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MITOGENOME ANNOUNCEMENT

The complete chloroplast genome of *Laurocerasus zippeliana* (Rosaceae)

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ABSTRACT

Laurocerasus zippeliana is a widely known landscape plant with high adaptability. We report herein the complete chloroplast genome sequence of *L. zippeliana* assembled from Illumina high-throughput sequencing data. With a total length of 158,940 bp, the complete chloroplast genome was a typical quadripartite circle: two inverted repeats (IRs) of 26,339 bp for each, a large single-copy (LSC) region of 87,339 bp, and a small single-copy (SSC) region of 18,923 bp. A total of 110 unique genes were identified, consisting of 78 protein-coding genes, 28 tRNA genes, and 4 rRNA genes. Phylogenetic analysis confirmed the position of *L. zippeliana* within the order Rosales.

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Laurocerasus zippeliana; landscape plant; complete chloroplast genome; automated assembly

Laurocerasus zippeliana (Miq.) Browicz (synonym of *Prunus zippeliana* Miq.), a perennial evergreen tree in Rosaceae with high ornamental value at all season, can grow vigorously on acidic or slightly alkaline soil, even on dry and barren limestone under high temperature (Peng et al. 2008), which makes it an ideal germplasm resource for landscape application in scenic zones and cities under the condition of extensive cultivation. However, genomic resources of this species are extremely scarce. Our research focused on the assembly of complete chloroplast genome sequence, which can provide some genetic basis for its introduction, improvement and application.

A sample of *L. zippeliana* was collected in Guangzhou Institute of Forestry and Landscape Architecture (113.347°E, 23.236°N), Guangdong province, China, and deposited at Sun Yat-sen University Herbarium (SYS; specimen code SYS-Bore-2018-07-20). Genomic DNA was extracted from mature fresh leaves through modified CTAB method (Doyle and Doyle 1987) and purified to construct a DNA library with the insertion size of ~400 bp. High-throughput sequencing with paired-end 150 bp was performed on an Illumina Hiseq X10 platform. We finally got 5.77 Gb of sequence data, which were then fed into NOVOPlasty (Dierckxsens et al. 2017) to assemble the complete chloroplast genome sequence, using a partial *rpl*16 gene sequence (GenBank accession No. AB254502.1) of *Prunus zippeliana* as a seed during this seed-and-extend algorithm. After being stitched into a synthetic loop, the chloroplast genome was automatically annotated by an online website DOGMA (Wyman et al. 2004) and double-check by Geneious version 11.1.5 (Kearse et al. 2012), followed by manual adjustment and confirmation.

The complete chloroplast genome sequence of *L. zippeliana* (GenBank accession MK168018) was 158,940 bp in length constituting a typical quadripartite circle: two inverted repeats (IRs) of 26,339 bp for each, a large single-copy (LSC) region of 87,339 bp, and a small single-copy (SSC) region of 18,923 bp. A total of 110 unique genes were identified, comprising 78 unique protein-coding genes (12 of them contain a single or more intron(s), while 6 are duplicated in the IR), 28 unique tRNA genes (7 are duplicated in the IR), and 4 rRNA genes (all of which duplicated in the IR).

To infer the explicit phylogenetic position of *L. zippeliana*, a maximum-likelihood (ML) tree was constructed with the chloroplast genomic sequences of 32 species from five orders (Rosales, Fagales, Cucurbitales, Fabales and Celastrales) based on GTRGAMMA substitution model (Stamatakis 2014) with 1000 bootstrap replicates after aligned with MAFFT v7.307 (Katoh and Standley 2013). As shown in Figure 1, *L. zippeliana* is sister to *Prunus takesimensis* and clustered within the group consisting of the species that belong to Rosaceae.

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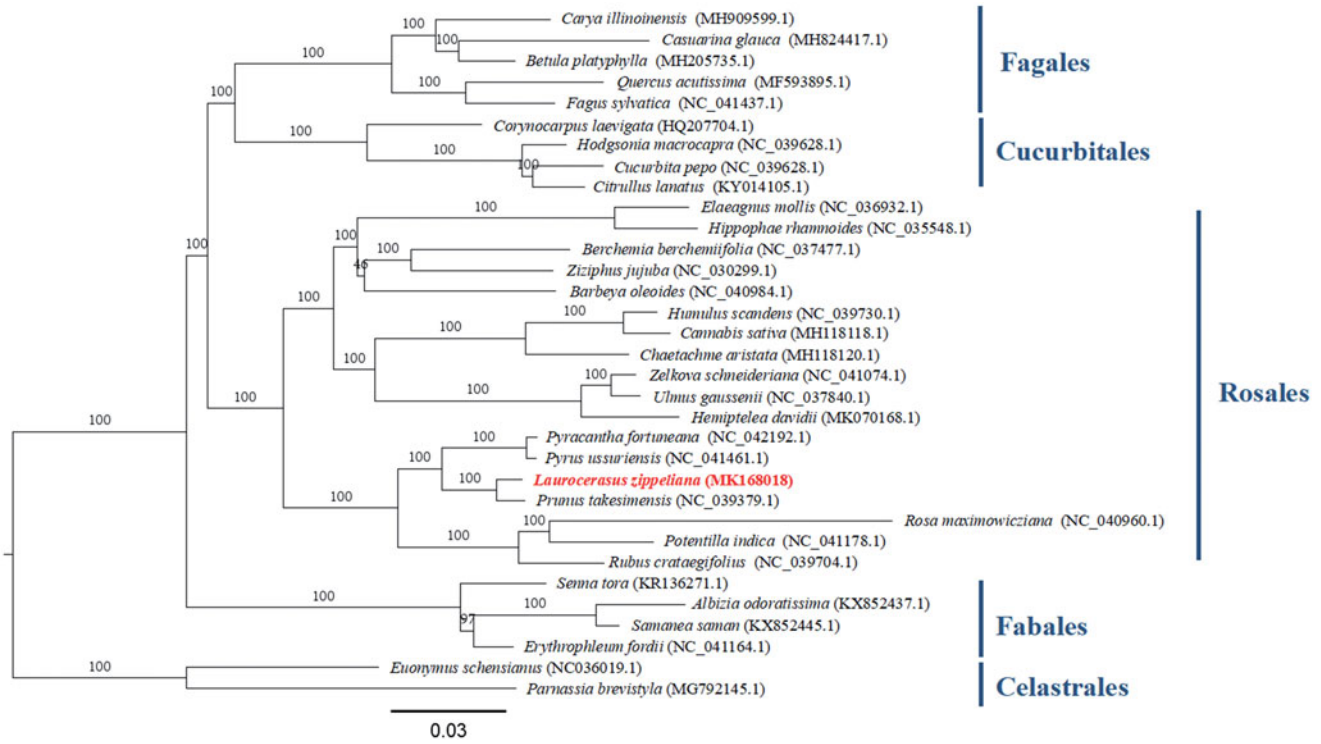

Figure 1. Maximum-likelihood tree showing the phylogenetic position of *Laurocerasus zippeliana* based on the complete chloroplast genome sequences. Bootstrap support values (1000 replicates) are shown next to the nodes. Scale is substitutions per site.

Disclosure statement

No potential conflict of interest was reported by the authors.

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