The complete chloroplast genome of *Aucuba obcordata* (Rehder) Fu ex W. K. Hu et Soong (Garryaceae) from China

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**ABSTRACT**

*Aucuba obcordata* is an endemic species and traditional Chinese medicine in China. The complete chloroplast genome sequence of *A. obcordata* was generated by de novo assembly using whole genome next generation sequencing. The complete chloroplast genome was 157,993 bp in length, contained four parts: a large single copy (LSC) region of 87,317 bp, a small single copy (SSC) region of 18,483 bp, and two inverted repeat (IRs) regions of 26,094 bp each. The genome annotation contained a total of 113 genes, including 79 protein-coding genes, 30 tRNA genes, and four rRNA genes. The overall GC content was 37.8%. Phylogenetic analysis of chloroplast genomes clustered *A. obcordata* with *Eucommia ulmoides* Oliver.

*Aucuba obcordata* (Rehder) Fu ex W. K. Hu et Soong, a member of Garryaceae (APG IV 2016), is endemic to China (Xiang and Boufford 2005). The leaves of *A. obcordata* can be used as a traditional Chinese medicine for treating dysmenorrhea, irregular menstruation, traumatic injury, and scald (Editorial Committee of Chinese Materia Medica 1999). Meanwhile, *A. obcordata* is cultivated in gardens because of its evergreen habit, shiny leaves and brightly colored fruits.

*Aucuba* Thunb. is phylogenetically close to the America genus *Garrya* Lindl. (Bremer et al. 2001; APG IV 2016). It contains only ten species in the world with seven of them being endemic to China (Xiang and Boufford 2005). The taxonomy and genetic structure of *A. obcordata* is complicated due to its wide distribution, diverse leaf-form, dioecy and ambiguous interspecific boundary with *A. albopunctifolia* Wang. In the present study, we sought to sequence the complete chloroplast genome of *A. obcordata* and expand our understanding of the diversity of *Aucuba* chloroplast genomes. Our studies could also provide basic data for the medicinal species conservation and is essential for studying the phylogeny and evolution of the genus *Aucuba*, family Garryaceae and order Garryales.

Total genomic DNA was extracted from strain leaves of *Aucuba obcordata* (Yi Tong TY2934, GUCM) collected from wild of Guangdong province (E113’54’1.84”; N23’44’35.26”), China, using the DNeasy Plant Maxi kit (Qiagen, Valencia, CA). An Illumina paired-end library was constructed and sequenced using the Illumina HiSeq 2500 platform (Illumina Inc., San Diego, CA). The PE reads were assembled using GetOrganelle pipeline (Jin et al. 2018). The filtered plastid reads were transferred to the Bandage software (Wick et al. 2015) for visualization processing. The complete plastid genome was annotated and compared with the reference sequence of *Cornus controversa* Hemsl. artificially in Geneious 7.1.4 (Kearse et al. 2012). The final complete plastome was deposited into GenBank (GenBank Accession no. MN015608).

The complete chloroplast genome of *A. obcordata* is 157,993 bp in length and has a typical quadripartite structure, consisting of a large single copy region (LSC) of 87,317 bp, a small single region (SSC) of 18,483 bp, and two inverted repeat regions (IRa and IRb) of 26,094 bp. Genome annotation revealed 113 functional genes in the chloroplast genome, including 79 protein-coding genes, four ribosomal RNA (rRNA) genes, and 30 transfer RNA (tRNA) genes. Seventeen of the genes are duplicated in IR regions. The overall GC content of the circular genome is 37.8% while the corresponding values of the LSC, SSC, and IR region are 35.9%, 31.5%, and 43%, respectively.

Based on the chloroplast genomes of 17 species, we constructed a Maximum-likelihood (ML) tree by RAxML-HPC2 on XSEDE (8.2.12) on CIPRES Science Gateway (https://www.phylo.org/). The ML tree (Figure 1) revealed that the phylogenetic placement of *A. obcordata* was sister to *Eucommia ulmoides* Oliver and the phylogenetic relationships of the analysed species were consistent with previous results (APG IV 2016). Our results can provide a reference for other
Aucuba species and can be subsequently used for species identification, phylogenetic analysis and cp genomic studies of the genus Aucuba.

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Disclosure statement

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References

Angiosperm Phylogeny Group IV. 2016. An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG IV. Bot J Linn Soc. 181:1–20.

Bremer K, Backlund A, Sennblad B, Swenson U, Andreasen K, Hjertson M, Lundberg J, Backlund M, Bremer B. 2001. A phylogenetic analysis of 100+ genera and 50+ families of euasterids based on morphological and molecular data with notes on possible higher level morphological synapomorphies. Plant Syst Evol. 229:137–169.

Editorial Committee of Chinese Materia Medica, State Administration Bureau of Traditional Chinese Medicine. 1999. Chinese Materia Medica (Zhonghua Bencao). Vol. 15. Shanghai: Shanghai Science & Technology Press; p. 737.

Jin JJ, Yu WB, Yang JB, Song Y, Yi TS, Li DZ. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. bioRxiv. 4:256479.

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. 28:1647–1649.

Wick RR, Schultz MB, Zobel J, Holt KE. 2015. Bandage: interactive visualization of de novo genome assemblies. Bioinformatics. 31:3350–3352.

Xiang QY, Boufford DE. 2005. Aucubaceae. In: Wu ZY, Raven P, Hong DY, editors. Flora of China. Vol. 14. Beijing: Science Press; St. Louis: Missouri Botanic Garden Press; p. 222–226.