

Characterisation of microbial endophytes from wild grapevine (*Vitis vinifera* subsp. *sylvestris*)

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While a large number of studies aim at analyzing the microorganisms found in crops, using either a classical microbiology approach or more novel, DNA-based techniques, little is known on the selective forces affecting these microbial communities during the process of domestication or if and how they shaped plant-associated microbes. We are interested in elucidating how domestication has influenced bacteria and fungi colonizing the grapevine endosphere, and how these modifications interfere with plant physiology, growth and health.

We isolated microbial endophytes from *V. vinifera* subsp. *sylvestris* plants obtained from different areas of Italy and analysed the isolates for important traits related to interaction with the plant host, social behaviour, tolerance to antibiotics and their production, biocontrol.

In addition, a DNA-dependent approach was adopted to fingerprint microbial communities in wild grapevine plants and to compare them to non-domesticated plants. Automated Ribosomal Intergenic Spacer Analysis (ARISA) was used to assess variability and identity of the non-culturable microbial fauna. Both geographical origin and plant genotype were considered.

The ability of some of these isolates to colonize domesticated grapevines was investigated to assess their viability for reintroduction in cultivated grapevines.

Diversity of endophytic bacterial communities in *Pinus flexilis* foliage

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The relationship between forest trees and the endophytic bacteria is likely to be one of the world's most wide-spread symbioses, yet, we presently have limited knowledge of bacterial diversity and function within forest trees. Using 454 pyrosequencing with primers targeting bacterial 16S rRNA genes, we explored the diversity of foliar endophytic bacteria associated with mature *Pinus flexilis* in Niwot Ridge, CO. The endophytic community from 6 individuals of *P. flexilis* sampled at two sites were all dominated by *Alphaproteobacteria* (50-70%), with little variation in bacterial richness and OTU abundance among and within individuals. The dominant genera were an unclassified Acetobacteraceae, *Gluconacetobacter* sp., and *Acetobacter* sp., together making up 45-60% of total bacteria in the sample. These genera have been identified as nitrogen fixers in other plants. The presence of endophytic nitrogen fixers was confirmed with PCR amplification of the nitrogenase reductase gene, *nifH* in each sample. This suggests that *P. flexilis* endophytic communities are dominated by a core community of nitrogen-fixing endophytes. Thus, although commonly attributed to soil bacteria, nitrogen-fixation in forests could also be carried out by endophytes.