



Case Study

Characterization of the complete chloroplast genome sequence of *Vitis vinifera* 'Guifeimeigui'

Li Liu, Yang Yang, Xiujie Li* and Bo Li*

Shandong Academy of Grape, Shandong Academy of Agricultural Sciences, Jinan, China

Received: 01 October, 2021

Accepted: 03 December, 2021

Published: 04 December, 2021

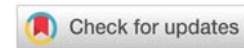
***Corresponding authors:** Xiujie Li, Shandong Academy of Grape, Shandong Academy of Agricultural Sciences, Jinan, China, Email: lixujie-2007@163.com

Bo Li, Shandong Academy of Grape, Shandong Academy of Agricultural Sciences, Jinan, China, Email: sdtalibo@163.com

Keywords: *Vitis vinifera* 'Guifeimeigui'; Chloroplast genome; Illumina sequencing; Phylogeny

Copyright: © 2021 Liu L, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

<https://www.peertechzpublications.com>



Introduction

Vitis vinifera 'Guifeimeigui' is a diploid table grape, a Eurasian species. This research first reported the complete chloroplast (cp) genome of *Vitis vinifera* 'Guifeimeigui'. The size of the complete cp genome is 160,928 bp and its GC content is 37.38%, including a pair of inverted repeats (26,353 bp each) separated by large (89,150 bp) and small (19,072 bp) single-copy regions. It encodes 85 genes, including 40 protein coding genes, 37 transfer RNA genes (tRNA), and 8 ribosomal RNA genes (rRNA). The Maximum Likelihood (ML) phylogenetic tree demonstrated that *Vitis vinifera* 'Guifeimeigui' is close to *Vitis vinifera*.

'Guifeimeigui' (*V. vinifera*) is a table grape cultivar, well known for pleasant flavors of rose, bred by a science researcher of Shandong Academy of Grape [1], Shandong Academy of Agricultural Sciences. It shows strong disease resistance and wide adaptability. It has a special rose aroma and is suitable for facilities cultivation in China. Besides, *V. vinifera* 'Guifeimeigui' is an early maturing variety. Thus, it is widely used for breeding grapes against disease and with early maturity. This high-quality assembly based on Illumina short reads sheds light on *Vitis* phylogeny and evolution and provides accurate genetic information for future research on *Vitis* species.

The sample of *V. vinifera* 'Guifeimeigui' was collected from a vineyard in Zhonggong, Jinan, China (E116°59'7"; N36°28'42"). We used fresh leaves to extract total genomic a DNA with

DNeasy Plant Mini kit (Qiagen, Valencia, CA, and USA) and constructed the library with an average length of 300bp using Illumina TruSeq™ Nano DNA Sample Prep Kit. The DNA library (paired-end, PE=150bp) was sequenced on Illumina NovaSeq 6000 platform (Illumina, San Diego, CA). The resulting reads were quality-filtered using Trimmomatic v0.39 [2]. 4.38Gb clean reads were obtained in total and used to assemble the cp genome with NOVOPlasty v4.2 software [3]. The cp genome of *V. acerifolia* (MG66484.8) serves as the reference for assembly and annotation by GeSeq [3]. The complete cp genome sequence of *V. vinifera* 'Guifeimeigui' had been deposited into GenBank (No. MZ569033) and the SRA number is SRR15114330. In addition, the sample was stored at the Laboratory of Molecular Biology, Shandong Academy of Grape, Shandong Academy of Agricultural Sciences (Voucher specimen: GFMG20210416) (Li Liu, Email: 15153871569@163.com).

Chloroplast length of *V. vinifera* 'Guifeimeigui' was 160,928 bp, consisting of a large single-copy region (LSC, 89150 bp), and a small single-copy region (SSC, 19072 bp) (Figure 1). LSC and SSC are separated by a pair of inverted repeats (IRRs, 26,353 bp each). The cp genome encodes 85 genes, including 40 protein coding genes, 37 transfer RNA genes (tRNA), and 8 ribosomal RNA genes (rRNA) and 37.38% overall GC content (Figure 1). The overall GC content was very similar to that of other complete chloroplast genomes from *V. vinifera* [4,5]. Six protein-coding genes (rpl2, rpl23, ycf2, ndhB, rps7, rps12), seven tRNA genes (trnI-CAU, trnL-CAA, trnV-GAC, trnI-GAU,

trnA-UGC, trnR-ACG, trnN-GUU) and all rRNA genes (rrn4.5, rrn5, rrn16, and rrn23) were located at the IR regions. The GC content of the LSC (35.31%) and SSC (31.65%) regions was lower than those in the IRa region (42.96%) and the IRb region (42.97%). Therefore, the relatively high GC content of the IR regions was mostly attributable to the four rRNAs and tRNAs [6,7].

To investigate the phylogenetic position of *V. vinifera* 'Guifeimeigui' and other 17 *V.* species, a maximum likelihood phylogenetic tree was constructed (Figure 2) through the PhyML [8,9]. The result revealed that *V. vinifera* 'Guifeimeigui' is situated within the same branch as *V. vinifera* (MN149615), which suggested that 'Guifeimeigui' has more traits of the *V. vinifera*.

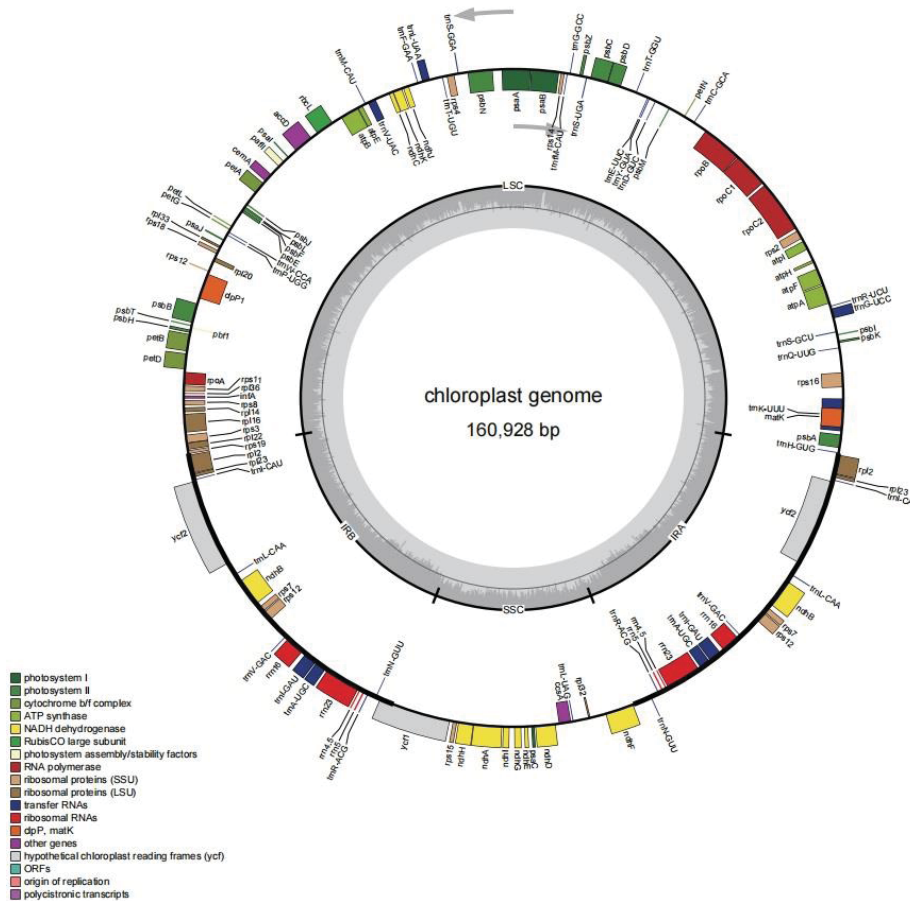


Figure 1: Gene map of *Vitis vinifera* 'Guifeimeigui' chloroplast genome.

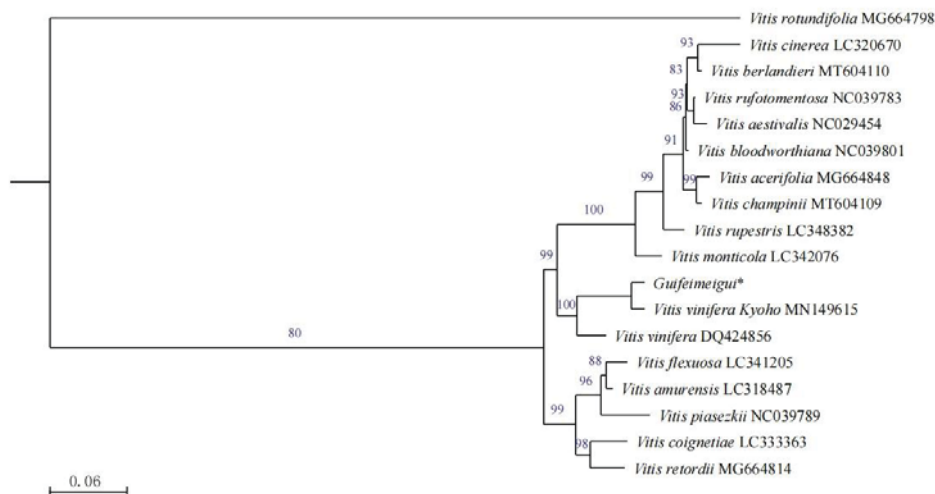


Figure 2: A maximum likelihood phylogenetic tree was constructed using chloroplast genome sequences of *Vitis vinifera* 'Guifeimeigui' and other 17 *Vitis* species.

Acknowledgments

The authors would like to thank TopEdit (www.topeditsci.com) for linguistic assistance during the preparation of this manuscript.

Funding

This study was funded by the Natural Science Foundation of Shandong Province (Grant No. ZR201807090168), New Variety Breeding of High-Quality Characteristic Fruit Trees (Grant No. 2020LZGC008), and Integrated Research and Demonstration of Key Techniques of Facility Cultivation of High Quality and Efficiency Grape (2020ZX010).

Data availability

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. MZ569033, or available from the corresponding author.

References

1. Li KY (2015) 14 grape varieties suitable for early cultivation in solar greenhouse. *Gansu Agricultural Science and Technology* 74-77.
2. Bolger AM, Lohse M, Usadel B (2014) Trimmomatic: a flexible trimmer

for Illumina sequence data. *Bioinformatics* 30: 2114-2120. [Link: https://bit.ly/3pqqGf0](https://bit.ly/3pqqGf0)

3. Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, et al. (2017) GeSeq-Versatile and accurate annotation of organelle genomes. *Nucleic Acids Res* 45: W6-W11. [Link: https://bit.ly/3rtmApb](https://bit.ly/3rtmApb)
4. Guo DH, Li D, Li H, Wang S, Wang L, et al. (2020) The complete chloroplast genome sequence of *Vitis vinifera* Muscat Hamburg. *Mitochondrial DNA B Resour* 5: 117-118. [Link: https://bit.ly/3rv76RB](https://bit.ly/3rv76RB)
5. Zhang L, Guo D, Liu M, Dou F, Ren Y, et al. (2021) The complete chloroplast genome sequence of *Vitis vinifera* × *Vitis labrusca* 'Shenhua'. *Mitochondrial DNA B Resour* 6: 166-167. [Link: https://bit.ly/3ogWjbl](https://bit.ly/3ogWjbl)
6. Shen X, Wu M, Liao B, Liu Z, Bai R, et al. (2017) Complete chloroplast genome sequence and phylogenetic analysis of the medicinal plant *Artemisia annua*. *Molecules* 22: 1330. [Link: https://bit.ly/3pr2Hw6](https://bit.ly/3pr2Hw6)
7. Asaf S, Khan AL, Khan MA, Waqas M, Kang SM, et al. (2017) Chloroplast genomes of *Arabidopsis halleri* ssp. *gemmaifera* and *Arabidopsis lyrata* ssp. *petraea*: Structures and comparative analysis. *Scientific Reports* 7: 7556. [Link: https://go.nature.com/3lcE5QF](https://go.nature.com/3lcE5QF)
8. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, et al. (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of phylml 3.0. *Systematic Biology* 59: 307-321. [Link: https://bit.ly/3ly8COZ](https://bit.ly/3ly8COZ)
9. Kumar S, Stecher G, Tamura K (2016) MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol* 33: 1870-1874. [Link: https://bit.ly/3oiYFqx](https://bit.ly/3oiYFqx)

Discover a bigger Impact and Visibility of your article publication with Peertechz Publications

Highlights

- ❖ Signatory publisher of ORCID
- ❖ Signatory Publisher of DORA (San Francisco Declaration on Research Assessment)
- ❖ Articles archived in worlds' renowned service providers such as Portico, CNKI, AGRIS, TDNet, Base (Bielefeld University Library), CrossRef, Scilit, J-Gate etc.
- ❖ Journals indexed in ICMJE, SHERPA/ROMEO, Google Scholar etc.
- ❖ OAI-PMH (Open Archives Initiative Protocol for Metadata Harvesting)
- ❖ Dedicated Editorial Board for every journal
- ❖ Accurate and rapid peer-review process
- ❖ Increased citations of published articles through promotions
- ❖ Reduced timeline for article publication

Submit your articles and experience a new surge in publication services (<https://www.peertechz.com/submission>).

Peertechz journals wishes everlasting success in your every endeavours.