Complete plastome sequence of *Hoya pottsii* Traill and *Hoya liangii* Tsiang (Apocynaceae)

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**ABSTRACT**

*Hoya* is the largest genus (about 350–450 species) within Apocynaceae. It is a subshrub or liana, epiphytic or epilithic. Most species grow in tropical and subtropical South and Southeast Asia. Here we report and characterize the complete plastid genome sequence of *Hoya pottsii* Traill and *Hoya liangii* Tsiang in an effort to provide genomic resources useful for promoting its systematics research. The complete plastome of *H. pottsii* is 161,565 bp in length, including two Inverted Repeat (IR) regions of 24,657 bp, a Large Single-Copy (LSC) region of 92,532 bp, and a Small Single-Copy (SSC) region of 19,719 bp. The plastome contains 115 genes, consisting of 81 unique protein-coding genes, 30 unique tRNA genes, and 4 unique rRNA genes. The overall A/T content in the plastome of *H. pottsii* is 62.40%. The complete plastome of *H. liangii* is 162,989 bp in length, including two IR regions of 24,841 bp, a LSC region of 93,292 bp, and a SSC region of 20,015 bp. The plastome contains 115 genes, consisting of 81 unique protein-coding genes, 30 unique tRNA genes, and 4 unique rRNA genes. The overall A/T content in the plastome of *H. liangii* is 62.30%. The complete plastome sequence of *H. pottsii* and *H. liangii* will provide a useful resource for the conservation genetics of the two species as well as for the phylogenetic studies of *Hoya*.

**Introduction**

*Hoya* is the largest genus (about 350–450 species) within Apocynaceae. It is a subshrub or liana, epiphytic or epilithic. Most species grow in tropical and subtropical South and Southeast Asia (Lamb and Rodda 2016). There are 38 species and one variety in China, and most of them are distributed in southwestern China (Zhang et al. 2015). The leaves of *H. pottsii* are used for the treatment of fractures and swellings and for draining off pus and promoting new growth. They both have typical quadruplicate structure of angiosperms, containing two Inverted Repeats (IRs) of 24,657 bp in *H. pottsii* and 24,841 bp in *H. liangii*, a Large Single-Copy (LSC) region of 92,532 bp (*H. pottsii*) and 93,292 bp (*H. liangii*), a Small Single-Copy (SSC) region of 19,719 bp (*H. pottsii*) and 20,015 bp (*H. liangii*). The plastome of *H. pottsii* and *H. liangii* contains 115 genes, consisting of 81 unique protein-coding genes (7 of which are duplicated in the IR), 30 unique tRNA genes (7 of which are duplicated in the IR), and 4 unique rRNA genes. Among these genes, 5 pseudogenes (*rpoC1*, *accD*, *ycf2*, *ndhH*, *ycf1*) in *H. pottsii* and 6 pseudogenes (*rpoC2*, *accD*, *ycf2*, *ycf1*, *ndhH*, *ycf1*) in *H. liangii*, 14 genes possessed a single intron and 3 genes (*ycf3*, *clpP*, *rps12*) had 2 introns. The gene *rps12* was found to be trans-spliced, as is typical of angiosperms. The overall A/T content in the plastome of *H. pottsii* is 62.40%, which the corresponding value of the LSC, SSC, and IR region were 64.10%, 68.20%, and 56.80%, respectively. The overall A/T content in the plastome of *H. liangii* is 62.30%, which the...
corresponding value of the LSC, SSC, and IR region were 64.10%, 68.20%, and 56.80%, respectively.

We used RAxML (Stamatakis 2006) with 1000 bootstraps under the GTRGAMMAI substitution model to reconstruct a maximum likelihood (ML) phylogeny of 16 published complete plastome of Apocynaceae, using Gentiana veitchiorum (Gentianaceae) as outgroup. The phylogenetic analysis indicated that H. pottsii and H. liangii are close to C. wilfordii and Asclepias nivea within Apocynaceae respectively (Figure 1). Most nodes in the plastome ML trees were strongly supported. The complete plastome sequence of H. pottsii and H. liangii will provide a useful resource for the conservation genetics of the two species as well as for the phylogenetic studies of Hoya.

Disclosure statement

No potential conflict of interest was reported by the authors.

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References

Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads - a baiting and iterative mapping approach. Nucleic Acids Res. 41: e129

Jang W, Kim KY, Kim K, Lee SC, Park HS, Lee J, Seong RS, Shim YH, Sung SH, Yang TJ. 2016. The complete chloroplast genome sequence of Cynanchum auriculatum Royle ex Wight (Apocynaceae). DNA Seq. 27: 4549–4550.

Lamb A, Rodda M. 2016. A Guide to Hoyas of Borneo [M]. Borneo: Natural History Publications; p. 1–13.

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

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

Zhang JF, Bai L, Xia NH, et al. 2015. Hoya yingjiangensis (Asclepiadoideae, Apocynaceae), a new campanulate flowered species from Yunnan, China. J. Phytotaxa. 219:283–288.

Zhu ZX, Mu WX, Wang JH, Zhang JR, Zhao KK, Friedman CR, Wang HF. 2018. Complete plastome sequence of Dracaena cambodiana (Asparagaceae): a species considered “Vulnerable” in Southeast Asia. Mitochondrial DNA Part B: Resources. 3(2):620–621.