



*XXII Convegno Nazionale
Società Italiana di Patologia Vegetale
(SIPaV)*

*La patologia vegetale tra produttività
e sostenibilità*

BOOK OF ABSTRACTS

Edited by: Taglienti A., Tomassoli L., Infantino A.

Roma, 19-20-21-22 Settembre 2016

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COMPARING CHESTNUT CULTIVARS AND THE WILD-TYPE FOR THEIR SUSCEPTIBILITY TO THE NUT ROT CAUSED BY *GNOMONIOPSIS CASTANEAE*.

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The emerging nut rot caused by the fungal pathogen *Gnomoniopsis castaneae* stands among the most detrimental threats to chestnut (*Castanea* spp.). The goal of this study was comparing a large selection of chestnut cultivars and the wild-type of *C. sativa* for the levels of susceptibility to *G. castaneae*. In 2013, up to 40 nuts per tree were collected from 85 chestnut cultivars and from the wild-type growing in the Chestnut Regional Repository of Chiusa Pesio (Italy). The sampling was partially replicated in 2014 for validation purpose. Isolation trials and molecular analyses were performed to assess the incidence of *G. castaneae* at tree level. The incidence of each cultivar was compared to the incidence of the wild-type, assumed as reference population, through an innovative approach based on the Pearson system of generalized frequency curves and on Monte Carlo simulations. In the wild-type, the incidence of *G. castaneae* increased from 2013 (4.8%) to 2014 (19.6%) and a similar trend was also observed, on average, in the chestnut cultivars (up to +29.7%). Cultivars significantly more susceptible ($P < 0.05$) than the wild-type (22% of the total number of cultivars in 2013 and 55% in 2014) were detected by definite integration of curves associated with the Pearson system. The validation analysis revealed no significant association between the most susceptible cultivars detected in 2013 and 2014 (odds ratio 2.85; 0.18-176.61 95% CI), suggesting that the susceptibility to *G. castaneae* is substantially homogeneous between the chestnut cultivars and the wild-type.

COMPETITION ASSAYS REVEAL A NOVEL PUTATIVE BIOCONTROL AGENT: *PAENIBACILLUS PASADANENSIS* STRAIN R16. A. Passera, P. Casati, G. Venturini, F. Penaca, F. Quaglino, P.A. Bianco. Università degli Studi di Milano, DISAA, Milano, Italia. E-mail: alessandro.passera@unimi.it

Since European policies aim to reduce the environmental impact of agriculture and implement sustainable containment strategies for diseases, research of novel biocontrol agents is very important. In this study, the plant growth promoting potential and biocontrol effect against three important plant pathogenic fungi (*Botrytis cinerea*, *Fusarium verticillioides*, and *Phomopsis viticola*), exerted by the novel candidate biocontrol agent *Paenibacillus pasadenensis* strain R16, isolated during previous investigation carried out to characterize the microbiome of diseased and healthy plants, were assessed *in vitro*. Biochemical assays to determine plant growth promoting potential gave negative results in regard to siderophore production and phosphate solubilization, and positive results for ACC-deamination, IAA production, and activity of catalase and chitinase. Biocontrol assays showed that strain R16 is very effective against *B. cinerea* in several tests, reducing mycelial growth both in dual-culture and through volatile substances only, as well as reducing infection rate on berries and inhibiting conidia germination. Strain R16 also showed good biocontrol potential also against *P. viticola*, but was ineffective toward *F. verticillioides*.

Obtained results proved for the first time the efficient biocontrol activity against fungal pathogens and putative plant growth promotion traits of *P. pasadenensis* strain R16, opening an interesting scenario for further studies investigating the application of this endophytic bacterium as a biocontrol agent in open field.

SYNERGISTIC EFFECT OF TRICHODERMA AND CHITOSAN APPLICATION IN TOMATO FOR THE CONTROL OF CUCUMBER MOSAIC VIRUS INFECTION.

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Soil and plant environments are characterized by a wide range of microorganisms able to interact with host plants and, in some cases, to differentially induce susceptibility or resistance to pathogens. Plant viruses cause chlorosis and necrosis, so decreasing plant growth and productivity. Differently, many fungi are able to trigger a beneficial relationship with plants. *Trichoderma* spp. are endophytic symbionts able to modify plants metabolism, increasing nutrient uptake by plants and photosynthetic efficiency, and protecting them from pathogens. A biopolymer able to elicit plant-immunity is chitosan, derived by the deacetylation of chitin, a component of some fungal

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-PHRESO 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}. ¹Dipartimento di Agraria, Università degli studi di Napoli Federico II, Via Università 100 - 80055 Portici, Napoli, Italy. ²EnvixLab, Dipartimento Bioscienze e Territorio, Università del Molise, Pesche, Italy. ³CNR, Istituto per la Protezione Sostenibile delle Piante, UOD Portici, Italy. ⁴School 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