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MICROSATELLITE LOCI ASSOCIATED WITH PLANT HEIGHT IN UKRAINIAN BREAD WHEAT VARIETIES (TRITICUM AESTIVUM L.)

Plant height (PH) is one of the critical traits for the adaptation of bread wheat (*Triticum aestivum* L.) to diverse climatic environments and the cultivation in various regions and cropping seasons. PH variation in Ukrainian as well as in European wheat cultivars is mainly controlled by the *Rht-D1* and *Rht-B1* semi-dwarfing genes (Chebotar, 2006; Chebotar et al., 2010), but also by other medium- or small-effect quantitative trait loci (QTL) and potentially epistatic QTL enabling fine adjustments of plant height (Wьrschum et al., 2015). Other major genes conferring reduced height are *Rht8* on 2D (Korzun et al., 1998; Chebotar et al., 2010) and the photoperiod regulator *Ppd-1* (Shaw et al., 2012). According to Zanke et al. (2014) a wide range of loci in the genome are available to breeders for modulating PH in wheat. In the study of Bellucci et al. (2015) 6 QTLs for PH were mapped, among which one QTL was previously reported, while the remaining QTLs constituted new genomic regions linked to trait variation.

In our research we determined genetic diversity among a group of 48 bread winter wheat varieties (250 bread wheat lines) of PBGI breeding by SSR markers. The variability of PH was determined in the field conditions during four growing seasons (2010-2011, 2011-2012, 2012-2013, 2013-2014). The main goal of this work was focused on finding marker trait associations (MTAs) in the investigated varieties. As a result 17 MTAs were found to be stable in three – four growing seasons and 22 MTAs were proved to be significant in two growing seasons. Overall 17 SSR markers were associated with the larger value of PH while 22 alleles were associated with the smaller value of PH. In our research there was detected that marker *Xgwm408*-5B showed significant associations with PH. According to Leonova et al., the *Xgwm408*-5B was shown to be in close linkage to the vernalization response gene *Vrn-B1* on 5BL. Brbaklic et al. (2013) identified that the QTL located near microsatellite marker *Xgwm18*-1B explained about 23% of the total variability for PH but in our study this marker did not have any association with PH in our breeding material in climatic conditions of southern Ukraine. Zanke et al. (2014) reported the detection of 34 SSR alleles located on different wheat chromosomes which were associated with PH, 16

SSR alleles were reducing the PH while 18 SSR alleles were enhancing it, among them allele $Xgwm357_{128}$ was significantly associated with PH and proved to be one of the most PH reducing alleles. In our study no MTAs were found between *Xgwm357* and PH. Overall, 12 SSR markers associated with PH have locations on chromosomes 2A, 3A, 5A, 1B, 3D, 4D, 6D and 7D. Confirmation of MTAs in Ukrainian breeding material under climatic conditions of southern Steppe opens new opportunities for using the pointed microsatellite markers for MAS.

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CULTURE IN VITRO AS A TEST SYSTEM FOR DETERMINING DEGREE THE PHYTO STABILITY OF ISOGENIC BY GENES VRN LINES OF SOFT WHEAT

It is known, that duration of ontogenesis, type of development (spring/winter) and speed of development in soft wheat *Triticum aestivum* L. determined by the system of *VRN* genes (Stelmach et al., 2000; Cockram et al., 2007). One of the factors limited the productivity of soft wheat is affection by vascular diseases induced by different types of micromycete of g. *Fusarium* (Grutcyk, 2013). *In vitro* is a modern model system in phytobiological research and in present days is widely used in cell selection for receiving stable to diseases plant varieties (Bavol et al., 2009; Kornya, 2011). Thus, in forming of resistance to plant pathogens, age, plant ontogenesis phase put through biotic stress are of the essence, it is interesting to learn predetermination by genes of wheat development rates in forming of biological mechanisms of resistance to biotic stress. The aim of our work is to research the influence of exometabolites phytopathogens of g. *Fusarium* on callus cultures isogenic wheat lines differ by development rates. The objects of research were near isogenic by genes *VRN* lines (NILs) of soft wheat *Triticum aestivum* L., Mironovskaya 808 sort and phytopathogenic micromycetes *Fusarium oxysporum* and *Fusarium moniliforme*. Primary callus cultures of isogenic lines were obtained using in the capacity of explants mature embryo. The cultivation was conducted in nutrient medium Murashige and Skoog (MS) containing growth stimulant – 2,4-D (2 mg/l) in thermostat with temperature 26°C in the darkness. Phytopathogens exometabolites influence g. *Fusarium* was researched by adding cultural filtrate of micromycetes into nutrient medium MS in the ratio 1:20. The cultivation of callus cultures