

GENETIC DIVERSITY OF RUSSIAN ADVANCED WHEAT CULTIVARS REVEALED WITH SSR MARKERS

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A quick and reproducible tool for cultivar identification is useful to assess in certified seed production programs and to resolve legal conflicts over the recognition of a seed stock (Mangini et al., 2009). In order to obtain plant breeders' rights (PBR) the new variety has to pass the distinctness-uniformity-stability (DUS) criteria in which the candidate breeding lines are compared with existing cultivars on the basis of a series of morphological traits. Although these traits are informative and practical, they exhibit a polygenic control and are subject to environmental influences. Seed storage protein electrophoresis is included in the DUS testing guidelines, but the low level of polymorphism limits the ability to distinguish different genotypes. The resolving power of DNA markers is significantly higher allowing to prove that a new variety is unique from all other varieties that have already been described and that all individuals are as identical as possible.

As a part of research project initiated in 2011 we are developing a molecular identification key for 320 wheat cultivars registered in Russian Federation and the Republic of Belarus using SSR markers. A subset of 24 cultivars was randomly selected from the 320 cultivars and screened with 84 genomic SSR primers (Xbarc, Xgwm). At the present stage of project the SSRs with high discriminating ability were further analysed on a set of 96 genotypes. The power of each primer to distinguish among the studied genotypes was estimated by Polymorphism Information Content and the Resolving power. With the selected markers 96 genotypes were easily discriminated. A molecular identification key to distinguish Russian advanced wheat cultivars using SSR-profiling is discussed. We suggest the reproducible fingerprint system for the identification of Russian hexaploid wheat cultivars that could be employed in certified seed production programs to identify sources of seed contamination, and to distinguish cultivars with similar phenotype.