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Li-Zhi Gao
Chinese Academy of Sciences

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MITOGENOME ANNOUNCEMENT

The complete chloroplast genome sequence of the *Phyllostachys sulphurea* (Poaceae: Bambusoideae)

Ju Gao[1] and Li-zhi Gao[1,2]

[1]*Faculty of Life Science and Technology, Kunming University of Science and Technology, Kunming, China and* [2]*Plant Germplasm and Genomics Center, Germplasm Bank of Wild Species in Southwest China, Kunming Institute of Botany, the Chinese Academy of Sciences, Kunming, China*

Abstract

The complete nucleotide sequence of the *Phyllostachys sulphurea* chloroplast genome (cpDNA) was determined in this study. The cpDNA was 139,731 bp in length, containing a pair of 21,798 bp inverted repeat regions (IR), which were separated by small and large single copy regions (SSC and LSC) of 12,879 and 83,256 bp, respectively. The *P. sulphurea* cp genome encodes 129 predicted functional genes; 110 are unique (77 protein-coding genes, 29 tRNA genes, 4 rRNA), 19 are duplicated in the IR regions and one gene extended into the IR region in the junctions between IR and SSC. 43.06% of the genome sequence encodes proteins. The *P. sulphurea* cp genome is AT-rich (61.11%). In these genes, fourteen genes contained one intron, while one gene had two introns.

Keywords

Bambusoideae, chloroplast genome, *P. sulphurea*

History

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Bambusoideae is one of the largest subfamilies in the grass family (Poaceae). There are about 150 genera and 1225 species. Bamboos are of notable economic significance and have a long history of varied uses, ranging from food to raw materials for furniture and housing around the world. The cpDNA sequences are increasingly used for resolving the deep phylogeny of plants because of their low rates of nucleotide substitutions and structural changes (Jansen et al., 2007; Moore et al., 2010; Soltis et al., 2004; Wu & Ge, 2012). At present, 12 complete cp genomes belonging to Bambusoideae have been available in NCBI GenBank (http://www.ncbi.nlm.nih.gov/genbank) (Burke et al., 2012; Wu et al., 2009; Wu & Ge, 2012; Zhang et al., 2011), while the *P. sulphurea* cp genome has not been sequenced. Here we report the sequence and characteristics of complete chloroplast genome of *P. sulphurea*, which was sequenced by using high-throughput sequencing of Illumina's Genome Analyzer, assembled using the CLC Genomic Workbench v3.6 (2010) and deposited into GenBank with the accession number KJ722540. The new data will help to determine the phylogenetic placement of Bamboos and fill gaps in our understanding of Bambusoideae biology.

The *P. sulphurea* cp genome is a typical double-stranded circular DNA with 139,731 bp in length, exhibit the quadripartite structure common to most land plant cp genomes (Kim et al., 2006; Raubeson & Jansen, 2005; Wang et al., 2013; Zhang et al., 2011) with large single copy regions (LSC, 83,256 bp) and small single copy regions (SSC, 12,879 bp) separated by two copies of the inverted repeat (IR, 21,798 bp) (Figure 1). It encodes 129 predicted functional genes; 110 are unique, 19 are duplicated in the IR regions. Among the 110 annotated unique genes, including 77 unique proteins coding genes, 29 tRNA genes and 4 rRNA genes. 43.06%, 2.05%, and 6.58% of the genome sequence encode proteins, tRNAs, and rRNAs, respectively, whereas the remaining 48.31% are non-coding and filled with introns and intergenic spacers. Similar to other cp genomes (Gao et al., 2009; Raubeson et al., 2007; Yang et al., 2010), the *P. sulphurea* cp genome is also AT-rich (61.11%), and the values vary slightly among defined sequences of non-coding, protein-coding, tRNA, and rRNA, where their A+T contents are 64.41%, 60.48%, 47.56%, and 45.27%, respectively. The four rRNA genes are all located in the IR. Twenty-one tRNA genes are located in the single-copy region, whereas the others are located in the IR. 15 genes containing introns, *ycf3* contains two introns, and the rest of the gene contains an intron; *rps12* is trans-spliced, one of its exons is in the LSC region (5′ end) and the two reside in the IR regions (3′ end) separated by an intron; *ndhH* extended into the IR region in the junctions between IR and SSC. Gene *matK* was located within the intron of *trnK-UUU*, and *ycf68* was located within the intron of *trnI-GAU*. In *P. sulphurea* cp genome, the pairs of genes *atpB-atpE*, *psbC-psbD* and *ndhC-ndhK* had 4 bp, 53 bp and 10 bp overlapping regions, respectively.

Correspondence: Li-zhi Gao, Faculty of Life Science and Technology, Kunming University of Science and Technology, Kunming 650500, China. Tel/Fax: +86-871-65223277. E-mail: Lgao@mail.kib.ac.cn

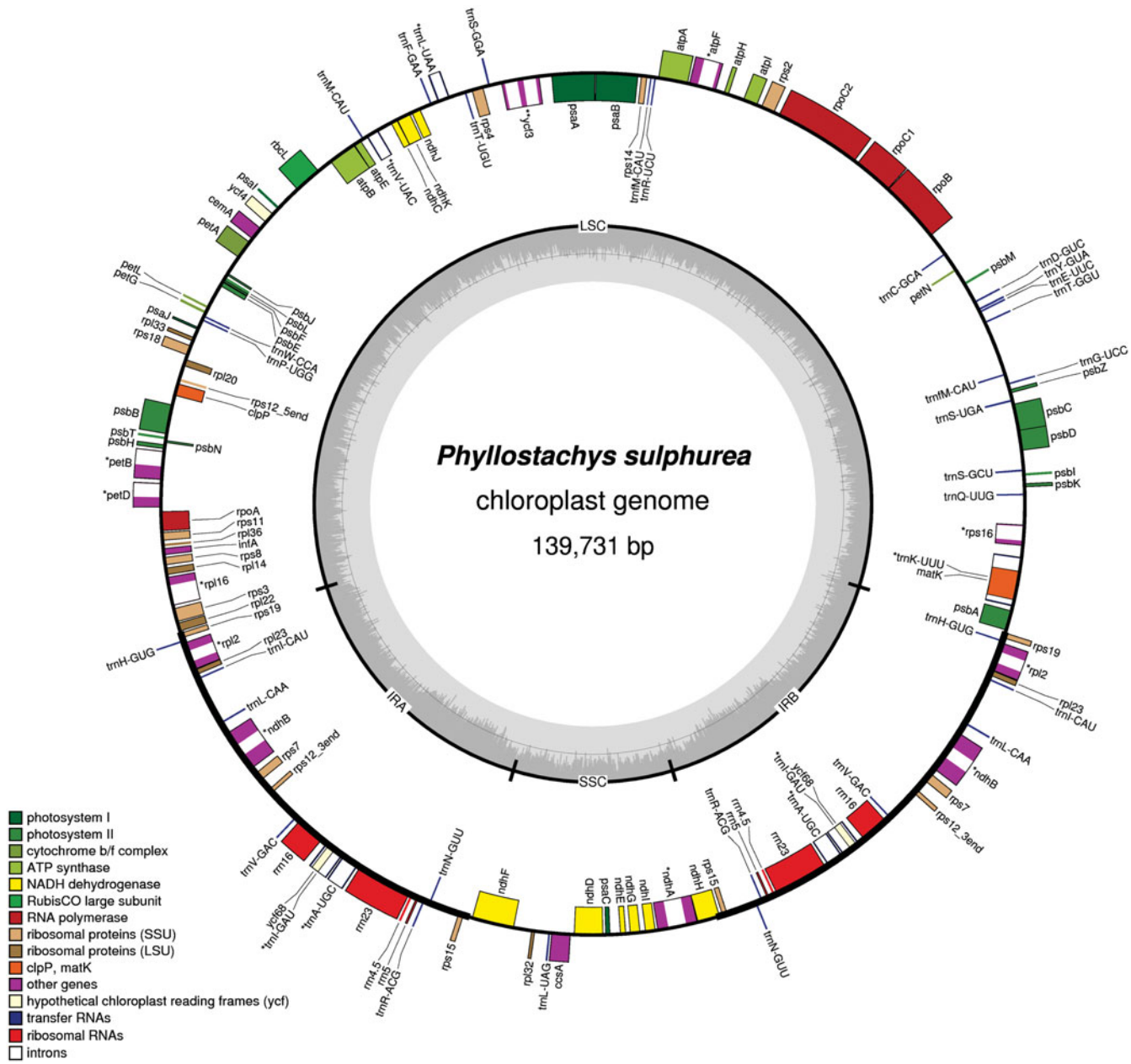

Figure 1. Gene maps of *P. sulphurea* cp genome. The inner circle shows the quadripartite structure of the genome: the two copies of the inverted repeat (IR_A and IR_B) and the large and small single-copy regions (LSC and SSC). Genes inside the circle are transcribed in a clockwise direction, and genes outside of the circle are transcribed counterclockwise. Genes belonging to different functional groups are color coded. Dashed area in the inner circle indicates the GC content of the chloroplast genome.

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Declaration of interest

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