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Protocols for "The draft genome assembly of the critically endangered Nyssa yunnanensis, a plant species with extremely small populations endemic to Yunnan Province, China"



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We use this protocol and it's working

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Abstract

Nyssa yunnanensis is a deciduous tree species in the family Nyssaceae within the order Cornales. As only eight individual trees and two populations have been recorded in China's Yunnan province, this species has been listed among China's national Class I protection species since 1999 and also among 120 PSESP (Plant Species with Extremely Small Populations) in the *Implementation Plan of Rescuing and Conserving China's Plant Species with Extremely Small Populations(PSESP)* (2011-2-15).

We have assembled the draft genome assembly of *N. yunnanensis*. Using 10X Genomics linked-reads sequencing data, we carried out the *de novo* assembly and annotation analysis. The *N. yunnanensis* genome assembly is 1475 Mb in length, containing 288,519 scaffolds with a scaffold N50 length of 985.59 kb. Within the assembled genome, 799.51 Mb was identified as repetitive elements, accounting for 54.24% of the sequenced genome, and a total of 39,803 protein-coding genes were predicted.

With the genomic characteristics of *N. yunnanensis* available, our study might facilitate future conservation biology studies to help protect this extremely threatened tree species. Protocols used include DNA-extraction, DNA Sequencing using the BGI-SEQ 500 (now known as DNBSEQ-G50) sequencer, and sequencing of 10X linked-reads.

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Protocol



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RNA extraction for plant samples using CTAB-pBIOZOL

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