

A chromosome-scale genome assembly of the Mongolian oak (*Quercus mongolica*)

Wanfeng Ai¹, Mei Mei¹, Xiaolin Zhang¹, Lijie Zhang¹, Xiaoyi Han¹, Hao Zhan¹, and
Xiujun Lu¹

¹Shenyang Agricultural University

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Abstract

Quercus mongolica (Fagaceae) is an important ecological and economic tree species in East Asia. It has excellent biological characteristics, such as hardwood, strong resistance to biotic and abiotic stresses. The availability of a high-quality genome will help to further reveal the underlying mechanisms. Here we assemble the first chromosome-level reference genome of *Q. mongolica*. The final assembled genome was 809.84 Mb with contig and scaffold N50s of 2.64 Mb and 66.74 Mb, respectively. Hi-C scaffolding anchored twelve pseudochromosomes, accounting for 95.65% of the assembled genome. Moreover, 68.5% and 5.4% of the genomic sequence were transposon elements and tandem repeat elements, respectively. A total of 36,553 protein-coding genes were predicted, of which 94.89% were functionally annotated. Comparative genomics analysis indicated that *Q. mongolica* was more closely related to *Q. robur* than to either *Q. lobata* or *Q. suber*. *Q. mongolica* and *Q. robur* diverged ~10.2 Mya. *Q. mongolica* had undergone two whole-genome duplications which occurred earlier than *Q. robur*. We identified multiple genes in 38 positive selection genes, including pyridoxal reductase 1 (PLR1) and switch subunit 3 (SWI3B). In addition, we identified 496 genes related to wood formation, 88 WRKY genes, and 124 NAC genes in *Q. mongolica*. This genomic information will be an important molecular resource for further exploring the biological characteristics and adaptive evolution of *Q. mongolica*. Meanwhile, the genomic resource from Asian oak will also contribute to the study of the taxonomy, evolution and conservation of *Quercus* species.

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