

Analysis of repetitive DNA sequences in genomes of *Porodaedalea niemelaei*, *P. chrysoloma* and *Armillaria borealis*

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Motivation and Aim: We are interested in the evolution of the fungi genes and genomes. Repetitive DNA sequences may play significant role in determining the structure and evolution of genes and genomes. Therefore, it is very important to identify and study them in the fungi genomes, such as *Porodaedalea* and *Armillaria* that are among the most important fungi in boreal and temperate forests.

Methods and Algorithms: The *P. niemelaei* genome was sequenced and annotated using the PacBio technology by the US DoE Joint Genome Institute (JGI) in collaboration with Department of Forest Genetics and Forest Tree Breeding, Georg-August University of Göttingen, Germany and Laboratory of Forest Genomics, Siberian Federal University (SFU), Russia. The length of the full genomic assembly was 53 Mbp. The genome assembly of *P. chrysoloma* was obtained from the JGI fungal database (<http://genome.jgi.doe.gov/programs/fungi/index.jsf>). The length of the full genomic assembly was 44 Mbp. The *A. borealis* genome was sequenced and annotated in the Laboratory of Forest Genomics, SFU using Illumina HiSeq 2000. The length of the full genomic assembly was 66 million Mbp.

Results: In total, 161 highly repetitive elements (REs) including 127 unknown REs were found in the *P. niemelaei* genome, 122 REs including 94 unknown REs were found in the *P. chrysoloma* genome, and 886 REs including 835 unknown REs – in the *A. borealis* genome.

Conclusion: Known as well as mostly unknown repetitive elements were identified in the *Porodaedalea* and *Armillaria* genomes. Their study and comparison with other genomes of basidiomycetes will help us better understand the functional and evolutionary role of REs and to reveal their evolutionary relationships.

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