**ABSTRACT**

*Rhododendron kawakamii* is endemic in Taiwan island and is a unique and epiphytic species. Here, we report its complete chloroplast genome. The length of the *R. kawakamii* chloroplast genome is 230,777 bp, with a large single-copy region of 146,155 bp, a small single-copy region of 72,082 bp, and a pair of inverted repeat regions (IRA) of 6,270 bp each. The genome contains 77 protein-coding genes, 29 transfer RNA genes, and four ribosomal RNA genes. In addition, the genome contains 81 simple sequence repeats. Phylogenetic analysis revealed that *R. kawakamii* is genetically related to *R. datiandingense*.

**RESULTS**

*Rhododendron*, in the Ericaceae family, is a large and extremely diverse genus, containing more than 1000 species worldwide (Shrestha et al. 2018). *Rhododendron kawakamii* Hayata is endemic to Taiwan island. Unlike the other *Rhododendron* species on the island, which are either shrubs or trees, *R. kawakamii* is epiphytic (Tsai et al. 2012) and naturally distributed in the forest between 1500 and 2600 m. Molecular data supported its uniqueness in the phylogeny and showed that it formed an independent cluster in section *Vireya* of subgenus *Rhododendron* (Tsai et al. 2003, 2012). Both natural and artificial hybridization among *Rhododendron* species are common due to their low reproduction barriers (Kaul et al. 1986; Milne et al. 2010), which is particularly true in section *Vireya*, possibly as a result of adaptive radiation events (Milne et al. 2010). Crossing experiments indicate that *R. kawakamii* could also hybridize with *R. santapauii* and produce viable seeds (Kaul et al. 1986). As approximately 70% of *Rhododendron* are classified as endangered or need conservation (Shrestha et al. 2018), and hybridization presents a grave threat to species integrity (Zhang, Qin, et al. 2020b), we report the complete chloroplast genome of *R. kawakamii* to provide a germplasm resource for its evolution and conservation studies.

Fresh leaves of *R. kawakamii* were collected from the Shanlinxi forest recreation area (N23°38'7.8", E120°47'29.3"). A voucher specimen was deposited at the Herbarium of Taiwan Forest Research Institute (https://taif.tfri.gov.tw/tw/index.php, Chien-Fan Chen, chenc@tfri.gov.tw) under the voucher number 511025. The genomic DNA of *R. kawakamii* was extracted by the CTAB (cetyltrimethylammonium bromide) method. The extracted DNA was sequenced using the Illumina HiSeq X Ten system. The sequences were then used to assemble the chloroplast genome of *R. kawakamii* by Fast-Plast 1.2.8 (McKain and Wilson 2017). After assembly, the genome was polished by Pilon 1.24 (Walker et al. 2014) twice. The polished genome was subsequently annotated with CPGAVAS2 (Shi et al. 2019), GeSeq (Tillich et al. 2017), and PGA (Qu et al. 2019). The annotated genome is now available in GenBank under the accession number MW762686. Phylogenetic analysis was perform using maximum likelihood in PhyloSuite 1.2.2 (Zhang, Gao, et al. 2020a) with the concatenated protein sequences of 77 chloroplast coding genes for *R. kawakamii* and the other 17 species.

The *R. kawakamii* chloroplast genome was 230,777 bp in length with a GC content of 35.10%. The genome showed a large single-copy region of 146,155 bp, a small single-copy region of 72,082 bp, and two copies of inverted repeat regions of 6,270 bp each. After annotation, a total of 110 genes were identified in the *R. kawakamii* chloroplast genome, including 77 protein-coding genes, 29 transfer RNA genes, and four ribosomal RNA genes. Furthermore, a total of 81 simple sequence repeats (SSR) were discovered in the genome. These SSRs included 76 mononucleotides (A/T), 3 dinucleotides (A/T), 3 dinucleotides (TA) and 2 trinucleotides (AAT/ATT). Phylogenetic analysis revealed that *R. kawakamii* was genetically related to *R. datiandingense* (Figure 1).

For the 18 species analyzed in phylogeny, a total of 90 protein-coding genes were annotated in their chloroplast genome.
genomes (Table S1), in which clpP, lhbA, orf23, orf28, orf34, orf39, orf46, ORF63, orf64, orf222, ycf1, ycf2, and ycf68 genes were not identified in R. kawakamii chloroplast genome. The orf23, orf28, orf34, orf39, ORF63, orf64, and orf222 genes were only annotated in two Oryza species, and their functions were unknown. For clpP, lhbA, ycf1, ycf2 and ycf68 genes, they also extensively missed in the other Rhododendron species. clpP gene is a proteolytic subunit of the ATP-dependent Clp protease (Shikanai et al. 2001), may be related to the development of plant (Shikanai et al. 2001; Moreno et al. 2017). lhbA encodes a structural protein of the light-harvesting antenna, may be related to maintenance of stable antenna complexes (Ruf et al. 2000). ycf1, ycf2 and ycf68 genes are in ycf gene family and their functions generally unknown (Logacheva et al. 2017; Siipiko et al. 2020), although ycf2 gene is a putative ATPase (Huang et al. 2017). How these missed genes in R. kawakamii chloroplast are functionally related to the growth of R. kawakamii needs further study in the future.

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

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Data availability statement
The genome sequence data that support the finding of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov] under the accession number MW762686 and is also accessible at https://doi.org/10.13140/RG.2.2.36349.69600. The associated BioProject, SRA, and Bio-Sample numbers for reads are PRJNA701862, SRR13987606, and SAMN17915251 respectively.

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Figure 1. Phylogenetic tree for Rhododendron kawakamii and 17 additional species. The GenBank accession numbers are shown in parentheses. Bootstrap values are shown at nodes.
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