Application of molecular markers for plant breeding and variety investigation and diversification

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Introduction

The application of molecular markers has enabled breeders to select superior genotypes for traits that are difficult to select based solely on phenotype or to pyramid desirable combinations of genes into a single genetic background. Since the 1990s SSR markers have been extensively used in constructing genetic linkage maps, QTL mapping, marker-assisted selection (MAS) and germplasm analysis in plants. Most of the important agronomic traits are polygenic or controlled by multiple QTLs (Campbell et al. 1999). MAS for the improvement of such traits is a complex and difficult task because it is related to many genes or QTLs involved, QTL x Environment interaction and epistasis. Usually, each of these genes has a small effect on the phenotypic expression of the trait and expression is affected by environmental conditions. Over the past three decades, the total number of the proposed molecular markers reached such a level, which makes it possible to construct high density genetic maps. In the present study, we have applied microsatellite markers (Röder et al. 1998, 2002) for the association with major loci connected with controlling of main wheat agronomical and morphological characteristics in a core collection from modern Ukrainian bread wheat varieties (Kolesnyk et al. 2013).

Material and Methods

The analyzed material consists of 48 bread winter wheat varieties (*Triticum aestivum* L.) originated in Plant Breeding and Genetic Institute (PBGI) and registered in State Register of plant varieties suitable for dissemination in Ukraine during different years: Hospodynia (2007), Scarbnytsia (2007), Kosovytsia (2008), Antonivka (2008), Zamozhnist' (2008), Blahodarka odes'ka (2009), Misiia odes'ka (2009), Dal'nyts'ka (2005), Yednist' (2008), Kiriia (2004), Liona (2005), Kuial'nyk (2003), Poshana (2004), Zaporuka (2008), Bunchuk (2009), Podiaka (2008), Oksana (2007), Zahrava odes'ka (2010), Epokha odes'ka (2010), Lytanivka (2008), Sluzhnytsia odes'ka (2009), Hoduval'nutsia odes'ka (2009), Istyna odes'ka (2010), Zmina (2007), Dovira (2009), Krasen' (2009), Otaman (2008), Borvii

(2010), Turunchuk (2008), Diuk (2008), Nebokrai (2011), Khyst (2013), Pylypivka (2011), Zorepad (2011), Zhaivir (2010), Uzhynok (2010), Hurt (2013), Dobrochyn (2013), Vatazhok (2011), Pol'ovyk (2009), Holubka odes'ka (2011), Kniahynia O'lha (2011), Lebidka odes'ka (2 samples, 2011), Zhuravka odes'ka (2011), Bezmezhna (2008), Lastivka odes'ka (2011). Varieties Albatros odes'kyi (1990) and two collection samples of variety Bezosta 1 (1955) were taken into research as standard (etalon) samples according to recommendation of Ukrainian Institute of Examination of Plant Varieties of Ministry of Agriculture and Food of Ukraine as a national standards provided for distinctness, uniformity and stability (DUS) of new varieties of bread wheat (*Triticum aestivum* L.) for the purpose of granting the Breeders' Right.

It is assumed that in consequence of breeding these varieties are adapted to the conditions of a certain region, i. e. the genetic basis of such varieties is respectively narrowed compared to the complete gene pool of the culture. Each year the obtained grain material was analysed for a number of morphological and colorimetric characteristics (grain area projected on a plane, perimeter, length, and width, circularity, grain color intensity) by the optical methods using the digital images of kernels. In addition important agronomical traits (heading time, plant height, 1000 kernel weight, awn size, ear color, ear size) were evaluated during three growing seasons.

Results and Discussion

Genetic diversity in studied varieties of interest was evaluated based on (i) allelic richness (range of allele size and number of alleles per locus) as a measure of genetic variation; (ii) presence of specific alleles found in one variety but absent in others as a measure of genetic distinctiveness and uniformity; and (iii) PIC of each SSR marker as a measure of genetic diversity. A total of 114 alleles were detected at 17 SSR markers among the 48 winter bread wheat varieties, and the number of alleles per locus ranged from 4 to 10 with an average of 6.7. Allelic polymorphism was manifested by the occurrence of numerous alleles per SSR locus appearing in the whole pool of varieties, and by their frequency varying. The largest number of alleles (10) was found at Xgwm155-3A, Xgwm325-6D and Xbarc126-7D loci, whereas only four alleles were detected at Xgwm190-5D locus in the investigated varieties. Besides, the average PIC value was 0.67 with a range of 0.48 (Xgwm190-5D) − 0.84 (Xgwm155-3A).

On the studied material there was confirmed the previously shown presence of statistically significant associations of allelic state revealed by microsatellite loci with the expressiveness of a number of parameters of agronomical and morphological traits. There was determined the hereditary nature of some associations found in previous years. Development of research in this area is promising in terms of a more complete disclosure of genetic predetermination of the key breeding traits (plant height, photoperiod response, resistance to various diseases). Based on the

experimental results of this study, the practical cooperation with the department of wheat breeding has been started in order to improve the variety control while breeding and primary seed production and to increase the competitive ability of Ukrainian varieties on the global seed market.

Acknowledgements

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