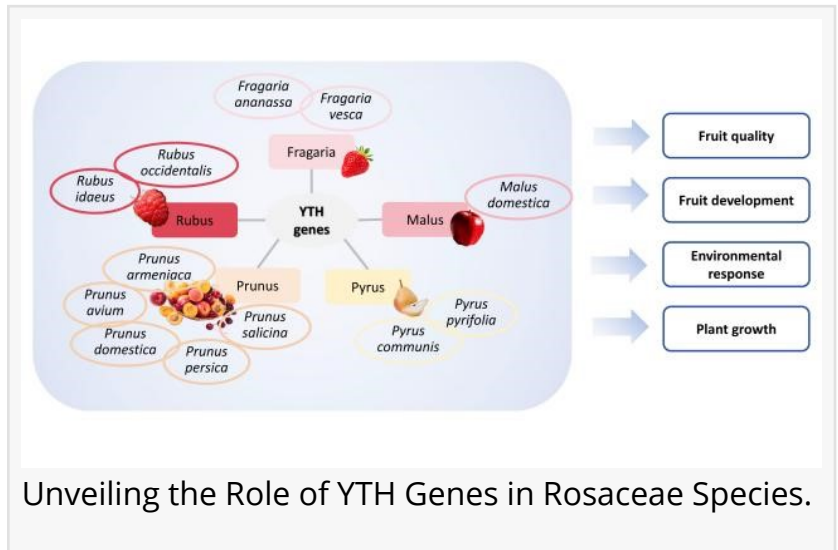


YTH Genes Unveiling Their Secret Role in Fruit Development

GA, UNITED STATES, February 5, 2025 /EINPresswire.com/ -- In a study, researchers have successfully identified and characterized 185 [YTH](#) genes across twelve species in the Rosaceae family, revealing new insights into the regulatory mechanisms of N6-methyladenosine (m6A) and its impact on plant development and fruit quality. This pivotal discovery paves the way for potential breakthroughs in enhancing fruit flavor and improving plant resilience to environmental stress, offering exciting prospects for agricultural research and crop improvement.



The Rosaceae family, which includes economically valuable fruits such as apples, strawberries, and peaches, has long been a focus of agricultural research. However, the role of YTH domain proteins—key players in recognizing N6-methyladenosine (m6A) modifications in RNA—has remained largely unexplored in these species. Understanding the functions of these proteins is crucial for improving fruit quality and enhancing plant resilience, making it essential to study the YTH genes within Rosaceae species more comprehensively.

On January 13, 2025, a study (DOI: [10.1093/fqsafe/fyae050](https://doi.org/10.1093/fqsafe/fyae050)) published in the Food Quality and Safety marked a significant advancement in understanding the YTH genes in Rosaceae species. Researchers from Zhejiang University and Chongqing University unveiled 185 YTH genes across twelve species, offering insights into the genetic mechanisms behind fruit development and quality.

Using a sophisticated genomic approach, the researchers identified YTH genes and analyzed their expression patterns across the twelve species of Rosaceae. By conducting Profile Hidden Markov Model (HMM) searches against protein databases, they pinpointed 185 YTH domain proteins, which were subsequently classified into two subfamilies: YTHDF and YTHDC. The team also constructed phylogenetic trees and performed conserved motif analyses to better understand the evolutionary relationships and functional domains of these proteins. In-depth

expression profiling of YTH genes in *Fragaria vesca*, *Malus domestica*, *Prunus persica*, and *Rubus idaeus* revealed tissue-specific patterns of gene activity, highlighting their role in plant and fruit development. Notably, the study revealed that the expression of PpYTHDFC1 and PpYTHDFE1 in peaches was significantly affected by MeJA treatment, pointing to a potential role in mitigating chilling injury during cold storage. Moreover, overexpressing PpYTHDFE1 in tomatoes resulted in increased organic acid accumulation and a decreased sugar-to-acid ratio, demonstrating a direct effect on fruit flavor. These findings not only close a critical gap in our understanding but also open exciting new avenues for genetic improvements in fruit crops, with the potential to enhance both fruit quality and plant adaptability.

“Deciphering the YTH genes in Rosaceae species represents a monumental step forward in plant epigenetics,” said Dr. Ying Gao from Chongqing University. “Our detailed identification and analysis of these genes provide a solid foundation for understanding how m6A modifications regulate plant processes, impacting fruit development and quality. This study not only deepens our understanding of plant molecular biology but also offers valuable insights for breeding programs focused on improving fruit characteristics and boosting crop resilience to environmental stressors.”

The implications of this research are far-reaching. By manipulating YTH genes, scientists could develop fruit varieties with enhanced flavor profiles and improved resistance to environmental challenges. Such advancements could pave the way for more sustainable farming practices and higher-quality produce, ultimately transforming the horticulture industry and benefiting consumers worldwide.

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