

Genetic diversity of facultative bread wheat from the VIR collection

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Motivation and Aim: Facultative bread wheat (*Triticum aestivum* L.) is cultivated in different countries of the world and adapted to wide range of environments. In Russia this wheat is used as an insurance crop. For expanding of genetic basis for breeding of facultative wheat not only in the North-Caucasian region, where this wheat is cultivated, but also in other regions, it was essential to assess its world genetic diversity, to understand, how it is represented in the VIR collection, and to form core-set for usage in breeding and basic researches. The aim of our study was to use molecular markers to characterize the major alleles of genes responsible for vernalization response and photoperiod sensitivity and to elucidate the relationships between some biological or agronomic traits and allelic variations of these genes.

Methods and Algorithms: According to GRIS [1], 2116 accessions of facultative bread wheat are known in the world, among them 651 – in the VIR collection. We have formed a representative sample of 345 accessions, which were evaluated in spring- and autumn-sown in the North-West region of Russia (t. Pushkin). From this sample 243 accessions (256 biotypes) were chosen for molecular studies. Total DNA was extracted from the six seedlings, descendants of the one plant (genotype). PCR was performed using allele-specific molecular markers for determination the main allele-types for *Vrn*- and *Ppd*-genes [2].

Results: A total 15 alleles for *Vrn-A1*, *Vrn-B1*, *Vrn-D1*, *Vrn-B3*, *Ppd-D1* genes, and for *Vrn-D1* promoter region were observed. Frequencies of dominant alleles were varied from 0.8 % (*Vrn-B3*) to 36.7 % (*Vrn-B1a*), whereas of recessive alleles – from 43.8 % (*vrn-b1*) to 94.5 % (wild type of *Vrn-D1* promoter region). The amplified products of other sizes for genes *Vrn-A1* and *Vrn-B3* were found in 18 biotypes. No products characteristic for individual genes were detected in 52 biotypes. Four biotypes were heterozygous. In total, 64 allelic compositions were identified in 256 biotypes. The most frequent composition was *vrn-A1 Vrn-B1c vrn-D1 vrn-B3 Ppd-D1b* wild type of *Vrn-D1* promoter region, which was revealed for biotypes from Russia, Kursk region. The genotypes with alleles *Vrn-B1c* had shorter heading than *Vrn-B1a*. The degree of overwintering of biotypes was mainly related to geographic origin of accessions, from which the biotypes were isolated.

Conclusion: The core-set of facultative bread wheat comprising 256 biotypes is maintained the wide genetic diversity not only alleles of *Vrn*- and *Ppd*-genes but also the other traits. It can be used for wheat improvement and conducting basic researches.

References

1. <http://wheatpedigree.net/>
2. <http://maswheat.ucdavis.edu/protocols/Vrn/index.htm>