

Activation of retrotransposition in grapevine

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Abstract (250 words)

Retrotransposons, particularly of the Ty-Copia and Ty-Gypsy superfamilies, represent the most abundant and widespread transposons in many plant genomes. Grapevine is no exception and it is clear that these mobile elements have played a major role in the evolution of Vitaceae genomes. While speculation abounds around the possible role of transposons in plant genomes, outside of the rather obvious involvement of retrotransposition in fueling genome expansion, there is little clarity of the actual role these elements have in both developing new genetic variation and in modulating epigenetic responses within genomes to changing climate. To this end we have been exploring de-novo assembled Sauvignon blanc and Pinot noir genomes with a view to catalogue retrotransposon loci to determine the structural intactness and thus age of insertion variation across a small number of clonal lineages of these 2 varieties in an attempt to identify 'live' TE loci. Combining insights into insertional patterns with both short and long read transcriptome data has highlighted that only a small number of families and within these families and an even smaller number of discrete loci are responsible for ongoing retrotransposition. We are currently exploring means to alter the epigenomic landscape of grape genomes to allow heightened retrotransposon activity and thus mobilization. We will present how we are tracking this mobility using virus-like protein particle analysis (VLP-seq) to both identify families actively transposing and to study the genomic and epigenomic impact of this mobility prior to purifying selection.

Keywords: Grapevine, Transposon, Genomics, Epigenomics, Climate Adaptation