**Περίληψη Διατριβής στα αγγλικά**

Grapevine phyllosphere and carposphere harbors microbial communities whose assemblage mechanisms are under the direct influence of the inner and outer plant environment. The epiphytic grapevine microbiome has a notable influence on plant performance and physiology and further on the vinification process and final wine quality. Its structure and composition can vary significantly depending on different vineyard mediated factors with clear reflections both on plant health and on the winemaking process. In this thesis we aimed to disentangle the factors and conditions that determine the composition of the epiphytic (phyllospheric and carpospheric) grapevine microbiome and the wood grapevine microbiome, with the latter focusing on its role in the establishment of grapevine trunk diseases (GTDs). Further, we determined, under near full scale spontaneous and commercial vinification conditions, the influence of vineyard mediated and vinification associated factors on microbial succession and on the antioxidant, antimutagenic and anticancer profile of the produced wines facilitating the establishment of correlations between vinification microbiome and wine properties. Finally, we explored in spontaneous and inoculated vinifications microbial succession (via amplicon and the metabolic pathways and functions employed by the vinification microbiota to cope with the fermentation conditions and lead to the production of wine (via metatranscriptomic analysis).

Firstly, we assessed the wood microbiome of grapevines asymptomatic and symptomatic to GTDs in three major Greek cultivars each cultivated at geographically different zones. We noticed that biogeography/cultivar (lumped factor) was the main determinant of both fungal and bacterial communities, while the GTD status, differentiated asymptomatic from symptomatic vines only in the cultivar Xinomavro, demonstrating its higher resistance towards GTDs an d thus complex interactions of cultivar biogeography. Moreover, we observed a cultivar dependent association of *P. chlamydospora*, *Κ. variispora*, *Fomitiporia spp* and *Diaporthe* all previously proposed as GTDs causal agents with symptomatic grape vines suggesting their direct involvement in the establishment of GTDs. Random forest analysis identified *P. chlamydospora*, *Κ. variispora*, along with *Cladosporium spp*. and *A. alternata* as early and accurate predictors of GTDs, offering a valuable microbiome mediated analytical tools for early identification of GTDs in vineyards. As for the bacterial microbiome, the notable negative co-occurrence of *Bacillus* and *Streptomyces* with *Phaemoniella*, *Phaeoacremonium* and *Seimatosporium*, members of the GTD pathobiome, in asymptomatic grape vines suggested a potential suppressive role of these bacterial towards GTDs that needs to be further verified through directed isolation and further characterization of their suppressive potential in vitro and in planta.

Secondly, we analyzed, via amplicon sequencing, the epiphytic (carposphere and phyllosphere) grapevine microbiome in four emblematic Greek grapevine cultivars, at different geographical scales aiming to unravel the effects of different structural factors on the composition of the grapevine microbiome. When looking at larger geographical scales, across different viticultural zones biogeography was the main determinant of the epiphytic fungal and bacterial communities. However, at regional scales, within the same viticultural zone of Aigialeia, cultivar becomes the most important determinant factor. When the analysis was performed separately for each of the two studied cultivars in the viticultural zone of Aigialeia (cv. Roditis and Sideritis) strong effects of the terroir units were evident. In addition, the epiphytic fungal grapevine microbiota exhibited stronger responses to the studied factors and clear distance decay patterns at both studied scales, unlike the bacterial community which showed weaker responses to the confounding factors and weak distance decay patterns.

Thirdly, we extended our study and we investigated the effects of vineyard mediated factors on vinification microbiome under different vinification strategies, directly relevant to current winemaking practices. We showed that under realistic scale wise and process wise wine making practices, vineyard mediated factors, such as cultivar and vintage, remain operative along the vinification process, unlike terroir whose effect, although significant at start (in vineyard and early fermentation stages), becomes less important as fermentation progresses. The strategy of vinification employed also strongly influenced the composition of the vinification microbiota, with the effect varying between fungi and bacteria. The fungal community showed a universal pattern of NS yeasts and filamentous fungi dominating at the early stages of fermentation being displaced, though by indigenous or inoculated Saccharomyces strains as the fermentation progresses. On the other hand, bacterial community succession varied, with the most common pattern mirrored in an initially rich in AAB bacterial community replaced by *Oenococcus* at the end of fermentation. Vintage and vinification type were also the stronger determinants of the antioxidant, anticancer and antimutagenic profile of the produced wines. Further analysis identified significant and universal across cultivars, positive correlations between members of the vinification microbiota like the NS yeasts *Torulaspora debrueckii* and *Lachancea quebecensis* with the anticancer and the antioxidant properties of wines. These findings could be exploited towards a microbiota modulated vinification process that will lead to high quality wines with desirable properties and enhanced regional identity.

Finally, we evaluated, in spontaneous and commercial vinifications (both being amended with preservatives) with grapes of the Greek cultivar Vidiano, the composition and succession of the fungal and bacterial microbiome and explored, via metatranscriptomic analysis, the metabolic pathways and functions employed by the vinification microbiome along the fermentation. The stage of vinification was identified as the most important structural factor of the vinification microbiome while the type of vinification process employed also contributed but to a lower extent, being most probably a result of the universal use of preservatives in both vinifications. The fungal community showed a wide phylogenetic diversity of NS yeasts and *Saccharomyces* at early fermentation stages which was replaced by the complete dominance of inoculated or indigenous *Saccharomyces* strains as the fermentation progressed. The bacterial community was composed of LAB and AAB, with *Oenococcus* showing a progressive increase along the fermentation process. Metatranscriptomic analysis reinforced the strong influence of vinification stage on the metabolic activity of the microbiome. When data from the different fermentation stages were analyzed separately, we noted strong signatures of the different vinification strategies employed (spontaneous and inoculated) at the first and middle stages of fermentation. Overall, we noted upregulation of genes mostly originated from *S. cerevisiae* and other yeasts that were associated with stress response mechanisms, transportation, glycolysis and ethanol production in line with the biochemical environment of fermentations.

The results of this thesis have serious practical implications for grapevine plant health (Chapter 2 and 3) and the wine making sector (Chapter 3, 4 and 5), while it offered benchmarking knowledge and diagnostic tools that could be further optimized and used in the vineyard management and the wine making process.