

## APULIAN OLIVE GERMPLASM AS POTENTIAL SOURCES OF RESISTANCE TO XYLELLA FASTIDIOSA

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The olive tree (*Olea europaea* subsp. *europaea* var. *europaea*) represents the cornerstone crop of Apulian economic system based on the production of oil and table olives. During the last years, the high genetic variability of Apulia's olive germplasm is being exposed to a risk of genetic erosion due to social, economic, and climatic changes. In addition, since 2013, the spread of the gram-negative bacterium *Xylella fastidiosa* subsp. *pauca*, which is responsible for the olive tree rapid decline syndrome (OQDS), has menaced Apulia's olive biodiversity, damaging the regional economy and landscape heritage.

To reduce the impact of *Xylella fastidiosa*, breeding programs have been started to identify agronomically interesting traits and new sources of tolerance or resistance.

So far, two cultivars "Leccino" and "FS17" (also known as "Favolosa") showed resistance to *X. fastidiosa* in contrast to the susceptible cultivars "Cellina di Nardò" and "Ogliarola salentina". In addition, recent studies have shown a moderate tolerance in "Frantoio," "Toscanina," "Termite di Bitetto," "Maiatica," "Dolce di Cassano," "Oliastro," "Nociara," and "Nocellara Etnea."

This study aims to investigate the variability of interactions with *X. fastidiosa* of a large panel of Apulian olive genotypes.

Sixty olive samples (50 cultivars and 10 unknown genotypes) were grown up in an experimental field, following a randomized block with 5 replicates, located in the west part of the infected area in province of Lecce, and they were inoculated with *X. fastidiosa*. Monitoring of colony-forming units (CFU) by RealTime-PCR assay allowed to identify a different behavior of the genotypes to the infection, based on the Cq values. A preliminary subset of most promising tolerant genotypes (PT) including both cultivars and unknown, was identified and characterized by molecular analysis with a set of 10 SSR markers. The allelic profiles were compared with the molecular profiles deposited in the Di.S.S.P.A database consisting of about 600 olive genotypes widespread in the Mediterranean basin. Lynch and Ritland Method (LRM), Neighbor-joining and STRUCTURE analysis allowed to highlight cases of synonymy and homonymy, evaluate the genetic relationships between unknown olive genotypes and cultivars, and investigate the genetic structure of this Apulian olive germplasm.