Beyond *Xylella*, Integrated Management Strategies for Mitigating *Xylella fastidiosa* impact in Europe

Practice abstract 6 - Extended version

Genomic and molecular insights into olive resistance to *Xylella fastidiosa*: Comparative analysis of Apulian cultivars *Ogliarola Salentina* and *Leccino*

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Genomic and molecular insights into olive resistance to *Xylella fastidiosa:* Comparative analysis of Apulian cultivars *Ogliarola salentina* and *Leccino*

Olive Quick Decline Syndrome (OQDS), caused by the xylem-dwelling bacterium ***Xylella fastidiosa,*** poses a severe threat to Mediterranean olive production, with highly susceptible local cultivars such as ***Ogliarola salentina*** experiencing dramatic decline and mortality. By contrast, the cultivar ***Leccino*** shows partial resistance; however, the underlying genetic and immune determinants of this resistance are poorly understood, limiting breeding and management strategies for durable control of OQDS.

How will BeXyl make a difference?

The **BeXyl project** aims to identify the genetic bases of resistance to Xylella fastidiosa by combining high-resolution genomic analyses with functional molecular studies in olive cultivars with contrasting susceptibility.
Specific goals are:

- Generate high-quality genome assemblies for ***Ogliarola salentina*** and ***Leccino***
- Develop stem tissue and suspension cell cultures for olive
- Identify differences in immune receptor genes and defence responses associated with resistance.

Olive tree (***Olea europaea***) in Puglia, Italy. The picture of this 80 years-old tree was taken in Sept 2019. It shows symptoms of the olive quick decline syndrome in the right branch, which is the cultivar Ogliarola salentina and highly susceptible to ***Xylella fastidiosa***. The left branch was grafted about 50 years ago onto the susceptible rootstock (white binding). This scion originates from the ***Leccino*** cultivar, showing decent levels of resistance to the infection.

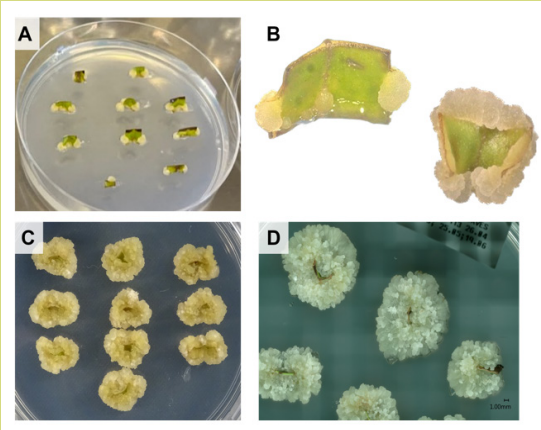


Taken from : Silke Robatzek et al. (2024). New Phytol, 242: 30-32. https://doi.org/10.1111/nph.19549

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Methods: The project uses advanced DNA sequencing methods and bioinformatic tools to build detailed genetic maps at chromosome-scale of ***Ogliarola salentina*** and ***Leccino***. These maps help scientists predict which defence-related genes (immune receptors) are present in each cultivar and identify those that may be involved in plant resistance against ***Xylella fastidiosa***.
To study how these genes function, scientist use well-known laboratory model plants and have also developed special olive tissue and cell cultures. These laboratory systems allow researchers to introduce selected genes into plants and to study defence responses in a controlled way, helping to understand how resistance to the bacterium is activated.

Induction and development of stem cell cultures from olive leaf explants.Leaves from the cultivars ***Leccino*** and ***Ogliarola Salentina*** were used as explants to induce stem cell formation. (A) After two weeks of culture, stem cell tissue began to develop along the leaf margins. (B) Close-up images showing emerging stem cell structures from the leaf explants. (C) Stem cell cultures after six weeks of growth. (D) Stem cell cultures after eight weeks of cultivation. These cultures serve as a platform for immune response profiling and downstream molecular analyses. Interestingly, the two olive cultivars differ in their requirements to induce and maintain stem cell cultures. For details see Robatzek, S., do Valle Capelli, N. & Tisserant, C. Das Rätsel um *Xylella fastidiosa* und die Immunität des Olivenbaums. Biospektrum 31, 357–359 (2025). https://doi.org/10.1007/s12268-025-2507-8



Outcomes: By comparing the genetic information of the two olive cultivars, researchers identified clear differences in immune receptor gene families and presence/absence patterns that help explain why one olive cultivar is more resistant to the disease than the other.
In addition, the tissue and cell culture systems developed in the project provide practical laboratory tools to test these defence mechanisms and to better understand how olive plants respond to infection

Impact:This integrated genomic and molecular approach advances the understanding of genetic resistance to *Xylella fastidiosa* in olive and establishes foundational resources for breeding and biotechnological improvement. The insights gained will support the development of resistant olive cultivars and promote sustainable ways to manage the disease, directly contributing to the resilience of Mediterranean olive

More Information

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