

The complete chloroplast genome sequence of *Mikania micrantha* (Asteraceae), a noxious invasive weed to South China

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ABSTRACT

It is the first report on complete chloroplast genome of *Mikania micrantha* (Asteraceae), a noxious invasive weed to South China. The genome is a circular molecule of 152,092 bp in length with 37.58% average GC content, and includes a large single copy region (83,793 bp), a small single copy region (18,287 bp), and two inverted repeat regions (25,006 bp). The *M. micrantha* cp genome encodes 135 unique genes, including 90 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. ML tree based on 16 complete cpDNA from Asteraceae indicated that *M. micrantha* has a close sister relationship with *Ageratina adenophora* and *Praxelis clematidea*. The complete cpDNA of *M. micrantha* provides useful molecular data for further phylogenetic and evolutionary analysis.

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Asteraceae; chloroplast genome; *Mikania micrantha*; noxious invasive weed

Mikania micrantha (Asteraceae) is one of the top 10 worst weeds in the world known as a mile-a-minute weed. It is an extremely fast growing, long-lived herbaceous vine. It was introduced to Hong Kong in 1884 (Zhang et al. 2004). After naturalization, *M. micrantha* has rapidly spread through the Pearl River Delta since 1984, due to lack of natural enemy (Huang et al. 2015). The species is a noxious invasive weed to South China. It not only kills other plants by blocking the light, twinning, smothering and preventing forest tree regeneration (Zhang et al. 2004), but also competes for water and nutrients with coexisting natives (Wang et al. 2004). Currently, studies on *M. micrantha* focus in investigation of basic features such as the biological characteristics (Hu & But 1994), photosynthetic activity (Wen et al. 2000), allelopathy (Shao et al. 2003), and genetic variation (Wang et al. 2008). However, its characteristics of chloroplast genome remain unresolved. Here, we reported the complete cp genome sequences of *M. micrantha*, which will contribute to elucidate adaptive evolutionary mechanism.

The leaves were from bamboo garden (N: 23°5'37.41", E: 113°17'43.94"), Sun Yat-sen University, Guangdong Province, China, and the specimen is stored in Herbarium of Sun Yat-sen University (SYSU; voucher: L Huang 201408). We sequenced the complete cp genome by using Illumina HiSeqTM 2500 platform (Illumina Inc., San Diego, CA), which generated a total of 4.73 GB of 150-bp paired-end clean reads. Velvet (V 1.2.07) was used to assemble *de novo* sequences from clean reads (Zerbino & Birney 2008). A total length of 127,801 bp in ten chloroplast contigs were obtained through

BLAST to the published invasive species cpDNA sequences in Asteraceae. PCR amplification was applied to bridge the gaps. The initial annotation of the assembled chloroplast genome was executed with Dual Organellar GenoMe Annotator (DOGMA) to predict protein coding genes, transfer RNA (tRNA) genes, and ribosome RNA (rRNA) genes. Furthermore, we performed BLASTN to determine accurate annotation of gene positions. Based on complete chloroplast sequences of 15 species corresponding to 15 different genera in Asteraceae, a maximum likelihood tree was constructed to explore phylogenetic relationship of *M. micrantha* using RAXMLGUI v.1.3 with 1000 bootstrap replicates (Silvestro & Michalak 2012). *Trachelium caeruleum* (Campanulaceae) was used as outgroup.

The complete cp genome of *M. micrantha* is a circular molecule of 152,092 bp in length with 37.58% average GC content (GenBank accession no. KX154571), and includes a large single copy region (LSC, 83,793 bp), a small single copy region (SSC, 18,287 bp), and two inverted repeat regions (IR, 25,006 bp). The *M. micrantha* cp genome contains 135 unique genes, including 90 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Among these genes, two (*clpP* and *ycf3*) contained two introns, which were located in LSC. In addition, 19 genes embraced one introns. ML result with 98% bootstrap showed that *M. micrantha* has a close sister relationship with *Ageratina adenophora* and *Praxelis clematidea* (Figure 1). The complete cpDNA of *M. micrantha* provides useful molecular data for further phylogenetic and evolutionary analysis.

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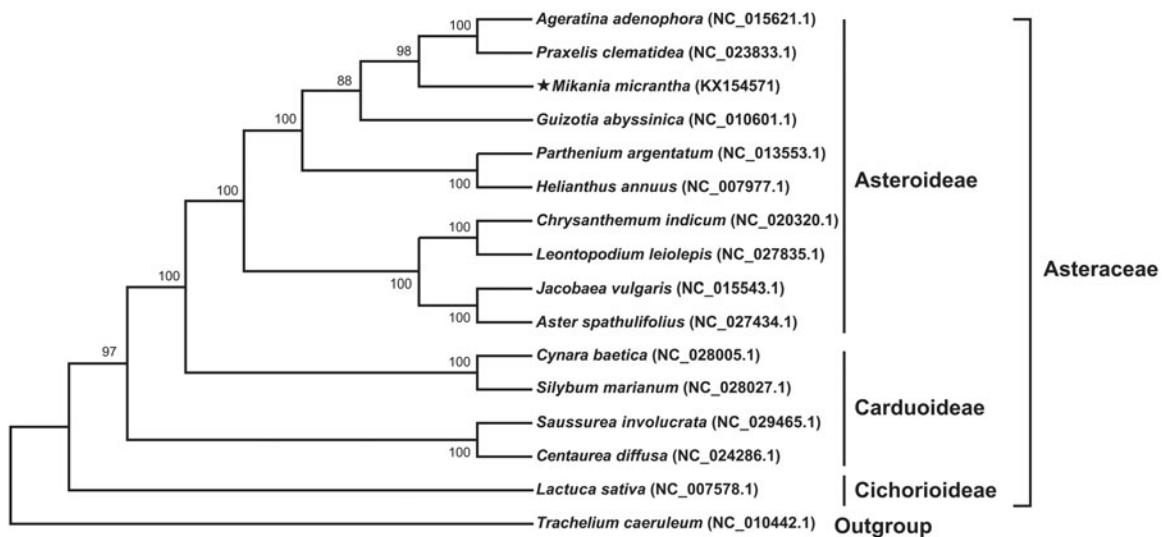


Figure 1. The ML phylogenetic tree based on complete chloroplast genome sequences of 15 species in Asteraceae and *Trachelium caeruleum* as outgroup. The complete chloroplast genome sequences were downloaded from GenBank, and the accession numbers were shown in the tree. ML bootstrap support values were indicated at the nodes.

Disclosure statement

The authors declare no conflict of interests. The authors alone are responsible for the content and writing of the paper.

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