

The complete chloroplast genome sequence of *Vitis vinifera* Muscat Hamburg

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ABSTRACT

Vitis vinifera Muscat Hamburg is Eurasian species, which is widely cultivated all over the world. In this study, the complete chloroplast genome of *V. vinifera* Muscat Hamburg is assembled for the first time. The chloroplast genome is 160,915 bp in length, and comprises a 19,072 bp small single copy region and an 89,135 bp large single copy region, which are separated by a pair of inverted repeat regions. The chloroplast genome contains 133 genes, including 88 CDSs, 8 rRNA genes and 37 tRNA genes. The phylogenetic tree analysis showed that *V. vinifera* Muscat Hamburg was the closest to *V. vinifera*.

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Vitis vinifera Muscat Hamburg could be used as both fresh and for wine making. The famous producing regions are mainly concentrated in Tianjin, Hebei, and Shandong provinces in China. The variety has high sugar content, strong aroma and good coloration (Tsevdou et al. 2019). The complete chloroplast genome of *V. vinifera* Muscat Hamburg was

assemble at the first time (GenBank; MN561034) according to whole-genome high-throughput sequencing data. It offers useful information for the resistance breeding of grapevine.

Genomic DNA was extracted from leaves of *V. vinifera* Muscat Hamburg grown at the Modern Engineering Training Center (31°11'N, 121°29'W) and stored at the Center for

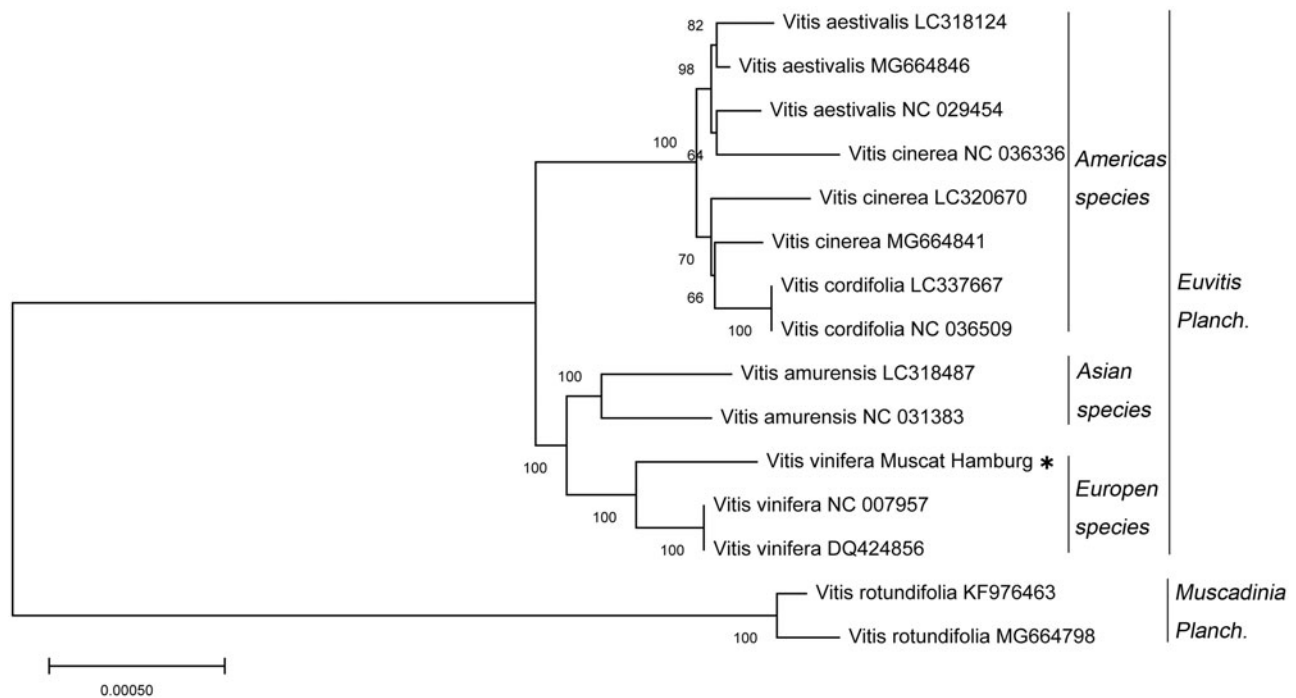






Figure 1. A neighbor-joining (NJ) phylogenetic tree was constructed by using 15 *Vitis* species. *indicate *Vitis* variety in this study.

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Viticulture and Enology, Shanghai Jiao Tong University, storage number was 'Muscat Hamburg'. The Rapid Plant Genomic DNA Isolation Kit (Sangon Biotech, China) was used to extract gDNA. Paired-end reads were sequenced by HiSeq PE150 sequencing platform (Illumina, CA, USA). In total, 3.52 Gb clean reads were obtained. A5-MiSeqv20150522 (Coil et al. 2015) and SPAdesv3.9.0 (Bankevich et al. 2012) software were used to assemble the complete chloroplast genome. The *V. vinifera* chloroplast genome sequence (DQ424856) was used as a reference (Jansen et al. 2006) and the GeSeq was used to annotate gene (Tillich et al. 2017).

The *V. vinifera* Muscat Hamburg chloroplast genome is 161,065 bp in length, comprising a pair of inverted repeat regions (26,354 bp each) that are separated by a 19,072 bp small single copy region and an 89,135 bp large single copy region. The chloroplast genome contains 133 single genes, including 88 protein coding genes (CDS), 8 rRNA and 37 tRNA genes. The grape genome is 37.38% GC and 62.62% AT. The majority of genes are single copy in the chloroplast genome, but 5 CDS (*rps12*, *rps19*, *rp123*, *ycf2* and *ycf15*), 8 tRNAs (*trnG-GCC*, *trnI-CAU*, *trnL-CAA*, *trnV-GAC*, *trnI-GAU*, *trnA-UGC*, *trnR-ACG* and *trnN-GUU*) and 4 rRNAs (*rrn-16*, *rrn-23*, *rrn4.5* and *rrn5*) occur as double copies.

A neighbor-joining (NJ) phylogenetic tree was constructed by using 15 *Vitis* species through the MEGA X (Kumar et al. 2018) to identify the phylogenetic position of *V. vinifera* Muscat Hamburg within the Vitaceae. The phylogenetic tree showed that the 15 *Vitis* species are clustered into two orders (Figure 1), which is consistent with the result of Xie et al. (2017). The *V. vinifera* Muscat Hamburg was phylogenetically closer to *V. vinifera* than species in other genera. It also closer to Asian species and European species within the family Vitaceae.

Disclosure statement

There are no conflicts of interest for all the authors including the implementation of research experiments and writing this article.

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