The complete chloroplast genome of *Chimonobambusa utilis* (Keng) P. C. Keng, known as ‘the king of bamboo shoots’

Liangjun Xiao, Tao Wu, Yongjian Liao, and Tian Xu

Institute of Economic Forest, Yunnan Academy of Forestry and Grassland, Kunming, China

**ABSTRACT**

The whole chloroplast (cp) genome sequence of *Chimonobambusa utilis* (Keng) P. C. Keng has been characterized using Illumina pair-end sequencing. The complete cp genome (GenBank accession: OK040769) was 139,540 bp in length, containing a large single copy region (LSC) of 83,133 bp and a small single copy region (SSC) of 12,811 bp, which were separated by a pair of 21,798 bp inverted repeat regions (IRs). The genome contained 133 genes (114 unique), including 86 protein-coding genes (81 unique), 39 tRNA genes (29 unique), and eight rRNA genes (four unique). The overall GC content of *C. utilis* cp genome is 38.88%. Phylogenetic analysis of 32 cp genomes within the supertribe Bambusatae suggests that *C. utilis* is closely related to *C. quadrangularis*.

*Chimonobambusa utilis* (Keng) P. C. Keng 1948 is a kind of tall bamboo with a stalk as high as 10 m and diameter of 2–4 cm. It is an endemic bamboo species in Southwest China, mainly distributed in an altitude range of 1000–2100 m in Sichuan, Guizhou, Yunnan provinces and Chongqing municipality, with abundant natural resources and large preservation area (Li and Chris 2006; Ding et al. 2011). This bamboo is a rich source of nutrients, natural bioactive compounds and antioxidants. The young shoots of *C. utilis* are formed in September, and end in November, lasting for 60–70 days. They are famous all over the world for their unique fresh, fragrant, tender, and crisp quality, and are known as ‘the king of bamboo shoots’ (Ren et al. 2021). It is also a good raw material for papermaking and bamboo weaving. The genus *Chimonobambusa* includes about 37 species (Li and Chris 2006), but NCBI database currently only records a few chloroplast (cp) genome data from six species of this genus. The cp genome sequence of *C. sichuanaensis* has been used to determine evolutionary relationships and to clarify the classification status of the species (Zhao et al. 2021). In this study, we report and characterize the complete cp genome of *C. utilis*, which will provide genomic data for further research.

Fresh and healthy leaves of a single plant of *C. utilis* were collected from Jinfo Mountain, Nanshan District, Chongqing municipality, China (N 29°1’11”, E 107°10’37”, altitude: 2080 m). The voucher specimen (Wu20210049) was deposited in the Herbarium of Yunnan Academy of Forestry and Grassland, Kunming, China (http://www.ynlyr.org.cn/, Wu Tao, ynfwt@126.com). *C. utilis* in current research did not belong to the endangered or protected species. The experimental materials were collected complying with relevant institutional guidelines and national legislation. The samples were collected without causing harm to the plant habitat or the bamboos themselves. The total genomic DNA was isolated using DNAsecure Plant Kit (Beijing Tiangen Biotech Company, Beijing, China). The concentration and integrity of the DNA were analyzed by Invitrogen Qubit Fluorometers (Thermo Fisher Scientific, Waltham, MA) and agarose gel electrophoresis. A shotgun library with an insert size of 150 bp was prepared and sequenced using the Illumina Hiseq 2500 (Illumina, San Diego, CA). Approximately, 2.1 Gb raw data of 150 bp paired-end reads were obtained. The raw reads were filtered to obtain high-quality clean reads by using NGS QC Toolkit v2.3.3 with default parameters (Patel and Jain 2012). Plastomes were de novo assembled by GetOrganelle (Jin et al. 2020). The genome sequence was annotated using the published *C. hejiangensis* cp genomes (NC053872) as references, then adjusted and confirmed with Geneious Prime 2020.0.5 (Kearse et al. 2012). The annotated genomic sequence was then deposited into GenBank with the accession number OK040769. The complete cp genome sequences of 32 species from the four tribes, Bambuseae, Dendrocalameae, Melocanneae, and Shibataeeae in supertribe Bambusatae were aligned using MAFFT (Katoh and Standley 2013), and a maximum-likelihood (ML) tree was established based on whole cp genome sequences using the RAxML8 (Stamatakis 2014) with GTR GAMMA 1 nucleotide model and 1000 bootstrap replicates, in order to ascertain the phylogenetic status of *C. utilis*.

The complete cp genome of *C. utilis* is 139,540 bp in length, containing a pair of inverted repeats (IRs) of 21,798 bp, a small single copy (SSC) of 12,811 bp, and a large single copy (LSC) of 83,133 bp. The overall GC content of the cp genome is 38.88%, the ones of the LSC, SSC, and IR were...
36.95%, 33.22%, and 44.22%, respectively. A total of 133 genes (114 unique ones) in the cp genome were annotated, including 86 protein-coding genes (81 unique), 39 tRNA genes (29 unique), and eight rRNA genes (four unique). ML phylogenetic analysis revealed that *C. utilis* is closely related to *C. quadrangularis* (Figure 1). The newly characterized complete cp genome of *C. utilis* will provide essential resources for further study on the evolution and genetic diversity.

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*Ethics statement*: The plant material of this study is a kind of bamboo, *Chimonobambusa utilis*, which is not a threatened or endangered species. The collection of plant material was carried out in accordance with guidelines provided by our institution, Yunnan Academy of Forestry and Grassland. The authors of this manuscript are willing to undertake relevant ethical responsibilities.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**ORCID**

Liangjun Xiao  [http://orcid.org/0000-0003-4851-1574](http://orcid.org/0000-0003-4851-1574)
Data availability statement

The complete chloroplast genome generated for this study has been deposited in GenBank with accession number OK040769, which is openly available in GenBank of NCBI at website (https://www.ncbi.nlm.nih.gov/). All high-throughput sequencing data files are available from the GenBank Sequence Read Archive (SRA) accession number: SRR15725928. The associated BioProject and BioSample numbers are PRJNA760964 and SAMN21240067, respectively.

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