

of quality in an interspecific context in the genus *Vitis*Léonie CHRETIEN, Komlan AVIA, Raymonde BALTENWECK, Patricia CLAUDEL, Éric DUCHÊNE, Philippe HUGUENEY, Camille RUSTENHOLZ

UMR1131 Santé de la Vigne et Qualité du Vin, équipe Génomique et Métabolisme de la Vigne

INRAE Colmar, Université de Strasbourg

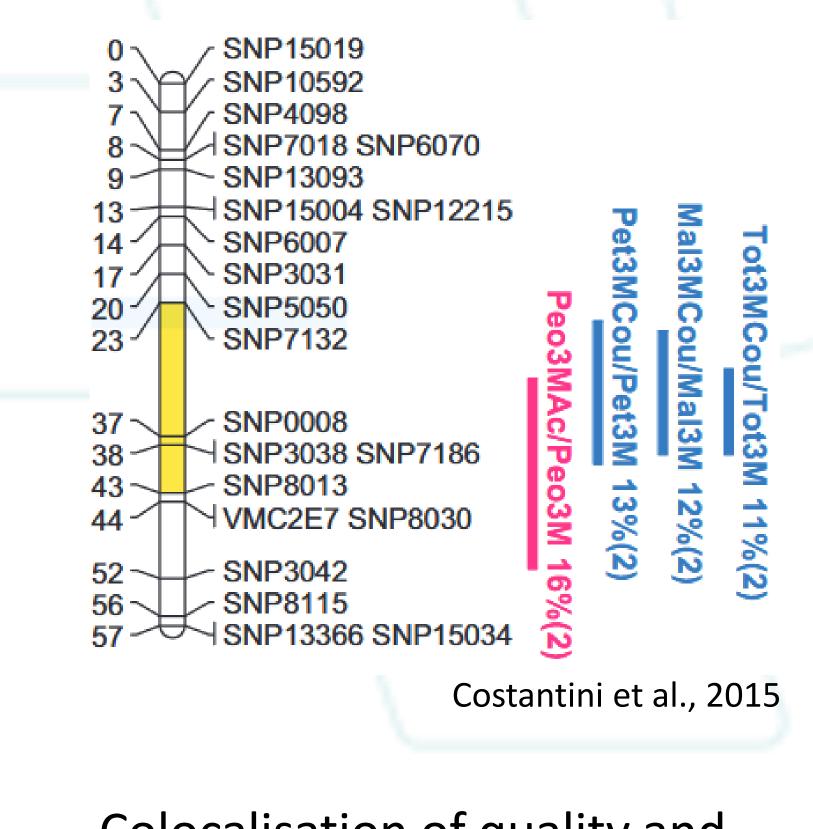
Context

In France, viticulture is the **second largest consumer of pesticides**, particularly fungicides. A breeding program initiated in 2000 at INRAE Colmar led to the registration of **11 grapevine varieties** carrying resistance genes to **downy and powdery mildew**, reducing fungicide use from ~12 to only **1–2 treatments per year**. However, selection has mainly focused on **disease resistance**, while **grape and wine quality traits** were not directly targeted. The aim of my PhD project is to study whether quality related **Quantitative Trait Loci (QTLs)** and resistance QTLs are genetically linked and to understand how meiotic recombination could be leveraged to combine all traits of interest in the frame of the breeding programs.

Axis 1: Identification of linkage between quality and resistance QTLs

Axis 2: Identification of genomic factors influencing interspecific recombination

Interspecific Grapevine Populations **Phenotypic Data Chromosome Painting Data** i there will there will there will there Genotyping 20 Mb Wine tasting GC- / LC-MS Delame et al., 2019 Sequencing Characterization of recombination **QTL** Detection **High-density Genetic** hot- and coldspots Maps SNP15019 SNP10592 Recombinaison rate SNP4098 SNP15019 SNP7018 SNP6070 SNP10592 SNP13093



Colocalisation of quality and resistance QTLs?

SNP4098 SNP7018 SNP6070 SNP13093 SNP15004 SNP12215 SNP6007 SNP3031 SNP5050 SNP7132 37 SNP0008 → SNP3038 SNP7186 SNP8013 YVMC2E7 SNP8030 52 SNP3042 ___/ SNP8115 57 SNP13366 SNP15034 Costantini et al., 2015

Recombinaison rate High Low Hybrid Hybrid parent 1 parent 2 Putative factors influencing recombination: - Chromosome structure

- Parental haplotype divergence

Perspectives

Long-read sequencing of hybrid parental genomes will enable their *de novo* diploid phased assembly, allowing the precise detection of structural variants (e.g., inversions) that are often missed with short-read data.

Costantini, L., Malacarne, G., Lorenzi, S., Troggio, M., Mattivi, F., Moser, C., Grando, M.S., 2015. New candidate genes for the fine regulation of the colour of grapes. J. Exp. Bot. 66, 4427–4440. https://doi.org/10.1093/jxb/erv159

Delame, M., Prado, E., Blanc, S., Robert-Siegwald, G., Schneider, C., Mestre, P., Rustenholz, C., Merdinoglu, D., 2019. Introgression reshapes recombination distribution in grapevine interspecific hybrids. Theor. Appl. Genet. 132, 1073–1087. https://doi.org/10.1007/s00122-018-3260-x







