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## **PHENOTYPICAL AND GENETIC EVALUATION OF SOFT WHEAT FOR GRAIN WEIGHT**

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Soft wheat (*Triticum aestivum* L.) is one of the most important food crops, providing a significant proportion of the calories and protein consumed by humans. Grain yield of wheat depends to a large extent on the architecture of the plant, in particular on the weight of 1000 seeds, which, along with the main elements of productivity, ultimately determine the yield potential [1].

Grain weight per spike plays a significant role in yield formation, because it directly affects harvest index. Grain weight per plant directly reflects the efficient use of nutrients and their translocation from vegetative into generative parts of a plant [2].

The Serbian scientist V. Kobilisky, investigating the correlation between productivity elements of wheat yield, pointed out that there was a highly significant positive correlation between grain yield and grain weight per spike.

Grain weight can be influenced by various agrotechnical measures, as well as growth and development factors during the filling period, especially if there is a genetic base. The decisive influence on the mass of 1000 grains of soft wheat is provided by the conditions of moisture supply and mineral nutrition during the wax ripeness period [3].

So, there is a genetic difference between varieties, and it is important to find the carriers of this genetic information associated with grain weight when creating a new source material [4].

Of all the yield components, grain weight is the most stable and heritable trait, so it is an important breeding target for genetically improving wheat yield [5].

This is the reason for the popularity of studies of the grain weight factor. One of the authors who studied the effect of grain weight on wheat yield is M.S. Savitsky, Doctor of Agricultural Sciences, professor, who, while studying grain weight, revealed that a long vegetation period in wheat varieties in the flowering-wax ripeness phases affects the accumulation of more nutrients in grains, thereby increasing their weight per 1000 seeds [6].

The productivity of wheat in Northern Kazakhstan in conditions of lack of

moisture remains within 10-12 c/ha, therefore, work in the direction of increasing the elements of productivity is relevant.

The purpose of this research was to study the collection and hybrid material, as well as the selection of promising genotypes by means of the weight of 1000 grains and genetic screening using the marker *Triticum aestivum* isolate 3A serine carboxypeptidase-like 33 (GS5), linked to the grain weight [7].

The research was carried out in 2022 in the dry steppe zone of Northern Kazakhstan.

The dry steppe zone of Northern Kazakhstan is characterized by a sharply continental climate. According to average long-term data, precipitation falls within the range of 280-300 mm per year. The frequency of drought is 20%, i.e. drought has a probability of occurring once every 5 years. The recurrence of a severe drought, when the yield is reduced by 50% or more, is 2%, i.e. has a probability of occurring once every 50 years. In the arid dry steppe zone, both spring and summer droughts can occur. At the same time, in recent years, there has been a negative trend associated with drought, i.e. drought manifestations are increasing every year [8].

During the study, 124 collection specimens and 64 hybrid specimens were studied.

The results of structural analysis made it possible in the field to identify the best genotypes on the basis of productivity and grain weight.

The weight of 1000 grains in the collection ranged from 28,1 g to 47,4 g, among hybrids varied from 27,85 g to 42,0 g, while standard samples showed the following results on average for nursery: Astana (early ripe variety) -32.4 g; Akmola 2 (mid-season variety) – 36,85 g.; Shortandinskaya 95 improved (medium-late variety) – 42,6 g.

The phenotype of the plant may vary from year to year, as it is associated with the place of growth and weather conditions, especially in the conditions of the sharply continental arid climate of Northern Kazakhstan. Based on this, it is important to carry out the selection by an integrated approach to studying the problem.

Based on the results of a study by domestic and foreign scientists, the main genes linked to grain weight of wheat have been identified, among the most effective is the *TaGW* (*Triticum aestivum* Grain Weight) gene. The *TaGW* gene group determines the coarseness of wheat and increases yield. *TaGW2-A1*, located on chromosome 6A, encodes RING-type E3 ubiquitin ligase, is responsible for the mass of 1000 grains and a lower content of IAA (the main natural auxin) [9].

In particular, the *TaTGW-7A* gene (*TaTGW-7Ab*, *TaTGW-6*) located on the 7A chromosome leads to an increase in the mass of 1000 grains and the length of the grain, encoding IAA-glucose hydrolase. *TaGW8B1* is positively associated with grain size in soft wheat. The *TaGW8-B1a* gene does not have a 276 b.p. InDel in the first intron, while the *TaGW8-B1b* gene has a 276 b.p. InDel. Carriers of the *TaGW8-B1a* gene have a significantly greater width and length of the nucleus, and a greater mass of 1000 grains. [10].

In our studies, collection samples and hybrid material were screened for the

*TaGW8* gene and a positive result was obtained on wheat samples.

DNA was isolated from collection and hybrid samples using the CTAB method [11].

The concentration was determined on *NanoDrop 2000* (Thermo fisher scientific, USA). Amplification of marker genes was carried out in a final reaction volume of 15 µl containing: 15 mMSe buffer, 2 mM dNTP, 50 mMgCl<sub>2</sub>, 10 pmol forward and reverse primers, 1U TaqDNA polymerase, DNA at a concentration of 20 ng/µl. PCR was performed under the following thermal cycling conditions with differences in annealing temperatures: 95°C for 5 min, 95°C for 30 sec, 60°C for 30 sec, 72°C for 40 sec. and final elongation 5 min. at 72°C. Separation of the amplification products was carried out on a 1% agarose gel with the addition of ethidium bromide. The results obtained were documented using the *GelDoc gel documentation system* (VilberLourmat, France) [12].

Using the primer (TaGW8-P2~TaGW8-P7) developed for the *TaGW8B1* gene, samples, that did not have an insert in the first intron 276 b.p. long, were picked out: varieties XN 04, XN 08, XN 10 and Wyalkatchem, the mass of which in the field varied from 40 g to 42,4 g [9].

At the same time, hereditary information on the *TaGW8-B1a* gene was transferred to the hybrid XN 04 x Aktyubinka from the maternal form of the XN 04 variety of chinese selection, the weight of 1000 seeds of the hybrid in the field in 2022 was 40,6 g; to the hybrid XN 10 x Karagandinskaya 22, the hereditary information for the *TaGW8-B1a* gene was transferred from the maternal form of the XN 10 variety, the weight of 1000 seeds of the hybrid in the field in 2022 was 41,2 g.

As a result of phenotypical and genetic selection in terms of grain weight, varieties XN 04, XN 08, XN 10 (China) and Wyalkatchem (Australia) can be recommended as a promising source material.

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