Epidemiology and Ecogenomics of Regulated Prunus Diseases in Cova da Beira

Eva Garcia[1,2], Daniela Figueira[1,2], João Trovão[1,2], Anabela Barateiro3, Cristina Ramos[3], Preciosa Fragoso[3], Sandra Lopes[3] , Alexandra Camelo[1,4], Inês Brandão[1,4], António Veríssimo[2], Christophe Espírito-Santo[1,4], Joana Costa[1,2]

[1] University of Coimbra, Centre for Functional Ecology, Associate Laboratory TERRA, Department of Life Sciences, Coimbra, Portugal
[2] Instituto Pedro Nunes - Laboratório de Fitossanidade (Fitolab), Portugal,
[3] APPIZEZERE – Associação de Proteção Integrada e Agricultura Sustentável do Zêzere
[4] CATAA - Centro de Apoio Agro-Alimentar de Castelo Branco, Portugal.

Theme VI

Introduction

Diagnostic challenges are increasing as globalisation and climate change favour the introduction of new plant pests. *Xylella fastidiosa, Xanthomonas arboricola, Pseudomonas syringae* and *Monilinia fructicola* are important pests affecting *Prunus* production with significant losses. Two different *Prunus* production systems were analysed: old orchards of *P. dulcis* and coexisting orchards of *P. avium* and *P. persica*, where significant areas of *P. dulcis* have recently been established. The high density of genetically heterogeneous Prunus sp. in which pests can coexist favours the development of highly adapted strains and/or the occurrence of coevolutionary phenomena associated with the spread and emergence of new diseases. This coexistence of phylogenetically close strains with drastically different phenotypes is a critical diagnostic challenge.

Objective

In this context, the aim was to conduct molecular epidemiology studies by characterizing the microbiota *of P. avium* and *P. persica* leaves and flowers using the Oxford Nanopore Technologies (ONT) long-read sequencing platform to identify bacteria and fungi. This strategy aims to detect the introduction and impact of pathogens on the structure and functions of the microbiota, and to identify taxonomic groups relevant to modulating the microbiota as part of potential bio-based solutions for disease control.

Methods

1. Sampling in Cova da Beira orchards of *P. avium* and *P. persica*
2. Processing of flowers and leaves (collected in spring and autumn)
3. DNA extraction by the CTAB method
4. 16S rDNA and ITS18S-ITS1-5.8S-ITS2-28S amplification
5. Long chain sequencing ONT
6. Identification with NCBI curated platform

Results *preliminarY*

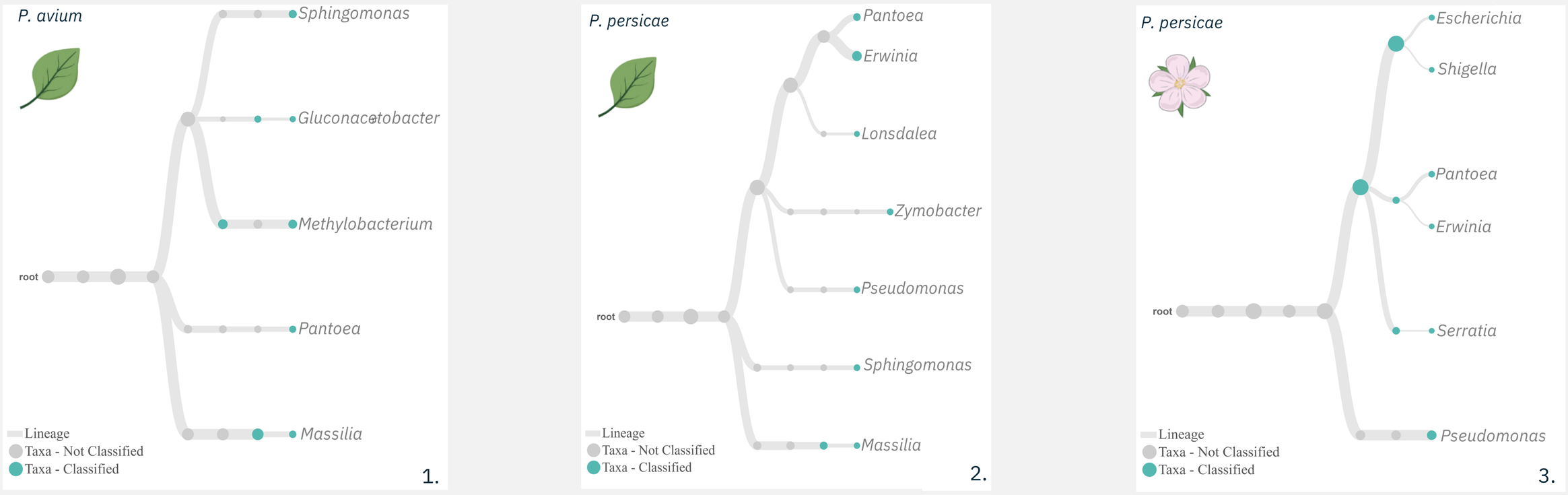

Figure 1: Identification by 16S rDNA sequencing of *P. avium* (1) and *P. persica* (2) leaf samples and *P. persica* flowers (3) using the EPI2ME platform..

Discussion *preliminary*

Preliminary results showed that, in contrast to the leaf microbiome among *Prunus* species, significant differences were found between the flower and leaf microbiomes. Important pathogen-related groups were detected with significant impact on the microbiome structure, supporting the use of this approach for large screening phytosanitary surveys.Foi possível identificar um microbioma comum a folhas e flores das espécies de *Prunus* sp. analisadas – *Massilia* sp., *Pantoea* sp. e *Sphingomonas* sp.

Organized by:
CATAA CENTRO DE APOIO TECNOLÓGICO AGRO ALIMENTAR
CENTRE FOR FUNCTIONAL ECOLOGY
TERRA Laboratory for sustainable land use and ecosystem services
IPN INSTITUTO PEDRO NUNES
UNIVERSIDADE D COIMBRA
CNCFS Centro Nacional de Competências dos Frutos Secos
fct Fundação para a Ciência e a Tecnologia
XylOut