

High-quality haplotype-resolved genome assemblies of ring-cup oak (*Quercus glauca*) provide insight into the demographic dynamics of a dominant tree in East Asia subtropics evergreen broadleaved forests

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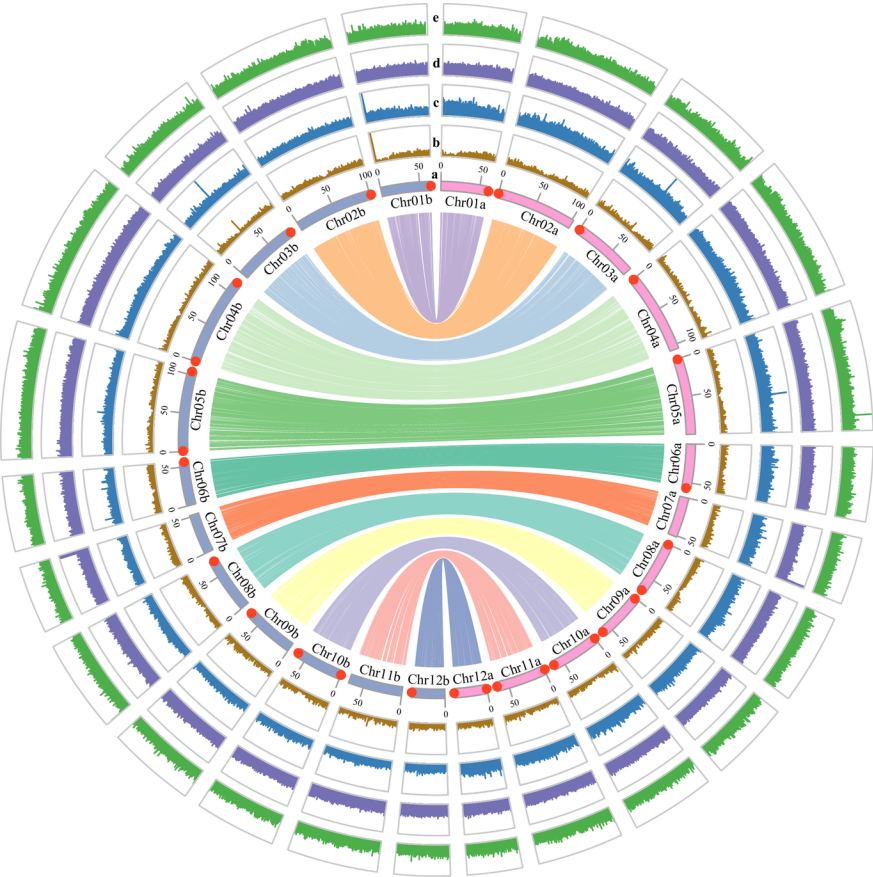
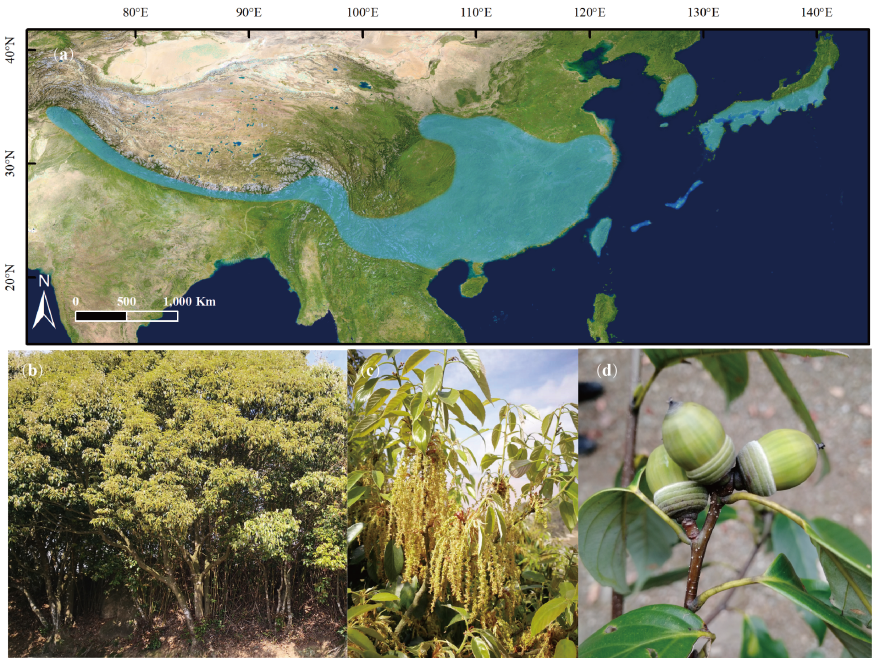
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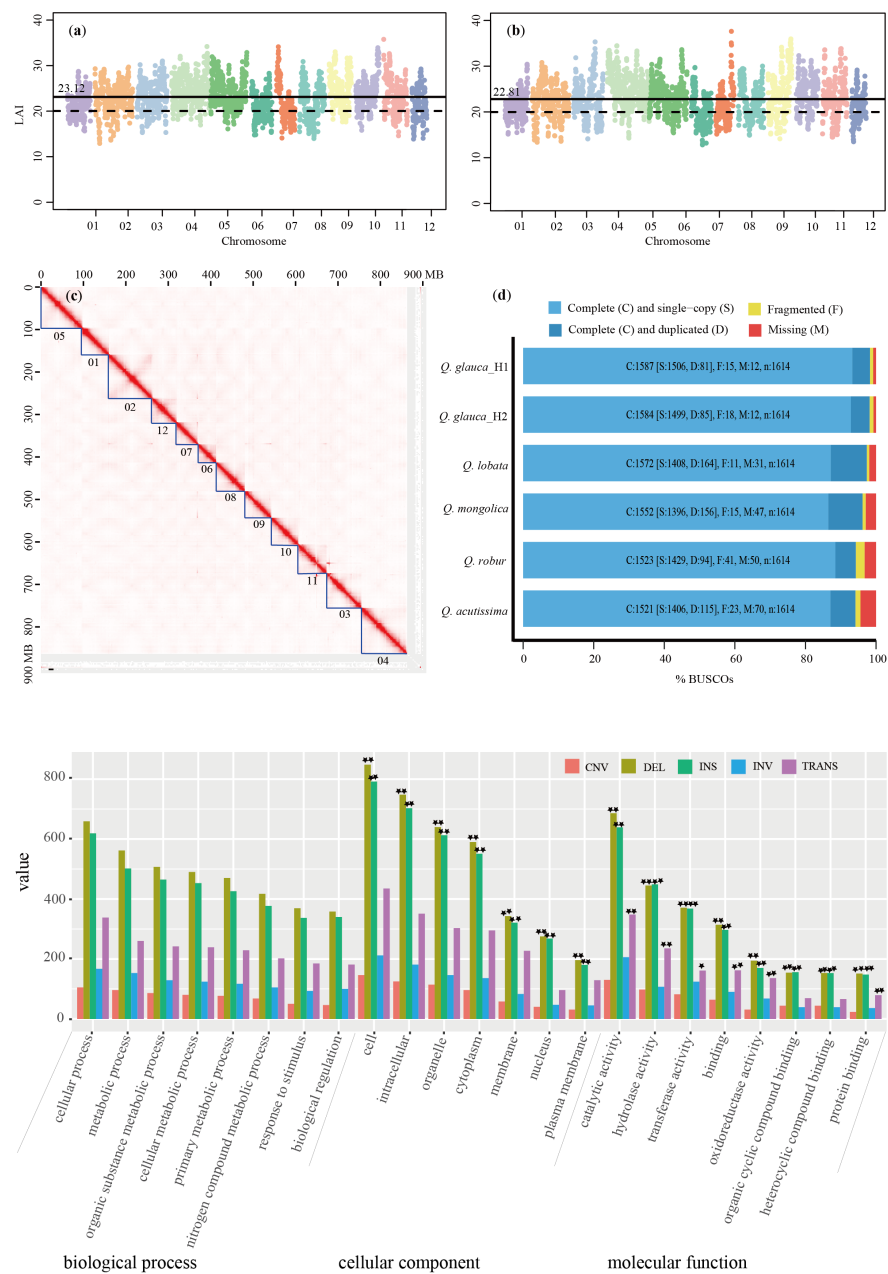
Abstract

Quercus section *Cyclobalanopsis* is a dominant woody lineage in East Asian evergreen broadleaved forests. Regardless of its significant ecological and economic importance, little was known on the genome of this unique oak group. *Quercus glauca*, also known as ring-cup oak, is the most widespread tree in section *Cyclobalanopsis*. In this study, a high-quality haplotype-resolved reference genome of *Q. glauca* was generated from PacBio CCS and Hi-C reads. The genome size, contig N50, and scaffold N50 of *Q. glauca* are 902.8 Mb, 7.6 Mb, and 69.3 Mb, respectively, for haplotype1, and 913.2 Mb, 7.2 Mb, and 71.5 Mb, respectively, for haplotype2. The LTR Assembly Index of the *Q. glauca* genome was more than 22. A total of 37,460 and 38,312 protein-coding genes were predicted in haplotype1 and haplotype2, respectively. Homologous chromosomes of *Q. glauca* had excellent gene pair collinearity. A total of 905 R-genes were detected in *Q. glauca*. The divergence between *Q. glauca* and *Q. suber* occurred about 44.6 million years ago, agreeable to the earliest fossil records of section *Cyclobalanopsis* found in East Asia. The global climate change before the late Miocene and local climate change since the Pliocene were the main causes of the effective population size change of *Q. glauca*. The high-quality genome assembly of the most widespread species of section *Cyclobalanopsis* can provide essential genomic resources for unraveling the evolution mystery of the main oak lineages, and to promote the application of genomic data on the interspecific introgression, local adaptation, and speciation studies of oaks.

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