

## Assembling of the Siberian larch mitochondrial genome using long nucleotide sequence reads, the largest currently known mitogenome

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Plants have very large mitochondrial genomes (mitogenomes) varying from 200 Kbp to 11.3 Mbp. They have also very complex structure in plants. So far, only a few mitochondrial genomes have been sequenced and published in conifers. We succeeded a high-quality assembly of the Siberian larch (*Larix sibirica* Ledeb.) mitogenome using both short and long nucleotide sequencing reads generated by the Illumina HiSeq2000 and MinION (Oxford Nanopore Technologies) sequencers, respectively, and a hybrid approach based on the MaSuRCa pipeline. To select mitochondrial sequences from nuclear and plastid sequences, assembled contigs were mapped to the nucleotide database of complete and partial plant mitogenomes. The final assembly of the Siberian larch mitogenome consists of 9 contigs with a total length of 11,662,539 bp (N50 = 3,031,766 bp). The longest contig is 4,008,762 bp, the shortest – of 24,767 bp. Finally, 40 protein-coding, 34 tRNA, and 3 rRNA genes were annotated. This mitogenome is currently the largest one.