

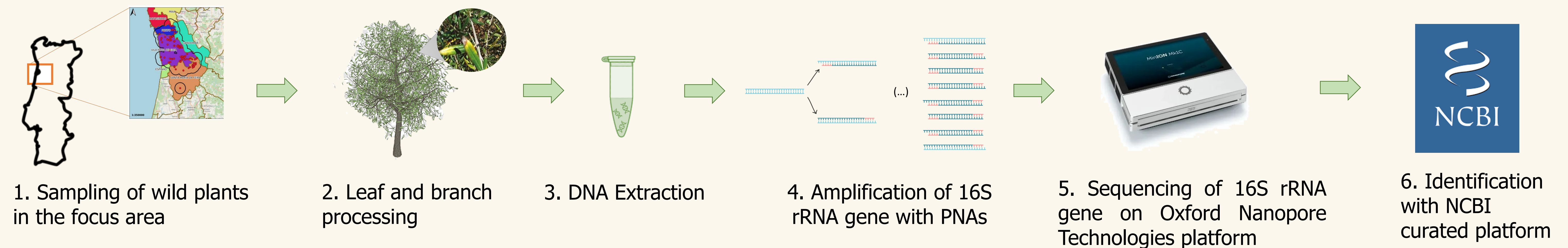
Introduction

Xylella fastidiosa (Xf) is a phytopathogenic bacterium responsible for a wide range of diseases with high economic, environmental and social impacts. The plant-associated microbiome plays a central role in maintaining fitness, but little is known about the diversity and structure of these endophytic microbial communities. It is therefore essential to study this diversity and the interactions between endophytes and plants in order to understand the biotechnological potential of these microorganisms.

Objective

In this context, we aim to characterise the structural diversity of endophytic microorganisms in wild plant species susceptible to Xf infection and present in the demarcated area of Portugal.

Methods



Results preliminary

Table 1. Most common species in each of the wild host species.

Sample	Host	Most Abundant Species				
42B	<i>Adenocarpus sp.</i>	<i>Caballeronia sordidicola</i>	<i>Caballeronia terrestris</i>	<i>Massilia putida</i>	<i>Burkholderia catarinensis</i>	<i>Massilia pinisoli</i>
43L	<i>Lavandula dentata</i>	<i>Ralstonia pickettii</i>	<i>Bacillus mycoides</i>	<i>Delftia lacustris</i>	<i>Staphylococcus epidermis</i>	<i>Staphylococcus saccharolyticus</i>
45L	<i>Dimorphoteca</i>	<i>Xylella fastidiosa</i>	<i>Ralstonia pickettii</i>	<i>Xanthomonas campestris</i>	<i>Duganella zoogloeoides</i>	<i>Delftia lacustris</i>
45B	<i>Dimorphoteca</i>	<i>Xylella fastidiosa</i>	<i>Ralstonia pickettii</i>	<i>Staniera cyanosphaera</i>	<i>Aliterella antarctica</i>	<i>Loriellopsis cavernicola</i>
46B	<i>Gazania sp.</i>	<i>Xylella fastidiosa</i>	<i>Staniera cyanosphaera</i>	<i>Aliterella antarctica</i>	<i>Loriellopsis cavernicola</i>	<i>Caballeronia sordidicola</i>
85L	<i>Cytisus scoparius</i>	<i>Xylella fastidiosa</i>	<i>Liberibacter crescens</i>	<i>Diplorickettsia massiliensis</i>	<i>Xanthomonas campestris</i>	<i>Pseudomonas boreopolis</i>
193L	<i>Dimorphoteca</i>	<i>Aliterella antarctica</i>	<i>Xylella fastidiosa</i>	<i>Staniera cyanosphaera</i>	<i>Caballeronia sordidicola</i>	<i>Ralstonia pickettii</i>
193B	<i>Dimorphoteca</i>	<i>Aliterella antarctica</i>	<i>Staniera cyanosphaera</i>	<i>Xylella fastidiosa</i>	<i>Loriellopsis cavernicola</i>	<i>Caballeronia sordidicola</i>
197L	<i>Gazania sp.</i>	<i>Aliterella antarctica</i>	<i>Staniera cyanosphaera</i>	<i>Ralstonia pickettii</i>	<i>Loriellopsis cavernicola</i>	<i>Xylella fastidiosa</i>
198L	<i>Dimorphoteca</i>	<i>Staniera cyanosphaera</i>	<i>Aliterella antarctica</i>	<i>Xylella fastidiosa</i>	<i>Caballeronia sordidicola</i>	<i>Loriellopsis cavernicola</i>
198B	<i>Dimorphoteca</i>	<i>Xylella fastidiosa</i>	<i>Caballeronia sordidicola</i>	<i>Aliterella antarctica</i>	<i>Staniera cyanosphaera</i>	<i>Stenotrophomonas rhizophila</i>
199B	<i>Adenocarpus sp.</i>	<i>Caballeronia sordidicola</i>	<i>Caballeronia terrestris</i>	<i>Caballeronia udeis</i>	<i>Terriglobus aquaticus</i>	<i>Staphylococcus saccharolyticus</i>

Legend: R - Branches; L - Leaves

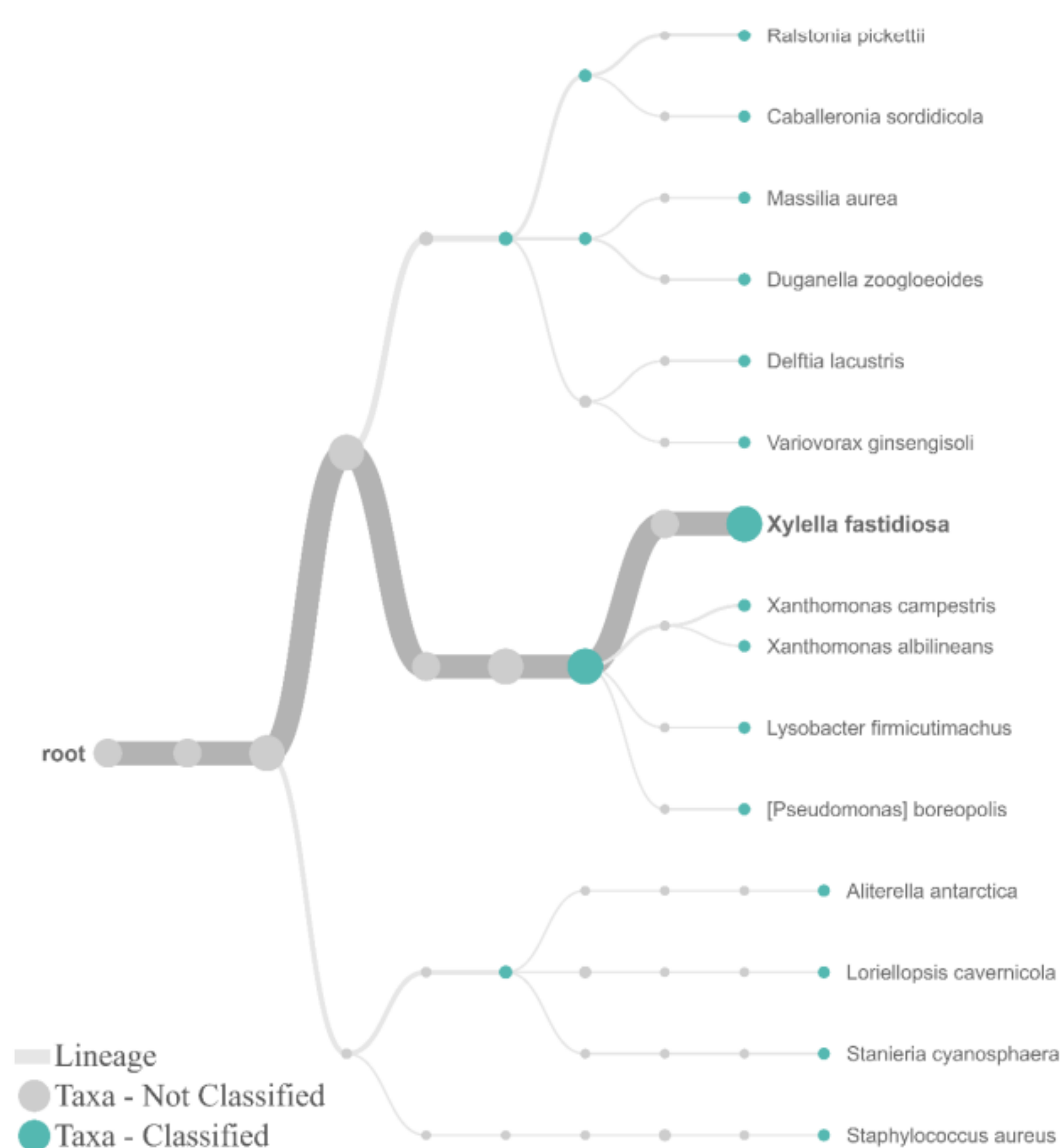


Figure 1. Identification by metabarcoding of the 16S rRNA gene of sample 45L using the EPI2ME platform.

Discussion preliminary

The results suggest a functional importance of some core groups of the microbiome, related to the ability to degrade toxic substances, fix nitrogen and promote plant growth. They may also help to explain the lack of visible symptoms and signs of decline in these wild plants, suggesting that certain taxonomic endophyte groups may help to model infection. Notably, this is the first study in wild plants and the identification of relevant clusters contributes to the understanding of the impact of Xf on microbiome dysbiosis in nature.