

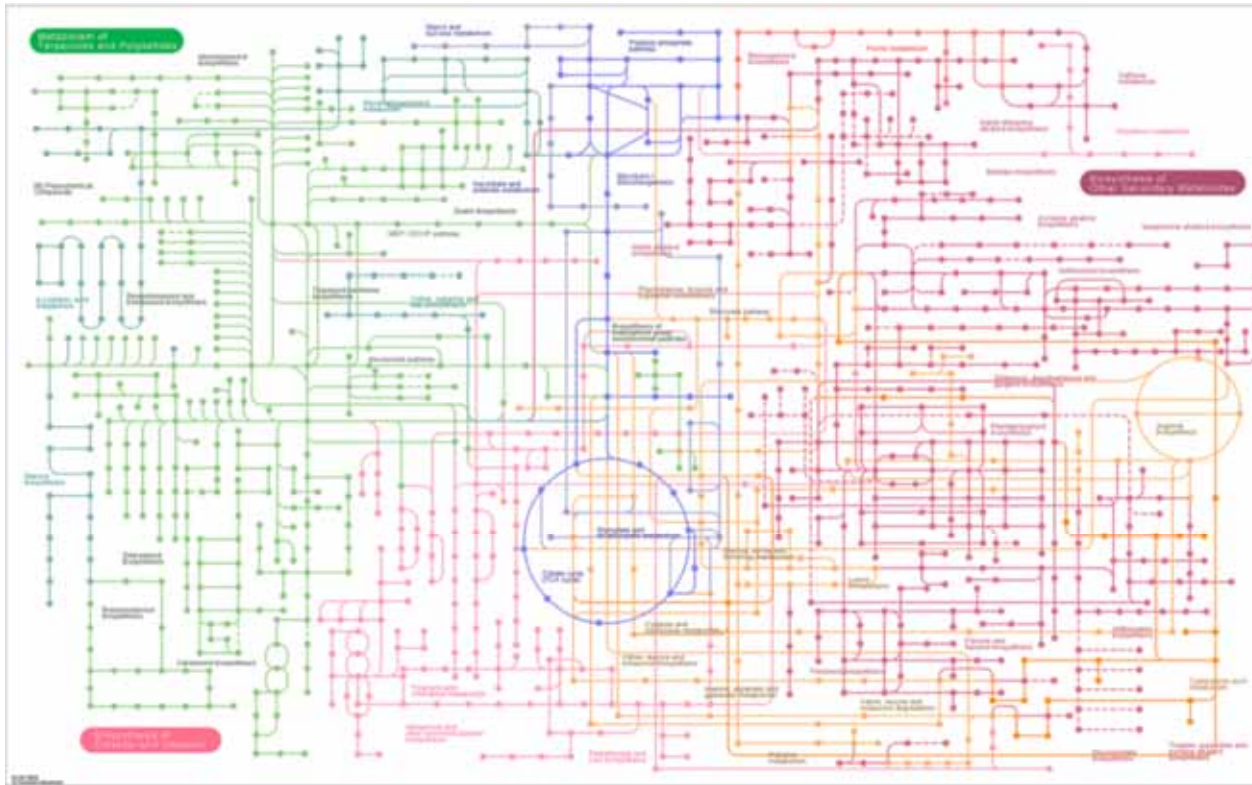


Genetic analysis of grapevine secondary metabolism using non-targeted metabolomics



Thuy-Thanh TRUONG – INRA Grand Est Colmar – France

Secondary metabolism is a major contributor to wine quality



- Color
- Structure
- Aroma

Which genes are involved in grape aroma biosynthesis?

**Riesling
(RI)**

- Fruity
- Mineral



x



**Gewurztraminer
(GW)**

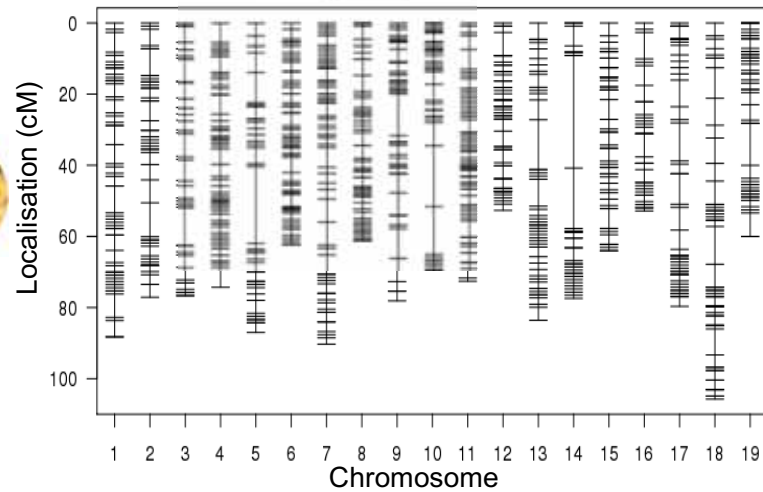
- Floral
- Spicy
- Exotic fruits

383 progenies in a vineyard of 7000 m² since 2006

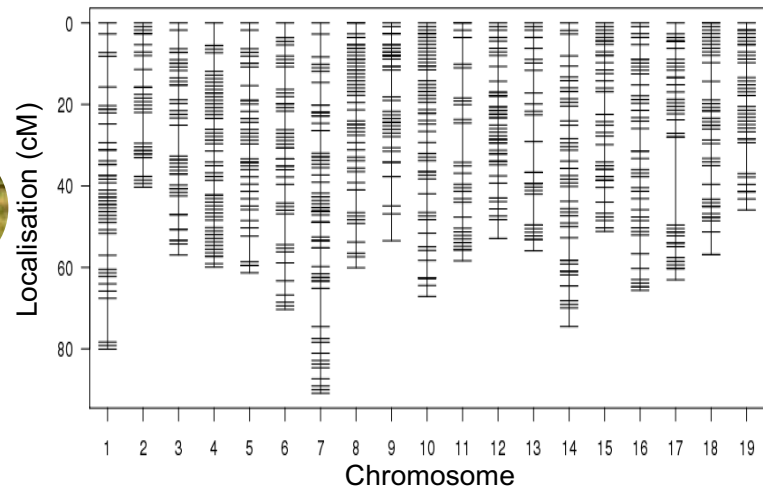


Genetic data

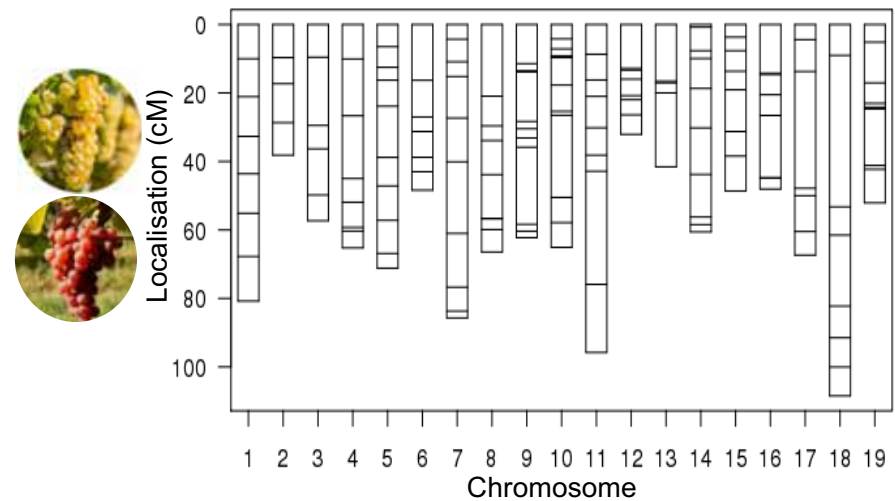
RI map : 953 SNP



GW Map : 806 SNP



Consensus map: 157 SSR



→ **1916 genetic markers**

High resolution metabolic phenotyping

Ultra High Pressure Liquid Chromatography –
High Resolution Mass Spectroscopy
(UHPLC-HRMS)



RI x GW
population



UHPLC-HRMS
Orbitrap

→ Untargeted analyses

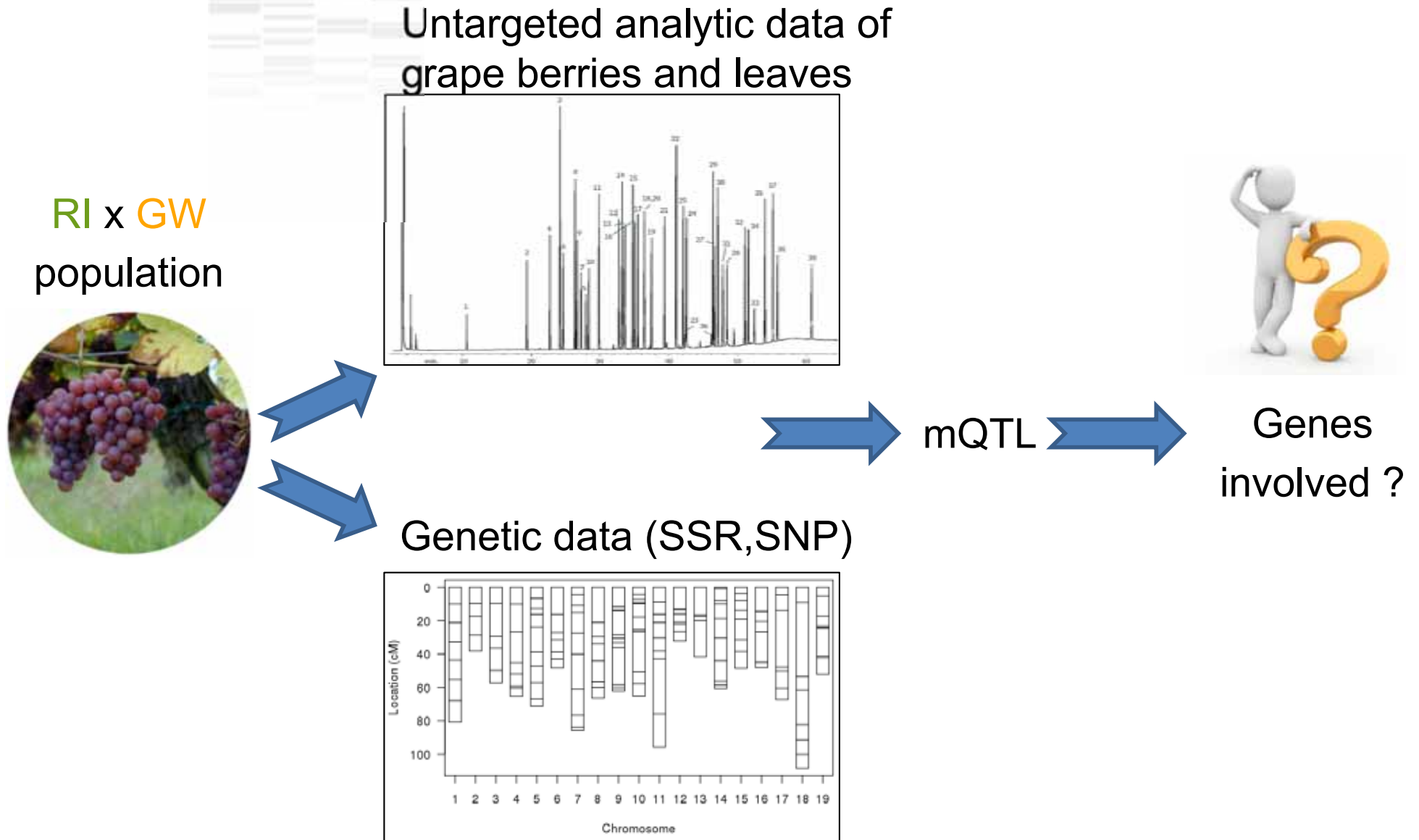


8030 ions



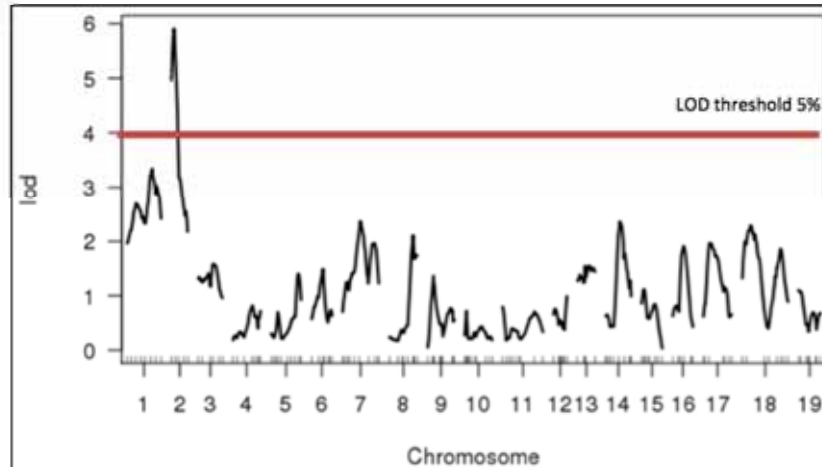
2215 ions

Metabolic Quantitative Trait Loci (mQTL) analysis



Identification of candidate genes

mQTL



Physical position: annotated genes on PN40024



Identification of candidate genes

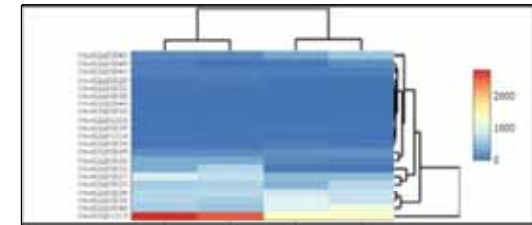
Physical position: annotated genes on PN40024



Annotated
function

RI and GW
genomic sequences

RI and GW RNAseq



Candidate genes

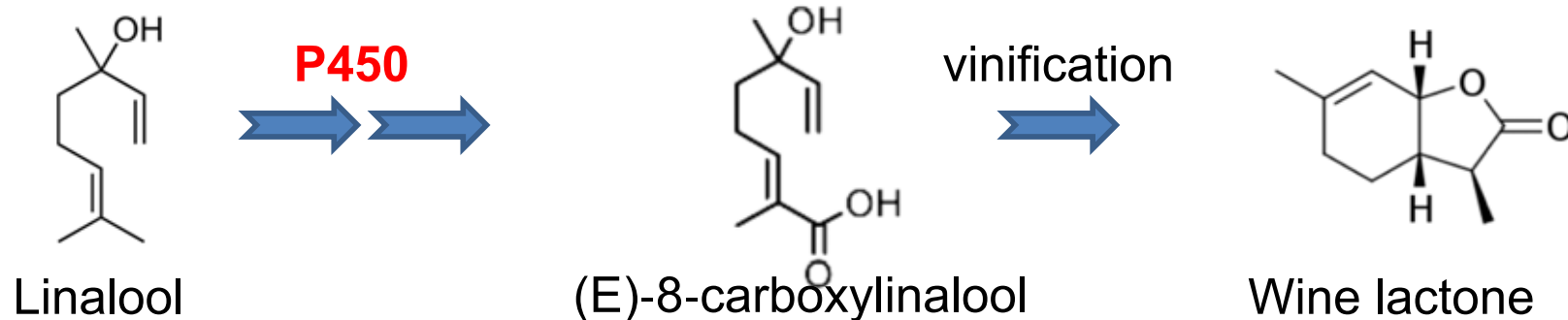
Functional characterization

A successful approach (Ilc et al., 2017)

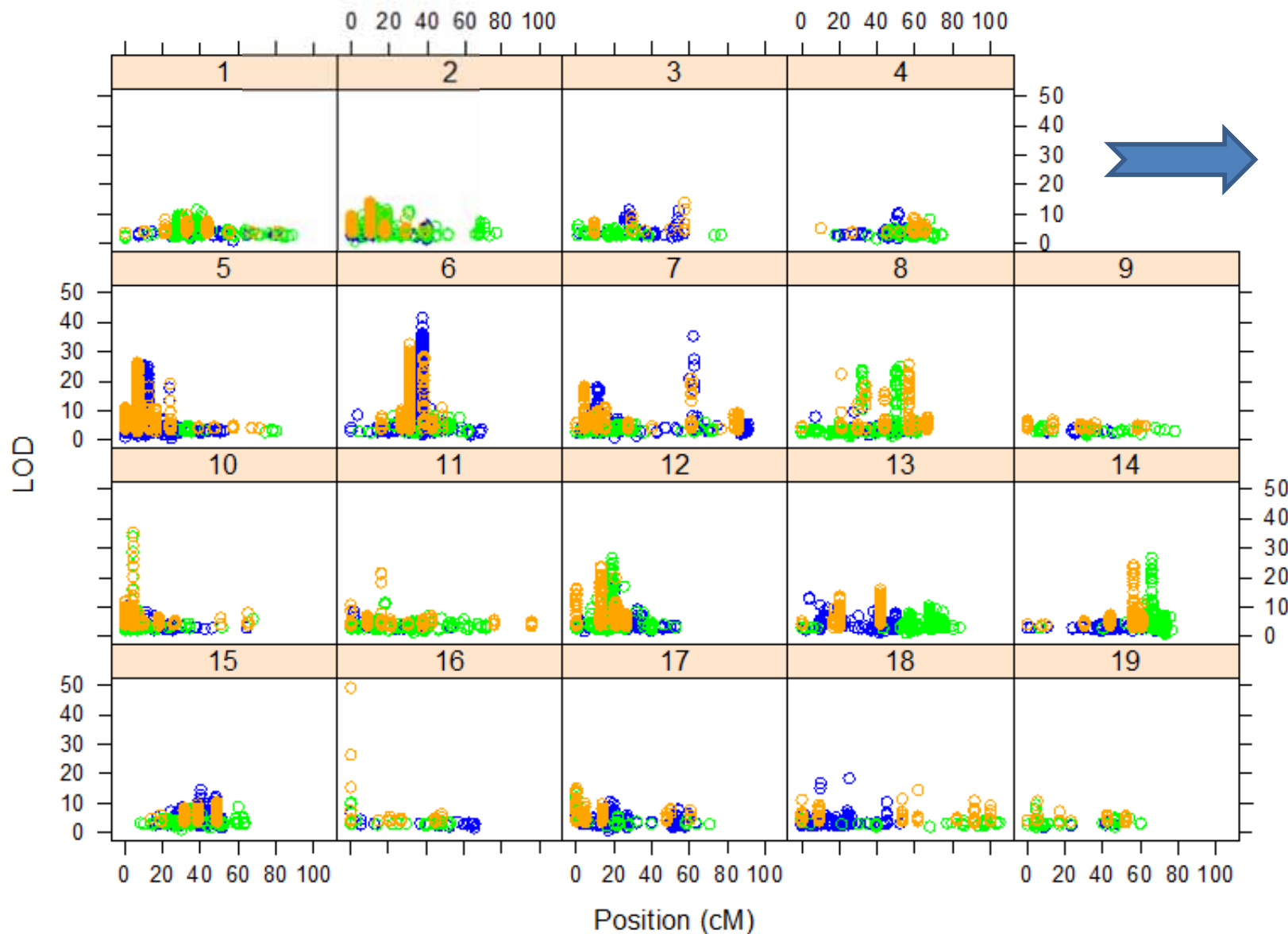
A grapevine cytochrome P450 generates the precursor of wine lactone, a key odorant in wine

Tina Ilc¹, David Halter², Laurence Miesch³, Florian Lauvoisard³, Lucie Kriegshauser¹, Andrea Ilg², Raymonde Baltenweck², Philippe Hugueney², Danièle Werck-Reichhart¹, Eric Duchêne² and Nicolas Navrot¹

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Thousands of mQTL distributed all over the genome



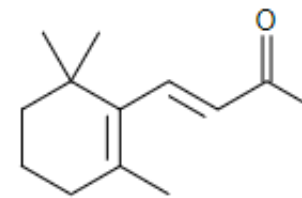
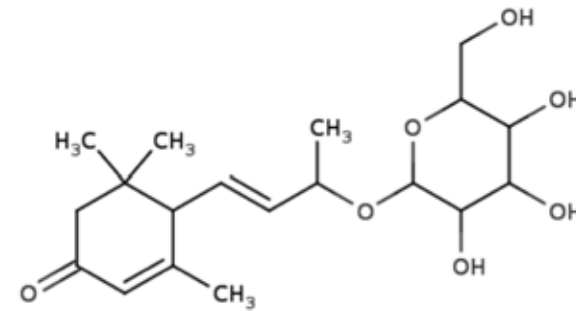
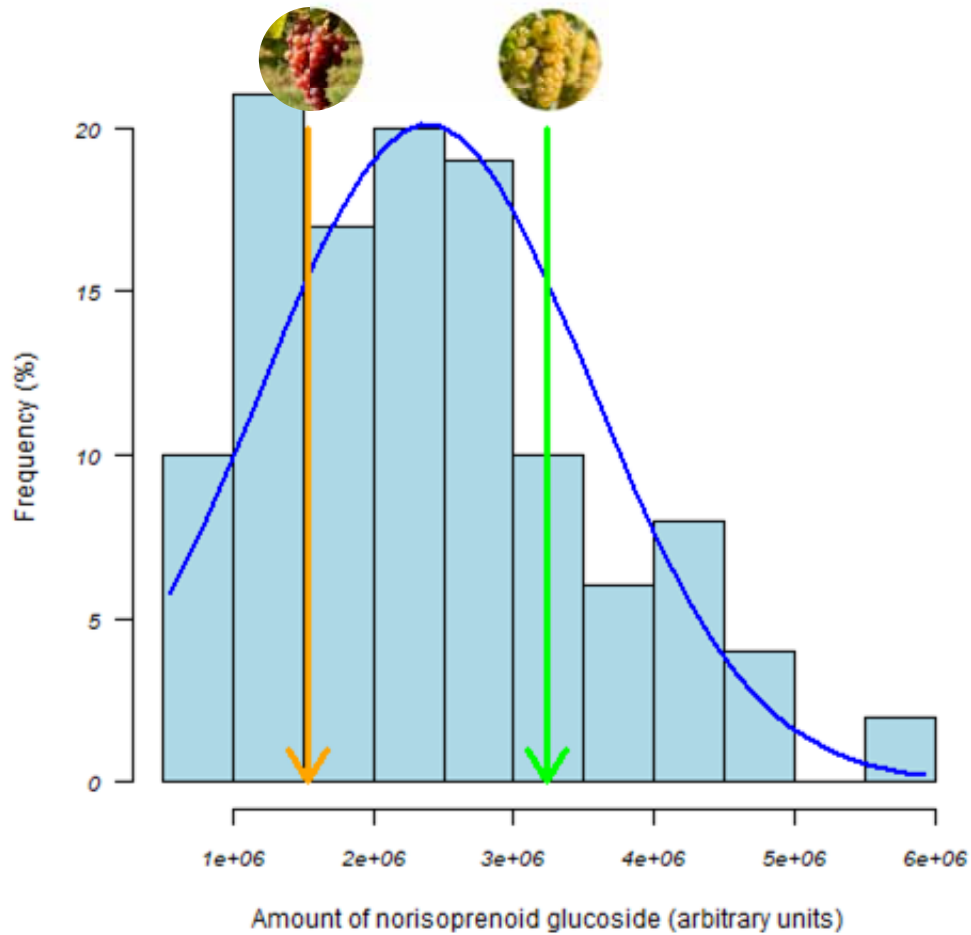
**Focus on
QTL for
aroma
compounds**

*p < 0.05
genome wide*

A QTL on chr1 for the content of a norisoprenoid glucoside



Segregation



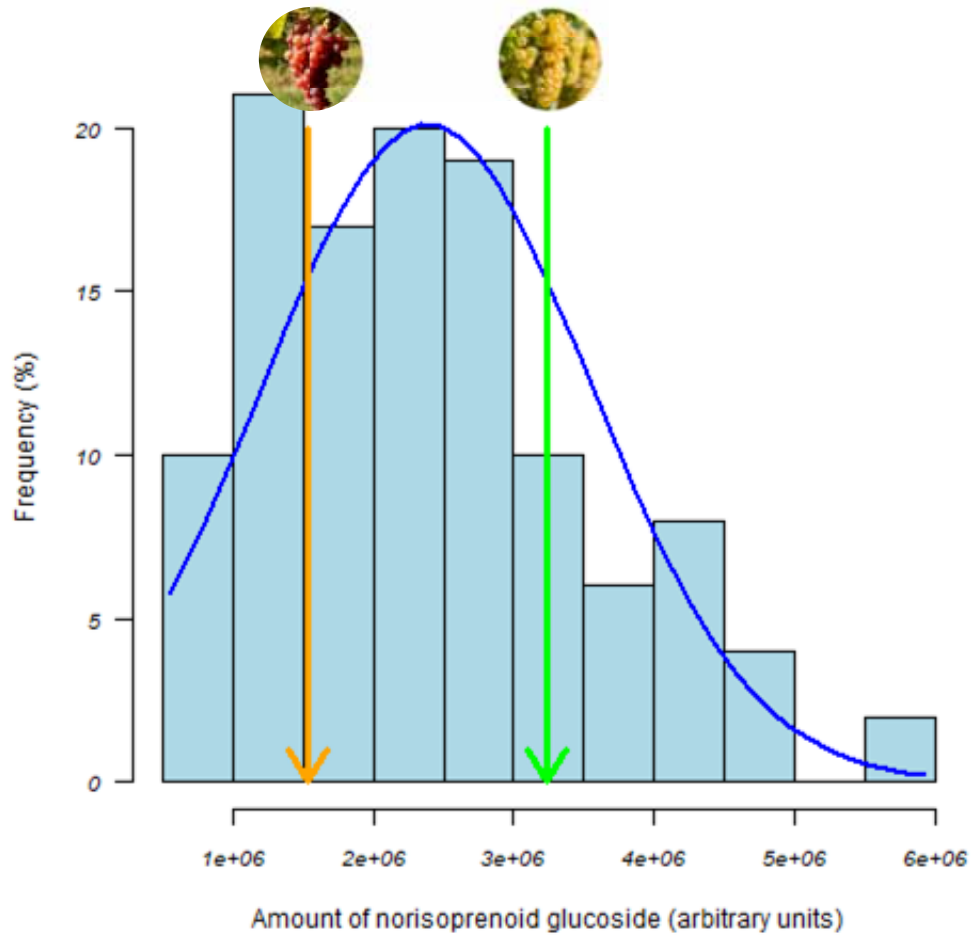
β -Ionone



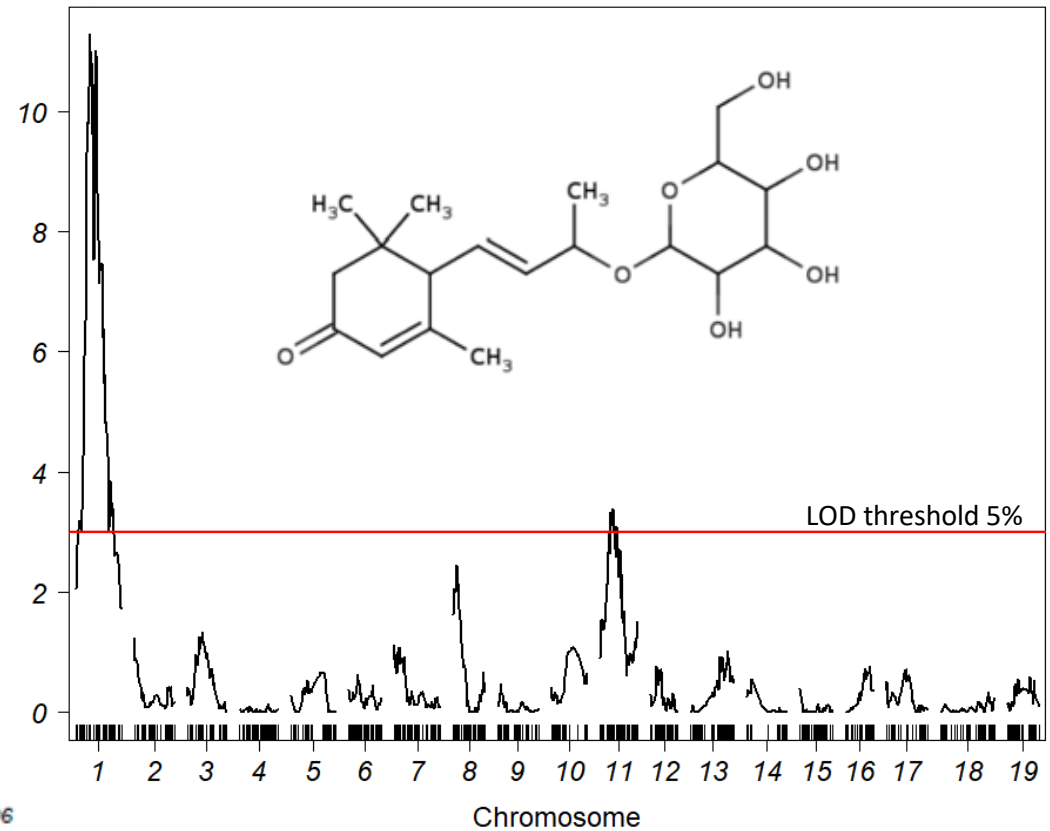
A QTL on chr1 for the content of a norisoprenoid glucoside



Segregation



QTL analysis (RI map)

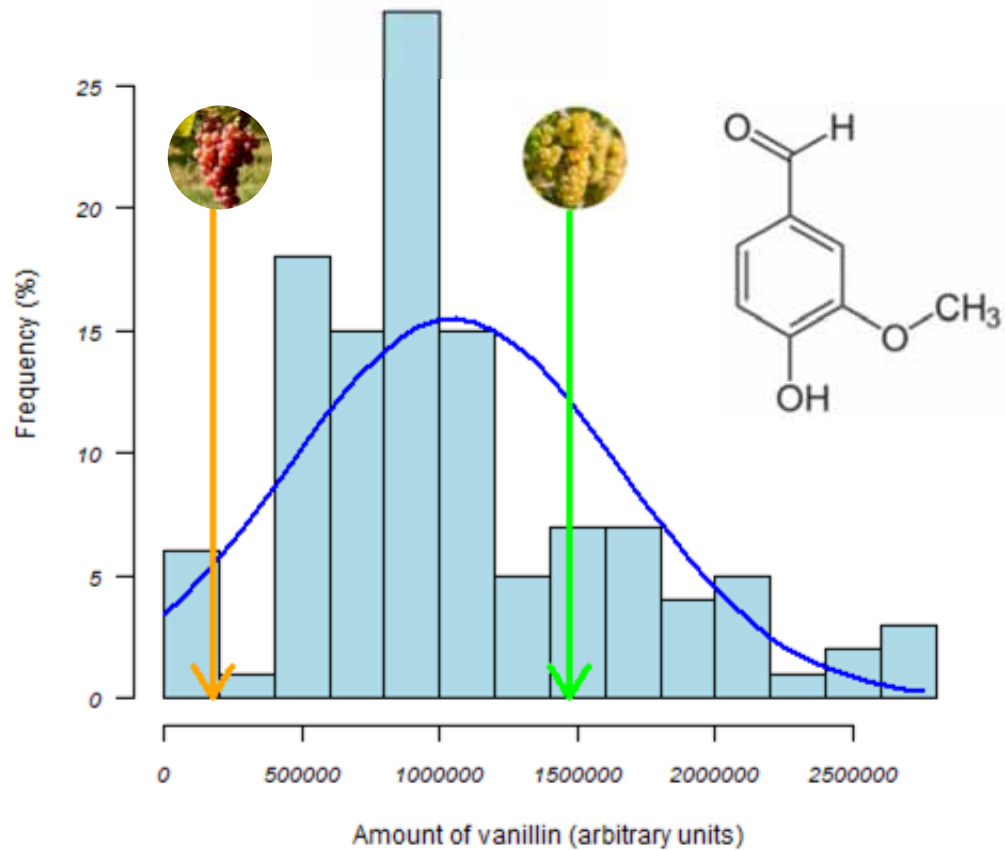


Explained variance : 37%

A QTL on chr2 for vanillin content



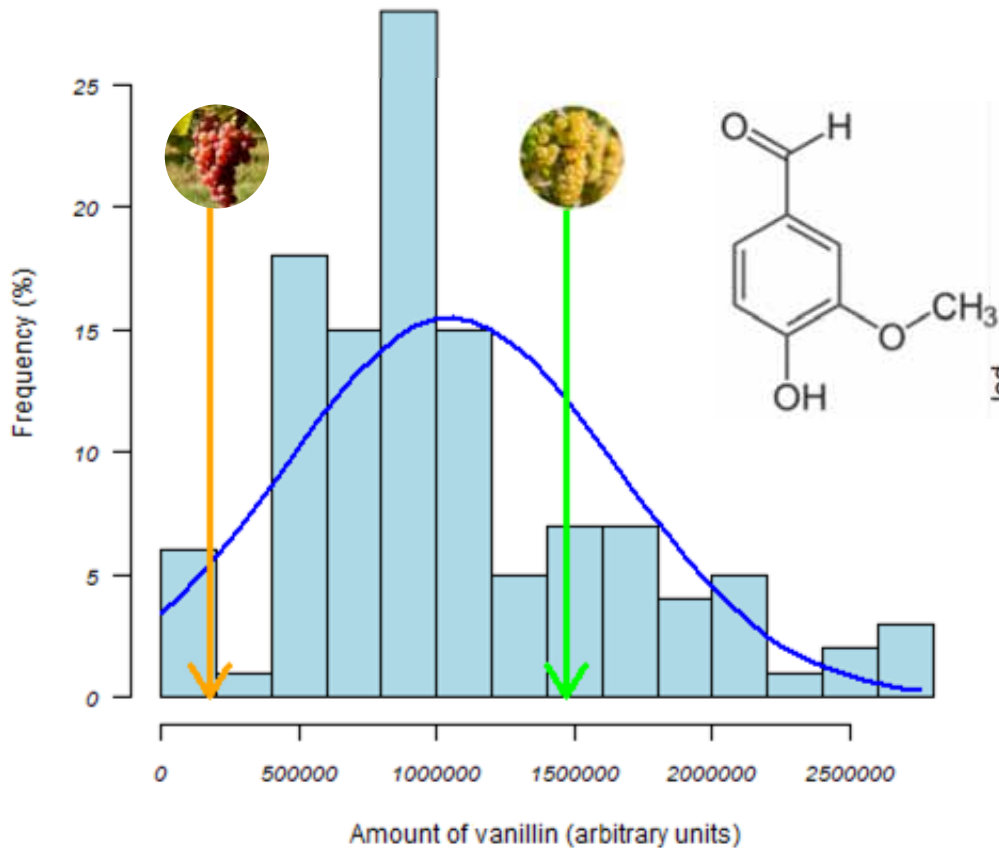
Segregation



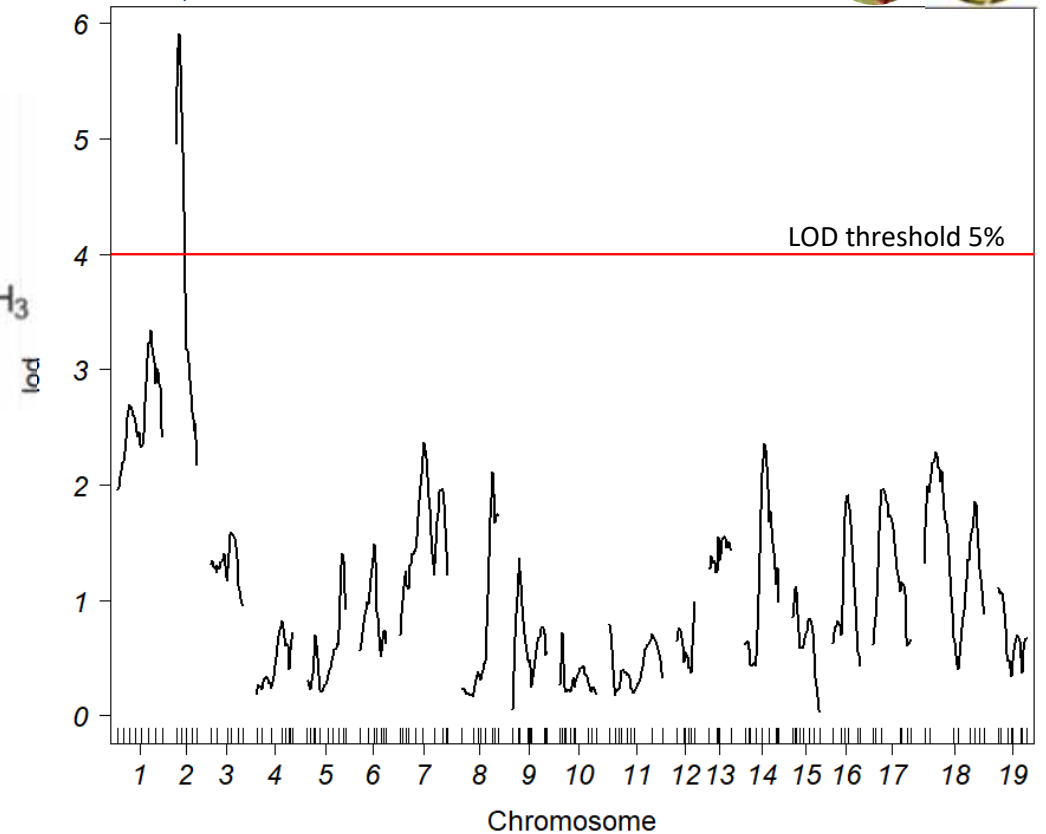
A QTL on chr2 for vanillin content



Segregation



QTL analysis (SSR map)



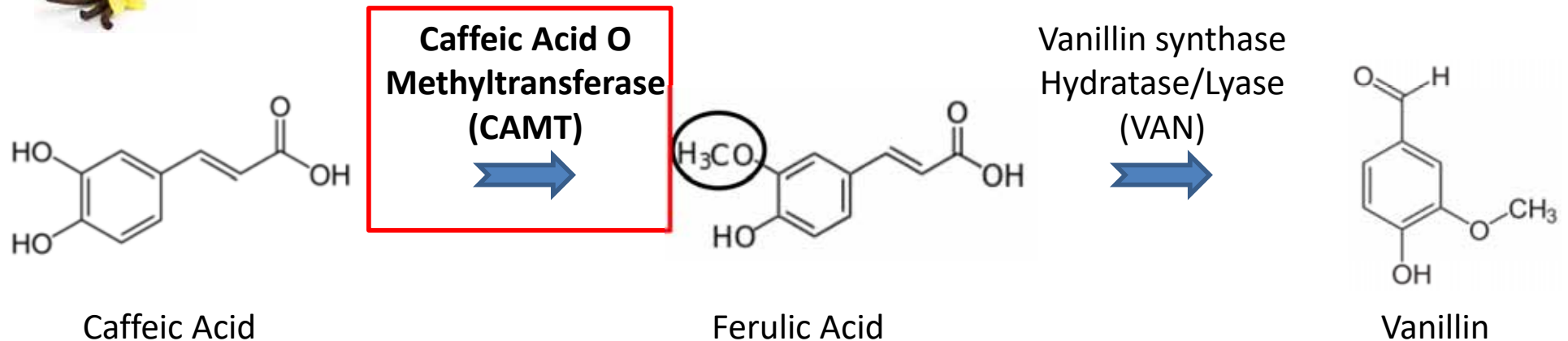
Explained variance: 17%

Identification of candidate genes

Physical location of the QTL on PN40024



Gallage *et al.*, 2014

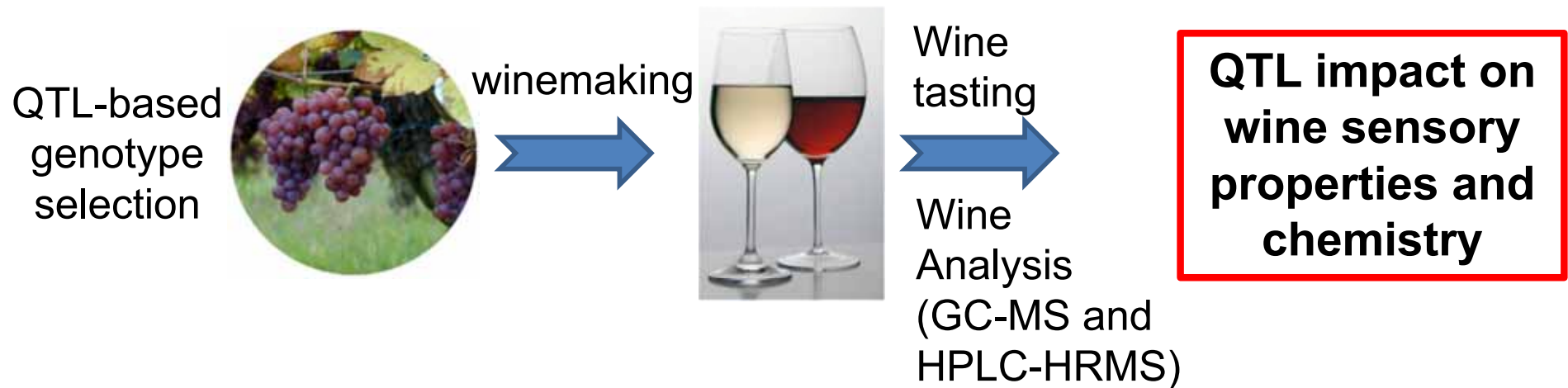


RI and GW have different CAMT protein isoforms

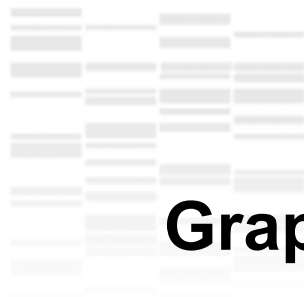
Activities under characterization

Conclusion and perspectives

- Thousands of QTL : candidate genes related to aroma under investigation
- High impact QTL for wine aroma ?
→ QTL validation through winemaking



- Use of genetic markers linked to aromatic characteristics for grapevine breeding



Acknowledgements

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