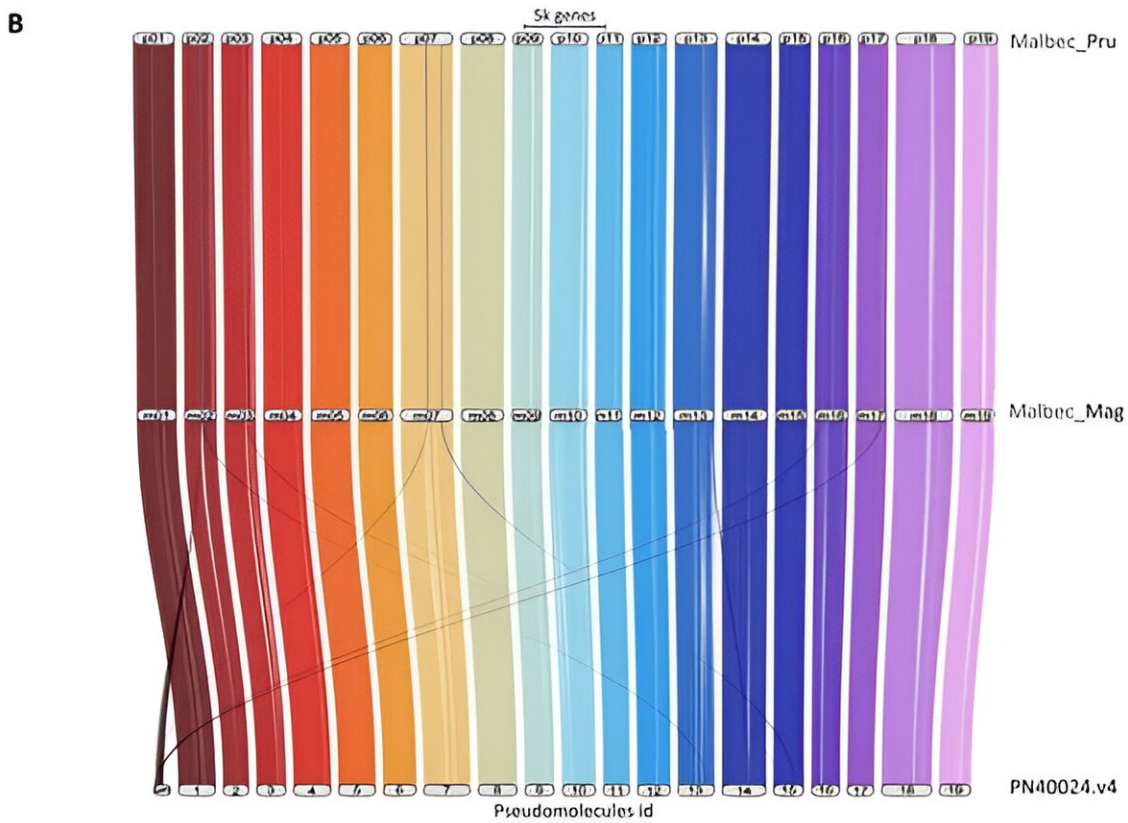
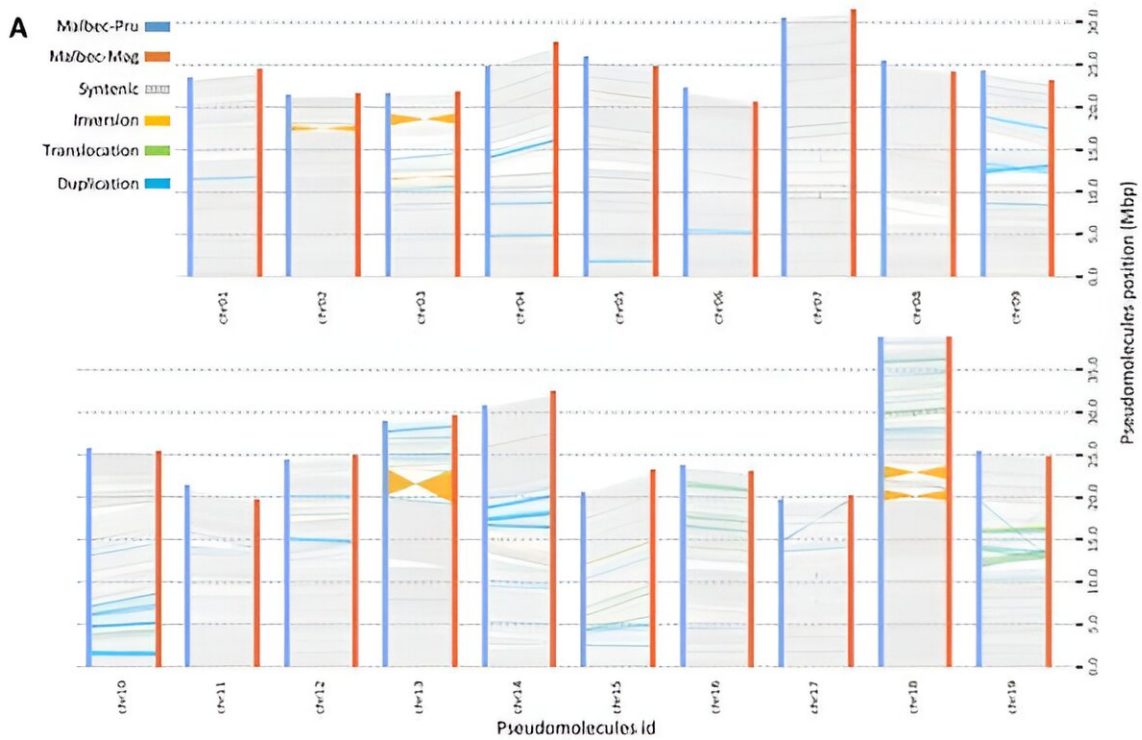


# **From vine to wine: Decoding Malbec's genetic diversity for clonal excellence**

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Synteny analysis based on the comparison of the 19 pseudomolecules assembled

for Malbec haplophases. Credit: *Horticulture Research* (2024). DOI: 10.1093/hr/uhae080

Grapevine genomes, known for their high heterozygosity, present significant challenges for accurate assembly. Traditional approaches often focus on nearly homozygous lines, which fail to capture the full genetic diversity of complex cultivars like Malbec.

Understanding clonal phenotypic variation, which significantly impacts wine quality, adds to this complexity. To address these challenges, a detailed and accurate genomic assembly is essential for comprehending the [genetic mechanisms](#) driving clonal variation and contributing to the unique attributes of the Malbec [grapevine](#).

A team of researchers from the Instituto de Biología Agrícola de Mendoza, Instituto de Ciencias de la Vid y del Vino, and Max Planck Institute for Biology Tübingen, among others, have [published](#) a study in the journal *Horticulture Research* on March 14, 2024. This study presents the first diploid genome assembly of the Malbec grapevine, leveraging advanced sequencing technologies to resolve the two haplotypes inherited from its parental cultivars.

The study achieved a high-quality genome assembly of the Malbec grapevine using advanced PacBio long-read sequencing and trio binning techniques. This method enabled the separation and assembly of the two haplotypes inherited from Malbec's parent cultivars, Prunelard and Magdeleine Noire des Charentes.

The assembled genome revealed significant polymorphic regions and provided detailed gene model annotations for both haplotypes. Transcriptomic analysis of Malbec clonal variants uncovered differences

in [gene expression](#), particularly highlighting the higher anthocyanin content in certain clones. This increased anthocyanin content was associated with heightened abscisic acid responses, leading to the overexpression of genes involved in phenylpropanoid metabolism and abiotic stress responses.

These findings underscore the critical role of haplotype-resolved assemblies in understanding the genetic basis of clonal variation and its impact on traits essential for [wine quality](#) and grapevine adaptability.

Dr. Luciano Calderón, one of the lead researchers, stated, "This genome assembly not only enhances our understanding of Malbec's [genetic diversity](#) but also provides a valuable resource for studying the [molecular mechanisms](#) underlying clonal variation. It opens up new possibilities for breeding and improving grapevine cultivars."

The assembled genome of Malbec offers a comprehensive reference for future genetic studies and breeding programs aimed at improving grapevine cultivars. By understanding the genetic basis of traits like berry composition and stress responses, researchers can develop more resilient and high-quality grapevines, ultimately benefiting the [wine industry](#) and addressing challenges posed by climate change.

**More information:** Luciano Calderón et al, Diploid genome assembly of the Malbec grapevine cultivar enables haplotype-aware analysis of transcriptomic differences underlying clonal phenotypic variation, *Horticulture Research* (2024). [DOI: 10.1093/hr/uhae080](https://doi.org/10.1093/hr/uhae080)

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