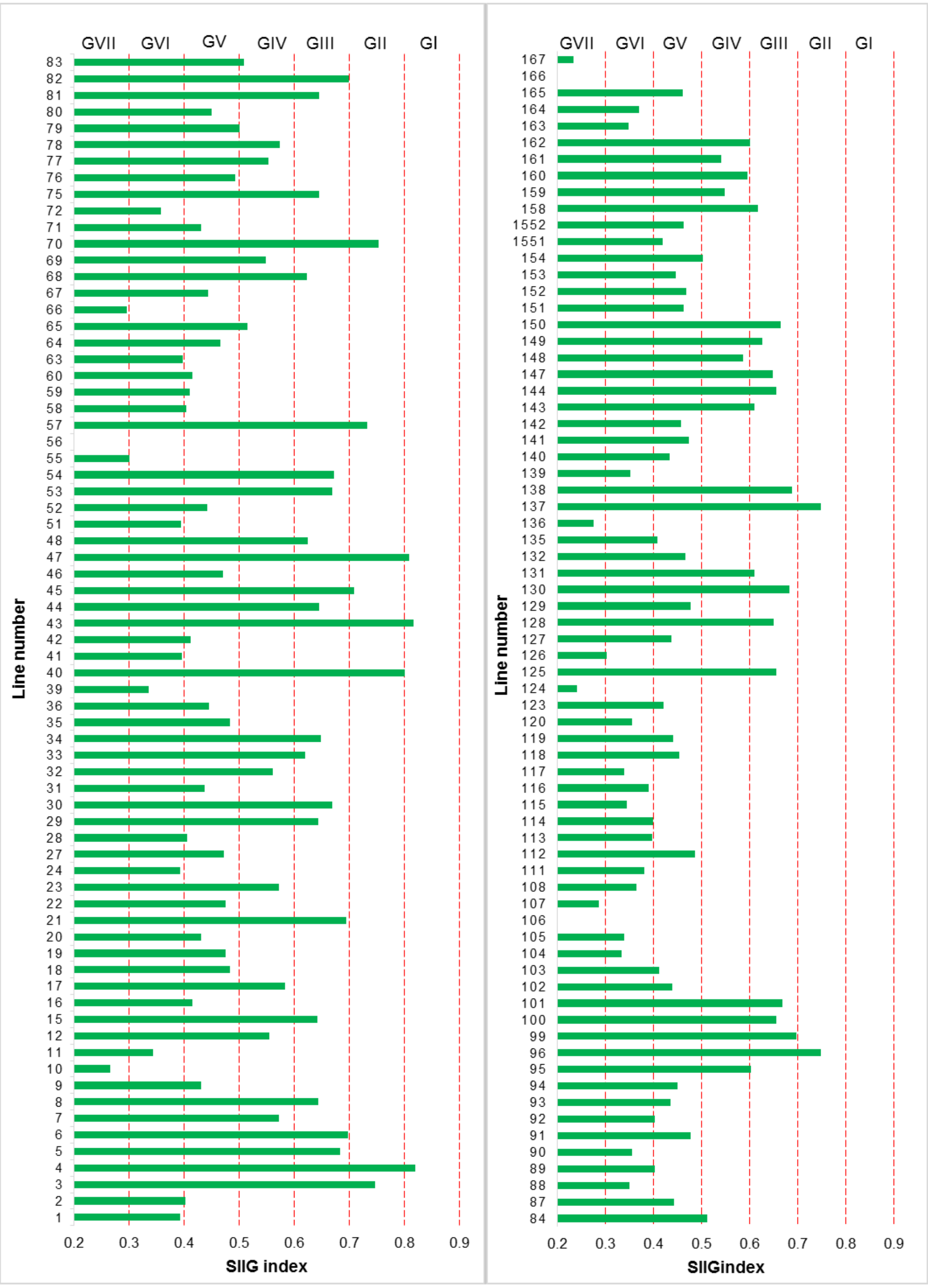

Figure 1. Grouping of 140 barley advanced lines based on SIIG index.

Table 4. Correlation analysis among different morphological traits and SIIG index.

Traits	SIIG	R/T	E.G.V	DHE	F.L.L	PLH	G/S	TKW	GY
SIIG	1								
R/T	0.81**	1							
E.G.	0.48**	-0.04^{ns}	1						
DH	0.21**	0.09^{ns}	0.11^{ns}	1					
F.L.	0.32**	0.12^{ns}	0.03^{ns}	0.29**	1				
PLH	0.19*	0.13^{ns}	0.13^{ns}	0.09^{ns}	0.15^{ns}	1			
G/S	0.83**	0.98**	-0.02^{ns}	0.08^{ns}	0.14^{ns}	0.13^{ns}	1		
TK	0.07^{ns}	-0.14^{ns}	0.25**	0.15^{ns}	0.04^{ns}	0.09^{ns}	-0.16^{ns}	1	
GY	0.35**	-0.17*	0.76**	0.195*	0.01^{ns}	0.19*	-0.13	0.46**	1

* , **, and ^{NS}: significant at 5% , 1% probability levels and non-significance respectively.

In group III, there were 34 lines whose average grain yield, number of seeds per spike, flag leaf length, and early growth vigor were 3617.04 kg/ha, 53.20, 9.22 cm, and 7.29, respectively.

The mean of grain yield and early growth vigor of this group were lower than those of the control cultivars. Group IV with 16 lines had the average grain yield, number of seeds per spike, flag leaf length, 1000-seed weight, plant height, and early growth vigor of 3772.08 kg/ha, 42.29, 9.48 cm, 37.61 g, 91.31 cm, and 6.25, respectively. In group V with 51 lines, the average grain yield, the number of seeds per spike, flag leaf length, 1000-seed weight, plant height, and early growth vigor were 4102.27 kg/ha, 26.05, 8.65 cm, 37.77 g, 89.51 cm, and 7.04, respectively. In group VI, there were 22 lines with an average grain yield, the number of seeds per spike, flag leaf length, 1000-seed weight, plant height, and early growth vigor were 3393.09 kg/ha, 22.18, 8.91 cm, 37.61 g, 91.04 cm, and 5.36, respectively. In group VII, there were eight lines with average grain yield, the number of seeds per spike, flag leaf length, 1000-seed weight, plant height, and early growth vigor of 2482.5 kg/ha, 22, 7.79 cm, 37.42 g, 80.54 cm, and 2.5, respectively. According to the results, the average grain yield of lines in groups I and II was higher than that of both control cultivars and the other lines groups.

The results of correlation analysis between traits used and SIIG index (Table 4) showed that SIIG correlation coefficients observed with all traits were significantly positive. The highest positive correlations were observed between SIIG with the number of grains per spike (0.83), spike type (0.81), early growth vigor (0.48), grain yield (0.35), flag leaf length (0.32), days to heading (0.21), and plant height (0.19), respectively. Nevertheless, no significant correlation was observed between grain yield with some grain yield components such as the number of grains per spike and flag leaf length. We used all traits entered/un-entered in the regression model along with the standardized regression coefficient for each trait as optimal weight, in order to select the best lines in terms of grain yield and other traits using the ASIIG method, and calculated the ASIIG values for each line (Table 2). Whenever the value of this index is closer to one, the genotype will be more desirable. Here, the value of ASIIG for line 47 was calculated 0.907 and therefore, had the most similarity to the ideal genotype. Lines 3, 4, 43, 45, 21, 96, 137, 40 and 54 with ASIIG values of 0.856, 0.852, 0.849, 0.847, 0.84, 0.8, 0.79, 0.756 and 0.732, respectively, and also with a minimum distance to the ideal genotype were placed in the next ranks (Table 2). Also, according to Figure 2 plots and the creation of ideal quarters and graphic grouping established between the lines, only lines 47, 3, 43, 45, 137, 96, and 40 were placed in the ideal quarter. The lines 106, 166, 167, 56, 124 with the ASIIG values of 0.069, 0.075, 0.097, 0.156 and 0.220 were in non-ideal quarter, respectively.

The SIIG index in selecting the best lines in terms of grain yield and seven more traits entered the regression model simultaneously and separated the studied 140 advanced lines of barely into seven groups. According to the results, the average grain yield of lines located in groups I and II were higher than the grain yield of both control cultivars and the lines located in other groups in rainfed conditions. These results showed that the SIIG index can simultaneously classify the studied lines and determine their distances based on several traits. According to Table 2, we observed that as the value of SIIG decreases, the value of grain yield, the number of seeds per spike, flag leaf length, and vigor decrease. We could not observe a significant difference in the value of days to heading, plant height, and 1000-seed weight. This indicated that the SIIG index could simultaneously select high-yielding barely lines with

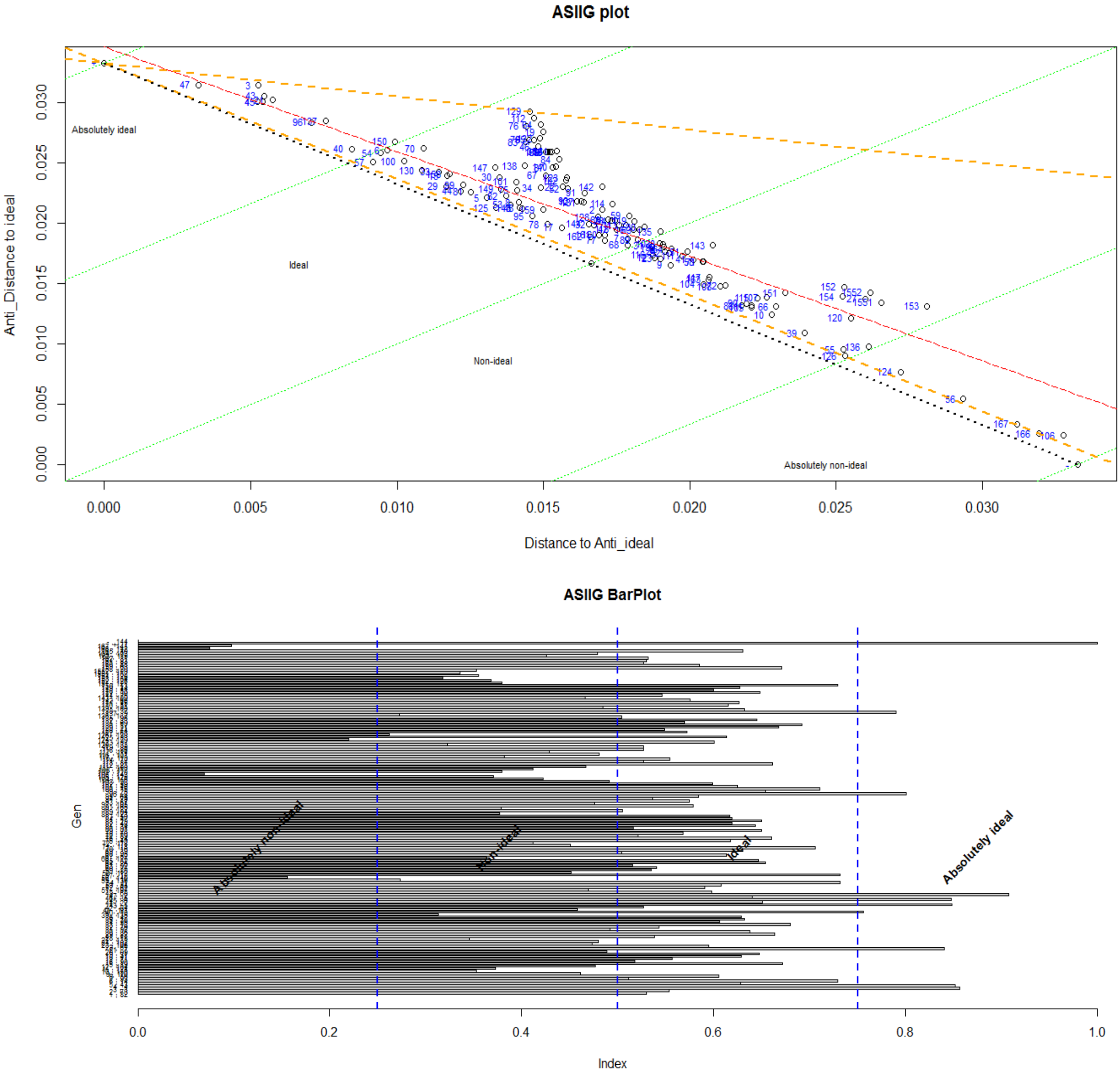

Figure 2. Grouping of 140 barley advanced lines based on ASIIG index.

more seeds per spike, flag leaf length, and early growth vigor.

Based on the results of correlation analysis between traits and SIIG index (Table 4), there were no significant relationships between grain yield with some grain yield components such as the number of grains per spike and flag leaf length. Therefore, selection based on grain yield alone may not lead to identifying lines with other desirable traits. On the other hand, there was positively significant relationships between SIIG with grain yield and other traits affecting grain yield. Therefore, the SIIG index used in this study has been more efficient than single-trait selections. Tadili *et al.* (2020) studied drought tolerance in 18 advanced durum wheat lines under rainfed and supplementary irrigation conditions, and based on the SIIG method, they performed the selection of superior lines. Zali and Barati (2020) investigated genetic diversity and selected high-yielding lines with desirable agronomic characteristics using the SIIG index from 108 pure barley lines along with four controls. Their results showed that the SIIG index, by integrating different traits, selects the desired genotypes more effectively; therefore, the lines with the highest the SIIG values were the superior lines, and the lowest SIIG values were the weakest lines in this research. They evaluate the efficiency of SIIG index in selecting the best lines in terms of grain yield, 1000-seed weight, plant height, days to flowering, and days to ripening simultaneously; where they classified the studied lines according to the SIIG index into six groups. On the other hand, the genotypes with SIIG index close to one were drought-tolerant, and with SIIG index close to zero were drought-sensitive genotypes. The conclusion showed that the selection index of the ideal genotype is a selective model and is used to select the most appropriate genotype among genotypes in different environments. Researchers can use either the SIIG method to convert drought tolerance indices, different traits to a single index, or other stability analysis parameters and select superior genotypes confidently and accurately. Yagoutipour *et al.* (2017) evaluated 20 bread wheat genotypes using other drought tolerance indices and SIIG index to identify drought-tolerant genotypes. They indicated the efficiency of the SIIG index in selecting drought-tolerant genotypes. Researchers obtained similar results regarding the application of the SIIG index by an experiment to evaluate salinity tolerance indices and choose the ideal genotype among several new cultivars and lines of safflower (Haghighatnia and Alhani 2020). Based on the fact that using an indicator alone in selecting stable or ideal genotypes is not a suitable choice, it is better to evaluate the stability of genotypes using several indices. Additionally, by increasing the number of indices, it may be difficult for the researcher to select the appropriate genotype; therefore, all parametric statistics simultaneously evaluate the stability of genotypes. Moqaddas Zadeh Ahrab *et al.* (2018) investigated the interaction of genotype×environment on tuber grain yield of 15 potato genotypes in six environments based on parametric stability methods using SIIG technique to identify stable potato genotypes with high grain yield. By using the SIIG index, some researchers have integrated different methods of stability analysis, where they introduce Cooper and Lilian canola genotypes as stable genotypes (Zali *et al.,* 2015). Ramzi *et al.* (2018) used this index to evaluate the tolerance of advanced durum wheat lines under aluminum stress conditions. They identified 20 lines with the highest rank and 20 lines with the lowest level among 100 studied lines.

Comparing the grouping results of SIIG with ASIIG methods, both methods showed high similarities in selecting the best lines. In SIIG method, lines 4, 43, 47, 40, 70, 96, 137, 3, 57 and 45, also in ASIIG method, lines 47, 3, 4, 43, 45, 21, 96, 137, 40 and 54 were identified as the best/ideal lines. Therefore, these two methods are compatible in selecting the best lines. ASIIG method, because of the participation of all traits commensurate with its importance and weight in the quantity and quality of the crop end product, was more suitable for separating the desired lines.

CONCLUSION

The coefficient of variation for agronomic traits showed a wide range of variations and diversity among 140 advanced lines. The highest variation was related to grain yield, followed by seeds per spike, flag leaf area, and plant height. The results of the SIIG index, based on the traits entered into the regression model, showed that lines 4, 43, 47, 40, 70, 96, 137, 3, 57, and 45 with the highest SIIG values, are the most tolerant lines under rainfed conditions with the highest grain yield. In the ASIIG method, in addition to the best lines identified by the SIIG method, lines 21 and 54 were also found as the best lines. Also, according to ASIIG plots and the creation of ideal quarters, only lines 47, 3, 43, 45, 137, 96, and 40 were placed in the ideal quarter.

ACKNOWLEDGMENTS

This research supported by Kohgiluyeh-Boyerahmad Agricultural and Natural Resources Research and Education Center and Imam Komeini International University. We thanks Behrouz Vaezi for helpful agricultural operations.

Conflict of interest

The authors declare that they have no conflict of interest with any organization in relation.

REFERENCES

Abdel-Ghani A. H., Neumann K., Wabila C., Sharma R., Dhanagond S., Owais S. J., Borner A., Graner A., and Kilian B. (2015). Diversity of germination and seedling traits in a spring barley (*Hordeum vulgare* L.) collection under drought simulated conditions. *Genetic Resources and Crop Evolution,* 62(2): 275-292.

Addisu A., and Shumet T. (2015). Variability, heritability and genetic advance for some yield and yield related traits in barley (*Hordeum vulgare* L.) landraces in Ethiopia. *International Journal of Plant Breeding and Genetics*, 9(2): 68-76.

Alemayehu F., and Parlevliet J. E. (1997). Variation between and within Ethiopian barley landraces. *Euphytica,* 94(2): 183.

Al-Karaki G. N. (2001). Germination, sodium, and potassium concentrations of barley seeds as influenced by salinity. *Journal of Plant Nutrition*, 24(3): 511-522.

Brachi B., Meyer C. G., Villoutreix R., Platt A., Morton T. C., Roux F., and Bergelson J. (2015). Coselected genes determine adaptive variation in herbivore resistance throughout the native range of *Arabidopsis thaliana*. *Proceedings of the National Academy of Sciences*, 112(13): 4032-4037.

Derbew S., Elias U., and Hussein M. (2013). Genetic variability in barley (*Hordeum vulgare* L.) landrace collections from southern Ethiopia. *International Journal of Science and Research*, 12(2): 125-131.

Draper N. R., and Smith H. (1998). Applied regression analysis. (3th Ed.). New York: Wiley, (Chapter 6).

Drikvand R., Samiei K., and Hossinpor T. (2011). Path coefficient analysis in hull-less barley under rainfed condition. *Australian Journal of Basic and Applied Sciences*, 5(12): 277-279.

Ebrahim S., Shiferaw E., and Hailu F. (2015). Evaluation of genetic diversity in barley (*Hordeum vulgare* L.) from Wollo high land areas using agromorphological traits and hordein. *African Journal of Biotechnology*, 14(22): 1886-1896.

Evans L. T., and Fischer R. A. (1999). Yield potential: its definition, measurement, and significance. *Crop Science*, 39(6): 1544-1551.

FAO. (2015). FAOSTAT - Food and Agriculture Organization of the United Nations. [Online] Available: http://faostat3.fao.org (Verified in Feb 2, 2017).

Haghighatnia H., and Alhani F. (2020). Evaluation of irrigation water salinity tolerance indices in new cultivars and lines of safflower. *Air, Iranian Soil and Water Research*, 51(7):1811-1821. (In Persian with English Abstract).

Haseneyer G., Stracke S., Paul C., Einfeldt C., Broda A., Piepho H. P., Graner A., and Geiger H. H. (2010). Population structure and phenotypic variation of a spring barley world collection set up for association studies. *Plant Breeding*, 129(3): 271-279.

Hwang C. L., and Yoon K. P. (1981). Lecture notes in economics and mathematical systems. In: Multiple Attribute Decision Making, Springer-Verlag Berlin Heidelberg58-191 ,.

Jabbari M., Fakheri B. A., Aghnoum R., Nezhad N. M., Ataei R., and Koochakpour Z. (2019). Association mapping of morphological and physiological traits of flag leaf related to drought tolerance in barley. *Journal of Neotropical Agriculture*, 6(2): 7-18.

Jalata Z., Ayana A., and Zeleke H. (2011). Variability, heritability and genetic advance for some yield and yield related traits in Ethiopian Barley (*Hordeum vulgare* L.) landraces and crosses. *International Journal of Plant Breeding and Genetics*, 5(1): 44-52.

Kerwin R., Feusier J., Corwin J., Rubin M., Lin C., Muok A., Larson B., Joseph B., Francisco M., Weinig C., Kliebenstein D., and Copeland D. (2015). Natural genetic variation in *Arabidopsis thaliana* defense metabolism genes modulates field fitness. *Elife*, 4: e05604.

Leilah A. A., and Al-Khateeb S. A. (2005). Statistical analysis of wheat yield under drought conditions. *Journal of Arid Environments*, 61(3): 483-496.

Mishra B. N., and Shivakumar B. G. (2000). Barley in: techniques and management of field crop production. Agrobios. Rothere, PS (Ed.), India.

Mohtashami R. (2015). The correlation study of important barley agronomic traits and grain yield by path analysis. *In Biological Forum*, 7(1): 1211-1219.

Moqaddaszadeh Ahrab M., Asghari Z., Hassanpanah D., and Nasser Z. (2015). Assessing the interaction of genotype×environment of potato genotypes (*Solanum tuberosum* L.) using parametric statistics and the selection index of ideal genotype (SIIG) technique. The First National Conference on Modern Ideas in Agriculture and Natural Resources, 14 November, Ardabil, Iran, 887-891.

Naceur A. B., Chaabane R., El-Faleh M., Abdelly C., Ramla D., Nada A., and Sakr M. (2012). Genetic diversity analysis of North Africa's barley using SSR markers. *Journal of Genetic Engineering and Biotechnology*, 10(1): 13-21.

Newman C. W., and Newman R. K. (2006). A brief history of barley foods. *Cereal Foods world*, 51(1): 4-7.

Ramzi E., Asghari A., Khomari S., and Mohammaddoust e Chamanabad H. (2018). Investigation of durum wheat (*Triticum turgidum* L. subsp. durum Desf) lines for tolerance to aluminum stress condition. *Journal of Crop Breeding*, 10(25): 63-72.

Shakhatreh Y., Haddad N., Alrababah M., Grando S., and Ceccarelli S. (2010). Phenotypic diversity in wild barley (*Hordeum vulgare* L. ssp. spontaneum (C. Koch) Thell.) accessions collected in Jordan. *Resources and Crop Evolution*, 57(1): 131-146.

Shrimali J., Shekhawat A. S., Kumari S. (2017). Genetic variation and heritability studies for yield and yield components in barley genotypes under normal and limited moisture conditions. *Journal of Pharmacognosy and Phytochemistry*, 6(4): 233-235.

Tadili S., Asghari A., Karimzadeh R., Sofalian O., and Mohammaddoust C. H. (2020). Evaluation of drought stress tolerance in advanced lines durum wheat using the selection index of ideal genotype (SIIG). *Journal of Crop Ecophysiology*, 1(14): 45-62.

Taghizadeh A., Aminian dehkordi R., and Zeinanloo A. (2020). Estimation of compatibility of some olive cultivars and genotypes in Tarom climate conditions using non-parametric methods . *Iranian Journal of Horticultural Science*, 51(3): 657-688.

Wada Y., Wisser D., Eisner S., Florke M., Gerten D., Haddeland I., Hanasaki N., Masaki Y., Portmann F. T., Stacke T., and Tessler Z. (2013). Multimodel projections and uncertainties of irrigation water demand under climate change. *Geophysical Research Letters*, 40(17): 4626-4632.

Yacoubi I., Nigro D., Sayar R., Masmoudi K., Seo Y. W., Brini F., Giove S. L., Mangini G., Giancaspro A., Marcotuli I., Colasuonno P., and Gadaleta A. (2020). New insight into the North-African durum wheat biodiversity: phenotypic variations for adaptive and agronomic traits.

Genetic Resources and Crop Evolution, 67(2): 445-455.

Yagoutipour A., Farshadfar E., and Saeedi M. (2017). Assessment of durum wheat genotypes for drought tolerance by suitable compound method. *Environmental Stress in Crop Sciences*, 10(2): 247-256. (In Persian with English Abstract).

Zali H., and Barati A. (2020). Evaluation of selection index of ideal genotype (SIIG) in other to selction of barley promising lines with high yield and desirable agronomy traits. *Journal of Crop Breeding,* 12(34): 93-104.

Zali H., Hasanloo T., Sofalian O., Asgharii A., and Enayati Shariatpanahi M. (2019). Identifying drought tolerant canola genotypes using selection index of ideal genotype. *Journal of Crop Breeding,* 11(29): 117-126. (In Persian).

Zali H., Hassanloo T., Sofalian O., Asghari A., and Zeinalabedini M. (2017). Appropriate strategies for selection of drought tolerant genotypes in canola. *Journal of Crop Breeding,* 8(20): 90-77. (In Persian).

Zali H., Hasanloo T., Sofalian O., Asghari A., and Zeinalabedini M. (2016). Drought stress effect on physiological parameter and amino acids accumulations in canola. *Journal of Crop Breeding,* 8(18): 191. (In Persian).

Zali H., Sofalian O., Hasanloo T., Asgharii A., and Hoseini S. M. (2015). Appraising of drought tolerance relying on stability analysis indices in canola genotypes simultaneously, using selection index of ideal genotype (SIIG) technique: Introduction of new method. *In Biological Forum*, 7(2): 703.

Zeng X. Q. (2015). Genetic variability in agronomic traits of a germplasm collection of hulless barley. *Genetics and Molecular Research*, 14(4): 18356-18369.

SUPPLEMENTAL DATA

Supplementary Table 1. Pedigree of 140 barley advanced lines with line number and their source (ICARDA).

Line no.	Source	Pedigree
1	Iran	Khorram as check
2	Iran	Fardan as check
3	IBYT-HI (2018-19)	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA1/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1 CBSS07Y00497S-4T-05CJ-05CH-04CJ-0CH
4	IBYT-HI (2018-19)	CIRU/ZIGZIG CBSS07Y00322S-14T-05T-05CJ -05CH-3CJ-0CH
5	IBYT-HI (2018-19)	CANELA//LIMON/BICHY2000 CBSS07Y00382S-4T-05T-05CJ -05CH-5CJ-0CH
6	IBYT-HI (2018-19)	BERMEJO//CAPUL/TOCTE CBSS06Y00313S-13Y-1M-05T-05CJ-05T-3CJ-0CH
7	IBYT-HI (2018-19)	S95031002008N/H87010008N H99075001 09/4H0018-0MR
8	IBYT-HI (2018-19)	MSEL/LOGAN-BAR CBSS03B00016S-0M-0Y-0M-0Y-1M-0Y
9	IBYT-HI (2018-19)	AJO 61/6/Vmorales ICB09-1494-0AP-0TR-0AP-0TR
10	6thGSBYT(2018-19)	WABAR2242//LIMON/BICHY2000 CBSS07Y00242S-7T-05T-05CJ -05CH-3CJ-0CH
11	6thGSBYT(2018-19)	LIMON/BICHY2000//DEFRA/DESCONOCIDA-BAR CBSS05Y00036S-6Y-0M-0Y-0M-4AP
12	6thGSBYT(2018-19)	IPA7/4/AwBlack/Aths//Arar/3/9Cr279-07/Roho/5/Rhn-03//Lignee527/As45 ICB03-0079-0AP-5AP-0AP
15	IBON-HI(2018-19)	RIHANE-03 As46//Avt/Aths (Sel,02L-1AP-3AP-0AP)
16	IBON-HI(2018-19)	AZAF/MSEL/4/PFC8562//ATAH92/GOB/3/CANELA CITV10B095S- 0100T-0100CJ-9CH-04CJ-0CH
17	IBON-HI(2018-19)	CHAMICO/TOCTE//CONGONA/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1 CBSS07Y00423S-8T-05T-05CJ -05CH-3CJ-0CH
18	IBON-HI(2018-19)	COMINO/3/MATICO/JET//SHYRI/4/ALELI/5/L.P/SHYRI M00080001 08/1G0043
19	IBON-HI(2018-19)	ALELI/SCARLETT CBSS05M00148S-2M-0Y-0M-0AP-0TR
20	IBON-HI(2018-19)	CANELA//LIMON/BICHY2000 CBSS07Y00382S-13T-05T-05CJ -05CH-1CJ-0CH
21	IBON-HI(2018-19)	RIHANE-03 As46//Avt/Aths (Sel,02L-1AP-3AP-0AP)
22	IBON-HI(2018-19)	CANELA//LIMON/BICHY2000 CBSS07Y00382S-14T-05T-05CJ -05CH-1CJ-0CH
23	IBON-HI(2018-19)	CIRU//BREA/DL70/3/SUMBARD400 CBSS07Y01027T-A-0AP-0AP
24	IBON-HI(2018-19)	H92013289Z\H93003203Z J02037004 09/2T0127
27	IBON-HI(2018-19)	LBIRAN/UNA80//LIGNEE640/3/PUNGSANCHAPSSALBORI CBSS07Y00052S-23T-05CJ-05T-05CJ - 010CH-CH2-0CH
28	IBON-HI(2018-19)	TR653/H92020115X J00038005 09/3T0021
29	IBON-HI(2018-19)	GLORIA-BAR/COPAL//M104 CBSS07Y00004S-3T-05CJ-05T-05CJ -010CH-CH3-0CH
30	IBON-HI(2018-19)	VMorales/6/ORGE618 CBSS06Y00274S-11Y-0M-0AP-0TR
31	IBON-HI(2018-19)	CANELA/ECU1.31 CBSS07Y00391S-18T-05T-05CJ -05CH-3CJ-0CH

Supplementary Table 1 (Continued). Pedigree of 140 barley advanced lines with line number and their source (ICARDA).

Line no.	Source	Pedigree
32	IBON-HI(2018-19)	LBIRAN/UNA80//LIGNEE640/3/PUNGSANCHAPSSALBORI CBSS07Y00052S-31T-05CJ-05T-05CJ - 010CH-CH3-0CH
33	IBON-HI(2018-19)	ADABELLA/ESMERALDA/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5 /PETUNIA 1 CBSS07Y01054T-G-05T-05CJ-05T-05CJ - 010CH-CH4-0CH
34	IBON-HI(2018-19)	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1 CBSS07Y00497S-41T-05CJ-05CH-04CJ-0CH
35	IBON-HI(2018-19)	J09072 F3 10/030575 H97034002/J99048002-0MR
36	IBON-HI(2018-19)	AJO 61/6/Vmorales ICB09-1494-0AP-0TR-0AP-0TR
39	IBON-HI(2018-19)	CANELA//LIMON/BICHY2000 CBSS07Y00382S-23T-05T-05CJ -05CH-3CJ-0CH
40	IBON-HI(2018-19)	GLORIA-BAR/IAR.H.485//ALOE/3/CABUYA M00009001 08/1G0018
41	IBON-HI(2018-19)	CANELA/CONLON F10166-0MR
42	IBON-HI(2018-19)	BR2/MERIT,B//MSEL F09446 09/D30363-0MR
43	IBON-HI(2018-19)	NISKA/H00057 H01023001 09/2S0001
44	IBON-HI(2018-19)	RIHANE-03 As46//Avt/Aths (Sel,02L-1AP-3AP-0AP)
45	IBON-HI(2018-19)	LA MOLINA 94/FOSTER F10199-0MR
46	IBON-HI(2018-19)	G09107 F3 10/030601 G08110/TR06676-0MR
47	IBON-HI(2018-19)	ATAH92/GOB//PETUNIA 2 M99147001 08/2G0014
48	IBON-HI(2018-19)	LBIRAN/UNA80//LIGNEE640/6/Vmorales ICB09-1620-0AP-0TR-0AP
51	IBON-HI(2018-19)	CANELA//E.QUEBRACHO/W9338 CBSS07Y00384S-25T-05T-05CJ -05CH-1CJ-0CH
52	6th GSBON(2018-19)	G09111 F3 10/030605 G08114/TR06676-0MR
53	6th GSBON(2018-19)	LBIRAN/UNA80//LIGNEE640/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1 CBSS07Y00060S-44T-05CJ-05T-05CJ - 010CH-CH3-0CH
54	6th GSBON(2018-19)	LA MOLINA 96/6/Vmorales CBSS05Y00158S-25Y-0M-0Y-0M-4AP
55	6th GSBON(2018-19)	CLE150/W89.11369//CHERI/3/CANELA F10191-0MR
56	6th GSBON(2018-19)	DEFRA/E.QUEBRACHO//DEFRA/E.QUEBRACHO/3/LEO-B F09808 09/D30759-0MR
57	6th GSBON(2018-19)	Avt/Attiki//MAtt733371/3/Aths/Lignee686/4/Lignee527/NK1272//JLB70-63 ICB02-0689-0AP-5AP-0AP-0MC
58	6th GSBON(2018-19)	CANELA//LIMON/BICHY2000 CBSS07Y00382S-9T-05T-05CJ -05CH-2CJ-0CH
59	6th GSBON(2018-19)	BARONESE/5/ESCOBA/3/MOLA/SHYRI//ARUPO*2/JET/4/ALELI/6/MSEL/7/LIMON/AZAF M06445 F6 08/030381-0MR
60	6th GSBON(2018-19)	CEV 96060//BUCK M8.88/E.ACACIA/3/CANELA F10192-0MR
63	6th GSBON(2018-19)	AZAF/MSEL/4/PFC8562//ATAH92/GOB/3/CANELA CITV10B095S- 0100T-0100CJ-9CH-04CJ-0CH
64	6th GSBON(2018-19)	J09062 F3 10/030565 H97042002/H97075001-0MR
65	6th GSBON(2018-19)	J09058 F3 10/030561 H97006017/BUSBY-0MR
66	6th GSBON(2018-19)	MSEL//BUCKM8.88/E.ACACIA/3/MSEL//PERLE/BOWMAN CITV10B087S- 0100T-0100CJ-2CH-04CJ-0CH
67	6th GSBON(2018-19)	MSEL/LOGAN-BAR CBSS03B00016S-0M-0Y-0M-0Y-1M-0Y
68	6th GSBON(2018-19)	Alanda/Hamra//Alanda-01 ICB97-0930-0AP-18AP-3TR-4AP-0AP-3AP-0AP
69	6th GSBON(2018-19)	CANELA//LIMON/BICHY2000 CBSS07Y00382S-5T-05T-05CJ -05CH-3CJ-0CH

Supplementary Table 1 (Continued). Pedigree of 140 barley advanced lines with line number and their source (ICARDA).

Line no.	Source	Pedigree
70	6th GSBON(2018-19)	CHAMICO/TOCTE//CONGONA/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1 CBSS07Y00423S-8T-05T-05CJ -05CH-3CJ-0CH
71	6th GSBON(2018-19)	CANELA//LIMON/BICHY2000 CBSS07Y00382S-31T-05T-05CJ -05CH-3CJ-0CH
72	6th GSBON(2018-19)	BISON 136/CANELA CBSS07Y00807S-37T-05T-05CJ -05CH-1CJ-0CH
75	6th GSBON(2018-19)	VMorales/6/M9846//CCXX14.ARZ3/PACO/3/PALTON CBSS04B00043S-3M-0Y-0M-0Y-2M-0AP
76	6th GSBON(2018-19)	J09072 F3 10/030575 H97034002/J99048002-0MR
77	6th GSBON(2018-19)	Nadawa/Rhn-03//Saida ICB04-0706-0AP-1AP-0AP-0MC
78	6th GSBON(2018-19)	CIRU/3/LEGACY//PENCO/CHEVRON-BAR CBSS07Y00326S-27T-05CJ-05T-05CJ - 010CH-CH2-0CH
79	Mrocco nurseries-Gonbad(2018-19)	Melusine/Aleli/3/Matico/Jet//Shyri/4/Canela/5/Cerise/Shyri//Aleli/3/Mpyt169-1Y/Laurel//Olmo/4/Canela ICB11-0128-0MC-0MC-0MC-2MR
80	Mrocco nurseries-Gonbad(2018-19)	CEV 96060/3/ARUPO/K8755//MORA/4/CANELA
81	Mrocco nurseries-Gonbad(2018-19)	VLB 118
82	Mrocco nurseries-Gonbad(2018-19)	SARA1-BAR/CAPUCHONA 20
83	Mrocco nurseries-Gonbad(2018-19)	Melusine/Aleli/3/Matico/Jet//Shyri/4/Canela/5/Gobernadora HIICB10-0053-0AP-0TR-0MR-6MR
84	Mrocco nurseries-Gonbad(2018-19)	Litani/Chigwell HIICB10-0200-0AP-0TR-0MR-8MR
87	Mrocco nurseries-Gonbad(2018-19)	Melusine/Aleli/3/Matico/Jet//Shyri/4/Canela/5/Reem HIICB10-0055-0AP-0TR-0MR-11MR
88	Mrocco nurseries-Gonbad(2018-19)	Cerise/Shyri//Aleli/3/Mpyt169.1Y/Laurel//Olmo/4/Canela/5/Horonera HIICB10-0092-0AP-0TR-0MR-2MR
89	Mrocco nurseries-Gonbad(2018-19)	Xena/CANELA/DEFRA HIICB10-0354-0AP-0TR-0MR-19MR
90	Mrocco nurseries-Gonbad(2018-19)	Xena/DWRUB52 HIICB10-0362-0AP-0TR-0MR-12MR
91	Mrocco nurseries-Gonbad(2018-19)	Melusine/Aleli/3/Matico/Jet//Shyri/4/Canela/5/HOLKR HIICB10-0057-0AP-0TR-0MR-11MR
92	Mrocco nurseries-Gonbad(2018-19)	LOGAN-BAR/MSEL//AZAF/3/MADRE SELVA HIICB10-0555-0AP-0TR-0MR-14MR
93	Mrocco nurseries-Gonbad(2018-19)	Litani/Chigwell HIICB10-0200-0AP-0TR-0MR-3MR
94	Mrocco nurseries-Gonbad(2018-19)	Melusine/Aleli/3/Matico/Jet//Shyri/4/Canela/5/EFES28 HIICB10-0077-0AP-0TR-0MR-18MR
95	Mrocco nurseries-Gonbad(2018-19)	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1/6/GLORIA-BAR/COPAL/7/TOCTE IBM12CH178-10CH-05CJ-010CH-1CJ-0CH-0MR
96	Mrocco nurseries-Gonbad(2018-19)	PETUNIA 2/M111/5/ESMERALDA/3/SLLO/ROBUST//QUINA/4/M104 HIICB12-549-0TR-0MR-0MR-0MR-7MR
99	Mrocco nurseries-Gonbad(2018-19)	ATACO/BERMEJO//HIGO/3/CALI92/ROBUST/4/PETUNIA1/5/PETUNIA1/CHINIA/3/ATACO/BERMEJO//HIGO/6/ZIGZIG/3/M9846//CCXX14.ARZ3/PACO/7/M122 HIICB12-500-0TR-0TR-0MR-0MR-3MR
100	Mrocco nurseries-Gonbad(2018-19)	RD2668/7/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA1/6/ZIGZIG/4/EGYPT4/TERAN78//P.STO/3/QUINA HIICB12-033-0TR-0TR-0MR-0MR-1MR
101	Mrocco nurseries-Gonbad(2018-19)	SUMBARD400/5/ESMERALDA/3/SLLO/ROBUST//QUINA/4/M104 HIICB12-323-0TR-0MR-0MR-0MR-7MR
102	Mrocco nurseries-Gonbad(2018-19)	BICHY2000//GOB/HUMAI10/3/Sebastian HIICB12-192-0TR-0TR-0MR-0MR-2MR

Supplementary Table 1 (Continued). Pedigree of 140 barley advanced lines with line number and their source (ICARDA).

Line no.	Source	Pedigree
103	Mrocco nurseries-Gonbad(2018-19)	Xena//Canela HIICB12-083-0TR-0MR-0MR-0MR-10MR
104	Mrocco nurseries-Gonbad(2018-19)	MSEL/LA MOLINA 95//SHAKIRA HIICB12-219-0TR-0MR-0MR-0MR-7MR
105	Mrocco nurseries-Gonbad(2018-19)	PFC9214//PENCO/CHEVRON-BAR/7/ATACO/BERMEJO//HIGO/3/CALI92/ROBUST/4/PETUNIA 1/5/PETUNIA 1/CHINIA/3/ATACO/BERMEJO//HIGO/6/ZIGZIG/3/M9846//CCXX14.ARZ 3/PACO HIICB12-013-0TR-0TR-0MR-0MR-8MR
106	Mrocco nurseries-Gonbad(2018-19)	LEGACY /4-1MBN11 ICM13CH29-29CH-05CJ-010CH-0MR
107	Mrocco nurseries-Gonbad(2018-19)	BICHY2000//GOB/HUMAI10/3/SHAKIRA HIICB12-221-0TR-0MR-0MR-0MR-4MR
108	Mrocco nurseries-Gonbad(2018-19)	PFC9214//PENCO/CHEVRON-BAR/8/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1/6/M111/7/LEGACY/3/SVANHALS-BAR/MSEL//AZAF/GOB24DH HIICB12-016-0TR-0MR-0MR-0MR-6MR
111	Mrocco nurseries-Gonbad(2018-19)	BICHY2000//GOB/HUMAI10/3/CONCHITA HIICB12-246-0TR-0MR-0MR-0MR-9MR
112	Mrocco nurseries-Gonbad(2018-19)	MSEL/PFC9214//Zacatecas 9 IBM12CH214-9CH-05CJ-010CH-4CJ-0CH-0MR
113	Mrocco nurseries-Gonbad(2018-19)	MADRE SELVA/7/STANDERBAR/API/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1 ICM13CH18-64CH-05CJ-010CH-0MR
114	Mrocco nurseries-Gonbad(2018-19)	MSEL/LA MOLINA 95//BRS195/ND19098-1 HIICB12-445-0TR-0TR-0MR-0MR-6MR
115	Mrocco nurseries-Gonbad(2018-19)	BREA/DL70//CABUYA/3/MADRE SELVA ICM13CH62-2CH-05CJ-010CH-0MR
116	Mrocco nurseries-Gonbad(2018-19)	PFC9214//PENCO/CHEVRON-BAR/7/ATACO/BERMEJO//HIGO/3/CALI92/ROBUST/4/PETUNIA 1/5/PETUNIA 1/CHINIA/3/ATACO/BERMEJO//HIGO/6/ZIGZIG/3/M9846//CCXX14.ARZ 3/PACO HIICB12-013-0TR-0MR-0MR-0MR-4MR
117	Mrocco nurseries-Gonbad(2018-19)	SARA1-BAR/CAPUCHONA 20/3/PFC9214//PENCO/CHEVRON-BAR HIICB12-526-0TR-0MR-0MR-0MR-4MR
118	Mrocco nurseries-Gonbad(2018-19)	SHYRI/3/ZHEDAR#1/SHYRI//OLMO
119	Mrocco nurseries-Gonbad(2018-19)	Xena/3/MSEL//DEFRA/CL128 HIICB10-0359-0AP-0TR-0MR-0MR
120	Mrocco nurseries-Gonbad(2018-19)	MSEL//LIMON/BICHY2000 CBSS06Y00152S-1Y-0M-05T-05CJ-05T-1CJ-0CH-0MR
123	Mrocco nurseries-Gonbad(2018-19)	SVANHALS-BAR/MSEL//AZAF/GOB24DH/3/NE167/CLE176
124	Mrocco nurseries-Gonbad(2018-19)	OPS 66/CANELA
125	Mrocco nurseries-Gonbad(2018-19)	ROBUST//GLORIA-BAR/COPAL/3/MAHIGAN/4/PETUNIA 2/5/ESMERALDA/ROBUST CICJ1011B075S-050CJ-8CH-04CJ-05CH-5CJ-0CH-0MR
126	Mrocco nurseries-Gonbad(2018-19)	CANELA//ATAH92/GOB CBSS07Y00375S-17T-05T-05CJ -05CH-5CJ-0CH
127	Mrocco nurseries-Gonbad(2018-19)	H92020078/TR232//I95039 H97042002 09/6T0006
128	Mrocco nurseries-Gonbad(2018-19)	BT554/MAHIGAN H98080003 09/500012
129	Mrocco nurseries-Gonbad(2018-19)	MSEL/LOGAN-BAR CBSS03B00016S-0M-0Y-0M-0Y-1M-0Y

Supplementary Table 1 (Continued). Pedigree of 140 barley advanced lines with line number and their source (ICARDA).

Line no.	Source	Pedigree
130	Mrocco nurseries-Gonbad(2018-19)	BISON 110.3/3/SVANHALS-BAR/MSEL//AZAF/GOB24DH
131	Mrocco nurseries-Gonbad(2018-19)	TRADITION//PENCO/CHEVRON-BAR
132	Mrocco nurseries-Gachsaran(2018-19)	J08040/MERIT 57 J08053 F3-0TR-3MR
135	Mrocco nurseries-Gachsaran(2018-19)	SHENMAI NO.3/SCARLETT//CANELA F09120 09/D30020-0AP-0TR-13MR
136	Mrocco nurseries-Gachsaran(2018-19)	110122/Impala//Birence/3/ArabiAbiad/4/5604/1025/5/SB73358B1041613//ER/Apm/6/WI2291/Bgs//Hml-02/7/MADRE SELVA ICB09-1932-0AP-0AP-0TR--0AP-0TR-6MR
137	Mrocco nurseries-Gachsaran(2018-19)	CABUYA/4/GLORIABAR/COPAL//BEN.4D/3/S.PB/5/PETUNIA1/6/P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA 1 M06427 F6 08/030380-0TR-8MR
138	Mrocco nurseries-Gachsaran(2018-19)	Hma02//110122/CM67/3/Alanda/5/Rhn03//Lignee527/NK1272/4/Lignee527/Chn01/3/Alanda/6/Rhn//Bc/Coho/3/DeirAlla106//Api/EB89-8-2-15-4/5/CM67/3/Apro//Sv02109/Mari/4/Carbo ICB09-0613-0AP-0AP-025AUB-2AUB-0MR
139	Mrocco nurseries-Gachsaran(2018-19)	Chigwell//SHAKIRA HIICB12-112-0TR-0MR-0MR-0MR-2MR
140	Mrocco nurseries-Gachsaran(2018-19)	CANELA//E.ACACIA/DEFRA/4/CLI18/E.QUEBRANCHO//E.QUEBRANCHO/NCL95109/3/CANELA RSI/ICJ11-12B017S-81CJ-05CH-05CJ-10CH-0CJ-0MR
141	Mrocco nurseries-Gachsaran(2018-19)	MP103MQ/11MQ51 UCD13-118-0UCD-0UCD-0MR-0MR-2MR
142	Mrocco nurseries-Gachsaran(2018-19)	Melusine/Aleli/3/Matico/Jet//Shyri/4/Canela/5/CANELA ICB11-0162-0MC-0MC-0MC-10MR
143	SPII nurseries-Gonbad(2018-19)	Rhn03/Eldorado/5/Rhn03//Lignee527/NK1272/4/Lignee527/Chn01/3/Alanda/6/Rhn03/Eldorado/5/Rhn-03//Lignee527/NK1272/4/Lignee527/Chn-01/3/Alanda
144	SPII nurseries-Gonbad(2018-19)	Rhn-03/Eldorado/5/Rhn-03//Lignee527/NK1272/4/Lignee527/Chn-01/3/Alanda/6/ALISO/CI3909-2//FALCON-BAR/3/HIGO
147	SPII nurseries-Gonbad(2018-19)	Rihane03/3/As46/Aths*2//Aths/Lignee686/6/Rhn03/Eldorado/5/Rhn03//Lignee527/NK1272/4/Lignee527/Chn-01/3/Alanda
148	SPII nurseries-Gonbad(2018-19)	Rihane03//Lignee527/Aths/6/Rhn03/Eldorado/5/Rhn03//Lignee527/NK1272/4/Lignee527/Chn-01/3/Alanda
149	SPII nurseries-Gonbad(2018-19)	Lignee527/NK1272//JLB70063/3/Rhn03/6/Rhn03/Eldorado/5/Rhn03//Lignee527/NK1272/4/Lignee527/Chn-01/3/Alanda
150	SPII nurseries-Gonbad(2018-19)	Roho/4/Zanbaka/3/ER/Apm//Lignee131/5/Otis/7/IPA7/5/Api/CM67//Mona/3/DI//Asse/CM65-1W-B/4/Asl-02/6/Aths
151	SPII nurseries-Gonbad(2018-19)	7028/2759/3/6982//Ds/Apro/4/Arizona5908/Aths//ArabiAbiad*2/5/Menuet/ArabiAbiad//WI2198/6/Arar/Rihane-03//Osiris
152	SPII nurseries-Gonbad(2018-19)	Nadawa/Rhn03/3/Lignee527/Rihane//Arar/9/Saida/6/Cita'S'/4/Apm/RI//Manker/3/Maswi/Bon/5/Copal'S'/7/Malouh/8/Birka
153	SPII nurseries-Gonbad(2018-19)	Nadawa/Rhn03/3/Lignee527/Rihane//Arar/9/Saida/6/Cita'S'/4/Apm/RI//Manker/3/Maswi/Bon/5/Copal'S'/7/Malouh/8/Birka
154	SPII nurseries-Gonbad(2018-19)	Nadawa/Rhn-03/3/Lignee527/Rihane//Arar/7/AwBlack/Aths//Arar/3/9Cr279-07/Roho/6/Alanda-01/5/CI01021/4/CM67/U.Sask.1800//Pro/CM67/3/DL70
155-1	SPII nurseries-Gonbad(2018-19)	Rihane03/3/As46/Aths*2//Aths/Lignee686/5/Lignee527/NK1272/4/Avt/Attiki//Aths/3/Giza121/Pue
155-2	SPII nurseries-Gonbad(2018-19)	Rhn-03/3/Mr25-84/Att//Mari/Aths*3-02/4/Rhn-03/Lignee527/7/Rhn03/3/Mr2584/Att//Mari/Aths*3-02/6/Lignee527//Bahtim/DL71/3/Api/CM67//Mzq/5/Alanda-01/4/WI2291/3/Api/CM67//L2966-69

Supplementary Table 1 (Continued). Pedigree of 140 barley advanced lines with line number and their source (ICARDA).

Line no.	Source	Pedigree
158	SPII nurseries-Gonbad(2018-19)	Alanda/Hamra//Alanda-01/7/Alanda/5/Aths/4/Pro/Toll//Cer*2/Toll/3/5106/6/Baca'S'/3/AC253//CI08887/CI05761
159	SPII nurseries-Gonbad(2018-19)	Alanda-01/3/Alanda//Lignee527/Arar/6/Alanda-01//Gerbel/Hma/5/Chn-01/3/Arizona5908/Aths//Bgs/4/Lignee640/Bgs//Cel
160	SPII nurseries-Gonbad(2018-19)	Soffet no.9//SLB21-81/SLB22-74
161	SPII nurseries-Gonbad(2018-19)	JLB70-20/SenS//Aths/Lignee686/6/U.Sask.1766/Api//Cel/3/Weeah/4/Arar/5/Aths
162	SPII nurseries-Gachsaran(2018-19)	GLORIA-BAR/IAR.H.485//ALOE/3/CABUYA
163	SPII nurseries-Gachsaran(2018-19)	WI2737/4/Alger/Ceres//Sls/3/ER/Apm/5/Onslow/Tipper
164	SPII nurseries-Gachsaran(2018-19)	Harrington/Arta/4/Leb71/CBB37//Leb71/CBB29/3/Lignee527/Chn-01
165	SPII nurseries-Gachsaran(2018-19)	Leb71/CBB37//Leb71/CBB29/3/Lignee527/Chn01/4/Mo.B1337/WI2291//Moroc9-75
166	SPII nurseries-Gachsaran(2018-19)	ICARO/MORA/5/Melusine/Aleli/3/Matico/Jet//Shyri/4/Canela
167	SPII nurseries-Gachsaran(2018-19)	FIRAT/3/Mo.B1337/WI2291//Moroc9-75