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BOOK OF ABSTRACTS

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AN ECTOMYCORRHIZAL FUNGUS MAY DECREASE THE SUSCEPTIBILITY OF *PINUS SYLVESTRIS* TO THE NATIVE PATHOGEN *HETEROBASIDION ANNOSUM* BUT NOT TO THE EXOTIC *H. IRREGULARE*. **L. Giordano[1,2], E. Zampieri[1], G. Lione[1], A. Vizzini[3,4], J.V. Colpaert[5], R. Balestrini[4], P. Gonthier[1].** *[1]University of Torino, Department of Agricultural, Forest and Food Sciences (DISAFA), Largo Paolo Braccini 2, I-10095 Grugliasco (TO), Italy. [2]University of Torino, Centre of Competence for the Innovation in the Agro-Environmental Field (AGROINNOVA), Largo Paolo Braccini 2, I-10095 Grugliasco (TO), Italy. [3]University of Torino, Department of Life Sciences and Systems Biology (DBIOS), Viale P.A. Mattioli 25, I-10125 Torino, Italy. [4]Institute for Sustainable Plant Protection, CNR, Torino Unit, Viale P.A. Mattioli 25, I-10125 Torino, Italy. [5]Universiteit Hasselt, Centrum voor Milieu-Kunde (CMK), Agoralaan Gebouw D, 3590 Diepenbeek, Belgium. E-mail: paolo.gonthier@unito.it*

In the last century, the intensification of global trade has greatly enhanced the likelihood of biological invasions resulting in increasing threats to native ecosystems. The North American root rot agent *Heterobasidion irregulare* Garbel. et Otrosina was accidentally introduced in central Italy in 1944 where the Eurasian congener *H. annosum* (Fr.) Bref. is also present. *H. irregulare* has become invasive colonizing pine and oak stands along 103 km of coastline west of Rome. Although many studies have focused on factors driving biological invasions, very little is known on the role played by native mycorrhizal fungi in modulating host tolerance to non-native pathogens. The aim of this study was to compare the level of susceptibility of *Pinus sylvestris* L. to *H. irregulare* and *H. annosum* between plants mycorrhized and non-mycorrhized with the native ectomycorrhizal fungus *Suillus luteus* (L.) Roussel. Inoculation experiments were performed with three pathogen genotypes per species on seven-month-old mycorrhized and non-mycorrhized seedlings. To assess the level of host susceptibility, seedlings were inspected every day and scored depending on their time to death. The resulting survival curves pointed out that mycorrhizae reduced significantly the level of host susceptibility to the native pathogen, but not to the exotic one. Besides, non-mycorrhized plants were equally susceptible to both pathogens. These findings suggest that a symbiont-mediated mechanism of tolerance might protect the host plant from a native pathogen, but may fail in the presence of a non-native one. In this model system, this mechanism may confer an additional competitive advantage to *H. irregulare*.

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PROMOTER CHARACTERIZATION OF THE *VviATL156* GENE INVOLVED IN GRAPEVINE RESISTENCE TO *PLASMOPARA VITICOLA*. **P. Ariani, D. Danzi, A. Regaiolo, A. Polverari, E. Vandelle.** *Università degli Studi di Verona, Strada Le Grazie 15, 37135 Verona (VR), Italy. E-mail: elodiegenevieve.vandelle@univr.it*

Despite a lot of efforts to overcome the susceptibility of grapevine (*Vitis vinifera*) to pathogens, in particular *Plasmopara viticola*, by crossing with wild relatives, traditional breeding did not lead so far to significant results. Thus, to allow the development of new plant breeding techniques to improve premium cultivars, we are currently studying the resistance mechanisms evolved in naturally resistant American grapes. We selected *VviATL156* as candidate gene specifically upregulated in the resistant *V. riparia* upon downy mildew infection and generated stable transformed grapevines (*V. vinifera* cv. Shiraz) constitutively expressing it. *VviATL156* encodes to downy mildew. However, knowledge about the specific regulation of candidate genes is crucial to identify a truly promising gene, not severely affected by the genomic background in which it is introduced. In this context, the *VviATL156* regulative regions from both resistant and susceptible grapevine species were cloned and sequenced. Bioinformatics analyses allowed to define the core promoter structures and *cis*-acting element compositions. An extra TATA-box was predicted in the *V. riparia* sequence, together with some over-represented *cis*-acting elements, likely related to disease resistance. The promoters were then functionally characterized in stably transformed *Arabidopsis thaliana* plants, under physiological conditions and in response to hormones and pathogen infection. Moreover, promoter *trans*-activation by specific transcription factors was evaluated in a Dual Luciferase Assay experiment in transiently transformed *Nicotiana benthamiana*.

STUDY OF THE MOLECULAR DIALOGUE BETWEEN GRAPEVINE INFLORESCENCE/BERRY AND *BOTRYTIS CINEREA* DURING THE INITIAL, QUIESCENT, AND EGRESSION INFECTION STAGES. **Z.H. Mehari[1,4,5], S. Pilati[1], P. Sonego[1], G. Malacarne[1], U. Vrhovsek[1], K. Engelen[1], P. Tudzynski[2], M. Zottini[3], E. Baraldi[4], C. Moser[1].** *[1]Research and Innovation Centre, Fondazione Edmund Mach, 38010 San Michele all'Adige (TN), Italy. [2]Institute for Biology and Biotechnology of Plants, Westf. University of Muenster, Muenster, Germany. [3]Università di Padova, Italy. [4]Università di Bologna, Laboratorio di Biotecnologie Vegetali, Bologna, Italy. [5]Ethiopian Institute of Agricultural Research, A.A., Ethiopia. E- mail: claudio.moser@fmach.it*

Grapes quality and yield are affected by gray mould disease caused by the necrotrophic fungus *Botrytis cinerea*. Primary infections are mostly initiated at blooming by air-borne conidia but the fungus often remains quiescent from bloom until maturity, when it causes grey mould. Molecular analyses of the interaction between *B. cinerea* and the flower/berry of grapevine (*Vitis vinifera* L.) were carried out using confocal microscopy plus integrated transcriptomic and metabolic analysis of the host and the pathogen. Open flowers from fruiting cuttings of cv. Pinot Noir were infected with GFP-labeled *B. cinerea* and samples taken at 24 and 96 hours post inoculation (hpi), 4 and 12 weeks post inoculation (wpi) were studied. Penetration of the flower epidermis by *B. cinerea* at 24 hpi coincided with an increased expression of fungal genes encoding virulence factors and induced a rapid defense reaction in the flowers involving genes associated with the accumulation of PR proteins, stilbenoids, reactive oxygen species and cell wall reinforcement. At 96 hpi the transcriptional reaction appeared largely diminished both in the host and in the pathogen. Afterwards, infected berries continued their development without any visible symptom, although the presence of *B. cinerea* could be ascertained. Nonetheless, at the transcriptional level, both the fungus and the hard-green berries displayed to be transcriptionally active. At 12 wpi, the egressed *B. cinerea* expressed almost all virulence and growth-related genes enabling the pathogen to colonize the berries. In response to egression, ripe berries reprogrammed different defense responses, though ineffectively.

METABOLOMIC AND TRANSCRIPTOMIC PROFILES IN HEALTHY AND ONION YELLOW DWARF VIRUS INFECTED 'ROSSA DI TROPEA' ONIONS. **A. Tiberini[1], F. Mercati[2], F. Araniti[1], A. Ciampa[4], G. Micali[1], S.B. Grande[1], A. Taglienti[3], M.R. Abenavoli[1], M.T. Dell'Abate[4], F. Sunseri[1], L. Tomassoli[3],**