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Haplotype-Resolved genome assembly of the Microvine

Samuel Talbot[1]*, Steven Carrell[2], Brent Kronmiller[2], Satyanarayana Gouthu[1], Luca Bianco[3], Paolo Fontana[3], Mickael Malnoy[3], and Laurent G. Deluc[1&4]

[1]Department of Horticulture, Oregon State University, Corvallis, USA,
[2]Center for Quantitative Life Sciences, Oregon State University, Corvallis, USA,
[3]Foundation Edmund Mach, San Michelle All'addige, Italy.
[4]Oregon Wine Research Institute, Oregon State University, Corvallis, USA,.

*Corresponding Author: sam.talbot@oregonstate.edu

Developing a tractable genetic engineering and gene editing system is an essential tool for grapevine. We initiated a plant transformation and biotechnology program at Oregon State University using the grape microvine system (*V. vinifera*) in 2018 to interrogate gene-to-trait relationships using traditional genetic engineering and gene editing. The microvine model is also used for nanomaterial-assisted RNP, DNA, and RNA delivery. Most reference genomes and annotations for grapevine are collapsed assemblies of homologous chromosomes and do not represent the specific microvine cultivar '043023V004' under study at our institution. We used a trio-binning method combining PacBio HiFi and parental Illumina reads to develop a high-quality, haplotype-resolved microvine genome. This genome was refined using chromosome scaffolding with high-throughput chromosome conformation capture (Hi-C). To evaluate genome quality, we compared this genome with our own highly curated microvine genome, which was produced using a combination of Oxford Nanopore and PacBio Sequel I sequencing. While the new genome retains considerable large-scale structural synteny with existing grape genomes, it also revealed significant differences between haplotypes. The phasing approach has elucidated the unique allelic contributions of essential gene families like *GRAS*, which contribute to the microvine dwarfing, or MYB, involved in regulating pigment accumulation in berries. The roles of additional gene variants, alongside associated alternative-splicing events, provide insights into the dynamic regulation of these key gene families across haplotypes. This comprehensive genomic resource will accelerate the functional characterization of complex molecular gene interactions, enhance molecular marker development, and improve the precision of genome editing tools in grapevine research.

Keyword: Microvine, HiFi, Haplotype-resolved genome, trio-binning method