Characterization of the complete chloroplast genome sequence of the endangered species Platycrater arguta (Hydrangeaceae)

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\textbf{ABSTRACT}

Platycrater arguta is a rare and endangered shrub species endemic to East Asia. Here, we report the complete chloroplast (cp) genome structure and its taxonomic position within Hydrangeaceae to promote its conservation and restoration. The complete cp genome of \textit{P. arguta} was 157,810 bp in length and contained a large single-copy region (LSC) of 86,823 bp and a small single-copy region (SSC) of 18,735 bp, as well as a pair of inverted repeat (IR) regions of 26,126 bp, each. 113 unique genes are predicted in this cp genome, including 79 protein-coding genes, 30 transfer RNA (tRNA) genes and 4 rRNAs. Maximum-likelihood (ML) phylogenetic analysis based on 79 shared cp CDS (coding DNA sequences) of 19 species reveals a close relationship between \textit{P. arguta} and Schizophragma hydrangeoides.

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to tribe Hydrangeeae of subfamily Hydrangeoideae and closely related to Schizophragma hydrangeoides Sieb. et Zucc.

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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 MT610904. The raw sequencing reads used in this study were deposited in the Sequence Read Archive (SRA) under accession number PRJNA659226.

References
Ao CQ. 2008. Pre-zygotic embryological characters of Platycrater arguta, a rare and endangered species endemic to East Asia. J Plant Biol. 51(2):116–121.

Chen LX, Brown KR, Yi XG, Sun ZS. 2019. Complete chloroplast genome of Prunus emarginata and its implications for the phylogenetic position within Prunus sensu lato (Rosaceae). Mitochondrial DNA Part B. 4(2):3402–3403.

Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochem Bull. 19:11–15.

Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45(4):e18.

Fu LG. 1989. Rare and endangered plants in China. Shanghai (China): Hanghai Education Publishing House.

Hufford L, Moody ML, Soltis DE. 2001. A phylogenetic analysis of Hydrangeaceae based on sequences of the plastid gene matK and their combination with rbcL and morphological data. Int J Plant Sci. 162:835–846.

Liu LX, Li R, Worth JRP, Li X, Li P, Cameron KM, Fu CX. 2017. The complete chloroplast genome of Chinese bayberry (Morella rubra, Myricaceae): implications for understanding the evolution of Fagales. Front Plant Sci. 8:968.
Qi XS, Yuan N, Comes HP, Sakaguchi S, Qiu YX. 2014. A strong ‘filter’ effect of the East China Sea land bridge for East Asia’s temperate plant species: inferences from molecular phylogeography and ecological niche modelling of Platycrater arguta (Hydrangeaceae). BMC Evol Biol. 14(1):41.

Qiu YX, Qi XS, Jin XF, Tao XY, Fu CX, Naiki A, Comes HP. 2009. Population genetic structure, phylogeography, and demographic history of Platycrater arguta (Hydrangeaceae) endemic to East China and South Japan, inferred from chloroplast DNA sequence variation. Taxon. 58:1226–1241.

Soltis DE, Xiang QY, Hufford L. 1995. Relationships and evolution of Hydrangeaceae based on rbcL sequence data. Am J Bot. 82: 504–514.

Stamatakis A. 2006. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics. 22(21):2688–2690.

Wang S, Xie Y. 2004. China species red list. Vol. 1. Beijing (China): Higher Education Press.

Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organelar genomes with DOGMA. Bioinformatics. 20(17):3252–3255.