Microbial diversity at different stages of wine making has been studied for many years in the quest to understand the wine ecology and the role of different microorganisms in grape must fermentation. However, none of the methods used provide comprehensive genetic information to allow for detailed analysis of the metabolic activities and interdependencies underlying the wine microbiota and the resulting impact on the organoleptic properties of wine. My research combines metagenomics, traditional microbiological analyses as well as community fingerprinting methods (e.g. T-RFLP and ARISA) to evaluate functional diversity and microbial interactions during wine making, with special focus on genes encoding antimicrobial peptides and proteins (e.g. killer toxins and cell wall lytic enzymes). Isolation and oenological characterization of non-Saccharomyces yeasts is also of special interest due to the growing interest of these yeasts as starter cultures in co-fermentation with *Saccharomyces cerevisiae*.