The complete plastid genome sequence of *Vaccinium japonicum* (Ericales: Ericaceae), a deciduous broad-leaved shrub endemic to East Asia

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**ABSTRACT**

We here sequenced the complete plastid genome (plastome) of *Vaccinium japonicum* (Ericaceae), a deciduous broad-leaved shrub endemic to East Asia. This species has considerable practical economic value. The plastome of *V. japonicum* is assembled as a single contig (187,213 bp). A large single copy (104,637 bp) and a small single copy (3,000 bp) of the genome are separated by a pair of inverted repeats (39,788 bp). The genome consists of 135 genes, which include 88 protein coding, eight ribosomal RNA, and 39 transfer RNA genes. The plastome of *V. japonicum* is similar to that of *Vaccinium macrocarpon* in gene content and order. Our phylogenetic analysis revealed the phylogenetic position of *V. japonicum* in a highly supported clade of the genus *Vaccinium* together with other four congener, *V. bracteatum*, *V. vitis-idaea*, *V. uliginosum* and *V. macrocarpon*.

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2010). The maximum likelihood (ML) analysis was performed with RAxML v.8.0 (Stamatakis, 2014) using default parameters and 1000 bootstrap replicates. For the RAxML tree, the general time-reversible (GTR) model of nucleotide substitution was used with the Gamma model of rate heterogeneity.

The *V. japonicum* plastome is 187,213 bp long, with two inverted repeat (IR) regions (39,788 bp each) that separate a large single copy (LSC) region (104,637 bp) and a small single copy (SSC) region (3000 bp). The genome has a pair of enlarged IR regions and an extremely shortened SSC region, which contains only a single gene—*ndhF*. In total, 135 genes, which include 88 protein-coding, eight ribosomal RNA, and 39 transfer RNA genes, were annotated. The GC content in overall, LSC, SSC, IR regions are 36.7%, 35.7%, 29.3%, and 38.4%, respectively. The most similar plastome, compared to *V. japonicum* (187,213 bp) in gene content and order, is *V. macrocarpon* (176,045 bp), despite the length difference.

The ML tree shows that all five *Vaccinium* species, *V. bracteatum*, *V. vitis-idaea*, *V. uliginosum*, *V. macrocarpon* and *V. japonicum*, are a monophyletic group with a 100% bootstrap value (Figure 1). This suggests that the complete plastome sequenced in this study is a valuable input to the genomic resources of Ericaceae and can be utilized in future evolutionary studies.

**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 findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov/) under the accession no. MW006668. The associated Sequence Read Archive (SRA) number is PRJNA681995.

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