Relevancy of genomic and gene-based variation in distinguishing of elite barleys

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Abstract: Two types of microsatellite markers generated by polymerase chain reaction have been used for proofing of their differentiation competence. The one generated microsatellite variation outside and the other within the coding DNA sequences – genomic and gene-based markers, respectively. Both were tested in the set of 62 elite winter and spring barley cultivars. Variation related to 13 genomic and 11 gene-based analyzed loci revealed 61 genomic and 35 gene-based alleles. Polymorphism was higher at the genomic SSR loci, genetic similarity indices based on variation at genomic and gene-based loci were 0.133–0.958 and 0.048–1.0, respectively. There were exposed markers specific for individual cultivars but also unexpected alleles within analyzed barleys. Variation at the analyzed loci reflected its linkage with winter and spring growth habit, respectively. The probability index, which is an important indicator of usable differentiation competence of the markers, significantly correlated with the index of diversity.

Key words: microsatellite, genomic, gene-based, barley, diversity index, probability index.

Abbreviations: DI, diversity index; EST, expressed sequence tags; PI, probability index; PIC, polymorphic information content; SSR, simple sequence repeat.

Introduction

Eukaryotic genomes are saturated with simple sequence repeats – microsatellites located outside and within the coding DNA sequences. The concept of microsatellite appeared 16 years ago (LITT & LUTY, 1989). Simple sequence repeats (SSRs) and short tandem repeats (STRs) designate also the same occurrence. Analysis of variation in plant microsatellites (SSR) have begun by RFLP (restriction fragment length polymorphism) analysis using oligonucleotide DNA probes containing short repeat motif (WEISING et al., 1989). The polymerase chain reaction – PCR (MULLIS & FALOONA, 1987) proposed a simpler tool for observation of variation also in plant microsatellites. Occurrence of microsatellites in genome, their information value and identification simplicity have made them the optimal markers for theoretical studies in gene location, linkage genetics, physical mapping, population studies, and differentiation of cultivars (MORGANTE & OLIVIERI, 1993) required also in practical uses, e.g. distinguishing, uniformity, and stability of new released cultivars, effective conservation and exploitation of genetic diversity, germplasm characterization, etc.

Differentiation of cultivars is more difficult in modern cereal and also barley cultivars than in landraces or old cultivars. The main reason is that during past decades a limited number of elite parental components were used for breeding of new advanced cultivars. The extent of genetic variation was constantly reduced and genetic uniformity increased. Standard traits and characteristics used for cereal cultivars differentiation, i.e. morphological, anatomical, and agronomical traits do not provide sufficient level of variation. Also protein polymorphism is not often a sufficient discrimination parameter for cereal cultivar differentiation (GÁLOVÁ et al., 2003). This is the main reason why differentiation of plant cultivars converted to molecular markers.

DNA markers development for barley followed common progress in DNA techniques in plants. PCR approach followed development in DNA fingerprinting and restriction fragment length polymorphisms (BECKMANN & SOLLER, 1983; ZHANG et al., 1992; PECCHIONI et al., 1993). PCR-based detection of DNA polymorphism has begun in barley by primers derived from gene sequences (D'OVIDIO et al., 1990; WEINING & LANDRIDGE, 1991). The so-called sequence-tagged-site markers have been used in barley genome