

cell walls. Chitosan improves the host hypersensitive response by the expression of pathogenesis-related proteins and the synthesis of secondary metabolites. *Trichoderma harzianum* T-22 (T22) induces defense responses against *Cucumber mosaic virus* Fny (CMV) in *Solanum lycopersicum*. On this basis, the aim of this work was to determine if the combination T22-chitosan has an antiviral activity against CMV in tomato plants. Plant physiological parameters (gas exchange, chlorophyll content and fluorescence) were followed throughout the experiment. Furthermore, ELISA test was employed to detect CMV. Results indicate that plants treated with T22 and chitosan had a strong attenuation of viral load, a higher chlorophyll content and a better photosynthetic performance compared to the untreated plants. Further investigations are in progress to determine plant antioxidant responses. In conclusion, combined treatment based on T22 and chitosan represents a highly effective strategy against CMV, embracing the criteria of sustainable agricultural practice and public health protection.

THE EU RESEARCH PROGRAMS IN RESPONSE TO THE XYLELLA FASTIDIOSA EMERGENCY. D. Boscia, M. Saponari. CNR Istituto per la Protezione Sostenibile delle Piante (IPSP), SS Bari - 70126 Bari, Italy. E-mail: donato.boscia@ipsp.cnr.it

The identification in 2013 of a large outbreak of *Xylella fastidiosa* (*Xf*) in olive groves in the Salento peninsula (southern Italy) has resulted in a plant health emergency of unprecedented proportions for the EU. Afterwards, in 2015 numerous *Xf* outbreaks were identified in Corsica and France. Because of the complexity of the *Xf*-associated diseases, the management and the control of the infections rely on deep knowledge of the hosts, of the biology and genetics of the isolate(s), and on their interactions with the autochthonous insect vector population(s), the climate conditions and the agriculture practices. As such, the EU Commission mobilized resources within the EU framework programme for research and innovation Horizon 2020. At the end of 2015, the project Pest Organisms Threatening Europe (POnTE) started covering among the other emerging pathogens the topic of *Xf*, whereas in 2016 (i) a dedicated H2020 action for *Xf* (Spotlight on critical outbreak of pests: the case of *Xylella fastidiosa*) has been launched, and (ii) a targeted *Xf*-project has been set within the EU-PHRESKO network. These actions involve very large Consortiums with ambitious work-plans covering basic and applied researches on prevention, detection, surveillance and innovative control strategies for *Xf*

and its vector(s). The multi-actor approach ensured by these large Consortiums will facilitate interactions among research groups, share previous experiences, establish new and strengthen current collaborations among European and non-European research organizations, and increase awareness about scientific work previously done. Best practices to manage the EU resources are put in place in order to maximize the efforts while avoiding research duplications.

POTENTIAL DISTRIBUTION OF XYLELLA FASTIDIOSA AND ITS INSECT VECTOR PHILAENUS SPUMARIUS IN THE MEDITERRANEAN BASIN. L. Bosso¹, M. Di Febbraro², G. Cristinzio¹, A. Zoina³, D. Russo^{1,4}. ¹ Dipartimento di Agraria, Università degli studi di Napoli Federico II, Via Università 100 - 80055 Portici, Napoli, Italy. ² EnvixLab, Dipartimento Bioscienze e Territorio, Università del Molise, Pesche, Italy. ³ CNR, Istituto per la Protezione Sostenibile delle Piante, UOD Portici, Italy. ⁴ School of Biological Sciences, University of Bristol, Woodland Road BS8 1UG, Bristol, United Kingdom 4. E-mail: luciano.bosso@unina.it

Xylella fastidiosa is a xylem-limited gram negative bacterium causing a high number of severe diseases to many agricultural and forestry plants. *Philaenus spumarius* is the principal insect vector of this pathogen bacterium in Italy. We developed a Maxent model to detect the potential distribution of *X. fastidiosa* and *P. spumarius* in the Mediterranean basin. Maxent models achieved excellent levels of predictive performance as can be seen from AUC, TSS and AUC_{diff} values for both the organisms. Species distribution models showed a high probability of *X. fastidiosa* in Portugal, Spain, Italy, Southern France, Corsica, Albania, Montenegro, Greece and Turkey as well as all countries of Northern Africa and the Middle East. Maxent models also showed that *P. spumarius* was widespread in all countries of Europe, Northern Africa and the Middle East. *P. spumarius* could spread *X. fastidiosa* in all countries of the Mediterranean basin but, cold winter temperature seems to limit the spread of this pathogen bacterium in all countries located beyond the south of France. Our study highlights that *X. fastidiosa* may overcome the current boundaries outside Italy. Given the potentially high risk, the Phytosanitary Services of the listed nations are considering stringent phytosanitary measures to avoid the introduction of the bacterium in their own countries.

MONITORING OF XYLELLA FASTIDIOSA IN AN ITALIAN PEST-FREE AREA