BENEFICIAL MICROBE–PATHOGEN-PLANT INTERACTIONS: THE RECOGNIZED ROLE OF SECONDARY METABOLITES. **F. Vinale[1*], M. Ruocco[1], R. Marra[1,2], N. Lombardi[1,2], A. Pascale[1,2], S. Lanzuise[1,2], R. Varlese[2], G. Manganiello[2], D. Stellitano[1], F. Zecca[3], S.L. Woo[1,2], M. Lorito[1,2].** *[1]CNR – Istituto per la Protezione Sostenibile delle Piante, Via Università 133, 80055 Portici, Italy. [2]Dipartimento di Agraria, Università degli Studi di Napoli 'Federico II', Via Università 100, 80055, Portici, Italy.[3]Dipartimento di Management, Università di Roma "La Sapienza", Via del Castro Laurenziano 9 - 00161 Roma. E-mail: f.vinale@ipp.cnr.it*

Microbial secondary metabolites are chemically different natural compounds of low molecular weight produced during processes of competition with other micro- and macro-organisms, symbiosis, parasitism or pathogenesis. Beneficial microbes typically produce bioactive molecules involved in the interactions with plant and pathogens. Some secondary metabolites with antibiotic activity have been associated to the biological control of plant pathogens and pests. The production of secondary metabolites depends on: i) the compound considered; ii) the species and the strain; iii) the occurrence of other microorganisms; iv) the equilibrium between elicited biosynthesis and biotransformation rate; and v) the growth conditions. In addition to direct toxic activity against phytopathogens, biocontrol-related metabolites may also increase disease resistance, and/or enhance root, stem, shoot and leaf vegetative growth.

Metabolomic analysis of the interactions between plants, fungal phytopathogens and beneficial microbes has aided in the identification of new bioactive metabolites that positively affect plant metabolism. Recently, we have found a new *Trichoderma* polyketide, named cremenolide, with strong antifungal activity. This compound alone or in combination with other known metabolites (i.e. 6-penthyl-a-pyrone or harzianic acid) improve growth and/or health of different plant species. We have effectively tested several *Trichoderma* metabolites from *in vitro* conditions all the way to the field, and developed new active ingredients for use as biostimulators and disease inhibitors, both alone and in combination with the living beneficial microbes. Agrobiochemicals of this new class should be available on the market in few years and become very useful IPM tools.

FIMICOLOUS FUNGI: AN UNDEREXPLORED RESERVOIR OF NEW COMPOUNDS TO BE EMPLOYED FOR THE CONTROL OF PLANT PATHOGENS. **S. Sarrocco[1], S. Diquattro[1], F. Avolio[2], A. Cimmino[2], A. Andolfi[2], G. Puntoni[1], F. Doveri[1], A. Evidente[2], G. Vannacci[1].** *[1] Dipartimento di Scienze Agrarie, Alimentari e Agro-ambientali, Università di Pisa, Via del Borghetto 80 - 56124 Pisa, Italy. [2] Dipartimento di Scienze Chimiche, Università degli Studi di Napoli Federico II, Via Cintia 4 - 80126 Napoli, Italy. E-mail: sabrina.sarrocco@unipi.it*

Herbivorous mammals dung support a large variety of fimicolous fungi and the number of new genera and species is constantly increasing. Dung is a complex ecosystem and to win the struggle for life, these fungi produce a plethora of bioactive secondary metabolites to compete with other organisms. Fimicolous fungi and their bioactive metabolites are mostly evaluated for a possible use in medicine. Very few information are available about their possible exploitation in agriculture against plant pathogens.

Five coprophilous (*Auxarthron umbrinum*, *A. concentricum*, *Cleistothelebolus nipigonensis*, *Neogymnomyces virgineus* and *Rodentomyces reticulatus*) Italian isolates collected from dung of different herbivores, were investigated. "*In vitro*" antibiosis tests showed positive results against several fungal plant pathogens on different growth media. A solid culture on rye flour was extracted by methanol-water (5% sodium chloride) and this latter, successively, with n-hexane and dichloromethane. Extracts and the corresponding aqueous fractions were tested on PDA against eight plant pathogenic fungi. A very good inhibitory activity of some *C. nipigonensis* and *N. virgineus* extracts was recorded and further fractions obtained by column chromatography were successfully tested against *Alternaria* sp., *Botrytis cinerea*, *Fusarium graminearum* and *Sclerotinia sclerotiorum*. A further chromatography of the selected bioactive fractions will allow to detect the compounds responsible of this activity and to determine their structures.

Data here obtained suggest the possibility to discover novel metabolites to be used in the management of plant disease and highlight how fimiculous fungi could represent a marvellous unexplored reservoir of new bioactive compounds.

MINING THE GENOME OF *LYSOBACTER CAPSICI* AZ78 TO IDENTIFY THE MECHANISMS INVOLVED IN THE BIOLOGICAL CONTROL OF *PHYTOPHTHORA INFESTANS* AND *PLASMOPARA VITICOLA*. **G. Puopolo[1], P. Sonego[2], K. Engelen[2], I. Pertot[1].** *[1]Department of Sustainable Agro-Ecosystems and Bioresources, Research and Innovation Centre, Fondazione Edmund Mach, 38010 S. Michele all'Adige (TN), Italy. [2]Department of Computational Biology, Research and Innovation Centre, Fondazione Edmund Mach, 38010 S. Michele all'Adige (TN), Italy. E-mail: gerardo.puopolo@fmach.it*

The use of biological control microorganisms to protect plants against pathogenic oomycetes may contribute to make crop production more sustainable. Recently, we showed that *Lysobacter capsici* AZ78 effectively controls grapevine downy mildew and tomato late blight incited by *Plasmopara viticola* and *Phytophthora infestans*, respectively. Furthermore, we proved that this bacterial strain can be combined with copper based fungicides for controlling both the plant pathogenic oomycetes. In order to investigate the mechanisms that can be involved in the antagonism of *L. capsici* AZ78, the genome of this bacterium was sequenced through Illumina GAIIX system.

The *L. capsici* AZ78 draft genome is constituted of 6.3 Mb with a 66.43% GC content. Mining the annotated *L. capsici* AZ78 genome showed the presence of genes coding for chitinases, glucanases, lipases, xilanases and a high amount of proteases, lytic enzymes that can be potentially involved in the control of plant pathogenic microorganisms. Furthermore, the analysis revealed also that *L. capsici* AZ78 genome contains genes responsible for the production of non-ribosomally synthesized peptides with antibiotic activity. Interestingly, *L. capsici* AZ78 genome encompasses genes involved in resistance to drugs and heavy metals as cadmium, cobalt, copper and zinc.

The availability of the whole genome of *L. capsici* AZ78 represents a first step in unravelling the biology of the biological control bacteria belonging to the genus *Lysobacter* and, moreover, will provide the basis for analysing the interaction between this biocontrol bacterium and plant pathogenic oomycetes.

BIOCONTROL ACTIVITY OF A NOVEL ENDOCHITINASE FROM *METSCHNIKOWIA FRUCTICOLA* EXPRESSED IN *PICHIA PASTORIS* AGAINST POSTHARVEST PATHOGENS OF FRUITS. **H. Banani, D. Spadaro, M.L. Gullino, A. Garibaldi.** *AGROINNOVA – Centro di Competenza per l'Innovazione in Campo Agroambientale, Università di Torino, Largo Paolo Braccini 2 (ex- Via L. da Vinci 44), Grugliasco (TO), Italy. E-mail: davide.spadaro@unito.it*

Metschnikowia fructicola strain AP47 was isolated from the carposphere of temperate fruits and showed a high efficacy in controlling *Monilinia* spp. on stone fruits, however its mechanism against postharvest pathogens is still unclear.