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Mobilizing endogenous transposable elements for grapevine improvement: a genomic and epigenomic approach in New Zealand Sauvignon Blanc

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Abstract (250 words)

Efforts to improve the New Zealand wine industry's climate resilience and sustainability through grapevine improvement are limited by germplasm availability and a reliance on Sauvignon Blanc exports. To address this, we are working to generate a population of 12,000 individuals with unique genetic traits, from which to select future clones for major export varieties.

Sauvignon Blanc plantlets are being regenerated from embryogenic callus, using an approach designed to mobilise endogenous transposable elements as mutagens. Alongside early phenotypic characterisation, whole-genome genotyping and epigenotyping is being conducted using nanopore sequencing. To facilitate this, we produced a phased diploid telomere-to-telomere (T2T) assembly of the clone progenitor. Each 500 Mb haplotype exhibits over 99% completeness and accuracy (QV ~60), with genic and repetitive elements annotated.

To evaluate the robustness of methylation signals to experimental parameters, we used low-coverage nanopore skim sequencing. Genomic and epigenetic variations in New Zealand's commercial germplasm were similarly characterised. Preliminary analysis of the initial clone set promises insights into mutational processes operating in this collection, which we expect to be dominated by transposable element movement and epigenetic dysregulation.

This research aims not only to enrich the clonal diversity for future New Zealand viticulture but also to shed light on aspects of transposon mutagenesis, epigenetic variability, and the function of mutated genes. It is anticipated that these findings will contribute to crop improvement efforts both in New Zealand and internationally, by advancing the understanding of somatic variability and epigenomics in agriculture.

Keywords: somatic mutations, transposable elements, nanopore sequencing, epigenetics