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P46 – Genetic analysis of grapevine (*Vitis vinifera*) wood composition

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Abstract

Grapevine woody stems represent a valuable source of polyphenols with a broad spectrum of health benefits. In contrast to the large number of studies about genetic determinants of grape berry composition, few works have investigated the genetic bases of grapevine wood composition.

In this work, we have used both targeted and non-targeted metabolomic approaches to perform a global metabolic quantitative trait loci (mQTL) analysis with a progeny from a cross between 'Riesling' (Ri) and 'Gewürztraminer' (Gw).

Analysis of woody canes extracts using high performance liquid chromatography coupled to mass spectrometry has revealed genetic variability in the Ri x Gw progeny for metabolites from different families such as stilbenoids and flavonoids. High-density genetic maps based on single nucleotide polymorphism (SNPs) allowed the detection of significant mQTLs for a large number of metabolites, including major polyphenols.

This poster presents information about the detected QTLs impacting the accumulation of major grapevine wood polyphenols. Furthermore, characterization of major determinants of grapevine wood composition may provide bases for a better understanding of sensitivity to wood diseases such as grapevine trunk diseases.

Keywords: Grapevine, wood, metabolomics, genetics, QTLs