

Speciation genomics identifies candidate genomic regions responsible for reproductive isolation in chestnut trees

July 7 2020, by Zhang Nannan



Fruit of Chinese chestnut (*Castanea mollissima*). Credit: SUN Yongshuai

Chinese chestnut trees are thought to be critical for resurrecting wild American chestnut and European chestnut trees. Knowledge of

speciation genomics may be of great value to the chestnut forest restoration in Europe and America.

In a study published in *Nature Communications*, researchers from Xishuangbanna Tropical Botanical Garden (XTBG) used phylogenetic control, the exclusiveness of [barrier](#) alleles in the hybrid lineage, and backward simulations to identify/test candidate [genomic regions](#) responsible for [reproductive isolation](#) between *Castanea mollissima* and variety *henryi* of *Castanea henryi*.

The researchers produced a high-quality genome assembly for *C. mollissima* using nanopore sequencing data and high-throughput chromosome conformation capture (Hi-C) short reads, and characterized evolutionary relationships among related chestnut taxa.

Based on population genomic datasets, they found that *C. henryi* var. *omeiensis* had a distinct genetic structure, and that both of the parental lineages contributed substantial genomic material to the hybrid lineage.

Then the researchers tested the polygenic barrier model and identified candidate barrier genomic regions between *C. henryi* var. *henryi* and *C. mollissima*.

Further, they tested the hypothesis of homoploid hybrid speciation for *C. henryi* var. *omeiensis* using multiple population genomic approaches and simulation-based tests. Barrier effects in candidate regions separating *C. mollissima* and *C. henryi* var. *henryi* would continue to exclude unfit mixed alleles from *C. henryi* var. *omeiensis*. That is, the hybrid lineage had inherited preexisting genetic barriers from its two parents and supported the hypothesis of homoploid hybrid speciation.

"Our study highlights the importance of using phylogenetic information in identifying molecular segments involved in reproductive isolation, and

further we find the non-uniform distribution of reproductively barrier loci across the chestnut genome," said Dr. Sun Yongshuai, principal investigator of the study.



Fruit of *Castanea henryi*. Credit: SUN Yongshuai

More information: Yongshuai Sun et al. Genomic basis of homoploid hybrid speciation within chestnut trees, *Nature Communications* (2020). [DOI: 10.1038/s41467-020-17111-w](https://doi.org/10.1038/s41467-020-17111-w)

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