

# Tendencies in baking quality of common wheat varieties realised in Ukraine and their influence on allele frequency of storage protein genes

Zlatska AV, Shovhun OO, Shytikova Yu.V, Korol.V

<sup>1</sup> *Ukrainian Institute for Plant Varieties Examination, 15 Henerala Rodimtseva Str., Kyiv 03041, Ukraine.*

*E-mail: zlatska@hotmail.com, azlatska@sops.gov.ua*

## INTRODUCTION

End-use quality of wheat grains became one of the most important requests for breeders from the industry in many countries over the world, because of consumers needs. In some states the limited factor is amount of grain protein content, in others gluten or starch characteristics. Traditionally since the end of 19<sup>th</sup> and beginning of 20<sup>th</sup> centuries Ukraine was the famous exporter of high quality wheat grains with gluten content up to 35-45%. It was achieved by utilization traditional landraces and old varieties with extensive type of cultivation and low yield (1,2-1,6 tones per hectare) [1]. However at the beginning of 1960's the situation was changed because of introduction of new intensive type of agriculture as well as new intensive type varieties. In this period the average gluten content decreased up to 22-24%, however yield increase by two or three times. Since this period, national genetics and breeding programs in the former Soviet Union have opened in order to study the genetic mechanism, which formed end-use quality of wheat as well as improving these characteristics in common winter wheat [1].

In 1973 only six strong winter wheat varieties were grown in the entire former Soviet Union [2], including four that were developed by Ukrainian breeding institutes: Myronivska 808, Myronivska yubilejna, Odeska 51 and Kooperatorka. Currently in Ukraine in National register of varieties suitable for dissemination in Ukraine there are more than 90 strong varieties [3]. Strong varieties have grain protein content better than 14%, and alveograph-W from 314 up to 480. There are several fillers with 12-13% of grain protein content, less than 25% gluten content and 202-219 for alveograph-W. Among current varieties, 8% have intermediate bread-making characteristics and are considered valuable.

The aim of present studies was to analyze the allele frequency of the genetic system which has the main influence on bread-making quality in common wheat: high molecular weight glutenins (HMG), gliadins and puroindoline genes *PinA* and *PinB*. The study includes the breeding history in Ukraine up to the present and projects the possibilities of future breeding successes for improvement of the quality characteristics in wheat varieties in particular this agro-climatic region.

## MATERIAL AND METHODS

*Materials* of present investigation was more than 200 common winter wheat varieties planted in the Ukraine since the end of 19<sup>th</sup> century.

*Methods.* High molecular weight glutenins have been separated using the SDS-PAGE electrophoresis method [4]. Allele identification was performed according to catalogues developed by Payne and Lawrence [5]. For identification of allele *al* with over expressed unit 7<sup>oc</sup> the PCR based approach has been applied with specific primers to the MAR section the gene [6]. Gliadins have been studied in A-PAGE according to procedure of Metakovsky [7]. Alleles of puroindoline genes were identified using PCR methods with specific primers for particular known mutations as described Pogna et al. [8].

## RESULTS AND DISCUSSION

*Puroindolines.* Investigation of alleles of puroindoline genes allowed us to make conclusions about their highly conserved nature. The cultivars had the allele *PinB1b* that is the marker of particular mutation of this gene related to formation of hard grains due to disturbance of links between starch granules and cell membrane. Only several of tested varieties had allele *PinB1a* and the most of them had Western European common wheat varieties in pedigree.

In the *PinA1* locus the main allele found was *PinA1a* with only few cultivars carrying *PinB1a* with the allele *PinA1b*. Because these were identified in old landraces planted in the Ukraine at the end of 19<sup>th</sup> and beginning of 20<sup>th</sup> centuries we conclude that those mutations appeared in our territory many years ago and were spontaneously selected by peasants.

*High molecular weight glutenins.* Analysis of alleles of three loci and HMG in tested varieties also showed very low levels of polymorphism. At the *Glu-A1* locus mainly alleles *a* and *b* have been found out. In the *Glu-B1* locus there were identified mainly *c* and *b* alleles. Other alleles such as *d*, *e* occurred very rarely and in appeared in which had a gene pool derived from foreign varieties. Most of these varieties were short-lived (one or two years) because they appeared to be not very suitable for further utilization. In *Glu-D1* locus mainly (96%) allele *d* was detected. It was important to note that a decrease in the number of lines with of allele *b* of *Glu-B1* locus in the line strong wheats -valuable wheats – fillers

accompanied an increase in the frequency of allele *c*. This suggests that for this particular wheat population the locus defined by the allele *b* has an important influence on bread-making quality performance. The wheats with allele formulas *bcd* as well as *acd* appeared in all quality groups suggesting these combinations of alleles despite they influence end-use quality, however do not play the key role. The high level of conservatism of loci in tested population can be explained by particular benefits of wheats with such allele compositions in this particular environment, in which those wheats perform their end-use quality much better than wheats with other allele compositions.

The same phenomenon of conservatism of particular allele (*GluD1f*) in particular environment as a result of neutral selection for winter habit and artificial selection for flour hardness has been found out in Japanese populations of wheats, where the *GluD1f* allele occurs much more frequently (Nakamura and Fujimaki [9]).

Screening of our populations of wheats has been carried out for allele *al* ( $7^{oe} + 8$ ) of *Glu-B1* locus. This allele was first identified in the Canadian extra strong wheat Glenlea [10] and has been described in USA and Australian varieties [11,12] and old Hungarian landraces [13]. It is known as well that this particular mutation occurred at the old Ukrainian variety Galychanka and moved with emigrants at the end of 19<sup>th</sup> and beginning of 20<sup>th</sup> centuries to spread all over the world [14]. Our results indicated that this allele did not occur in wheat varieties plants released in Ukraine since 1920 up to 2000. However in several modern varieties and some lines it has appeared again (variety Selyanka Fig. 1).

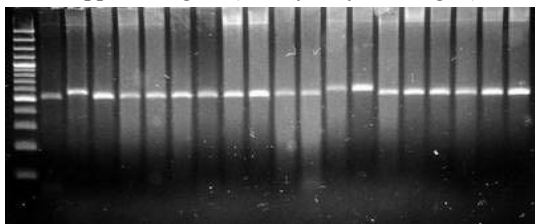


Fig. 1. 1 – Marker 100 bp, 2 - Chinese spring, 3 – Glenlea, 4 – Poshana, 5,6 – Remeslivna, 7,8 – Zolotokolosa, 9,10 – Strumok, 11,12 – Stanychna, 13,14 – Selyanka, 15,16 – Elegia, 17,18 – Suputnytsya, 19,20 – Renan.

Interestingly appearance of this allele in variety cannot explain its bread-making characteristics, because we did not found out any significant differences between group of current Ukrainian wheats that have this allele and group of strong wheat varieties with good end-use characteristic and varieties without this gene. Only one exception was revealed the variety Panna with 16% of grain protein content, 34% of gluten content and 580 alveograph-W. However this variety had mainly lower yield than those other one with good characteristics of bread-making quality.

*Gliadins*. Alleles of gliadins appeared to be more flexible to the changes in breeding strategies if compare to puroindolines and glutenin loci. It was found out that wheat varieties at the beginning of 20<sup>th</sup> century had different alleles in *Gli-A1* locus compared to wheats of the 1960's and 1970's and current. Wheats from the beginning of the 20<sup>th</sup> century mainly had alleles *o* and *m* as well as one allele that was not be mentioned in catalogue of Metakovsky [7]. Currently such alleles, with exception of allele *o*, are not possible to find out in realised wheat varieties. Varieties with allele *o* mainly are fillers with generally poor quality. Since the 1960's and 1970's the dominant allele has become allele *b* of locus *Gli-A1*. Up to the end of 20<sup>th</sup> century it was in many cases only one allele in population of strong wheat varieties released in Ukraine. Since beginning of the 20<sup>th</sup> century, as a result of the introduction a new gene pool from world collections, new and rare alleles appeared in population of strong wheat varieties. However these varieties had a limited period of release compared to those with allele *b* in *Gli-A1* locus. It was observed that within wheat quality groups the gradation from strong wheat – valuable to filler correlates with an increased frequency of this allele and increasing of the frequency of allele *o* and others which are normally only rarely detected.

Several years ago populations of winter wheats in Ukraine appeared with the 1A/1R translocation with a gliadin allele specific for this translocation, which has not been mentioned in catalogue of Metakovsky [7]. This translocation does not decrease the end-use quality of wheat varieties when compare to 1B/1R translocation.

In locus *Gli-B1* we observed a situation which is differed from that observed during the study of *Glu-B1* alleles of our tested varieties when there were several alleles which quantity was different in groups of wheats with different quality characteristics. Since the end of 19<sup>th</sup> century and up to now, the dominated allele of this locus is *b*. During all the history of breeding there was several other alleles that appeared in the population of wheat varieties. Those alleles had both positive and negative influence on bread-making quality however their utilization was not so long. Negative selection was performed to eliminate the alleles with negative influence, however it was not so clear why new allele with positive influence did not increase their frequency in varietal population. Long term work (15 years) with artificial populations produced by mixture of varieties and near isogenic lines clearly revealed the negative nature selection against some of those new alleles with positive influence on bread-making quality [15]. Recently in populations of strong wheats in Ukraine a new allele *c* of *Gli-B1* locus with very strong positive influence on bread-making quality has been detected. In the gradation of quality groups of wheat: strong wheat – valuable – filler, there was observed a decrease in the frequency allele *Gli-B1 b* and increasing frequency of allele *l* and others which are normally rarely observed.

In locus *Gli-D1* also showed the phenomenon of domination of particular alleles during the whole breeding history of wheat. This occurred mainly in population of varieties released in Ukraine in the last hundred years with reference to alleles *j*, *g* and *b*. From time to time populations of varieties realised in Ukraine appeared to carry other alleles in that locus. They mainly were introduced from genetic sources of other regions in the world otherwise which is much more rarely by spontaneous mutation. The frequency of the alleles depended on the different groups of wheat, as defined by quality, but were generally shared among varieties with almost the same characteristics of end-use quality.

Alleles found in three loci of *Gli-2* were more polymorphic, did not have any significant links with bread-making quality in our population of varieties.

The results of our investigations clearly showed high level of conservatism in alleles of three main genetic systems which have the most powerful influence on bread-making quality in populations of common winter wheat varieties grown in the Eastern European region. Despite of the changing in breeding programs during the century and differences in end use quality, which very often led to involving the germplasm of other region and of course with other allele composition it was very rare observed the changing in allele composition of genes *Gli-1*, *Gli-2*, *Glu-1*, *PinA* and *PinB* and quantity of their alleles in population of strong wheat varieties in particular region. On the other hand investigation of our varieties showed that it is impossible to explain the end-use characteristics of those varieties only by allele composition of those three genetic systems. So, there are other genetic systems which all together form those characteristics of bread wheat which we named end-use quality. Another point is that alleles *Gli-1*, *Gli-2*, *Glu-1*, *PinA* and *PinB* which perform well in one agro-climatic environment may not always be useful in other environments because of negative natural selection effects. However the identification of genes which perform well in all environments, such as *Glu-D1d*, *Glu-B1a1* etc., suggests that such genetic systems with universal performance have a decreases linkage with surrounding loci that have negative interactions to new environmental conditions.

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