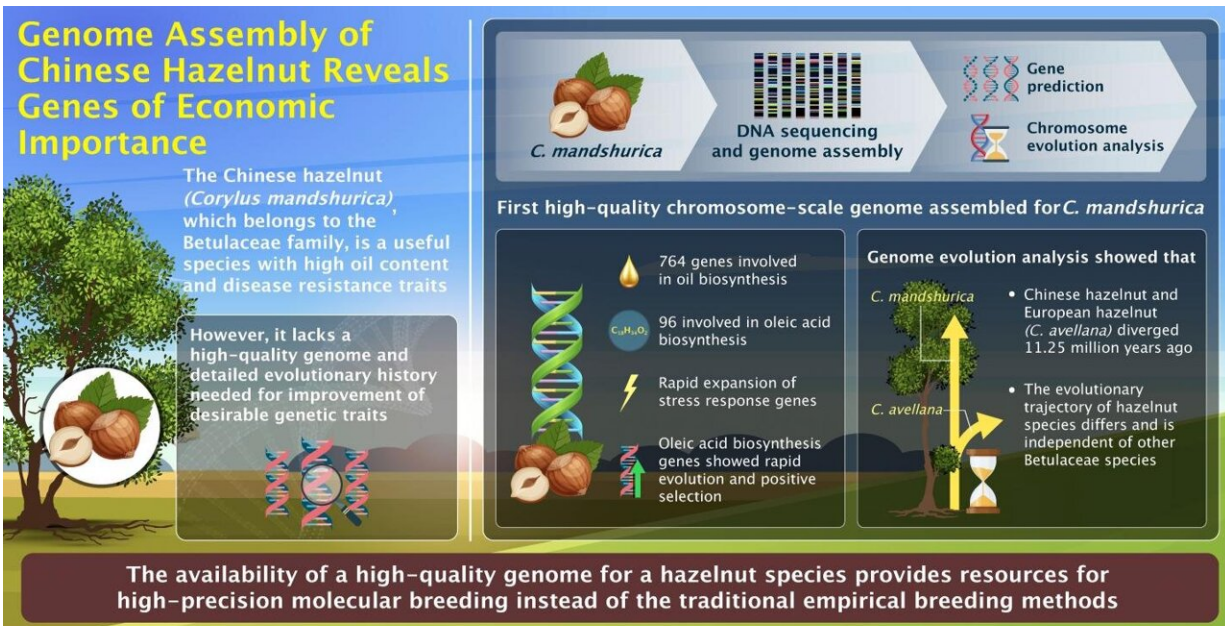


# Chinese hazelnut: The newest piece in the hazelnut genome puzzle

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The *Corylus mandshurica* genome provides insights into the evolution of Betulaceae genomes and hazelnut breeding  
 Li et al. (2021) | Horticulture Research  
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The ability of a high-quality genome for a hazelnut species provides resources for high-precision molecular breeding instead of the traditional empirical breeding methods. Credit: Horticulture Research

Humans have been breeding plants for their economic value for thousands of years. Traditionally, plant breeding techniques included cumbersome and time-consuming techniques like grafting and hybridization to enhance traits of economic value like disease resistance

and high nutrition content. Now, with the ability to edit plant DNA using revolutionary gene-editing tools, particularly the CRISPR-Cas9 system, it is possible to enhance traits of economic value in plants easily and more efficiently than by using traditional techniques. But for that, it is necessary to sequence whole genomes of economically important crops and identify all the genes controlling these desirable traits.

Hazelnut is an important commercial crop, being the fourth largest grown nut in the world. It is widely used for its [oil content](#) and pleasant flavor for the large-scale preparation of chocolates and cookies.

Hazelnut oil has an important healthy fatty acid called oleic acid, which reduces the risk of cardiovascular diseases. Chinese [hazelnut](#) (*Corylus mandshurica*) has proven to be a useful species because of its high oil content and disease resistance traits. However, it lacks a high-quality genome and information about [genes](#) involved in traits like oil synthesis and stress resistance.

A study published in *Horticulture Research* by a team of scientists from China led by Dr. Ying Li and Dr. Yong-Zhi Yang detailed a comprehensive and enhanced genome of the Chinese hazelnut. As Dr. Li explains, "If the genome of each species is a [jigsaw puzzle](#), our study completed the puzzle of a hazelnut species with high quality and found several key pieces related to the quality of the hazelnut fruit." They identified 764 genes involved in oil biosynthesis, of which 96 are directly involved in oleic acid biosynthesis.

The ability to grow in stressful conditions is another important trait that plant breeders try to enhance in their crops. Apart from several genes that they found for oil biosynthesis, Dr. Li's team also found many genes involved in stress resistance. Of them, ten genes related to oil biosynthesis and 38 genes related to stress response undergoing positive nature selection or rapid evolution in the Chinese hazelnut. Since this is the first high-quality genome for this species, researchers also tried to

understand how chromosomes have changed between the ancestral Betulaceae karyotype and five Betulaceae species, including Chinese hazelnut. They found that the evolutionary trajectory of hazelnut species is different from and independent of other Betulaceae [species](#).

The low quality of the genetic resources available for hazelnut has long prevented its widespread use in [plant breeding](#). "The new high-quality reference genome presented here constitutes a valuable resource for molecular breeding and genetic improvement of the important agronomic properties of hazelnuts," Dr. Yang concludes.

Without a doubt, this new genetic resource can be expected to guide future breeding efforts and improvements for hazelnut crops worldwide.

**More information:** Ying Li et al, The *Corylus mandshurica* genome provides insights into the evolution of Betulaceae genomes and hazelnut breeding, *Horticulture Research* (2021). [DOI: 10.1038/s41438-021-00495-1](#)

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