

Figueira, D^{1,2*}, Garcia, E^{1,2}, Marrão, R³, Santos, A, E³, Espírito-Santo, C^{1,4}, Bento, A³, Costa, J^{1,2}

1 Centre for Functional Ecology, Associate Laboratory TERRA, Department of Life Sciences, University of Coimbra, Portugal
2 Fitolab - Instituto Pedro Nunes, Laboratory for Phytopathology, Coimbra, Portugal
3 CNCFS - Centro Nacional de Competências dos Frutos Secos, Bragança, Portugal
4 CATAA - Centro de Apoio Agro-Alimentar de Castelo Branco, Portugal.

Introduction

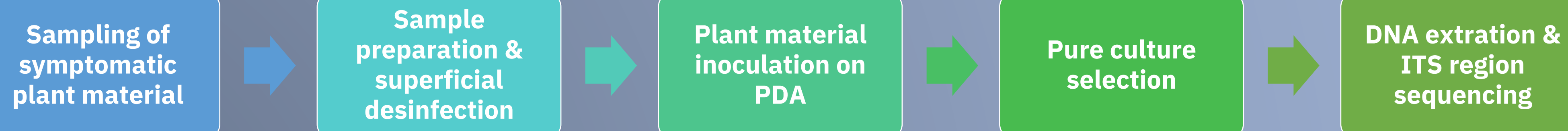
The impact of plant diseases has increased dramatically due to intensification, globalisation and climate change, accounting for more than 15% of total losses despite investments in protection and control. *Prunus* production is no exception and is severely affected by the occurrence of diseases whose intensity and severity are increasing, without all the aetiological agents having been identified. In this context, the XylOut project aims to characterise diseases in almond orchards using culture-dependent methods and to study their epidemiology using long-chain sequencing from Oxford Nanopore Technologies (ONT). The work presented concerns a survey of the diversity of potentially phytopathogenic fungi in almond trees using cultivation-dependent methods.



Figure 1. Location of almond orchards selected for the study and associated symptoms.

Methodology

Almond orchards were selected along a gradient of intensity of good practices and disease incidence to collect plant material for isolation of potentially pathogenic fungi and characterisation of the mycobiota. Molecular identification was based on ITS region amplification and NCBI Blast tools.



Results preliminary

Several organisms associated with the occurrence of diseases in almond trees were isolated, belonging to the genera *Alternaria*, *Epicoccum*, *Fusarium*, *Botryotinia*, *Diaporthe*, *Monilinia* and *Nigrospora*. Moniliosis, caused by *Monilinia laxa*, was found in almost all orchards sampled (Fig. 2). Stem cankers associated fungi were also isolated, namely *Diaporthe amygdali* and *Dothiorella iberica*. Of particular note, is the presence of *Dothiorella iberica* (Fig. 2), a fungus of the *Botryosphaeriaceae* family, which is responsible for stem cankers that cause severe damage to almond trees and whose impact is unknown in Portugal. Saprophytic fungi and some yeasts were also identified, namely *Pithomyces chartarum*, *Sordaria fimicola*, *Nigrospora pyriformis* and *Aureobasidium pullulans*.

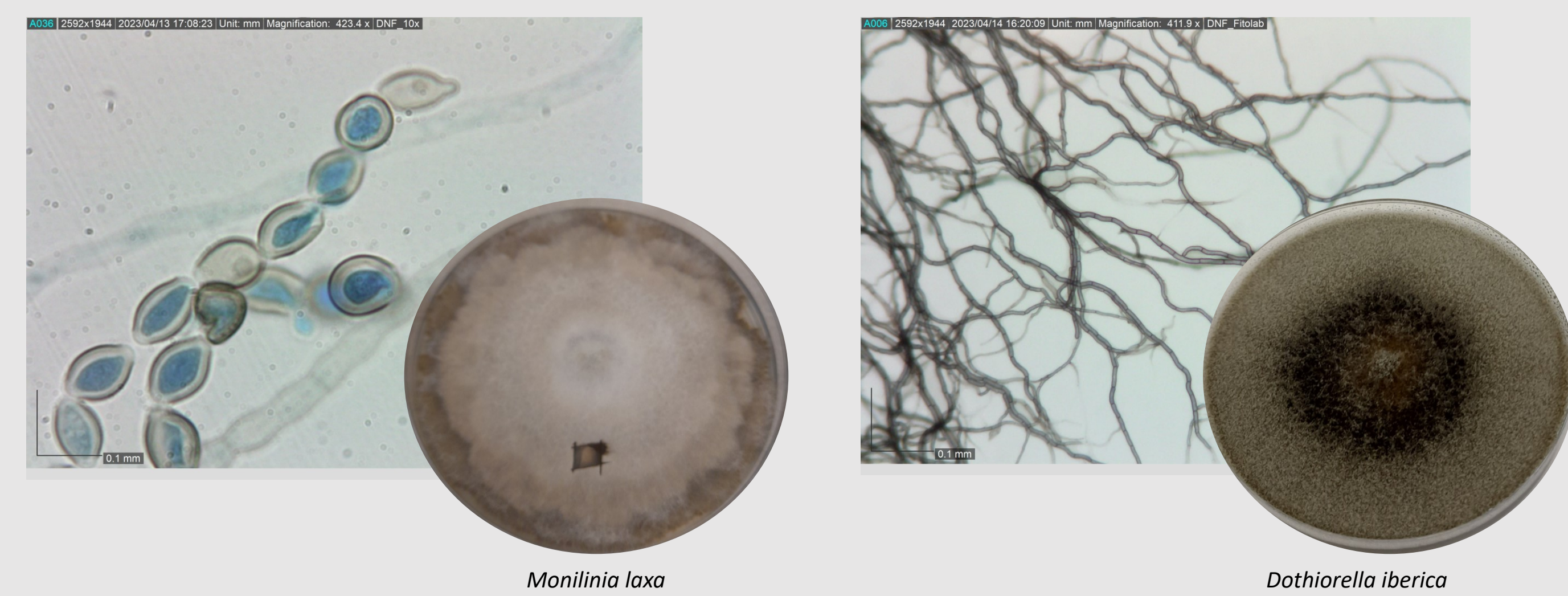
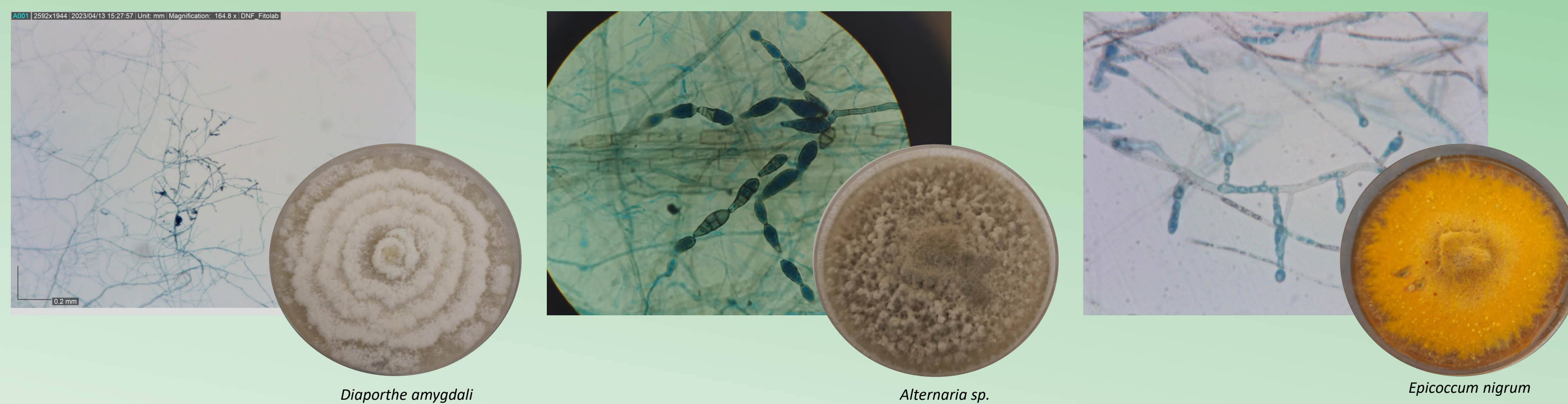


Figure 2. Morphology and mycelial structure of fungal cultures isolated from almond trees.



Conclusions

The characterisation of the mycobiota present in the almond trees of the northern region of Portugal is still ongoing. The next samplings will take into account the diversity found in order to reinforce its monitoring. In addition, the application of long-chain sequencing from ONT will provide new insights into the epidemiology of almond tree diseases.