



## Characterization of the first complete chloroplast genome of *Amaranthus hybridus* (Caryophyllales: Amaranthaceae) with phylogenetic implications

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### ABSTRACT

In the present study, the complete chloroplast genome of *Amaranthus hybridus* was sequenced and assembled. The complete chloroplast genome of *Amaranthus hybridus* is 150,709 in size, with the GC content of 36.56%. The chloroplast genome of *Amaranthus hybridus* contained 86 protein-coding genes (PCGs), eight ribosomal RNA (rRNA) genes, and 37 transfer RNA (tRNA) genes. Phylogenetic analysis based on combined chloroplast gene dataset indicated that the *Amaranthus hybridus* exhibited a close relationship with *A. hypochondriacus* and *A. caudatus*.

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### KEYWORDS



Weed; chloroplast genome; phylogenetic analysis; molecular marker

The genus *Amaranthus* contains some of the most agronomically important weeds (Montgomery et al. 2020), some of them are used as leafy vegetables, and the others are used for sources of grain or ornamental value (Viljoen et al. 2018). *Amaranthus* is a promising nutritious food source concerning by more and more researchers, just like the tartary buckwheat with high nutritional value (Song et al. 2016; Xiang et al. 2016, 2019a, 2019b). The genus *Amaranthus* comprises approximately 60 species, which are distributed throughout the world (Stetter and Schmid 2017). It is difficult to classify *Amaranthus* species accurately only by morphology. Organelle genomes, including mitochondrial genomes and chloroplast genomes, have been widely used for the phylogeny of eukaryotes (Yang et al. 2019; Li et al. 2019a, 2019b, 2020a; Wang et al. 2020b). So far, the chloroplast genome of *Amaranthus hybridus* has not been sequenced. The complete chloroplast genome of *Amaranthus hybridus* sequenced in this study will promote the understanding of phylogeny and evolution of the genus *Amaranthus*.

The specimen (*Amaranthus hybridus*) was collected from Sichuan, China (102.43E; 31.51N), and then we stored the specimen in Collection Center of Chengdu University (no. ZLX\_w7). The complete chloroplast genome of *Amaranthus hybridus* was sequenced and *de novo* assembled according to methods previously described (Li et al. 2018a, 2018b). Briefly, we extracted the total genomic DNA of *Amaranthus hybridus* using a Plant DNA Kit (D3485-00, Omega Bio-Tek, Norcross, GA). Then, the genomic DNA was purified using a Gel Extraction Kit (Omega Bio-Tek, Norcross, GA). The purified


DNA was stored in Chengdu University (no. DNA\_ZLX\_w7). Sequencing libraries of *Amaranthus hybridus* were constructed using a NEBNext® Ultra™ II DNA Library Prep Kit (NEB, Beijing, China). Whole genomic sequencing (WGS) of *Amaranthus hybridus* was then conducted using the Illumina HiSeq 2500 Platform (Illumina, San Diego, CA). The chloroplast genome of *Amaranthus hybridus* was *de novo* assembled using SPAdes 3.9.0 (Bankevich et al. 2012; Li et al. 2020b). The obtained complete chloroplast genome of *Amaranthus hybridus* was annotated using GeSeq (Tillich et al. 2017).

The complete chloroplast genome of *Amaranthus hybridus* is 150,759 bp in length. The base compositions of the *Amaranthus hybridus* chloroplast genome were as follows: A (31.40%), T (32.04%), G (17.97%), and C (18.60%). The complete chloroplast genome of *Amaranthus hybridus* contains 86 protein-coding genes (PCGs), eight ribosomal RNA (rRNA) genes, and 37 transfer RNA (tRNA) genes (Table S1). To investigate the phylogenetic status of the chloroplast genome of *Amaranthus hybridus*, we constructed a phylogenetic tree for 20 species. The protein coding region of 13 genes conserved in the 20 species was used to construct a combined chloroplast gene set (Wang et al. 2020a, 2020c; Wu et al. 2021). The Bayesian inference (BI) method was used to construct the phylogenetic tree based on combined PCGs of chloroplast genome as described by previous methods (Li et al. 2020c, 2021; Cheng et al. 2021). The chloroplast genome of *Oryza sativa* was used as the outgroup (KM103369). The chloroplast genome of *Amaranthus hybridus* exhibited a close

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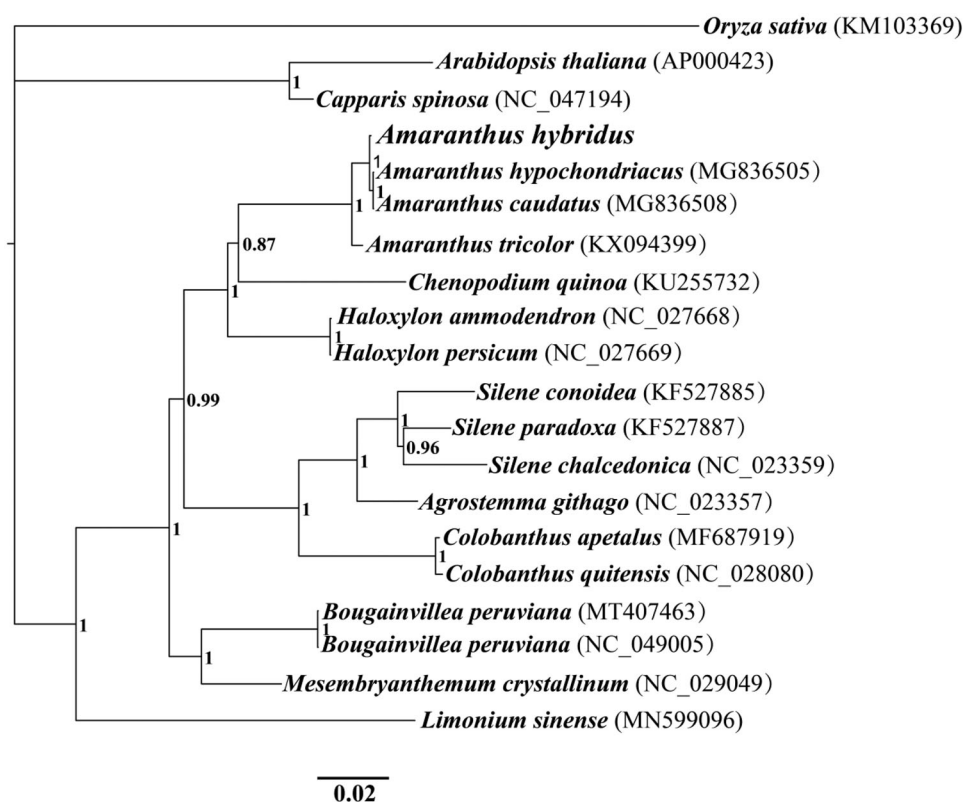
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**Figure 1.** Bayesian phylogenetic analysis of 20 species based on the combined protein-coding genes of chloroplast genome. Accession numbers of chloroplast sequences used in the phylogenetic analysis are listed in brackets after species. Support values are Bayesian posterior probabilities (BPP).

relationship with that of *A. hypochondriacus* and *A. caudatus* (Hong et al. 2019) (Figure 1).

## Disclosure statement

The authors have declared that no competing interests exist.

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## Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov/> under the accession no. MT993471. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA716742, SRR14055740, and SAMN18450400, respectively.

## References

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, et al. 2012. SPAdes: a

- new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol.* 19(5):455–477.
- Cheng J, Luo Q, Ren YH, Luo Z, Liao WL, Wang X, Li Q. 2021. Panorama of intron dynamics and gene rearrangements in the phylum *Basidiomycota* as revealed by the complete mitochondrial genome of *Turbinellus floccosus*. *Appl Microbiol Biotechnol.* 105(5):2017–2032.
- Hong SY, Cheon KS, Yoo KO, Lee HO, Mekapogu M, Cho KS. 2019. Comparative analysis of the complete chloroplast genome sequences of three *Amaranthus* species. *Plant Genet Resour.* 17(3):245–254.
- Li Q, He X, Ren Y, Xiong C, Jin X, Peng L, Huang W. 2020a. Comparative mitogenome analysis reveals mitochondrial genome differentiation in ectomycorrhizal and asymbiotic amanita species. *Front Microbiol.* 11: 1382.
- Li Q, Liao M, Yang M, Xiong C, Jin X, Chen Z, Huang W. 2018a. Characterization of the mitochondrial genomes of three species in the ectomycorrhizal genus *Cantharellus* and phylogeny of *Agaricomycetes*. *Int J Biol Macromol.* 118(Pt A):756–769.
- Li Q, Ren Y, Shi X, Peng L, Zhao J, Song Y, Zhao G. 2019a. Comparative mitochondrial genome analysis of two ectomycorrhizal fungi (*Rhizopogon*) reveals dynamic changes of intron and phylogenetic relationships of the subphylum *Agaricomycotina*. *Int J Mol Sci.* 20(20): 5167.
- Li Q, Ren Y, Xiang D, Shi X, Zhao J, Peng L, Zhao G. 2020b. Comparative mitogenome analysis of two ectomycorrhizal fungi (*Paxillus*) reveals gene rearrangement, intron dynamics, and phylogeny of *Basidiomycetes*. *IMA Fungus.* 11(1):12.
- Li Q, Wang Q, Chen C, Jin X, Chen Z, Xiong C, Li P, Zhao J, Huang W. 2018b. Characterization and comparative mitogenomic analysis of six newly sequenced mitochondrial genomes from ectomycorrhizal fungi (*Russula*) and phylogenetic analysis of the *Agaricomycetes*. *Int J Biol Macromol.* 119:792–802.
- Li Q, Wu P, Li L, Feng H, Tu W, Bao Z, Xiong C, Gui M, Huang W. 2021. The first eleven mitochondrial genomes from the ectomycorrhizal fungal genus (*Boletus*) reveal intron loss and gene rearrangement. *Int J Biol Macromol.* 172:560–572.
- Li Q, Xiang D, Wan Y, Wu Q, Wu X, Ma C, Song Y, Zhao G, Huang W. 2019b. The complete mitochondrial genomes of five important

- medicinal *Ganoderma* species: features, evolution, and phylogeny. *Int J Biol Macromol.* 139:397–408.
- Li Q, Yang L, Xiang D, Wan Y, Wu Q, Huang W, Zhao G. 2020c. The complete mitochondrial genomes of two model ectomycorrhizal fungi (*Laccaria*): features, intron dynamics and phylogenetic implications. *Int J Biol Macromol.* 145:974–984.
- Montgomery JS, Giacomini D, Waitthaka B, Lanz C, Murphy BP, Campe R, Lerchl J, Landes A, Gatzmann F, Janssen A, et al. 2020. Draft genomes of *Amaranthus tuberculatus*, *Amaranthus hybridus* and *Amaranthus palmeri*. *Genome Biol Evol.* 12(11):1988–1993.
- Song C, Xiang DB, Yan L, Song Y, Zhao G, Wang YH, Zhang BL. 2016. Changes in seed growth, levels and distribution of flavonoids during tartary buckwheat seed development. *Plant Prod Sci.* 19(4):518–527.
- Stetter MG, Schmid KJ. 2017. Analysis of phylogenetic relationships and genome size evolution of the *Amaranthus* genus using GBS indicates the ancestors of an ancient crop. *Mol Phylogenet Evol.* 109:80–92.
- 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(W1):W6–W11.
- Viljoen E, Odeny DA, Coetzee MPA, Berger DK, Rees DJG. 2018. Application of chloroplast phylogenomics to resolve species relationships within the plant genus *Amaranthus*. *J Mol Evol.* 86(3–4):216–239.
- Wang X, Jia LH, Wang MD, Yang H, Chen MY, Li X, Liu HY, Li Q, Liu N. 2020a. The complete mitochondrial genome of medicinal fungus *Taiwanofungus camphoratus* reveals gene rearrangements and intron dynamics of *Polyporales*. *Sci Rep.* 10(1):16500.
- Wang X, Song A, Wang F, Chen M, Li X, Li Q, Liu N. 2020b. The 206 kbp mitochondrial genome of *Phanerochaete carnosae* reveals dynamics of introns, accumulation of repeat sequences and plasmid-derived genes. *Int J Biol Macromol.* 162:209–219.
- Wang X, Wang YJ, Yao W, Shen JW, Chen MY, Gao M, Ren JN, Li Q, Liu N. 2020c. The 256 kb mitochondrial genome of *Clavaria fumosa* is the largest among phylum *Basidiomycota* and is rich in introns and intronic ORFs. *IMA Fungus.* 11(1):26.
- Wu P, Bao Z, Tu W, Li L, Xiong C, Jin X, Li P, Gui M, Huang W, Li Q. 2021. The mitogenomes of two saprophytic *Boletales* species (*Coniophora*) reveals intron dynamics and accumulation of plasmid-derived and non-conserved genes. *Comput Struct Biotechnol J.* 19: 401–414.
- Xiang DB, Ma CR, Song Y, Wu Q, Wu XY, Sun YX, Zhao G, Wan Y. 2019a. Post-anthesis photosynthetic properties provide insights into yield potential of tartary buckwheat cultivars. *Agronomy.* 9(3):149.
- Xiang DB, Song Y, Wu Q, Ma CR, Zhao JL, Wan Y, Zhao G. 2019b. Relationship between stem characteristics and lodging resistance of Tartary buckwheat (*Fagopyrum tataricum*). *Plant Prod Sci.* 22(2): 202–210.
- Xiang DB, Zhao G, Wan Y, Tan ML, Song C, Song Y. 2016. Effect of planting density on lodging-related morphology, lodging rate, and yield of tartary buckwheat (*Fagopyrum tataricum*). *Plant Prod Sci.* 19(4): 479–488.
- Yang LX, Li Q, Zhao G. 2019. Characterization of the complete chloroplast genome of *Chenopodium* sp. (Caryophyllales: Chenopodiaceae). *Mitochondrial DNA B Resour.* 4(2):2574–2575.