

## Intragenomic polymorphism of internal transcribed spacer ITS1 in the locus 35S rRNA of polyploid *Avena* species

Rodionov A.V.<sup>1,2\*</sup>, Krainova L.<sup>2</sup>, Gnutikov A.A.<sup>1,3</sup>, Mikhailova Y.<sup>1</sup>, Machs E.M.<sup>1</sup>, Shneyer V.S.<sup>1</sup>, Loskutov I.G.<sup>3</sup>, Muravenko O.V.<sup>4</sup>

<sup>1</sup> Komarov Botanical Institute, RAS, St. Petersburg, Russia

<sup>2</sup> Department of Cytology and Histology, St. Petersburg State University, St. Petersburg, Russia

<sup>3</sup> N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR), St. Petersburg, Russia

<sup>4</sup> Engelhardt Institute of Molecular Biology, RAS, Moscow, Russia

\* e-mail: avrodionov@mail.ru

Using sequence-tagged Roche 454 platform, we studied intragenomic polymorphism of ITS1, a spacer region of the multiple 35SrRNA genes in four polyploid *Avena* species. Comparison of ITS1 sequences from the diploid species, earlier sequenced by Sanger approach, allowed to detect two indels specific for all ITS1 of C-genome diploid species. It enabled easily identifying rare C-subgenome-specific ITSs among hundreds of ITS1 reads characteristic for the A-subgenomes. Instead of expected 50 % C-variant reads of 35S rDNA in *A. insularis* (karyotype AACC or CCDD) and 33 % C-variant reads in hexaploids *A. fatua*, *A. ludoviciana* and *A. sterilis* (all AACCCDD), the actual rate consisted only about 4 % in *A. insularis* and 2–3 % C-variant reads in hexaploid genomes. The C-genome-originated 18S (fragment), ITS1 and 5.8S (small fragment) were 10 times more variable than the same sequences originated from to A-genome. Some of the sequences of C-subgenomes contained deletions, including deletions in the 18S rRNA region. As for the origin of C-subgenome ITS1s in the polyploid species, some sequences revealed similarity to the ITS1 variants of either *A. macrostachya* (Cm) or *A. ventricosa* (Cv), but the core variant of C-subgenome ITS1 on the genetic tree is approximately equidistant from all the present-day C-genome diploid species. The A-type ITS1 of *A. insularis* is represented by few families, one of which is close to the A-genomes of *A. longiglumis*, *A. hirtula* and *A. wiestii*. As for hexaploids, there are two more frequent families of A-type rDNA reads in their genomes. We believe that one of them, represented by a higher number of reads, is located in NORs of D- and another one in NORs of A-subgenomes.

**Acknowledgements:** This study was supported by the RFBR KOMFI 17-00-00340 (17-00-00336, 17-00-00337, 17-00-00338).