

MARKER-ASSISTED SELECTION AS A PERSPECTIVE APPROACH FOR THE ESTIMATION OF WINTER WHEAT BREEDING MATERIAL

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In the new European platform "Plants for the Future" until 2025 in the field of genomics and biotechnology of plants, one of the priorities is to increase the efficiency of breeding. A promising way to solve this problem is a selection using markers. The term "Marker-Assisted Selection" was first used in literature in 1986. Numerous MAS strategies have been developed, including the use of marker backcrossing with genetic backcross selection and enrichment of favorable alleles in early generations, selection for quantitative traits using QTL markers [1].

Marker-assisted selection, now widely use to provide quick selection at next genes: *Rht* (reduced height genes); *Ppd* (photoperiod sensitivity genes); *Vrn* (vernalization response genes); *Lr* (leaf rust resistance); *Sr* (stem rust resistance); *Yr* (yellow (stripe) rust resistance genes); *Pch* (eyespot resistance genes); *Wx* (waxy proteins genes); *Su1* (chlorotoluron resistance genes); *Sbm* (soil-borne cereal mosaic virus resistance genes); *Sm* (resistance to orange wheat blossom midge) and others.

Poltava Breeding Program have been started in 1970's; from that time have been created 28 winter wheat varieties and numerous of breeding lines. For few last years, breeding material has been estimated as by agronomic parameters, yield, quality and as by molecular markers [2].

The genetic diversity of local breeding program (Poltava Research Plant Breeding Centre) was screened using 10 SSR markers, covering all the three genome and at least 9 chromosomes [3]. It helps to highlight genetic differences between all accessions and between the lines resulting from a unique combination of crosses. In addition, was conducted estimation of genetic similarity of PSAA WW breeding material by UPGMA clustering. According to the results of the analysis of genetic similarity, varieties were structured into five groups. It is can be useful for the selection of appropriate parents for crossing.

It is known, TDF_076_2D gene of moderate resistance to pathogens of ear fusarios present in Ariivka, Vilshana, Zelenyi hai, Karmelyk, Lutenka, Orzhytsia, Orzhytsia nova,

Orlyk napivkarlykovyi, Pabatka, Poltavchanka, Radyvonivka, Samara 2, Sanzhara, Tsarychanka [4]. According to analysis of varieties in which determined resistance allele, may show a lower degree of damage Fusarium head blight in the field, as well as be a serve as gene sources for selection using molecular markers.

Markers of gene sensitivity *Tsn1* to the *Pyrenophora tritici-repentis* were detected in next varieties: Orzhytsia nova, Radyvonivka, Sanzhara and Karmelyk. Resistance genes *Pm8*, *Sr31*, *Lr26*, *Yr9* have been detected in Ariivka, Orzhytsia nova, Pabatka and Vilshana biotype [5]. Wheat-rye translocation 1BL.1RS was detected in Ariivka, Orzhytsia nova, Pabatka and Vilshana.

According to authors [6] Levada, Tsarychanka, Lyutenka and Orzhytsia varieties were carriers *Ppd-A1b*, *Ppd-B1b*, *Ppd-D1a*, *Rht8c*, *Rht-B1a*, *Rht-D1b*, *Pina-D1a*, *Pinb D1b*, *Wx-A1a*, *Wx-B1a*, *Wx-D1a* alleles, and the cultivar Sydor Kovpak – *Ppd-A1b*, *Ppd-B1b*, *Ppd-D1a*, *Rht8c*, *Rht-B1a*, *Rht-D1a*, *Pina-D1a*, *Pinb-D1a/b*, *Wx-A1a*, *Wx-B1a/b*, *Wx-D1a*.

Therefore, using of molecular markers help quick to indicate varieties and breeding lines with valuable agronomic traits. Marker-assisted selection is a perspective approach for the estimation of the genetic diversity of local breeding programs and can be useful for the selection of appropriate parents for crossing.

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