

MITOGENOME ANNOUNCEMENT

The complete chloroplast genome sequence of *Chikusichloa aquatica* (Poaceae: Oryzeae)

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Abstract

The complete chloroplast sequence of the *Chikusichloa aquatica* was determined in this study. The genome consists of 136 563 bp containing a pair of inverted repeats (IRs) of 20 837 bp, which was separated by a large single-copy region and a small single-copy region of 82 315 bp and 33 411 bp, respectively. The *C. aquatica* cp genome encodes 111 functional genes (71 protein-coding genes, four rRNA genes, and 36 tRNA genes): 92 are unique, while 19 are duplicated in the IR regions. The genic regions account for 58.9% of whole cp genome, and the GC content of the plastome is 39.0%. A phylogenomic analysis showed that *C. aquatica* is closely related to *Rhynchoryza subulata* that belongs to the tribe Oryzeae.

Keywords

Chikusichloa aquatica Koidz, chloroplast genome, Oryzeae

History

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The tribe Oryzeae (Poaceae) contains economically important genera, *Oryza* L. with approximately 23 species and *Zizania* L., which is disjunctly distributed in eastern Asia and eastern North America. Increasing attention has been paid for studying the phylogeny of *Oryza* and its closely related genera in the tribe Oryzeae (Guo & Ge, 2005). The chloroplast DNA (cpDNA) sequences are more and more used for resolving the deep phylogeny of plants (Jansen et al., 2007; Moore et al., 2010; Soltis et al., 2004; Wu & Ge, 2012). At present, a total of eight complete cp genomes belonging to Oryzeae have been published (Brozynska et al., 2014; Mariac et al., 2014; Masood et al., 2004; Tang et al., 2004; Waters et al., 2012; Wu & Ge, 2012).

In this study, we report and characterize the complete chloroplast genome of *Chikusichloa aquatica* Koidz, one important member of the tribe Oryzeae. About 20 g fresh mature leaves were collected to isolate the cpDNA (Shi et al., 2012). Approximately 10 µg purified cpDNA was used for library construction and sequencing on the Illumina Genome Analyzer IIx platform (Germplasm Bank of Wild Species, Kunming Institute of Botany, the Chinese Academy of Sciences (CAS), Kunming, China). Sequence data were then filtered and assembled into the complete cp genome with SOAPdenovo software (Li et al., 2009). Annotation of the assembled genome was performed with Dual OrganellarGenoMe Annotator (DOGMA) to predict protein-coding genes, transfer RNA (tRNA) genes, and ribosome RNA (rRNA) genes (Wyman

et al., 2004). The complete cp genome sequence together with gene annotations was submitted to the GenBank under the accession number of KR078265. To perform phylogenomic analysis we included a total of 13 complete chloroplast genomes together with the obtained cp genome sequence in this study. Maximum likelihood analyses were implemented in RAxML version 7.0.4 (High Performance Computing Center, KIB, CAS, Kunming, China) (Stamatakis, 2006). RAxML searches relied on the general time reversible (GTR) model of nucleotide substitution with the gamma model of rate heterogeneity. Non-parametric bootstrapping as implemented in the “fast bootstrap” algorithm of RAxML used 1000 replicates.

The complete plastome of *C. aquatica* has a total length of 136 563 bp with a typical quadripartite structure (Li et al., 2014). It possesses a pair of inverted repeats (IRa and IRb) of 20 837 bp that separate a large single copy (LSC) region of 82 315 bp and a small single copy (SSC) region of 33 411 bp. The GC content of whole cp genome is 39.0%, with the IRs having higher GC content (44.4%) than LSC (37.2%) and SSC (33.4%) regions due to the presence of GC-rich rRNA genes. The genic regions account for 58.9% of the genome and include 130 genes: 92 are unique, while 19 are duplicated in the IR regions. Among these genes, 71 genes are protein-coding, four are rRNA genes, and 36 are tRNA genes of which eight are present in the IRs. Sixteen genes contain one intron, and two genes have two introns. Phylogenomic analysis showed that *C. aquatica* is closely related to *Rhynchoryza subulata* that is also a member of the tribe Oryzeae (Figure 1). This newly determined cp genome sequence will provide valuable data for understanding the phylogeny and diversification of the tribe Oryzeae and exploiting useful germplasms for rice genetic improvement programs.

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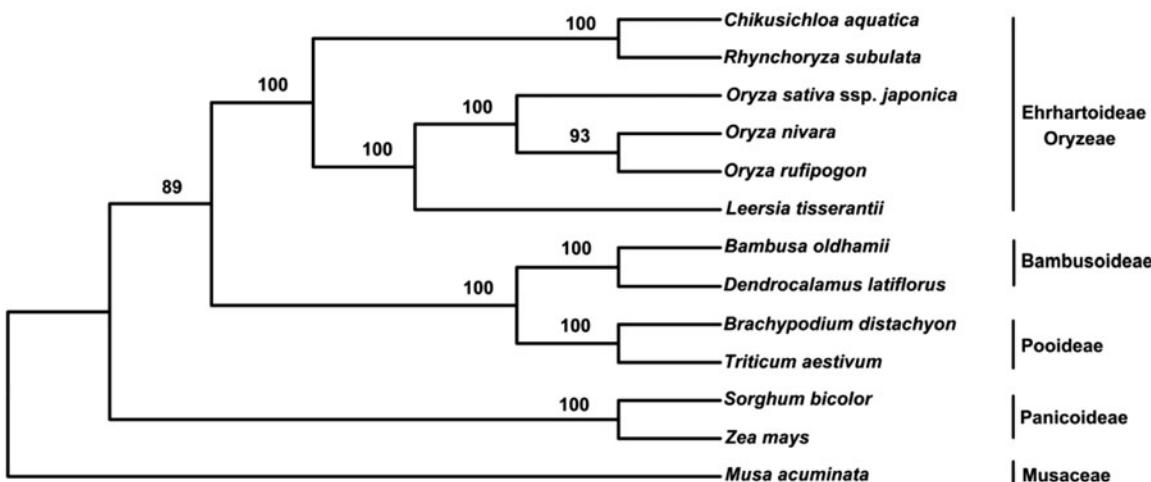


Figure 1. Maximum likelihood phylogenetic tree based on complete chloroplast genome sequences from 12 Poaceae and 1 Musaceae species. Accession numbers: *Chikusichloa aquatica* KR078265, *Rhynchospora subulata* JN415114, *Oryza sativa* ssp. *japonica* AY522330, *Oryza nivara* NC_005973, *Oryza rufipogon* NC_017835, *Leersia tisserantii* JN415112, *Bambusa oldhamii* NC_012927, *Dendrocalamus latiflorus* NC_013088, *Brachypodium distachyon* NC_011032, *Triticum aestivum* NC_002762, *Sorghum bicolor* NC_008602, *Zea mays* NC_001666, and *Musa acuminata* HF677508.

Declaration of interest

The authors report that they have no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This work was supported by the Top Talents Program of Yunnan Province (20080A009), Project of Innovation Team of Yunnan Province, Hundred Oversea Talents Program of Yunnan Province, and Hundred Talents Program of Chinese Academy of Sciences (CAS) to L. Z. Gao.

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