

## The complete plastid genome sequence of *Quercus acuta* (Fagaceae), an evergreen broad-leaved oak endemic to East Asia

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### ABSTRACT

We are reporting the complete plastid genome (plastome) of *Quercus acuta*, an evergreen broad-leaved oak endemic to East Asia. This species is important for maintaining the warm-temperate evergreen forest biome in East Asia. The *Q. acuta* plastome is 160,522 base pairs (bp) long, with two inverted repeat (IR) regions (25,839 bp each) that separate a large single copy (LSC) region (90,199 bp) and a small single copy (SSC) region (18,645 bp). The phylogenetic tree shows that *Quercus acuta* is closely related to *Quercus sichouensis* with strong bootstrap support.

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The genus *Quercus* L. is one of the most abundant and economically important woody plant genera in the Northern Hemisphere (Manos et al. 1999). Its evolutionary success is attributed to the species diversity, which varies among geographic regions and follows ecological divergence within each region (Han et al. 2020; Hipp et al. 2020). *Quercus* species can be locally endemic or widespread, extending from the equator to the boreal regions of Europe and from sea level to 4000 m in China (Kremer and Hipp 2020). *Quercus* section *Cyclobalanopsis* species dominate in the subtropical and warm-temperate evergreen broad-leaved forests of East Asia (Deng et al. 2018) where species such as *Quercus acuta* Thunb. and *Quercus hondae* Makino maintain a high degree of endemism (Qian and Ricklefs 2000).

To date, many plastid genomes (plastomes) have been sequenced for *Quercus* and have provided useful phylogenetic information to solve the taxonomic problems attributed to hybridization (Yang et al. 2016). However, *Cyclobalanopsis* plastome sequence availability is scarce, especially when considering their high level of endemism in East Asia. *Quercus acuta* is known as an evergreen broad-leaved oak tree endemic to the warm-temperate regions of East Asia, such as China, Korea and Japan. This species is an important resource for maintaining regional forest biomes (Lee and Choi 2010). However, their distribution in China, along with taxonomic problems, still remains controversial (Ohashi et al. 2006; Deng et al. 2008). Therefore, the plastome sequence for this species will be an important basis for improving our understanding

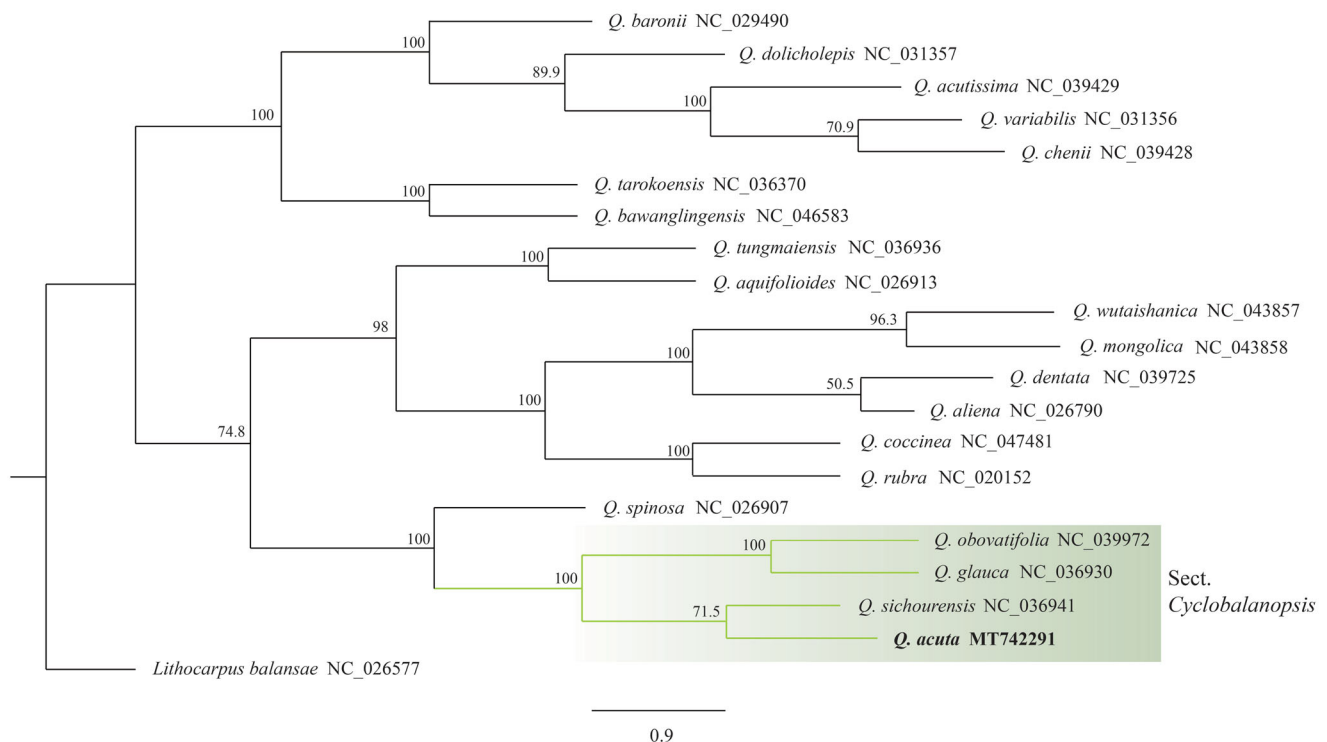
of the evolutionary process and solving taxonomic problems in inter/intra species within especially section *Cyclobalanopsis*.

*Quercus acuta* samples were collected from Jeju Island, South Korea (N33°19'11", E126°37'25"). The voucher specimen (MFDS-C-7840) was stored in the herbarium at the Korea Institute of Oriental Medicine (KIOM: [sgyang81@kiom.re.kr](mailto:sgyang81@kiom.re.kr)). The DNA library was constructed and sequenced on the MGI-seq 2000 platform (LAS, Seoul, Korea) and generated 71,993,390 raw reads (150 bp paired-end). The *Q. acuta* plastid genome was constructed using NOVOPlasty 4.1 (Dierckx et al. 2017), with the *Q. gilva* *rbcl* gene sequence (Zeng et al. 2019; MK986651) as the seed. The sequence was checked by reference mapping using Geneious 10.2.3 (Kearse et al. 2012), on which 86,571 reads were assembled with an 80X coverage. The annotation was separately performed in Geneious 10.2.3 (Kearse et al. 2012), and was manually corrected for the start and stop codons and for the intron/exon boundaries. The annotated plastome sequence was deposited in GenBank (accession number: MT742291). The phylogenetic tree was constructed by downloading the complete plastome sequences of 20 related species (*Quercus*: 19 species, *Lithocarpus*: 1 species) from the NCBI database and alignments were performed with MAFFT (Kato and Toh 2010). The maximum likelihood (ML) analysis was performed with RAxML v.8.0 (Stamatakis 2014) using default parameters and 1000 bootstrap replicates. For RAxML tree, the general time-reversible (GTR) model of nucleotide

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**Figure 1.** A phylogenetic tree (RAxML) using the plastome sequences of 21 species, with *Lithocarpus balansae* as the outgroup. The numbers above each node indicate the bootstrap value with 1000 replicates.

substitution was used with the Gamma model of rate heterogeneity.

The *Q. acuta* plastome is 160,522 bp long, with two inverted repeat (IR) regions (25,839 bp each) that separate a large single copy (LSC) region (90,199 bp) and a small single copy (SSC) region (18,645 bp). This is the second shortest reported *Quercus* plastome. It contains 130 genes that encode 85 proteins, eight ribosomal RNAs, and 37 transfer RNAs, and the G+C content is 36.9% overall, 34.8% in the LSC region, and 42.8% in the IR regions. The gene content and order were comparable to other published *Quercus* plastome (Yang et al. 2016; Zeng et al. 2019). The phylogenetic tree (Figure 1) shows that *Q. acuta* is closely related to *Q. sichouensis*, with strong bootstrap support. Section *Cyclobalanopsis*, comprised of *Q. acuta*, *Q. sichouensis*, *Q. glauca*, and *Q. obovatifolia*, form a monophyletic sister clade to *Q. spinosa*. These data are useful for the phylogenetic and evolutionary studies of *Quercus* and Fagaceae.

## Disclosure statement

No potential conflict of interest was reported by the author(s).

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## Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI (accession no. MT742291) at <https://www.ncbi.nlm.nih.gov>. All high-throughput sequencing data files are available from

the GenBank Sequence Read Archive (SRA) accession number: SRR13068430.

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