

Effectiveness of microsatellites in differentiation of elite wheat cultivars

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Abstract: In order to reveal genetic diversity and discriminate 44 winter and spring bread wheat genotypes, fifteen microsatellite markers were used. Fifteen primer pairs amplified altogether 94 different alleles with an average number of 6.33 alleles per locus. The diversity index (DI) of the tested microsatellite markers ranged from 0.375 to 0.849 with an average of 0.68 and the polymorphic information content (PIC) ranged from 0.305 to 0.844 with an average of 0.65. This is generally considered sufficient for this purpose. The dendrogram, based on the hierarchical cluster analysis using UPGMA algorithm, was prepared. Forty-four wheat cultivars were grouped into two major clusters. Cluster I contained 5 genotypes all bred in Slovakia and had in their pedigree cultivars Nebojská, Kavkaz and Aurora. Cluster II with 39 genotypes was subdivided into three subclusters. Two subclusters (IIIa and IIIb) of subcluster IIb contained mostly in the pedigree cultivar Mironovskaja 808 coming from the Czech Republic. Subcluster IIIc included 5 cultivars all bred in Slovakia which had cultivar Kavkaz in their pedigree. Clustering partially reflects pedigree and origin of the wheat genotypes.

Key words: wheat, *Triticum aestivum*, genetic diversity, microsatellite, diversity index, polymorphic information content.

Abbreviations: DI, diversity index; PIC, polymorphic information content.

Introduction

Bread wheat (*Triticum aestivum* L.) belongs to the most important crop species cultivated in the Slovak Republic. It has three genomes A, B and D with more than 80% of repetitive DNA (RÖDER et al., 1998). This makes bread wheat a difficult material for genome-wide studies. Different markers, based on proteins (GÁLOVÁ et al., 2003) and also DNA, have been developed to assess genetic diversity in wheat. There is generally a low level of polymorphism in wheat relative to other cereal species (rice, maize or barley) and this means that a larger numbers of markers is usually necessary to screen (LANGRIDGE et al., 2001). Recently PCR-based marker systems, such as AFLP (BARETT & KIWELL, 1998) and microsatellites, appear most promising. Microsatellites are simple sequences with the basic repetitive unit of 1–6 base pair. They have been proposed as one of the most suitable markers. They are codominant, locus-specific and showed high level of polymorphism and reproducibility (RÖDER et al., 1995, 1998; GUPTA et al., 2002). Efforts have been made to develop microsatellite or SSR (simple sequence repeats)

maps in wheat; at the beginning by RÖDER et al. (1998) and PESTSOVA et al. (2000) in Germany who mapped 279 and 55 microsatellite loci, respectively. Another 50 SSR loci were mapped by STEPHENSON et al. (1998). There were mapped additional 144 SSR loci (belonging to 137 microsatellites) in Australia by HARKER et al. (2001) and 66 SSR loci by GUPTA et al. (2002). Recently SOMMERS et al. (2004) mapped 1235 microsatellite markers which put on a consensus map. Assessment and application of microsatellite markers in hexaploid wheat is also well-documented (PLASCHKE et al., 1995; BRYAN et al., 1997; PRASAD et al., 2000; STACHEL et al., 2000; CHRISTIANSEN et al., 2002; HUANG et al., 2002; RÖDER et al., 2002; AKKAYA & BUYUKUNALBAL, 2004; ROUSSEL et al., 2004).

The national list of recommended bread wheat includes yearly about fifty cultivars more or less similar in morphological and agronomical traits and perhaps genetically consistent. Their appearance occasionally does not allow to fulfil the requirements for basic characteristic of new-released cultivars, i.e. distinguishing. Therefore the aim of this study was to assess genetic differences within the set of registered winter and spring

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