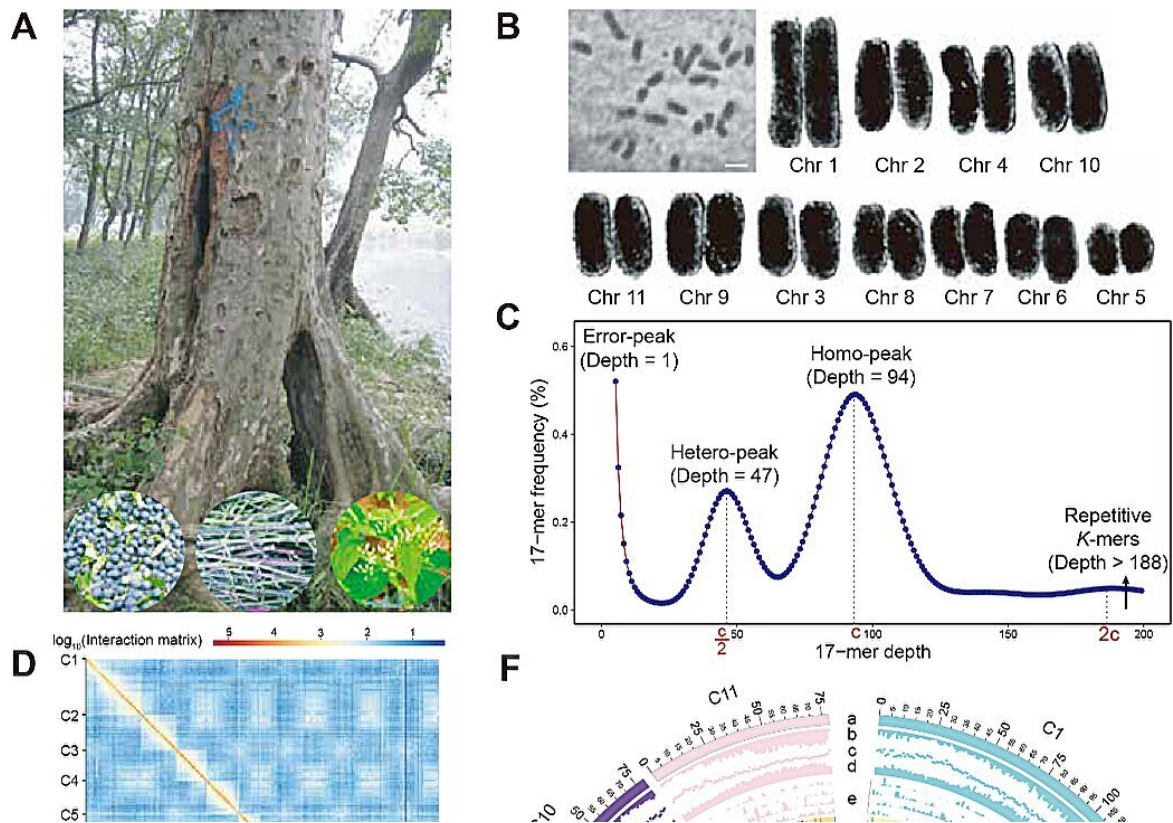


# Chinese team completes the genome assembly of *Cornus wilsoniana*

November 24 2023



High-quality assembly and genome features of *C. wilsoniana*. Credit: *Horticulture Research*

*Cornus wilsoniana* ( $2n=22$ ) is a common shrub in the northern temperate zone of China. It blooms white flowers in spring and produces purple-

black berries in autumn. This tree has a unique mottled bark texture that makes it particularly eye-catching in winter, earning it the common name "ghost dogwood." Due to its peeling bark in winter, it is commonly known as "Guangpi tree" in China.

The fruit of *C. wilsoniana* is rich in oil and can be used to extract edible oil. The oil content of the fruit can reach up to 55% and contains abundant unsaturated fatty acids. Compared to other edible oils, it has hypolipidemic effects. Therefore, the fruit oil of *C. wilsoniana* can not only serve as a well-balanced dietary oil, but also helps control blood lipids.

Meanwhile, owing to its strong stress resistance, it can play a huge role in afforestation, sand-fixation and soil conservation.

In September 2023 [Horticulture Research](#) published an article titled "[A chromosome-level genome assembly provides insights into \*Cornus wilsoniana\* evolution, oil biosynthesis and floral bud development](#)," which was completed by the collaboration of Prof. He Zhenxiang, Prof. Dijun Chen, Prof. Ming Chen and Prof. Liangbo Zhang's group.

This study accomplished the chromosome-level genome assembly of *C. wilsoniana*, laying the foundation for evolutionary analysis and genetic research of key traits in this species.

This study obtained the chromosome-level genome sequence of *C. wilsoniana* using PacBio HiFi and Hi-C sequencing technologies. The [genome size](#) is about 843.51 Mb, with a contig N50 of 4.49 Mb and scaffold N50 of 78.00 Mb.

A total of 30,474 [protein-coding genes](#) were annotated. Comparative genomics analysis identified that the genome of *C. wilsoniana* has experienced one whole genome triplication event (WGT- $\gamma$ , 115.86 Mya)

and one whole genome duplication event (WGD, 44.90 Mya).

The researchers also explored the origin of *C. wilsoniana* chromosomes and reconstructed its karyotype evolution history.

Collinearity analysis revealed that *C. wilsoniana* shares similar [genome](#) structures with *C. controversa* ( $2n=20$ ), and they both belong to the genus *Cornus* in the Cornaceae family, completing divergence about 12.46 Mya.

Transcriptomic analysis found that FAD2 gene family members play a key role in regulating the oleic to linoleic acid ratio in *C. wilsoniana* oil. Additionally, 33 MADS transcription factor genes highly correlated with the flowering process of *C. wilsoniana* were identified by transcriptomic and metabolomic techniques.

This research provides valuable resources for germplasm innovation and genetic improvement of *C. wilsoniana*.

**More information:** Zhenxiang He et al, A chromosome-level genome assembly provides insights into *Cornus wilsoniana* evolution, oil biosynthesis and floral bud development, *Horticulture Research* (2023). [DOI: 10.1093/hr/uhad196](https://doi.org/10.1093/hr/uhad196)

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