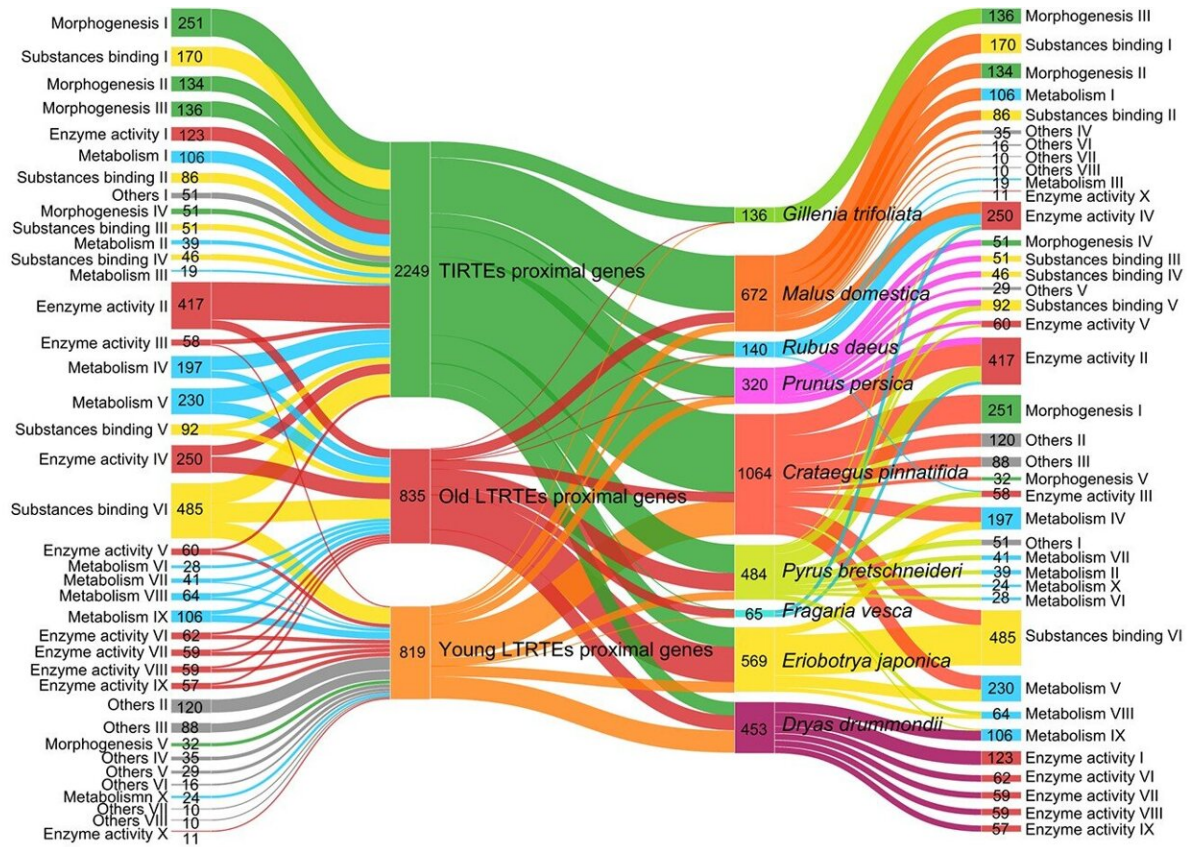


The hidden drivers of evolution: Transposable elements in Rosaceae genomes

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GO term classification

<p>Morphogenesis</p> <ul style="list-style-type: none"> I: organism reproduction II: shoot system morphogenesis III: phyllome development IV: apoplast V: extracellular space 	<p>Substances binding</p> <ul style="list-style-type: none"> I: cis-regulatory region sequence-specific DNA binding II: RNA polymerase II transcription regulatory region sequence-specific DNA binding III: tetrapyrrole binding IV: iron ion binding V: heme binding VI: ADP binding 	
<p>Enzyme activity</p> <ul style="list-style-type: none"> I: protein dimerization activity II: monooxygenase activity III: carbon-oxygen lyase activity IV: oxidoreductase activity V: glucuronosyltransferase activity VI: nuclease activity VII: endonuclease activity VIII: ribonuclease activity IX: endoribonuclease activity X: terpene synthase activity 	<p>Metabolism</p> <ul style="list-style-type: none"> I: protein autophosphorylation II: amine metabolic process III: sterol biosynthetic process IV: secondary metabolite biosynthetic process V: phenylpropanoid metabolic process VI: indole-containing compound metabolic process VII: flavone biosynthetic process VIII: lignin metabolic process IX: DNA integration X: oxylipin metabolic process 	<p>Others</p> <ul style="list-style-type: none"> I: response to chitin II: response to metal ion III: ion transmembrane transporter activity IV: acid transport V: transmembrane signaling receptor activity VI: C4-dicarboxylate transport VII: response to herbivore VIII: pentose transmembrane transporter activity

Sankey diagram illustrating the inferred functions of TE-proximal genes. The width of connections between each vertical block represents the gene count, delineating GO term classifications associated with TE-proximal genes, the number of genes adjacent to three distinct types of TEs, genes categorized across nine species, and the GO term classifications of TE-proximal genes. Credit: *Horticulture Research* (2024). DOI: 10.1093/hr/uhae118

Transposable elements are mobile DNA sequences that play a crucial role in plant genome architecture and gene regulation. They drive genome size variation and affect gene expression by altering regulatory networks. Despite their significance, the diverse and dynamic roles of transposable elements (TEs) are not well understood.

To address these complexities, in-depth studies are necessary to explore TE activity, distribution, and their effects on [gene regulation](#). This research focuses on the Rosaceae family, aiming to uncover the impact of TEs on genome evolution and functional diversity.

Conducted by a team from Northwest A&F University, this study was [published](#) on April 26, 2024, in *Horticulture Research*. The researchers investigated [transposable elements](#) in 14 Rosaceae genomes, examining their distribution, transposition activity, expression patterns, and influence on differentially expressed genes. The goal is to provide comprehensive insights into how TEs shape genome evolution and gene regulation in Rosaceae.

The study analyzed 14 representative Rosaceae genomes, revealing distinct evolutionary patterns of long terminal repeat retrotransposons (LTR-RTs) and their effects on [genome size](#) and gene expression. Genes near recent TE insertions were associated with adversity resistance, while those near older insertions were linked to morphogenesis, enzyme activity, and metabolic processes.

The research highlights diverse responses of LTR-RTs to various conditions, demonstrating their significant role in plant genome evolution. Additionally, 3,695 pairs of syntenic differentially expressed [genes](#) (DEGs) near TEs in apple varieties were identified, suggesting that TE insertions contribute to varietal trait differences. This analysis

provides new insights into the role of TEs in shaping the genomic landscape and regulatory mechanisms within the Rosaceae family.

Dr. Yaqiang Sun, one of the corresponding authors, stated, "Our findings underscore the pivotal role of transposable elements in shaping the genomic architecture and functional diversity within the Rosaceae family. This research provides a valuable resource for future studies on genome evolution and the regulatory mechanisms of TEs."

The insights from this study have significant implications for [plant breeding](#) and genetic engineering. Understanding the role of TEs in gene regulation and genome evolution can help develop new strategies for crop improvement, particularly in enhancing stress resistance and optimizing desirable traits in Rosaceae species. This research also sets the stage for further exploration of TEs in other plant families, contributing to a broader understanding of plant [genome](#) dynamics.

More information: Ze Yu et al, Transposable elements in Rosaceae: insights into genome evolution, expression dynamics, and syntenic gene regulation, *Horticulture Research* (2024). [DOI: 10.1093/hr/uhae118](https://doi.org/10.1093/hr/uhae118)

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