The complete chloroplast genome sequence of Laplacea alpestris and its phylogenetic position

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Laplacea Kunth, with ca. 30 species, mainly distributed in South and Central America, Malaya, Indonesia (Kobuski 1949, 1950). The genus was built in 1822 based on the type species (L. speciosa Dyer) from Peru (Humboldt et al. 1822). The systematic position of Laplacea changed significantly among different taxonomic treatments based on morphological and floral ontogenic evidence, and even was included in Gordonia s.l. (Airy Shaw 1936; Sealy 1958; Keng 1962; Ye 1990; Tsou 1998). Molecular phylogenetic analysis based on rbcL and matK, and the chloroplast genome sequences suggested that only Gordonia brandegeei H. Keng nom. nov. (=Laplacea grandis) (Keng 1980) should be retained in Gordonia s.s., other species from Laplacea were members of Theaceae (Prince and Parks 2001; Yu et al. 2017). However, only scarce species were included in previous studies and only one chloroplast genome was reported for Laplacea (Laplacea fruticosa, Yu et al. 2017). In this study, we present the complete chloroplast genome sequence of Laplacea alpestris Dyer using Illumina sequencing technology.

Leaf sample of L. alpestris was obtained from the Herbarium of University of Florida (FLAS, voucher FLAS 180,103), the specimen was collected from Massif de la Selle of Haiti. Genomic DNA was isolated using a modified CTAB approach (Doyle and Doyle 1987). The 150 bp pair-end reads were sequenced based on the Illumina Hi-Seq 2500 platform. Totally, 14,086,309 reads in size of 4.71 G were obtained for the next analysis. The chloroplast genome was de novo assembled by GetOrganelle script (Jin et al. 2020), with SPAdes version 3.10.1 as assembler (Bankevich et al. 2012), and visualized the paths of the cp genome using Bandage (Stamatakis 2014) was used to build a maximum likelihood phylogenetic tree. Sequences were aligned using MAFFT version 7.407 (Katoh and Standley 2013) with the Auto algorithm. RAxML (Stamatakis 2014) was used to build a maximum likelihood (ML) tree, and bootstrap support (BS) were calculated using 1000 replicates. The maximum likelihood phylogenetic tree revealed that L. alpestris and L. fruticosa formed a monophyletic clade (BS = 100%), which was closely related to Apterosperma oblata (Figure 1).

To confirm the phylogenetic position of L. alpestris, we conducted the phylogenetic analysis by combining the chloroplast genome of L. alpestris and other 55 species (including 50 ingroups from Theaceae and 5 outgroups). Sequences were aligned using MAFFT version 7.407 (Katoh and Standley 2013) with the Auto algorithm. RAxML (Stamatakis 2014) was used to build a maximum likelihood (ML) tree, and bootstrap support (BS) were calculated using 1000 replicates. The maximum likelihood phylogenetic tree revealed that L. alpestris and L. fruticosa formed a monophyletic clade (BS = 100%), which was closely related to Apterosperma oblata (Figure 1). However, only species of Laplacea from Central and South America were studied till
now (i.e. *L. alpestris*, *Laplacea fruticosa*, and *Laplacea portoricensis*) (Prince and Parks 2001; Yu et al. 2017), whether species from Southeast Asia will fall into *Laplacea* or *Gordonia* s.s. need further researches. The complete chloroplast genome of *L. alpestris* would be useful for the genetic diversity studies of this species and provided new molecular data to illuminate the phylogenetic relationships within Theaceae.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Data availability statement**

The data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov, reference number MT916289.
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