

The complete chloroplast genome and phylogenetic analysis of *Veratrum mengtzeanum* Loes. F. (Liliaceae)

Li-Jun Han^{a*}, Ying-Ying Liu^{a,b*}, Ying-Min Zhang^a, Cong-Wei Yang^a, Zi-Gang Qian^{a,c} and Guo-Dong Li^{a,c}

^aFaculty of Traditional Chinese Pharmacy, Yunnan University of Chinese Medicine, Kunming, China; ^bYunnan Institute for Food and Drug, Kunming, China; ^cYunnan Key Laboratory for Dai and Yi Medicines, Yunnan University of Chinese Medicine, Kunming, China

ABSTRACT

Veratrum mengtzeanum Loes. F. is a medicinal plant belonging to the genus *Veratrum* (Liliaceae). In the present study, we assembled and characterized the complete chloroplast (cp) genome of this species. The chloroplast genome is 152,051 bp in length, with one large single copy (LSC) region and one small single copy (SSC) region of 82,112 bp and 17,544 bp, respectively; two inverted repeat (IR) regions of 26,198 bp. It contains 131 annotated genes, including 85 protein-coding genes (PCGs), 38 transfer RNA (tRNA) genes, and 8 ribosomal RNA (rRNA) genes. Phylogenetic analysis indicated that *V. mengtzeanum* was closely related to *Veratrum japonicum* with 100% bootstrap value.

ARTICLE HISTORY

Received 3 November 2019
Accepted 9 November 2019

KEYWORDS

Veratrum mengtzeanum;
chloroplast genome;
Liliaceae; phylogenetic analysis

Veratrum mengtzeanum Loes. F., a perennial herb, endemic to southwest China, is a medicinal and poisonous plant belonging to the genus *Veratrum* (Liliaceae). It grows under the forest or beside the hill sided-road with altitude of 1200–3200 m (Yin et al. 2014). There are about 43 species of the genus *Veratrum* in the world (Gu et al. 2018), most of which are used as the medicinal plants (Yin et al. 2016). The roots and rhizomes of *V. mengtzeanum* have been used as traditional folk medicine named “Pimacao” in Yunnan province, used for treating traumatic injuries, fracture, paraplegia, epilepsy, rheumatic pain and traumatic hemorrhage (Li et al. 2019). It is the main component of the renowned traditional Chinese medicine, “Yunnan Baiyao”. To date no study has been carried out on the genome of *V. mengtzeanum*. To provide a rich genetic information and improve *V. mengtzeanum* molecular breeding in the future, we report and characterize the complete chloroplast genome sequence of *V. mengtzeanum* (GenBank accession number: MN589932).

Fresh leaves of *V. mengtzeanum* were collected from Gejiu (N23°21', E103°10'), Honghe Hani and Yi Autonomous Prefecture of Yunnan, China and voucher specimens (5325030256) were deposited in Herbarium of Yunnan University of Chinese Medicine. Firstly, the genomic DNA was extracted using the plant DNA extraction kit (Bioteke Corporation, China). Then genome sequencing was performed on the Illumina HiSeq 2500 platform with a library

construction. Secondly, we de novo trimmed and assembled the raw data of 3 Gb based on NOVOPlasty (Dierckxsens et al. 2017). And the complete cp genome we obtained was annotated with the online annotation tool GeSeq (Tillich et al. 2017).

The complete cp genome of *V. mengtzeanum* is 152,051 bp, including a large single copy (LSC) region of 82,112 bp and a small single copy (SSC) region of 17,544 bp, separated by a pair of inverted repeat (IR) regions of 26,198 bp. The overall GC content of the whole plastome, LSC, SSC and IR regions are 37.8%, 35.8%, 31.5%, 42.9%, respectively. The cp genome has 131 annotated genes, including 85 protein-coding genes, 38 tRNA genes, and eight rRNA genes. A total of 64 SSRs were detected using the online software IMEx (Mudunuri and Nagarajaram 2007). The number of mono-, di-, tri-, tetra-, penta-, and hexanucleotides SSRs are 44, 11, 3, 5, 1, and 0, respectively.

To further infer the phylogenetic position of *V. mengtzeanum*, plastome of 25 representative species were obtained from NCBI to construct the plastome phylogeny, with two species of Araceae and Colocasia as outgroups. All the plastomes were aligned using MAFFT v.7 (Katoh and Standley. 2013). And we used the RAXML (Stamatakis 2014) with 1000 bootstrap replicates for supporting the branches evaluated under the GTR model. The phylogenetic tree shows that *V. mengtzeanum* was closer to *V. japonicum* compared with other species (Figure 1).

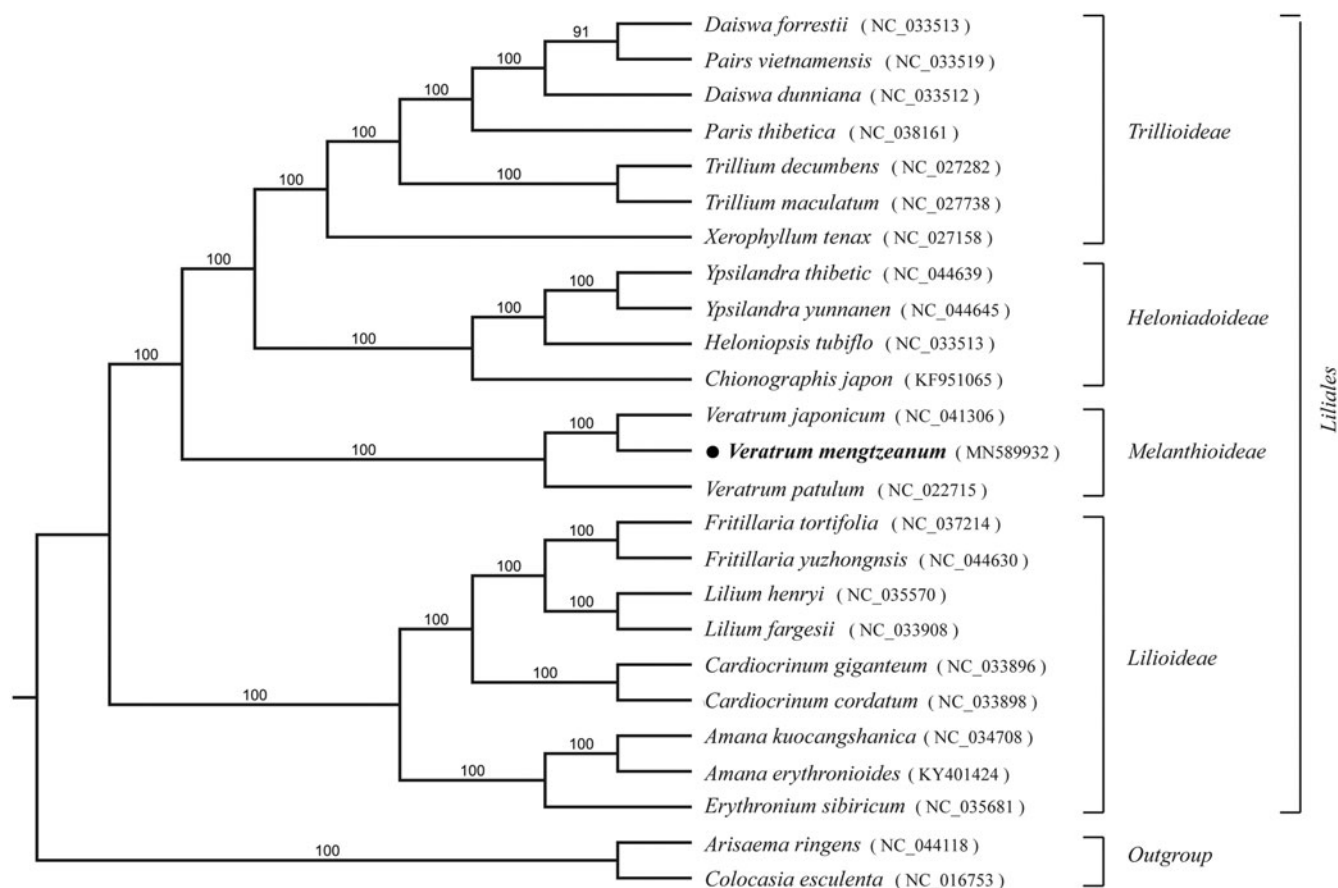


Figure 1. The Maximum likelihood phylogenetic tree inferred from 25 chloroplast genomes. Bootstrap support values >50% are indicated next to the branches. GenBank accession numbers are given in figure.

In summary, the complete cp genome from this study provides significant insight for elucidating the phylogenetic relationship of taxa genus *Veratrum*.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the Yunnan Provincial Science and Technology Department – Applied Basic Research Joint Special Funds of Yunnan University of Traditional Chinese Medicine [no. 2018FF001(-039)], the major project of science and technology in Yunnan Province [2018ZF010-1], and Special subsidies for public health services of TCM “the national survey of TCM resources” [DSS, MOF. No 66/2017].

References

- Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. *Nucleic Acids Res.* 45:e18.
- Gu LS, Yang XL, Li Y, Liu T, Jin YS. 2018. Advances in research of ecophysiological for *Veratrum*. *Chin Wild Plant Resources.* 37(6): 53–56.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol.* 30:772–780.
- Li Q, Zhao YL, Long CB, Zhu PF, Liu YP, Luo XD. 2019. Seven new veratramine-type alkaloids with potent analgesic effect from *Veratrum taliense*. *J Ethnopharmacol.* 244:112–137.
- Mudunuri SB, Nagarajaram HA. 2007. IMEx: imperfect microsatellite extractor. *Bioinformatics.* 23(10):1181–1187.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30: 1312–1313.
- Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq-versatile and accurate annotation of organelle genomes. *Nucleic Acids Res.* 45: W6–W11.
- Yin ZL, Tan WH, Yang XY, Zhang J. 2014. The advances in research of three plant sources of Pimacao. *Yunnan J Tradit Chin Med Materia Med.* 35(3):60–61.
- Yin ZL, Xie H, Zhang J. 2016. A Preliminary study on biological characteristics of *Veratrum Nigrum*. *Yunnan J Tradit Chin Med Materia Med.* 37: 54–57.