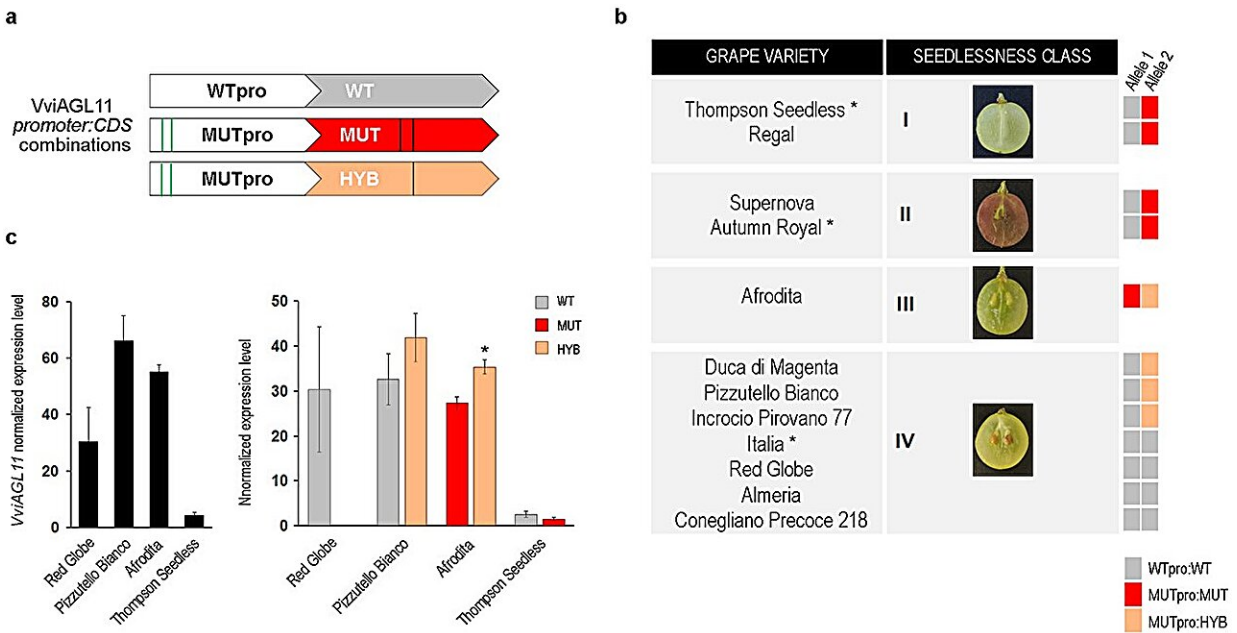


Unlocking the genetic secrets of grape seedlessness

December 21 2023



VviAGL11 gene sequencing and expression analyses. Credit: *Horticulture Research*

Seedlessness in table grapes is a key breeding target, mainly results from stenospermocarpy, linked to the Thompson Seedless grape variety. Advances in genetic research have identified the VviAGL11 gene, one of the MADS-box transcription factor family, as crucial in this process.

This gene, related to seed development, has a specific mutation

(Arg197Leu) strongly associated with seedlessness. Despite significant progress in understanding the genetic aspects of stenospermocarpy, the functional mechanisms of VviAGL11 in inducing seedlessness in grapes remain unclear, presenting a primary focus for ongoing research.

In June 2022, *Horticulture Research* published a research article titled "[VviAGL11 self-regulates and targets hormone- and secondary metabolism-related genes during seed development](#) ."

In this study, the full gene sequence of VviAGL11 was first isolated and sequenced from nine grapevine varieties. Researchers identified three main CDSs: seeded (wild type, WT), seedless (mutated, MUT), and hybrid (HYB) and two main types of promoters (i) seeded (wild type promoter, WTpro) and seedless (mutated promoter, MUTpro).

Notably, a full association was found between WT promoter and WT CDS, and MUT promoter with either MUT or HYB CDS. Expression level assessments revealed the highest total VviAGL11 expression in Pizzutello Bianco, a variety with the HYB allele. In contrast, Thompson Seedless showed the lowest total expression.

VviAGL11 was shown to regulate its own transcription in a specific promoter-CDS manner. GUS fluorimetric assays demonstrated that both WT and MUT CDSs could activate the WT promoter, while all CDSs activated the MUT promoter, with the HYB CDS showing the strongest induction.

Transcriptomic assays on ovules and seeds identified differentially-expressed genes (DEGs) between seeded (SD) and seedless (SL) varieties at various developmental stages, identifying 2,490 upregulated and 851 downregulated genes in seed development stage S3.

Upregulated genes have been shown to primarily participate in protein

metabolism and modification, nucleic acid metabolism, and transport. On the contrary, downregulated genes do not specifically represent any functional categories and mainly participate in "signaling pathways" and "stress responses."

Finally, to identify VviAGL11 [target genes](#), a multi-VviAGL11 co-expression analysis was conducted, leading to the identification of a methyl jasmonate esterase, an indole-3-acetate beta-glucosyltransferase, and an isoflavone reductase as top candidate targets. In vivo experiments further confirmed VviAGL11's role in regulating these genes, demonstrating its significant influence in seed development and the seedlessness trait in grapevines.

In conclusion, this study on VviAGL11 in grapevines revealed three distinct promoter-CDS combinations influencing gene expression and seedlessness. By examining VviAGL11 alleles, researchers demonstrated that VviAGL11 self-activates in specific combinations and identified key target genes involved in hormone signaling and secondary metabolism.

These findings indicate that the wild type VviAGL11 CDS activates crucial [genes](#) in [seed development](#). The study highlights a novel regulatory mechanism linking VviAGL11 haplotypes with seedlessness, suggesting potential applications in grapevine breeding for seedlessness and fruit size optimization.

More information: Alessandra Amato et al, VviAGL11 self-regulates and targets hormone- and secondary metabolism-related genes during seed development, *Horticulture Research* (2022). [DOI: 10.1093/hr/uhac133](#)

Provided by Plant Phenomics

Citation: Unlocking the genetic secrets of grape seedlessness (2023, December 21) retrieved 21 June 2024 from <https://phys.org/news/2023-12-genetic-secrets-grape-seedlessness.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.