

## WINTER BARLEY GRAINS QUALITY VARIATION UNDER WATER-LIMITING CONDITIONS

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### Abstract

*The variation of some grain quality parameters has been caused by the use of a desiccant within a set of 16 winter barley genotypes (varieties and advanced lines), which led to the characterization of the indices, namely the one thousand kernel weight (TKW), protein content (P), starch content (S) and seed size (S I+II). These induced drought conditions have provided results regarding the possibility of growing certain genotypes under restrictive water conditions (field conditions) that can register both high yield and appropriate grain quality parameters. The performed analysis of the results revealed significant differences between genotypes, in terms of the influence of treatment applied and also the interaction between genotype and treatment. Results have been obtained regarding the identification of valuable genetic resources for the translocation of assimilates in water-limiting conditions but also the characterization of genotypes concerning the high stability of quality indices. These genotypes have a high content of carbohydrates in the stem and leaves at the beginning of the grain-filling period but also a high rate of translocation to the grains.*

**Key words:** winter barley varieties, quality indices, drought, desiccation.

### INTRODUCTION

The yield level of cereals decreases significantly during the period with low rainfall as a result of the stress caused by drought and due to the varieties being less adapted to this phenomenon, therefore the availability of water is one of the factors that significantly limit productivity (Robinson et al., 2016). Also, the thermal stress manifested after anthesis leads to some changes regarding the grain weight and size and accumulation of seed compounds which can negatively influence the grain quality (Martínez-Subirà et al., 2021).

Among the most effective methods to simulate drought stress in different species, in the postanthesis phase, chemical desiccation is recommended because it inhibits photosynthesis and thus manifests the ability to fill the grains with reserves from the stem and leaves (Blum, 1983).

When plants are treated with different desiccants such as magnesium chloride

Mg(ClO<sub>4</sub>)<sub>2</sub>, sodium chloride (NaClO<sub>3</sub>), potassium iodide (KI), potassium chlorate (KClO<sub>3</sub>), the varieties that translocate a greater amount of carbohydrates reserve to grains are able to maintain a stable grain weight under drought conditions.

Dogan et al., in 2012, studied the effect of post-anthesis stress in the mobilization of reserves from the stem to grains in triticale and showed that some lines were more drought resistant than the other genotypes in respect of the rate of grain reduction (using potassium chlorate as desiccant agent).

During the 2013-2014 period (Petcu et al., 2014), another research was carried out on winter barley on the reduction of the thousand kernel weight as well as on the cuticular transpiration and the stress tolerance index, following the application of potassium iodide. Ongom et al. (2016) also obtained good results which suggested that the stress technique based on desiccants could be used in the sorghum breeding domain.

Barley grain size can be reduced by lack of precipitation and high temperature after anthesis and to improve end-use efficiency (Wang et al., 2021), it has to enhance the barley seed size because this quality parameter correlates with protein and starch content (Yu et al., 2017). The exposure of a barley plant to a high temperature (35°C) reduces the conversion of sucrose to starch by less than 30% more than a barley plant grown under normal conditions during the grain-filling stage (Wallwork et al., 1998).

Kand et al. (2009) experimented with 148 barley cultivars under high temperatures during the grain-filling period and observed that both protein and starch synthesis were affected. The starch from seeds is the first largest chemical component which counts approximately 60-80% and protein is the second component from the barley grain and could reach from 8 to 20% (Evers et al., 1999).

Therefore, assessing genotype x environment interaction using some parametric and non-parametric stability indices can help to identify barley varieties with superior behavior across growing conditions (Pour-Aboughadareh et al., 2023).

The purpose of this testing was to characterize some winter barley genotypes from the point of view of drought tolerance with reference to the one thousand kernel weight, the stability of the quality indices, i.e., protein and starch content, the size of the seeds, as well as the identification of sources valuable for the translocation of assimilates in limited water conditions for use as parents in the winter barley breeding program.

## MATERIALS AND METHODS

In order to evaluate grain quality parameters of barley variety and lines under drought stress, an experiment in the winter barley experimental field of NARDI Fundulea (16 genotypes) during the two seasons (2014-2015 and 2015-2016 period) was conducted. The same genotypes were included in this experiment as checks and treatments. Using a 5-liter hand-held pressure pump sprayer, potassium iodide (0.4% concentration) was applied to the 16 winter barley genotypes (varieties and perspective lines) on 2 rows of 1 m length after

2 weeks from anthesis as the stage of plant development, respecting the differences between the genotypes regarding the flowering date. The neighboring rows were shielded to avoid applying the desiccant on the other rows and to be able to spray the plant up to the flag leaf inclusive. At full maturity, the rows treated with desiccant and the control rows were manually harvested and threshed, after which the mass of 1000 grains (TKW) with the Contador grain counting machine, the protein (P%) and starch (S%) content with the Infratech 1241 NIR analyzer were determined.

The size of barley seeds (plump grains or assortment I and II expressed in %) was measured using one hundred seeds grams ( $\pm 0.1$  g) of each sample (two replications) which was passed through three consecutive sieves ( $> 2.8$  mm,  $> 2.5$  mm,  $> 2.2$  mm) using a sieve shaker (Sortimat) for 3 minutes ( $\pm 10$  s). The sample collected in each sieve was weighed, the percentages were recorded and only the 2.8 mm and 2.5 mm were used in this analysis (the seeds used in the malting process). The percentage of reduction in the case of TKW and assortment I (seeds  $> 2.8$  mm) and increase in the values of the analyzed parameters (protein, starch, and assortment II - seeds  $> 2.5$  mm) was determined based on the formula:

$\% \text{ KI} = (\text{Gc}-\text{Gd})/\text{Gc} \cdot 100$  (Petcu et al., 2014),  
where: % KI - the percentage of KI reduction,  
Gc - control weight, Gt - treated weight.

The obtained values for each index were analyzed with Statistical Analysis Step-By-Step Using a Statistical Calculator (Dhakre and Bhattacharya, 2018), and the stability of the quality indices at the grain level using the STABILITYSOFT program (Pour-Aboughadareh et al., 2019).

Two statistical parameters were obtained namely regression coefficient ( $b_i$  - Finlay and Wilkinson, 1963) and coefficient of variance ( $\text{CV}_i$  - Francis and Kannenberg, 1978) to assess genotype stability by relating genotypic responses (TKW, protein and starch content, seed size) to environmental conditions (rainfall stress due to desiccant), and one non-parametric Kang's rank-sum ( $\text{KR}$  - Kang, 1988) which can explain environment and phenotype relative to the limited water condition (abiotic factor).

## RESULTS AND DISCUSSIONS

The desiccant inhibits photosynthesis and the ability of the genotype to fill the grains with the reserves in the stem is manifested.

Within a set of 16 winter barley genotypes (varieties and perspective lines), the variation of some quality parameters was caused by using a desiccant called potassium iodide (KI-0.4%), which led to the characterization of the indices of grain quality, namely thousand kernel weight (TKW), protein content, starch, and grain size (assortment I and II, 2.8 and 2.5 mm).

The analysis of the obtained results revealed significant differences, regarding the influence of the genotype and the applied treatment on TKW and the treatment on the starch content (Table 1).

Table 1. The value of probability and significance (TKW, protein, and starch content)

Check	TKW		Protein		Starch	
	p-value	sign.	P-value	sign.	p-value	sign.
Source						
Genotypes	0.004	** 1%	0.120	ns	0.648	ns
Replications	0.000	** 1%	0.600	ns	0.317	ns
Treatment	TKW		Protein		Starch	
Source						
Genotypes	0.035	* 5%	0.182	ns	0.738	ns
Replications	0.000	** 1%	0.563	ns	0.009	** 1%

\*, \*\*significant for p = 5% and p = 1%, ns - nonsignificant

Table 2. The value of probability and significance (assortment I and II, 2.8 and 2.5 mm)

Check	Assortment I		Assortment II	
	p-value	sign.	p-value	sign.
Source				
Genotypes	0.0001	** 1%	0.0060	** 1%
Replications	0.0001	** 1%	0.1960	ns
Treatment	Assortment I		Assortment II	
Source				
Genotypes	0.0007	** 1%	0.0006	** 1%
Replications	0.0084	** 1%	0.0060	** 1%

\*, \*\*significant for p = 5% and p = 1%, ns - nonsignificant

In the case of grain size (Table 2), the influence of genotype was significant for both 2.8 mm and 2.5 mm grain sizes. The analysis carried out showed significant differences between the genotypes, thus, in the case of TKW, the barley varieties with six rows of grains Dana, Univers, Ametist, Lucian, and the F 8-10-12 line were noted, as well as the varieties with two rows of

grains Artemis and Gabriela (Table 3) with the highest values.

The TKW parameter showed a reduction from 1.3% (Smarald variety) to 10.4% (DH 267-66 line) and it has to be underlined 9 genotypes registered values over 42.0 g (Table 3).

The grain protein and starch deposition are limited by water availability during the growing season. Under limited water growing conditions, the converted sucrose quantity to starch is reduced and therefore the TKW but at the same time, the protein was diluted by starch according to Emebiri et al., 2001.

Under the same test conditions, the protein content and the starch content did not decrease below 9.5% and 60%, respectively (standards required by the malt and beer industry). Regarding assortment I (Table 4), in every studied case this parameter (> 2.8 mm seed size) showed a reduction between 1.3% (six-row Dana variety) and 40.6% (two-row DH 267-66 line).

The smallest reduction (from 41.7 to 37.8%) of the six-row Lucian variety (9.4%) compared with the highest (41.4%) for the six-row F 8-10-12 line was registered by the assortment II (> 2.5 mm seed size).

The regression coefficient value of individual genotypes was suggested by Finlay and Wilkinson (1963) as the response to the favourability/unfavorability of the plant-growing environment.

There are three situations: the genotype is well adapted to all growing environments when this coefficient is almost 1 or does not differ from 1 (the regression intercept is large) and when the  $bi \geq 1$  (the regression intercept is large), the genotype is widely adapted). A  $bi > 1$  shows that genotypes have good behavior in favorable environments, whereas a  $bi < 1$  describes good adaptability in unfavorable environments (the intercept is large. According to these, a characterization of the studied parameters was performed.

Regarding the reduction or/and increase in seed quality parameters and size under drought conditions, a barley genotype can be characterized as adapted to unfavorable environments when the regression coefficient  $b < 1$  and the regression intercept is large. When  $b > 1$  the barley variety is adapted to favorable

Table 3. Experimental data comparison before and after the desiccant treatment (TKW, protein, and starch content)

No.	Genotypes	TKW (g)		Reduction (%)	Protein (%)		Reduction/Increase (%)	Starch (%)		Reduction/Increase (%)
		Check	Treatment		Check	Treatment		Check	Treatment	
1	Dana	46.7	43.9	5.9	12.3	11.9	-3.3	61.5	61.9	-0.73
2	Cardinal	39.8	38.1	4.2	10.8	10.2	-5.6	62.9	63.0	-0.24
3	Univers	46.9	42.2	10.0	10.8	11.0	+1.9	62.8	62.6	+0.32
4	Ametist	46.4	44.6	3.8	11.4	11.7	+2.6	62.4	61.5	+1.44
5	Smarald	39.4	39.4	1.3	11.5	11.4	-0.4	62.8	63.0	-0.40
6	Simbol	44.0	39.8	9.5	11.5	11.2	-2.6	62.9	62.8	+0.16
7	F8-19-10	42.7	39.0	8.7	10.7	10.5	-2.3	63.3	62.9	+0.63
8	F8-3-01	39.2	38.5	1.8	11.5	11.6	+0.9	62.6	61.9	+1.04
9	Lucian	43.4	41.5	4.5	12.3	12.6	+2.0	62.6	62.0	+0.96
10	Onix	43.3	40.5	6.4	12.2	12.0	-2.0	62.8	63.0	-0.32
11	F8-10-12	48.5	46.0	5.2	12.0	12.2	+1.7	61.5	61.7	-0.24
12	Andreea	45.7	43.0	6.0	12.7	12.5	-1.6	62.8	62.2	+0.96
13	Artemis	51.2	48.0	6.3	12.8	12.4	-2.7	62.3	62.2	+0.16
14	DH267-66	47.5	42.6	10.4	11.5	11.8	+3.1	63.2	62.9	+0.48
15	Gabriela	52.8	48.6	8.0	13.3	12.6	-5.3	61.8	62.2	-0.65
16	DH315-10	47.1	45.3	3.8	14.0	13.4	-4.3	62.5	62.5	0.00
Mean		45.2	42.5	6.0	11.9	11.8	2.6	62.5	62.3	
R <sup>2</sup>		0.91	0.91		0.65	0.62		0.47	0.57	
CV (%)		6.02	6.77		8.03	7.87		1.34	1.35	
LSD (5%)		5.56	5.87		1.95	1.89		1.71	1.72	

Table 4. Experimental data comparison before and after the desiccant treatment (assortment I and II)

No.	Genotypes	Assortment I (> 2.8 mm)		Reduction (%)	Assortment II (> 2.5 mm)		Reduction/Increase (%)
		Check	Treatment		Check	Treatment	
1	Dana	44.8	44.2	-1.3	36.9	38.2	+3.5
2	Cardinal	54.8	47.5	-13.4	28.1	34.7	+23.5
3	Univers	66.9	58.4	-12.7	24.0	25.8	+7.5
4	Ametist	67.1	47.7	-28.9	25.6	31.2	+21.9
5	Smarald	49.3	47.7	-3.2	25.9	28.4	+9.7
6	Simbol	45.9	26.2	-42.9	34.8	40.3	+15.8
7	F8-19-10	32.8	29.5	-10.0	41.9	35.7	-14.8
8	F8-3-01	42.2	33.6	-20.4	32.4	36.8	+13.6
9	Lucian	43.5	33.5	-23.0	41.7	37.8	-9.4
10	Onix	58.3	39.5	-32.3	31.4	39.7	+26.4
11	F8-10-12	65.2	40.4	-38.1	26.8	37.9	+41.4
12	Andreea	52.5	37.5	-28.7	38.5	47.8	+24.2
13	Artemis	75.4	67.3	-10.7	19.6	20.4	+4.1
14	DH267-66	50.3	29.9	-40.6	39.7	43.8	+10.3
15	Gabriela	86.2	66.0	-13.5	9.5	23.8	+22.7
16	DH315-10	66.2	58.7	-11.3	24.9	31.3	+25.7
Mean		35.51	65.05		37.82	18.19	
R <sup>2</sup>		0.89	0.92		0.87	0.80	
CV (%)		26.36	9.18		19.23	26.86	
LSD (5%)		19.09	12.17		14.83	9.96	

Table 5. Variation of coefficient of regression ( $b_i$ ), coefficient of variation (CV $_i$ ), and Kang's rank-sum (KR) of TKW, protein, and starch content

Genotype	TKW (g)	$b_i$	CV $_i$	KR	P (%)	$b_i$	CV $_i$	KR	S (%)	$b_i$	CV $_i$	KR
Dana	45.3	1.010	4.29	4	12.1	2.618	2.63	7	61.7	-2.370	0.45	15
Cardinal	38.9	0.606	2.99	14	10.5	3.782	4.38	16	63.0	-0.593	0.11	6
Univers	44.6	1.727	7.46	10	10.9	-1.164	1.29	15	62.7	1.481	0.28	6
Ametist	45.5	0.643	2.72	8	11.6	-1.745	1.83	13	62.0	5.333	1.02	15
Smarald	39.4	0.050	0.60	15	11.5	0.582	0.61	6	62.9	-1.185	0.22	8
Simbol	41.9	1.543	7.08	13	11.3	2.036	2.18	10	62.8	0.889	0.16	3
F8-19-10	40.9	1.359	6.40	11	10.6	1.455	1.67	12	63.1	2.370	0.44	3
F8-3-01	38.8	0.257	1.27	15	11.5	-0.291	0.30	9	62.3	4.148	0.79	13
Lucian	42.4	0.716	3.25	9	12.4	-1.455	1.42	8	62.3	3.556	0.68	11
Onix	41.9	1.010	4.64	7	12.1	1.455	1.46	1	62.9	-0.889	0.16	8
F8-10-12	47.2	0.918	3.74	3	12.1	-1.164	1.16	4	61.6	-0.889	0.17	12
Andreea	44.3	1.010	4.38	4	12.6	1.164	1.12	3	62.5	3.556	0.67	10
Artemis	49.6	1.176	4.56	2	12.6	2.327	2.24	5	62.3	0.593	0.11	1
DH267-66	45.0	1.819	7.77	11	11.7	-1.745	1.82	13	63.0	2.074	0.39	3
Gabriela	50.7	1.543	5.86	1	12.9	4.364	4.10	10	62.0	-2.074	0.39	14
DH315-10	46.2	0.661	2.75	6	13.7	3.782	3.36	2	62.5	0.055	0.15	2

Table 6. Variation of  $b_i$  (coefficient of regression), CV $_i$  (coefficient of variation), and KR (Kang's rank-sum) of grain size (assortment II and I)

Genotype	S I (%)	$b_i$	CV $_i$	KR	S II (%)	$b_i$	CV $_i$	KR
Dana	44.5	0.047	0.90	15	37.6	0.296	2.50	5
Cardinal	51.1	0.607	10.16	6	31.4	1.463	14.80	7
Univers	62.7	0.699	9.55	1	24.9	0.390	4.97	13
Ametist	57.4	1.599	23.85	6	28.4	1.254	14.01	6
Smarald	48.5	0.132	2.33	12	27.1	0.550	6.43	11
Simbol	36.1	1.624	38.56	14	37.5	1.220	10.32	2
F8-19-10	31.2	0.272	7.49	16	38.7	-1.370	11.23	12
F8-3-01	37.9	0.712	16.08	10	34.6	0.973	8.93	2
Lucian	38.5	0.824	18.32	6	39.7	-0.880	7.03	7
Onix	48.9	1.556	27.27	9	35.5	1.844	16.47	10
F8-10-12	52.8	2.047	33.21	11	32.4	2.478	24.31	13
Andreea	45.0	1.242	23.66	4	43.2	2.078	15.28	4
Artemis	71.4	0.666	7.99	1	20.0	0.174	2.75	15
DH267-66	40.1	1.686	36.01	13	41.8	0.917	6.97	1
Gabriela	76.1	1.671	18.82	4	16.6	3.180	60.68	16
DH315-10	62.5	0.617	8.45	3	28.1	1.432	16.17	7

conditions and when  $b_i \geq 1$  and the regression intercept is large, the variety is widely adapted. The most desirable genotypes are considered the genotypes with low environmental variance and with a low coefficient of variation (CV $_i$ ) as suggested by Francis and Kannenberg (1978). Kang's rank-sum (Kang, 1988) is a parameter

that gives a weight of 1 to both yield and stability statistics in order to identify high-yielding and stable genotypes and uses both yield and intercepts as selection criteria. The genotype with the highest yield and lower intercepts is assigned a rank of 1, the ranks are

added for each genotype and those with the lowest rank-sum are the most desirable.

The studied winter barley varieties and advanced lines from this experiment varied widely in the TKW (0.050 Smarald variety and 1.819 DH 267-66 line), protein content (0.582 Smarald variety and 4.364 Gabriela variety), and starch content (0.593 Artemis variety and 5.333 Ametist variety) regression coefficient (Table 5), while the CVi was low (for TKW from 0.60 to 7.08, for protein content from 0.30 to 4.10 and for starch content from 0.11 to 1.02). A coefficient of variation below 10 shows very good stability of the parameters under drought conditions. The KR sum showed a good environment and phenotype relative to the abiotic-induced factor for Gabriela, Artemis, F 8-10-12, Andreea, and Dana genotypes regarding TKW. The lowest protein rank sum was registered by the Onix, DH 315-10, Andreea, F 8-10-12, and Artemis genotypes while for starch content the best genotypes were Artemis, DH 315-10, DH 267-66, Simbol, and F 8-19-10 (Table 5).

The grain size regression coefficient also widely varied (both sizes) and the CVi of assortment I ranged between 2.33 (Smarald variety) and 38.56 (Simbol variety), only six genotypes registered a CVi below 10 while a number of sixteen between 10,16 and 38.56 (Table 6).

The genotype stability by relating genotypic responses was different regarding assortment II due to a higher variation of CVi (2.75-60.68) and it is observed that some genotypes had a lower CVi than in the case of assortment I meaning a higher percent of grain >2.5 mm. Regarding the KR sum for assortment I (Table 6), the best genotypes are Univers, Artemis, Gabriela, DH 315-10, and Andreea while for assortment II, the DH 267-66, F 8-3-01, Simbol, and Andreea.

## CONCLUSIONS

Comparing parameter values, among tested genotypes, some of them were sensitive and others were tolerant to water-limiting conditions.

Significant results regarding the identification of valuable genetic resources for the translocation of assimilates under water-

limiting conditions, for use as parents in the breeding program, as well as the characterization of varieties and lines with reference to the high stability of grain weight, were obtained.

These winter barley genotypes have a high content of carbohydrates in the stem and leave at the beginning of the grain filling period, but also a high rate of translocation to seed. Furthermore, for the varieties and lines with high stability of grain weight (TKW), it is necessary to study the individual contribution of the stem, leave, and spike and also in order to establish if the spike partially compensates the photosynthesis through palea and awns.

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