# Using nanopore skim-sequencing to characterise regional epigenetic variability in New Zealand Sauvignon Blanc

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**Abstract (250 words)**

Recent advancements in genomic sequencing technologies have enabled more detailed and direct studies of DNA methylation, which can help characterise epigenetic variations in plants. The Grapevine Improvement team at the Bragato Research Institute is studying the use of Oxford Nanopore sequencing to identify epigenetic changes associated with environmental differences among clonally-propagated grapevines.

This study involved sequencing DNA from the same Sauvignon Blanc clone, sourced from diverse New Zealand viticultural regions, using the PromethION platform. New base-calling models were used to characterise cytosine methylation in various contexts (CG, CHG, and CHH) alongside adenosine methylation. Subsampling revealed that low-depth skim sequencing (0.1x) is sufficient to distinguish genome-wide methylation profiles, with geographic location emerging as the predominant factor influencing epigenetic traits. The method of sample preservation, whether immediate snap-freezing or initial storage in desiccant, did not have a significant effect on the results.

This research demonstrates the potential of low-depth nanopore sequencing for assessing epigenetic variability as influenced by environmental factors in plants. The approach holds promise for the investigation of the mechanisms that drive the expression of location-specific agronomic traits, forecasting climate-related epigenetic shifts, and facilitating the development of technologies aimed at inducing targeted epigenetic modifications.

**Keywords:** Nanopore sequencing, epigenetics, DNA methylation