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# The draft genome and multi-omics analyses reveal new insights into geo-herbalism properties of *Citrus grandis* ‘Tomentosa’

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## Highlights

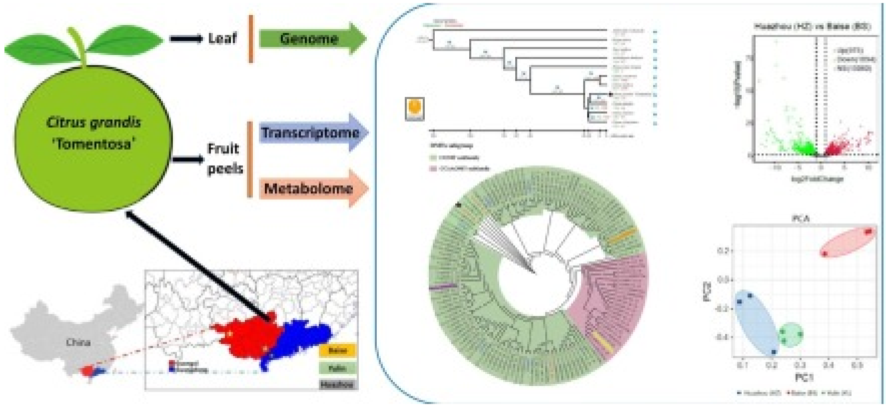
- The first high-quality genome of *Citrus grandis* ‘Tomentosa’ (HJH) is presented.
- Genome size is 359.29 Mb (N50: 9.12 Mb), encoding 30,238 protein-coding genes.

- No recent whole-genome duplication (WGD) is detected.
- Nobiletin content is identified as a potential indicator of geo-herbalism.
- Nobiletin synthesis is found to be regulated by *CtgOMT1*.

## Abstract

*Citrus grandis* ‘Tomentosa’ (CGT) (Huajuhong, HJH) is a widely used medicinal plant, which is mainly produced in Guangdong and Guangxi provinces of South China. Particularly, HJH from Huazhou (HZ) county of Guangdong province has been well-regarded as the best national product for geo-herbalism. But the reasons for geo-herbalism property in HJH from HZ county remains a mystery. Therefore, a multi-omics approach was applied to identify the nature of the geo-herbalism in CGT from three different regions. The comprehensive screening of differential metabolites revealed that the Nobiletin content was significantly different in HZ region compared to other regions, and could be employed as a key indicator to determine the geo-herbalism. Furthermore, the high-quality genome (N50 of 9.12 Mb), coupled with genomics and transcriptomics analyses indicated that CGT and *Citrus grandis* are closely related, with a predicted divergence time of 19.1 million years ago (MYA), and no recent WGD occurred in the CGT, and the bioactive ingredients of CGT were more abundant than that of *Citrus grandis*. Interestingly, Nobiletin (Polymethoxyflavones) content was identified as a potential indicator of geo-herbalism, and O-methyltransferase (OMT) genes are involved in the synthesis of Polymethoxyflavones. Further multi-omics analysis led to the identification of a novel *OMT* gene (*CtgOMT1*) whose transient overexpression displayed significantly higher Nobiletin content, suggesting that *CtgOMT1* was involved in the synthesis of Nobiletin. Overall, our findings provide new data resources for geo-herbalism evaluation, germplasm conservation and insights into Nobiletin biosynthesis pathways for the medicinal plant *C. grandis* ‘Tomentosa’.

## Graphical Abstract



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## Keywords

*Citrus grandis*; Genome; Metabolomics; Transcriptomics; Geo-herbalism; Nobiletin; *CtgOMT1*

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## Data availability

The data sets generated and analyzed during the current study are available in the CNGB Nucleotide Sequence Archive (CNSA: https://db.cngb.org/cnsa) under the accession number CNP0002121.

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[1] Contributed equally

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