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Assessment of environment effect on yield component in barley (*Hordeum vulgare* L.) genotypes under rainfed conditions

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Purpose. This research was carried out to assess barley genotypes yield and quality parameters under various environmental conditions. **Methods.** The experiments were set up with 25 barley genotypes in a completely randomized blocks design with four replications at four locations in the 2018–2019 cycles in the Trakia region, Turkey. Data on grain yield, plant height, days of heading, 1000-kernel weight, test weight, protein ratio and grain uniformity were investigated. **Results.** The combined ANOVA revealed significant differences ($p < 0.01$) among genotypes and environments for all parameters investigated. In the study genotype G4 (8514 kg ha^{-1}) had a higher yield followed by G9 (8369 kg ha^{-1}). The highest thousand kernel weight was 52.0 g in G14 and the test weight was 75.1 kg in G5. There was a significant difference among genotypes for protein ratio and genotype G22 had a higher protein ratio, followed by G23 and G24. The grain uniformity in barley is an essential parameter and G14 had a higher ratio of grain uniformity. Correlation analyses showed that a negative correlation was determined between grain yield with days of heading ($r = -0.506^{**}$), plant height ($r = -0.583^{**}$), and protein ratio ($r = -0.542^{**}$). 1000-kernel weight and test weight were significantly positively correlated ($r = 0.708^{**}$). Grain uniformity had a positive correlation with 1000-kernel weight ($r = 0.898^{**}$) and test weight ($r = 0.539^{**}$). Protein ratio was positively associated with plant height ($r = 0.692^{**}$). According to stability analysis genotypes G9, G3, G15, G2, and G17 were adaptable to less fertile environmental conditions. It was determined that G10 and G16 were well adaptable to all environmental conditions and also were ideal in terms of higher-yielding ability and stability. **Conclusions.** While genotype G9 has high yield potential, G10 and G16 have high adaptability to different environmental conditions. The environmental effect was found to be very important according to the parameters examined. Early and short genotypes have higher yield potential. Environment E4 was the ideal environment because located close to the first concentric circle in the environment-focused biplot. Therefore, it should be regarded as the most suitable to select widely adapted barley genotypes.

Keywords: *barley; genotypes; yield component; environment effect; G×E interaction.*

Introduction

Barley (*Hordeum vulgare* L.) is the primary cereal in many areas of the Trakya region and is essential for the livelihoods of many farmers. Barley is an annual cereal crop grown in environments ranging the many areas. Because of various environmental conditions during the growing season (October-June), in weather conditions, some biotic and abiotic stress factors could reduce grain yield [1]. Barley is one of the more important cultivated crops in the Mediterranean region, where drought and high temperatures during the grain filling stage are the main abiotic stresses limiting its production [2]. Climate change presents geographically varied risks to barley production. Due to the large proportion of barley used for animal feed, it is not surprising that the effect of future shocks to supply has been assessed mainly from food security or feed use perspective [3]. Improving crop yields is essential to meet the increasing pressure of global food demands. The loss of high-quality land, the slowing in annual yield increases of major cereals, increasing fertilizer use, and the effect of this on the environment indicate that we need to develop new strategies an increase grain yields with less impact on the environment. One strategy that could help address this concern is by narrowing the yield gaps of major crops using improved genetics and management [4, 5]. Grain yield in barley is a complex character depending on a large number of environmental, agronomic and physiological characteristics. Grain yields also depend upon other yield components [6]. Genotype × trait biplot analysis is highlighted among the multivariate methodologies because it assesses genotypes based on multiple traits and identifies those that are superior to the desired variables; these can be used as parents in breeding programs or even as possible commercial cultivars. A quick and practical visualization of the genetic correlation between traits is also provided by this analysis [7]. The long-term value of a genotype depends not only on its absolute productivity or the possession of some other desirable traits but also on its ability to maintain sufficient levels of these traits under different environmental conditions. Experiments that include testing cultivars for several years under a range of locations (or treatments) require analysis of genotype-environment interaction (GE) in addition to the analysis of means [8]. GGE biplot analysis has been widely used to determine performance stability in multilocation trials when identifying superior genotypes [9, 10]. G × E 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 stability of the breeding materials [11]. Barley grain is used primarily as an energy and protein source for animal feed. The high protein content is desirable for feed production. Variations in weather conditions, environmental effects, soil fertility and pest management can affect barley grain quality significantly [12].

The aim of the study. It was to investigate and compares yield quality and physiological parameters under various rainfed environment conditions by using four experiments and advanced genotypes.

Material and methods

The experiments were set up in 2018–2019 growing cycles at four locations in the Trakya region, Turkey. The research was carried out on a total of 25 barley genotypes. A randomized complete block design (RCBD) with four replications was used. Each plot had 6 meters long, in 6 rows, spaced 0.17 meters apart. Sowings were performed by using a plot drill and a seed rate of 500 seeds m^2 and fertilizer 170 kg ha^{-1} N and 40 kg ha^{-1} P_2O_5 was used.

Data on; grain yield (kg ha^{-1}), plant height (cm), days of heading, 1000-kernel weight (g), test weight (kg), protein ratio (%), and grain uniformity (%) were investigated. The parameter days to heading (DH) was estimated from 1st January to the moment when 50% of main stems in a plot had at least half of emerged ears. The parameter plant height of ten randomly taken plants was measured at harvest maturity from the ground level to the tip of the tallest spike in centimeters and averaged. Thousand kernel weights and test weight [13], protein ratio [14, 15] were investigated.

The data were subjected to analysis of variance (ANOVA) according to the statistical methods [16] and mean performance and LSD of all genotypes were calculated for the comparison of means [17]. The differences between genotype means of parameters were tested by the L.S.D test (0.05). Letter groupings were generated by using a 5% level of significance. The regression equations were also calculated [18, 19]. Regression graphs were used to predict the adaptability of genotypes and the correlations between the quality parameters were determined by Pearson’s correlation analysis.

Results and discussion

The results of the variance analysis (ANOVA) of the research are presented in Table 2. The combined ANOVA revealed significant differences ($P < 0.01$) among genotypes for all parameters investigated, and significant differences ($P < 0.01$) for all traits among environments (Table 1).

Table 1

Combined analysis of variance for barley genotypes across four environments for parameters

Parameters	Genotypes			Environments		
	SS	MS	F Ratio	SS	MS	F Ratio
Grain yield (GY)	735541.0	30647.5	6.05**	3217541.0	1072514.0	50.46**
Days of heading (DH)	982.86	40.95	8.30**	3116.20	1038.73	210.49**
Plant height (PH)	5066.94	211.12	5.01**	5064.35	1688.12	40.02**
1000-kernel weight (TKW)	3460.11	144.17	26.90**	666.39	222.13	41.45**
Test weight (TW)	629.33	26.22	9.52**	75.36	25.12	9.12**
Protein ratio (PRT)	39.90	1.66	3.29**	50.69	16.90	33.47**
Grain uniformity (GU)	23406.10	975.25	10.30**	2464.31	821.44	8.68**

*, ** Significant at $p < 0.05$ and $p < 0.01$ respectively. ns: non-significant. SS: Sum of square, MS: Mean of square.

Due to various environmental conditions, grain yield is a complex character depending on a large number of environmental, agronomic and physiological characteristics [6]. There was a significant difference among genotypes for yield across four environments. In the study genotype G4 (8514 kg ha^{-1}) had a higher yield followed by G9 (8369 kg ha^{-1}). There was a highly significant difference ($p < 0.01$) in the thousand kernel weights of barley genotypes. The highest thousand kernel weight was 52.0 g (G14) and the lowest was 29.0 g (G10) across four environments. The mean test weight of genotypes indicated that the highest test weight was 75.1 kg in G5, whereas, the lowest test weight was observed in G17 (64.7 kg). There was a significant difference among genotypes for protein ratio. The maximum and lowest protein ratio varied from 12.4% to 10.0%. Genotype G22 had a higher protein ratio, followed by G23 and G24. The grain uniformity in barley is an essential parameter and the uniformity of grain depends to a large extent on the structure of the genotype of the spikes. There was a highly significant difference among genotypes for grain uniformity and the minimum was 49.85% and a maximum of 96.0%. Genotypes G14 had a higher ratio of grain uniformity (Table 2). Earliness is a favourable character in barley production areas, especially for second crop cultivation in the same growing year. In the study, the earliest heading was in G3 and the latest was in G11. Stem length and solidness are the most essential selection criteria in barley breeding study, being a direct component of lodging resistance. In the study, the lowest and highest plant height varied from 95.0 cm to 122.3 cm over four environments. The mean plant height was 106.9 cm (Table 2).

Table 2

Mean grain yield and parameters investigated across four environments in 2018–2019 cycles

Genotype	GY	DH	PH	TKW	TW	PRT	GU
1	*2*	*3*	*4*	*5*	*6*	*7*	*8*
G1	7605d-g	109.0c-f	105.0e-ı	46.5b-e	72.5bcd	11.6a-d	90.1abc
G2	8128abc	106.5e-ı	96.5ıj	48.3bc	72.8abc	10.3fgh	89.4abc
G3	8208abc	106.0f-ı	95.0j	48.7b	73.3abc	10.0h	88.9abc
G4	8514a	106.8e-ı	97.8hıj	45.0def	71.5cde	10.7c-h	86.3a-d
G5	7817cde	105.5ghı	110.0c-f	44.1ef	75.1a	11.3b-f	85.3a-d
G6	8118abc	108.5c-g	103.3f-j	46.7b-e	72.9abc	10.6e-h	87.3a-d
G7	8203abc	108.5c-g	104.5e-ı	36.5gh	69.6efg	10.6d-h	58.4ghı
G8	7764c-f	103.8ı	107.0d-g	42.3f	72.2bcd	10.6d-h	67.3efg
G9	8369ab	107.0d-h	103.3f-j	45.1c-f	71.8b-e	10.2gh	81.9bcd
G10	8043a-d	105.5ghı	98.0g-j	29.0ı	70.2def	10.3fgh	34.0j

Continuation of the Table 2

1	*2*	*3*	*4*	*5*	*6*	*7*	*8*
G11	7148gh	118.5a	102.8f-j	47.8bcd	74.0ab	10.9c-h	84.5a-d
G12	8015bcd	110.8c	97.3hıj	38.1g	70.4def	11.1c-g	63.2f-ı
G13	7417e-h	106.3f-ı	109.8c-f	45.9b-e	73.8abc	11.5a-e	90.3abc
G14	7379e-h	105.3hı	109.0def	52.0a	72.7bc	11.7abc	96.0a
G15	8169abc	105.5ghı	111.3c-f	44.1ef	72.1bcd	11.1c-g	79.1cde
G16	8089a-d	106.8e-ı	112.8b-e	38.5g	67.3gh	11.5a-e	85.6a-d
G17	8041a-d	110.0cd	106.3d-h	30.7ı	64.7ı	11.4a-e	49.8ı
G18	7025h	109.5cde	118.3abc	43.9ef	67.7gh	10.7c-h	79.2b-e
G19	7287fgh	109.5cde	105.5d-ı	37.2gh	69.1fgh	10.8c-h	63.7fgh
G20	7771c-f	108.3c-h	114.5a-d	44.9def	72.0bcd	11.4b-e	88.5a-d
G21	7188gh	110.3c	104.8e-ı	34.4h	68.3fgh	11.4b-e	52.0hı
G22	7481e-h	114.0b	110.3c-f	34.0h	68.9fgh	12.4a	74.8def
G23	7380e-h	111.3bc	120.8ab	38.3g	67.2h	12.2ab	74.9def
G24	7040h	111.3bc	122.3a	48.1bcd	70.3def	12.2ab	92.9ab
G25	7774c-f	106.5e-ı	107.3def	42.1f	73.0abc	11.4b-e	74.9def
Mean	7759	108.4	106.9	42.1	70.9	11.1	76.7
CV (%)	49.3	2.04	6.07	5.5	2.34	6.39	12.6
LSD (0.05)	9.2	3.12	9.13	3.26	2.33	1	13.69

GY: Grain yield (kg ha^{-1}), DH: days of heading, PH: Plant height (cm), TKW: 1000-kernel weight (g), TW: Test weight (kg), PRT: Protein ratio (%), GU: Grain uniformity (%).

Correlation coefficients were determined by Pearson’s correlation analysis and given in Table 3. Correlation analyses showed that a negative correlation was determined between grain yield with days of heading ($r = -0.506$**), plant height ($r = -0.583$**), and protein ratio ($r = -0.542$**). There was no correlation between grain yield and 1000-kernel weight. The results revealed that test weight was negatively slightly correlated with days of heading and plant height. 1000-kernel weight and test weight was significantly positively correlated ($r = 0.708$**). Grain uniformity had a positive correlation with 1000-kernel weight ($r = 0.898$**) and test weight ($r = 0.539$**). Protein ratio was positively associated with plant height ($r = 0.692$**).

Table 3

Correlation coefficients among yield and other parameters in 2018–2019

Parameters	GY	DH	PH	TKW	TW	PRT
DH	−0.506**					
PH	−0.583**	0.165				
TKW	−0.067	−0.150	0.047			
TW	0.138	−0.276	−0.313	0.708**		
PRT	−0.542**	0.370	0.692**	−0.108	−0.280	
GU	−0.081	−0.049	0.244	0.898**	0.539**	0.174

Significance at *: $P < 0.05$; **: $P < 0.01$; GY. Grain yield (kg ha^{-1}), DH: days of heading, PH: Plant height (cm), TKW: 1000-kernel weight (g), TW: Test weight (kg), PRT: Protein ratio (%), GU: Grain uniformity.

Genotype environment interaction is the main issue in improving high-yielding and stable genotypes across variable environments. Several methods of measuring the stability of genotypes tested across a range of environments have been proposed. Genotypes with high average yield (x), regression coefficient (b) equal to one, mean of squares leaving the regression (S^2d) close to zero, high coefficient of determination (R^2), positive coefficient of determination (a) and high are considered as stable genotypes. The stability parameters of the genotypes are presented in Table 3. Genotypes G4, G9 and G3 had higher yield potential across four environments. Genotypes G12 was very stable due to the highest determinations coefficient (R^2). In the study, the regression coefficients (b) values varied between 0.60 (G17) and 1.57 (G18) among genotypes. The variation in the b value showed a wide range of stability in genotypes. Genotypes G11, G21, G14 and G25 had optimum b values. Across four locations, a total of 11 genotypes had the highest positive intercept values (a). This result showed that genotypes G9, G3, G15, G2, and G17 were well adaptable to less fertile environmental conditions. It was determined that G10 and G16 were well adaptable to all environmental conditions and also were ideal in terms of higher-yielding ability and stability. In the study, the lowest standard deviation was determined in G23 and G17 according to grain yield in barley genotypes (Table 4).

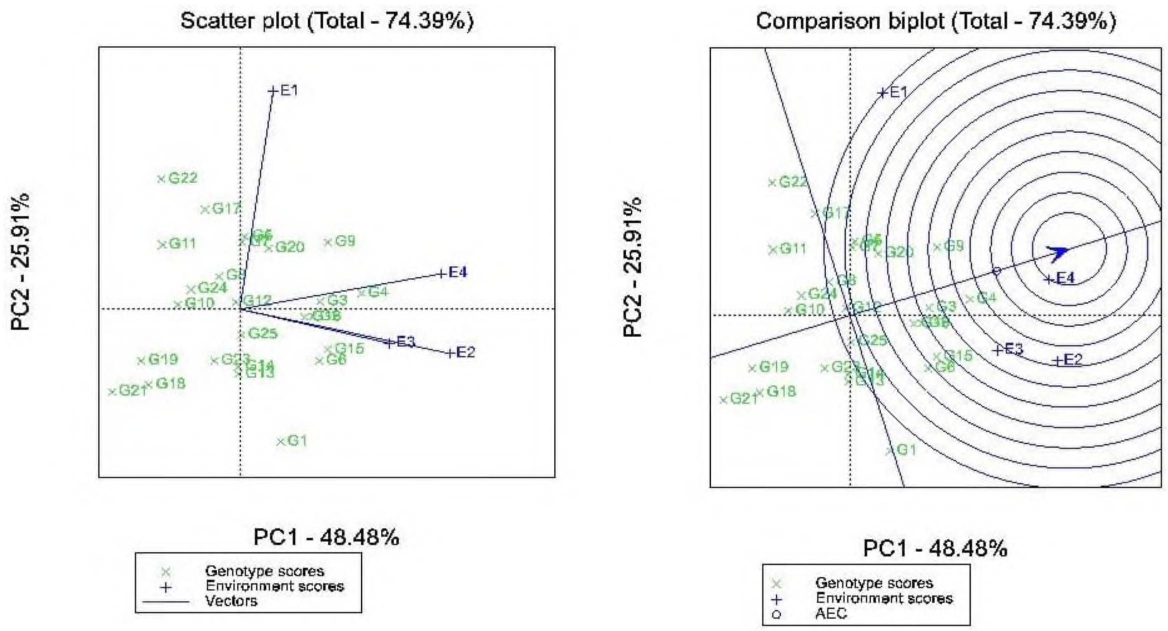
Table 4

The stability parameters and standard deviation of the barley genotypes across four environments

No	Genotype	X	R^2	b	S^2d	a
1	G1	7605 ± 102.9	0.66	0.81	453.6	135.41
2	G2	8128 ± 99.3	0.75	0.83	307.3	168.13
3	G3	8208 ± 101.5	0.61	0.77	497.7	225.16
4	G4	8514 ± 89.6	0.92	0.83	81.1	208.11
5	G5	7817 ± 141.7	0.90	1.30	244.6	−226.46
6	G6	8118 ± 137.5	0.82	1.20	429.6	−120.37
7	G7	8203 ± 156.8	0.88	1.42	361.6	−282.84
8	G8	7764 ± 87.1	0.89	0.79	105.9	161.36
9	G9	8369 ± 87.6	0.82	0.77	169.8	241.88
10	G10	8043 ± 103.2	0.96	0.97	57.8	48.21
11	G11	7148 ± 141.7	0.86	1.27	346.4	−271.18
12	G12	8015 ± 121.3	0.99	1.16	22.1	−101.83
13	G13	7417 ± 89.9	0.81	0.78	190.1	134.69
14	G14	7379 ± 113.7	0.96	1.07	71.7	−95.12
15	G15	8169 ± 97.6	0.84	0.87	185.3	145.03
16	G16	8089 ± 94.3	0.98	0.90	26.7	111.26
17	G17	8042 ± 77.5	0.64	0.60	271.4	339.48
18	G18	7025 ± 167.9	0.94	1.57	201.3	−518.79
19	G19	7287 ± 123.2	0.96	1.16	81.8	−174.52
20	G20	7771 ± 100.6	0.90	0.92	130.4	63.36
21	G21	7188 ± 101.6	0.98	0.97	31.2	−33.18
22	G22	7481 ± 175.3	0.72	1.43	1094.8	−362.56
23	G23	7380 ± 74.8	0.79	0.64	147.9	240.69
24	G24	7040 ± 98.0	0.87	0.88	155.8	19.03
25	G25	7774 ± 113.2	0.96	1.07	59.6	−54.97

X: mean yield, R^2: coefficient of determinations, S^2d: Deviation from regression, a: intercept value, b: regression coefficient

The genotype and environment interaction varieties were evaluated according to GGE biplot analysis across 4 environmental conditions. Obtained GGE biplot analysis results are explained below. About the discriminating power of environments can be obtained by the environment-vector view of the GGE-biplot. A long environmental vector reflects a high capacity to discriminate the genotypes. Furthermore, the cosine of an angle between vectors of two environments approximates the correlation between them. A wide obtuse angle indicates a strong negative correlation, an acute angle indicates a positive correlation while a close-to-90° angle indicates a lack of correlation [7, 20]. With the longest vectors from the origin, environments E1 were the most discriminating while E3 was the least discriminating. While there was a very high positive correlation between E3 and E2, these two locations were also positively correlated (Fig. 1a).

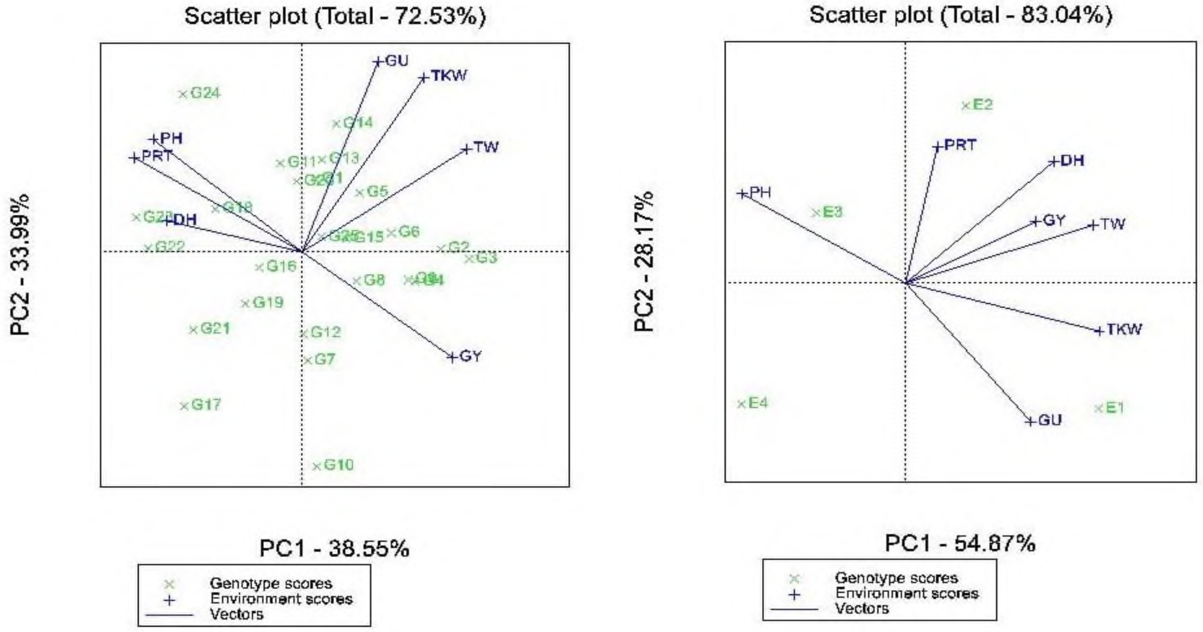


1a

1b

Fig. 1. GGE biplot for the evaluation of the relationships among the four environments (1a), and GGE biplot with scaling focused on environments, for the evaluation based on the ideal environment of genotypes across four environments (1b)

The ideal environment is representative and has the highest discriminating power [7]. Similarly to the ideal genotype, the ideal environment is located in the first concentric circle in the environment-focused biplot, and desirable environments are close to the ideal environment. In the study, Environment E4 was the ideal environment. Therefore, it should be regarded as the most suitable to select widely adapted genotypes (1b).



2a

2b

Fig. 2. The GGE biplot to show which genotypes performed best in which environments and a genotype by trait biplot represent genotypes measured for parameters (2b) and the relationship among test environments and genotypes based on parameters investigated (2b)

The angle between the vector of any genotype and any trait gives information about the state of the genotypes. According to this description, plant height was positively correlated with protein ratio and days of heading. Grain yield was negatively correlated with PH, DH and protein ratio. Among other parameters, there was a positively highly correlation between grain uniformity and 1000-kernel weight (Figure 2a). With the longest vectors from the origin, traits GU, TKW, DH, TW and PH were the most discriminating. PRT was moderately discriminating, while GY was least discriminating. Considering the angles between parameter vectors, parameter results in GY and TW were strongly correlated, similarly to those obtained in grain yield and days of heading.

Conclusions

The environment affected the characters examined in the study at different rates. In the study, there were significant differences among genotypes and environments for all parameters investigated. Genotypes G4 and G9 had a higher yield. The highest thousand kernel weight was in G14 and the test weight was in G5. There was a significant difference among genotypes for protein ratio and genotype G22 had a higher protein ratio, followed by G23 and G24. The grain uniformity in barley is an essential parameter and G14 had a higher ratio of grain uniformity. Correlation analyses showed that a negative correlation was determined between grain yield with days of heading, plant height, and protein ratio. 1000-kernel weight and test weight were significantly positively correlated. Grain uniformity had a positive correlation with 1000-kernel weight and test weight. The protein ratio was positively associated with plant height. According to stability analysis genotypes G9, G3, G15, G2, and G17 were adaptable to less fertile environmental conditions. It was determined that G10 and G16 were well adaptable to all environmental conditions and also were ideal in terms of higher-yielding ability and stability. While genotype G9 has high yield potential, G10 and G16 have high adaptability to different environmental conditions. The environmental effect was found to be very important according to the parameters examined. Early and short genotypes have higher yield potential. Environment E4 was the ideal environment because located close to the first concentric circle in the environment-focused biplot. Therefore, it should be regarded as the most suitable to select widely adapted barley genotypes.

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Мета. Оцінка показників урожайності та якості генотипів ячменю за різних умов навколишнього середовища. **Методи.** У дослідженні було використано 25 генотипів ячменю. Схема експерименту − повністю рандомізовані блоки з чотирма повторами у чотирьох місцях у регіоні Тракія (Туреччина) впродовж 2018–2019 рр. Визначали врожайність зерна, висоту рослин, дату колосіння, масу 1000 зерен, насипну вагу, вміст білка й вирівняність зерна. **Результати.** За допомогою комбінованого методу ANOVA було виявлено значні відмінності ($p < 0{,}01$) усіх досліджуваних показників між генотипами й середовищами. Генотип G4 (8514 кг/га) мав вищу врожайність, за ним був G9 (8369 кг/га). Найвищий показник маси 1000 зернин мав G14 − 52,0 г, а найвищу насипну вагу G5 − 75,1 кг. Генотипи значно відрізнялися за вмістом білка: генотип G22 мав найвищий вміст білка, за ним слідували G23 і G24. Однорідність зерна ячменю є важливим параметром, і генотип G14 мав вищий коефіцієнт однорідності зерна. Кореляційний аналіз виявив негативну кореляцію між урожайністю зерна й датою колосіння ($r = -0{,}506^{**}$), висотою рослин ($r = -0{,}583^{**}$) і вмістом білка ($r = -0{,}542^{**}$). Маса 1000 зерен і насипна вага корелювали істотно позитивно ($r = 0{,}708^{**}$). Однорідність зерна мала позитивну кореляцію з масою 1000 зерен ($r = 0{,}898^{**}$)

і насипною вагою ($r = 0{,}539^{**}$). Вміст білка позитивно корелював із висотою рослин ($r = 0{,}692^{**}$). За результатами аналізу стабільності генотипи G9, G3, G15, G2 і G17 виявилися адаптованими до менш сприятливих умов середовища. Було визначено, що G10 і G16 добре адаптуються до будь-яких умов навколишнього середовища, а також є ідеальними з точки зору високої врожайності та стабільності. **Висновки.** Генотип G9 має високий потенціал урожайності, а G10 і G16 мають високу адаптивну здатність до різних умов середовища. Вплив навколишнього середовища на досліджувані показники виявився значним. Вищий потенціал урожайності мають ранні й низькорослі генотипи. Середовище E4 виявилося ідеальним, оскільки воно було розташоване близько до першого концентричного кола парних ділянок середовищ, тому його слід розглядати як найбільш придатне для відбору генотипів ячменю з широкою адаптивною здатністю.

Ключові слова: *ячмінь; генотипи; складова врожайності; вплив середовища; G×E взаємодія.*

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Насіннєва продуктивність алоплазмотичних ліній на основі стерильних цитоплазм *Beta patula* і *B. maritima* за апозиготичного способу репродукції насіння

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Мета. Вивчити вплив цитоплазматичного геному заміщених ліній з новою плазмою від диких видів *Beta patula і B. maritima* і апозиготичних ліній А4–А8 з *S vulgaris* цитоплазмою Оуена на основні чинники апозиготичної репродукції насіння, насіннєву продуктивність, схожість роздільноквітковість, стерильність залежно від генетичного походження матеріалу. **Методи.** Дослідження проведено з використанням польових, лабораторних, статистичних методів в лабораторії цитогенетики ІБКіЦБ, лабораторії апоміксису і поліплоїдії Ялтушківської ДСС, лабораторії адаптивної селекції Веселоподільської ДСС. Отримане апозиготичне насіння в умовах безпилкового режиму за методикою ІБКіЦБ з використанням просторової ізоляції і пергаментних ізоляторів. Під час цвітіння насінників у кожної рослини визначали її фенотип за стерильністю пилку та роздільноквітковістю. Класифікацію рослин проводили за Оуеном (1945), ідентифікуючи рослини чс-0 типу, чс-1 типу, чс-2 типу. Роздільноквітковість насінників оцінювали візуально за наявністю роздільноплідних плодів на центральних пагонах. У 2021 р. коренеплоди заміщених ліній Веселоподільської ДСС посаджені в умовах безпилкового режиму на дослідному полі ІБКіЦБ. Досліджена насіннєва продуктивність при апозиготії, враховуючи кількість зав'язаних плодів на відрізку 10 см при 5 повторах для кожного насінника. Схожість визначалась на 10-ту добу, енергія проростання − на 5-ту добу. **Результати.** Нові джерела цитоплазматичної чоловічої стерильності (ЦЧС) виділені в лабораторії цитогенетики на основі генетичної моделі аналізуючого схрещування, з використанням диференціації і добору за маркерними зчепленими генами забарвлення гіпокотелю $R+r-$, однолітнього і дволітнього циклу розвитку $B+b-$. Аналізаторами природи стерильності використані закріплювачі стерильності цукрових буряків, домінантні гомозиготи за рецесивними генами антоціанового забарвлення,