

The complete chloroplast genome of *Juniperus squamata* (Cupressaceae), a shrubby conifer from Asian Mountains

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ABSTRACT

The complete chloroplast genome of *Juniperus squamata*, a shrubby conifer of ornamental value, is determined in this study. The complete chloroplast genome size is 127,792 bp in length. The genome contains 118 genes, including 82 protein-coding genes, 32 transfer RNA genes, and four ribosomal RNA genes (16S ribosomal RNA, 23S ribosomal RNA, 4.5S ribosomal RNA, and 5S ribosomal RNA). It does not contain inverted repeat (IR) sequence. The overall GC content of *J. squamata* cpDNA is 35.1%. The phylogenetic analysis suggests its close relationship with *J. recurva* and *J. tibetica* from Himalaya and the Qinghai-Tibet Plateau, respectively. The genome may contribute to evolutionary studies of conifers.

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Juniperus squamata, also known as flaky juniper, is a conifer of the genus *Juniperus*, which consists of approximately 75 species and belonging to Cupressaceae (Adams 2014). This species is a shrub or small tree up to 12 meters tall, and it has a wide distribution in Asia and it is found in China, Afghanistan, Bhutan, North India, N Myanmar, Nepal, and Pakistan (Fu et al. 1999). It grows at an altitude of 1340 to 4850 meters and can grow in forests, thickets, valleys and roadside in mountain areas (Fu et al. 1999; Farjon 2005). Although this species is widely cultivated in Europe and North America as ornamental plant appreciating its bluish foliage and compact habit (Farjon 2005), genomic background of this species is lacking. Here, we assembled and characterized the complete chloroplast genome of *J. squamata* using the Illumina paired-end sequencing data.

Fresh leaves were collected from Kangding, Sichuan province, China (coordinates: 30°00.31N, 101°52.12E), and the dried leaf materials and voucher specimen were deposited at College of Life Sciences, Sichuan University (Sample No. MaoKS-2017-002A-1). Total genomic DNA was extracted by modified CTAB method (Doyle 1987) and prepared for high-throughput sequencing. As a result, we obtained high-quality clean reads for the cp genome assembly. The reads were assembled into contigs using NOVO-Plasty (Dierckxsens et al. 2017), and *J. microsperma* was used as a reference (Tso et al. 2018). Then, the cp genome was annotated using Plann (Huang and Cronk 2015). Then, we corrected the annotated

results in Geneious (Kearse et al. 2012). Finally, we chose chloroplast genome of 18 species to do alignments by MAFFT (Katoh and Standley 2013). An ML tree with 100 bootstrap replicates was constructed by RAXML v8 (Stamatakis 2014) based on the alignments of 78 common coding region of 18 cp genome of Cupressaceae species. The whole chloroplast genome of *J. squamata* was submitted to GenBank under Accession Number MK085509.

The cp genome sequence of *J. squamata* was 127792 bp long. It is circular DNA, which contains 118 genes, including 82 protein-coding genes, 32 transfer RNA genes, and four ribosomal RNA genes (16S ribosomal RNA, 23S ribosomal RNA, 4.5S ribosomal RNA, and 5S ribosomal RNA). The cp genome, which includes 117 single copy genes and one duplicated gene (trnQ-UUG). The overall GC content of *J. squamata* cpDNA is 35.1%. This genome does not contain inverted repeat (IR) sequence, which is consistent with the results of the previously published Cupressaceae species (Guo et al. 2016; Li et al. 2016; Tso et al. 2018; Miao et al. 2019; Song et al. 2019).

The phylogenetic analysis of 18 cp genomes suggests a close relationship among *J. squamata*, *J. recurva*, and *J. tibetica* (Figure 1), agree with previous studies based on nine chloroplast DNA fragments (Mao et al. 2010). The cp genome of this species will facilitate evolutionary studies of conifers as well as genetic studies of this bluish shrubby juniper.

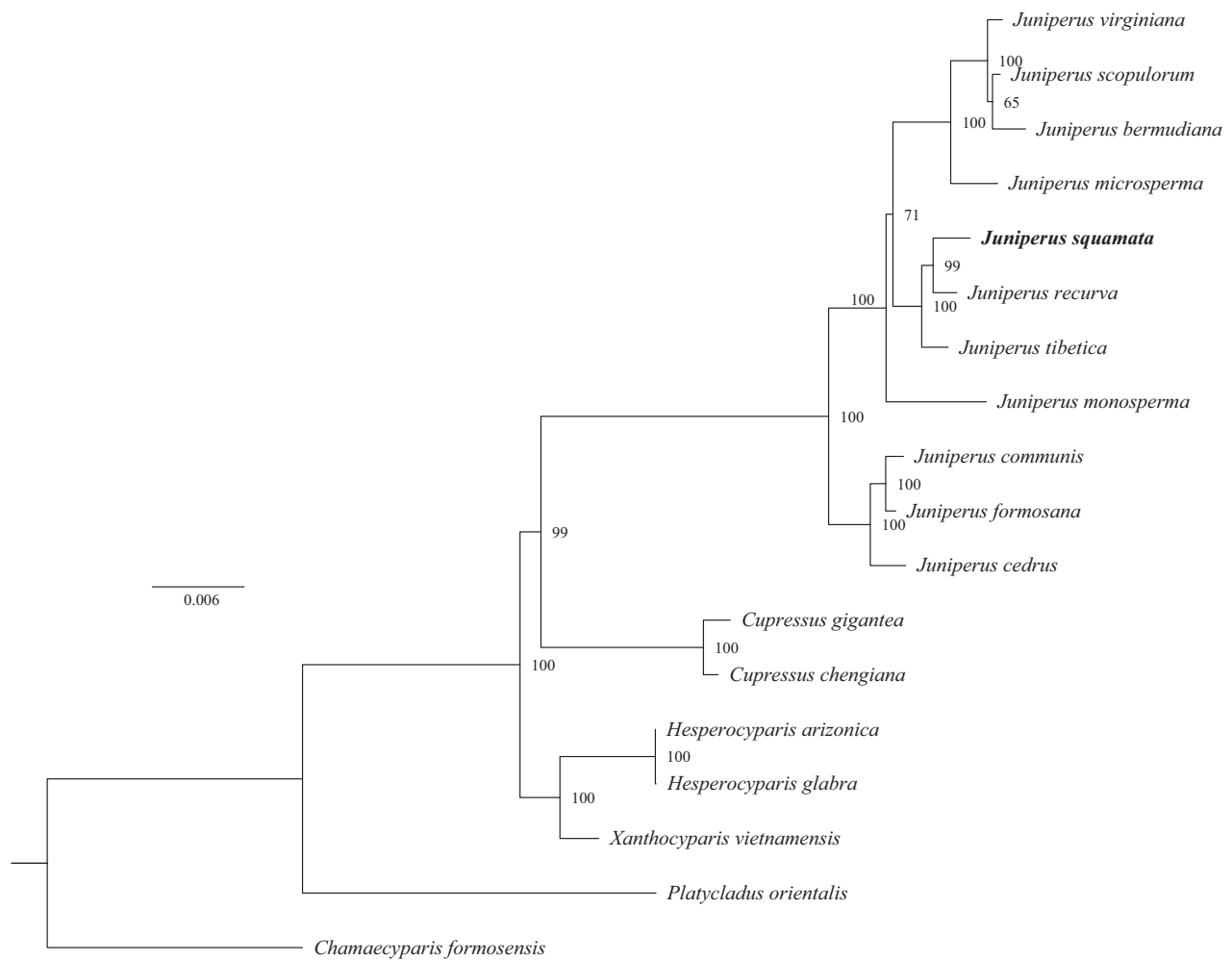


Figure 1. The phylogenetic tree based on the 18 complete chloroplast genome sequences. Accession numbers: *Cupressus chengiana* (NC_034788.1), *Cupressus gigantea* (NC_028155.1), *Xanthocyparis vietnamensis* (KX832629.1), *Hesperocyparis glabra* (KX832624.1), *Hesperocyparis arizonica* (MH121048), *Chamaecyparis formosensis* (NC_034943.1), *Juniperus monosperma* (KF866298.1), *Juniperus bermudiana* (KF866297.1), *Juniperus formosana* (KX832625.1), *Juniperus virginiana* (KF866300.1), *Juniperus microsperma* (MG878380.1), *Juniperus scopulorum* (NC_024023.1), *Juniperus squamata* (MK085509), *Juniperus tibetica* (MK135439), *Juniperus recurva* (MK375217), *Juniperus cedrus* (NC_028190), *Juniperus communis* (NC_035068), and *Platycladus orientalis* (KX832626).

Disclosure statement

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