



The first study to discover population-level genomic structural variants (SVs) in wild populations of *Eucalyptus viminalis*.

Zixiong Zhuang (Australian National University); Ashley Jones (Australian National University); Scott Ferguson (Australian National University); Justin Borevitz (Australian National University).

Rapid advancements in long-read sequencing technologies have enabled us to discover large structural variations in eukaryotic genomes. Algorithms for discovering structural variants (SVs) via read mapping have proliferated in recent years with the increase in computing power and accessible long-read sequencing. Here we present the first discovery and characterisation of structural variants in wild populations of *Eucalyptus viminalis*, an ecologically important species. *Eucalyptus* species are highly heterogeneous, which result in noisy alignments, making reliable discovery of SVs challenging. Using a combination of recently developed bioinformatics tools, we have discovered ~300,000 structural variants (multi-nucleotide polymorphisms) among 45 *E. viminalis* individuals. After transcriptome discovery using direct RNA sequencing, we have observed that most instances of the terpene synthase (TPS) gene family (important for oil production and tree defence) are avoided by SVs, but some TEs were observed to be inserted into the intronic regions of certain TPS genes. Together, this study establishes our foundational understanding of SVs in wild populations of *E. viminalis* and provides insights into pangenomic studies of *Eucalyptus* in the future.

Zixiong Zhuang: u7192444@anu.edu.au