The Heritability of Some Qualitative and Quantitative Traits at One Set of Spring Barley Genotypes

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Abstract

Work collections are subjected to a renewal process, therefore a regular evaluation is needed inorder to appreciate the genetic advance of the existing variability at collection level and further to identify valuable genotypes in terms of morphoproductive and qualitative traits (protein, starch). The barley intended for brewing must correspond to some qualitative parameters, of which proteins and starch content are of major importance. For this purpose, a study was conducted to assess the variability and heritability indicators corresponding to the two traits at 48 barley genotypes. The genotypes that were the subject of this study were sown in three experimental years 2013, 2014 and 2016. The mean values of 2013 year was 13.71 compared with only 10.77, and 11.27 in 2014 and 2016. The significant value of the heritability coefficient along with the genetic advantage of 0.81 indicates the success of selection work for this important chemical trait.

Keywords: *Barley, starch, protein, coefficient of variation*

INTRODUCTION

The primary domains in which barley is used are forage and beer brewing. To a lesser extent, the grains and the plant are used in nutrition, especially in forms with a high amount of active biochemical substances. In compliance with these aspects, the directions towards quality improvement are:

1. obtaining varieties intended for animal feed, with a high amount of proteins and rich in essential amino acids;

2. creating breeds suitable for the brewing industry (low protein content and high amount of starch, with raised germinative energy and high TKW);

3. identifying and creating genotypes with a high content of β-glucans and other components beneficial to human health.

Improving and obtaining new superior crops for the brewing industry is much more difficult than improving the quality of those for forage.

Many authors support the concept that protein content affects malt quality in several ways: nutritional yeast production, beer precipitation and enzyme activity (See *et al.*, 2002, Clancy *et al.*, 2003 quote by Shengguan Cai *et al.*, 2013). The role of proteins in beer production is mentioned by other authors, which show their importance in nutritional yeast production, foam formation and in determining the flavour of the brewing. (Bishop 1930; Chen *et al.*, 2006; Steiner *et. al.,* 2011 cited by Mekonnen *et al.,* 2012).

Shengguan Cai *et al.,* 2013 have demonstrated a close correlation between protein content and malt quality parameters, an imperative requirement being to obtain new barley genotypes with high protein content stability.

As a result of some studies conducted in our country regarding the varietal qualities of the grains according to the genetic factor and the ecological conditions, it was found that a difficult

problem in breeding barley for beer in the ecology of our country is the relatively high level of protein content. Considering these statements it can be concluded that varieties of the barley plant and barley specially designated for the brewing industry must only be grown in those areas where there is a greater climatic constant conditions, which ultimately leads to the achievement of stable productions for the brewing industry (Neguț, 1982).

Production is probably the most complex trait and, compared to other quantitative traits, the most difficult to assess in early selection, mainly due to the high heterozygosity state and the large number of major and minor genes involved in the heredity. Although it was initially believed that composing elements of production had a less complex influence and that the division of production into these component would improve the selection for this trait, they did not have the expected results. As a result of studies, it was concluded that the elements of production also have a complex influence.

The production of barley varieties is closely related to the variability of the initial breeding material, and implicitly, in the collection of germplasm. Tested collections are subject to processes of structural change in inputs, requiring a periodic assessment in order to estimate the genetic progress of new genotypes and the variability existing at the collection level in order to identify those genotypes of high morpho-productive and quality traits (protein, starch).

Even in areas specific to the spring barley culture, the increasing incidence of climate change requires special attention towards increasing the quantitative and qualitative stability the new genotypes crops.

MATERIAL AND METHOD

The germoplasm collection at ARDS Turda has about 550 genotypes in its structure. Relatively recent germoplasm collection has been improved with new West European breeds suitable to the beer industry. These genotypes were analyzed alongside other native or foreign genotypes in terms of qualitative and quantitative indicators. A total of 48 genotypes were taken into consideration, of which 29 of foreign origin, 8 of autochthonous origin as well as 11 older lines created in Turda.

The genotypes were sown in three experimental years 2013, 2014 and 2016 in rows with the length of 1 meter in 5 replication. Phenotypic and genotypic variance was calculated on the basis of Comstock and Robinson's proposed relations in 1952, and the calculation methods proposed by Sing and Chaudhri, 1985, were chosen to determine the genotypic and phenotypic coefficient of variation. The narrow-sense heritability was calculated on the basis of the relationship proposed by Werner, 1952. Estimation of the qualitative parameters was done with the TANGO-NIR device, the samples resulting from the milling of grains from 100 ears of barley from the five rehearsals.

RESULTS AND DISCUSSIONS

Most breeders and technicians agree that a major role in the quality of crops is played by the environment and farming technology. It is important to note that during the three year experiment the same technology (pre-emergence plant, dose and type of fertilizer) was used in the improvement field. Accounting for this, it can be concluded that the qualitative differences between genotypes are solely due to the hereditary and environmental factors.

The average protein content experienced a significant fluctuation in experimental years, from 13.71% in 2013 to 10.77% in 2014 and 11.27% in 2016 (Tab. 1). The highest performance on this important qualitative asset are recorded for the Kervana genotype, which in 2013 achieved 16.14% proteins. These results justify and reinforce previous assertions about the role of the environment in the quantitative achievement of protein content.

The differences between the minimum and maximum values as well as the coefficient of variation values indicate that genotypes can be identified at the level of the 48 genotypes which, in various combinations, lead to some negative or positive transgressions and obviously to the reduction or increase of the protein content of new genotypes.

As it is already known, the average starch content trend is inversely proportional to the protein content. The coefficient of variation suggests a slight variation in the average level of starch. However, the significant variation between the minimum and maximum values indicate the

Table 1. Variability of protein and starch content in the 48 studied genotypes (Turda 2013, 2014 and 2016)

| Years	Mean	Minimum	Maximum	s%
Proteine content (%)				
2013	13.71±0.14	11.01 (Odisey)	16.14 (Kervana)	7
2014	10.77±0.11	9.28 (Chronicle)	12.39 (To2057/96)	6.91
2016	11.27±0.12	9.45 (Belgravia)	13.10 (To2021/91)	7.4
Starch content (%)				
2013	47.32±0.25	43.55 (To2023/91)	51.35 (Sulilly)	3.59
2014	51.60±0.26	47.46 (Daciana)	56.31(Prima)	3.48
2016	56.70±0.30	52.94 (Tremois)	61.47 (To2264/92)	3.65
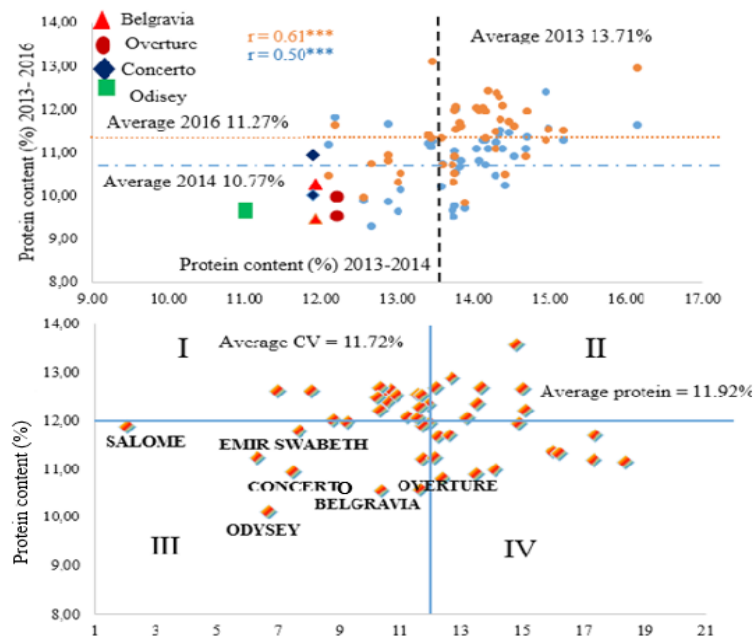
Figure 1. Stability of protein content expressed as repeatability degree and by the coefficient of variation (Turda 2013, 2014 and 2016)

possibility of identifying valuable genes, which could lead to the increase of the starch content in the new genotypes.

The correlation of the annual values of protein content to the 48 genotypes can be seen as a repeatability coefficient with a particular importance for the breeder. High values of the correlation coefficient "r" directly suggest character stability and indirectly heritability. By comparing the annual values of protein content in the years 2014 and 2016 with those of the year 2013, genotypes with a high degree of stability and low yearly fluctuations be identified.

In this regard, the Odisey genotype is of interest, as in all three experimental years it had the lowest variations in protein content – 11.01 (2013)/9.71 (2014) and 9.61 (2016) (figure 1). Even under the conditions of 2013, which can be considered a particularly favorable year for the accumulation of proteins, this genotype records the lowest values. The significant increase in the percentage of protein in 2013 is due to the significant amounts of rainfall recorded in May and June, which led to a qualitative depreciation in beer industry. The important role of precipitation in these months in favoring protein accumulation processes is also confirmed in the speciality study.
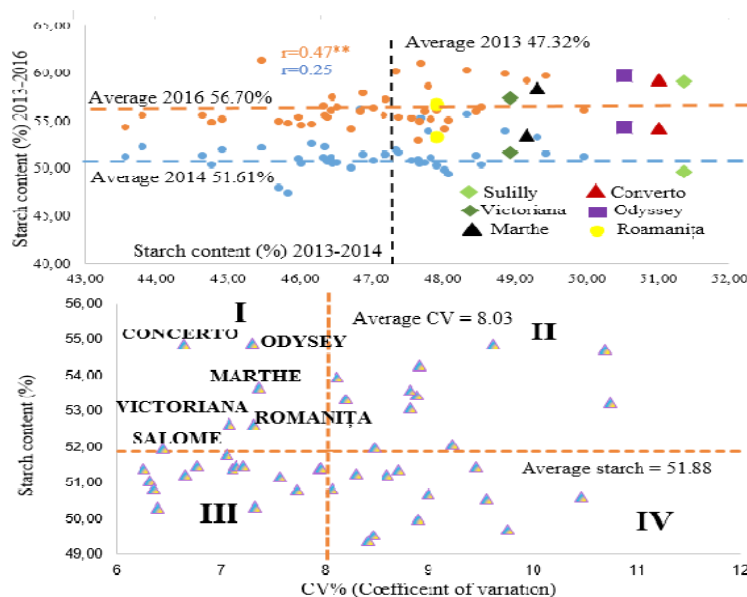
Figure 2. Stability of starch content expressed as repeatability degree and by the coefficient of variation (Turda 2013, 2014 and 2016)

Concerto, Overture and Belgravia genotypes can also be noted in this regard.

For comparison, we used another stability assessment method proposed by Francis and Kannenberg (1978) based on the coefficient of variation, the stability of the genotypes being based on its average. The four genotypes mentioned above as having a high protein content are found in quadrant III, all genotypes in this quadrant have coefficients of variation (CV%) and protein content below average. The lowest CV values of protein content are recorded for the Salome genotype, but it shows quite high values of protein content, close to average. The smallest percentage of protein is recorded by Odysey genotype having an average protein percentage of only 10%.

Genotypes placed in quadrant IV do not have high protein stability and may experience significant fluctuations, therefore these genotypes, under environmental conditions favorable to protein accumulation, can record values above 12.5%. These genotypes could be part of a hybridization program to eventually improve the stability of protein content or to address technological measures to reduce protein content: lower doses of nitrogen or a possible cultivation on less fertile land but only after a prior identification of genotypes that behave favorably on these lands.

Genotypes placed in quadrant I have good stability of proteins with values below the coefficient of variation, but above protein average.

In turn, these genotypes could be improved by specific hybridization steps with low protein content forms for the production of brewing varieties. The good stability of these genotypes indicates their use in hybrid combinations with other genotypes with lower stability and high protein content of another destination, namely animal feed, for example with the genotypes in quadrant II. The genotypes placed in this quadrant have low protein content but are noticeable by the high values of this chemical property.

Regarding the starch content, we used the same measures to estimate the stability of the analyzed genotypes.

The values of the correlation coefficients "r" for the annual starch content determination of 0.47 and 0.25 reflect the fact that besides the genotype and the environment has an important involvement in the assimilation of starch into the grain.

In other research at Fundulea on genotypes of autumn barley and spring barley with two rows in different localities, a mention a contribution of genotype to the starch content of 20-30% (Neguț, 1982). Therefore, the correlation coefficient „r" of the annual starch content values in this study defines quite accurately the heritability of this trait.

Again, we notice that the Concerto and Odyssey genotypes do not record large differences from one year to the next, being placed above the

Table 2. The variation of protein and starch content in the 48 analyzed genotypes (Turda 2013, 2014, 2016)

Nr. crt.	Source of variance	SPA	GL	s^2	F
			Protein		
1	Total	1025.54	429		
2	Years (Y)	713.80	2	356.90	18853.87***
3	Genotypes(G)	223.91	47	4.76	574.78***
4	Y x G	85.41	94	0.91	109.62***
5	Error (Y)	0.08	4	0.018	
6	Error (G)	2.34	282	0,008	
			Starch		
1	Total	7938.23	429		
2	Years (Y)	6259.28	2	3129.64	9985.54***
3	Genotypes(G)	963.01	47	20.49	61.59***
4	Y x G	620.88	94	6.61	19.86***
5	Error (Y)	1.25	4	0.31	
6	Error (G)	93.81	282	0.33	

Table 3. The influence of the year factor on the content of proteins and starch

	Year	Protein (%)	%	Starch (%)	%
1	Mean (Check)	11.92	100	51.90	100
2	2013	13.71	115***	47.39	91[000]
3	2014	10.77	90[000]	51.61	99[0]
4	2016	11.27	95[000]	56.70	109***
DL p 5%	0.05			DL p 5% 0.18	
DL p 1%	0.07			DL p 1% 0.30	
DL p 0,1%	0.14			DL p 0,1% 0.57	

average of each year, and in the quadrant I, below the coefficient of variation average. Therefore these two genotypes are should be used for the qualitative improvement of in the Turda's beer breewing program. A fairly favorable reaction to the stability of starch and even of proteins can be attributed to the native genotype Romanița, with values above the average for the starch content in all three years and below the average in the coefficient of variation. It is also worth noting that the Marthe, Victoriana and Salome genotypes have good starch stability.

The variants placed in quadrant II have a high starch content but appear to interact much more strongly with the environment in the formation of this trait, or are more sensitive to environmental fluctuations.

Adaptability can also be defined as a limit of resistance of plants to adverse factors such as pests, weed infestation of crops, diseases, drought, salinity or low temperatures.

The largest share of the total protein and starch content variation is the year and genotype factors. The values of sample F show a significant involvement of these factors in the variance of the two chemical components. As years advance, genotypes appear to behave quite differently suggesting a more significant reaction of starch at different climatic conditions.

The climatic conditions of 2016 showed a favorable influence on the quality of barley for beer brewing, as can be seen from the significant negative differences in the percentage of proteins compared to the base sample and the very significant positive increases of the starch content.

Table 4. The reaction of genotypes on the average protein and starch content of the studied genotypes (Turda 2013, 2014, 2016)

Nr	Genotypes	Protein (%)	Diference	Starch	Diference
1	Check	11.92	100	51.90	100
2	Turdeana	11.67	97.9^{000}	49.54	95.5^{000}
3	Daciana	11.70	98.2^{000}	49.37	95.1^{000}
4	Roamanița	11.22	94.1^{000}	52.62	101.4^{**}
5	Prima	11.23	94.2^{000}	53.08	102.3^{***}
6	Farmec	11.70	98.2^{000}	50.82	97.9^{000}
7	Adina	11.37	95.4^{000}	52.01	100.2
8	Victoriana	11.15	93.5^{000}	52.65	101.4^{**}
9	Marthe	11.18	93.8^{000}	53.69	103.5^{***}
10	Chronicle	10.89	91.4^{000}	53.46	103^{***}
11	Belgravia	10.55	88.5^{000}	53.97	104^{***}
12	Odyssey	10.11	84.8^{000}	54.87	105.7^{***}
13	Overture	10.57	88.7^{000}	54.28	104.5^{***}
14	Concerto	10.95	91.9^{000}	54.86	105.7^{***}
15	Tatum	10.80	90.6^{000}	53.59	103.3^{***}
16	Sulilly	11.24	94.4^{000}	54.46	104.9^{***}
17	Salome	11.87	99.6^{000}	52.46	101.1^{*}
18	Arupo	12.65	106.2^{***}	50.69	97.7^{000}
19	Magnif	11.94	100.2	50.81	97.9^{000}
20	Anni	12.47	104.6^{***}	54.72	105.4^{***}
21	Ello	12.22	102.5^{***}	54.84	105.7^{***}
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The year 2014 was also a favourable year for beer quality, but the average values of starch content were slightly lower, with significant negative differences compared to the experiment's average. Concerning protein content, the year 2014 had the greatest impact on protein depletion. The strong negative correlation between starch and protein is also reflected in the data presented in Tab. 3.

Although the protein content values have a superior variability coefficient to that of starch, correlating to a higher value scattering around the average, the differences between the minimum and maximum values in starch are superior, obtaining values for the genetic and phenotypic variation above the protein average values. Hence, the values of the heritability index, in the broad sense, of starch are slightly inferior to the protein values, but in both cases they indicate a pronounced heredity. Both the phenotypic variance and the phenotypic

coefficient of variation follow an ascending path compared to the genotypic variance and the genotypic coefficient of variation (Tab. 4).

The heritability coefficient values, for both; protein (0.81) and starch content (0.68), indicates significant genetic control of the variation of the two properties (Tab. 5). The variety can be defined as a population of individuals with a more or less uniform genofound. The variation of traits is related with the genetic factors, environment and the experimental errors. The only one which is hereditary transmitted and that we find in the progeny is the genetic variation. The heritability index allows to determine the contribution of the genotype and the environment in the phenotypic manifestation of a trait. The size of the heritability coefficient has a significant variation, or it can be said that the heritability is relative, being valid only for the genotypes and the environmental conditions in which and for which it was estimated

Tab 5. Heritability in norow sense (H²), genetic advance (AG), coefficients of variation genotypic (CVG), phenotypic (CVP) and residual variance (CVR)

	$\sigma^2 g$	CVG%	$\sigma^2 p$	CVP%	$\sigma^2 r$	CVR%	H²	AG	AG% over the mean
Proteine%									
	0.43	5.5	0.53	6.11	0.019	1.16	0.81	0.81	6.8
Starch %	1.54	2.39	2.28	2.90	0.31	1.07	0.68	2.17	4.18

σ²g, σ²p, σ²r - genotypic, phenotypic, residual variance, CVG%, CVP%, CVR%- coefficient of genotypic, phenotypic and residual variance; H² - , heritability coefficient in broad sense, AG- genetic advance, AG%- genetic advance over the mean

Table 6. The mean values of the grain weight/ear for parental populations, F1, F2, BCI, BCII in a system of backcrossings at spring barley

	Populations					
Combination	P1	P2	F1	F2	BCI	BCII
CB1 (Rubin x Jubileu)	1.1	1.49	1.08	1.32	1.38	1.5
CB2 (Prima x Vienna)	1.34	1.27	1.37	1.39	1.69	1.51
CB3 (Thuringia x Salome)	0.99	1.11	1.24	0.93	1.28	1.49
CB4 (Adina x Anabelle)	1.29	1.05	1.48	1.2	1.5	1.3

before. Based on the heritability coefficient it may be calculated other indicators, such as genetic advantage, genetic advantage over the average, and the repeatability coefficient that predict much more eloquently the expected effects of selection. Hence, the heritability coefficient in tandem with a genetic advantage over the high average can accurately enough predict the expected effects of the selection.

Addisu and Shumet (2015) also point out that the superiority of the genetic advantage expressed in percent must be associated with a high heritability to anticipate the effects of selection. The two researchers claim that the genetic advantage expressed as a percentage over the average yields more accurate results compared to the genetic advantage.

As well a Panse (1957) cited by Dyulgerova and Valcheva (2014) states that a high heritability associated with a high genetic advance indicates the additive effects of the gene, while a high heritability accompanied with a small genetic advance indicates the non-aitive effects of genes for controlling the trait. Higher values of genetic advantage over the average are recorded at the level of protein content being coupled as well with the highest values of heritability (Tab. 5). An almost similar situation can also be reported in the case of starch. Consequently, in order to improve

the two traits, rigorous selection work could lead to favorable results.

Production is the most complex trait, being the ultimate result of all metabolic and physiological processes in the plant under the strong control of the environmental conditions. In view of these assertions it can be said with certainty that the improvement of this trait requires complex efforts. It was thought that the improvement of the elements production components would require less effort but the determinism of these components is complex being governed by the action of the polygene. Based on these considerations, some morphological components of the production were analyzed in four hybrid combinations.

The performance of one of the most important trait of production, namely grain weight/ spike, is shown in Tab. 6, with the parents recording values between 0.99 and 1.49 g / spike. At backcross generations, grain weights are superior to F1 and F2, as well as parental populations suggesting the additive effect of genes involved in controlling this trait. The superiority of the F2 generation compared to F1 in two of the four combinations indicates the presence of transgressional segregation phenomena for this trait. From the point of view of this traits, it is remarked BCI from the combination (Prima x Vienna) x Prima with

Table 7. The mean values of genetic parameters estimated for grains number and grains weight at Spring Barley (Turda 2017)

Trait	Dominance $\frac{F1}{HP} * 100$	Heritability coefficient in broad sense (H) by Mahmoud și Kramer (1951)	Heritability coefficient in narrow sense (h^2) by WARNER (1952)
Grains number	95.5	0.81	0.42
Grains weight	97	0.65	0.56

the highest average grain weight / spike. Also, in three of the four combinations, a heterosis effect in the F1 generation can be noted, registering higher grain weights compared to the average of the best parent (Table 6).

The degree of dominance, expressed as a ratio between the F1 average and the average of the best parent expressed in percent, shows a partial dominance towards a complete dominance for the two traits (Tab. 7).

Viewed as a simple parameter, the heritability coefficient is of no great importance in the appreciation of some traits, but along with the selection pressure and the existing variability, it can provide information on the probability of transmission of the genes to be obtained in the new genotype. The calculation method proposed by Mahmoud and Kramer (1951) was used to determine the heredity coefficient in a broad sense, the values corresponding to the two traits of production reflecting an important participation of the genotype in their formation (Tab. 7).

Regarding the mean values of heritability in a narrow sense (h2), it can be stated that the grain weight/spike has a average heritability to more higher of 0.56, and the number of grains/spike has a reduced heritability of 0.42 (Tab. 7)

CONCLUSIONS
The high values of the dominance to overdominance for the grain weight suggest the complexity of this direct component of production, as Falconer's (1969) claims tht overdominance can be manifested at a higher level in the case of complex characters.

The success of the selection work, largely depends on the speed and certainty of the evaluation of the segregants from combinations

and the fidelity with which the phenotype reflects the genotype.

The fairly high values of heritability index (h^2) indicate important genetic conditioning as well as a major contribution of genotype in phenotypic expression of grain weight.

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