Identification and characterization of trunk pathogens of seedlings in forest nurseries **THROUGH HIGH-THROUGHPUT** Amplicon **SEQUENCING**

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BACKGROUND

- Forest nurseries are having a key role in the detection of plant pests and diseases for the building of healthy forest stands (Wingfield et al., 2015).
- Trunk disease (TD) pathogens are aggressive species that colonize the xylem and phloem of their host and cause plant decay (Mora-Sala et al., 2018).
- High-throughput amplicon sequencing (HTAS) is the method used routinely for the detection of microbial communities of different environmental samples (Tremblay et al., 2018).

OBJECTIVES

1.Detect the fungal community (mycobiome) presented in vascular tissue in tree seedlings by the use of HTAS

2.Describe the relationship between the incidence of fungal genera presented in vascular tissue of European beech (*Fagus sylvatica L*.; *FS*), English oak (*Quercus robur L*.; *QR*), and Sessile oak (*Quercus petrea L*.; *QP*) and

3.Evaulate the influence of soil type on fungal diversity in plant and nursery location.





CONCLUSIONS

This study revealed the different distribution patterns and assembly mechanisms of interaction of fungal diversity between the seedlings of three species (*FS, QP, QR*), nursery locality, soil type, and plant sample site. For evaluation of detected genera as phytopathologically problematic is necessary to continue in research of particular fungal isolates associated with TD. To fulfill Koch's postulates, the specific isolates should be inoculated into the wood of non-infected plants.

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