

Chromosome genome assembly and annotation of *Artocarpus Nanchuanensis* with Nanopore and Hi-C sequencing data

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Abstract

The *A.nanchuanensis* (*Artocarpus Nanchuanensis*, Moraceae) is an evergreen *Artocarpus* genus representative tree species in the northernmost natural distribution and one of the extremely endangered tree species in China. In this study, we obtained a high-quality chromosome-scale genome assembly and annotation for *A.nanchuanensis* using inter-grated approaches, including Illumina, Nanopore sequencing platform as well as Hi-C. A total of 128.71 gigabases (Gb) raw Nanopore Sequel reads were generated from 20 kb libraries. After filtering, 123.38 Gb clean reads were obtained, giving 160.34x coverage depth. The final assembled *A.nanchuanensis* genome was 769.44 Mb with a contig N50 of 2.09 Mb, and 99.62% (766.50 Mb) of the assembly data was assigned to 28 pseudochromosomes. Gene modelling predicted 41,636 protein-coding genes, of which 95.10% were annotated. The gene annotation completeness was evaluated by BUSCO, and 94.44% conserved genes could be found in the assembly data. The disclosure of *A.nanchuanensis* genome sequence information provides an important resource to expand our understanding of the molecular mechanism in its unique biological processes and nutritional, medicinal benefits.

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