

# The microbiome of xylem sap associated with almond leaf scorch disease caused by *Xylella fastidiosa* in South-East Spain

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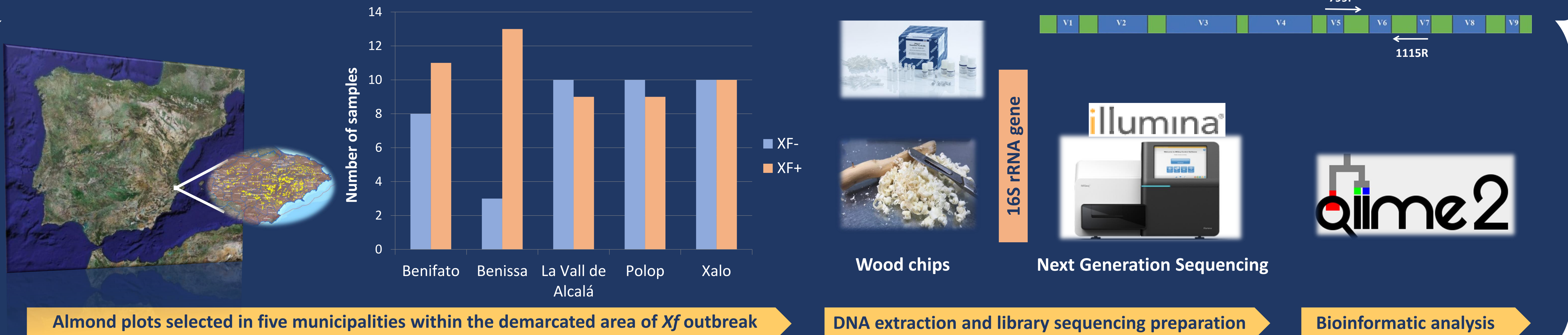
## State of Art

*Xylella fastidiosa* (*Xf*) is one of the most harmful emerging plant pathogenic bacteria and represents an important threat to agriculture, forestry and landscape worldwide. In June of 2017, *Xf* was reported in almond trees in the province of Alicante, Spain. Metagenomics is a valuable methodology to study the impact of causal agents of plant diseases and their interaction with others naturally occurring microorganism, as part of innovative approaches to mitigate or control the disease. Moreover, endophytic bacteria seem to be a promising biocontrol solution.

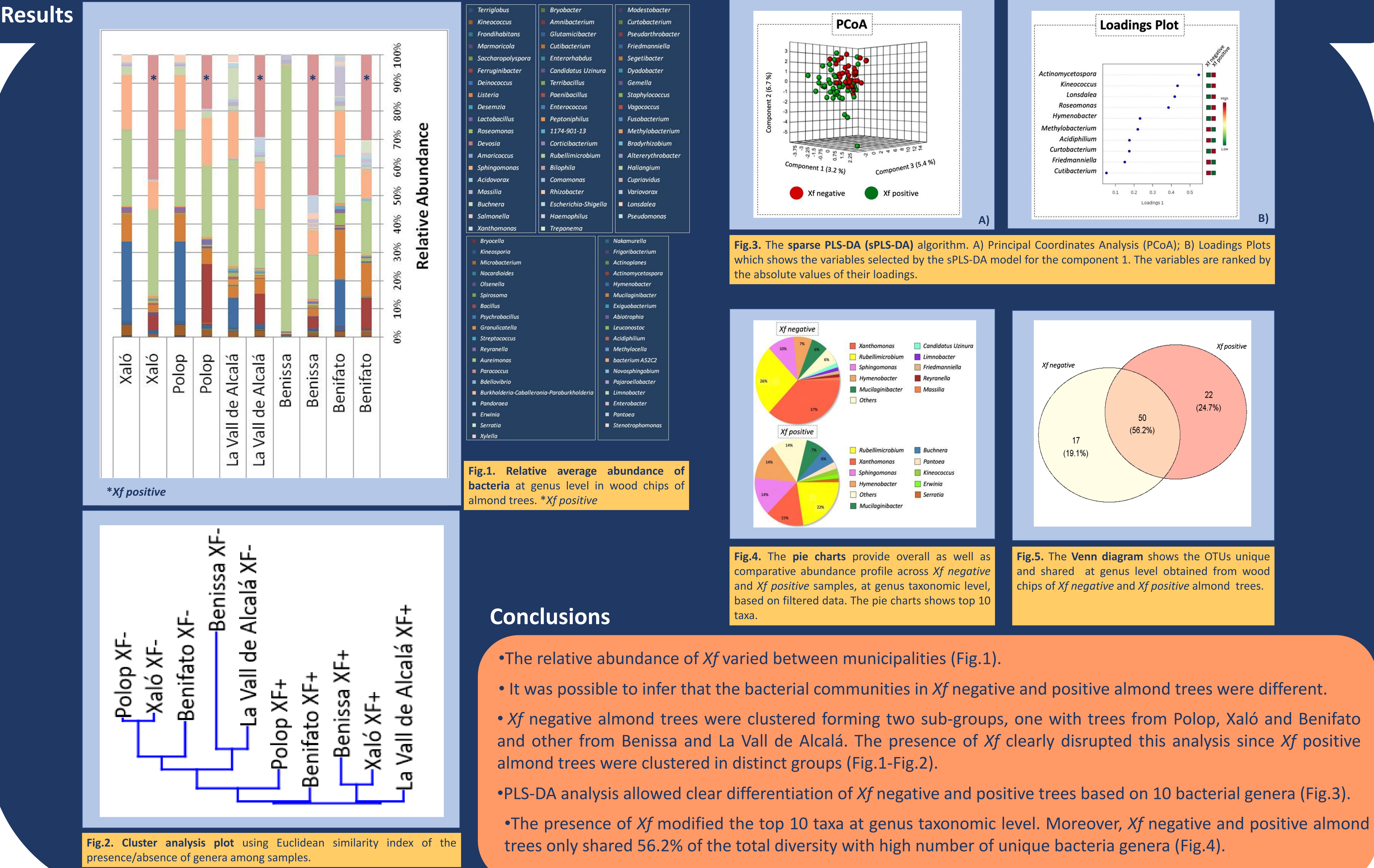
## Objective

Compare the xylem sap microbiota of *Xf* positive and *Xf* negative almonds trees to identify groups of microorganisms that could potentially modulate the almond leaf scorch disease.

## Material & Methods



## Results



## Conclusions

- The relative abundance of *Xf* varied between municipalities (Fig.1).
- It was possible to infer that the bacterial communities in *Xf* negative and positive almond trees were different.
- *Xf* negative almond trees were clustered forming two sub-groups, one with trees from Polop, Xaló and Benifato and other from Benissa and La Vall de Alcalá. The presence of *Xf* clearly disrupted this analysis since *Xf* positive almond trees were clustered in distinct groups (Fig.1-Fig.2).
- PLS-DA analysis allowed clear differentiation of *Xf* negative and positive trees based on 10 bacterial genera (Fig.3).
- The presence of *Xf* modified the top 10 taxa at genus taxonomic level. Moreover, *Xf* negative and positive almond trees only shared 56.2% of the total diversity with high number of unique bacteria genera (Fig.4).

## Acknowledgments

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