

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.

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To assess the presence of the xylem-limited bacterium *Xylella fastidiosa* subsp. *pauca* strain CoDiRO in olive trees, a specific sampling method was evaluated. Symptomatic and symptomless plants were randomly selected in four olive orchards located in the province of Lecce (Southern Italy). The crown of each plant was subdivided into a lower and an upper portion; four samples were collected from each layer in the main four cardinal directions. A total of eight samples per plant, composed of one- or two-year-old asymptomatic twigs, were collected next to branches showing leaf-scorch symptoms. In this preliminary study, the null hypothesis was tested. i.e. there is no difference between the lower and the upper portions of the tree canopy and across the four cardinal directions. Samples (472), collected from 60 plants belonging to 11 different olive cultivars, were tested by qPCR. Out of 236 samples taken from the upper and lower parts of the canopy only 38,1% of lower samples, in contrast to 56,8% taken from the upper crown layer, were positive to the bacterium. The McNemar test determined that there is a statistically significant difference in the proportion of positive samples between the upper and lower crown ($p < 0,001$). The Cochran's Q test was performed to evaluate differences in the four cardinal directions. The null hypothesis suggesting there is no difference across cardinal directions was confirmed ($p = 0,097$). Based on these preliminary results, it appears that sampling should be directed to the upper part of the canopy. However, further studies are needed to improve the efficiency of the sampling technique.

23. IDENTIFICATION OF PUTATIVE EFFECTOR GENES OF 'CANDIDATUS PHYTOPLASMA AURANTIFOLIA' IN INFECTED LIME AND PRELIMINARY SUBCELLULAR LOCALIZATION OF ONE OF THEM IN NICOTIANA BENTHAMIANA. Ananbestani¹, M. Morano¹, S. Palmano¹, A. Carra¹, M. Vallino¹, C. Marzachi¹. ¹*CNR, Istituto per la Protezione Sostenibile delle Piante, Torino, Italy. E-mail: ameneh.ananbestani@ips.cnr.it*

Phytoplasma are phytopathogenic bacteria that induce several specific symptoms in the infected plants

through secretion of effector proteins that induce changes in the architecture and defense response. Witches'-broom disease (WBDL) is an important disease of lime in Southern Iran. The disease is caused by 'Candidatus Phytoplasma aurantifolia', for which full genome sequence is not available. To identify putative WBDL effector genes, the fully sequenced genome of the close relative peanut witches'-broom phytoplasma (PnWB) was mined using an appropriate pipeline. Primers were designed according to the retrieved genes, and total DNA of WBDL-infected lime was amplified with the PnWB-specific primer pairs. Eight putative effector genes were identified, and their similarity to PnWB homologs ranged from 50% to 100%. *In vivo* transcription of these putative effectors in infected limes was monitored. Bands of expected sizes were detected for five putative effector genes but not for the others, suggesting that only some of these putative effector genes maybe active, at least under the experimental conditions of this study. Two of these putative effector genes (WBDLEff64 and WBDLEff99), were expressed at high levels during 'Ca. P. aurantifolia' infection of lime, and both were selected for determination of their subcellular localization through a standard *Agrobacterium*-mediated transient transformation. The infiltrated leaves, harvested 72 h after infiltration, were examined by confocal laser-scanning microscopy (CLSM). Preliminary CLSM showed that GFP-WBDLEff64 was excluded from the cell nucleus and predominantly localized within the cytoplasm, suggesting a role for this protein at this cellular compartment.

24. PHYTOPATHOLOGICAL PROBLEMS IN POPLAR SHORT ROTATIONS FOR BIOENERGY PRODUCTION. N. Anselmi¹, A. Giorcelli². ¹*Dipartimento per la Innovazione nei sistemi biologici, agroalimentari e forestali (DIBAF), University of Tuscia, Via San Camillo de Lellis s.n.c. - 01100 Viterbo, Italy.* ²*Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Unità di Ricerca per le produzioni legnose fuori foresta, Strada Frassineto 35 - 15033 Casale Monferrato (AL), Italy. E-mail: anselmi@unitus.it*

Poplar short rotation, with high density of plants, are a very good opportunity for production of bioenergy. However, they present several characteristics that may induce disease attacks: high moisture and prolonged periods of wetness of the leaves in connection with limited gas exchanges and lack of light; constant sprouting of green tissue during the most part of the growing season; high competition for water and nutri-