



Homeostasis and Genotypic Resultant for the Main Spike Characters of Two-rowed Barely

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Article info	Abstract
<p>Original: 2 June. 2015 Revised: 10 August. 2015 Accepted: 30 August. 2015 Published online: 20 March. 2016</p> <p>Key Words:</p> <p><i>Two-rowed barley, Homeostasis and Genotypic Resultant Analysis, Main spike characters.</i></p>	<p>Five genotypes of two-rowed barley (<i>Hordeum distichum</i> L.) named MORA, ABN-B, Arabi Aswad, Clipper and Bohoth H1 with their twenty F₁ progeny were evaluated in Kurdistan Region-Iraq at three different locations, Erbil-Grdarasha, Garmian-Kalar and Sulaimani-Qilyasan during the winter season 2011-2012 using Randomized Completely Block Design (RCBD) with three replications in order to study the homeostasis and genotypic resultant growth and spike characters. The results revealed highly significant effects due to genotypes × locations in most of the studied characters with exception of flag leaf length, spike length, and grain weight / spike. Parent 1 was the best genotype which had the highest homeostasis values for five characters no. of grain / spike (0.936), flag leaf length (0.915), peduncle diameter (0.962), spike length (0.933) and no. of spikelets / spike (0.975), while the hybrid (1×2) had the highest homeostasis values for three characters flag leaf length (0.985), spike length (0.988), and no. of spikelets / spike (0.990). So the homeostasis of these genotypes needs to be better evaluated in a set of environments tested across different years. Very high genotypic resultant values were obtained for no. of grain / spike (1.135 by the hybrid 2×5), flag leaf length (1.074 by the hybrid 5×4), spike length and no. of spikelets / spike (1.061 and 1.059, respectively by the hybrid 2×5) indicating these genotypes having high performances at different environments and should be not ignored in future studies.</p>

Introduction

The performance of a particular variety is result of its genetic constitution and environment in which it has been grown. It is possible that a particular variety may not give the same performance under different environments or different varieties may respond differently to a specific environment [1].

Genotype × environment interactions are of major importance, because they provide information about the effect of different environments on cultivar performance and have a key role for assessment of performance homeostasis of the breeding materials [2].

Barley is most widely adapted cereal grain species with good drought, cold, and salt tolerance and it constitutes the second agricultural commodity in Iraq and Iraq-Kurdistan rejoins after wheat. It is the best known crop grown worldwide under varying agro climatic situations for food, feed and forage. Barley in recent years has been the fourth most- produced cereal after maize, rice and wheat with average of 8 years (2000 – 2008) by 140, 672, 609 and 598 million Mt, respectively [3].

Grain yield is a complex character made up of the interaction between different yield components and the environmental effects. There is an increasing number of phenotypic homeostasis measures used to

assess the response of genotypes when grown in different environments. El-Sahookie and Al-Rawi, (2011) summarized genotype-by-environment (G × E) interaction through homeostasis and genotypic resultant [4].

A variety is considered sufficiently stable when there is no evidence to indicate that it lacks uniformity or fails to conform to the essential characteristics of its description in different submissions or in different tests.

The objective of this investigation was to examine, for a multi- location barley test, the genotype × environment interactions for main spike characters in population of two-rowed barley genotypes with respect to selection of genotypes under condition of Kurdistan region -Iraq.

Materials and Methods

This study was conducted at three environments in Iraqi Kurdistan region, Erbil-Grdarasha (36° 07' 14" N, 44° 00' 23" E and 419 masl), 10 Km south of Erbil city, Garmian - Kalar (34° 21' 558" N, 45° 22' 681" E and 178 masl) and Sulaimani - Qlyasan (35° 34' 307" N, 45° 21' 992" E and 765 masl), 3 Km North west of Sulaimani city during the winter growing season 2010-2011. Five varieties and Pedigrees of two-rowed barley (*Hordeum distichum* L.), namely, MORA, ABN-B, Arabi Aswad, Clipper, and Bohoth H1 were cultivated. The origin and pedigree of these genotypes are presented in Table (1). Each cross was plants in four rows, 0.75 m apart and 5 m long with 0.25 m between plants. At full maturity, the central two rows of each plot (excluding the borders and 0.5 m from each end) were harvested manually in each environment. Measurements were taken on the following parameters (the average of the main spikes of 5 plants / plot): no. of grains / spike, flag leaf length (cm), average grain weight (mg), peduncle length (cm), peduncle diameter (mm), spike length (cm), spike weight (g), no. of spikelets / spike, and grain weight / spike (g).

One set of diallel crosses was made during the growing season in 2010-2011 in full diallel mating design to produce 20 F₁ hybrids Table (2). Grains of F₁ generation and their parents were grown in the following growing season 2011–2012 by using Randomized Completely Block Design (RCBD) with three replications. Each experimental unit was three rows of 2 meter length, 40 cm apart and 20 cm between plants within a row.

Soil samples were analyzed at the laboratory of Soil and Water Department, Faculty of Agricultural Sciences, University of Sulaimani as shown in Appendix (1).

The Metrological data obtained from Erbil, Kalar, and Sulaimani metrological stations during the growing season 2011–2012 from October to May at three environments were shown in Appendix (2).

Statistical analysis:

Once all genotypes data were collected, data from 25 genotypes were utilized to perform all statistical analysis as a general test. Combined analysis of variance across environments was conducted according to Al-Mohammad and Al-Yonis (2000). [5]. Homeostasis and genotypic resultant were calculates according to the following equations [6].

$$\text{Homeostatis (H)} = 1 - \frac{S}{\bar{X}_i} \quad \text{Where,}$$

$$S: \text{ The Standard Deviation, } S = \sqrt{S^2} = \sqrt{\frac{\sum X_i^2 - \frac{(\sum X_i)^2}{n}}{n-1}}$$

i : The value of genotype,

\bar{X}_i : The average character value across studied environments.

$$\text{Genotypic Resultant (GR)} = \left(1 - \frac{S}{\bar{X}_i} \right) \times \left(\frac{\bar{X}_i}{\bar{X}_{..}} \right) \text{ Where,}$$

\bar{X}_i : The average character value crossing studied environments,

\bar{X}_j : The average character value for particular environment crossing genotypes,

$\bar{X}_{..}$: The general mean of particular character for all genotypes and all environments.

Table 1: The origin and pedigree of the genotypes

No.	Pedigree or name	Source	Origin
1	MORA/NB1054/3/MOLA/SHYRI//ARUPO*2/JET/4/... CBSS99M00293T-G- 5M-1Y-1M-0Y,	Sulaimani Agricultural Research Center	ICARDA
2	ABN-B/KA-B//RAISA/3/ALELI/4/LIMON/5/... CBSS99M00228 T-K-6M-1Y- 1M-0Y	Sulaimani Agricultural Research Center	ICARDA
3	Arabi Aswad	Kalar Agricultural Research Center	ICARDA
4	Clipper (Proctor*Prior A)	Erbil Agricultural Research Center	Australia
5	Bohoth H1	Erbil Agricultural Research Center	ICARDA

Table 2: Studied Breeding Materials

No.	Diallel, Reciprocal Crosses and Parents No.	Parentage		
1	1 × 2	MORA	×	ANB-B
2	2 × 1	ANB-B	×	MORA
3	1 × 3	MORA	×	Arabi Aswad
4	3 × 1	Arabi Aswad	×	MORA
5	1 × 4	MORA	×	Clipper
6	4 × 1	Clipper	×	MORA
7	1 × 5	MORA	×	Bohoth H1
8	5 × 1	Bohoth H1	×	MORA
9	2 × 3	ANB-B	×	Arabi Aswad
10	3 × 2	Arabi Aswad	×	ANB-B
11	2 × 4	ANB-B	×	Clipper
12	4 × 2	Clipper	×	ANB-B
13	2 × 5	ANB-B	×	Bohoth H1
14	5 × 2	Bohoth H1	×	ANB-B
15	3 × 4	Arabi Aswad	×	Clipper
16	4 × 3	Clipper	×	Arabi Aswad
17	3 × 5	Arabi Aswad	×	Bohoth H1
18	5 × 3	Bohoth H1	×	Arabi Aswad
19	4 × 5	Clipper	×	Bohoth H1
20	5 × 4	Bohoth H1	×	Clipper
21	1	MORA		
22	2	ANB-B		
23	3	Arabi Aswad		
24	4	Clipper		
25	5	Bohoth H1		

Results and Discussion

Appendix (3) confirms the presence of highly significant interaction due to genotypes \times environments for the characters no. of grains / spike, average grain weight (mg), peduncle length (cm), peduncle diameter (mm), spike weight (g), and no. of spikelets / spike which demonstrate the presence of genotype and environmental differences governing the expression of these characters and the significant contribution of genotypes \times environments interactions in influencing genotype performance, while this interaction were not significant for the characters flag leaf length (cm), spike length (cm), and grain weight / spike (g). This is in agreement with Sinebo, (2005) who obtained highly significant GE interaction by sixteen barley genotypes in three sowing date with three seasons for the characters no. of grain / spike, grain weight and flag leaf length; Rodriguez *et al.*, (2008) for no. of grains / spike; Jalata *et al.*, (2011) for no. of spikelets / spike and no. of grains / spike [7], [8] and [9].

Table (3- a and b) represents the means of the studied characters across locations; the hybrid (5 \times 1) recorded the maximum no. of grains / spike, peduncle diameter (9mm), spike weight (g), no. of spikelets / spike, and grain weight (g) with 37.78, 1.88, 2.33, 39.67, and 1.961 respectively. Parent 1 obtained the maximum values for the characters no. of grains / spike, peduncle length (cm), and no. of spikelets / spike with 33.11, 29.12 and 35.33 respectively, and the highest values recorded by the parent 5 for the characters flag leaf length (cm), peduncle diameter (mm), spike weight (g) and grain weight / spike (g) with 16.39, 1.89, 1.98 and 1.67 respectively. These results confirm that parents 1 and 5 have the best combiner as showed the highest values for most of the studied characters, and reflected in their cross (5 \times 1) which gave the best values for the desirable characters as mentioned previously. The hybrid (5 \times 1) also showed high homeostasis and genotypic resultants for the mentioned characters which means that this genotype was more stable and had a good performance across environments. According to Elsahookie (1990), if the value of homeostasis is more than 85% it means that this genotype was stable across environments, and if the value of genetic resultant was high and close to unity, it means that the genotype has a good performance across different environments [10].

Figure (1) confirms mean values of Homeostasis and genotypic resultant for the studied characters. In general, the characters no. of grains / spike, average grain weight, peduncle diameter, spike length, no. of spikelets / spike should be stable and close to high genotypic resultant with average values (0.895 and 0.902), (0.851 and 0.852), (0.930 and 0.930), (0.892 and 0.864) and (0.952 and 0.9952) respectively, while the characters flag leaf length, peduncle length, spike weight, and grain weight / spike showed the lowest unstable and genotypic resultant average values (0.826 and 0.793), (0.614 and 0.617), (0.751 and 0.749), and (0.785 and 0.750) respectively. These results is in accordance with Elsahookie (1990), Elsahookie (1995), and Elsahookie and Al-Rawi (2011), who mentioned that the stability of the genotypes depending on the value of homeostasis, if more than 85% it means that this genotype was stable across environments, and the value of genetic resultant was high and close to unity, it means that the genotype has a good performance across different environments. [4], [6], and [10].

Table 3- a: Means of the studied characters across locations

Char.	No. of grains / spike				Flag leaf length (cm)				Average grain weight (mg)				Peduncle length (cm)				Peduncle diameter (mm)			
	Erb.	Gar.	Sul.	Means	Erb.	Gar.	Sul.	Means	Erb.	Gar.	Sul.	Means	Erb.	Gar.	Sul.	Means	Erb.	Gar.	Sul.	Means
1 × 2	34.33	36.67	36.67	35.89	11.57	11.23	11.33	11.38	37.80	48.97	54.67	47.14	21.27	32.93	41.67	31.96	1.50	1.63	1.50	1.54
2 × 1	31.67	32.00	36.33	33.33	9.37	11.93	11.80	11.03	38.30	45.23	52.40	45.31	19.07	27.27	41.87	29.40	1.37	1.58	1.50	1.48
1 × 3	22.00	31.67	23.00	25.56	11.73	11.57	13.37	12.22	46.27	37.50	55.70	46.49	16.43	23.20	40.27	26.63	1.36	1.56	1.43	1.45
3 × 1	25.33	23.33	27.00	25.22	12.27	10.93	12.23	11.81	47.97	50.13	58.50	52.20	14.57	26.03	40.80	27.13	1.43	1.48	1.52	1.48
1 × 4	34.33	36.67	37.00	36.00	11.80	15.27	18.73	15.27	42.83	46.17	65.93	51.64	16.23	33.03	44.47	31.24	1.53	1.67	1.91	1.70
4 × 1	32.33	36.33	38.33	35.67	10.60	13.93	15.87	13.47	43.27	51.37	62.50	52.38	16.33	29.17	43.57	29.69	1.68	1.99	1.74	1.80
1 × 5	31.33	36.00	38.33	35.22	11.80	15.67	14.77	14.08	42.77	51.63	65.20	53.20	24.17	34.77	44.47	34.47	1.54	1.81	1.69	1.68
5 × 1	34.00	40.00	39.33	37.78	12.53	13.67	14.63	13.61	42.93	51.07	60.53	51.51	21.77	34.63	42.30	32.90	1.76	1.97	1.90	1.88
2 × 3	25.33	27.33	19.00	23.89	9.67	14.47	9.97	11.37	40.50	51.57	59.50	50.52	15.23	30.83	36.80	27.62	1.31	1.54	1.33	1.40
3 × 2	25.67	22.67	24.33	24.22	9.47	12.80	13.17	11.81	39.83	56.57	55.20	50.53	16.03	30.80	40.87	29.23	1.34	1.47	1.40	1.41
2 × 4	30.00	34.33	35.33	33.22	9.63	15.37	58.77	27.92	44.83	56.87	61.03	54.24	16.33	28.63	42.63	29.20	1.57	1.78	1.78	1.71
4 × 2	28.67	36.67	36.67	34.00	10.60	14.87	13.03	12.83	44.63	52.73	60.07	52.48	12.53	29.60	43.63	28.59	1.43	1.82	1.76	1.67
2 × 5	35.00	37.33	37.00	36.44	12.13	14.80	13.90	13.61	38.00	47.57	59.37	48.31	24.77	33.47	44.70	34.31	1.64	1.84	1.72	1.73
5 × 2	35.00	36.67	38.67	36.78	12.40	16.93	18.60	15.98	44.83	46.53	59.23	50.20	24.47	30.57	44.83	33.29	1.59	1.79	1.76	1.71
3 × 4	18.33	23.33	26.33	22.67	11.50	13.63	13.80	12.98	50.40	60.37	52.40	54.39	16.83	24.03	39.70	26.86	1.42	1.60	1.66	1.56
4 × 3	27.00	37.67	33.67	32.78	13.03	17.47	15.50	15.33	49.20	51.13	58.30	52.88	17.63	30.47	41.93	30.01	1.56	1.80	1.72	1.69
3 × 5	18.67	15.00	25.33	19.67	12.80	13.80	12.87	13.16	48.77	51.03	57.10	52.30	23.50	29.73	39.37	30.87	1.59	1.72	1.60	1.64
5 × 3	18.67	23.67	25.67	22.67	13.80	14.80	18.47	15.69	54.13	54.63	60.27	56.34	22.57	29.73	40.97	31.09	1.58	1.60	1.75	1.64
4 × 5	30.00	32.00	35.33	32.44	11.67	14.93	18.23	14.94	45.73	53.23	57.73	52.23	15.53	28.57	40.27	28.12	1.72	1.79	1.97	1.83
5 × 4	31.67	32.33	36.00	33.33	14.93	16.50	17.50	16.31	44.67	54.53	63.70	54.30	17.77	29.87	40.00	29.21	1.63	1.76	2.01	1.80
1	30.67	34.33	34.33	33.11	9.47	11.20	10.20	10.29	35.90	41.37	46.90	41.39	22.77	28.77	35.83	29.12	1.43	1.54	1.52	1.50
2	29.67	32.33	35.00	32.33	7.33	12.27	12.77	10.79	40.30	44.43	54.50	46.41	16.77	29.23	40.87	28.96	1.27	1.46	1.46	1.40
3	27.33	30.00	33.33	30.22	11.93	14.10	15.37	13.80	45.53	51.10	56.10	50.91	17.57	19.57	32.57	23.23	1.32	1.41	1.49	1.41
4	27.33	32.33	33.00	30.89	9.63	14.67	15.87	13.39	50.07	49.40	57.60	52.36	13.50	21.83	35.57	23.63	1.71	1.96	1.90	1.86
5	28.33	34.00	32.67	31.67	14.77	16.80	17.60	16.39	45.57	52.57	58.90	52.34	18.57	27.07	38.97	28.20	1.91	1.98	1.78	1.89
Means	28.51	31.79	32.71	31.00	11.46	14.14	16.33	13.98	44.20	50.31	58.13	50.88	18.49	28.95	40.76	29.40	1.53	1.70	1.67	1.63
SD	5.03	6.06	5.73	5.25	1.79	1.87	9.21	3.41	4.47	4.97	4.21	3.37	3.62	3.79	3.07	2.82	0.16	0.18	0.19	0.16

To be continued

Table 3- b: Means of the studied characters across locations

<i>Characters</i>	<i>Spike length (cm)</i>				<i>Spike weight (g)</i>				<i>No. of spiklets / Spike</i>				<i>Grain weight / spike (g)</i>			
	<i>Erb.</i>	<i>Gar.</i>	<i>Sul.</i>	<i>Means</i>	<i>Erb.</i>	<i>Gar.</i>	<i>Sul.</i>	<i>Means</i>	<i>Erb.</i>	<i>Gar.</i>	<i>Sul.</i>	<i>Means</i>	<i>Erb.</i>	<i>Gar.</i>	<i>Sul.</i>	<i>Means</i>
<i>1 × 2</i>	11.00	11.17	10.90	11.02	1.47	2.06	2.30	1.94	38.67	38.67	38.00	38.44	1.29	1.80	2.00	1.70
<i>2 × 1</i>	9.83	10.90	10.83	10.52	1.37	1.67	2.27	1.77	36.33	35.67	38.67	36.89	1.21	1.45	1.90	1.52
<i>1 × 3</i>	9.07	10.23	11.37	10.22	1.11	1.44	1.78	1.44	36.67	35.67	38.00	36.78	1.01	1.20	1.28	1.16
<i>3 × 1</i>	9.93	9.93	42.53	20.80	1.31	1.46	2.02	1.60	37.00	34.00	38.33	36.44	1.21	1.17	1.58	1.32
<i>1 × 4</i>	9.97	11.43	12.37	11.26	1.64	1.96	3.08	2.23	37.00	37.67	39.33	38.00	1.47	1.69	2.44	1.87
<i>4 × 1</i>	10.43	11.63	11.43	11.17	1.61	2.13	2.78	2.17	36.33	38.67	39.67	38.22	1.40	1.87	2.40	1.89
<i>1 × 5</i>	10.53	12.10	12.57	11.73	1.53	2.18	2.97	2.23	36.33	39.67	40.00	38.67	1.34	1.84	2.50	1.89
<i>5 × 1</i>	11.17	12.10	12.37	11.88	1.68	2.40	2.90	2.33	37.33	41.33	40.33	39.67	1.46	2.04	2.38	1.96
<i>2 × 3</i>	9.50	11.70	10.50	10.57	1.23	1.75	1.55	1.51	31.67	38.00	36.00	35.22	1.03	1.41	1.13	1.19
<i>3 × 2</i>	9.70	11.33	10.80	10.61	1.25	1.64	1.76	1.55	34.33	36.67	36.67	35.89	1.02	1.28	1.34	1.22
<i>2 × 4</i>	10.43	12.07	11.23	11.24	1.56	2.27	2.53	2.12	36.33	37.67	37.67	37.22	1.34	1.95	2.16	1.82
<i>4 × 2</i>	10.30	12.63	11.10	11.34	1.57	2.26	2.58	2.14	33.67	39.00	38.00	36.89	1.28	1.93	2.20	1.81
<i>2 × 5</i>	11.87	12.33	12.00	12.07	1.57	2.10	2.65	2.10	38.67	39.00	38.67	38.78	1.33	1.78	2.20	1.77
<i>5 × 2</i>	11.40	12.17	12.67	12.08	1.71	2.00	2.76	2.15	37.33	38.00	40.33	38.56	1.57	1.71	2.29	1.86
<i>3 × 4</i>	9.90	10.60	11.33	10.61	1.02	1.83	1.91	1.59	34.67	33.67	37.00	35.11	0.92	1.41	1.38	1.24
<i>4 × 3</i>	10.13	12.30	12.80	11.74	1.55	2.29	2.58	2.14	35.00	39.00	40.67	38.22	1.33	1.93	1.96	1.74
<i>3 × 5</i>	9.87	10.53	10.77	10.39	1.21	1.59	2.02	1.61	32.33	35.67	37.33	35.11	0.91	1.16	1.45	1.17
<i>5 × 3</i>	10.87	10.93	11.77	11.19	1.34	1.72	2.16	1.74	35.67	34.00	39.00	36.22	1.01	1.29	1.55	1.29
<i>4 × 5</i>	9.13	9.47	10.23	9.61	1.73	2.07	2.63	2.14	33.67	33.67	35.67	34.33	1.37	1.70	2.04	1.70
<i>5 × 4</i>	11.00	10.17	10.50	10.56	1.62	2.12	2.89	2.21	34.33	33.67	37.00	35.00	1.40	1.76	2.29	1.82
<i>1</i>	9.10	10.40	9.67	9.72	1.20	1.70	1.90	1.60	34.33	35.67	36.00	35.33	1.10	1.42	1.61	1.38
<i>2</i>	9.07	11.13	11.53	10.58	1.30	1.65	2.23	1.73	32.33	36.00	36.33	34.89	1.19	1.44	1.91	1.51
<i>3</i>	8.77	9.70	10.47	9.64	1.35	1.87	2.21	1.81	30.67	32.33	34.00	32.33	1.24	1.53	1.87	1.55
<i>4</i>	7.50	9.67	8.87	8.68	1.54	1.92	2.33	1.93	31.33	34.67	35.67	33.89	1.37	1.60	1.90	1.62
<i>5</i>	8.60	9.70	10.33	9.54	1.44	2.07	2.44	1.98	32.67	35.00	36.33	34.67	1.29	1.79	1.92	1.67
<i>Means</i>	9.96	11.05	12.44	11.15	1.44	1.93	2.37	1.91	34.99	36.52	37.79	36.43	1.24	1.61	1.91	1.59
<i>SD</i>	0.99	0.98	6.34	2.19	0.20	0.27	0.42	0.28	2.27	2.34	1.73	1.84	0.18	0.27	0.40	0.27

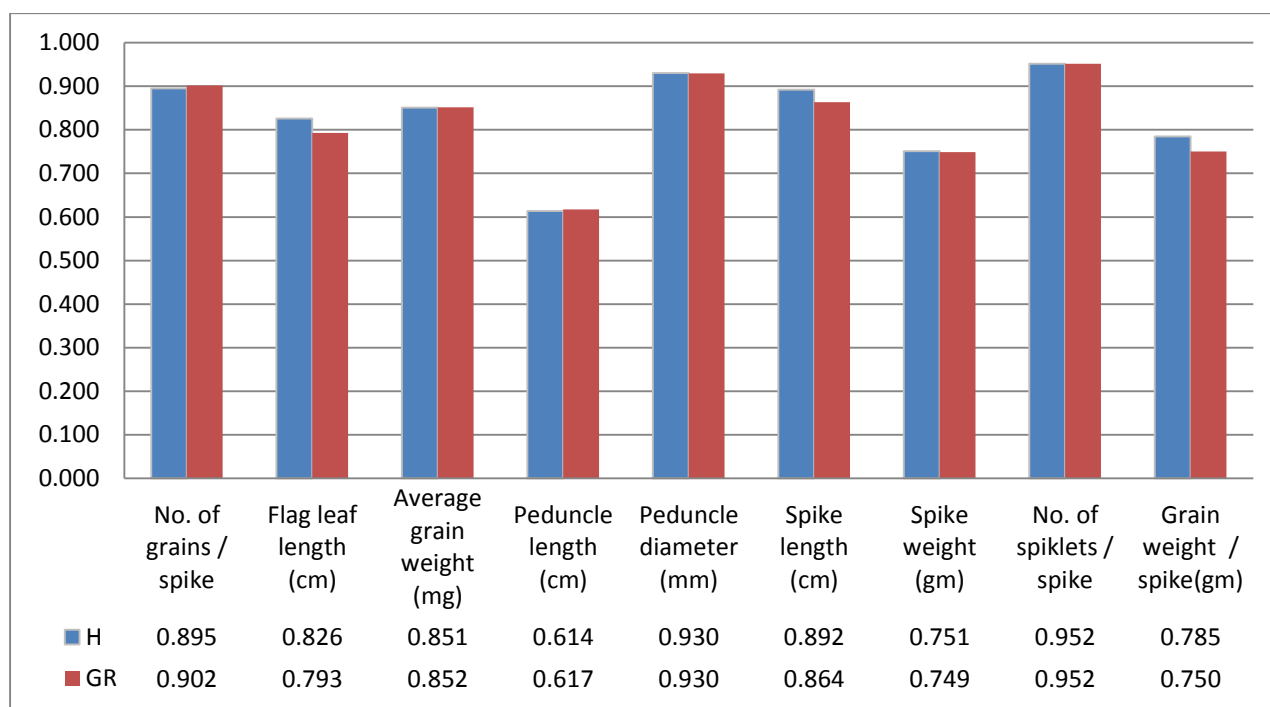


Figure 1: Main spike character means of homeostasis (H) and genotypic resultants (GR) for barley genotypes across environments

Table (4) represents homeostasis and genotypic resultant for the studied characters. According to the no. of grain / spike, the hybrid (2×5) versus all hybrids and parent (1) versus all parents had the greatest homeostasis and genotypic resultant values with 0.965 and 1.135, 0.936 and 1.000, respectively indicating that these genotypes having the highest stable yield performances among the studied environments.

The hybrid (1×2) versus all hybrids and parent (1) versus all parents had the greatest homeostasis values for flag leaf length with 0.985 and 0.915 respectively, while the hybrid (5×4) versus all hybrids and the parent (5) versus all parents had the greatest genotypic resultant values of 1.074 and 1.068 respectively, indicating these genotypes were more stable than the other genotypes across environments.

Average grain weight it should be stable because it had height homeostasis and genotypic resultant, the hybrid (5×3) versus all hybrids and parent (4) versus all parents had the greatest homeostasis values with 0.940 and 0.913 respectively, while the same hybrid versus all hybrids and the same parent versus all parents had the greatest genotypic resultant values of 1.040 and 0.939 respectively.

Various homeostasis and genotypic resultant values concerning peduncle length were obtained and this character was not stable across environments. However, the hybrid (3×5) versus all hybrids and parent (1) versus all parents had the greatest homeostasis values with 0.714 and 0.775 respectively, while the hybrids (1×5) and (2×5) versus all hybrids and the same parent versus all parents had the greatest genotypic resultant values of 0.827 and 0.768 respectively.

Peduncle diameter possessed high homeostasis across environments due to high genotypic resultant values, the hybrid (3×1) versus all hybrids and parent (1) versus all parents had the greatest homeostasis values with 0.970 and 0.962 respectively, while the hybrids (5×1) versus all hybrids and the parent (5) versus all parents had the greatest genotypic resultant values of 1.082 and 1.095 respectively.

Table 4: Main spike characters homeostasis (H) and genotypic resultants (GR) of barely genotypes across environments

Gen.	Genetic Pars.	No. of grains / spike	Flag leaf length (cm)	Average grain weight (mg)	Peduncle length (cm)	Peduncle diameter (mm)	Spike length (cm)	Spike weight (gm)	No. of spikelets / Spike	Grain weight / spike (gm)
1 × 2	H	0.962	0.985	0.818	0.680	0.954	0.988	0.780	0.990	0.784
	GR	1.114	0.802	0.758	0.739	0.902	0.976	0.794	1.045	0.838
2 × 1	H	0.922	0.869	0.844	0.607	0.926	0.943	0.741	0.957	0.769
	GR	0.991	0.686	0.752	0.607	0.840	0.890	0.686	0.969	0.738
1 × 3	H	0.792	0.919	0.804	0.539	0.932	0.887	0.769	0.968	0.882
	GR	0.653	0.803	0.735	0.488	0.826	0.814	0.580	0.977	0.648
3 × 1	H	0.927	0.936	0.893	0.515	0.970	0.095	0.767	0.939	0.830
	GR	0.754	0.791	0.917	0.476	0.877	0.177	0.641	0.939	0.691
1 × 4	H	0.960	0.773	0.758	0.545	0.888	0.893	0.661	0.968	0.728
	GR	1.114	0.844	0.770	0.580	0.925	0.901	0.771	1.010	0.857
4 × 1	H	0.914	0.802	0.816	0.541	0.909	0.942	0.729	0.955	0.736
	GR	1.052	0.773	0.840	0.546	1.003	0.944	0.828	1.002	0.876
1 × 5	H	0.899	0.856	0.788	0.705	0.920	0.909	0.675	0.948	0.693
	GR	1.021	0.862	0.824	0.827	0.946	0.957	0.786	1.006	0.827
5 × 1	H	0.913	0.923	0.829	0.685	0.941	0.947	0.735	0.948	0.763
	GR	1.113	0.899	0.839	0.766	1.082	1.009	0.895	1.032	0.943
2 × 3	H	0.818	0.763	0.811	0.597	0.908	0.896	0.827	0.908	0.833
	GR	0.630	0.621	0.805	0.561	0.775	0.849	0.655	0.878	0.625
3 × 2	H	0.938	0.827	0.816	0.573	0.955	0.922	0.829	0.962	0.860
	GR	0.733	0.699	0.811	0.570	0.821	0.877	0.673	0.948	0.660
2 × 4	H	0.915	0.038	0.845	0.549	0.928	0.927	0.762	0.979	0.767
	GR	0.980	0.076	0.901	0.546	0.970	0.935	0.845	1.001	0.879
4 × 2	H	0.864	0.833	0.853	0.455	0.876	0.895	0.759	0.923	0.737
	GR	0.948	0.765	0.880	0.443	0.895	0.911	0.850	0.935	0.839
2 × 5	H	0.965	0.900	0.778	0.709	0.943	0.980	0.743	0.995	0.755
	GR	1.135	0.877	0.739	0.827	1.000	1.061	0.818	1.059	0.841
5 × 2	H	0.950	0.799	0.843	0.686	0.936	0.947	0.747	0.959	0.794
	GR	1.127	0.914	0.832	0.777	0.980	1.026	0.843	1.015	0.929
3 × 4	H	0.822	0.901	0.903	0.565	0.922	0.932	0.687	0.951	0.780
	GR	0.601	0.837	0.965	0.516	0.880	0.887	0.571	0.917	0.608
4 × 3	H	0.836	0.855	0.909	0.595	0.930	0.879	0.752	0.924	0.794
	GR	0.884	0.938	0.945	0.607	0.964	0.926	0.844	0.969	0.871
3 × 5	H	0.734	0.958	0.918	0.741	0.957	0.955	0.750	0.927	0.771
	GR	0.465	0.901	0.943	0.778	0.958	0.890	0.631	0.894	0.569
5 × 3	H	0.841	0.843	0.940	0.702	0.943	0.955	0.763	0.930	0.789
	GR	0.615	0.947	1.040	0.742	0.949	0.958	0.696	0.924	0.639
4 × 5	H	0.917	0.780	0.884	0.560	0.929	0.941	0.788	0.966	0.803
	GR	0.960	0.834	0.907	0.536	1.039	0.811	0.884	0.911	0.863
5 × 4	H	0.930	0.921	0.825	0.619	0.892	0.960	0.709	0.950	0.753
	GR	1.000	1.074	0.880	0.615	0.983	0.909	0.820	0.912	0.864
1	H	0.936	0.915	0.867	0.775	0.962	0.933	0.775	0.975	0.814
	GR	1.000	0.674	0.705	0.768	0.880	0.813	0.650	0.946	0.707
2	H	0.918	0.722	0.843	0.584	0.921	0.875	0.729	0.936	0.760
	GR	0.957	0.557	0.769	0.575	0.788	0.830	0.659	0.897	0.725
3	H	0.901	0.874	0.896	0.649	0.942	0.912	0.763	0.948	0.798
	GR	0.878	0.863	0.897	0.513	0.811	0.789	0.722	0.842	0.779
4	H	0.900	0.753	0.913	0.529	0.930	0.874	0.794	0.933	0.836
	GR	0.897	0.721	0.939	0.425	1.058	0.680	0.801	0.868	0.855
5	H	0.906	0.911	0.873	0.637	0.946	0.908	0.746	0.946	0.800
	GR	0.926	1.068	0.898	0.611	1.095	0.777	0.774	0.901	0.841

Spike length was stable because it had height homeostasis and genotypic resultant, the hybrid (1×2) versus all hybrids and parent (1) versus all parents had the greatest homeostasis values with 0.988 and 0.933 respectively, while the hybrid (2×5) versus all hybrids and the parent (2) versus all parents had the greatest genotypic resultant values of 1.061 and 0.830 respectively.

Spike weigh should be not stabile across environments due to low genotypic resultant values. However, the hybrid (3×2) versus all hybrids and parent (4) versus all parents had the greatest homeostasis values with (0.829 and 0.794) respectively, while the hybrids (5×1) versus all hybrids and the same parent versus all parents had the greatest genotypic resultant values of 0.895 and 0.801 respectively.

There were high homeostasis and genotypic resultant values for no. of spiklets / spikes. The hybrid (1×2) versus all hybrids and parent (1) versus all parents had the greatest homeostasis values with 0.990 and 0.975 respectively indicating these genotypes having more homeostasis performance among the environments than others, while hybrid (2×5) versus all hybrids and the same parent versus all parents had the greatest genotypic resultant values with 1.059 and 0.946 respectively.

For the character Grain weight / spike, the hybrid (1×3) versus all hybrids and parent (4) versus all parents had the greatest homeostasis values with 0.882 and 0.836 respectively indicating these genotypes having more homeostasis among divers environments than others, while hybrid (5×1) versus all hybrids and the same parent versus all parents had the highest genotypic resultant values with 0.905 and 0.820 respectively indicating these genotypes having the highest stable grain weighing performances among the different environments. Kaczmarek *et al.* (2002) for grain weight in three environments and two years suggested that effects of heterozygous loci are more stable in contrasting environments than effects of homozygous loci [11].

Conclusions

Despite the fact that the various homeostasis methods are indicative, Elsahookei (1995) method provides useful information for achieving definitive results and the identification of mega-environments and wining genotypes are indispensable. The best recommended genotypes according to this investigation were the cross (5×1) which gave the maximum for most of the desirable characters such as no. of grains / spike, spike weight (g), no. of spikelets / spike, and grain weight (g) with the best homeostasis and genotypic resultants across the investigated locations.

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Appendix 1: Soils physical and chemical properties at three environments in the date of sowing season 2011-2012

<i>Soil Properties</i>	<i>Erbil – Gdrarasha</i>	<i>Garmian – Kalar</i>	<i>Sulaimani – Qilyasan</i>
<i>PSD</i>	Silty clay loam	Silty clay	Silty clay
<i>Sand %</i>	9.94	12.6	5.83
<i>Silt %</i>	52.06	45.9	42.07
<i>Clay %</i>	38.50	41.5	52.10
<i>pH</i>	8.22	7.35	7.13
<i>Organic Matter %</i>	0.30	1.35	2.13
<i>Total Nitrogen %</i>	0.25	0.089	0.15
<i>Available Phosphate (ppm)</i>	3.20	5.50	4.49

Appendix 2: The Metrological data at Erbil, Kalar, and Sulaimani environments during the growing season 2011-2012.

Period	Erbil – Grdarasha			Garmian – Kalar			Sulaimani – Qilyasan		
	Temp. C°		Rainfall mm	Temp. C°		Rainfall mm	Temp. C°		Rainfall mm
	Max.	Min.		Max.	Min.		Max.	Min.	
Oct	36.32	9.81	10.4	37.4	10.9	1.5	33.0	15.0	37.3
Nov	22.7	8.0	5.6	23.0	9.0	3.2	21.0	8.0	54.1
Dec	22.9	8.0	4.6	22.9	8.0	67.8	17.0	8.0	48.0
Jan	16.3	-4.8	43.7	17.5	-1.0	21.2	14.7	-5.7	94.2
Feb	17.4	-0.4	33.6	20.9	2.0	53.5	15.5	-0.6	96.5
Mar	24.0	-1.7	56.6	29.5	8.5	27.3	21.1	-2.2	141.4
Apr	34.1	10.2	12.7	36.5	14.8	11.0	30.5	6.1	34.0
May	39.5	15.9	9.4	41.0	20.8	5.3	35.5	13.7	36.0
Jun	40.2	18.5	—	42.1	24.5	—	38.6	16.8	—
Total	—	—	176.3	—	—	190.8	—	—	541.5

Appendix 3: Mean squares of combined analysis of variance across environments

S.O.V	d.f	MS								
		No. of grains / spike	Flag leaf length (cm)	Average grain weight (mg)	Peduncle length (cm)	Peduncle diameter (mm)	Spike length (cm)	Spike weight (gm)	No. of Spiklets / Spike	Grain weight / spike (gm)
Environments	2	365.560 **	447.334 *	3657.848 **	9308.669 **	0.648 **	115.362 n.s	16.34 7**	147.444 **	9.581 *
Block / Environments =E(a)	6	13.027	81.257	2.003	0.663	0.002	39.555	0.006	0.782	1.087
Genotypes / Environments	72	94.910 **	91.599 n.s	62.443 **	36.871 **	0.092 **	42.174 n.s	0.286 **	13.652 **	1.344 n.s
Genotypes	24	248.139 **	104.800 n.s	101.949 **	71.390 **	0.238 **	43.096 n.s	0.686 **	30.475 **	1.949 **
Genotypes x Environments	48	18.296 **	84.998 n.s	42.690 **	19.612 **	0.019 **	41.714 n.s	0.086 **	5.241 **	1.041 n.s
Error / Environments =E(b)	144	3.939	79.817	1.126	0.356	0.002	40.410	0.016	3.116	1.002

