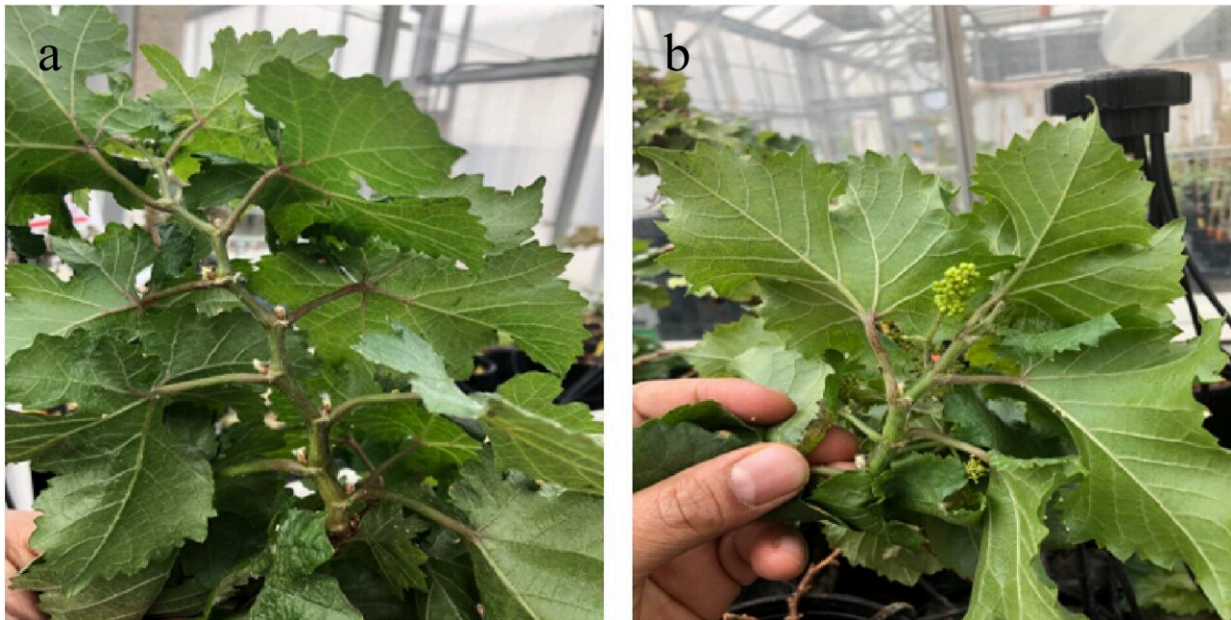


Unraveling the unique role of DELLA proteins in grapevine flowering

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Pixie shoot trait characteristics. (a) Pixie shows a monopodial growth, producing few, if any, lateral branches from the axillary buds. (b) Pixie has a precocious flowering habit, producing inflorescences and bunches starting in the first year of its growth, and even in the younger/upper portion of its main branch. Credit: *Fruit Research* (2024). DOI: 10.48130/frures-0024-0004

The transition from vegetative to reproductive stages in plants involves both internal and external cues, with grapevines (*Vitis vinifera* L. cv. Pixie) presenting a unique case. Research shows that a mutation in the

grapevine's DELLA proteins enhances the conversion of tendrils to inflorescences, diverging from DELLA's typical role in suppressing flowering in annual plants.

While DELLA proteins regulate [plant growth](#) by interacting with various genes and environmental signals, the specific mechanisms and genes targeted by VvDELLA1 in grapevine to promote flowering, in contrast to its usual growth-restrictive functions in other species, warrant further exploration.

Fruit Research [published](#) a paper online titled "Transcriptome analysis unveils a potential novel role of VvAP1 in regulating the developmental fate of primordia in grapevine."

To explore the differential gene expression induced by the gain-of-function VvDELLA1 in L1 dwarf grape mutants, RNA sequencing (RNAseq) profiling was conducted on shoot apices from four mutant cultivars and the wild-type Pinot Meunier. These shoot apices included various developmental structures, and the samples were collected from vines grown hydroponically for over two years.

Pairwise comparisons between each mutant and the wild-type identified thousands of differentially expressed genes (DEGs) across the cultivars, with a significant number of these DEGs being common across three or four mutants, indicating a robust differential expression pattern linked to the VvDELLA1 mutation.

The analysis showed a broad range of expression changes among these DEGs, with some exhibiting up to 550-fold differences compared to the wild type. Gene Ontology (GO) analysis of up-regulated DEGs highlighted their involvement in fundamental cellular processes and biosynthesis pathways, while down-regulated DEGs were associated with processes like defense response and reproduction.

The study also focused on genes within the gibberellin (GA) pathway, noting significant regulatory patterns, particularly with GA2ox genes showing substantial downregulation, suggesting a pivotal role of VvDELLA1 in GA-mediated pathways. Importantly, it was found that the positive regulatory gene VvAP1 and the flowering inhibitory factor VvTFL1a related to flower development were significantly downregulated in mutants, further indicating the complex regulatory complexity of grapevine unique flower development.

The investigation into GA [pathway](#) genes and flowering regulation underscores VvDELLA1's central role in modulating these pathways, disrupting conventional growth patterns, and promoting the unusual development of inflorescences in L1 dwarf mutants.

In conclusion, this study provides insights into the complex regulatory mechanisms disrupted by the VvDELLA1 mutation. It highlights the mutation's impact on flowering and hormonal response pathways, offering a deeper understanding of grapevine's unique developmental processes and the pivotal role of VvDELLA1 in diverging these processes from typical patterns observed in other plants.

More information: Jie Arro et al, Transcriptome analysis unveils a potential novel role of VvAP1 in regulating the developmental fate of primordia in grapevine, *Fruit Research* (2024). [DOI: 10.48130/frures-0024-0004](#)

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