

## The complete chloroplast genome of the invasive and Cd-hyperaccumulator herb *Bidens pilosa* L. (Asteraceae)

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### ABSTRACT

*Bidens pilosa* is an annual invasive and Cd-hyperaccumulator herb. The complete chloroplast genome sequence of the *B. pilosa* is 150,542 bp in length, which is composed of a large single-copy region of 83,542 bp, a small single-copy region of 17,624 bp and a pair of inverted repeat regions of 24,688 bp. It encodes a set of 114 genes, consisting of 80 protein coding, 30 tRNA and 4 rRNA genes. Among all of these genes, 2 genes possess double introns, and 16 genes have a single intron. Phylogenetic analysis showed that *B. pilosa* clustered together with *Marshallia obovata*.

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### KEYWORDS

*Bidens pilosa*; chloroplast genome; Cd-hyperaccumulator; phylogenetic analysis

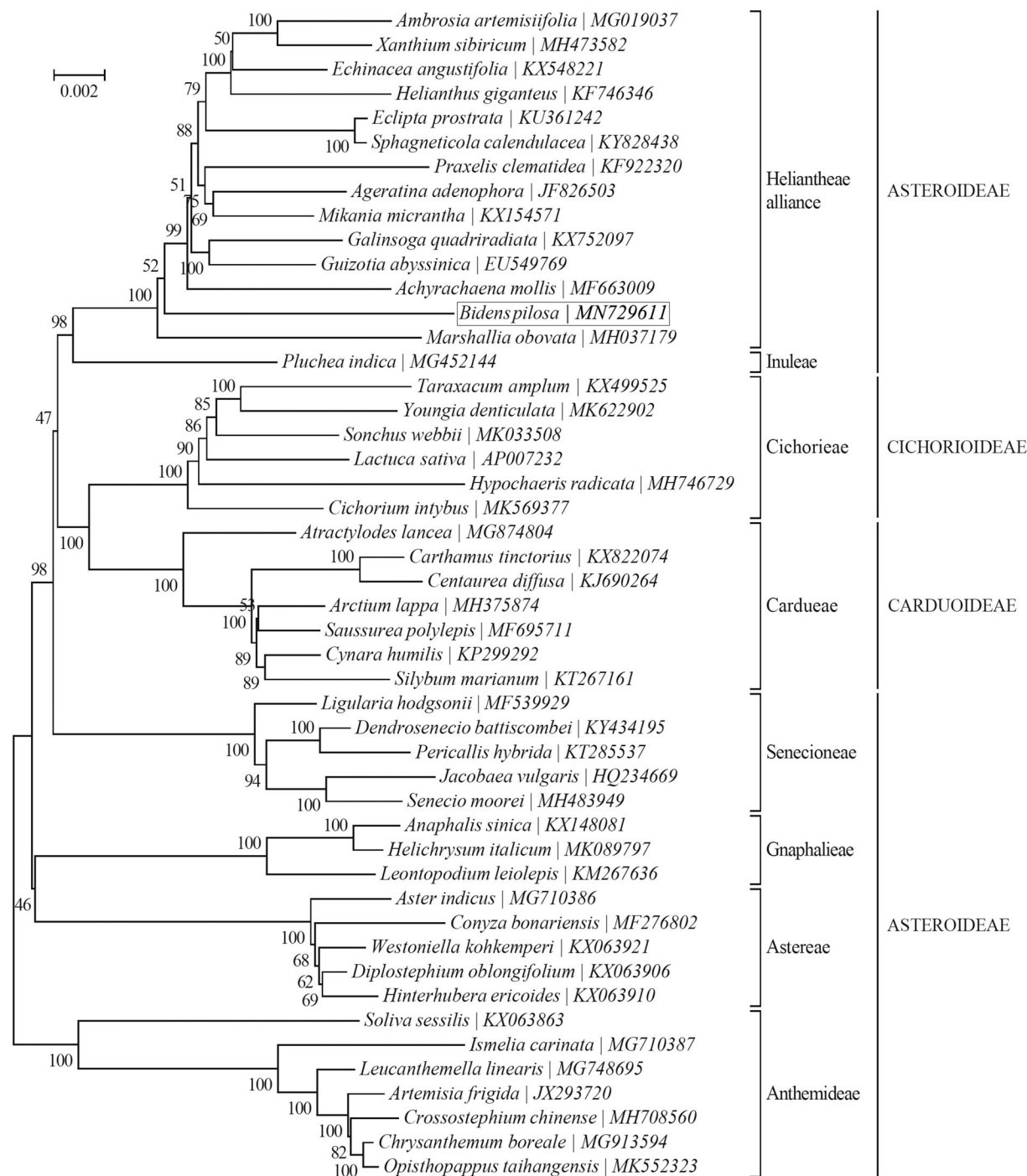
*Bidens pilosa* L. (Asteraceae) is an annual invasive and Cd-hyperaccumulator herb. It is originated from tropical America (Reddy and Singh 1992). At present, it is distributed in the tropics and subtropics of Asia and America. This non-native plant is introduced into China in 1857, and now it is widely distributed in China. This invasive species can produce a large population within one to two generations after spreading to a new habitat for its high seed germination rate, efficient reproductive ability and strong phenotypic plasticity to light, temperature and nitrogen (Chauhan et al. 2019). This invasive species can directly or indirectly damage the survival of local species, agricultural production and biodiversity through interspecific competition and allelopathy (Zhang et al. 2019). *B. pilosa* can be used as the staple food or an ingredient in food for animal or human consumption (Bartolome et al. 2013) and the components of medicinal herbs to treat more than 40 diseases in humans and animals (Hsu et al. 2009; Lai et al. 2015). *B. pilosa* is a cadmium super enrichment plant and an arsenic exclusion species (Sun et al. 2009; Dai et al. 2017). It also has a strong tolerance to the combined pollution of arsenic and cadmium (Sun et al. 2009).

Fresh leaves of *B. pilosa* were obtained from the Xunyangba Town, Ningshan County, Ankang City, Shaanxi Province of China (108°32'22"E, 33°32'38"N) with voucher specimen deposited at the Herbarium of Hunan University of Humanities, Science and Technology (RW2019100501). After

total genomic DNA extraction, high-throughput DNA sequencing (pair-end 150 bp) was conducted on an Illumina HiSeq X Ten platform and the sequence data were used for the assembly of cp genome with MITObim v1.9 (Hahn et al. 2013). The cp genome of *Eclipta prostrata* (KU 361242) (Park et al. 2016) was included as the initial reference.

The complete chloroplast genome of *B. pilosa* (MN 729611) is 150,542 bp in length, containing a large single copy region of 83,542 bp, a small single copy region of 17,624 bp and a pair of inverted repeat regions of 24,688 bp. The overall AT-content of the whole plastome is 62.50%. A total of 114 genes are predicted in the genome, including 80 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Among all of these genes, 2 genes (*clpP* and *ycf3*) possess double introns, and 16 genes (*atpF*, *ndhA*, *ndhB*, *petB*, *petD*, *rpl2*, *rpl16*, *rpoC1*, *rps12*, *rps16*, *trnA-UGC*, *trnG-UCC*, *trnI-GAU*, *trnK-UUU*, *trnL-UAA* and *trnV-UAC*) have a single intron.

To further investigate the phylogenetic position of *B. pilosa*, a neighbor-joining (NJ) analysis was constructed based on the concatenated chloroplast protein-coding sequences of 47 other Asteraceae species using MEGA7 (Kumar et al. 2016) with 1000 bootstrap replicates. The phylogenetic tree showed that *B. pilosa* clustered together with *Marshallia obovata* (Figure 1). This study identified the whole chloroplast genome sequence of *B. pilosa*, which may provide valuable resources for the genetic research and important guidance



**Figure 1.** Phylogeny of 48 species within the family Asteraceae based on the neighbor-joining (NJ) analysis of the concatenated chloroplast protein-coding sequences. The support values are based on 1000 random replicates, and are placed next to the branches. The tribe- and subfamily-level taxonomy is also shown.

for the scientific management and efficient utilization of *B. pilosa*.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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