



## Characterization of complete chloroplast genome of *Amentotaxus yunnanensis* (Taxaceae), a species with extremely small populations in China

Jia Ge, Guiqi Bi & Guifen Luo

To cite this article: Jia Ge, Guiqi Bi & Guifen Luo (2019) Characterization of complete chloroplast genome of *Amentotaxus yunnanensis* (Taxaceae), a species with extremely small populations in China, *Mitochondrial DNA Part B*, 4:1, 1765-1767, DOI: [10.1080/23802359.2019.1607592](https://doi.org/10.1080/23802359.2019.1607592)

To link to this article: <https://doi.org/10.1080/23802359.2019.1607592>



© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 06 May 2019.



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



Article views: 190



View related articles [↗](#)



View Crossmark data [↗](#)



Citing articles: 1 View citing articles [↗](#)

## Characterization of complete chloroplast genome of *Amentotaxus yunnanensis* (Taxaceae), a species with extremely small populations in China

Jia Ge<sup>a,b</sup>, Guiqi Bi<sup>c</sup> and Guifen Luo<sup>a,b</sup>

<sup>a</sup>Yunnan Key Laboratory for Integrative Conservation of Plant Species with Extremely Small Populations, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China; <sup>b</sup>Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China; <sup>c</sup>Agricultural Synthetic Biology Center, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China

### ABSTRACT

*Amentotaxus yunnanensis* H. L. Li (Taxaceae) is a threatened plant species and a typical Plant Species with Extremely Small Population (PSESP). In this study, we sequenced the whole chloroplast (cp) genome of *A. yunnanensis*. The results showed that the plastid genome is 137,594 bp in size. In total, 118 unique genes were annotated, including 83 protein-coding genes, 31 tRNA genes, and four rRNA genes. The phylogenetic tree based on 24 cp genomes of Taxaceae support the close relationships of the genera *Amentotaxus* and *Torreya*.

### ARTICLE HISTORY

Received 27 March 2019  
Accepted 6 April 2019

### KEYWORDS

*Amentotaxus yunnanensis*;  
chloroplast genome; Plant  
Species with Extremely  
Small Population (PSESP)



Conifers have dominated forests for more than 200 million years and are very important for the ecosystem and human society (Nystedt et al. 2013). Taxaceae is a small family of conifers comprises of six genera (including *Amentotaxus*, *Austrotaxus*, *Cephalotaxus*, *Pseudotaxus*, *Taxus*, and *Torreya*) and about 35 species (Elpe et al. 2018). The genus *Amentotaxus* Pilg. consists of six species, one of them *Amentotaxus yunnanensis* H. L. Li (vernacular name Yunnan Catkin Yes) occurs in China, Laos and Vietnam and was categorized as Vulnerable (VU) in the Red List (Thomas et al. 2017). Moreover, this species has also been listed as a Plant Species with Extremely Small Population (PSESE) needing urgent rescue action by the local Government of Yunnan (Sun 2013). As a typical PSESP, *A. yunnanensis* is of huge ecological, scientific, cultural, and economic importance. However, this species has received very limited research and conservation attention so far. In the present study, we report and characterized the complete plastome of *A. yunnanensis*. The obtained results will be fundamental for the further conservation of this threatened species.

Plant material of *A. yunnanensis* (voucher: CL2018035) was collected from Xichou, Yunnan Province of China (23°24'19" N, 104°50'48" E). The individual was cultivated in Kunming Botanical Garden, Kunming Institute of Botany, CAS. An herbarium specimen was stored in Yunnan Key Laboratory for Integrative Conservation of Plant Species with Extremely Small Populations, Kunming Institute of Botany, CAS. The

complete cp genome sequencing was performed on the Illumina HiSeq X platform (Illumina Inc, San Diego, CA, USA), assembled into the complete cp genome by NOVOPlasty version 2.6.2 (Dierckxsens et al. 2016) with *A. argotaenia* (Accession no.: NC\_027581) as the reference. Annotated was performed using the tools DOGMA (Wyman et al. 2004) and plann 1.1 (Huang and Cronk 2015). *Amentotaxus yunnanensis* cp genome was deposited in Genbank under the Accession no.: MK675813.

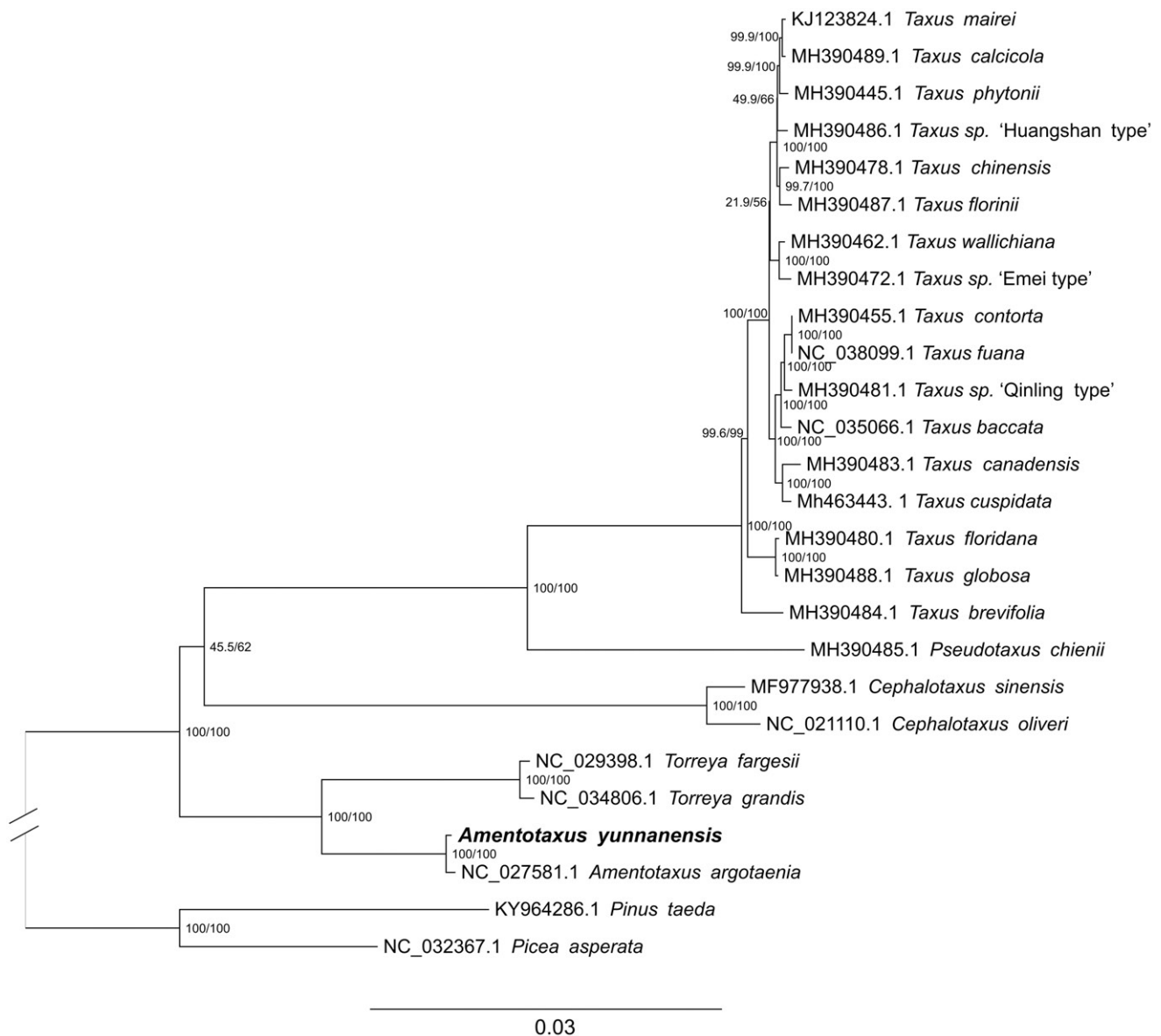
The complete cp genome of *A. yunnanensis* is 137,594 bp in length. Similar to other conifers, the studied species does not contain IRs. The total GC content was 35.9%. In total, 118 unique genes were annotated, including 83 protein-coding genes, 31 tRNA genes, and four rRNA genes. Sixteen genes contained a single intron (comprising 10 protein-coding and six tRNA genes) and *ycf3* encoded two introns.

To study the phylogenetic position of *A. yunnanensis* 23 cp genomes from Taxaceae were selected for analyses using *Pinus taeda* and *Picea asperata* (Pinaceae clade) as outgroup. The genome-wide alignment of all cp genomes was done by HomBlocks (Bi et al. 2018), resulting in 76,554 positions in total. The whole genome alignment was analyzed using IQ-TREE version 1.6.6 (Nguyen et al. 2014) under the TIM3 + F + R3 model. The tree topology was verified under both 1000 bootstrap and 1000 replicates of SH-aLRT test. Phylogenetic analysis revealed that the genera *Amentotaxus*

**CONTACT** Guifen Luo  [lgf@mail.kib.ac.cn](mailto:lgf@mail.kib.ac.cn)  Yunnan Key Laboratory for Integrative Conservation of Plant Species with Extremely Small Populations, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China

© 2019 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 obtained using ML analysis of 24 cp genomes of Taxaceae. *Pinus taeda* and *Picea asperata* were used as outgroup. The ML consensus tree is shown with bootstrap supports indicated by numbers beside the branching point.

and *Torreya* form a sister group to the other genera of Taxaceae (Figure 1).

Projects: Urgent Rescuing Conservation of *Amentotaxus yunnanensis*, a Plant Species with Extremely Small Population.

## Acknowledgements

We are grateful to Lei Cai for collecting the samples.

## Disclosure statement

No potential conflict of interest was reported by the authors.

## Funding

This work was supported by the Science & Technology Basic Resources Investigation Program of China: Survey and Germplasm Conservation of Plant Species with Extremely Small Populations in Southwest China [grant No. 2017FY100100], and Yunnan Provincial Wildlife Conservation

## References

- Bi G, Mao Y, Xing Q, Cao M. 2018. HomBlocks: a multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. *Genomics*. 110:18–22.
- Dierckxsens N, Patrick M, Guillaume S. 2016. NOVOPlasty: *de novo* assembly of organelle genomes from whole genome data. *Nucleic Acids Res*. 45:e18.
- Elpe C, Knopf P, Stützel T, Christian S. 2018. Diversity and evolution of leaf anatomical characters in Taxaceae *s.l.*—fluorescence microscopy reveals new delimitating characters. *J Plant Res*. 131:125–141.
- Huang DI, Cronk Q. 2015. Plann: a command-line application for annotating plastome sequences. *Appl Plant Sci*. 3:apps.1500026.
- Nguyen LT, Schmidt HA, Haeseler A, Minh BQ. 2014. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol Biol Evol*. 32:268–274.

- Nystedt B, Street NR, Wetterbom A, Zuccolo A, Lin Y-C, Scofield DG, Vezzi F, Delhomme N, Giacomello S, Alexeyenko A, et al. 2013. The Norway spruce genome sequence and conifer genome evolution. *Nature*. 497:579–584.
- Sun WB. 2013. Conserving Plant Species with Extremely Small Populations (PSESP) in Yunnan: a practice and exploration. Kunming: Yunnan Science and Technology Press; p. 11–14.
- Thomas P, Gao L, Phan KL. 2017. *Amentotaxus yunnanensis*. The IUCN Red List of Threatened Species 2017. e.T118076066A96812158. <http://dx.doi.org/10.2305/IUCN.UK.2017-2.RLTS.T118076066A96812158.en>. Downloaded on 24 January 2019.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics*. 20: 3252–3255.