

Rapid and reliable molecular detection of *Diplodia sapinea* on pine tree

Stehliková D.¹, Luchi N.², Pepori A. L.², Pecori F.², Migliorini D.², Santini A.²

¹ - University of South Bohemia, Faculty of agriculture and technology (USB FAT), Na Sádkách 1780, 37005, České Budějovice, Czech Republic

² - Institute for Sustainable Plant Protection, National Research Council (IPSP-CNR), Via Madonna del Piano, 10, I-50019 Sesto Fiorentino (Firenze), Italy

Background

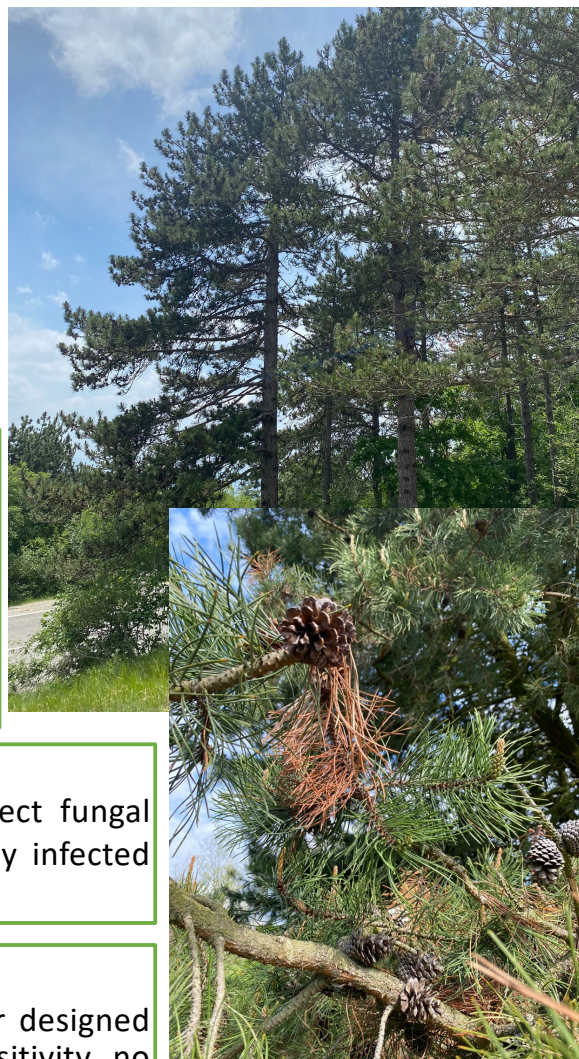
One of the major worldwide spread plant pathogen causes shoot tip dieback on pine trees is fungus *Diplodia sapinea*. In last years disease is more dominant in northern Europe too (Brodde et al. 2019). *D. sapinea* attacks can cause serious economic damage and sensitive monitoring methods are needed.

Objectives

The mainly aim was optimized qLAMP and qPCR to detect fungal pathogens in DNA from pure mycelium and from naturally infected woody plant tissues.

Methods

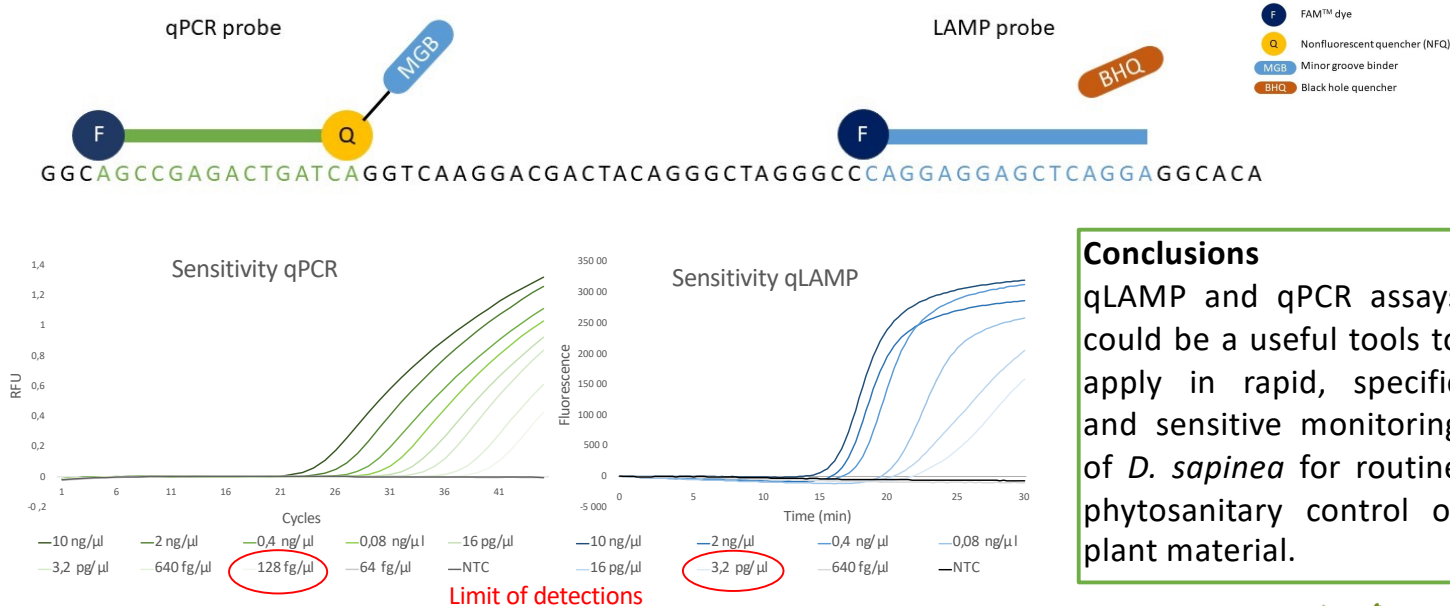
The mating type (*MAT1*) gene (Lopes et al. 2018) used for designed specific probes and primers with high specificity and sensitivity, no cross reactivity to other species of *Botryosphaeriaceae*.



Symptomatic plants of *Pinus sylvestris* affected by *D. sapinea* (Monte Morello – Tuscany, IT)

Results

MAT1 gene



Conclusions

qLAMP and qPCR assays could be a useful tools to apply in rapid, specific and sensitive monitoring of *D. sapinea* for routine phytosanitary control of plant material.

References:

Brodde, L., Adamson, K., Julio Camarero, J., Castaño, C., Drenkhan, R., Lehtijärvi, A., ... & Oliva, J. (2019). Diplodia tip blight on its way to the north: drivers of disease emergence in northern Europe. *Frontiers in Plant Science*, 1818.

Lopes, A., Linaldeddu, B. T., Phillips, A. J., & Alves, A. (2018). Mating type gene analyses in the genus *Diplodia*: From cryptic sex to cryptic species. *Fungal Biology*, 122(7), 629-638.

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