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

Practice abstract 6

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.

Comparative genomic analyses using advanced DNA sequencing and bioinformatic tools, generated chromosome-scale genome maps for both cultivars. These analyses revealed clear differences in immune receptor gene families between the two cultivars, helping to identify defence-related genes and immune receptors that may contribute to resistance.

Functional analyses are carried out using model plants and olive tissue and cell culture systems developed within **BeXyl.** These platforms provide valuable laboratory tools to test defence mechanisms and to better understand how olive plants respond to Xylella fastidiosa infection.

Impact: This work improves understanding of genetic resistance to *Xylella fastidiosa* in olive and provides key resources to support breeding of resistant olive cultivars and promote sustainable ways to manage the disease, directly contributing to the resilience of Mediterranean olive agroecosystems.

More Information

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