

See discussions, stats, and author profiles for this publication at: <https://www.researchgate.net/publication/350126197>

# The complete chloroplast genome sequence of *Achimenes cettoana* (Gesneriaceae)

Article in *Mitochondrial DNA Part B* · March 2021

DOI: 10.1080/23802359.2020.1847607

CITATIONS

0

READ

1

6 authors, including:



Shu Li

Guangxi Academy of Sciences

14 PUBLICATIONS 11 CITATIONS

[SEE PROFILE](#)



Zi-Bing Xin

Guangxi Institute of Botany, Chinese Academy of Sciences

25 PUBLICATIONS 26 CITATIONS

[SEE PROFILE](#)



Zhangjie Huang

Northeast Forestry University

15 PUBLICATIONS 6 CITATIONS

[SEE PROFILE](#)



Stephen Maciejewski

21 PUBLICATIONS 30 CITATIONS

[SEE PROFILE](#)

Some of the authors of this publication are also working on these related projects:



Taxonomy of the species-rich genus *Elatostema* [View project](#)



国家自然科学基金项目 (31860047), 中国科学院科技服务网络计划 (KFJ-3W-No1), 广西自然科学基金项目 (2017GXNSFAA198006), 广西科技计划项目 (桂科AB16380053), 广西科学院基本业务费项目 (2017YJJ23022), 广西喀斯特植物保育与恢复生态学重点实验室基金项目 (17-259-23) 和中国科学院植物资源保护与可持续利用重点实验室开放基金项目 [View project](#)



## The complete chloroplast genome sequence of *Achimenes cettoana* (Gesneriaceae)

Shu Li, Rui Liao, Zi-Bing Xin, Zhang-Jie Huang, Stephen Maciejewski & Fang Wen

To cite this article: Shu Li, Rui Liao, Zi-Bing Xin, Zhang-Jie Huang, Stephen Maciejewski & Fang Wen (2021) The complete chloroplast genome sequence of *Achimenes cettoana* (Gesneriaceae), Mitochondrial DNA Part B, 6:3, 705-707, DOI: [10.1080/23802359.2020.1847607](https://doi.org/10.1080/23802359.2020.1847607)

To link to this article: <https://doi.org/10.1080/23802359.2020.1847607>



© 2021 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 17 Mar 2021.



Submit your article to this journal [↗](#)



Article views: 29



View related articles [↗](#)



View Crossmark data [↗](#)

## The complete chloroplast genome sequence of *Achimenes cettoana* (Gesneriaceae)

Shu Li<sup>a,b</sup>, Rui Liao<sup>c</sup>, Zi-Bing Xin<sup>a,b</sup>, Zhang-Jie Huang<sup>a,b</sup>, Stephen Maciejewski<sup>b,d</sup> and Fang Wen<sup>a,b</sup>

<sup>a</sup>Guangxi Key Laboratory of Plant Conservation and Restoration Ecology in Karst Terrain, Guangxi Institute of Botany, Guangxi Zhuang Autonomous Region and Chinese Academy of Sciences, Guilin, PR China; <sup>b</sup>Gesneriad Conservation Center of China, Guilin Botanical Garden, Chinese Academy of Sciences, Guilin, PR China; <sup>c</sup>Hubei Provincial Key Laboratory for Protection and Application of Special Plant Germplasm in Wuling Area of China, Key Laboratory of State Ethnic Affairs Commission for Biological Technology, College of Life Science, South-Central University for Nationalities, Wuhan, PR China; <sup>d</sup>The Gesneriad Society, Philadelphia, PA, USA

### ABSTRACT

*Achimenes* Pers. is well known for its floral diversity and widely used in horticulture, but its phylogenetic position is still poorly understood. And most research about the complete chloroplast genome sequence focused on the Old World species; therefore, we think it is necessary to examine taxa of the New World in more detail. This study determined the complete chloroplast genome of *Achimenes cettoana* H.E. Moore. The cp genome was 153,011 bp in a total length containing two inverted repeats (IRs) of 25,162 bp separated by a large single-copy (LSC) region of 84,669 bp and a small single-copy (SSC) region of 18,018 bp. The whole cp genome of *A. cettoana* contains 112 genes, including 79 protein-coding genes, 29 *tRNA* genes, and four *rRNA* genes. This plastid genome is firstly reported in the New World Gesneriaceae, which will be a valuable resource for future studies on breeding, conservation genetics, and phylogeny of Gesneriaceae.

### ARTICLE HISTORY

Received 21 July 2020  
Accepted 3 November 2020

### KEYWORDS



*Achimenes*; chloroplast genome; phylogenetics

Based on molecular phylogenetic studies, the first detailed and overall classification of Gesneriaceae was made by Weber et al. (2013), three subfamilies were recognized: Sanangoioideae (monospecific with *Sanango racemosum* G.S. Bunting & J.A. Duke), Gesnerioideae, and Didymocarpoideae. Both Subfam. Sanangoioideae and Subfam. Gesnerioideae are distributed in the New World (*Titanotrichum* Soler. excluded), and Subfam. Didymocarpoideae is distributed in the Old World. *Achimenes* Pers. (belonging to the Subfam. Gesnerioideae) is an herbaceous genus of about 24 species (IPNI 2020; Tropicos 2020), distributed from southern Mexico through Central America (Roa et al. 2002; Roalson and Roberts 2016).

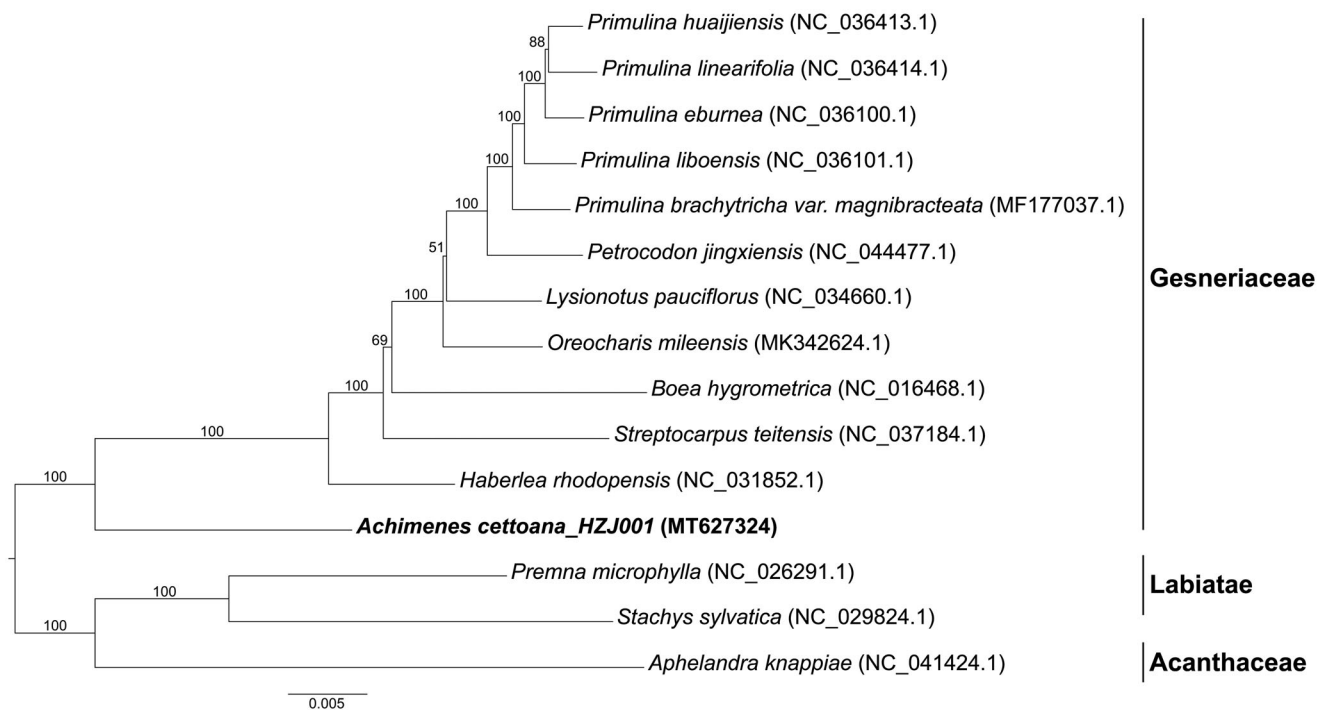
The DNA sequence of the chloroplast genome can be used as a valuable resource for future studies on breeding, conservation genetics and phylogeny. Within Gesneriaceae, all chloroplast genomes reported belong to Subfam. Didymocarpoideae and no complete chloroplast sequence for the New World Gesneriaceae have been published to date.

The members of the Gesneriad Society collected seeds of *Achimenes cettoana*, which grows on rocks in the stream of a shaded ravine, from Chiapas, Mexico (GPS: 16.74 N, 92.69 W). Then seeds were shared to GCCC, and were being cultivated in the nursery of GCCC since 2015. *Achimenes cettoana* is a compact plant and adapts well to cultivation (Moore 1961),

especially for a windowsill or under artificial light. The voucher specimen (HZJ001) was deposited at the Herbarium of Guangxi Institute of Botany, CAS (IBK). The chloroplast DNA of *A. cettoana* was extracted by the CTAB method (Doyle and Doyle 1987) and sequenced using the Illumina HiSeq 4000 sequencing platform (Majorbio Company (<http://www.majorbio.com/>), China). We used Map to Reference function in Geneious R11 (Kearse et al. 2012) to exclude nuclear and mitochondrial reads using the plastid genome of *Petrocodon jingxiensis* (GenBank-MK887172) as reference. Putative chloroplast reads were used for de novo assembling construction using Geneious R11. Generated contigs were concatenated into larger ones using the Repeat Finder function in Geneious R11. The original data were again mapped to the larger contigs to extend their boundaries until all contigs were able to concatenate to one contig. The inverted repeat (IR) region was determined using the Repeat Finder function in Geneious R11 and was inverted and copied to obtain the complete chloroplast sequence. DOGMA program was used for annotation of the complete chloroplast genome (Wyman et al. 2004) and the annotation was corrected with Geneious R11 (Kearse et al. 2012). The complete chloroplast genome of *A. cettoana* was 153,011 bp in length (MT627324), and the GC content was 38.2%. Large single-copy (LSC) and small single-copy (SSC) contained 84,669 bp and 18,018 bp, while IRs were

**CONTACT** Fang Wen  [wenfang760608@139.com](mailto:wenfang760608@139.com)  Guangxi Key Laboratory of Plant Conservation and Restoration Ecology in Karst Terrain, Guangxi Institute of Botany, Guangxi Zhuang Autonomous Region and Chinese Academy of Sciences, Guilin, PR China

© 2021 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.



**Figure 1.** Phylogenetic tree reconstructed by maximum likelihood (ML) analysis based on concatenated sequences of protein-coding genes from 15 taxa of Lamiales, numbers upon branches are assessed by ML bootstrap.

25,162 bp in length. The plastid genome included 79 protein-coding genes, 29 *tRNA* genes, and four *rRNA* genes.

To analyze the phylogenetic position of *A. cettoana*, the concatenated sequences of protein-coding genes of *A. cettoana* and 11 other species from Gesneriaceae were aligned using MAFFT version 7.307 (Kato and Standley 2013) and 3 species from Labiatae and Acanthaceae were selected as outgroup. A phylogenetic tree (Figure 1) was constructed with the maximum likelihood (ML) method and the TVM + F + R2 evolutionary model using RAxML (Stamatakis 2014). The result was congruent with previous studies that established that *Achimenes* is a member of the New World Gesneriaceae (Clark et al. 2012; Weber et al. 2013). The topology of this molecular tree supports the division of this subfamily and shows that *A. cettoana* is a representative of Subtr. Gloxiniinae and is a sister group of Gesneriinae (Clark et al. 2012). The newly reported chloroplast genome of *A. cettoana* allows developing markers for further studies on resolving the relationship within the Subfam. Gesnerioideae and particularly, the genus *Achimenes*.

## Acknowledgments

We would like to thank Michael LoFurno (Adjunct Professor, Temple University, Philadelphia, PA, USA) for his editorial assistance.

## Disclosure statement

No potential conflict of interest was reported by the author(s).

## Funding

This study was supported by Guilin Science and Technology Foundation. [20170107-2/20180107-6], Guangxi Science and Technology Project [Guike AD20159091], Basal Research Fund of GXIB [Guizhiye20009], 21st Talent project of 'Ten-Hundred-Thousand' in Guangxi, and the Foundation of Guangxi Key Laboratory of Plant Conservation and Restoration Ecology in Karst Terrain [19-050-6].

## 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 MT627324.

## References

- Clark JL, Funke MM, Duffy AM, Smith JF. 2012. Phylogeny of a neotropical clade in the Gesneriaceae: more tales of convergent evolution. *Int J Plant Sci.* 173(8):894–916.
- Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf material. *Phytochem Bull.* 19:11–15.
- IPNI. 2020. The international plant names index [accessed 3 July 2020]. <http://www.ipni.org>.
- Kato 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.
- Moore HE. 1961. *Achimenes cettoana* (Gesneriaceae). *Baileya.* 8:144.

- Roa AR, Skog LE, Ramirez A. 2002. Novae Gesneriaceae neotropicarum X: a new species of *Achimenes* from Mexico. *Novon*. 12(3):382–384.
- Roalson EH, Roberts WR. 2016. Distinct processes drive diversification in different clades of Gesneriaceae. *Syst Biol*. 65(4):662–684.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*. 30(9):1312–1313.
- Tropicos. 2020. Tropicos.org. Missouri botanical garden. [accessed 3 July 2020]. <http://www.tropicos.org>.
- Weber A, Clark JL, Möller M. 2013. A new formal classification of Gesneriaceae. *Selbyana*. 31(2):68–94.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics*. 20(17):3252–3255.
- Xin ZB, Fu LF, Fu ZX, Li S, Wei YG, Wen F. 2019. Complete chloroplast genome sequence of *Petrocodon jingxiensis* (Gesneriaceae). *Mitochondrial DNA Part B*. 4(2):2771–2772.