The complete chloroplast genome sequence of the threatened *Cypripedium calceolus* (Orchidaceae)

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**ABSTRACT**

The complete chloroplast genome of *Cypripedium calceolus*, a rare species in the family Orchidaceae, was reported in this study. The genome size is 175,122 bp in length, and contains four sub-regions: 97,486 bp of large single copy (LSC) and 22,260 bp of small copy (SSC) regions, separated by 27,688 bp of inverted repeat (IR) regions. A total of 133 genes were annotated, including 87 protein-coding genes, 38 tRNA genes and 8 rRNA genes. The GC content of this cp genome is 34.36%. Phylogenetic analysis revealed a close relationship between *C. calceolus* with *C. japonicum* and *C. formosanum*. This is the first complete cp genome for *C. calceolus* that would be useful for conservation and phylogenetic studies of this species.

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Figure 1. Phylogenetic relationship of 47 orchid species built by maximum-likelihood method based on complete chloroplast genomes, with Oryza genus as the outgroup. The branch support was determined by computing 1000 non-parametric bootstrap replicates.

Disclosure statement
The authors declare no competing financial interest. The authors alone are responsible for the content and writing of the paper.
Funding
This work was supported by the National Natural Science Foundation of China [31670378], Foundation of Liaoning “Xingliaoyingcai Plan” [XLYC1807180], and Foundation for the Youth Scholars of Shenyang Agricultural University [880416040].

References
Bi GQ, Mao YX, Xing QK, Cao M. 2018. HomBlocks: A multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. Genomics. 110(1):18–22.
Cameron KM, Chase MW, Whitten WM, Kores PJ, Jarrell DC, Albert VA, Yukawa T, Hills HG, Goldman DH. 1999. A phylogenetic analysis of the Orchidaceae: evidence from rbcL nucleotide sequences. Am J Bot. 86(2):208–224.
Fay MF. 2018. Orchid conservation: how can we meet the challenges in the twenty-first century? Bot Stud. 59(1):16.
Kim JS, Kim HT, Kim JH. 2014. The largest plastid genome of Monocots: a novel genome type containing AT residue repeats in the slipper orchid Cypripedium japonicum. Plant Mol Biol Rep. 33(5):1–11.
Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol. 33(7):1870–1874.
Lang KY, Chen XQ, Zhu GH. 1999. Flora reipublicae popularis sinicae Vol. 17. Beijing (China): Science Press, p. 34.
Lin CS, Chen JJW, Huang YT, Chan MT, Daniell H, Chang WI, Hsu CT, Liao DC, Wu FH, Lin SY, et al. 2015. The location and translocation of ndh genes of chloroplast origin in the Orchidaceae family. Sci Rep. 5(1):9040.
Luo J, Hou BW, Niu ZT, Liu W, Xue QY, Ding XY. 2014. Comparative chloroplast genomes of photosynthetic orchids: insights into evolution of the Orchidaceae and development of molecular markers for phylogenetic applications. PLoS One. 9(6):e99016.
Minasiewicz J, Znaniecka JM, Górniak M, Kawiński A. 2018. Spatial genetic structure of an endangered orchid Cypripedium calceolus (Orchidaceae) at a regional scale: limited gene flow in a fragmented landscape. Conserv Genet. 19(6):1449–1460.
Rankou H, Bilz M. 2014. Cypripedium calceolus. The IUCN Red List of Threatened Species. e.T16202143316125.
Talavera G, Castresana J. 2007. Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. Syst Biol. 56(4):564–577.