ASSEMBLY OF THE MITOCHONDRIAL GENOME OF SIBERIAN CEDAR (*PINUS SIBIRICA*)

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Most plants have two types of organelles with their own genome: mitochondria and chloroplasts. It is well known that mitochondrial genome is inherited over the maternal lines and is rather complex. Currently, mitochondrial genomes have been published only for four gymnosperms.

Isolation of intact mitochondria was carried out at the Laboratory of Plant Genetic Engineering, SIFiBR SO RAN. In the forest genomics laboratory of Siberian Federal University, the mitochondrial sequences of *Pinus sibirica* were obtained. Sequencing was performed on the IlluminaHiSeq 2000 platform. The contigs were assembled using the CLC BIO. 879595 scaffolds with a total length of 283.4 Mb were obtained.

Mitochondrial scaffolds were selected by aligning the genomic assembly with BLAST against a base of 3489 (143.5 Mb) complete and partial sequences of mitochondrial genomes of seed plants. As a result, 97 scaffolds with a total length of 3.1 Mb were selected.

Protein-coding genes were searched using BLAST in the Genomic Workbench CLC software by aligning the assembly against well-annotated cycad and ginkgo genomes, tRNA genes were detected using tRNA-scan and Aragorn, rRNA genes were detected using RNAmmer. 40 protein-coding genes were found located in 7 scaffolds, also 18 tRNA genes and 2 rRNA genes were found. The total length of the repeats was 0.2 Mb, which is 6.2% of the total assembly length using RepeatModeler, TEclass.

To compare with, the total assembly length for *Picea glauca* [1] is 5.9 Mb, *Pinus taeda* [2] is 1.2 Mb, *Picea abies* [3] is 4.3 Mb. We believe the difference in the size of the mitochondrial genome results both from the difference in sizes of the non-coding regions, and the number of genes.

References

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