agriculture

MDPI

Article

Adaptability and Stability of Irrigated Barley Genotypes in the Cerrado of the Federal District [†]

Rodolfo Thomé [1], Renato Amabile [2], Juaci Malaquias [2], Nara Souza [1], Gustavo Santos [1],*, João Melo [1], Arlini Fialho [1] and Mariana Santos [1]

[1] Faculdade de Agronomia e Medicina Veterinária (FAV), Campus Darcy Ribeiro, University of Brasília (UnB), ICC-Sul, Asa Norte, Brasília CEP 70910-900, DF, Brazil; dolfoagroplanufv@gmail.com (R.T.); narasouza@unb.br (N.S.); joaovictormelo29@gmail.com (J.M.); arlinirf@gmail.com (A.F.); mariana.alvess140@gmail.com (M.S.)

[2] Embrapa Cerrados, Rodovia BR-020, Km 18, Caixa Postal 08233, Planaltina CEP 73301-970, DF, Brazil; renato.amabile@embrapa.br (R.A.); juaci.malaquias@embrapa.br (J.M.)

* Correspondence: 231105620@aluno.unb.br

[†] This paper is a part of the Master's Thesis of Rodolfo Dias Thomé, presented at University of Brasília (UnB).

Abstract: Barley (*Hordeum vulgare* L.) is a significant cereal globally, widely used in human and animal food. Furthermore, it has a strong influence on genotype-by-environment interactions, being considered a highly adaptable crop. This study aimed to estimate the parameters of adaptability and stability for 17 barley genotypes, compared with two controls (BRS 180 and BRS 195) grown under irrigation in the Cerrado. The experiments were conducted from 2017 to 2020, from May to September, in two different experimental areas of Embrapa in the Federal District, Brazil. Five traits were evaluated: 1. Esti mated grain yield (kg ha^{-1}); 2. CL1—commercial classification of first grains (>2.5 mm) (%); 3. TGW—1000-grain weight (g); 4. plant height (cm); 5. cycle—days after emergence to earing (days). The data obtained were analyzed for normality and homogeneity of variance, subjected to individual and joint analysis of variance, with means compared by Tukey's test at 5% significance and the adaptability and stability parameters estimated for the genotypes. The coefficients of environmental variation (CV%) were generally low, indicating good experimental precision. The PFC 2006053 and PFC 2006054 genotypes have broad adaptability and high stability for most traits and outperformed the controls and the overall experiment average.

Keywords: quantitative genetics; *Hordeum vulgare* L.; genetic improvement

check for updates

Citation: Thomé, R.; Amabile, R.; Malaquias, J.; Souza, N.; Santos, G.; Melo, J.; Fialho, A.; Santos, M. Adaptability and Stability of Irrigated Barley Genotypes in the Cerrado of the Federal District. *Agriculture* **2024**, *14*, 1776. https://doi.org/10.3390/agriculture14101776

Academic Editor: Antonio Giovino

Received: 22 August 2024
Revised: 25 September 2024
Accepted: 30 September 2024
Published: 9 October 2024

1. Introduction

The Cerrado Biome, located on Brazil's Central Plateau, is considered the world's agricultural frontier and has immense potential, as it is almost entirely mechanized. The region is essential for food production and is considered the largest producer of grains and responsible for a large part of Brazil's total cereal production. With the development of technologies adapted to the region, new species such as quinoa, sunflower, and barley have been explored in the Cerrado.

Barley (*Hordeum vulgare* L.) was introduced to the Central–West region's in the 1970s as an alternative crop under irrigation, grown during the winter season since the crop has a good ability to adapt to the region soil and climate conditions. The Cerrado of the Central Plateau has the potential to produce barley at marketable levels, providing an opportunity for a new agricultural business. Brazil has a breeding program for irrigated barley in the Cerrado to meet the constantly growing demand and reduce the country's dependence on imported malt. Although there are already cultivars recommended for irrigated management in the Cerrado, such as BRS 180, BRS Sampa, BRS Deméter, BRS Savanna, BRS Manduri, and BRS 195 [1], there is a constant search for superior genotypes to promote efficiency more assertively in plant breeding and thus offer new cultivars to producers. Agronomic traits such as grain yield, 1000-grain weight, plant height, cycle, and commercial classification of first grains are essential for differentiating the most outstanding genotypes. These traits are the most important to improve. However, the environmental influence over the crop cycle must be considered, with the aim of high stability and adaptability [2,3].

Barley genotypes, like other plant species, present different phenotypes depending on the environmental condition in which it was planted. This is due to the influence of the environment on the genotypes, known as genotypes by environment interaction [4]. In this context, it is essential to determine the effects of adaptability and stability, and for this purpose, some methodologies were defined to facilitate genotype recommendations, such as the proposal by [5].

Several studies have already been carried out with this objective, such as those carried out by [6–8].

The objective of this study was to evaluate and select irrigated barley genotypes, using adaptability and stability parameters, to contribute to the barley breeding program under irrigation in the Cerrado of Central Brazil and, consequently, offer new genotypes for producers.

2. Materials and Methods

The experiments were conducted from May to September, from 2017 to 2020, under a center-pivot irrigation system in two different experimental areas of Embrapa in the Federal District: the Center for Innovation in Plant Genetics—Sucupira Farm (CIGV), Riacho Fundo II—DF, Estrada Parque Contorno Taguatinga/Gama, Km 03, at 15°54′55.4″ S, 48°02′16.3″ W, and an altitude of 1.100 m, on a soil classified as Typical dystrophic Red Latosol with clayey texture; and the Experimental Field of Embrapa Cerrados (CPAC), Planaltina-DF, located at 15°35′30″ S, 47°42′30″ W, and an altitude of 1007 m, on a soil classified as Typical dystrophic red latosol with clayey texture.

The genotypes used belong to the barley breeding program at Embrapa Cerrados. Nineteen brewing barley genotypes were used, 17 of which were dystic genotypes of Brazilian origin and two controls (BRS 180 and BRS 195).

The following rainfall rates were recorded in the first, second, third, and fourth years: 41 mm at CIGV, 123 mm, 27 mm, and 108 mm, respectively, and 46.5 mm, 129 mm, 46 mm, and 108 mm, respectively, at CPAC. These indexes show a low probability of rainfall that could damage the harvest or influence the quality of the barley grains. Concerning relative air humidity, during the years, the maximum values ranged from 80 to 98.6%, and the minimum values ranged from 11 to 34.7% (Table 1). The maximum temperatures ranged from 28.1 to 36.6 °C and the minimum from 5.8 to 15 °C over the four years (Table 1).

The experimental design used was randomized blocks with four replications. The plots comprised five rows, spaced 20 cm apart and three meters long, with a useful area of three square meters (m^2) for each plot with a density of 300 plants per m^2. In the sowing furrow, 16 kg ha^{-1} of N, 120 kg ha^{-1} of P_2O_5, and 64 kg ha^{-1} of K_2O were applied. When the fifth fully expanded leaf appeared, 40 kg ha^{-1} of N was applied, according to [9]. Irrigation was conducted based on the Cerrado Irrigation Monitoring Program [10].

Five traits were evaluated: 1. Yield—estimated grain yield (kg ha^{-1}); 2. CL1—commercial classification of first grains (>2.5 mm), in percentage (%) (transformed data) [11]; 3. TGW—1000-grain weight (g) [12]; 4. Height—plant height (cm); 5. Cycle—days from seedling emergence to inflorescence emergence (days). Evaluations of grain yield, commercial classification of first grains, and TGW were conducted at the Embrapa Cerrados Seed Laboratory.

1. Yield: the grains from the plot were harvested and standardized at the same moisture (13%) and then extrapolated to obtain the estimated yield in one hectare.

2. Commercial classification of first grains (CL1): grain size, referred to as commercial grain classification. Barley, whose whole, healthy grains are retained on the 2.5 mm wide oblong sieve. Data taken as a percentage (%).

3. 1000-grain weight (TGW): the harvested grain was standardized to 13% moisture, and 1000 seeds were counted and weighed on a precision scale to obtain the value in grams of the 1000-grain weight (g).

4. Plant height (Height): 10% of the plants in each plot were considered. The measurement consists of the base of the plant (soil) to the last grain of the ear in centimeters (cm).

5. Cycle: when 50% of the plants in the plot have reached the reproductive stage, measured in days after emergence (DAE).

Table 1. Characteristics of the environments studied and maximum and minimum temperature (°C), relative air humidity (%), and rainfall indices from May to September over four years of experiments.

		CIGV				**CPAC**			
Altitude		**1.100 m**				**1.007 m**			
Soil Classified		**Typical Dystrophic Red Latosol with Clayey Texture**				**Typical Dystrophic Red Latosol with Clayey Texture**			
C I G V		1st year		2nd year		3rd year		4th year	
		Max	Min	Max	Min	Max	Min	Max	Min
	RH	97.8	14.5	97.2	18	98.3	15.5	98.6	11
	T	35.3	8.6	34	8.4	34.9	5.8	36.6	9
	PI	41		123		27		108	
C P A C		1st year		2nd year		3rd year		4th year	
		Max	Min	Max	Min	Max	Min	Max	Min
	RH	80.0	33.3	83.3	34.6	81.4	31.8	82.8	34.7
	T	28.1	15	28.3	14.9	28.6	13.9	28.6	14.4
	PI	46.5		129		46		108	

RH—relative air humidity; T—temperature; PI—Precipitation Index.

The data obtained were subjected to the Shapiro Wilk and Bartlett tests, using the statistical software "R" i386 3.6.1, to verify the normality and homogeneity of the variances. The results of the tests, with the original data, were homogeneous in terms of variance and showed normality, except for CL1, which was collected in a percentage system and subjected to a transformation [CL1 = ARCOSINO(ROOT(Class1/100)] to obtain normality in the distribution of errors and homogeneity of variances. Subsequently, for all the traits, the data were submitted to individual and joint analysis of variance, and to estimate the adaptability and stability of the genotypes to regional conditions, the [5] method was used with the aid of the GENES software [13].

The data from each experiment were tested separately in the Genotype (G), Location (L), and Year (Y) combinations. To carry out the individual analysis of variance, the following statistical model was considered: $Y_{ij} = \mu + G_i + B_j + e_{ij}$, where: Y_{ij} = value obtained for the i-th genotype trait in the j-th block; μ = general average; G_i = effect of i-th genotype (i = 1, 2, . . ., g); B_j = effect of the j-th block (j = 1, 2, . . ., r); e_{ij} = random error (uncontrolled factors).

In the joint analysis of variance: $Y_{ijk} = \mu + G_i + B/A_{jk} + A_j + GA_{ij} + e_{ijk}$, where: Y_{ijk} = observed value of the i-th genotype, in the j-th environment and the k-th block; μ = general average; G_i = effect of the i-th genotype (i = 1, 2, . . ., g); B/A_{jk} = effect of block k within environment A_j (k = 1, 2, . . ., r); A_j = effect of j-th environment; (j = 1, 2, . . ., a); GA_{ij} = effect of interaction between i-th genotype and j-th environment; e_{ijk} = random error (uncontrolled factors).

To estimate the adaptability and stability of the genotypes, the Eberhart and Russel (1966) method was used. The model adopted by [5] is given by: $Y_{ij} = \beta_{oi} + \beta_{li} I_j + \delta_{ij} + \underline{\varepsilon}_{ij}$, where: Y_{ij}—average of the trait of genotype I in environment j; β_{oi}¯regression constant; given by $\beta_{oi} = \underline{Y}_i$; β_{li}—linear regression coefficient that measures the response of the i-th genotype to variation in environments; I_j- coded environmental index $\left(\sum_i I_j = 0\right)$, given by: $I_j = \frac{1}{g} \sum_i Y_{ij} - \frac{1}{ag} Y$; δ_{ij} = regression deviation; $\underline{\varepsilon}_{ij}$ = average experimental error. In addition to the regression, the deviation coefficient (σ^2_{di}), and the coefficient of determination (R2) of each genotype were used to define phenotypic stability.

3. Results

When considering each trait in the joint analysis of variance, it became clear that there was a significant interaction between genotypes (G) and environments (E), demonstrating the need to separate them into environments (E). This resulted in eight distinct environments in the combinations of two locations (L) and four years (Y) of experimentation (Table 2). The ratio between the largest and smallest residual mean square is in line with that suggested by [14], less than or equal to 7, for conducting the joint analysis of the data.

Table 2. Joint analysis of variance of 19 barley genotypes in two locations (CPAC and CIGV) in four years (2017 to 2020), totaling eight environments for the estimated grain yield (Yield), commercial first grain classification (CL1#), 1000-grain weight (TGW), plant height (Height), and cycle (Cycle).

S.V.	D.F.	Yield		CL1 $^{\#}$		TGW		Height		Cycle	
		MS	**F**	**MS**	**F**	**MS**	**F**	**MS**	**F**	**MS**	**F**
BLOCKS/ENV	24	2,868,347.86		0.0073		9.26		234.16		15.94	
BLOCKS	3	3,644,319.47		0.0063		12.15		255.52		26.57	
BL × ENV	21	2,757,494.78		0.0074		8.85		231.11		14.42	
GENOTYPES	18	12,250,526.65	3.13 **	0.1753	3.19 **	434.59	3.36 **	739.40	2.08 **	332.69	2.01 *
ENVIRONMENTS	7	183,793,935.75	64.08 **	0.2894	39.80 **	1563.42	168.78 **	4015.86	17.15 **	1315.24	82.53 **
GEN × ENV	126	3,908,010.37	9.21 **	0.0550	7.89 **	129.43	11.53 **	354.81	8.43 **	165.48	10.05 **
RESIDUE	432	424,278.24		0.0070		11.22		42.08		16.47	
TOTAL	607										
CV(%)		10.30		6.90		6.66		8.15		6.49	

(SV) source of variation; (BL) blocks; (GEN) genotypes; (ENV) environments; (DF) degrees of freedom; (MS) mean square; (CV) coefficient of variation. ** and * significant at 1% and 5% probability by the F-test. $^{\#}$ Data collected in percentage system and submitted to transformation [CL1 = ARCOSINE(ROOT(Class1/100)].

For all the traits, there were statistical differences between the genotypes, the environments, and the G × E interaction at 1% probability by the ANOVA F-test. The exception was the cycle, which showed a significant difference at 5% (*) probability only for Genotypes (Table 2).

The overall average yield for the experiment was 6326 kg ha^{-1}, far exceeding the national average of 3882 kg ha^{-1} in 2022 [15], an average that peaked over the last 15 years in 2016 at 3921 kg ha^{-1} (Table 3).

In the test of mean comparison, the best yields (kg ha^{-1}) were for PFC 2005141 (7413 kg ha^{-1}), PFC 2005143 (7166 kg ha^{-1}), PFC 2006054 (7082 kg ha^{-1}), and PFC 2005142 (6867 kg ha^{-1}) (Table 3). The genotypes PFC 2006053, PFC 2005145, and CEV 98046/MERIT had a significantly higher average than the general average. PFC 2004,216, PFC 2007105, and BRS 180 (6309 kg ha^{-1}) are in a third group, with only the BRS 180 cultivar failing to surpass the overall average of the experiment in absolute values, but in line with what was presented when the cultivar was launched, with an average of 6280 kg ha^{-1} [2], ratifying the potential of this work collection about genotypes already released for these environments, such as BRS Savanna [16], BRS Sampa [17], and BRS Deméter [16]. The other genotypes ranged from 6078 kg ha^{-1} for PFC 2007125 to 5116 kg ha^{-1} for PFC 2004345. The BRS 195 cultivar averaged 5596 kg ha^{-1} (Table 3).

Table 3. Average of 19 barley genotypes from the Class A group and estimates of adaptability and stability parameters using the [5] method in eight environments for estimated grain yield (Yield), commercial first grain classification (CL1), 1000-grain weight (TGW), plant height (Height), and cycle (Cycle).

Genotype (G)	Yield					CL1				
	Average (β_0) (kg ha^{-1})	**Tukey (5%)**	β_1	$\sigma_d^2(10^5)$	**R^2 (%)**	**Average (β_0) (%)**	**Tukey (5%)**	β_1	σ_d^2	**R^2 (%)**
BRS180	6309.44	cde	1.33 **	28.19 **	62.8	74	h	2.57 **	0.1017 **	22.11
BRS195	5596.48	fgh	0.96 ns	7.22 **	75.8	78	gh	0.76 ns	0.0059 **	25.24
CEV 98046/MERIT	6714.15	bc	0.81 *	7.95 **	67.45	87	cdef	1.41 ns	0.0003 ns	81.06
PFC 2003054	6071.44	def	0.95 ns	15.20 **	60.97	84	fg	1.66 **	−0.0001 ns	88.34
PFC 2004033	6052.54	def	0.83 **	3.55 **	81	88	abcdef	0.83 ns	0.0026 *	41.23
PFC 2004212	5812.99	efg	0.51 **	3.59 **	61.58	85	ef	0.53 ns	0.003 *	20.75
PFC 2004216	6453.40	cd	1.10 ns	6.49 **	81.8	87	bcdef	0.65 ns	0.0067 **	18.3
PFC 2004345	5116.15	h	1.10 ns	11.65 **	71.12	86	def	0.56 ns	0.0064 **	14.49
PFC 2005138	5984.69	defg	1.10 ns	6.37 **	81.24	91	abc	0.89 ns	0.0045 **	36.1
PFC 2005141	7412.72	a	1.35 **	1.67 *	94.98	91	abc	0.44 *	0.0001 ns	32.59
PFC 2005142	6867.27	abc	1.16 *	5.10 **	86.1	92	ab	0.68 ns	0.0006 ns	46.55
PFC 2005143	7165.55	ab	1.33 **	3.82 **	91.13	90	abcd	0.96 ns	0.001 ns	59.6
PFC 2005145	6814.72	bc	1.36 **	5.59 **	88.65	90	abcde	0.54 ns	0.0001 ns	40.95
PFC 2006053	6828.26	bc	0.88 ns	6.13 **	75.16	92	a	0.42 *	0.0007 ns	24.12
PFC 2006054	7082.34	ab	0.87 ns	2.63 **	85.17	91	abc	0.89 ns	0.0005 ns	61.29
PFC 2006134	5477.40	gh	0.52 **	4.81 **	56.25	88	abcdef	0.26 **	0.0005 ns	11.74
PFC 2007098	5912.95	defg	0.90 ns	7.59 **	72.16	92	a	0.27 **	0.0001 ns	14.23
PFC 2007105	6444.93	cd	0.88 ns	3.78 **	81.68	92	ab	0.29 **	0.0044 **	5.71
PFC 2007125	6077.55	def	1.16 *	21.81 **	62.22	78	gh	4.39 **	0.0376 **	68.58
General Average	6326.05					87.16				

Genotype (G)	Height					Cycle				
	Average (β_0) (cm)	**Tukey (5%)**	β_1	σ_d^2	**R^2 (%)**	**Average (β_0) (days)**	**Tukey (5%)**	β_1	σ_d^2	**R^2 (%)**
BRS180	80.21	bcde	2.37 **	489.79 **	40.84	54.88	h	2.26 **	284.29 **	26.36
BRS195	77.75	defg	0.13 **	65.94 **	1.26	66.36	abc	0.53*	12.94 **	24.77
CEV 98046/MERIT	84.3	ab	0.98 ns	39.13 **	54.63	62.15	defg	1.16 ns	2.53 ns	80.28
PFC 2003054	71.11	h	0.96 ns	52.68 **	47.13	66.79	ab	0.63*	2.77 ns	53.73
PFC 2004033	78.01	def	1.1 ns	44.38 **	57.71	64.91	abcd	0.85 ns	−2.06 ns	87.62
PFC 2004212	84.09	ab	1.16 ns	48.28 **	58.53	64.47	bcde	1.16 ns	5.57 *	73.81
PFC 2004216	71.19	h	0.91 ns	7.54 ns	73.73	64.22	bcdef	0.71 ns	0.39 ns	69.26
PFC 2004345	78.25	cdef	0.59 *	9.4 ns	51.98	68.23	a	0.22 **	10.28 **	6.33
PFC 2005138	76.7	efgh	1.15 ns	16.16 *	75.27	62.4	defg	0.74 ns	7.02 *	49.94
PFC 2005141	73.82	fgh	0.66 *	38.15 **	35.6	60.92	efg	1.03 ns	9.46 **	61.07
PFC 2005142	81.22	abcde	0.96 ns	58.5 **	45.15	61.59	defg	1.26 ns	15.38 **	61.99
PFC 2005143	83.77	abc	0.89 ns	−7.46 ns	94.11	60.72	fg	0.9 ns	6.93 *	59.9
PFC 2005145	84.29	ab	0.82 ns	23.7 **	54.57	61.74	defg	1.27 ns	10.51 **	68.93
PFC 2006053	79.53	bcde	0.57 *	73.34 **	19.06	60.92	efg	1.25 ns	3.65 ns	80.25
PFC 2006054	84.49	ab	0.99 ns	36.48 **	56.2	62.27	defg	0.79 ns	8.03 **	50.89
PFC 2006134	81.35	abcde	0.73 ns	8.79 ns	63	64.57	bcd	0.79 ns	14.57 **	40.16
PFC 2007098	82.73	abcd	0.68 ns	27.98 **	42.24	60.58	g	1.07 ns	5.11 *	71.41
PFC 2007105	86.48	a	1.09 ns	29.41 **	64.62	62.83	cdefg	1.28 ns	2.19 ns	83.97
PFC 2007125	72.2	gh	2.28 **	289.71 **	51.65	56.81	h	1.11 ns	326.75 **	7.01
General Average	79.55					62.49				

Genotype (G)	TGW				
	Average (β_0) (g)	**Tukey (5%)**	β_1	σ_d^2	**R^2 (%)**
BRS180	40.41	h	1.21 ns	170.16 **	16.86
BRS195	46.5	g	0.67 *	8.59 **	48.31
CEV 98046/MERIT	51.21	cde	0.61 **	20.34 **	28.04
PFC 2003054	49.14	defg	0.65 *	23.29 **	27.91
PFC 2004033	51.74	cd	0.80 ns	10.19 **	54.01
PFC 2004212	51.99	bcd	1.01 ns	4.50 *	76.92
PFC 2004216	47.41	fg	1.03 ns	14.33 **	59.61
PFC 2004345	48.16	fg	1.11 ns	13.57 **	64.43
PFC 2005138	54.89	ab	0.66 *	5.09 *	57.1
PFC 2005141	48.58	efg	1.13 ns	13.03 **	65.93
PFC 2005142	51.88	cd	1.03 ns	2.52 ns	82.65
PFC 2005143	50.1	cdef	1.30 *	6.97 **	80.53
PFC 2005145	50.29	cdef	1.18 ns	8.83 **	74.29
PFC 2006053	49.91	cdef	1.12 ns	49.59 **	36.66
PFC 2006054	56.16	a	1.07 ns	23.99 **	50.41
PFC 2006134	47.92	fg	0.90 ns	9.01 **	62.39
PFC 2007098	52.73	bc	0.96 ns	4.38 *	75.49
PFC 2007105	56.57	a	1.03 ns	−0.49 ns	91.72
PFC 2007125	49.82	cdef	1.53 **	213.05 **	20.69
General Average	50.28				

(β_1) Regression coefficient; (σ_d^2) coefficient of the deviations from the regression; (R^2) coefficient of determination; and (β_0) average. (*) significant at 5% probability by the F-test, (**) significant at 1% probability by the F-test, and (ns) not significant. Means in each row followed by the same letter do not differ statistically by the Tukey test at 5% probability. Data collected in percentage system and submitted to transformation [CL1 = ARCOSINE(ROOT(Class1/100)], except Mean (β_0).

For CL1, the overall average was around 87%, indicating that the genotypes generally have the potential to exceed the industry target (80%) and that stipulated by ORDINANCE No. 691 [11]. Since the aim is to produce malt, the commercial classification of the first grains provides similar grains to guarantee the uniform modification of the endosperm in the process. The two controls, BRS 180 and BRS 195, have an average score of 74% and 78%, respectively, followed by genotype PFC 2007125, also with 78%, the only representatives with an average score of less than 80% (Table 3). The best-placed materials with the best commercial ratings were, in the following order: PFC 2006053 (92%), PFC 2007098, PFC 2005142, PFC 2007105, PFC 2006054, PFC 2005141, PFC 2005138, PFC 2005143, PFC 2005145, PFC 2006134, and PFC 2004033 (88%) all had representatives in the first group, with only the first two standing out from the rest (Table 3). Several groups were formed as follows: PFC 2004216 (87%) represented the second group, CEV 98,046/MERIT (87%) the third, PFC 2004345 (86%) the fourth, PFC 2004212 (85%) the fifth, PFC 2003054 (84%) the sixth, BRS 195 (78%), and PFC 2007125 (78%) the seventh, and the control cultivar BRS 180 (74%) the eighth and final group, with some overlap (Table 3).

Another trait studied was 1000-grain weight (TGW). In this characteristic, we had the same eight groups but with alternating positions between the genotypes, such as PFC 2007105 (57 g), with the best TGW ranked fourth in absolute value in CL1, PFC 2006054 (56 g), which did not differ statistically from the first, ranked fifth in absolute value in CL1, and so on, as can be seen in Table 3.

It can be seen that the control cultivars had the worst development in this trait. The last placed isolate was BRS 180, which, being the only six-row malting barley representative, tends to have smaller grains regardless of yield and lower TGW. The overall average for this trait was 50.3 g, surpassing other studies conducted in the Cerrado [9,18] and even the launch of cultivars recommended for the region, such as BRS Savanna, which had an average of 45.7 g in four years and three different states [16].

For example, the overall average plant height was 79.55 cm, lower than when the control cultivar BRS 180 was released. This is not true for the BRS 195 cultivar, which was released as a dwarf (69 cm), but the Cerrado has greater heights, as in this experiment, with an average of 78 cm (Table 3). The presentation of this trait will be from the lowest to the highest heights since the aim of irrigated barley for the Cerrado is to use smaller genotypes to prevent the plants from lodging. The shortest materials were PFC 2003054 (71 cm) and PFC 2004216 (71 cm), followed by PFC 2007125 (72 cm) in the second group. The third and fourth groups were PFC 2005141 and PFC 2005138, respectively. The fifth group of averages comprised the cultivar BRS 195 and the genotype PFC 2004033. In sixth place was PFC 2004345, followed in seventh place by PFC 2006053 and the BRS 180 cultivar. Finally, a large group is represented by the genotypes PFC 2007105 (86 cm), PFC 2006054, CEV 98046/MERIT, PFC 2005145, PFC 2004212, PFC 2005143, PFC 2007098, PFC 2006134, and PFC 2005142 (81 cm) (Table 3).

As with height, the cycle will be presented in ascending order since the search to meet the market tends to select earlier materials, optimizing the agricultural system by including barley in winter planting in the Cerrado of Central Brazil. The BRS 180 cultivar (55 days), 6-row barley, was the earliest material in absolute values without differing statistically from PFC 2007125 (57 days). In a second group, with many representatives, we have the following genotypes ranging from 61 cm to 63 cm: PFC 2007098 (61 days), PFC 2005143, PFC 2005141, PFC 2006053, PFC 2005142, PFC 2005145, CEV 98046/MERIT, PFC 2006054, PFC 2005138, and PFC 2007105 (63 days), with overlaps but which do not differ statistically from each other, as seen by the letter "g" associated with the averages. The third group includes PFC 2004216 (64 days), PFC 2004212 (64 days), and PFC 2006134 (65 days). The fourth group includes the genotypes PFC 2004033 (65 days), BRS 195 (66 days), and PFC 2003054 (67 days), with one representative, BRS 195, which was the earliest for this trait at 60 days. In the last group was the latest genotype, PFC 2004345 (68 days), which had the longest cycle and the lowest average yield (Table 3). The genotypes in this experiment had a higher overall average than in the comparative studies by [9], 59.46 days, and [18], 57.6 days, but compensated for the longer cycle with a higher average grain yield.

For inferences about adaptability and stability, regression analysis was performed for each genotype, using the environmental index as an independent variable and the traits evaluated as dependent variables. The results of the analyses are shown in Table 3.

4. Discussion

When considering each trait by the ANOVA F-test, it became clear that there were statistical differences between the genotypes, the environments, and the G × E interaction at 1% probability for most of the characteristics, with the exception of Cycle, which showed a significant difference at 5% (*) probability only for Genotypes (Table 2). From the significant effect of environments, it can be inferred that the experiments were conducted in L × A combinations that showed the necessary variation to discriminate between the genotypes in the work collection. The significant effect of the genotypes × environments interaction makes it possible to conclude that the genotypes behaved differently in the various environments, alternating positions between them within the same trait studied. The G × E interaction was also evidenced by other authors in barley recently in different locations in the country, both in the Federal District and Pato Branco PR [19].

The significance of the interaction between genotypes and environments indicates the need to study the adaptability and stability of genotypes to identify genotypes with greater adaptability [20].

Following the proposal by [14], who considers coefficients of variation to be low when they are less than 10%, medium when they are between 10 and 20%, high when they are between 20 and 30%, and very high when they are higher than 30%, and knowing that these values are suggested for field experiments with crops, we can see that the average coefficients of variation (CV%) were generally less than 10% and therefore classified as "low," which indicates good experimental precision. For CL1 (6.9%), TGW (6.66%), height (8.15%), and cycle (6.49%), except for yield, where for this trait it was 10.3%, very close to the "low" level, but classified as "medium," which is understandable for a polygenic trait with data from a large number of environments (Table 2).

Studying adaptability for the yield trait in barley for two years (2017/2018) in four locations in the state of Paraná [19] obtained an average estimated grain yield of 5279 kg ha^{-1}, closer to the national average, which confirms the Cerrado ability to produce barley with high grain yields.

In a study conducted in the Federal District by [9] with 39 elite barley genotypes, the overall average of the genotypes for yield was 5614 kg ha^{-1}, which was 700 kg lower than in this experiment. Under similar conditions, [18] conducted an experiment and analyzed elite genotypes in the Cerrado under irrigation and obtained an average of 4249 kg ha^{-1} over 3 years, which was 2077 kg lower than the overall average of the collection in the current study, demonstrating the potential of this work collection for the environments studied. Another study in Ukraine, for example, obtained the highest average in three environments of approximately 7200 kg ha^{-1} for the most productive cultivar, Kzovan, and an overall average of 5940 kg ha^{-1} [21].

The Cerrado cultivars, BRS Savanna (87%) [16], BRS Sampa (73%) [17], and BRS Deméter (89%) [18], also showed high averages for the CL1 trait, but only BRS Deméter surpassed this experiment in the overall average. Authors in [9] obtained an overall average of 83.54%, higher than the 80% recommended by the Brazilian industry, while [18] obtained 73.1%, even though they were working with elite barley genotypes. This experiment demonstrated that in this trait, the work collection also has great genetic potential to participate in the development of brewing barley in the Cerrado.

Regarding the average plant height characteristic, although there were representatives with considerable height, even the highest averages were below the cultivars recommended for the Cerrado BRS Savanna (82 cm), BRS 180 (90 cm), and very close to BRS Deméter (80 cm). The only genotypes below the general average (79.55 cm) were BRS Sampa (77 cm) and BRS 195 (69 cm), among those recommended for the Cerrado. It should be noted that the genotypes with the highest yield also presented greater height, which makes it difficult to work on breeding for smaller sizes. This is the case with genotypes PFC 2005143, with the second highest absolute yield but the sixth tallest material, and PFC 2006054, with the third highest yield and the second tallest height. However, contrary to this understanding, genotype PFC 2005141 deserves to be highlighted, given its position as the best yield performer with an average of 7413 kg ha^{-1} and the fourth lowest height (74 cm). In the work by [9], the average height of the genotypes was 84.08 cm, and in that of [18], 75.7 cm.

A regression analysis was conducted for each genotype to make inferences about adaptability and stability (Table 3), using the environmental index as an independent variable and the traits evaluated as dependent variables [5]. In addition to the regression, the deviation coefficient (σ^2_{di}), the coefficient of determination (R^2) of each genotype was used to define phenotypic stability [11,22] and also to quantify the proportion of the variation in Y_{ij} that is explained by the linear regression.

We can see that for the yield, the genotypes CEV 98,046/MERIT, PFC 2004216, PFC 2005141, PFC 2005142, PFC 2005143, PFC 2005145, PFC 2006054, PFC 2007105, and PFC 2006053 showed average grain yield (β_0) above the general average ($\underline{x}$), $\beta_0 > \underline{x}$. Among these, the genotypes PFC 2004216, PFC 2006053, PFC 2006054, and PFC 2007105 had $\beta_0 > \underline{x}$ and the regression coefficient (β_1) equal to unity, $\beta_1 = 1$. This classifies these genotypes as having broad adaptability for the trait in question [5]. As for stability, no genotype for this trait had a regression deviation coefficient (σ^2_d) equal to zero, which would classify it as stable. However, as mentioned above, R^2 will help identify more predictable genotypes, even if they are not classified as stable, although according to [23], σ^2_d and R^2 provide the same information. PFC 2004216, PFC 2006054, and PFC 2007105 showed R^2 above 80%, which indicates that they have predictable linear behavior, as noted by the high index. PFC 2006053 reached 75% in R^2, with considerable predictability since its overall average exceeded that of the previously mentioned genotypes and could be considered adapted by this method. Finally, the genotypes PFC 2005141, PFC 2005142, PFC 2005143, and PFC 2005145 had excellent averages and R^2 above 80%; although they are not widely adaptable, they are adaptable to favorable environments. PFC 2005141 stood out in this regard, as it had the highest absolute average among the treatments (7412 kg ha^{-1}) and was considered to have restricted adaptability to favorable environments and, at a 5% probability level, would be considered stable by [23], given that R^2 = 94.98% (Table 3). It is important to note that the control cultivars did not reach the general average in the experiments and that only BRS 195 obtained $\beta_1 = 1$ and can be considered broad adaptability by this method, in addition to the fact that none of them were considered stable.

A fundamental trait for meeting industrial demand is the commercial classification of first grains. This trait had high overall average values, and almost all the genotypes reached the desired minimum, except for the two cultivars BRS 180 (74%) and BRS 195 (78%) and the genotype PFC 2007125 (78%). In addition, these genotypes above did not have a mean (β_0) above the general mean ($\underline{x}$), and the regression coefficient (β_1) was only equal to unity in the case of BRS 195, which indicates wide adaptation to the environments studied. As for the stability of these genotypes, none had a regression deviation coefficient (σ^2_d) equal to zero, which would classify them as stable, and they were not predictable because the R^2 in all cases was less than 69%. For the genotypes that had an average higher than the general average for the yield, two of them, CEV 98,046/MERIT (87%) and PFC 2004216 (87%), had a CL1 higher than 80% but lower than the general average (87.16%). Both were considered adapted $\beta_1 = 1$ and not stable $\sigma^2_d > 0$. The genotypes PFC 2005141, PFC 2005142, PFC 2005143, PFC 2005145, PFC 2006053, PFC 2006054, and PFC 2007105 cannot be separated by a group of averages in this regard and achieved 90% to 92% CL1 and grain yield above the general average. Of these, PFC 2005142, PFC 2005143, PFC 2005145, and PFC 2006054 had $\beta_1 = 1$ *and* $\sigma^2_{di} = 0$ and are therefore considered to have broad adaptability and high stability. The genotypes PFC 2005141, PFC 2006053, and PFC 2007105 had $\beta_1 < 1$ and were, therefore, classified as having restricted adaptability to unfavorable environments. The first two were considered stable by variance (σ^2_{di}), despite R^2 of 24% and 33%, respectively. PFC 2007105 could not be considered stable (Table 3).

For TGW, the genotypes CEV 98,046/MERIT and PFC2005138 were considered to have restricted adaptability to unfavorable environments but were unstable. Five others, PFC 2004033, PFC 2004212, PFC 2005145, PFC 2006054, and PFC 2007098 had $\beta_1 = 1$ but $\sigma^2_d > 0$, which reveals adapted but not stable genotypes for this trait (R^2 ranging from 50 to 77%, which shows low predictability). PFC 2005142 and PFC 2007105 stood out in terms of TGW. These genotypes were considered to have broad adaptability, high stability ($\beta_1 = 1$, $\sigma^2_{di} = 0\ e\ \beta_0 > \underline{x}$), and high predictability, with R2 > 80% in both cases. The other genotypes did not achieve $\beta_0 > \underline{x}$. The BRS 180 cultivar obtained $\beta_1 = 1$, proving to be widely adapted to the environments studied but was not considered stable. Both controls obtained an average < $\underline{x}$.

The lowest $\beta_0 > \underline{x}$ genotypes, which are objectives in irrigated barley breeding programs in the Cerrado, were BRS 195, PFC 2003054, PFC 2004033, PFC 2004216, PFC 2004345, PFC 2005138, PFC 2005141, PFC 2006053, and PFC 2007125. However, only the genotypes PFC 2003054, PFC 2004033, PFC 2004216, and PFC 2005138 had broad adaptability, and of these, only PFC 2004216 was considered stable. When BRS 195 was launched, its size was defined as a dwarf, at just 69 cm. For example, it is a cultivar that can be used as a parent for crosses. Although their height was greater than the general average, the genotypes PFC 2005143 and PFC 2006134 have been outstanding in other traits and should also be kept among the potential parents for crosses. The growth reducers already mentioned in this work can also be used for planting in the environments studied, as they were considered to have wide adaptability and high stability ($\beta_1 = 1$, $\sigma^2_{di} = 0$).

The crop cycle is an important trait that guides the planning of crops on the farm. Regarding this trait, earlier materials are sought for winter planting in the Cerrado under irrigation, which is why they will be highlighted in this paragraph. However, later materials with good traits are also of great value to the program if combined with other traits. The BRS 180 cultivar had the shortest absolute average cycle (55 days) without differing statistically from PFC 2007125 (57 days), although neither is considered an adapted and stable genotype. In the case of PFC 2007125, β_1 was equal to unity, demonstrating broad adaptation to these environments with low stability or predictability. For this trait, CEV 98,046/MERIT and PFC2006053 were considered to have wide adaptability and high stability ($\beta_1 = 1$, $\sigma^2_{di} = 0\ e\ \beta_0 < \underline{x}$). The genotypes PFC 2005138, PFC 2005141, PFC 2005142, PFC 2005143, PFC 2005145, PFC 2006054, and PFC 2007,098 showed $\beta_0 < \underline{x}$ and $\beta_1 = 1$ as desired and were therefore considered widely adapted to the environments but were not stable over the variations imposed with $\sigma^2_{di} > 0$.

The genotypes that deserve to be highlighted will be described in more detail below: PFC 2006053 obtained an estimated average grain yield of 6828 kg ha^{-1} ($\beta_0 > \underline{x}$), with a regression coefficient (β_1) equal to unity ($\beta_1 = 1$) and a coefficient of determination R^2 equal to 75.16%, despite the coefficient of the deviations from the regression being greater than zero ($\sigma^2_{di} > 0$). This classifies this genotype as having broad adaptability but low stability or predictability for this trait. This genotype showed 92% CL1 ($\beta_0 > \underline{x}$). Although it is not considered adapted to all the environments tested ($\beta_1 > 1$), it is considered a genotype with adaptability restricted to favorable environments when analyzed at a 1% probability level. For the TGW trait, this genotype had a lower average than the general average and was not considered stable but adapted to the growing conditions of the region representative of the environments tested. It had an average height lower than the general average but was very close to this average and was considered adapted to favorable environments with low predictability. Another benefit of PFC 2006053 was the earliness cycle. The average obtained was lower than the general one ($\beta_0 < \underline{x}$); it had a regression coefficient equal to unity ($\beta_1 = 1$) and a regression deviation coefficient equal to zero ($\sigma^2_{di} = 0$), considering this trait to have broad adaptability and high stability.

PFC 2006054 obtained an estimated average grain yield of 7.0824 kg ha^{-1} ($\beta_0 > \underline{x}$) with a regression coefficient (β_1) equal to unity ($\beta_1 = 1$) and a coefficient of determination

(R^2) equal to 85.17% despite the regression deviation coefficient being greater than zero ($\sigma^2_{di} > 0$). This classifies this genotype as having broad adaptability but low stability or predictability for this trait. This genotype had 91% CL1. It was adapted to all the environments tested and is considered a genotype with broad adaptability and high stability ($\beta_1 = 1,\ \sigma^2_{di} = 0\ e\ \beta_0 > \underline{x}$). For the TGW trait, this genotype had a higher average than the general average ($\beta_0 > \underline{x}$) and was not considered stable but adapted to the growing conditions of the region representative of the environments tested ($\beta_1 = 1\ e\ \sigma^2_{di} > 0$). As for the height, PFC 2006054 had an average greater than the general average ($\beta_0 > \underline{x}$), was considered adapted to all the environments tested ($\beta_1 = 1$), despite the coefficient of the regression deviations being greater than zero ($\sigma^2_{di} > 0$), with low stability or predictability. Also beneficial was the earliness cycle, which had a lower average than the general one ($\beta_0 < \underline{x}$), a regression coefficient equal to unity ($\beta_1 = 1$), but the coefficient of the regression deviations being greater than zero ($\sigma^2_{di} > 0$), with low stability or predictability.

PFC 2007105 obtained an estimated average grain yield of 6444 kg ha^{-1} ($\beta_0 > \underline{x}$) with a regression coefficient (β_1) equal to unity ($\beta_1 = 1$) and a coefficient of determination R^2 equal to 81.68%, despite the coefficient of the regression deviations being greater than zero ($\sigma^2_{di} > 0$), i.e., broad adaptability but low stability or predictability for this trait. This genotype showed 92% CL1 ($\beta_0 > \underline{x}$), but was not considered stable, had low predictability, and was adapted to unfavorable environments ($\beta_1 < 1$). The TGW trait was considered to have broad adaptability and high stability ($\beta_1 = 1,\ \sigma^2_{di} = 0\ e\ \beta_0 > \underline{x}$). Its height had an average greater than the general average ($\beta_0 > \underline{x}$), and it was considered adapted to all the environments tested ($\beta_1 = 1$), despite the coefficient of the regression deviations being greater than zero ($\sigma^2_{di} > 0$), with low stability or predictability, which is not desired in this program, but with all the potential of other traits, it is an excellent parent for crossbreeding. Concerning cycle, the mean was higher than the overall mean, but the regression coefficient was equal to unity, and the regression deviation coefficient was equal to zero, making it a genotype with broad adaptability and high stability ($\beta_1 = 1,\ \sigma^2_{di} = 0\ e\ \beta_0 > \underline{x}$).

5. Conclusions

There are superior and promising genotypes that can be explored in crossing blocks within the breeding program for irrigated barley in the Cerrado.

There was significant interaction between genotypes and environments, which allows us to conclude that the genotypes behaved differently in different environments, alternating positions between them within the same characteristic studied.

The PFC 2006053 and PFC 2006054 genotypes have broad adaptability and high stability for most traits and outperformed the controls and the general average of the other genotypes.

Author Contributions: Conceptualization, R.T., R.A. and N.S.; methodology, R.A., N.S. and J.M. (Juaci Malaquias); software, J.M. (Juaci Malaquias); validation, R.A.; formal analysis, R.T. and J.M. (Juaci Malaquias); investigation, R.T. and R.A.; data curation, R.A.; writing—original draft preparation, R.T.; writing—review and editing, G.S., J.M. (João Melo), A.F. and M.S.; supervision, R.A. and N.S.; project administration, R.A. and N.S.; funding acquisition, R.A. All authors have read and agreed to the published version of the manuscript.

Funding: The first author received a master's scholarship from CAPES.

Institutional Review Board Statement: Not applicable.

Data Availability Statement: The original contributions presented in the study are included in the article; further inquiries can be directed to the corresponding author.

Acknowledgments: Technical support from Embrapa Cerrados.

Conflicts of Interest: The authors declare no conflicts of interest. The funders had no role in the design of the study, the collection, analysis, or interpretation of data, the writing of the manuscript, or the decision to publish the results.

References

1. Amabile, R.F.; Faleiro, F.G.; Capettini, F.; Sayd, R.M.; Peixoto, J.R.; Guercia, R.F. Characterization and genetic variability of barley accessions (*Hordeum vulgare* L.) irrigated in the savannas based on malting quality traits. *J. Inst. Brew.* **2014**, *120*, 404–414.
2. Sayd, R.M.; Amabile, R.F.; Faleiro, F.G.; Montalvão, A.P.L.; Coelho, M.C. Agronomic characterization of high-yielding irrigated barley accessions in the Cerrado. *Pesqui. Agropecu. Bras.* **2017**, *52*, 84–94. [CrossRef]
3. Sturite, L.; Kronberga, A.; Strazdina, V.; Kokare, A.; Aassveen, M.; Bergjord Olsen, A.K.; Straumite, E. Adaptability of hull-less barley varieties to different cropping systems and climatic conditions. *Acta Agric. Scand. Sect. B—Soil Plant Sci.* **2018**, *69*, 1–11. [CrossRef]
4. Yue, H.; Gauch, H.G.; Wei, J.; Xie, J.; Chen, S.; Peng, H.; Bu, J.; Jiang, X. Genotype by Environment Interaction Analysis for Grain Yield and Yield Components of Summer Maize Hybrids across the Huanghuaihai Region in China. *Agriculture* **2022**, *12*, 602. [CrossRef]
5. Eberhart, S.T.; Russell, W. Stability parameters for comparing varieties 1. *Crop Sci.* **1966**, *6*, 36–40. [CrossRef]
6. Oroian, C.; Ugruțan, F.; Mureșan, I.C.; Oroian, I.; Odagiu, A.; Petrescu-Mag, I.V.; Burduhos, P. AMMI Analysis of Genotype × Environment Interaction on Sugar Beet (*Beta vulgaris L.*) Yield, Sugar Content and Production in Romania. *Agronomy* **2023**, *13*, 2549. [CrossRef]
7. Pereira, M.C.; Souza, N.O.; Nascimento, W.M.; da Silva, G.O.; da Silva, C.R.; Suinaga, F.A. Stability Evaluation for Heat Tolerance in Lettuce: Implications and Recommendations. *Plants* **2024**, *13*, 1546. [CrossRef] [PubMed]
8. Pour-Aboughadareh, A.; Barati, A.; Koohkan, S.A.; Jabari, M.; Marzoghian, A.; Gholipoor, A.; Shahbazi-Homonloo, K.; Zali, H.; Poodineh, O.; Kheirgo, M. Dissection of Genotype-by-Environment Interaction and Yield Stability Analysis in Barley Using AMMI Model and Stability Statistics. *Bull. Natl. Res. Cent.* **2022**, *46*, 19. [CrossRef]
9. Amabile, R.F.; Faleiro, F.G.; Capettini, F.; Peixoto, J.R.; Sayd, R.M. Genetic variability in elite barley genotypes based on the agro-morphological characteristics evaluated under irrigated system. *Ciência E Agrotecnologia* **2017**, *41*, 147–158. [CrossRef]
10. Embrapa Cerrados. Monitoramento da Irrigação no Cerrado. Available online: http://hidro.cpac.embrapa.br/index.php (accessed on 17 August 2023).
11. BRASIL. Ministério da Agricultura, Pecuária e Abastecimento. Portaria n. 691, de 22 November 1996. Brasília. Diário Oficial da República Federativa do Brasil, Brasília, DF, 26 November 1996, Seção 1. pp. 24751–24752. Available online: https://sistemasweb.agricultura.gov.br/sislegis/action/detalhaAto.do?method=visualizarAtoPortalMapa&chave=2140540241 (accessed on 27 November 2023).
12. BRASIL. Ministério da Agricultura, Pecuária e Abastecimento. Secretária de Defesa Agropecuária. In *Regras Para Análise de Sementes*; MAPA: Brasília, DF, Brazil, 2009; p. 395.
13. Cruz, C.D. Genes Software—extended and integrated with the R, Matlab and Selegen. *Acta Sci.—Agron.* **2016**, *38*, 547–552. [CrossRef]
14. Pimentel, G.F. *Curso de Estatística Experimental*, 15th ed.; Piracicaba: São Paulo, Brazil, 2022; p. 451.
15. CONAB. Boletim da Safra de Grãos. 2023. Available online: https://www.conab.gov.br/info-agro/safras/graos/boletim-da-safra-de-graos (accessed on 27 November 2023).
16. Stevens, W.B.; Sainju, U.M.; Caesar-Tonthat, T.; Iversen, W.M. Malt Barley Yield and Quality Affected by Irrigation, Tillage, Crop Rotation, and Nitrogen Fertilization. *Agron. J.* **2015**, *107*, 2107–2119. [CrossRef]
17. Minella, E.; Eichelberger, L.; Costamilan, L.M.; Scagliusi, S.M.M. BRS Sampa: Malting barley cultivar for irrigated production. *Crop Breed. Appl. Biotechnol.* **2015**, *15*, 43–44. [CrossRef]
18. Sayd, R.M.; Amabile, R.F.; Faleiro, F.G.; Coelho, M.C.; Montalvão, A.P.L. Genetic parameters and agronomic characterization of elite barley accessions under irrigation in the Cerrado. Acta Scientiarum. *Agronomy* **2019**, *41*, 12.
19. Kobata, S.G.K. Adaptabilidade e Estabilidade de Genótipos de Cevada e Relações de Causa e Efeito com o Rendimento de Grãos. Master's Thesis, Universidade Tecnológica Federal do Paraná, Paraná, Brazil, 2019.
20. Cruz, C.D.; Carneiro, P.C.S. *Modelos Biométricos Aplicados ao Melhoramento Genético*, 3rd ed.; Universidade Federal de Viçosa: Viçosa, Brazil, 2014; p. 585.
21. Solonechnyy, P. Adaptability and stability of spring barley cultivars in terms of performance. *News Poltava State Agrar. Acad.* **2014**, *4*, 48–53.
22. Hudzenko, V.M.; Demydov, O.A.; Kavunets, V.P.; Kachan, L.M.; Ishchenko, V.A.; Sardak, M.O. Assessment of ecological stability in yield for breeding of spring barley cultivars with increased adaptive potential. *Regul. Mech. Biosyst.* **2020**, *11*, 425–430. [CrossRef]
23. Pinthus, M.J. Estimate of genotypic value: A proposed method. *Euphytica* **1973**, *22*, 121–123. [CrossRef]