

MITOGENOME ANNOUNCEMENT



Complete mitochondrial genome of *Hemiptelea davidii* (Ulmaceae) and phylogenetic analysis

Hua-Bo Liu^{a,b,*}, Yang Zhao^{c,*}, Xing-Ze Zhang^b, Chao Sun^b and Ji-Chen Xu^a

^aNational Engineering Laboratory for Tree Breeding, Beijing Forestry University, Beijing, China; ^bForest Seedling Station of Yantai City, Yantai, China; ^cState Key Laboratory of Tree Genetics and Breeding, Research Institute of Forestry, Chinese Academy of Forestry, Beijing, China

ABSTRACT

Hemiptelea davidii (Hance) Planch is a potential valuable forest tree in arid sandy environments. Here, the complete mitochondrial genome of *H. davidii* was assembled using a combination of the PacBio Sequel data and the Illumina Hiseq data. The mitochondrial genome is 460,941 bp in length, including 37 protein-coding genes, 19 tRNA genes, and three rRNA genes. The GC content of the whole mitochondrial genome is 44.84%. Phylogenetic analyses indicated that *H. davidii* is close with *Cannabis* and *Morus* species.

ARTICLE HISTORY

Received 13 June 2019
Accepted 10 July 2019

KEYWORDS

Hemiptelea davidii;
mitochondrial genome;
phylogenetic analysis

Hemiptelea davidii (Hance) Planch belonging to *Hemiptelea* of Ulmaceae is a kind of shrub or small tree with a height up to 10 m, which mainly distributed in China. It could survive well in arid sandy environment and was then recognized as a potential valuable forest tree resource in low rainfall region

(Bai et al. 2008). Despite the complete chloroplast genomes for *H. davidii* have been reported in our previous study, the genetic information available for this species is still extremely scarce (Liu et al. 2019). Plant mitochondria plays essential role to supply the cell with metabolic energy and was also

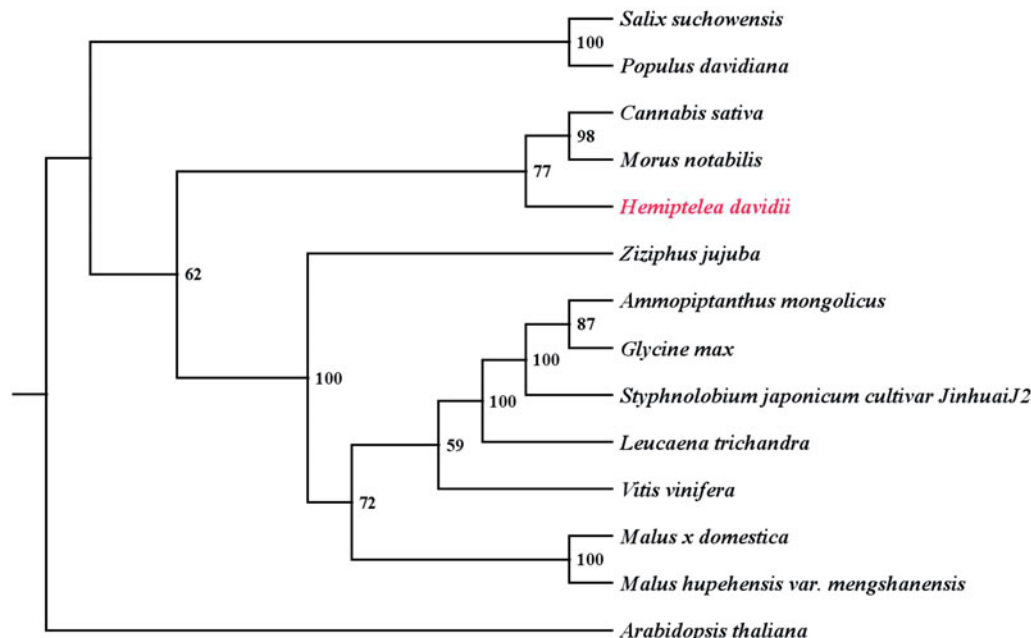


Figure 1. The phylogenetic tree of 14 plant mitochondrial genomes based on 10 common protein-coding genes using *Arabidopsis thaliana* as an out-group. Accession number: *Ammopiptanthus mongolicus* (MF683210), *Arabidopsis thaliana* (Y08501), *Cannabis sativa* (KU310670), *Glycine max* (JX463295), *Hemiptelea davidii* (MN061667), *Leucaena trichandra* (MH717173), *Malus hupehensis* var. *mengshanensis* (KR534606), *Malus x domestica* (NC_018554), *Morus notabilis* (MK301435), *Populus davidiana* (KY216145), *Salix suchowensis* (KU056812), *Styphnolobium japonicum* cultivar *JinhuaiJ2* (MG757109), *Vitis vinifera* (FM179380), and *Ziziphus jujuba* (KU187967). The number on each node indicates the bootstrap value.

involved in resisting adverse circumstances. Thus, we report the complete mitochondrial genome of *H. davidii* here in order to better understand their characteristics in response to the species status. The annotated mitochondrial genome has been deposited into GenBank under accession number MN061667.

In this study, the plant material were harvested from Yantai of Shandong Province (geographic coordinates: 37°9'50"N, 121°25'58"E), China and the specimen were conserved at Shandong Provincial Center of Forest Tree Germplasm Resources (voucher number: HD2016003). The mitochondria DNA was separated from fresh leaves using an improved method according to Chen et al. (2011) and then sequenced on the Illumina Hiseq 4000 platform and PacBio Sequel platform, respectively. The mitochondrial genome was assembled using a combination of the PacBio Sequel data and the Illumina Hiseq data using SPAdes v3.10.1 software (Antipov et al. 2016). The genome sequences were annotated using GeSeq (Tillich et al. 2017).

The *H. davidii* mitochondrial genome is assembled into a single circular-mapping molecule of 460,941 bp, with a GC content of 44.84%. The mitochondrial genome contains a total of 59 genes, including 37 protein-coding genes, 19 tRNA genes, and three rRNA genes. Of the protein-coding genes, *nad5* is the largest gene (2016 bp) while *atp9* is the smallest gene (225 bp).

Sequences of 10 common protein-coding genes (*cox1*, *cox2*, *cox3*, *matR*, *nad2*, *nad4*, *nad6*, *nad7*, *nad9*, and *rps3*) were aligned with the homologous genes in other 13 species using MAFFT (Katoh and Standley 2013). Phylogenetic analyses were performed using maximum-likelihood (ML) with RAxML based on GTRGAMMA model with 1000 bootstrap replicates (Silvestro and Michalak 2012). The phylogenetic

tree showed that *H. davidii* is close with *Cannabis* and *Morus* species (Figure 1), which is consistent with the evolutionary relationship of species.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the Forestry Science & Technology Innovation Project of Shandong Province [LYCX01-2018-01].

References

- Antipov D, Korobeynikov A, Mclean JS, Pevzner PA. 2016. HYBRIDSPADES: an algorithm for hybrid assembly of short and long reads. *Bioinformatics*. 32:1009–1015.
- Bai YP, Han DY, Dong YH, Zhao YJ, Li JD. 2008. Structural characteristics of *Hemiptelea davidii* community on Kerqin sandy land. *Chinese J Appl Ecol*. 19:257–260.
- Chen J, Guan R, Chang S, Du T, Zhang H, Xing H. 2011. Substoichiometrically different mitotypes coexist in mitochondrial genomes of *Brassica napus* L. *PLoS One*. 6:e17662.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol*. 30:772–780.
- Liu HB, Li WQ, Xie XM, Zhang XZ, Sun C, Xu JC, Lu YZ. 2019. The complete chloroplast genome of *Hemiptelea davidii* (Ulmaceae), the only species of the genus *Hemiptelea*. *Mitochondrial DNA B*. 4:229–230.
- Silvestro D, Michalak I. 2012. raxmlGUI: a graphical front-end for RAxML. *Org Divers Evol*. 12:335–337.
- Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq - versatile and accurate annotation of organellar genomes. *Nucleic Acids Res*. 45:W6–W11.