

Phenometabolomics of olive plants infected with *Xylella fastidiosa* using Nuclear Magnetic Resonance, high Resolution Mass Spectrometry, Hyperspectral Reflectance, and Integrative Chemometrics Analysis

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INTRODUCTION

Comparison of metabolic profiles and hyperspectral reflectances of Xf-infected olive plants can be exploited to identify infection markers and related wavelengths and set up early disease detection strategies through Remote Sensing.

MATERIALS & METHODS

Experimental design

- **Plants:** 100 young olive trees (3-4 years)
- **Variety:** Cellina di Nardò
- **Inoculum:** *X. fastidiosa* (ST53 strain)
 - Phaeoacremonium group:
 - *P. rubrigenum* (N20 strain)
 - *P. aleophilum* (B1a strain)
 - Pseudophaeoaniella group:
 - *P. oleae* (FvB4 strain)
 - *P. oleicola* (M24 strain)
 - *P. oleicola* (M51 strain)
- **Sample:** Number of mature leaves statistically significant (10-15)
- **Measurements:** spectral signatures, NMR and HRMS spectra, molecular analysis on the same leaves
- **Period:** December 2017 (2 years after inoculation)
- **Controlled climatic conditions:** 24 °C ± 2 °C; Relative Humidity over 80 %

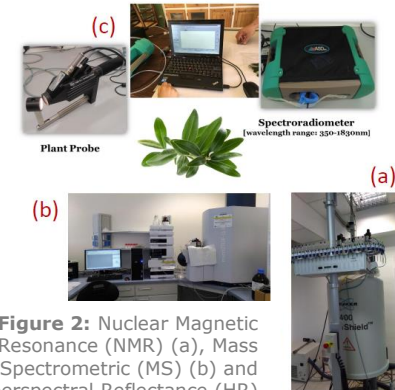
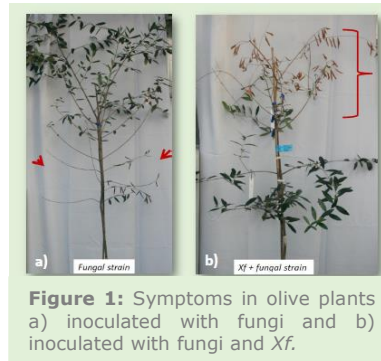


Figure 2: Nuclear Magnetic Resonance (NMR) (a), Mass Spectrometric (MS) (b) and Hyperspectral Reflectance (HR) (c) techniques used in this study

Trees undergo phenotypic and metabolic changes during the infection period, as demonstrated by a recent non-targeted metabolomic study under thermo-conditioned greenhouse of Xf-infected olive plants co-inoculated with xylem fungi (Jililat *et al.*, 2021). All acquired spectra were analyzed using statistical chemometric techniques.

RESULTS

Statistical characterization of primary (NMR) and secondary (MS) metabolites associated with Xf infection, in combination or not with fungal isolates, indicated that Xf-infected samples differed from those infected only with fungi and from the control (Jililat et al., 2021).

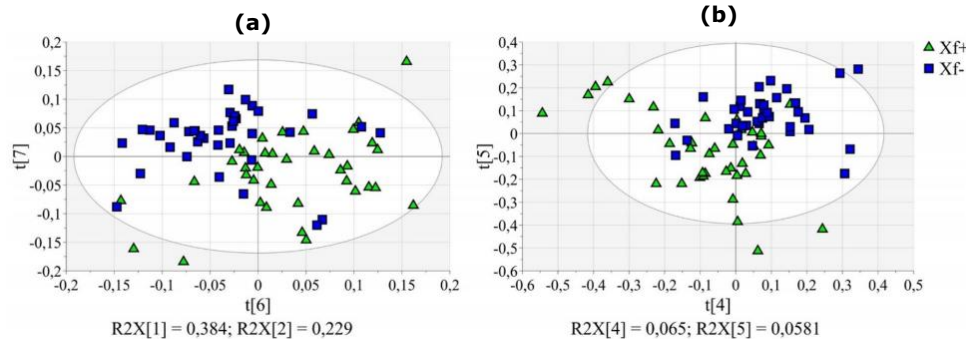


Figure 3: Principal Component Analysis (PCA) applied to NMR and MS data obtained from olive leaf analysis: (a) PCA applied to NMR data; (b) PCA applied to MS data.

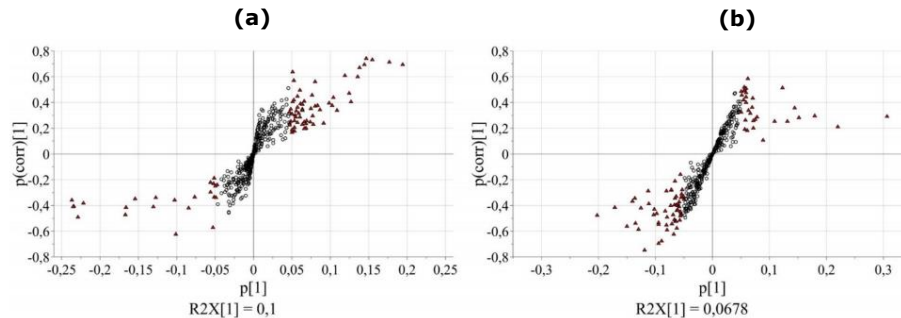


Figure 4: Identification of metabolites with the highest potential as biomarkers (red triangles) by applying Partial Least Square-Discriminant Analysis (OPLS-DA) to NMR (a) and MS (b) data.

RESULTS

- Higher amounts of **malic acid**, **formic acid**, **mannitol**, and **sucrose** were found in Xf-infected plants than in non-infected plants.
- In contrast, infected plants revealed lower amounts of **oleuropein** and **glucose**.

Signal	Metabolite	δ (ppm)	MMW	Correlated MS bucket [M-H] ⁺
1	Oleuropein	1.57, 2.49, 2.65, 5.76, 6.03, 7.51	540.184	539.182
2	Oleuropein aglycone	2.85 – 2.89, 8.91, 9.33	378.132	377.118
3	Malic acid	2.54, 2.75, 4.45	134.022	133.013
4	Mannitol	3.66 – 3.90	182.079	181.073
5	Glucose	3.25, 3.38 – 3.56, 3.65 – 3.90, 4.65 (anomeric-H β -glucose), 5.24 (anomeric-H α -glucose)	180.063	179.057
6	Sucrose	5.40, 4.21, 4.06	342.116	341.111
7	Aromatic compounds	6.80 – 7.00	-	-

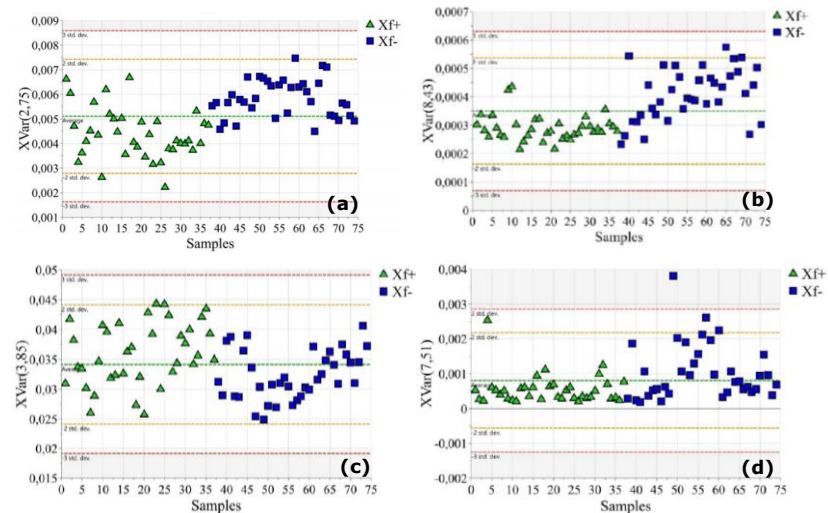


Figure 4. Assignment of relevant metabolites in the 1H NMR spectrum of *X. fastidiosa* infected leaves and statistic of the buckets attributable to malic acid (a), to formic acid(b), to mannitol(c) and to oleuropein (d). Xf+: samples of Xf-inoculated plants; Xf-: samples of uninoculated plants.

RESULTS

- Covariance matrices between NMR, MS, and HR methods were used to link HR spectral features with NMR and MS diagnostic signals.
- Several wavelength ranges *positively* and *negatively* related with the assigned metabolites were associated:

Visible: [480-520 nm]; [625-645 nm]

e [670-705 nm]

Infrared: [950-1000 nm]; [1165-1190 nm]

e [1420-1485 nm].

NMR/MS-HR covariance correlations for olive infected plants

