

8.9 **Culturome versus DNA metabarcoding: Diversity of grapevine endophytic mycobiome in old and young vines of different health status in New Zealand.**

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The grapevine harbours a diverse community of fungi in the woody trunk tissue, termed the “endophytic mycota”. These communities can have a profound effect on the vine’s physiology, health, growth, and ability to adapt to stress. Some of these include pathogenic fungi as the causal agents of grapevine trunk disease (GTD), with many considered latent pathogens. For GTD, understanding the factors affecting latency is still limited. This study aimed to compare the fungal endophyte community in young and old Sauvignon blanc vines, both symptomatic and asymptomatic for GTD, using culture-dependent and culture-independent approaches. Nine vineyards were sampled, with 60 mature vines (>10 years old) and 30 young vines (<9 years old) sampled. Each age group consisted of equal numbers of apparently healthy and symptomatic vines. Trunk cores were taken from each vine using a sterilised 4-mm drill bit after removing the bark with a knife. Fungal communities were characterized by isolation and metabarcoding of the ITS1 region. For the culturome, a collection of 2116 endophytic fungi were recovered, representing 42 fungal genera. Trunk microbiota was dominated by species of the genera *Alternaria*, *Aureobasidium*, *Diplodia*, *Epicoccum*, *Phaeoconiella*, *Eutypa*, *Botrytis*, *Cladosporium*, and *Diaporthe*. Differences in the taxa recovered into culture were observed between vines of different ages, and symptomology. In the metabarcoding approach, 1892 OTUs were obtained. The same fungal genera were identified as the most abundant using metabarcoding. Alpha diversity analysis revealed that greater diversity was detected in old compared to young vines and in asymptomatic compared to symptomatic trunks. Beta diversity analysis demonstrated significant differentiation in the fungal communities structure for both age and health status. This study has produced new baseline information on Sauvignon blanc endophytic mycota and further work will determine the impact of these microbial communities on the latency of GTDs.