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An in-depth evaluation of an olive genotype tolerant to *Xylella fastidiosa* which shares genetic traits with Tunisian cultivars

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INTRODUCTION & AIM

Since its first detection in 2013 in the Salento peninsula (southeastern Italy), *Xylella fastidiosa* subsp. *pauca* (*Xfp*) has emerged as a major phytopathological threat, causing the Olive Quick Decline Syndrome (OQDS). The epidemic has had a profound socio-economic and cultural impact: over 5 million olive trees are now unproductive, dead, or severely infected.

In Salento, where 85% of olive trees belong to the highly susceptible cultivars “Cellina di Nardò” and “Ogliarola Salentina”: the visual landscape has been transformed by widespread tree decline.

Among the most promising control strategies, replanting with resistant or tolerant cultivars, such as “Leccino” and “FS17” (“Favolosa”), is considered the most feasible. However, resistance is a complex trait, encompassing both the plant’s ability to restrict bacterial proliferation (resistance) and to mitigate symptom severity despite infection (tolerance).

A recent line of investigation has focused on a putatively resistant genotype named SX32, genetically related to Tunisian cultivars like “Chemlali Sfax” and “Sayali”. The aim of this study is the definition of the performance features of this presumably resistant plant, studied under conditions of high *Xfp* inoculum pressure to assess its agronomic and microbiological performance.

METHOD

The progression of symptoms and bacterial load in SX32 was evaluated and compared with those observed in the cultivars “Cellina di Nardò” and “Leccino”, across all four seasons. The extent of disease was measured using the pathometric scale proposed by Luvisi et al. (2017). Quantification of the bacterium through real-time PCR followed the procedure established by Harper et al. (2010), while bacterial concentration, expressed as CFU/ml, was calculated according to the method reported by D’Attoma et al. (2019).

Figure 1. Olive plant SX32

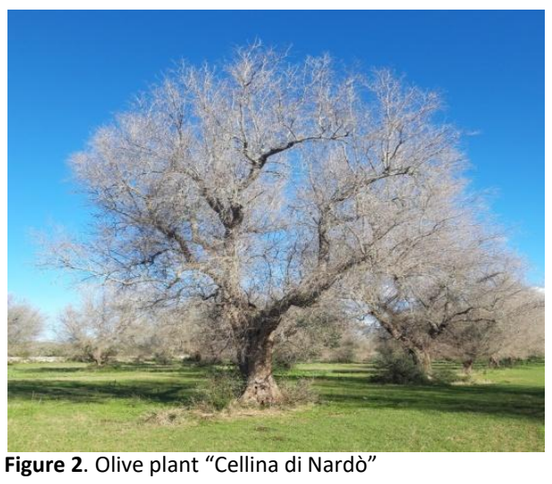

Figure 2. Olive plant “Cellina di Nardò”

RESULTS & DISCUSSION

The results reveal that SX32 exhibits minimal canopy symptoms and maintains a stable symptom profile across all four seasons. In contrast, “Cellina di Nardò” shows a progressive increase in symptom severity, peaking in autumn. Regarding bacterial load, SX32 displays concentrations ranging from 10^3 and 10^6 CFU/ml, with the highest values detected in winter and the lowest in summer. While “Cellina di Nardò” follows a similar seasonal trend, interestingly, “Leccino” presents the lowest bacterial count in winter and the highest in autumn, with values fluctuating between undetectable levels and 10^7 CFU/ml.

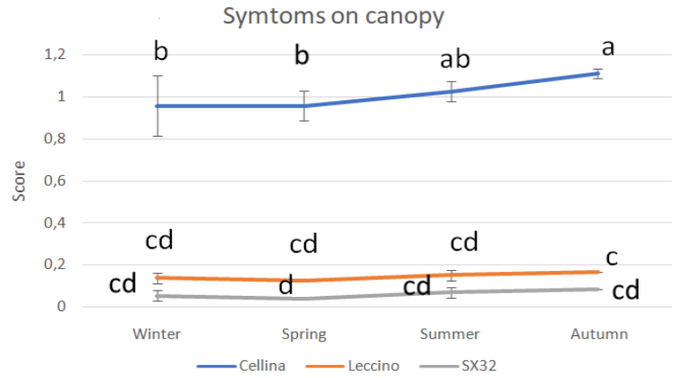

Figure 3. Symptoms on canopy of Cellina di Nardò, Leccino and SX32 in the four seasons

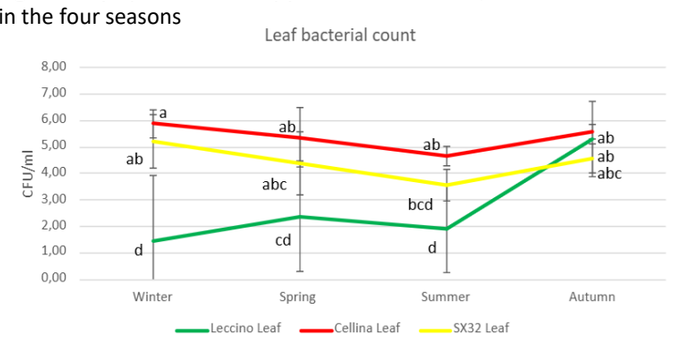

Figure 4. Leaf bacterial count of Cellina di Nardò, Leccino and SX32 in the four seasons

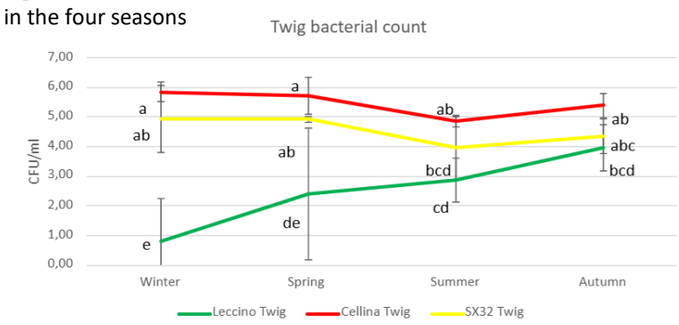

Figure 5. Twig bacterial count Cellina di Nardò, Leccino and SX32 in the four seasons

CONCLUSION

SX32 exhibits a remarkable level of tolerance to *Xf*, with minimal symptom expression, and is set to be further investigated as a potential source of additional resistance traits to *Xf*. Although the higher bacterial load observed in SX32 compared to “Leccino” was unexpected, it raises interest, as it may point to the involvement of xylem-associated endophytes that could play a role, directly or indirectly, in mitigating the pathogenic bacterium, thus allowing the plant to stay healthy despite the infection. Similar interactions have previously been documented in olive trees, involving microorganisms such as *Burkholderia*, *Quambalaria*, *Phaffia*, and *Rhodotorula*.

FUTURE WORK / REFERENCES

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