

experiments demonstrated that *OrfF* is required for expression of at least *TR11* and possibly other late-pathway genes (i.e. *TR13*, *TR17*, *TR13* and *TR18*) required for synthesis of TRI.

20. THE H2020 PONTE PROJECT WEB SITE: AN ONLINE RESOURCE FOR SCIENTIFIC DISSEMINATION ON EMERGING PEST DISEASES. M. Morelli¹, M. Saponari¹, D. Tavano¹, D. Boscia¹, A. Obradović². ¹CNR Istituto per la Protezione Sostenibile delle Piante (IPSP), SS Bari, 70126 Bari, Italy. ²University of Belgrade, Faculty of Agriculture, 11080 Belgrade, Serbia. E-mail: massimiliano.morelli@ipsp.cnr.it.

The International Research Consortium POnTE (Pest Organism Threatening Europe) is being funded by the European Commission under the Horizon 2020 programme to investigate four pathogens (i.e. *Xylella fastidiosa*, *Candidatus Liberibacter solanacearum*, *Hymenoscyphus fraxineus* and *Phytophthora* spp.) representing a major threat to strategic crops and natural landscapes in the EU, and to identify integrated management strategies for their containment. The wide range of studies conducted within the Project tasks on key emergent pests and the rising request for accessing up-to-date references over the Internet, suggested the need to provide a larger variety of real-time information about the project and its targets for a much wider variety of end-users. A WordPress-based web portal (www.ponteproject.eu) has been created by the Coordination Team to support collaborative platform functions, enhance the project's visibility and provide in a flexible manner a rapid dissemination of valuable information, fostering raise of general knowledge and public awareness on relevant themes in plant pathology. Answering to the modern challenges, accounting for an effective web-based pest information system, the resource is intended as an open-access platform to share scientific achievements, upload promotional material and fact sheets, communicate conferences and training courses, report press review and legislative regulations. A social media presence on Twitter and Facebook channels was set up from the early stages in order to enable a two-way communication with a web-active audience and work towards a continuous engagement of the major plant pathology networking platforms and institutional accounts. To keep Project partners and interested parties always informed of the web site updates and encourage frequent visits, a newsletter is being released on a weekly basis.

21. SURVEY FOR THE PRESENCE OF XYLELLA FASTIDIOSA SUBSP. PAUCA STRAIN CoDiRO IN THE NATIVE FLORA OF THE SALENTO PENINSULA. O. Potere¹, L. Susca¹, F. Civita¹, S. Marullo¹, G. Loconsole¹, M. Saponari², D. Boscia², V. Savino^{1,2}, P. La Notte². ¹Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti, Università degli Studi di Bari Aldo Moro, Via Amendola 165/A - 70126 Bari, Italy. ²Istituto per la Protezione Sostenibile delle Piante, CNR, SS di Bari, Via Amendola 165/A - 70126 Bari, Italy. E-mail: oriana.potere@uniba.it

Xylella fastidiosa subsp. *pauca* strain CoDiRO was identified as associated with the "Olive Quick Decline Syndrome", a devastating disease first observed in October 2013 in the southeastern Apulia. At least 350 plant species belonging to 75 families are reported as hosts of *X. fastidiosa*. These provide a source of inoculum for the vectors (xylem sap-feeding leafhoppers), thus playing a major epidemiological role and facilitating the entrenchment of the pathogen in the affected area. To investigate the CoDiRO strain host range in Salento, monthly samplings of the native flora of two heavily infected olive groves and of the side of adjacent roads were conducted from January 2014 onwards. One of the groves was grass-covered, whereas periodic tillage was performed in the other. Overall, more than 200 species of 50 families were sampled, observed for the presence of symptoms, photographed and identified. In the spring, *Philaenus spumarius* the main vector of the Salentinian *X. fastidiosa* strain was abundantly present on the herbaceous flora and shrubs at all sites. All samples, in pools of no less than 3 to 5 plants, were tested by DAS-ELISA and uncertain/positive results were verified by conventional and real time PCR. Bacterial isolates were obtained in axenic culture from some positive species. In a two-year survey, only *Euphorbia terracina* proved to be *Xylella*-positive among the herbaceous hosts, whereas some shrubs and subshrubs i.e. *Asparagus acutifolius*, *Cistus creticus*, *Myrtus communis*, *Phillyrea latifolia*, *Rhamnus alaternus* and *Rosmarinus officinalis* were infected. These results provide as strong indication that, rather than weeds, are the perennial shrubs that play a major role in the epidemiology of the *X. fastidiosa* in this area.

22. EVALUATION OF A SAMPLING METHOD FOR XYLELLA FASTIDIOSA DETECTION IN OLIVE TREES. L. Susca¹, O. Potere¹, V. Roseti¹, F. Civita¹, G. Loconsole¹, D.