

## Traçabilité génétique des bois de chêne de tonnellerie : vers une meilleure prédiction des propriétés organoleptiques?

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### Résumé

Aromatic compounds found in the wine mostly arise during the contact with oak wood barrels. Whisky-lactone which gives a coconut and a woody taste is the most important aromatic compound. Sessile and pedunculate oaks (*Quercus petraea* and *robur*) are widely used for wine maturation but these two species are characterized by a contrasted pattern for whisky-lactone. Identification of the genes involved in the biosynthesis of these compounds is of great importance to provide both (i) gene based diagnostic markers for species identification and (ii) homogenous batches of barrels. However, the molecular mechanisms involved in the biosynthesis of the aromatic compounds remain in their infancy in forest trees. To fill this gap, we implemented an experimental design on 20 sessile and pedunculate oaks. First, wood cores were sampled on each individual. The transition zone between heartwood and sapwood was immediately harvested and stored at -80°C until RNA extraction. The remaining wood was grinded and aromatic compounds quantified using GC/MS or LC-HRMS. This chemical approach confirmed the result previously obtained by [1] and [2] namely a higher whisky-lactone and QTT content in sessile oak and a higher Glu-BA content in pedunculate oak. Second, three sessile and pedunculate oak samples were selected according to the chemical data. Total RNA were extracted from the transition zone and its gene expression was investigated by RNAseq. We found that 97 genes were differentially regulated between the two species using the Deseq and the EdgeR packages. Among these genes, 9 and 4 were specifically expressed in the transition zone of sessile and pedunculate oaks respectively. A functional annotation was performed highlighting molecular functions potentially involved in the biosynthesis of the aromatic compounds.

### Références

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