

Identification of sequence type ST78 *Xylella fastidiosa* olive tree in Argentina

Tolocka, PA¹, Guzmán, FA², Paccioretti, MD¹, Roca, ME³, Otero, ML¹ y Haelterman, RM¹

1 INTA-CIAP-IPAVE-UFyMA.

2 AER-INTA, Villa Dolores. Córdoba.

3 SENASA-UNLaR. tolocka.patricia@inta.gob.ar

The most widely used technique for the molecular characterization of *Xylella fastidiosa*, the cause of olive quick decline syndrome in our country, is the *Multilocus sequence typing* (MLST) classification system technique, which defines the subspecies and the type of sequence (ST). This typing system involves seven constitutive genes named housekeeping (*leuA*, *petC*, *malF*, *cysG*, *holC*, *nuoL* and *gltT*). Until now, all olive trees samples analyzed in Argentina, were infected with the subspecies *pauca* ST69. The objective of this work was to perform a new type of characterization from a symptomatic plant from Cruz del Eje, Córdoba. Total DNA extraction was carried out according to the modified Murray and Thompson (1980) protocol, starting from symptomatic material. Next, all seven genes involved were amplified by PCR, and the products were purified, sequenced and analyzed using the Chromas Lite 2.0.1 and BioEdit version 7.2 programs. The sequences were compared with those available in the MLST *Xylella fastidiosa* database, confirming a new type sequence for olive trees, the ST78-Type. This ST also corresponds to the subspecies *pauca* and has been previously identified in almond plants of our country. This result confirms the presence of a single subspecies until now in our country, and the transmission of the same TS to different hosts.

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