

Complete chloroplast genome sequence of a white spruce (*Picea glauca*) genotype from eastern Canada

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ABSTRACT

Here we present the complete chloroplast genome sequence of white spruce (*Picea glauca*, genotype WS77111), a coniferous tree widespread in the boreal forests of North America. This sequence contributes to genomic and phylogenetic analyses of the *Picea* genus, part of ongoing research to understand their adaptation to environmental stress.

GENOME ANNOUNCEMENT

We sequenced, assembled, and annotated the chloroplast genome of white spruce (*Picea glauca* genotype WS77111), a dominant species in the Canadian boreal forest (1). Over tens of millions of years, conifers such as *P. glauca* have evolved to cope with adverse environmental conditions (2). However, climate change poses new challenges to the capacity of these trees to adapt to conditions such as prolonged drought and increased pressure from forest insect pests (3). *P. glauca* has three different genomes, a nuclear genome, a mitochondrial genome, and a plastid (i.e. chloroplast) genome. In general, chloroplast genomes are derived from the ancestral genomes of the microbial endosymbiont from which these organelles originated (4). The nuclear genome of *P. glauca* (WS77111) was published in 2015 (5).

A *P. glauca* (genotype WS77111) needle tissue sample was collected in southeastern Ontario (44°19'48"N, 78°9'0"W; elevation: 250m). The sample was sequenced at Canada's Michael Smith Genome Sciences Centre (GSC).

To sequence the sample, genomic DNA libraries were constructed according to GSC plate-based and paired-end library protocols on a Microlab NIMBUS liquid handling robot (Hamilton, USA), and sonicated into 400 bp fragments, as previously described (6-7). Pooled libraries were sequenced with paired-end 250 bp reads on an Illumina HiSeq2500 instrument in rapid mode.

To assemble the chloroplast genome, we generated various random subsamples of the full read set (0.75, 1.5, 3, 6, 12, 25, 50, 200 million read pairs), and assembled each subset with ABySS v2.1.0 (8) ($k=128$, $kc=3$). The 1.5M, 3M, and 6M read subsets produced the best ABySS chloroplast genome assemblies ($N50=3692$, 1313, 949, respectively), as determined by comparing these assemblies to the white spruce admix (PG29) chloroplast genome (NCBI accession NC_028594.1; (9)) using QUAST v5.0.0 (10). We then performed additional ABySS assemblies with varying k and kc parameters using these three subsets ($k=96$, 112, 128, 144, 160, $kc=3$, 4). The assembly with the fewest aligning contigs ($n=14$) and fewest misassemblies (1.5M read pairs, $k=96$, $kc=3$) was chosen for further scaffolding. Scaffolding the assembly using LINKS v1.8.5 (11) and the PG29 chloroplast genome joined the contigs into one piece. We then used Sealer (12) to close the scaffold gaps. We modified the start position of our assembly to match the PG29 reference using BLAST v.2.7.1 (13), and polished the final assembly with Pilon v1.22 (14).

The complete WS77111 chloroplast genome is 123,421 bp long, with 38.74% GC content. Using GeSeq (15) with several other *Picea* chloroplast genomes as reference (9, 16), we annotated 114 genes: 74 protein-coding, 36 tRNA-coding, and four rRNA-coding genes. Only *rps12*, *petB*, *petD*, *rpl16*, and *psbZ* required manual annotation. The genome map in Figure 1 was generated using OGDRAW v1.2 (17).

The assembly of this new chloroplast genome will enable further analysis of *Picea* phylogeny and genetics.

Accession number(s). The complete chloroplast genome sequence of *Picea glauca*, genotype WS77111 is available from Genbank under accession [MK174379](#), and the raw reads are in the SRA under [SRX525336](#). The annotations used as references were from *Picea abies* ([NC_021456](#)), *Picea asperata* ([NC_032367](#)), *Picea glauca* genotype PG29 ([NC_028594](#)), *Picea morrisonicola* ([NC_016069](#)), and *Picea sitchensis* ([NC_011152](#), [KU215903](#)).

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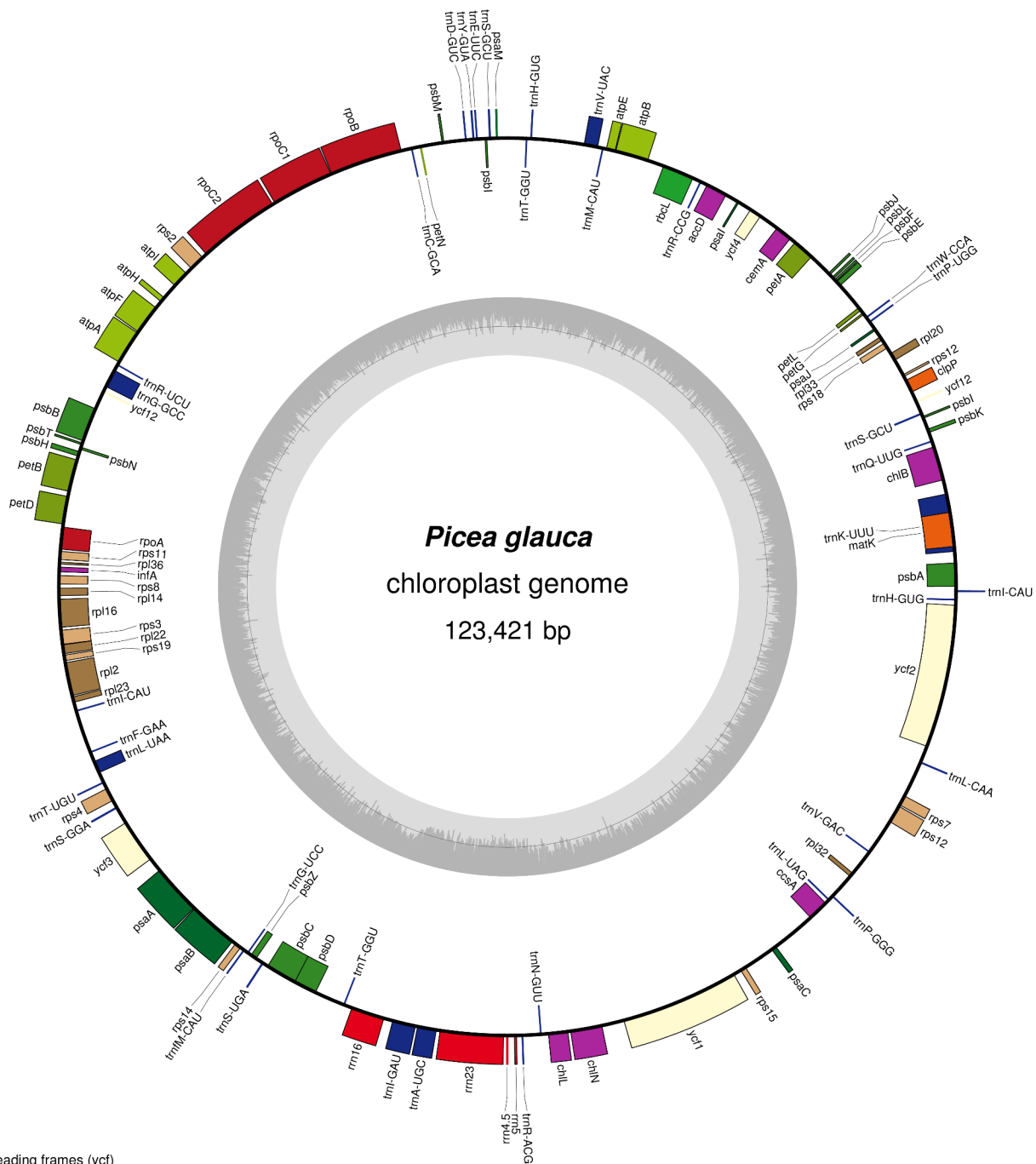
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Figure 1. The complete chloroplast genome of *Picea glauca* genotype WS77111

The *Picea glauca* chloroplast genome was annotated using GeSeq (15), and plotted using OGDRAW (17). The inner grey circle illustrates the GC content of the genome.

Picea glauca
chloroplast genome
123,421 bp



- photosystem I
- photosystem II
- cytochrome b/f complex
- ATP synthase
- NADH dehydrogenase
- RubisCO large subunit
- RNA polymerase
- ribosomal proteins (SSU)
- ribosomal proteins (LSU)
- clpP, matK
- other genes
- hypothetical chloroplast reading frames (ycf)
- ORFs
- transfer RNAs
- ribosomal RNAs
- origin of replication
- polycistronic transcripts
- introns