

The complete chloroplast genome sequences of *Barnardia japonica* (Thunb.) Schult. and Schult.f

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ABSTRACT

Barnardia japonica is an ornamental bulb with important medicinal usage. The complete chloroplast genome of *B. japonica* was newly sequenced in this study. The total chloroplast genome size of *B. japonica* was 156,129 bp. In total, 131 genes were identified, including 85 protein-coding genes, 8 rRNA genes, and 38 tRNA genes. Eighteen genes are containing introns (*clpP* and *ycf3* contained two introns) and 18 genes had two copies. The overall GC content of this genome was 37.7%. A further phylogenomic analysis of Asparagales, including 36 taxa, was conducted for the placement of genus *Barnardia*. The complete plastome of *B. japonica* will provide a valuable resource for further genetic conservation, phylogenomic, and evolution studies in the genus and family.

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Asparagaceae, according to the APG III system (APG III 2009), in the order of Asparagales, is a family of monocotyledonous flowering plants, including 114 genera with a total of ~2900 known species. *Barnardia* Lindley, is a small genus of bulbous flowering plants in the family Asparagaceae, subfamily Scilloideae. Only two species were included in this genus, *Barnardia japonica* and *Barnardia numidica*, which are mainly distributed in East Asia and Northwest Africa, Southwest Europe (Ali et al. 2012). *B. japonica* is heavily cultivated as an ornamental bulb showing attractive and sophisticated flowers. It also has been used for a wide range of medicinal applications to treat the rheumatism, cardiac, urinary infection, dermatological, and hemorrhoid disease (Chang 2017; Kayıran and Özkan 2017). Here, we assembled and characterized the first complete plastome of genus *Barnardia*. It will provide potential genetic resources for further evolutionary studies of the genus and other relatives in Asparagaceae.

Total DNA was extracted from fresh leaves of *Barnardia japonica* individual using DNA Plantzol Reagent (Invitrogen, Carlsbad). It is collected from Mingang, Wenzhou, Zhejiang, China (27°56'32.41"N, 120°31'34.06"E, Voucher No. WH1708010624, deposited at Zhejiang University). The plastome sequences were generated using Illumina HiSeq 2500 platform (Illumina Inc., San Diego, CA). In total, about 14.5 million high-quality clean reads (150 bp PE read length) were generated with adaptors trimmed. The CLC de novo assembler (CLC Bio, Aarhus, Denmark), BLAST, GeSeq (Tillich et al. 2017), and tRNAscan-SE v1.3.1 (Schattner et al. 2005) were used to align, assemble, and annotate the plastome.

The full length of *Barnardia japonica* chloroplast genome (GenBank Accession No. MH287351) was 156,129 bp and comprised of a large single copy region (LSC with 85,284 bp), a small single copy region (SSC with 18,429 bp), and two inverted repeat regions (IR with 26,208 bp). The overall GC content of the *B. japonica* cp genome was 37.7% and the GC content in the LSC, SSC, and IR regions are 35.8, 31.3, and 42.9%, respectively. A total of 131 genes were contained in the cp genome (85 protein-coding genes, 8 rRNA genes, and 38 tRNA genes). Eighteen genes had two copies, which included 6 PCG genes (*ndhB*, *rpl2*, *rpl23*, *rps12*, *rps7*, and *ycf2*), 8 tRNA genes (*trnA-UGC*, *trnH-GUG*, *trnI-CAU*, *trnI-GAU*, *trnL-CAA*, *trnN-GUU*, *trnR-ACG*, and *trnV-GAC*), and all 4 rRNA species (*rrn4.5*, *rrn5*, *rrn16*, and *rrn23*). Among the protein-coding genes, two genes (*clpP* and *ycf3*) contained two introns, and other ten genes (*atpF*, *ndhA*, *ndhB*, *petB*, *petD*, *rpl16*, *rpl2*, *rpoC1*, *rps12*, *rps16*) had one intron each.

Thirty-six chloroplast genome of Asparagales were fully aligned with MAFFT v7.3 (Kato and Standley 2013), and the maximum likelihood (ML) inference was performed using GTR+I+ Γ model with 1000 bootstrap replicates with RAxMLv.8.2.1 (Stamatakis 2014) on the CIPRES cluster service (Miller et al. 2010). The result revealed that *B. japonica* was most closely related to members of genus *Milla* with the current sampling extent (Figure 1). The newly characterized *B. japonica* complete chloroplast genome will provide essential data for further study on the phylogeny and evolution of the genus *Barnardia* and the family Asparagaceae.

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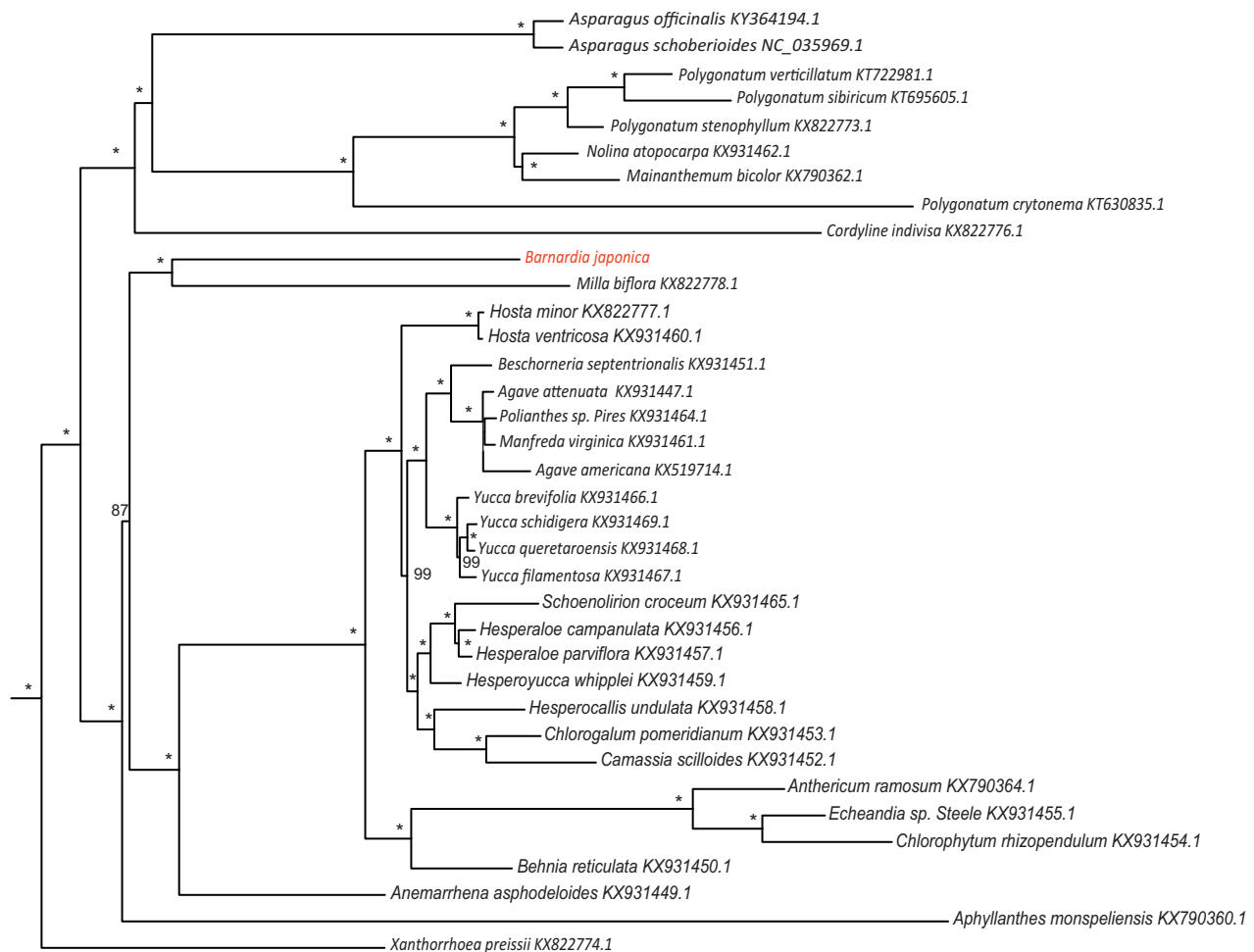


Figure 1. The best Maximum likelihood (ML) phylogram inferred from 36 chloroplast genomes in Asparagaceae (bootstrap value are indicated on the branches, "*" denotes a fully supported node).

Disclosure statement

No potential conflict of interest was reported by the authors.

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