



Abstracts of presentations at the XXIV Congress of the Italian Phytopathological Society

September 5-7, 2018. Department of Agricultural, Food and Environmental Sciences, Marche Polytechnic University, Ancona, Italy

Structure and dynamics of airborne fungal populations in organic and conventional vineyards

A. Abdelfattah¹, A. Ippolito², M. Wisniewski³, S. Pangallo¹, S. Scibetta¹, S. Mosca¹, M.G. Li Destri Nicosia¹, G.E. Agosteo¹, G. Magnano di San Lio¹, S.O. Cacciola⁴, L. Schena¹

¹Universita' degli Studi Mediterranea di Reggio Calabria, Reggio Calabria, Italy; ²Department of Soil, Plant, and Food Sciences, University of Bari Aldo Moro, Bari, Italy; ³USDA ARS, Kearneysville, WV, USA; ⁴Department of Agriculture, Food and Environment, University of Catania, Catania, Italy. E-mail: lschena@unirc.it

Recent studies have demonstrated the presence of a huge number of microorganisms in air samples. However, the relationship between the plant microbiome and the fungi present in the air surrounding the plant has not been intensively investigated. The structure and dynamics of airborne fungal communities associated to grapevine in organic and conventional vineyards were characterized in this study. Seven phyla, including Ascomycota, Basidiomycota, Zygomycota, Chytridiomycota and Glomeromycota, were identified. Overall, 638 fungal genera were detected with *Alternaria*, *Mycosphaerella* and *Stemphylium* representing about 70% of the total fungal community. Data analysis indicated that management practices had a significant impact on the structure of fungal community. However, population dynamics in organic and conventional farms showed the same trend. It appeared to be related prevalently to the biology of different taxa. Results of this study confirm the important role of circulating air in the spread and distribution of microorganisms. Epidemiological implications of population dynamics of important grapevine pathogens and useful fungal microorganisms, such as yeasts, over the growth season are discussed.

A new real-time loop-mediated isothermal amplification (LAMP) assay to rapidly detect *Phytophthora ramorum* and *P. lateralis* invasive plant pathogens

C. Aglietti¹, A. Santini², P. Bartolini², P. Capretti¹, N. Luchi²

¹Department of Agrifood Production and Environmental Sciences, University of Florence (DISPAA), Piazzale delle Cascine 28, I-50144 Firenze, Italy; ²Institute for Sustainable Plant Protection - National Research Council (IPSP-CNR), Via Madonna del Piano 10, I-50019 Sesto Fiorentino, Firenze, Italy. E-mail: nicola.luchi@ipsp.cnr.it

An effective framework for early warning and rapid response is a crucial element to mitigate or prevent the ecological and economic impacts of invasive plant pathogens. Molecular detection of these pathogens is now preferred for its greater sensitivity and specificity respect to classical tools. These analyses are generally PCR-based and require a well-equipped lab. Significant advantages in terms of prompt response to threats might be obtained by using an on-site detection tool. A real-time monitoring LAMP-based method has been optimized for a rapid and sensitive detection of *P. ramorum* and *P. lateralis*, two quarantine pathogens that cause mortality on forest trees and ornamental plants in Europe and North America, by using the Genie[®] II system. The assay was able to recognize each pathogen with a high level of specificity and sensitivity also in plant tissues (to 4 pg μL^{-1} of DNA) in only 30 minutes. Great simplicity, sensitivity, specificity, and minimum required equipment make the LAMP assay ideal for application in the field and for routine plant testing at ports of entry. The use of portable and handled instruments allows a fast analysis of the collected sample reducing the diagnosis time and may have implications for disease management and for the control of *P. lateralis* and *P. ramorum*.

Environmental genomics reveals the diversity of *Phytophthora* populations in phytocoenoses of “Complesso Speleologico Villasmundo-S. Alfio” Natural Reserve in Sicily

F. Aloï^{1,2}, A. Pane¹, F. La Spada¹, M. Evoli^{1,3}, R. Faedda¹, C. Stracquadanio³, L. Schena³, S.O. Cacciola¹

¹University of Catania, Department of Agriculture, Food and Environment (Di3A), via S. Sofia 100, 95123 Catania, Italy; ²University of Palermo, Department of Agricultural, Food and Forest Sciences, V.le della Scienze, Ed.4, 90128 Palermo, Italy; ³University Mediterranea of Reggio Calabria, Department of Agraria, Loc. Feo di Vito, 89122 Reggio Calabria, Italy. Email: olgacacciola@unict.it

The “Complesso Speleologico Villasmundo-S. Alfio” (Melilli, Siracusa) was established as a Natural Integral Reserve in 1998. It sits on a karstic calcareous subsoil and includes two deep river valleys delimiting a plateau. Because of its naturalistic and environmental features it has been recognized as a *Site of Community Importance* - SCI - (92/43/EEC). As part of a broader study aimed at investigating the causes of the decline of native vegetation in Natural Reserves in Sicily, the diversity of *Phytophthora* populations in six different phytocoenoses in this Natural Integral Reserve has been studied, including the riparian wood *Platanus-Salicetum pedicellate*, the termophylic evergreen wood *Pistacio-Quercetum ilicis*, the Mediterranean maquis *Myrto communis-*

Almond witches' broom (AlmWB) associated with '*Candidatus* Phytoplasma phoenicium' is one of the economically important diseases of almond in Iran and Lebanon. In 2012–2015 surveys of AlmWB, apricot yellows (AprY) disease was observed in Fars province of Iran. The characteristic symptoms of the disease were leaf yellowing, inward leaf curl, scorch of leaf margins, shortened internodes, production of rosettes at the tip of branches, decline, stunting, and death. Healthy bitter almond and apricot seedlings, grafted with shoots of AprY-affected trees, exhibited phytoplasma-type symptoms. The 16S rDNA fragment F2n/R2 was amplified by nested-PCR from both AprY-affected trees and grafted seedlings. Nucleotide sequence identity, presence of species-specific signature sequences, and phylogenetic analysis of 16S rDNA allowed the assignment of detected phytoplasma strains to the species '*Ca. P. phoenicium*'. *In vitro* and *in silico* RFLP analysis of the fragment F2n/R2 allowed the affiliation of AprY phytoplasma to a variant of subgroup 16SrIX-B. Within '*Ca. P. phoenicium*' (16SrIX-B) population strains, identified in this and previous studies, 16 genetic lineages were determined by the combination of 19 single nucleotide polymorphisms (SNPs) identified within 16S rDNA nucleotide sequences. Interestingly, AprY phytoplasma strains belong to a unique genetic lineage distinguished by the presence of three lineage-specific SNPs. This first report of '*Ca. P. phoenicium*' in association with AprY disease in Iran opens new perspectives on the epidemiology of AlmWB phytoplasma, suggesting its possible adaptation to other fruit trees.

A lipidomic approach to study the interaction of *Xylella fastidiosa* with *Olea europaea*

M. Salustri¹, V. Scala², N. Pucci², A. L'Aurora², V. Modesti², M. Scortichini³, M. Reverberi¹, S. Loreti²

¹Sapienza University, Dept. of Environmental Biology, P.le Aldo Moro 5, 00185 Roma, Italy; ²Council for Agricultural Research and the Analysis of Agricultural Economics (CREA), Research Centre for Plant Protection and Certification, Via C.G. Bertero 22, 00156 Roma, Italy; ³Council for Agricultural research and the Analysis of Agricultural Economics (CREA), Research Centre for Olive, Fruit Trees and Citrus, Via Torrino 3, 81100 Caserta, Italy. E-mail: valeria.scala@crea.gov.it

In the last years, *Xylella fastidiosa* became a severe threat for the European Community. In particular, *X. fastidiosa* subsp. *pauca* is associated with the Olive Quick Decline Syndrome, a disease causing severe losses in the Apulia region. So far, prevention is the most pursued strategy to restrain disease spread. Metabolomic studies, and specifically, in our case, the lipidomic ones, could provide useful information, either for prevention, detection (potential marker of infection) or for a possible remediation, i.e. by revealing pathogen pathways to be possibly blocked. In this study, naturally infected and healthy olive samples (cv. 'Ogliarola salentina') were collected in an affected olive orchard (Lecce and Taranto provinces, Apulia region) to investigate their lipidomic profile. In particular, HPLC-ToF untargeted analysis methods were used to acquire lipidome profiles and HPLC-MS/MS targeted methods to characterize and quantify different lipids. The untargeted analysis highlighted oxylipins, free fatty acids, glycerolipids and phosphoglycerolipids within the different lipid classes that were analysed. Based on these results, quantitative and semi-quantitative analysis of specific entities within each of these class of lipids both in healthy and infected samples was provided. A scenario has emerged, in which the Xf-infected olive samples presented at least one bacterium-specific lipid, i.e. 10-hydroperoxy-octadecenoic acid, and other host-pathogen shared lipids that are significantly higher in amount in comparison with healthy samples. To corroborate lipidomic profiles, the molecular quantification of bacterial charge through real time PCR is under way. This explorative approach will provide a robust basis for further targeted biological assays.

Enzyme production by solid state fermentation of *Cryphonectria parasitica* on agro-industrial residues

S. Savino¹, E. Monti¹, E. Gobbi^{1,2}

¹Unit of Biotechnology, Department of Molecular and Translational Medicine (DMMT), University of Brescia, 25123 Brescia, Italy; ²Agrifood and Environmental Microbiology Platform (PiMiAA), Department of Molecular and Translational Medicine, University of Brescia, 25123 Brescia, Italy. E-mail: emanuela.gobbi@unibs.it

A variety of microorganisms are used to produce biofuels, enzymes, vitamins, antioxidants, animal feed, antibiotics, and other products through solid state fermentation (SSF) of agro-industrial wastes. In a SSF process, microorganisms grow in an environment with no or a very low content of free water. Although its historical importance for humans has been known for thousands of years, recently this process has gained greater importance in circular economy. The aim of the present study was to investigate the capability of *Cryphonectria parasitica* (Murr.) Barr to grow and produce enzyme(s) on waste. Esterase, amylase, cellulase and laccase production by four newly isolated *C. parasitica* strains was obtained by means of solid state fermentation using commercially available wheat bran. Various physico-chemical parameters were optimized, such as fermentation period, moisture content and growth temperature, to guarantee a good colonization of the substrate. After liquid-solid extraction from fermented wheat bran, optimum fermentation conditions for esterase and amylase production were the following: growth at 25 °C, at a moisture content of 50% for 15 days. The results obtained suggest the feasibility of large-scale production of industrially relevant enzymes by *C. parasitica* in a SSF process of low-value materials. Furthermore, this SSF process offers notable economical and environmental advantages over submerged fermentation.

Tramesan, an eco-friendly approach against Septoria disease complex in wheat

V. Scala¹, C. Pietricola², L. Covarelli^{3,4}, M. Blandino⁵, V. Farina², G. Beccari³, F. Tini³, P. Cescutti⁶, B. Bellich⁶, A. Parroni², S. Zjalic⁷, J. Loncar⁷, M. Reverberi², A. Iori⁸

¹Consiglio per la Ricerca in Agricoltura e l'Analisi dell'Economia Agraria, Centro di ricerca Difesa e Certificazione, via C.G. Bertero 22, 00156 Roma, Italy; ²Dip. Biologia Ambientale, Università Sapienza, P.le Aldo Moro 5, 00185 Roma, Italy; ³Dip. di Agricoltura, Alimenti ed Ambiente, Università di Perugia, Borgo XX Giugno, 74, 06121 Perugia, Italy; ⁴Curtin University, Centre for Crop and Disease Management, Bentley, Perth, Australia; ⁵Università di Torino, Dipartimento di Scienze Agrarie, Forestali e Alimentari, Via Verdi 8, 10124 Torino, Italy; ⁶Università di Trieste, Dip. Scienze della Vita, via L. Giorgieri 1, Bdg C11, 34127 Trieste, Italy; ⁷Department of Ecology, Agronomy and Aquaculture, University of Zadar, Croatia; ⁸Consiglio per la Ricerca in Agricoltura e l'Analisi dell'Economia Agraria, Centro di ricerca Ingegneria e Trasformazioni agroalimentari, via Manziana 30, 00189 Roma, Italy. E-mail: massimo.reverberi@uniroma1.it

Wheat is the most cultivated cereal representing the main source of plant proteins in human food. However, up to 50% of worldwide wheat production may be lost because fungal diseases. The Septoria disease complex (STB) is critical, being *Parastagonospora nodorum*