


The complete chloroplast genome sequence of *Vitis amurensis* ‘Shuanghong’

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ABSTRACT

Vitis amurensis ‘Shuanghong’ is a hybrid offspring of wild grapes. This study first releases the complete chloroplast genome of *V. amurensis* ‘Shuanghong’ and subjected the sample to phlogenetic analysis. The chloroplast genome is 161,558 bp in length, and comprises a small single-copy region (19,336 bp) and a large single-copy region (89,744 bp), which are separated by a pair of inverted repeat regions. The chloroplast genome encodes 133 genes, including 88 CDSs, 8 rRNA genes, and 37 tRNA genes. The phylogenetic tree showed that *V. amurensis* ‘Shuanghong’ is most closely related to *Vitis vinifera*.

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Vitis amurensis ‘Shuanghong’; chloroplast genome; Illumina sequencing; phylogenetic analysis

Vitis amurensis ‘Shuanghong’ shows extremely strong cold-resistant and downy mildew resistance properties. So, it is widely used for breeding of grapes against downy mildew (Zhao Y et al. 2020). It is also an excellent wine brewing variety because of high anthocyanins content (Zhao Q et al. 2016). The complete chloroplast genome of *V. amurensis* ‘Shuanghong’ was assembled (GenBank; MT479164) and subject to phlogenetic analysis. It offers useful information for the resistance breeding of grapevine.

Genomic DNA was extracted from leaves of *V. amurensis* ‘Shuanghong’ grown at the Modern Engineering Training Center (31°11’N, 121°29’W) and stored at the Center for Viticulture and Enology, Shanghai Jiao Tong University, number was “Shuanghong”. This DNA was used for the preparation of a 400bp small-fragment DNA library and then sequenced using the HiSeq PE150 sequencing platform (Illumina, CA, USA). A total of 3.22 Gb clean reads were obtained. The complete chloroplast genome was assembled by A5-MiSeqv20150522 (Coil et al. 2015) and SPAdesv3.9.0 (Bankevich et al. 2012) software. The chloroplast genome of *V. vinifera* (GenBank; DQ424856) was used as a reference (Jansen et al. 2006) and the genome annotation also referred to the chloroplast genome of *V. vinifera*.

The *V. amurensis* ‘Shuanghong’ chloroplast genome is 161,558 bp in length, including two inverted repeat regions (26,239 bp each) that are separated by a small single-copy region (19,336 bp) and a large single-copy region (89,744 bp). The chloroplast genome contains 133 single genes, including 88 protein-coding genes (CDS), 8 rRNA, and 37 tRNA genes.

The GC content and AT content of the grape genome is 36.58% and 63.42%, respectively. Among these genes, the majority are single copy, whereas 8 CDS (*rp12*, *rp123*, *rps7*, *rps12*, *rps19*, *ycf2*, *ycf15*, *ndhB*), 7 tRNAs (*trnI-CAU*, *trnL-CAA*, *trnV-GAC*, *trnI-GAU*, *trnA-UGC*, *trnR-ACG*, *trnN-GUU*) and 4 rRNAs (*rrn4.5*, *rrn5*, *rrn-16*, *rrn-23*) occur as double copies.

A neighbor-joining (NJ) phylogenetic tree was constructed using 16 *Vitis* species through the MEGA X (Kumar et al. 2018). To identify the phylogenetic position of *V. amurensis* ‘Shuanghong’ within the family Vitaceae, the phylogenetic tree showed that the 16 *Vitis* species are clustered into two orders (Figure 1). The *V. amurensis* ‘Shuanghong’ was phylogenetically closer to *Vitis vinifera* of European species than species in other genera.

Disclosure statement



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

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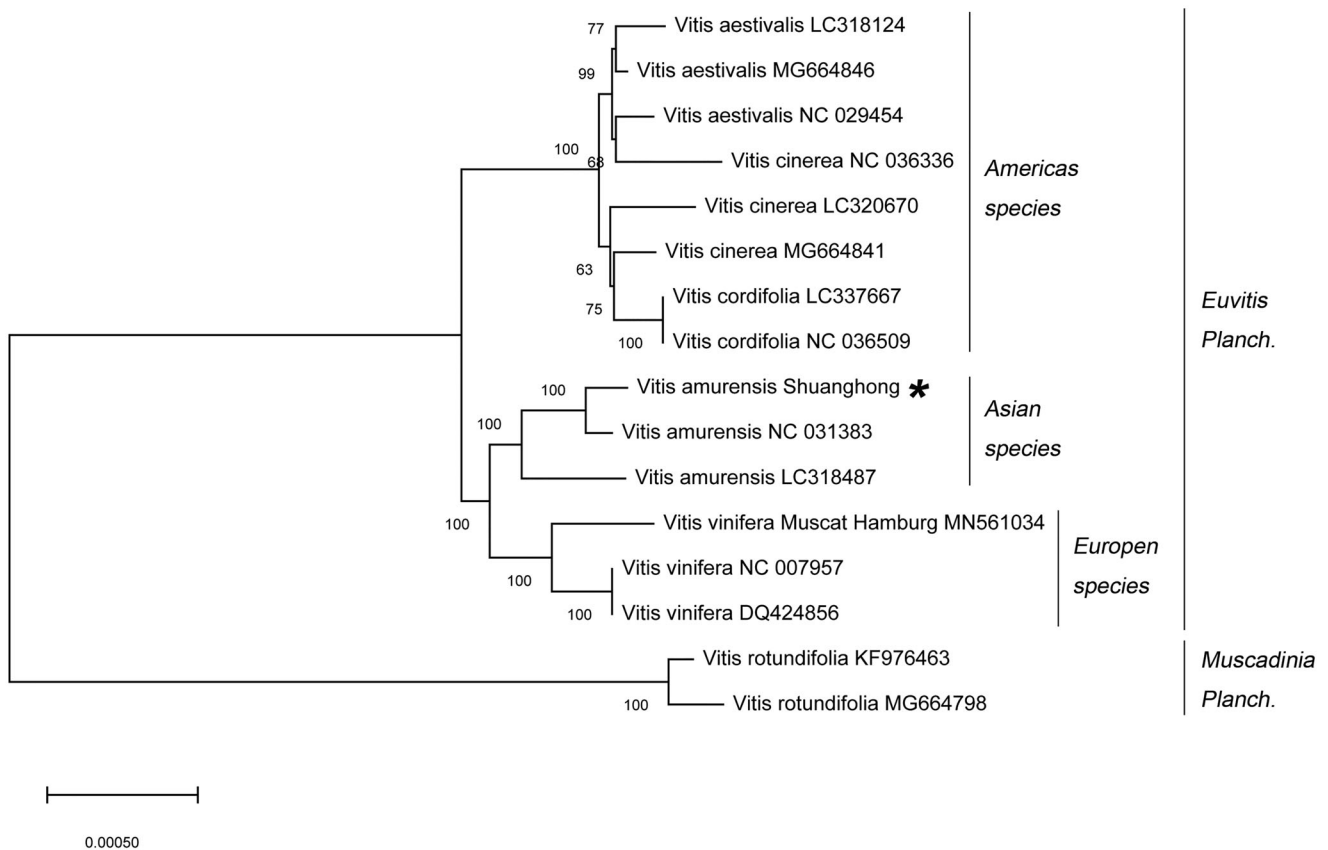


Figure 1. A neighbor-joining (NJ) phylogenetic tree was constructed by using 16 *Vitis* species. *Indicates *Vitis* variety in this study.

Data availability statement

The data that support the findings of this study are available in GenBank: MT479164 at <https://www.ncbi.nlm.nih.gov/genbank/>.

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