BIOLOGICAL YIELD CONTENT CORRELATED WITH YIELD COMPONENTS IN BARLEY (*Hordeum vulgare* L.) UNDER RAINFED CONDITIONS OF KURDISTAN- IRAQ

Asoz O. Abdullah[1]* Nariman S. Ahmad[2] Kamil M. Mustafa[2]
Lecturer Professor Assist. Professor
[1] Department of Field Crops and Medicinal Plants, College of Agricultural Engineering Science, Salahaddin University, Kurdistan- Iraq
[2] Department of Biotechnology and Crop Science, College of Agricultural Engineering Sciences, University of Sulaimani, Kurdistan-Iraq
Corresponding author: asoz.abdullah@su.edu.krd

ABSTRACT

Barley is the second cereal crop grown after wheat in the Kurdistan region of Iraq. Low rainfall and high-temperature impact barley yields. A study investigating an F_3 population of 100 segregated lines derived from a cross between Clipper, an Australian cultivar known for its high yield, and Local black, a cultivar recognized for its stress tolerance. The segregated F_3 lines were assessed under two different environmental conditions at the Grdarash research station in Erbil and the Qlyasan research station in Sulaimani. The field trial data for the F_3 population experienced analysis of variance and normality tests. Direct selection of high-yielding genotypes is challenging due to the complexity of the trait. Despite significant differences in yield among genotypes from various sources, genotypes showed no significant differences in harvest index (HI%). Location had a greater impact on yield-related traits of the segregated individuals, with temperature being a major influencing factor In Erbil, biological yield (BY) was significantly correlated with yield and its components, except for 1000-grain weight. In Sulaimani, BY was also significantly associated with yield and components, negatively correlated to HI%. Genetic effects were significant for BY but not HI%, with a negative genetic correlation between BY and HI% in Sulaimani. Significant impacts were observed on all attributes using regression analysis. except for 1000-grain weight, which had no significant correlation with BY or other traits. Biplot analysis indicated significant positive correlations between BY and yield-related traits, except for a negative %HI but insignificant correlation with 1000-grain weight.

Keywords: Barley, biological yield content, correlation, regression analysis.

محتوى الحاصل البيولوجي المرتبط بمكونات المحصول في الشعير(*Hordeum vulgare* L.) تحت ظروف الزراعة الديمية في كردستان العراق

اسوز عمر عبدالله [1] نريمان صالح احمد[2]* كامل محمود مصطفى[2]
مدرس استاذ استاذ مساعد
[1]: قسم المحاصيل الحقلية والنباتات الطبية/ كلية علوم الهندسة الزراعية/ جامعة صلاح الدين، كردستان العراق
[2]: قسم تكنلوجيا الحيوية والمحاصيل الحقلية/ كلية علوم الهندسة الزراعية/ جامعة السليمانية، كردستان العراق

المستخلص

الشعير هو محصول الحبوب الثاني الذي يزرع بعد القمح في إقليم كردستان العراق. انخفاض هطول الأمطار وارتفاع درجات الحرارة يؤثر على محصول الشعير. اجريت هذه الراسة باستخدام بذور الجيل الثالث لـ 100 سلالة منعزلة مشتقة من التهجين بين الصنفين Clipper x Local black . يتميز الصنف الاسترالى (Clipper) بالحاصل العالى فى حين ان الصنف المحلى Local black يتميز بتحمل الظروف القاسية. تم تقييم النباتات الجيل النعزالى الثالث فى بيئتين مختلفتين، الاولى فى اربيل (محطة ابحاث كردةرةش) والثانية فى السليمانية (محطة ابحاث قلياسان). شهدت بيانات التجربة الميدانية لمجموعة F_3 تحليل التباين والاختبارات الطبيعية. يعد الاختيار المباشر للأنماط الجينية عالية الحاصل أمرًا صعبًا بسبب تعقيد الصفات. على الرغم من الاختلافات الكبيرة في اللحاصل بين الأنماط الجينية من مصادر مختلفة، إلا أن الأنماط الجينية لم تظهر فروقًا كبيرة في مؤشر الحصاد HI ٪ . كان للموقع تأثير أكبر على الصفات المتعلقة بالحاصل للأفراد المنفصلين، حيث كانت درجة الحرارة عاملًا مؤثرًا رئيسيًا في أربيل، ارتبط الحاصل البيولوجي BY بشكل معنوي مع حاصل الحبوب ومكوناته، باستثناء وزن 1000 حبة في السليمانية، ارتبط أيضًا بشكل كبير بحاصل ومكوناتها، مع ارتباط سلبي مع BY كانت التأثيرات الوراثية مهمة بالنسبة لـ BY ولكن ليس HI٪ ، مع وجود ارتباط وراثي سلبي بين BY و HI ٪ في السليمانية. أظهر تحليل الانحدار تأثيرات كبيرة على جميع الصفات باستثناء وزن (1000) حبة، والتي لم يكن لها ارتباط كبير مع BY أو الصفات الأخرى. أشار تحليل Biplot إلى ارتباطات إيجابية كبيرة بين BY والصفات المرتبطة بالغلة، باستثناء نسبة HI٪ السلبية ولكن ارتباط غير مهم مع وزن (1000) حبة.

الكلمات المفتاحية: الشعير، محتوى الحاصل البيولوجي، الارتباط ، تحليل الانحدار.

Received:13/6/2024, Accepted:8/9/2024

INTRODUCTION

Barley (*Hordeum vulgare* L.) is a member of the Poaceae family, Triticaeae tribe, and *Hordeum* genus, which includes 32 species and 45 taxa. This genus comprises diploid (2n = 2x = 14), tetraploid (2n = 4x = 28), and hexaploid (2n = 6x = 42) types, all with a basic chromosome number of x = 7 (9, 31). Barley ranks fourth among cereal crops globally, following wheat, maize, and rice, and is among the top ten crop plants worldwide (2). The global production of barley is expected to reach 151.62 million metric tons in the 2022-2023 growing season (23). Developing and acquiring varieties that are resistant to challenging conditions and produce well across diverse environments is a key goal in the improvement program of this crop (14). *Hordeum vulgar*e is an ancient and crucial winter crop for the high mountain regions of the country. The crop is an annual cereal grown globally in temperate climate zones, adapted crops to different climatic conditions (5). It is primarily used as animal feed, as malting, human consumption (21, 27). One of the earliest domesticated cereals, barley is believed to have originated in the Fertile Crescent of the Middle East. However, Iraq is part of the Fertile Crescent, and being the center of domestication for this crop, the production is not at the required level to satisfy the current local demands on this crop (12). However, it is being considered as an important cereal worldwide after wheat, rice, and maize (25). This emphasizes the need for genetic improvement to enhance barley crop yield, especially given the current condition of aridity in Iraqi Kurdistan. Despite having a simple genetic system, barley is genetically diverse, making it an ideal model for cereal research. Molecular studies have revealed significant genetic similarities between barley, wheat, and rye (11). Many researchers (6, 24) have reported on the degree of association between yield and its components, as well as their use in barley selection. The improvement of grain yield through breeding relies on genetic diversity, a critical factor in any successful hybridization program. Quantitative traits, such as grain yield, are complex and influenced by numerous genes, both directly and indirectly, making direct selection challenging (8). In breeding programs, directly selecting for crop yields is paradoxical because yield is a complex trait influenced by multiple genes and various component traits (16). In genetic research, it is crucial to differentiate between genetic and environmental correlations among traits (13). Correlation coefficients measure the extent and direction of impacts on economic productivity, but using only simple correlation coefficients without accounting for interactions can mislead breeders (10, 18). Therefore, the current study was designed to assess the yield component characteristics as well as the genotypes and explore the correlations through simple and genetic correlations, regression analysis, and biplot analysis between biological yield and other traits in the yield components.

MATERIALS AND METHODS

Two barley cultivars were selected as parents for controlled crossing to create a segregated population for mapping. Clipper, an Australian variety known for its high yield, and Local Black, a domestic cultivar with black spikes and superior drought tolerance, were the parents of the cross. This cross (Clipper X Local Black) resulted in a total of 100 lines in an F3 segregation population. The F3-segregated lines were grown in two locations using a randomized complete block design (RCBD) with three replicates. The first trial started from November 23rd, 2019 to May 13th, 2020, at Salahaddin University's Grdarash Research Station, College of Agriculture, Engineering Sciences. The second trial ran from November 26th, 2019 to May 28th, 2020, at the Qlyasan Agricultural Research Station, University of Sulaimani. The individuals were planted in rows 150 cm long and 35 cm apart, with 15 grains sown per row, spaced 10 cm apart. Each replicate contained three rows, with a one-meter distance between them. In both locations, the data were taken as an average of five randomly selected plants per plot.

Site of application and planting process

Two locations were chosen for the planting of F2 lines in the current study. The original location was the Grdarash Research Station, which was a part of the Salahaddin University College of Agriculture and Engineering

Sciences. Grdarash is situated in the northern and central regions of the Erbil plain, primarily over 400 meters above sea level, according to the research. This plain is roughly bordered by the parallels N 360 06, 48.9, and E 0440 00, 45.0, and it is at a mean elevation of 412 meters. The average annual rainfall for the plain was more than 400 mm for that year (2019–2020) (29). The second site was the Qlyasan Agricultural Research Station, which is part of the College of Agricultural Engineering Sciences of the University of Sulaimani. It is located 2 kilometers north-west of Sulaimani city at Lat. 35o 34' 307"; N, long. 45o 21' 992"; E, 765 MASL. For that year, the plain receives more than 1000 mm of rainfall annually on average. The metrological information for both sites is displayed in Table 1.

Table 1. The research site's temperature and rainfall data of both locations in Erbil and Sulaimani (2019–2020).

Month	Erbil				Sulaimani			
	Rainfall (mm)	Temperature ^{o}C			Rainfall (mm)	Temperature ^{o}C		
		Minimum	maximum	Minimum		Minimum	maximum	Average
September	**0.00**	**24.90**	**36.60**	**31.00**	**0.00**	25.0	32.0	**28.93**
October	**24.70**	**20.20**	**30.90**	**25.30**	1.63	**17.00**	**30.00**	23.19
November	**4.20**	**11.60**	**22.60**	**16.60**	13.00	9.00	**19.00**	14.27
December	**55.10**	**8.50**	**16.10**	**11.90**	174.9	5.00	**13.00**	9.68
January	**97.10**	**5.70**	**13.00**	**8.90**	**249.3**	**2.00**	**13.00**	**6.97**
February	**66.30**	**6.90**	**14.20**	**10.30**	162.8	**4.00**	**11.00**	**10.30**
March	**127.50**	**11.90**	**20.50**	**16.00**	**321.3**	**5.00**	**13.00**	**9.74**
April	**21.30**	**15.10**	**24.80**	**20.00**	**142.0**	**8.00**	**20.00**	**14.77**
May	**11.60**	**21.30**	**32.30**	**27.20**	16.8	**18.00**	**31.00**	25.42
Total	**407.08**				**1082**			

Agro-Morphological Characteristics

Over the course of their lifetimes, several agronomic, yield, and component characteristics of the barley population in the experiment were documented. The characteristics that were looked at for the field trial produced the following outcome: The data were taken for biological yields (BY), grain number/plant (GN), grain weight/plant (GW), 1000-grain weight (1000-GW), spike number/plant (SN), spike weight (SW), spike length (SL), and % harvest index (%HI).

Statistical Analysis

For 102 genotypes, statistical analysis was carried out. It was decided where the variation came from and how the genotypes were compared. The findings were presented as mean, minimal, maximal, and standard deviation values (SD). At the probability level of 5%, the one-way analysis of variance (ANOVA) and Duncan multiple range tests were used. With the help of the statistical software "XLSTAT 2016," the data were subjected to statistical analysis. Principal component analysis (PCA) was used to distinguish between various genotypes. Simple correlations and genetic correlations were performed on the hybrids using SAS 9.4 software. Version 9.4 of the SAS software was used to conduct a combined analysis of variance (ANOVA) (SAS Institute Inc., 2014). The information was standardized using the NTSYS-PC program version 2.1 (22).

Soil Sampling

Before the experiment was set up, soil samples were randomly gathered from the land at a depth of 0 to 15 cm. The material was then brought to the lab. The dirt was then allowed to air dry before being sieved using a 2 mm pore size sieve. The physical and chemical characteristics of the soil at the two sites are displayed in Table 2.

Table 2. Some chemo-physical properties of the experiment soils of Grdarash and Qlyasan sites

Soil		Location	
		Qlyasan	Grdarash
Particle Size Distribution (PSD) g kg^{-1}	Sand	59.68	100.25
	Silt	619.17	515.00
	Clay	321.15	384.75
Textural Class		Silty clay loam	Silty clay
Bulk density Mg m-3*		1.40	1.45
pH		7.42	7.53
EC dS m-1 At 25 °C		0.38	0.38
Cation Exchange capacity (CEC) cmolc kg-1		49.82	46.50
Organic matter (OM) g kg-1		19.59	0.91
Total CaCO3 equivalent g kg-1		215.68	----
Soluble ions mmol L-1	Ca2+	2.0	----
	Mg2+	0.81	----
	Na+	0.46	----
	K+	0.156	----
	HCO3-	2.51	----
	SO42-	0.789	----
Micronutrients available form mg kg-1	Fe	2.08	----
	Zn	0.45	----
	Cu	3.01	----
	Mn	9.86	----
CaCO3 (g kg-1)	----	----	26.91
Gypsum (g kg-1)	----	----	1.01
Total N (ppm)	----	----	89.17
Total P (ppm)	----	----	5.36
Total K (ppm)	----	----	64.10
Available Nitrogen (mg kg-1)	----	----	59.67
Available Phosphorous (mg kg-1)	----	----	2.01
Soluble Potassium	----	----	0.94
Moisture content at field capacity	----	----	0.39
Moisture content at field capacity	----	----	0.22

RESULTS AND DISCUSSION

Modern improvements in crop breeding and management techniques have significantly boosted annual crop productivity by 0.8–1.2%. However, this rate of enhancement falls short of meeting the future food and biofuel needs projected for the global population in 2050, often referred to as the 2050 challenge (17). Extended periods of water scarcity, elevated temperatures, and decreased nutrient availability have been identified as key factors that adversely affect plant development (19). Despite collecting genotypes from various origins and sources, a combined analysis of variance (ANOVA) across two locations; table 3. reveals highly significant differences between the evaluated genotypes. According to this, the genotypes employed in this research exhibited divergence in yield and most yield-related traits. However, the genotypes were not significantly different for % HI, suggesting that these traits do not vary significantly among genotypes. The significant effects of locations on yield-related traits highlight the substantial differential hybrid responses across different locations. Temperature variation across these locations was thought to be a significant underlying cause of the genotype-location interaction affecting yield and yield-related traits. The impact of location was much greater than the gene effect for all traits, suggesting that location factors influence gene performance more significantly for these (30). Despite %HI not being significant, for every variable, the genotype effect's mean values were statistically significant and higher than the year effects, indicating that genotype performance is influenced by the kinds of hybrids that possess these qualities. Prior research conducted at Eskisehir in Turky found significant variations grain yield is an essential agricultural measure indicating the quantity of harvested grain per unit area of land. It is a crucial factor in crop production, as it directly represents the productivity and economic worth of the crop (7).

Table 3. Combined analysis of variance's mean squares for eight traits across two locations, evaluated using 100 lines of barley with two parents

S.O.V	DF	Mean Square							
		BY	GN	GW	1000GW	SN	SW	SL	%HI
Location	1	206530.6**	6726945**	19097.24**	1218.015**	13751.31**	1.816267**	23.19492*	71307.24*
Rep (Location)	4	3639.804**	610896.5**	2172.716**	144.9364**	334.2533**	0.701928**	24.55726**	23172.54$^{n.s}$
Gene	101	645.0942**	1820060**	5665.441**	82.73848**	32.27284**	0.089194**	4.863123*	43362.91$^{n.s}$
Location*Gene	101	525.5188**	1454277**	4472.114**	39.36712*	21.17351*	0.03015*	3.631746*	43501.68$^{n.s}$
Error	404	274.7324	8668.33	25.97792	34.33942	16.12951	0.022376	3.575098	44119.4
CV		40.34947	37.98866	37.261	10.35625	32.07474	11.5891	27.88044	449.584

*** and ** are significantly different at 0.05 and 0.01 levels of probability**

BY, Biological yield; GN, Grain Number; GW, Grain Weight;1000GW, Grain Weight; SN, Spike Number; SW, Spike Weight; SL, Spike Length; %HI, % Harvest Index

The findings on the phenotypic and genotypic correlations, along with the regression analysis between biological yield as well as qualities connected to yield, are summarized in (Table 4) for both locations. In Erbil, biological yield (BY) showed significant phenotypic correlations with yield and its components, except for the 1000-grain weight, which was not significant. In Sulaimani, BY was significantly correlated phenotypically with yield and its components, with harvest index (%HI) showing a negative significance, while 1000-GW and spike weight (SW) were not. In a study conducted by examining the causation among different yield traits, the research offers insights into the relationships between various factors that influence barley yield (26). In the current study, BY showed a highly significant genetic effect at both locations, but the effect on the %HI was not significant in Erbil. This suggests that the genetic influences on BY are independent of this trait. Additionally, there was a significantly negative genetic correlation between BY and HI in Sulaimani. Biological yield per plant and harvest index were negatively impacted by drought stress, leading to no seed yield at the highest level of water depletion, 70% (3). Regression analysis revealed substantial impacts on every characteristic being examined. This indicated that biological yield significantly impacted yield and yield components at both locations. However, for both locations, 1000-grain weight showed no significant correlation or regression with biological yield or other traits, except for harvest index, which was negatively significant in both locations. Researchers used stepwise regression to compare various traits. The regression model, significant at the one percent level, demonstrated that morphological traits have a direct impact on yield (20). The mentioned results in consistent with (4) on wheat.

Table 4. Regression analysis, genetic correlation, and Pearson correlation coefficient between biological yield content and other related traits at two different locations

Trait	Person Corr	Genetics Corr	Regression equation	R^2
		Erbil Location		
GN BY	0.88*	0.89**	y = 4.5498x + 80.429	0.78**
GW BY	0.89*	0.91**	y = 0.2545x + 4.1517	0.79**
1000GW BY	0.01	0.05*	y = 0.0013x + 55.098	0.00004^{ns}
SN BY	0.93*	1**	y = 0.188x + 6.1269	0.86**
SW BY	0.48*	0.43**	y = 0.0037x + 1.1192	0.23**
SL BY	0.22*	0.13**	y = 0.0072x + 6.5504	0.05*
%HI BY	-0.45*	0.0001ns	Y= -0.1084x + 39.543	0.20**
		Sulaimani Location		
GN BY	0.75*	0.048**	y = 4.7507x + 32.854	0.57**
GW BY	0.73*	0.88**	y = 0.276x + 1.8476	0.5353**
1000GW BY	-0.00112	0.8**	Y= -0.0012x + 58.2	0.000001^{ns}
SN BY	0.73*	0.74**	Y= 0.2417x + 2.3205	0.5289**
SW BY	0.160441	0.78**	Y= 0.0043x + 1.1405	0.0257*
SL BY	0.28*	0.014**	Y= 0.0949x + 4.4407	0.0786*
%HI BY	-0.311*	-0.681**	Y= -0.3744x + 44.614	0.097*

Principal Component Analysis (PCA)

As per the biplot analysis, for the Erbil location (Fig. 1), Eight indices were reduced to two independent components based on principal component analysis (PCA). Out of eight, two principal components (PCs) had eigenvalues greater than one, explaining 52.082% of the total variation. The first eigenvector had the greatest value of 4.167; however, the cumulating of the first two components contributed to the explanation of the relationship and transformed into PCs. The first two components account for 71.50% of the total variation, as indicated in the biplot graph and Scree plot of the components cumulatively. In contrast, the biplot analysis for the Sulaimani location was Out of eight, three principal components (PCs) had eigenvalues greater than one, explaining 43.38% of the total variation (Fig. 2), which accounted for 64.72% of the total variation (43.38% by PC1 and 21.34% by PC2). According to Yan (28), within the biplot, the cosine of the angle formed by any two or more trait vectors is an approximate representation of the correlation coefficient (15). Right angles (equal to 90°) show no association, obtuse angles (more than 90°) show a negative correlation, and acute angles (less than 90°) show a positive correlation. If the vector is small, there may be no correlation between the characteristic and other traits. In this research, a brief vector with acute angles (less than 90°) between BY and yield, as well as other traits at both locations, indicated a significant positive correlation (Figures 1 and 2). Conversely, an obtuse angle (greater than 90°) between BY and 1000GW suggested a negative correlation, which was not significant. Overall, the PCA results aligned with those from hierarchical clustering and were consistent with the pairwise analysis of genotype differences and similarities for the agro-morphological traits evaluated. These findings are supported by studies on lentil crops (1).

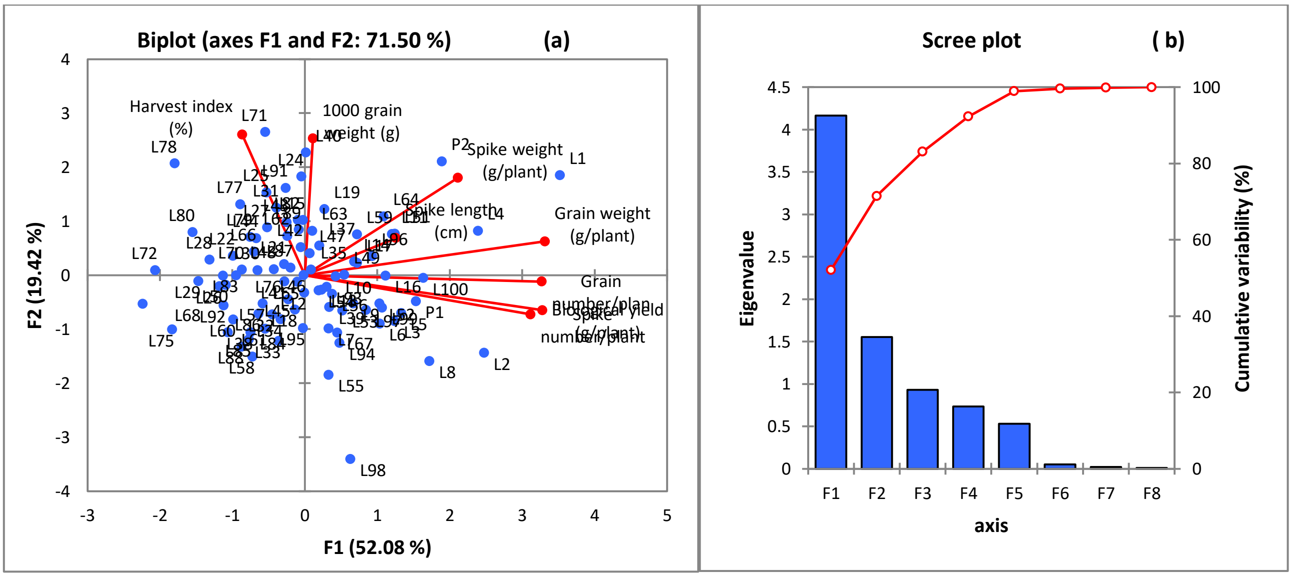

Figure 1. Principal component (PCA) of biplot diagram. (a) showing the distribution of the F_3 population derived from the cross Clipper X Local black (blue dots) based on data from eight evaluated traits (red dots). The scree plot (right) shows the variability given by eight principal components (F1- F8). BY, Biological yield; GN, Grain Number; GW, Grain Weight;1000GW, Grain Weight; SN, Spike Number; SW, Spike Weight; SL, Spike Length; %HI, % Harvest Index. (b) represents Scree plots of cumulative explained variance for the studied traits in Grdarash location

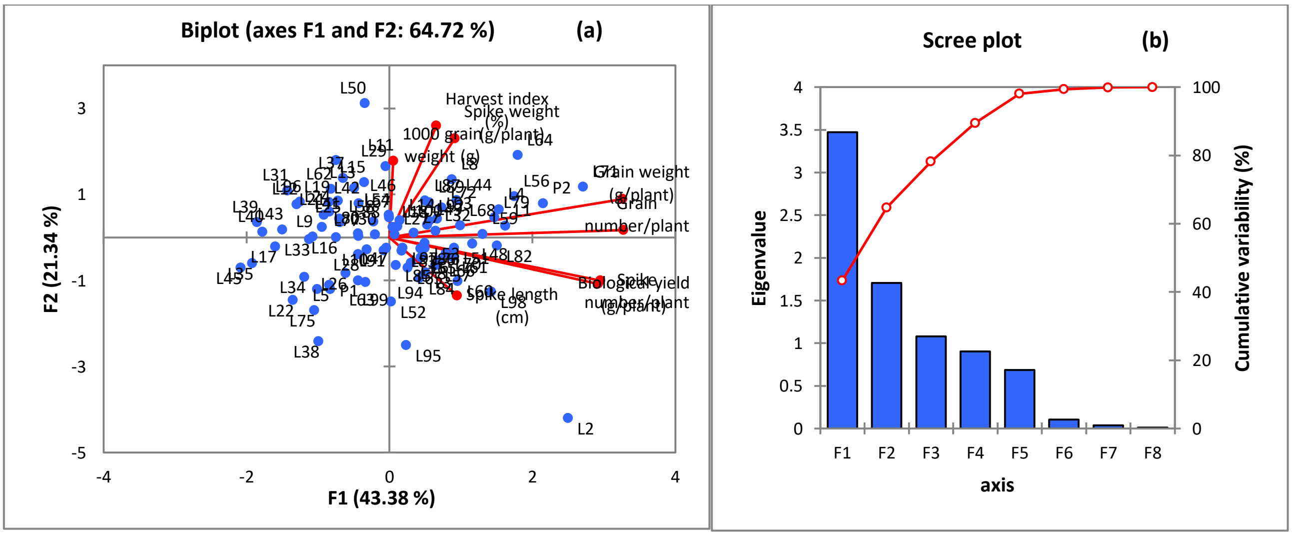

Figure 2. Principal component (PCA) of biplot diagram. (a) showing the distribution of the F_3 population derived from the cross Clipper X Local black (blue dots) based on data from eight evaluated traits (red dots). The scree plot (right) shows the variability given by eight principal components (F1- F8). BY, Biological yield; GN, Grain Number; GW, Grain Weight;1000GW, Grain Weight; SN, Spike Number; SW, Spike Weight; SL, Spike Length; %HI, % Harvest Index. (b) represents Scree plots of cumulative explained variance for the studied traits in Sulaimani location

The evaluated genotypes show significant differences in yield and yield-related traits, except for the harvest index (%HI), which appears consistent across genotypes. The influence of location on these traits is considerable, with environmental factors, especially temperature variation, playing a more crucial role than genetic factors. While genotype performance is affected by the type of hybrid, location has a stronger impact. Biological yield (BY) is strongly correlated with yield and its components in both locations, but the 1000-grain weight does not significantly correlate with yield or other traits. Regression analysis confirms that BY significantly affects yield and its components, while the 1000-grain weight does not have a notable impact.

REFERENCES

1. Ahmad, N.S., N. Moradi, J.G. Rafaat, and D.J. Mohammed, 2021. Genetic variability and heritability estimates of agronomic traits in lentil (Lens culinaris Medik.). Romanian Agricultural Research (38). https://doi.org/10.59665/rar3802

2. Akar, T., M. Avci, and F. Dusunceli, 2004. Barley: post-harvest operation. The Central Research Institute for field crops. Link: https://bit. ly/3mBBmV7. https://www.openknowledge.fao.org/handle/20.500.14283/au997e

3. Ali, K.A. and H. H. Hamad, 2021. Application of Some Drought Stress Indices to Study Response of Durum Wheat Triticum durum to Different Levels of Water Depletion. Tikrit Journal for Agricultural Sciences, 21 (1), 48-58. https://doi.org/10.25130/tjas.21.1.5

4. Al-Hassan, M. F. H. and J. W. Mahmoud. 2019. The contribution of the main stem and the primary tillering in three varieties of wheat under the influence of the five seed rates. Biochem. Cell. Arch. 19: 1353-60. DOI:10.35124/bca.2019.19.1.1353

5. Al-Khalaf, K., S. Lawand, and H. Al-Mahasneh. 2022. Genetic Relationship Between Some Barley Genotypes (*Hordeum vulgare* L.*)* Using SSR Technique (Microsatellite). Iraqi Journal of Agricultural Sciences, 53 (4), 890-900. https://doi.org/10.36103/ijas.v53i4.1601

6. Amardeep, L. and V. Singh, Piyushmalik (2017). Studies on correlation and path coefficients analysis in barley (*Hordeum vulgare* L.). Bulletin of Environment, Pharmacology and Life Sciences, 6 (12), 75-80. https://bepls.com/NOV_2017/17.pdf

7. Başçiftçi, Z. and N.G.A. Arpacıoğlu, 2021. Determination of Grain Yield and Some Yield Components of Some Two and Six Row Barley (Hordeum vulgare L.) Genotypes in Eskisehir Ecological Terms. International Journal of Agriculture Forestry and Life Sciences,5(2),211-216. https://dergipark.org.tr/en/download/article-file/2090007

8. Bhutta, W.M., T. Barley, and M. Ibrahim, 2005. Path-coefficient analysis of some quantitative characters in husked barley. https://hdl.handle.net/1807/5385

9. Bothmer, R.V., O. Seberg, and N. Jacobsen, 1992. Genetic resources in the Triticeae. Hereditas, 116 (1-2), 141-150. https://doi.org/10.1111/j.1601-5223.1992.tb00814.x

10. Del Moral, L.G., Y. Rharrabti, D. Villegas, and C.Royo, 2003. Evaluation of grain yield and its components in durum wheat under Mediterranean conditions: an ontogenic approach. Agronomy journal, 95 (2), 266-274. https://doi.org/10.2134/agronj2003.2660

11. Feuillet, C. and B. Keller, 2002. Comparative genomics in the grass family: molecular characterization of grass genome structure and evolution. Annals of botany, 89 (1), 3-10. https://doi.org/10.1093/aob/mcf008

12. Guo, Z., Y. Zhao, M.S. Röder, J. C., Reif, M. W. Ganal, D. Chen, et al. 2018. Manipulation and prediction of spike morphology traits for the improvement of grain yield in wheat. Scientific reports, 8 (1), 1-10. https://doi.org/10.1038/s41598-018-31977-3

13. Hailu, A., S. Alamerew, M. Nigussie, and E. Assefa, 2016. Correlation and path coefficient analysis of yield and yield associated traits in barley (*Hordeum vulgare* L.) germplasm. Advances in crop science and technology, 4 (2), 100216. https://doi.org/10.4172/2329-8863.1000216

14. Kallel, A., M. Ksibi, H. B. Dhia, and N. Khélifi, 2017. Recent Advances in Environmental Science from the Euro-Mediterranean and Surrounding Regions. https://doi.org/10.1007/978-3-319-70548-4

15. Khdir, S.A., N. S. Ahmad, E. Hama-Ali, and S. M. Abdullah. 2023. Genetic Diversity and Population Structure of Common Bean Genotypes Using Morphological Traits and SSR. Iraqi Journal of Agricultural Sciences, 54 (3), 792-805. https://doi.org/10.36103/ijas.v54i3.1762

16. Kobir, M., M., Rashid, M., Halder, M., Rahman, M., Akter, M., Hossain, et al. 2023. Genetic variability, correlation and path analysis for yield and its contributing traits in Barley (*Hordeum vulgar* L.). SAARC Journal of Agriculture, 21 (2), 15-25. https://doi.org/10.3329/sja.v21i2.69889

17. Li, H., A. Rasheed, , L.T. Hickey, and Z. He, 2018. Fast-forwarding genetic gain. Trends in plant science, 23 (3), 184-186. https://doi.org/10.1016/j.tplants.2018.01.007

18. Majumder, D. and A. Shamsuddin, 2008. Genetic variability, correlated response and path analysis of yield and yield contributing traits of spring wheat. Journal of the Bangladesh Agricultural University,6 (2). https://doi.org/10.3329/jbau.v6i2.4815

19. Morales, F., M. Ancín, D. Fakhet, J. González-Torralba, A. L. Gámez, A. Seminario, et al. 2020. Photosynthetic metabolism under stressful growth conditions as a bases for crop breeding and yield improvement. Plants, 9 (1), 88. https://doi.org/10.3390/plants9010088.

20. Mousavi, S.M.N. and J. Nagy, 2021. Evaluation of plant characteristics related to grain yield of FAO410 and FAO340 hybrids using regression models. Cereal Research Communications, 49 (1), 161-169. http://doi.org/10.1007/s42976-020-00076-3

21. Nashmi, R. J. and J. M. Naser. 2022. Improving the rheological and qualitative properties of bread wheat by barley-extracted pentosanes. Iraqi Journal of Agricultural Sciences, 53 (5), 1212-1222. https://doi.org/10.36103/ijas.v53i5.1635

22. Rohlf, F. 2000. NTSYS-PC, numerical taxonomy system for the PC ExeterSoftware, Version 2.1. Applied Biostatistics Inc Setauket, USA. https://doi.org/10.4236/psych.2010.12018

23. Shahbandeh, M. 2022. World barley production from 2008/2009 to 2021/2022. Statista, New York, NY, USA. https://doi.org/10.3390/molecules27227852 .

24.Tofiq, S.E., T.N.H., Amin, S.M.S. Abdulla, and D.A. Abdulkhaleq, 2015. Correlation and path coefficient analysis of grain yield and yield components in some barley genotypes created by full diallel analysis in Sulaimani region for F2 generation. International Journal of Plant, Animal and Environmental Sciences, 5(4),76-79. https://www.fortunejournals.com/ijpaes/admin/php/uploads/869_pdf.pdf

25. Tricase, C., V. Amicarelli, E. Lamonaca, and R.L. Rana, 2018. Economic analysis of the barley market and related uses. Grasses as food and feed, 10, 25-46.

26. Vitrakoti, D,. S. Aryal, S. Rasaily, B.R. Ojha, R. Kharel, and M. Sapkota, 2016. Study on genotypic response and correlation analysis of the yield and yield attributing traits of different barley (Hordeum vulgare) genotypes. International Journal of Applied Sciences and Biotechnology, 4 (4), 529-536. DOI: https://doi.org/10.3126/ijasbt.v4i4.16269

27. Wendt, T., I. Holme, C. Dockter, A.Preuß, W. Thomas, A. Druka, et al. 2016. HvDep1 is a positive regulator of culm elongation and grain size in barley and impacts yield in an environment-dependent manner. PLoS One, 11 (12), e0168924. https://doi.org/10.1371/journal.pone.0168924

28. Yan, W. 2001. GGEbiplot—A Windows application for graphical analysis of multienvironment trial data and other types of two-way data. Agronomy journal, 93 (5), 1111-1118. https://doi.org/10.2134/agronj2001.9351111x

29. Yaseen. K. Al-Timimi, and F. Y. Baktash. 2024. Monitoring the shift of rainfed line of 250 mm over Iraq. Iraqi Journal of Agricultural Sciences, 55(3), 931-940. https://doi.org/10.36103/h10cqh53

30. Zaid, I.U., Zahra, N., Habib, M., Naeem, M.K., Asghar, U., Uzair, M. et al. 2022. Estimation of genetic variances and stability components of yield-related traits of green super rice at multi-environmental conditions in Pakistan. Agronomy, 12 (5), 1157. https://doi.org/10.3390/agronomy12051157

31. Zhou, M. X. 2009. Barley production and consumption. In Genetics and improvement of barley malt quality (pp. 1-17). Berlin, Heidelberg: Springer Berlin Heidelberg. https://doi.org/10.1007/978-3-642-01279-2_1