

Characterization and phylogenetic analysis of the complete plastome of *Veronica undulata* (Plantaginaceae)

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ABSTRACT

Veronica undulata is a perennial herb, and the complete chloroplast genome (plastome) of *V. undulata* was determined in this study. The results showed that the plastome size of *V. undulata* was 151,178 bp, including a large single-copy region (68,533 bp), a small single-copy region (21,403 bp), and two inverted repeat regions (25,566 bp). The total GC content of the plastome was 38.1%. We annotated 115 unique genes in the plastome, including 81 protein-coding genes (PCGs), 30 tRNAs, and four rRNAs. Phylogenetic analysis showed that the species of *V. undulata* and *Veronica* clustered together.

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Veronica undulata is a perennial herb in the Plantaginaceae family (Albach and Chase 2001, 2004; Jensen et al. 2005). The species number in *Veronica* is very large, and many questions exist regarding the species classification of this genus (Albach et al. 2004). *V. undulata* was found on slopes flanking wetlands or ditches, which was widely distributed in China, Korea, Japan, Nepal, India, Pakistan, Afghanistan, Russian Federation, and the United States. As a large amphibious plant, *V. undulata* has important medicinal and ornamental value. Studies have shown that *V. undulata* was rich in iridoid glycosides (Taskova et al. 2010) and phenolic compounds (Li 1952; Boeger and Poulson 2003; Chen et al. 2003). *V. undulata* was previously reported to have cellular activity and anti-inflammatory activity (Saracoglu et al. 2011; Beara et al. 2015), which can help promote wound healing through hemostasis (Küpel et al. 2005; Harput-Hudaverdi et al. 2008). In addition, the extraction of *V. undulata* also contains anti-oxidant, anticholinergic, and anticancer activities (Stojković et al. 2013; Sharifi-Rad et al. 2018). Therefore, *V. undulata* is considered a potential source of functional ingredients with a wide range of biological activities and holds great promise for pharmacological applications (Frontela-Saseta et al. 2013; He et al. 2015). In this study, the plastome of *V. undulata* was reported, which will provide a basic genetic resource for studying this important species and determining its phylogenetic position.

The fresh leaves of *V. undulata* were collected from the Lushan area of Shandong Province (36°21'N, 118°4'E). The voucher specimens (20200709) of *V. undulata* were preserved at the College of Life Sciences, Shandong Normal University. The modified CTAB method was used for total plant DNA extraction (Doyle and Doyle 1987). Library preparation and

paired-end sequencing work were completed on the Illumina Novaseq platform at Novogene (Beijing, China). Plastome was assembled with the Organelle Genome Assembler (OGA, <https://github.com/quxiaojian/OGA>). Plastome was annotated by the Plastid Genome Annotator (PGA, <https://github.com/quxiaojian/PGA>) (Qu et al. 2019) and manually corrected using Geneious v8.0.2 (Kearse et al. 2012). To further determine the phylogenetic position of *V. undulata*, the maximum likelihood (ML) tree was reconstructed using RAxML v8.2.10 with the 1000 rapid bootstrap replicates and the GTRGAMMA substitution model, using the alignment matrix of 115 unique genes generated by MAFFT v7.313 (Katoh and Standley 2013; Stamatakis 2014).

The complete plastome of *V. undulata* (GenBank accession number: MW783683) was 151,178 bp in length. The plastome was a quadripartite structure consisting of two single-copy regions separated by a pair of 21,539 bp inverted repeats. The large and small single-copy regions were 80,455 bp and 12,849 bp, respectively. The total GC content was 38.1%. A total of 115 unique genes were annotated in this plastome, including 81 protein-coding genes (PCGs), 30 tRNAs, and four rRNAs. Phylogenetic tree analysis showed that the species of *V. undulata* and *Veronica* clustered together (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

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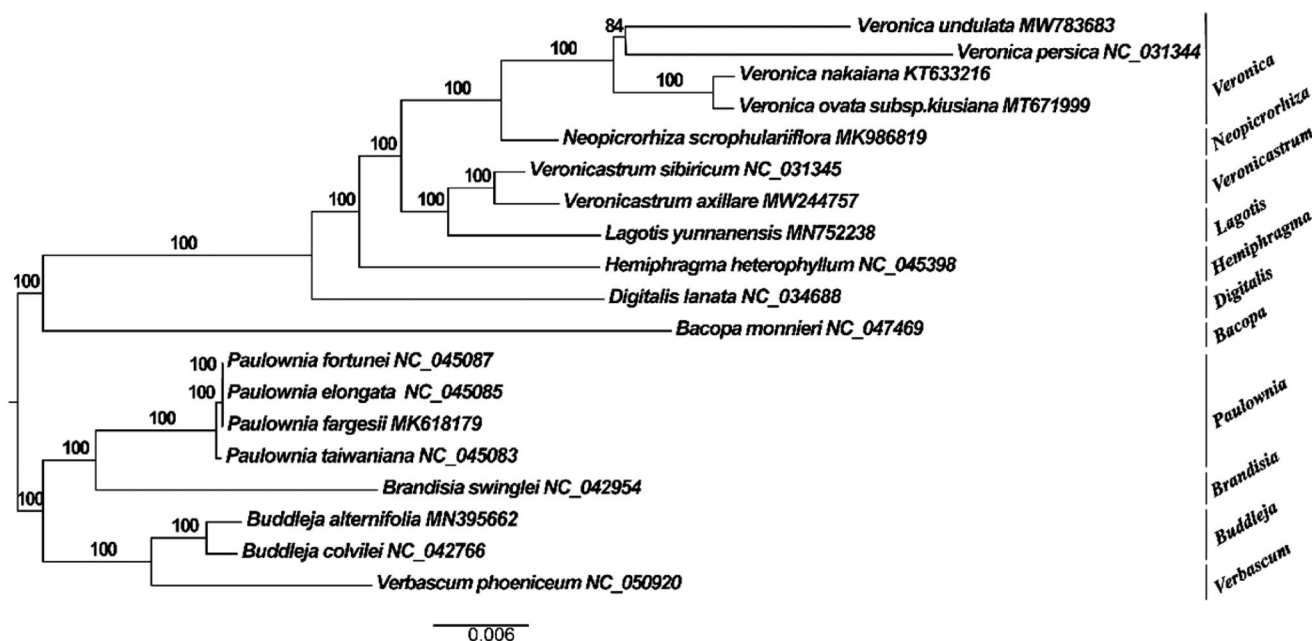


Figure 1. A maximum-likelihood (ML) tree inferred from 115 unique genes. *Paulownia*, *Brandisia*, *Buddleja* and *Verbascum* were used as outgroups. The numbers on branches are bootstrap support values.

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/>) under the accession no. MW783683. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA720311, SRR14162363, and SAMN18646670, respectively.

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