MITOCHONDRIAL DNA PART B
2020, VOL. 5, NO. 1, 895–896
https://doi.org/10.1080/23802359.2020.1717392

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MITOGENOME ANNOUNCEMENT

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The complete chloroplast genome sequence *Holmskioldia sanguinea* retz., an ornamental plant of Lamiaceae

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ABSTRACT

Holmskioldia sanguinea Retz. (Lamiaceae) is a widely cultivated ornamental plant. As a first report in the genus, we present the complete chloroplast genome sequence of *H. sanguinea* using genome skimming of paired-end NGS data. The total genome size measures 153,273 bp in length containing four subregions: 84,693 bp of large single-copy region, 17,330 bp small single-copy region, and a pair of inverted repeat regions, measuring 25,625 bp. The genome contains 115 genes including 80 protein-coding genes, 4 rRNAs, and 31 tRNAs. Phylogenetic analysis showed that *H. sanguinea* is a sister to *Scutellaria* in the subfamily Scutellarioideae of Lamiaceae.

ARTICLE HISTORY
Received 3 January 2020
Accepted 7 January 2020

KEYWORDS
Holmskioldia sanguinea; chloroplast genome; genome skimming; ornamental plant; Scutellarioideae

Holmskioldia Retz. is a monotypic genus and includes *H. sanguinea* Retz., which is distributed in southern Asia, Mauritius, Indonesia, and the West Indies (Atkins 1996). It is a scandent shrub with long brown-scarlet inflorescences. It has been unclear if this taxon is a member of Verbenaceae or Lamiaceae. However, recent molecular phylogenetic studies along with morphological studies suggest that *Holmskioldia* belong to Lamiaceae (Atkins 1996; Ryding 1995; Wagstaff and Olmstead 1997, 1998; Ryding 2007; Li et al. 2016), and is a sister to *Scutellaria* L. in the subfamily Scutellarioideae of Lamiaceae (Zhao et al. 2017; Safikhani et al. 2018).

We purchased *H. sanguinea* from the nursery and cultivated in the Sungshin University (N37°37′55.32″, E127°01′35.85″). A branch was used to prepare a voucher specimen (deposited in the herbarium of the Sungshin University; *Y. Lee 2019-001*, SWU). Total genomic DNA was extracted from fresh leaves using the GeneAll Plant SV Mini Kit (GeneAll Biotechnology Co. Ltd, Seoul, Korea) following the manufacturer's protocol. The whole-genome sequencing was conducted with paired-end reads (100 bp in each length) using the BGISEQ-500 sequencer (BGI, Shenzhen, China).

A total of 34,772,388 reads (3.5 Gbp) were produced. To obtain the chloroplast (cp) genome sequence, we mapped each paired-end read against a cp genome from *Scutellaria insignis* Nakai (GenBank accession: NC_028533), a previously reported sister to *Holmskioldia*, using Geneious (v9.0.5; Kearse et al. 2012) with the 'medium-low sensitivity option'. Subsequently, the quality of consensus sequences and their mapping condition were examined visually. Six specific primer pairs in the regions of *petG–psaJ*, *psbB*, *rpl23–ycf2*, *rpoA*, *rrn16*, and *rrn16–trnA*-UGG were designed (sequences not shown) for filling gaps. The PCR and Sanger sequencing were conducted with the condition from Song et al. (2019). The cp genome was annotated using GeSeq (Tillich et al. 2017). The annotated genome was compared with a cp genome of *S. insignis* in the alignment generated by MAFFT (v7.308; Katoh and Standley 2013) module in the Geneious (v9.0.5; Kearse et al. 2012).

The complete cp genome of *H. sanguinea* is 153,273 bp in length (GenBank accession: MN227130), containing a large single-copy (LSC) of 84,693bp, a small single-copy (SSC) of 17,330 bp, and a pair of inverted repeat (IR) regions of 25,625 bp. The genome includes 115 genes comprising 80 protein-coding genes, 4 rRNA genes, and 31 tRNA genes.

For the phylogenetic analysis, 11 representative cp genomes were selected from each subfamilies of Lamiaceae based on the phylogenetic information obtained from Li et al. (2016) (Figure 1). The phylogenetic tree (Figure 1) showed that *H. sanguinea* belongs to a clade of subfamily Scutellarioideae and is a sister to *Scutellaria*.

In this study, we report the complete cp genome sequence from *H. sanguinea*, a widely cultivated garden plant. This study will provide basic information elucidating the phylogeny and evolution of taxa in the subfamily Scutellarioideae. It also provides outgroup information for cp genome studies of *Scutellaria*, which is one of the largest genera in the Lamiaceae.

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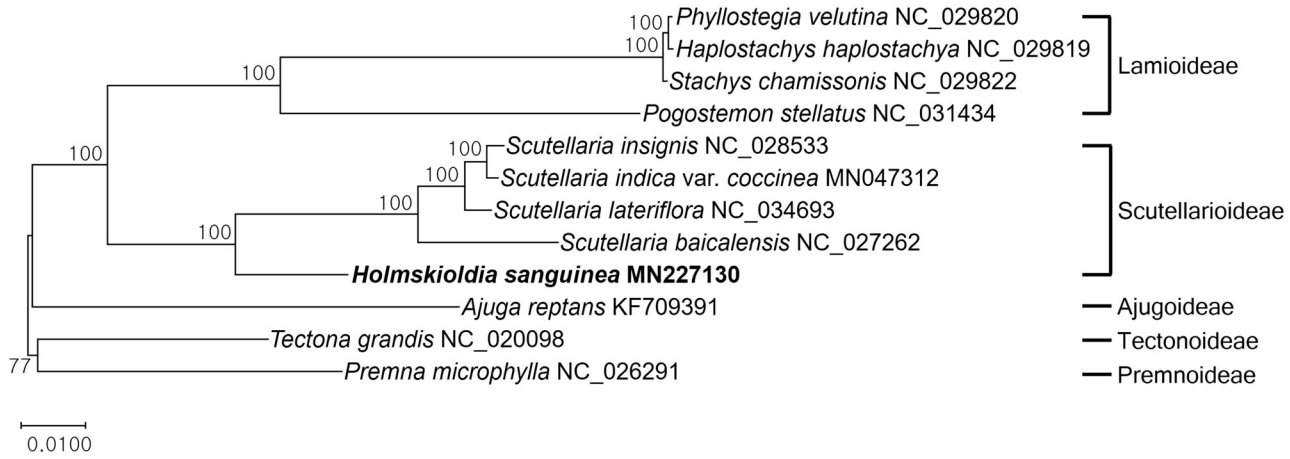


Figure 1. A maximum-likelihood tree based on a cp genome of *H. sanguinea* and 11 subfamilial cp genomes in Lamiaceae using raxmlGUI (v.1.5; Silvestro and Michalak 2012) with 1,000 bootstrap replications. The GTR + Gamma + I model was selected as the best model using a module of the model test in MEGA7 (Kumar et al. 2016). Numbers above the node indicate bootstrap values.

Disclosure statement

No potential conflict of interest was reported by the authors.

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References

Atkins S. 1996. *Holmskioldia sanguinea* Labiatae, formerly Verbenaceae. Bot Mag. 13:79–81.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12): 1647–1649.

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.

Li B, Cantino PD, Olmstead RG, Bramley GLC, Xiang CL, Ma ZH, Tan YH, Zhang DX. 2016. A large-scale chloroplast phylogeny of the Lamiaceae sheds new light on its subfamilial classification. Sci Rep. 6(1):34343.

Ryding O. 1995. Pericarp structure and phylogeny of the Lamiaceae–Verbenaceae complex. Plant Syst Evol. 198(1–2):101–141.

Ryding O. 2007. Amount of calyx fibers in Lamiaceae, relation to calyx structure, phylogeny and ecology. Plant Syst Evol. 268(1-4):45–58.

Safikhani K, Jamzad Z, Saeidi H. 2018. Phylogenetic relationships in Iranian *Scutellaria* (Lamiaceae) based on nuclear ribosomal ITS and chloroplast *trnL-F* DNA data. Plant Syst Evol. 304(9):1077–1089.

Silvestro D, Michalak I. 2012. raxmlGUI: a graphical front-end for RAxML. Org Divers Evol. 12(4):335–337.

Song E, Park S, Kim S. 2019. Primers for complete chloroplast genome sequencing in *Magnolia*. Appl Plant Sci. 7(9):e11286.

Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq – versatile and accurate annotation of organelle genomes. Nucleic Acids Res. 45:6–11.

Wagstaff SJ, Hickerson L, Spangler R, Reeves PA, Olmstead RG. 1998. Phylogeny in Labiatae s. l., inferred from cpDNA sequences. Plant Syst Evol. 209(3-4):265–274.

Wagstaff SJ, Olmstead RG. 1997. Phylogeny of the Labiatae and Verbenaceae inferred from *rbcL* sequences. Syst Bot. 22(1):165–179.

Zhao F, Liu ED, Peng H, Xiang CL. 2017. A new species of *Scutellaria* (Scutellarioideae, Lamiaceae) from Sichuan Province in southwest China. PeerJ. 5:e3624.