МЕТОДИ І РЕЗУЛЬТАТИ СЕЛЕКЦІЇ METHODS AND RESULTS SELECTION

UDC 631.52:633:114(477.72)

DOI: 10.30835/2413-7510.2022.271735

CORRELATIONS BETWEEN THE PROTEIN CONTENT IN GRAIN WITH ECONOMIC CHARACTERS IN WINTER BREAD WHEAT BREEDING ACCESSIONS OF HYBRID ORIGIN ON IRRIGATION

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The expression of the "protein content in grain" trait was studied in winter bread wheat lines, which were originated from late-ripening accessions of the Western European ecotype. Correlationregression models for relationships of the protein content in grain with the "anthesis - grain ripeness" interphase period length and grain yield in elite accessions grown in breeding nurseries were constructed.

Key words: varieties, hybrids, wheat, irrigation, breeding, yield, protein content in grain, earliness.

Introduction. In terms of food importance, wheat occupies a leading place in the world, as bread products for human nutrition are made from its grain. The quantitative and qualitative biochemical compositions of wheat grain determine its consumer value. Among the main indicators of the nutritional value of wheat grain, the protein content prevails, as wheat protein can compensate for limited consumption of animal products. Breeding is the most effective way to increase the protein share in the grain mass, therefore, when one breeds high-yielding varieties, it is necessary to strengthen control over the grain nutritional value indicators [1].

Literature Review and Problem Articulation. The grain production efficiency depends significantly on the breeding of modern high-yielding wheat varieties that are resistant to adverse growing conditions. Along with increasing the performance, another challenge for agrarian scientists is improving the winter bread wheat grain quality [2]. Even in the past, academician P. P. Lukianenko raised the problem of difficulties of combining high performance and high quality of wheat grain. At the same time, he emphasized that special difficulties might arise when varieties of the Western European ecotype would be involved in breeding [3].

It is well known that the wheat grain quality indicators are determined by both genotype and its phenotypic realization in agroecological gradients [4]. Inverse correlations between protein content and yield were observed. A.P. Orliuk studied in detail the wheat quality and relationships between grain quality parameters on irrigation. He reported data on correlations between the grain quality parameters and yield in wheat breeding lines, in particular, the protein content could be weakly, though significantly, oppositely directionally correlated with the wheat grain yield in some combinations [5].

Concurrent selection for grain yield and bread-making qualities is a serious problem in wheat breeding and several concepts have been developed to eliminate undesirable negative correlations between these traits. Possibilities of achieving simultaneous genetic improvement of grain yield, protein content, and protein quality are investigated to create varieties that would be more efficient in terms of resource use [6].

Genomic breeding indices based on regression deviations for the traits under investigation have shown great advantages in identifying resource-efficient genotypes that combine both high

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ISSN 1026-9959. Селекція і насінництво. 2022. Випуск 122.

yield capacity and relatively high quality. Thus, genomic breeding opens up opportunities for selection of many traits in early generations [7]. The very implementation of genomic breeding in many national and international plant breeding programs in recent years emphasizes the potential of this new tool for accelerating the genetic improvement of domestic plants [8].

Different predictive models have been proposed for genomic breeding, in particular, modeling the "marker – environment" interactions, when preliminary information on a conjugated trait is available earlier than that on the main trait, which is important to the breeder. Such approach is important for the breeder to carry out concurrent selection of the main agronomic traits, such as grain yield and protein content, which is a serious challenge in wheat breeding due to strong negative correlations between these traits [9].

As already mentioned, these correlations make simultaneous improvement of both traits difficult. Since the protein content in grain is an important determinant of the bread product quality [10], scientists strive to change these undesirable correlations by increasing the grain yield without drop in the protein content [11].

The protein output is considered a promising alternative criterion in selection, as it specifically evaluates the protein content/grain yield, because it is equivalent to total grain nitrogen yield, which has also been the focus of breeding studies in recent decades [12].

Researchers observed that some genotypes did not have negative correlations between the grain yield and protein content. Promising lines have been created; the protein contents in those lines are relatively higher than those one would expect from their grain yields. This linear regression of protein content at the grain yield limit has become commonly known as the grain protein deviation (GPD) [13]; it was generalized in the regression-residual method proposed by Hänsel [14] and can be considered as a method for estimating yield-adjusted protein content. These adjusted phenotypic values have already demonstrated a certain potential to mitigate the aforementioned negative relationship in a recurrent selection design [15]. For this purpose, one can calculate the grain protein deviation based on a graph by regressing unadjusted values of the protein content on the grain yield [13].

The implementation of genomic breeding in the breeding design of the creation of traditional lines was highly effective, as the grain yield was increased compared to results of traditional phenotypic selection according to data of one-year trial [16].

Classical phenotypic selection, even with low-quality data, can still outperform genomic selection, if data from several years and different ecological gradients are considered [17]. By combining the benefits of phenotypic selection based on previous yield trials with prior information on line performance, genomics-based selection resulted in a better prediction of the expression of the "protein content" and "grain yield" traits [18, 19].

Although strong negative genetic correlations are often observed between the grain yield and protein [20, 21], environmental effects can significantly alter the magnitude of this negative relationship, necessitating trials of genotypes in several environments [22].

The material presented in this article is a continuation of publications related to hybridization of local winter bread wheat varieties with later ripening short-stemmed genotypes of the Western European ecotype, with extended growing periods and certain interphase periods and with increased yield capacity [23].

Purpose and Objectives. To evaluate the expression of the "protein content in grain" trait in winter bread wheat lines derived from late-ripening accessions of the Western European ecotype; to construct correlation-regression models for the relationships of the protein content in grain with the "anthesis - grain ripeness" interphase period length and grain yield in elite accessions grown in breeding nurseries.

Material and Methods. The field studies were carried out at the Institute of Irrigated Agriculture of NAAS in 2019–2021. Modern winter wheat varieties bred at the Institute, collection specimens of the Western European ecotype, which had been introduced from France (registration numbers Kf1...16), and their hybrids were studied. Individual selections of elite plants from F_2 were brought to the control nursery and evaluated for protein content in grain, yield, "anthesis–ripeness" period and other economic characteristics. Biometric measurements, biochemical analyses, and yield records were conducted by traditional methods [24, 25]. The study methods were field, laboratory,

biochemical, breeding-genetic, and statistical. The studies were carried out under irrigation conditions at the pre-irrigation field moisture capacity (FMC) in the 0–50 cm soil layer of 75%.

Results and Discussion. We found that the minimum protein content in grain was within 11-12% (Table 1). The maximum protein content in grain (15.5–16.6%) was recorded in lines from hybrid populations Kf4-16 / Ovidii and Kf2-16 / Khersonska Bezosta. The combinations Kf2-16 / Khersonska Bezosta (14.74%) and Koshova / Kf2-16 (13.12%) were noticeable because of the mean values of the protein content in grain.

Table 1

Variability of the protein content in grain of the winter bread wheat breeding accessions in the control nursery (2019–2021)

the control nursery (2019–2021)											
Pedigrees of the	Parameters										
breeding accessions (hybrid population)	Specimen number	protein content in grain, min-max, (%)	mean ± standard error	coefficient of variation of the protein content in grain, %	correlation between the protein content in grain and the "anthesis - ripeness" period length, r	correlation between the protein content in grain and the yield, r					
Kf 2-16 / Ovidii	20	12.2–13.8	12.76 ±0.15	3.92	0.263	-0.358					
Kf4-16 / Ovidii	20	11.6–15.5	13.01 ± 0.34	8.46	0.413	0.333					
Kf2-16 /											
Khersonska	20	13.8–16.6	14.74 ± 0.25	5.56	-0.019	0.179					
Bezosta											
Koshova / Kf2-16	20	12.4–14.4	13.12 ± 0.18	4.42	-0.231	-0.065					
Кф5-16 /Ledia	20	11.3–14.1	12.10 ± 0.29	7.69	-0.281	0.609					
For all the combinations	600	11.6–16.6	13.14 ±0.17	8.88	-0.148	-0.036					

The coefficient of variability of the protein content in grain of the breeding accessions was low, which is typical of the "protein content in grain" indicator in general for all wheat breeding accessions. In the Kf4-16 / Ovidii (8.46%), Kf5-16 / Ledia (7.69%), Kf2-16 / Khersonska Bezosta (5.56%) hybrid combinations, it was slightly higher, indicating a possibility of effective of "protein content in grain"–driven selections. There may be a special prospect of selections from hybrid populations with high intra-population variability of the protein content in grain and high protein content (Kf2-16 / Khersonska Bezosta).

The correlation coefficient between the protein content in grain and the "anthesis–ripeness" period length in the breeding accessions showed a weak relationship between these traits. The correlation coefficients ranged -0.281 to 0.413, indicating "protein content in grain"–driven selections are possible in all groups with various lengths of the "anthesis–ripeness" period. The strongest positive correlation between these traits was observed in specimens of the Kf4-16 / Ovidii hybrid combination (r = 0.413); however, it should be noted that the specimens of this combination were characterized by the greatest variability range of the protein content in grain (11.6–15.5%) and the highest coefficient of variation (8.46%).

The correlation between the protein content in grain and the grain yield of the breeding accessions was also weak (from -0.358 to 0.333). The Kf5-16 / Ledia hybrid combination with the correlation coefficient between these traits of 0.609 became an exception. Nevertheless, it is noteworthy that this hybrid combination had the lowest protein content in grain, both the mean value (12.10%) and the range (11.3–14.1%). Such correlation between these traits indicates a possibility of concurrent selection for grain productivity and quality.

More detailed analysis of the correlation-regression relationships between the "anthesisripeness" interphase period and the protein content in grain in the general sample of the breeding accessions showed that there was a curvilinear dependence between these traits (Fig. 1). It was revealed that the maximum protein content in grain was mainly recorded in the breeding accessions with the "anthesis-ripeness" period length of 46–50 days. Exceedance over this limit led to a decrease in the protein content in grain in the breeding accessions.

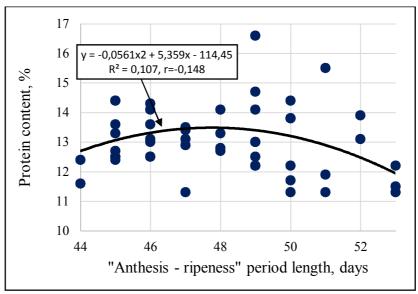


Figure 1. Correlation-regression model of the dependence between the "anthesis - ripeness" interphase period and protein content in grain in the general sample of the breeding accessions

The correlation-regression model of the relationship between the yield and protein content in grain in the general sample of the breeding accessions also showed that the curvilinear dependence between these traits was typical (Fig. 2). The curvilinear dependence significantly weakens the rectilinear correlations between these traits to minimum values, which was noted during analysis of the data in Table 1.

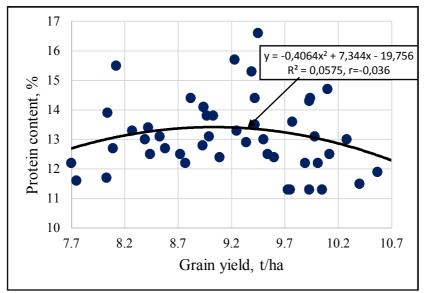


Figure 2. Correlation-regression model of the dependence between the yield and protein content in grain in the general sample of the breeding accessions

We analyzed the correlation-regression models of the dependence between the "anthesisripeness" interphase period and the protein content in grain in the breeding accessions selected from some hybrid populations. Thus, in the lines from the Kf2-16 / Ovidii hybrid population, an almost rectilinear relationship between these traits was established, albeit at a low level of significance (Fig. 3). The correlation coefficient was 0.263; however, there were no gradations in the "anthesis - ripeness" period related to the maximum protein content in grain in the families from this hybrid population, so it is possible to select genotypes with high protein content in grain in this hybrid population with various lengths of reproductive vegetation period.

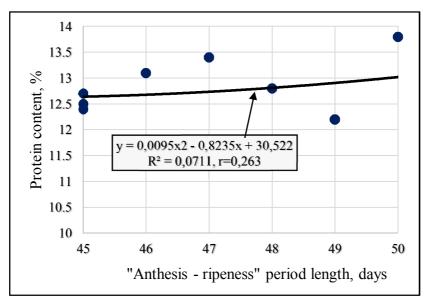


Figure 3. Correlation-regression model of the dependence between the "anthesis - ripeness" interphase period and protein content in the breeding accessions selected from the Kf2-16 / Ovidii hybrid population

The correlation-regression model of the dependence between the yield and protein content in grain in the breeding accessions selected from the Kf2-16 / Ovidii hybrid population showed that an increase in the grain yield led to a decrease in the protein content in grain, which worsens predictions of concurrent selection based on these two indicators (Fig. 4).

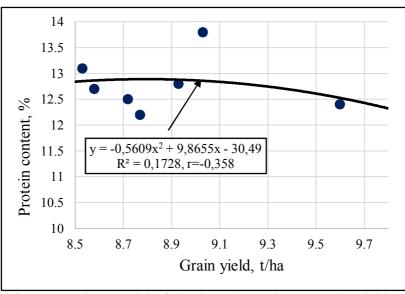


Figure 4. Correlation-regression model of the dependence between the yield and protein content in the breeding accessions selected from the Kf2-16 / Ovidii hybrid population

High performance (yield over 9.5 t/ha) is limited to the protein content in grain of 12–12.5%, and this is a considerable obstacle to selections for performance and grain quality in this population.

In the lines selected from the Kf4-16 / Ovidii hybrid population, the dependence between the length of the "anthesis-ripeness" period and the protein content in grain is mostly rectilinear (Fig. 5). It is possible to carry out effective selections of high-protein genotypes in groups with extended

lengths of the "anthesis–ripeness" period (50–52 days). This duration of the reproductive period of vegetation can ensure the protein content in grain of selected genotypes within 13.5–15.0%.

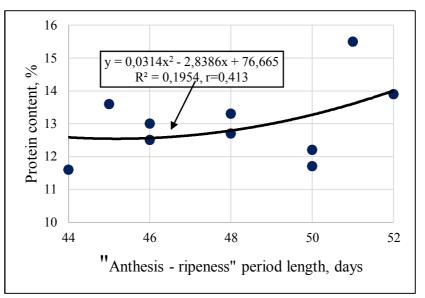


Figure 5. Correlation-regression model of the dependence between the "anthesis - ripeness" interphase period and protein content in the breeding accessions selected from the Kf4-16 / Ovidii hybrid population

The correlation-regression model of the dependence between the yield and protein content in grain in the breeding accessions selected from the Kf4-16 / Ovidii hybrid population also showed a mostly rectilinear relationship between these indicators (Fig. 6).

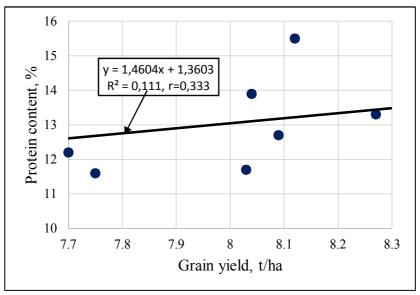


Figure 6. Correlation-regression model of the dependence between the yield and protein content in the breeding accessions selected from the Kf4-16 / Ovidii hybrid population

Such dependence provides encouraging predictions about concurrent selection based on these two traits. However, the yield capacity of the breeding accessions from this hybrid population is quite limited (8.2–8.5 t/ha), which is a significant problem of selections of promising new varieties from hybrid populations with such pedigree.

In the majority of the breeding accessions selected from different hybrid populations, the relationship between the protein content in grain and the "anthesis-ripeness" interphase period length was characterized by clear curvature, with certain maximum values of the protein content in grain (Fig. 7). The maximum protein content in grain was associated with certain values of the "anthesis - ripeness" period length. Thus, the maximum content of protein in grain in the breeding

accessions from the Kf2-16 / Khersonska Bezosta hybrid combination was recorded in the families with the "anthesis-ripeness" period of 47–49 days, and both reduction and extension of this period led to a decrease in the protein content in grain.

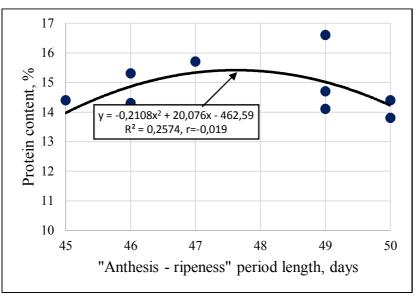


Figure 7. Correlation-regression model of the dependence between the "anthesis–ripeness" interphase period and protein content in the breeding accessions selected from the Kf2-16 / Khersonska Bezosta hybrid population

A similar pattern was observed for the protein content in grain of high-yielding representatives of the Kf2-16 / Khersonska Bezosta hybrid combination (Fig. 8).

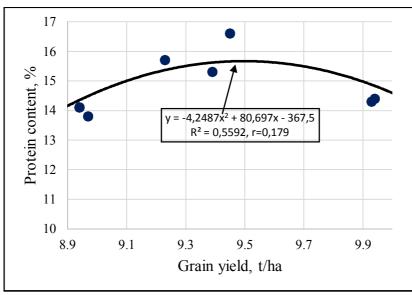


Figure 8. Correlation-regression model of the dependence between the yield and protein content in the breeding accessions selected from the Kf2-16 / Khersonska Bezosta hybrid population

Although the linear correlation was weakly positive (r = 0.179), as the grain yield approached the mark of 10 t/ha, the protein content in grain decreased. This hybrid combination was the most promising for selections to increase the performance and protein content in grain, although this combination was not free of "the higher grain yield, the lower protein content" tendency.

In general, it can be concluded that a parallel increase in the grain yield and protein content in grain upon individual selections from certain hybrid populations is not impossible; however, in most combinations, strong positive correlations between theses parameters are associated with lower grain yields in basic hybrid populations or with lower protein contents. The breeding potential of such combinations is low, if we only consider the yield capacity and protein content in grain.

Comprehensive evaluation of the promising accessions allowed for identification of lines combining valuable economic characteristics (Table 2).

The Kf2-16 / Khersonska Bezosta and Koshova / Kf2-16 hybrid populations turned out to be the most promising ones. By selections from these combinations, we managed to select lines that combine a high grain yield and protein content in grain. The grain yield of breeding accessions 18-681, 18-694, 18-704 (hybrid combination Kf2-16 / Khersonska Bezosta) amounted to 9.39...10.10 t/ha and the protein content in grain – to 14.7–16.6%. The accessions from the Koshova / Kf2-16 hybrid population yielded slightly less (9.40–9.77 t/ha) and contained less protein in grain (13.5–14.4%).

Table 2

terms of protein content in grain and other characteristics (2019-2021)											
Pedigree					Parameters						
of the	Line	Protein	Plant height		"Anthesis -	Spike length		Grain			
hybrid population	designa tion	content in grain, %	cm	CV, %	 ripeness" period length, day 	cm	CV, %	yield, t/ha			
Kf2-16 /	18-607	13.8	113.0	2.34	50	8.67	6.66	9.03			
Ovidii	18-626	13.4	103.3	2.96	47	8.09	8.35	8.42			
	18-629	13.1	93.6	3.43	46	8.33	6.93	8.53			
Kf4-16 /	18-644	13.6	97.0	1.11	45	9.67	5.97	7.67			
Ovidii	18-649	13.9	97.2	2.02	52	7.67	7.50	8.04			
	18-658	15.5	110.3	2.28	51	9.15	7.36	8.12			
Kf2-16 /	18-681	14.7	116.0	2.20	49	9.38	12.40	10.10			
Khersonsk	18-694	15.3	99.3	2.10	46	8.72	6.48	9.39			
a Bezosta	18-704	16.6	98.0	1.02	49	10.36	6.17	9.45			
Koshova /	18-706	13.6	101.3	1.51	46	10.60	7.11	9.77			
Kf2-16	18-720	13.5	106.5	2.37	47	10.48	6.28	9.42			
	18-728	14.4	96.1	3.76	45	10.39	7.06	9.40			
Kf5-16 /	18-752	13.0	109.2	0.92	49	11.13	6.93	10.28			
Ledia	18-752	14.1	82.4	4.91	48	10.14	14.29	10.80			
	18-776	13.1	102.6	3.53	52	11.01	6.93	9.98			
Khersonsk a Bezosta (check		13.8	95.3	-	47	9.24	-	8.47			
variety) LSD ₀₅								0.26			

Characteristics of the winter bread wheat breeding accessions, which had been originated from Western European specimens and were the best accessions in the control nursery in terms of protein content in grain and other characteristics (2019-2021)

The highest grain yield was recorded in specimens from the Kf5-16 / Ledia hybrid population (9.98–10.80 t/ha). However, high yields of the lines from this combination were not associated with high protein contents (the protein content in grain was 13.0-14.1%). This indicates that, after all, there is a problem of breeding combination of high grain productivity and protein content in grain, which was pointed out by researchers in publications [9–11].

A concurrent increase in the yield and protein content in grain, as mentioned in some publications [13, 14, 15], was also possible in our studies upon traditional "phenotypic selections"; however, such concurrent increase in these traits is more intrinsic to hybrid heterogeneous populations with low protein contents in grain and low yield capacity (Kf4-16 / Ovidii) or with low values of one of these traits (low protein content in grain in the Kf5-16 / Ledia representatives).

The "anthesis-ripeness" period of the best specimens lasted 45–52 days, and each original hybrid combination had its own optimum, which was associated with a high yield and protein content in grain. High values of the yield and protein content in grain were observed in the lines from the Kf2-16 / Khersonska Bezosta combination with the "anthesis-ripeness" period length of 46–49 days and in the lines from the Kf2-16 / Ovidii and Kf4-16 / Ovidii combinations with this period of 50...51 days. So, we can state that extension of the "anthesis-ripeness" period slightly increased the grain yields of the breeding accessions from some hybrid populations; however, analogous effect on the protein content in grain was insignificant.

Based on the above, when selecting for protein content in grain and grain yield, one should take into account possible correlation-regression models between these parameters and the "anthesis - ripeness" interphase period length. Under irrigation conditions, it was possible to use heterogeneous hybrid populations, in which correlations between the protein content in grain and the "anthesis - ripeness" reproductive interphase period length (Kf4-16 / Ovidii) or between the protein content in grain and yield (Kf5-16 / Ledia) were noted.

Conclusions. The expression of the "protein content in grain" trait in the breeding accessions selected from hybrid populations, which had been originated from Western European ecotypes of winter bread wheat, was analyzed; the correlation-regression models of the relationships between the protein content in grain, the grain yield and the "anthesis–ripeness" period were constructed.

A concurrent increase in the grain yield and protein content in grain through traditional selections is possible; however, such parallel enhancement of these traits is more suitable for heterogeneous hybrid populations with low protein contents grain and yields, or with low values of one of these traits (low protein content).

For each hybrid population from parents contrasting in vegetation length, it is necessary to develop a specific plan of selections with due account for intra-population correlation-regression models of yield capacity, protein content in grain and "anthesis–ripeness" period length.

The "anthesis–ripeness" period in the best accessions lasted 45–52 days, and each original hybrid combination had its own optimum, which was associated with a high yield and protein content in grain. Extension of the "anthesis–ripeness" period slightly increased the grain yields of the breeding accessions from some hybrid populations; however, analogous effect on the protein content in grain was insignificant.

Список використаних джерел

- 1. Колючий В.Т. Селекція пшениці озимої на якість зерна в Лісостепу України. *Селекція і насінництво*. 2011. Вип. 100. С. 160–171. DOI: <u>https://doi.org/10.30835/2413-7510.2011.66545</u>.
- Hellemans T., Landschoot S., Dewitte K. et al. Impact of crop husbandry practices and environmental conditions on wheat composition and quality: A review. *Journal of Agricultural and Food Chemistry*. 2018. V. 66, Iss. 11. P. 2491–2509. DOI: https://doi.org/10.1021/acs.jafc.7b05450.
- 3. Лукьяненко П.П. Выведение новых сортов озимой пшеницы интенсивного типа. Вестник сельскохозяйственной науки. 1970. № 4. С. 54–61.
- 4. Jurečka D. Přehled odrůd obilnin. Brno, 1998. 150 p.
- 5. Орлюк А.П. Адаптивний і продуктивний потенціали пшениці: монографія. Херсон: Наддніпрянська правда. 2002. 272 с.
- Michel S., Ametz C., Gungor H. et al. Genomic selection across multiple breeding cycles in applied bread wheat breeding. *Theor Appl Genet.* 2016. V. 129. P. 1179–1189. DOI: <u>https://doi.org/10.1007/s00122-016-2694-2</u>.
- Marulanda J.J., Mi X., Melchinger A.E. et al. Optimum breeding strategies using genomic selection for hybrid breeding in wheat, maize, rye, barley, rice and triticale. *Theor Appl Genet*. 2016. V. 129. P. 1901–1913. <u>https://doi.org/10.1007/s00122-016-2748-5</u>
- 8. Akdemir D., Jannink J. L., Isidro-Sánchez J. Locally epistatic models for genome-wide prediction and association by importance sampling. *Genet Sel Evol.* 2017. V. 49. P. 1–14.

DOI: <u>https://doi.org/10.1186/s12711-017-0348-8</u>.

- 9. Simmonds N.W. The relation between yield and protein in cereal grain. *J Sci Food Agric*. 1995. V. 67. P. 309–315. DOI: <u>https://doi.org/10.1002/jsfa.2740670306</u>.
- Gabriel D., Pftzner C., Haase N. et al. New strategies for a reliable assessment of baking quality of wheat-rethinking thecurrent indicator protein content. *J Cereal Sci.* 2017. V. 77. P. 126–134. DOI: <u>https://doi.org/10.1016/j.jcs.2017.08.002</u>.
- 11. DePauw R.M., Knox R.E., Clarke F.R. et al. Shifting undesirable correlations. *Euphytica*. 2007. V. 157. P. 409–415. DOI: <u>https://doi.org/10.1007/s10681-007-9379-5</u>.
- Ly D., Chenu K., Gaufreteau A. et al. Nitrogen nutrition index predicted by a crop model improves the genomic prediction of grain number for a bread wheat core collection. *F Crop Res.* 2017. V. 214. P. 331–340. DOI: <u>https://doi.org/10.1016/j.fcr.2017.09.024</u>
- Monaghan J. M., Snape J. W., Chojecki J. S., Kettlewell P. S. The use of grain protein deviation for identifying with cultivars with high grain protein concentration and yield. *Euphytica*. 2001. V. 122. P. 309–317. DOI: <u>https://doi.org/10.1023/a:1012961703208</u>.
- Hänsel H. Yield potential of barley corrected for disease infection by regression residuals. *Plant Breed.* 2001. V. 120. P. 223–226. DOI: <u>https://doi.org/10.1046/j.1439-0523.2001.00596.x</u>.
- Arief V.N., Lush D., Niu N. et al. Genetic gain in yield and protein over two cycles of a wheat recurrent selection program. *Breed Sci.* 2010. V. 60. P. 181–186. DOI: <u>https://doi.org/10.1270/jsbbs.60.181</u>
- 16. Sallam A.H., Smith K.P. Genomic selection performs similarly to phenotypic selection in barley. *Crop Sci.* 2016. V. 56. P. 1–11.DOI: <u>https://doi.org/10.2135/cropsci2015.09.0557</u>.
- 17. Belamkar V., Guttieri M.J., Hussain W. et al Genomic selection in preliminary yield trials in a winter wheat breeding program. *G3 Genes Genomes Genet*. 2018. V. 8. P. 2735–2747. DOI: <u>https://doi.org/10.1534/g3.118.200415</u>.
- Fiedler J.D., Salsman E., Liu Y. et al. Genome-wide association and prediction of grain and semolina quality traits in durum wheat breeding populations. *Plant Genome*. 2017. V. 10. P. 1–10. DOI: <u>https://doi.org/10.3835/plantgenome2017.05.0038</u>.
- Hayes B.J., Panozzo J., Walker C.K. et al. Accelerating wheat breeding for end-use quality with multi-trait genomic predictions incorporating near infrared and nuclear magnetic resonancederived phenotypes. *Theor Appl Genet*. 2017. V. 130. P. 2505–2519. DOI: https://doi.org/10.1007/s00122-017-2972-7.
- 20. Laidig F., Piepho H.-P., Rentel D. et al. Breeding progress, environmental variation and correlation of winter wheat yield and quality traits in German ofcial variety trials and on-farm during 1983–2014. *Theor Appl Genet*. 2017. V. 130. P. 223–245. DOI: <u>https://doi.org/10.1007/s00122-016-2810-3</u>.
- Thorwarth P., Piepho H.P., Zhao Y. et al. Higher grain yield and higher grain protein deviation underline the potential of hybrid wheat for a sustainable agriculture. *Plant Breed*. 2018. V. 137. P. 326–337. DOI: <u>https://doi.org/10.1111/pbr.12588</u>
- 22. Oury F.X., Godin C. Yield and grain protein concentration in bread wheat: How to use the negative relationship between the two characters to identify favourable genotypes? *Euphytica*. 2007. V. 157. P. 45–57. DOI: <u>https://doi.org/10.1007/s10681-007-9395-5/</u>
- 23. Жупина А.Ю., Базалій Г.Г., Усик Л.О. та ін. Успадкування висоти рослин гібридами пшениці озимої різного еколого-генетичного походження в умовах зрошення. *Аграрні інновації*. 2021. № 10. С. 122 –129. DOI: <u>https://doi.org/10.32848/agrar.innov.2021.10.19</u>.
- 24. Методика польових і лабораторних досліджень на зрошуваних землях / Вожегова Р. А. та ін. Херсон: Грінь Д. С., 2014. 286 с.
- 25. Базалій В.В. Принципи адаптивної селекції озимої пшениці в зоні Південного Степу: монографія. Херсон: Айлант. 2004. 244 с.

References

- 1. Koliuchyi VT. Winter wheat breeding for grain quality in the Forest-Steppe of Ukraine. Sel. Nasinn. 2011; 100: 160–171. DOI: <u>https://doi.org/10.30835/2413-7510.2011.66545</u>.
- 2. Hellemans T, Landschoot S, Dewitte K et al. Impact of crop husbandry practices and environmental conditions on wheat composition and quality: A review. Journal of Agricultural

and Food Chemistry. 2018; 66(11): 2491–2509. DOI: https://doi.org/10.1021/acs.jafc.7b05450

- 3. Lukyanenko PP. Breeding of new intensive winter wheat varieties. Vestnyk Selskokhozyaystvennoy Nauki. 1970; 4: 54–61.
- 4. Jurečka D. Overview of cereal varieties. Brno. 1998. 150 p.
- 5. Orliuk AP. Adaptive and productive potentials of wheat. Kherson: Naddniprianska Pravda. 2002. 272 p.
- Michel S, Ametz,C, Gungor H. et al. Genomic selection across multiple breeding cycles in applied bread wheat breeding. Theor Appl Genet. 2016; 129: 1179–1189. DOI: <u>https://doi.org/10.1007/s00122-016-2694-2</u>.
- Marulanda JJ, Mi X, Melchinger AE et al. Optimum breeding strategies using genomic selection for hybrid breeding in wheat, maize, rye, barley, rice and triticale. Theor Appl Genet. 2016; 129: 1901–1913. DOI: <u>https://doi.org/10.1007/s00122-016-2748-5</u>
- Akdemir D, Jannink JL, Isidro-Sánchez J. Locally epistatic models for genome-wide prediction and association by importance sampling. Genet Sel Evol. 2017; 49: 1–14. DOI: <u>https://doi.org/10.1186/s12711-017-0348-8</u>.
- 9. Simmonds NW. The relation between yield and protein in cereal grain. J Sci Food Agric. 1995; 67: 309–315. DOI: <u>https://doi.org/10.1002/jsfa.2740670306</u>.
- Gabriel D, Pftzner C, Haase N et al. New strategies for a reliable assessment of baking quality of wheat-rethinking thecurrent indicator protein content. J Cereal Sci. 2017; 77: 126–134. DOI: <u>https://doi.org/10.1016/j.jcs.2017.08.002</u>.
- 11. DePauw RM, Knox RE, Clarke FR et al. Shifting undesirable correlations. Euphytica. 2007; 157: 409–415. DOI: <u>https://doi.org/10.1007/s10681-007-9379-5</u>.
- Ly D, Chenu K, Gaufreteau A et al. Nitrogen nutrition index predicted by a crop model improves the genomic prediction of grain number for a bread wheat core collection. F Crop Res. 2017; 214: 331–340. DOI: <u>https://doi.org/10.1016/j.fcr.2017.09.024.</u>
- Monaghan JM, Snape JW, Chojecki JS, Kettlewell PS. The use of grain protein deviation for identifying with cultivars with high grain protein concentration and yield. Euphytica. 2001; 122: 309–317. DOI: <u>https://doi.org/10.1023/a:1012961703208</u>.
- 14. Hänsel H. Yield potential of barley corrected for disease infection by regression residuals. Plant Breed. 2001; 120: 223–226. DOI: <u>https://doi.org/10.1046/j.1439-0523.2001.00596.x</u>.
- 15. Arief VN, Lush D, Niu N et al. Genetic gain in yield and protein over two cycles of a wheat recurrent selection program. Breed Sci. 2010; 60: 181–186. DOI: https://doi.org/10.1270/jsbbs.60.181.
- 16. Sallam AH, Smith KP. Genomic selection performs similarly to phenotypic selection in barley. Crop Sci. 2016; 56: 1–11. DOI: <u>https://doi.org/10.2135/cropsci2015.09.0557</u>.
- 17. Belamkar V, Guttieri MJ, Hussain W et al. Genomic selection in preliminary yield trials in a winter wheat breeding program. G3 Genes Genomes Genet. 2018; 8: 2735–2747. DOI: <u>https://doi.org/10.1534/g3.118.200415</u>.
- Fiedler JD, Salsman E, Liu Y et al. Genome-wide association and prediction of grain and semolina quality traits in durum wheat breeding populations. Plant Genome. 2017; 10: 1–10. DOI: <u>https://doi.org/10.3835/plantgenome2017.05.0038</u>.
- 19. Hayes BJ, Panozzo J, Walker CK et al. Accelerating wheat breeding for end-use quality with multi-trait genomic predictions incorporating near infrared and nuclear magnetic resonancederived phenotypes. Theor Appl Genet. 2017; 130: 2505–2519. DOI: https://doi.org/10.1007/s00122-017-2972-7.
- Laidig F, Piepho H.-P, Rentel D et al. Breeding progress, environmental variation and correlation of winter wheat yield and quality traits in German ofcial variety trials and on-farm during 1983–2014. Theor Appl Genet. 2017; 130: 223–245. DOI: https://doi.org/10.1007/s00122-016-2810-3.
- Thorwarth P, Piepho HP, Zhao Y et al. Higher grain yield and higher grain protein deviation underline the potential of hybrid wheat for a sustainable agriculture. Plant Breed. 2018; 137: 326–337. DOI: <u>https://doi.org/10.1111/pbr.12588.</u>
- 22. Oury FX, Godin C. Yield and grain protein concentration in bread wheat: How to use the negative relationship between the two characters to identify favourable genotypes? Euphytica.2007; 157: 45–57. DOI: <u>https://doi.org/10.1007/s10681-007-9395-5</u>.

- Zhupyna AYu, Bazalii HH, Usyk LO et al.Inheritance of plant height by winter wheat hybrids of different ecological and genetic origins under irrigation conditions. Ahrarni Innovatsii. 2021;10: 122–129. https://doi.org/10.32848/agrar.innov.2021.10.19.
- 24. Vozhehova RA et al. Methods of field and laboratory studies on irrigated lands. Kherson: Hrin D. S. 2014.286 p.
- 25. Bazalii VV. Principles of the adaptive breeding of winter wheat in the Southern Steppe: monograph. Kherson: Ailant. 2004. 244 p.

CORRELATIONS BETWEEN THE PROTEIN CONTENT IN GRAIN WITH ECONOMIC CHARACTERS IN WINTER BREAD WHEAT BREEDING ACCESSIONS OF HYBRID ORIGIN ON IRRIGATION

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- **Purpose and Objectives**. To evaluate the expression of the "protein content in grain" trait in winter bread wheat lines derived from late-ripening accessions of the Western European ecotype; to construct correlation-regression models for the relationships of the protein content in grain with the "anthesis–grain ripeness" interphase period length and grain yield in elite accessions grown in breeding nurseries.
- **Material and Methods.** The field studies were carried out at the Institute of Irrigated Agriculture of NAAS in 2019–2021. Modern winter wheat varieties bred at the Institute, collection specimens of the Western European ecotype, which had been introduced from France (registration numbers Kf1...16), and their hybrids were studied. Individual selections of elite plants from F₂ were brought to the control nursery and evaluated for protein content in grain, yield, "anthesis–ripeness" period and other economic characteristics. Biometric measurements, biochemical analyses, and yield records were conducted by traditional methods. The study methods were field, laboratory, biochemical, breeding-genetic, and statistical. The studies were carried out under irrigation conditions at the pre-irrigation field moisture capacity (FMC) in the 0–50 cm soil layer of 75%.
- **Results and Discussion.** The expression of the "protein content in grain" trait in the breeding accessions selected from hybrid populations, which had been originated from Western European ecotypes of winter bread wheat, was analyzed; the correlation-regression models of the relationships between the protein content in grain, the grain yield and the "anthesis ripeness" period were constructed. The "anthesis–ripeness" period in the best accessions lasted 45–52 days, and each original hybrid combination had its own optimum, which was associated with a high yield and protein content in grain. Extension of the "anthesis–ripeness" period slightly increased the grain yields of the breeding accessions from some hybrid populations; however, analogous effect on the protein content in grain was insignificant.
- **Conclusions.** A concurrent increase in the grain yield and protein content in grain through traditional selections is possible; however, such parallel enhancement of these traits is more suitable for heterogeneous hybrid populations with low protein contents grain and yields, or with low values of one of these traits (low protein content). For each hybrid population from parents contrasting in vegetation length, it is necessary to develop a specific plan of selections with due account for intra-population correlation-regression models of yield capacity, protein content in grain and "anthesis–ripeness" period length.

Key words: varieties, hybrids, wheat, irrigation, breeding, yield, protein content in grain, earliness

КОРЕЛЯЦІЯ ВМІСТУ БІЛКА В ЗЕРНІ З ГОСПОДАРСЬКИМИ ОЗНАКАМИ У СЕЛЕКЦІЙНИХ ЗРАЗКІВ ПШЕНИЦІ М'ЯКОЇ ОЗИМОЇ ГІБРИДНОГО ПОХОДЖЕННЯ ЗА УМОВ ЗРОШЕННЯ

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- Мета та завдання досліджень. Встановити характер прояву ознаки «вміст білка в зерні» у ліній пшениці м'якої озимої, що створені з залученням пізньостиглих зразків західноєвропейського екотипу. Встановити кореляційно-регресійні моделі залежностей вмісту білка в зерні з тривалістю міжфазного періоду «цвітіння–стиглість зерна» та урожайністю зерна у елітних номерів в селекційних розсадниках.
- Матеріал і методи. Польові дослідження проведені в Інституті зрошуваного землеробства НААН у 2019–2021 рр. Об'єктом досліджень були сучасні сорти пшениці озимої селекції Інституту, колекційні зразки західноєвропейського екотипу, що були інтродуковані з Франції (номери реєстрації Кф1...16) та гібриди, створені за їх участі. Індивідуальні добори елітних рослин з F 2 були доведені до контрольного розсадника і оцінені за показниками вміст білка в зерні, урожайності, тривалості періоду «цвітіння– стиглість» та іншими господарськими ознаками. Біометричні виміри, біохімічні аналізи, обліки урожайності проводили за загальновизнаними методиками. Методи досліджень польові, лабораторні біохімічні, селекційно-генетичні, статистичні. Дослідження проводились в умовах зрошення за рівня передполивної вологості грунту в шарі 0–50 см 75% найменшої вологоємності.
- Результати та обговорення. Встановлено характер прояву ознаки «вміст білка в зерні» у селекційних номерів, що дібрані з гібридних популяцій за участі західноєвропейських екотипів пшениці м'якої озимої, кореляційно-регресійні моделі залежності вмісту білка в зерні, урожайності зерна та тривалості періоду «цвітіння–стиглість». Тривалість періоду «цвітіння–стиглість» коливалась у кращих номерів в межах 45–52 доби і в кожній вихідній гібридній комбінації були свої оптимуми, що детермінували високу урожайність та вміст білка в зерні. Подовження тривалості періоду «цвітіння–стиглість» дещо підвищує урожайність зерна у селекційних номерів, що дібрані з окремих гібридних популяцій, проте на білковість зерна такий вплив малозначущий.
- Висновки. Одночасне підвищення урожайності та вміст білка в зерні традиційними доборами можливе, проте таке синхронне підвищення цих ознак більш придатне для гібридних гетерогенних популяцій з заниженими параметрами прояву вмісту білка в зерні та урожайності, або ж за однією з ознак (низький вміст білка в зерні). Для кожної гібридної популяції, що створена за участі контрастних за тривалістю вегетації батьківських компонентів, необхідно розробляти специфічний план доборів з урахуванням внутрішньопопуляційних кореляційно-регресійних моделей урожайності, вмісту білка в зерні та тривалості періоду «цвітіння – стиглість».

Ключові слова: сорти, гібриди, пшениця, зрошення, селекція, урожайність, вміст білка в зерні, скоростиглість