The olive tree's blueprint: Key insights into high-quality oil production

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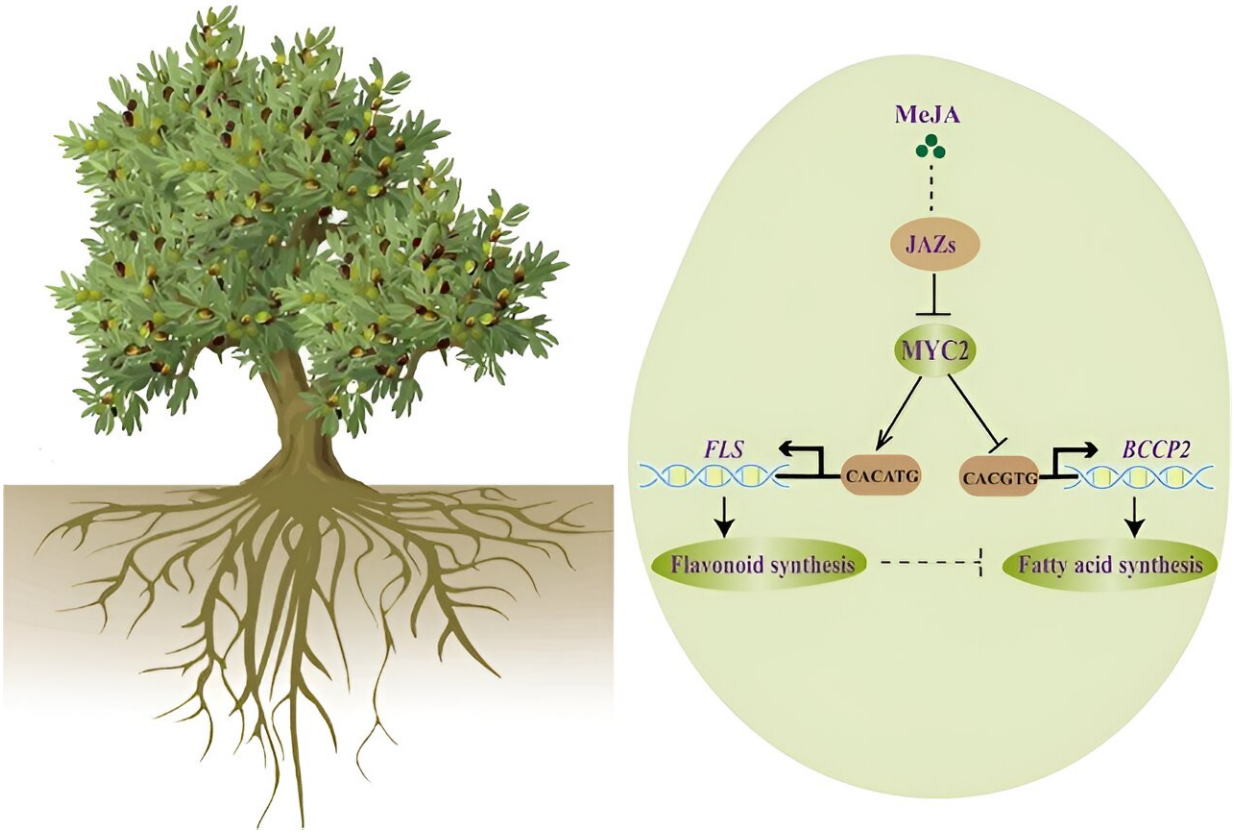

Model of MYC2 in the modulation of fatty acid and flavonoid biosynthesis under MeJA treatment. In the early stage of olive fruit development, accumulation of MeJA could decrease the expression of MYC2, which could repress fatty acid biosynthesis by downregulating the expression of BCCP2 though binding to the G-box within the promoter. Conversely, MYC2 was proved to directly bind to and activate the promoter of FLS, ultimately leading to an increase in flavonoid content. Credit: *Horticulture Research*

A pivotal study has decoded the genetic basis of olive oil production, revealing a key regulatory mechanism that shapes oil biosynthesis. By mapping the olive tree's genome and metabolic pathways, researchers have identified how MYC2, a critical transcription factor, orchestrates the balance between fatty acid and flavonoid synthesis. These insights open new avenues for breeding olives with superior oil profiles, catering to the growing demand for healthful dietary fats.

Renowned for its cardiovascular and cancer-preventive benefits, olive oil is a staple in healthy diets worldwide. However, the intricate biochemical pathways that drive oil production are influenced by complex genetic and developmental factors, complicating efforts to breed high-yield, high-quality varieties. Traditional methods fall short due to limited genomic resources, underscoring the need for deeper exploration into the molecular controls of oil biosynthesis in olives.

Published in *Horticulture Research*, scientists from Lanzhou University, Gansu Research Academy of Forestry Science and Technology, and Gansu Agricultural University unveiled a groundbreaking gap-free genome assembly of the olive cultivar known as Leccino. This study combines cutting-edge metabolomic and transcriptomic data to uncover how the MYC2 transcription factor regulates the interplay between fatty acid and flavonoid production, marking a significant advancement in understanding olive oil biosynthesis.

The research team achieved a telomere-to-telomere genome assembly of Olea europaea cv. Leccino, offering the highest level of accuracy and completeness recorded for olive genomes. By integrating time-course metabolomics and transcriptomics, the study identified MYC2 as a master regulator, inversely controlling fatty acid and flavonoid biosynthesis during early fruit development.

MYC2 suppresses fatty acid synthesis by downregulating BCCP2 and

boosts flavonoid production by activating FLS. This regulation is modulated by methyl jasmonate (MeJA) levels, highlighting a delicate balance in these pathways. The detailed genetic maps developed, including 115 genes linked to fatty acid biosynthesis, provide new targets for breeding olives with improved oil quality.

Professor Yongzhi Yang, a corresponding author, stated, "This study offers an in-depth look at the genetic and molecular framework governing oil biosynthesis in olives. Understanding MYC2's dual function enables us to refine these pathways, enhancing both yield and quality. Our findings set a new standard in olive genomics and open doors to innovative breeding strategies that meet the rising demand for premium olive oil."

The findings have significant potential to transform the olive oil industry. By pinpointing the genetic factors that drive oil biosynthesis, this research lays the groundwork for developing new olive varieties with enhanced oil content and health benefits. The high-quality genome assembly also serves as a vital tool for future research aimed at boosting disease resistance and environmental resilience in olives, supporting sustainable farming practices and addressing the global demand for high-quality olive oil.

More information: Jiaojiao Lv et al, The gapless genome assembly and multi-omics analyses unveil a pivotal regulatory mechanism of oil biosynthesis in the olive tree, *Horticulture Research* (2024). DOI: 10.1093/hr/uhae168

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