

The complete chloroplast genome sequence of a medicinal herb *Liriope platyphylla* (Asparagaceae)

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ABSTRACT

Liriope platyphylla is herbaceous perennial plant belonging to the Asparagaceae family and widely used both as ornamental plant and herbal medicine. The complete chloroplast genome of *L. platyphylla* was 156,754 bp in length, which was composed of four distinct parts; a large single copy (LSC) of 85,118 bp, a small single copy (SSC) of 18,680 bp, and a pair of inverted repeat regions (IRa and IRb) of 26,478 bp. A total of 130 genes including 83 protein-coding genes, 39 tRNA genes and 8 rRNA genes were identified. The phylogenetic tree showed that *L. platyphylla* has a close relationship with other Nolinoideae plants, especially with *Maianthemum dilatatum* and *Nolina atopocarpa*.

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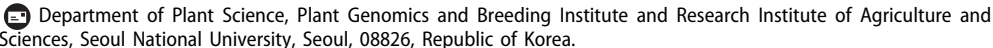
Liriope platyphylla is a perennial herb belonging to the Asparagaceae family, distributed in temperate regions of the Northern hemisphere, especially in East Asia (Lee et al. 1989). *L. platyphylla* has been used both as ornamental plant and herbal medicine. A root tuber of *L. platyphylla* has been proven the efficacy of anti-inflammatory, anti-asthmatic effects (Lee et al. 2005). It is also reported that aqueous extract of *L. platyphylla* has been shown to be effective in type 2 diabetes mellitus (Kim et al. 2012). These effects come from many bioactive substances contained in their tuber. Despite its medical importance, there is few genomic study of *L. platyphylla*. On this account, we completed and characterized the chloroplast genome sequence assembly of *L. platyphylla* using whole genome sequences and analyzed its relationship with other Asparagaceae species.

The plant sample was maintained and collected from Medicinal Plant Garden, College of Pharmacy, Seoul National University, Goyang, Korea (37°42'41.8"N, 126°49'07.2"E). Total genomic DNA was extracted from *L. platyphylla* leaves and stored in National institute of Biological Resources (42, Hwangyeong-ro, Seo-gu, Incheon, 22689, Korea) with collection number of NIBRGR0000608774. The whole genome sequencing was conducted using the Illumina Miseq platform (Illumina, San Diego, CA). The high quality paired-end reads of 3.38 Gbp were obtained and used for *de novo* assembly of the complete chloroplast genome. We followed the dnaLCW method (Kim et al. 2015a, Kim et al. 2015b) using CLC genome assembler (ver. 4.6, CLC Inc, Aarhus, Denmark). The

chloroplast genome was annotated by GeSeq (Tillich et al. 2017), followed by manual confirmation using Artemis program (Rutherford et al. 2000) and BLAST searches.

Complete chloroplast genome of *L. platyphylla* (GenBank Accession No. MK210628) was 156,754 bp in length, and separated into four distinct regions: a large single copy (LSC) (85,118 bp), a small single copy (SSC) (18,680 bp), and a pair of inverted repeats (IRa and IRb) (each 26,478 bp). In *L. platyphylla* chloroplast genome, a total of 130 genes including 83 protein-coding genes, 39 tRNA genes and 8 rRNA genes were identified through Ge-Seq annotation and BLAST tools (Tillich et al. 2017).

To carry out the phylogenetic tree, multiple alignment of complete chloroplast genome sequences with those of 28 species belonging to the Asparagaceae family and *Nicotiana tabacum* as an outgroup was initially performed, using MAFFT 7.0 (Kato and Standley 2013). Phylogenetic analysis was followed based on the aligned sequences for a neighbor-joining tree by maximum composite likelihood model with 1000 bootstrap replications of MEGA 7.0 (Kumar et al. 2016) (Figure 1). The phylogenetic tree informed that the family Asparagaceae was divided into Agavoideae, Brodiaeoideae, Asparagoideae, Lomandroideae, Nolinoideae, and Aphyllanthoideae subfamilies. The subfamily Nolinoideae, where *L. platyphylla* included, was sub-grouped into four genera, *Liriope*, *Polygonatum*, *Maianthemum*, and *Nolina*. More specifically, *L. platyphylla* was situated in company with *Maianthemum dilatatum* and *Nolina atopocarpa*.

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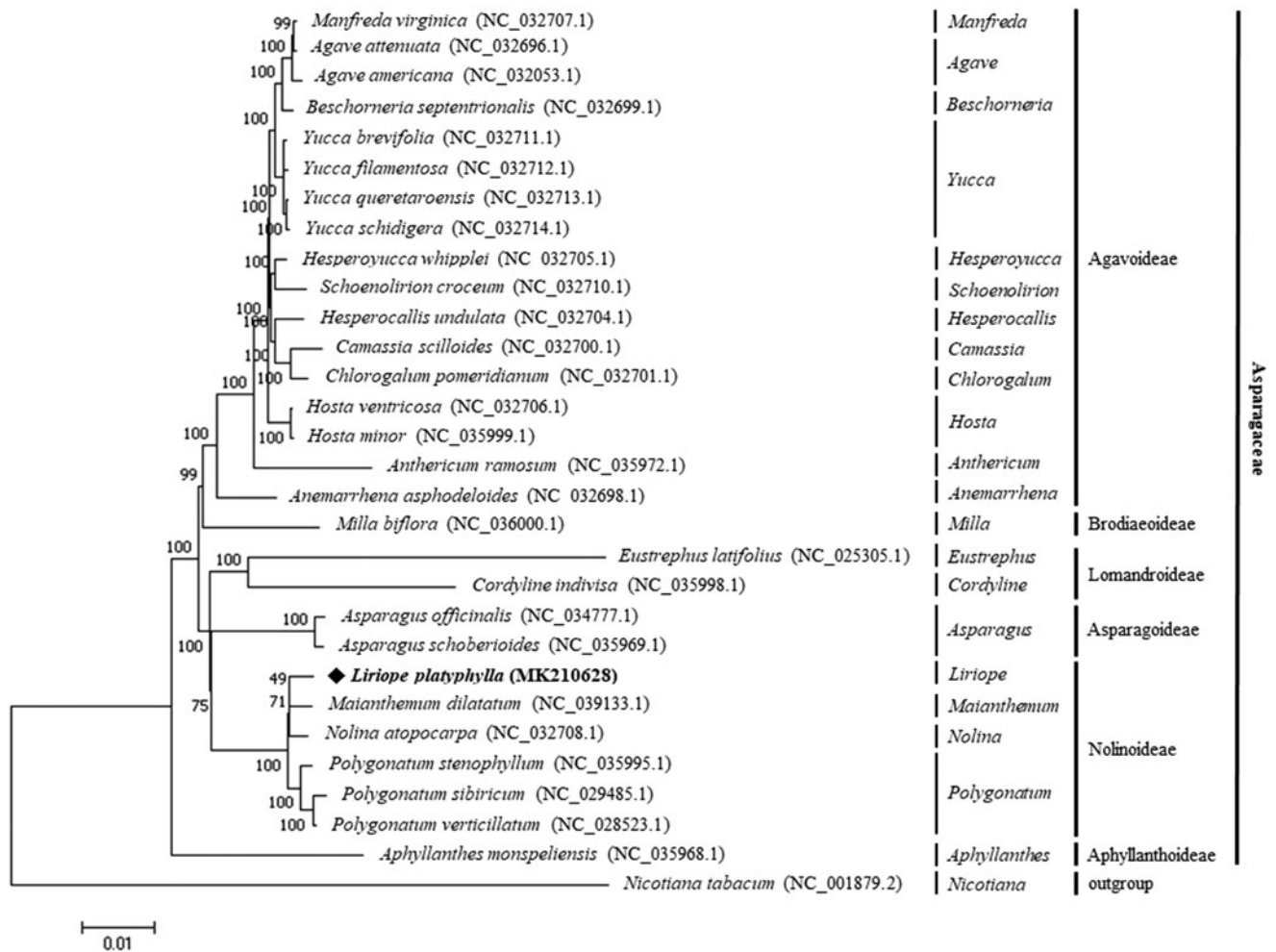


Figure 1. The phylogenetic tree was composed using chloroplast genome sequences of 29 species belong to the Asparagaceae family and *Nicotiana tabacum* as an outgroup. Using the Mega 7.0 software, a neighbor-joining tree was comprised with maximum composite likelihood model with 1000 bootstrap replications.

Disclosure statement

No potential conflict of interest was reported by the authors.

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