CHARACTERIZATION OF THE ROLE PLAYED BY *MAGNAPORTHE ORYZAE* POLYSACCHARIDE MONOOXYGENASES AND RELATED ENZYMES DURING INFECTION OF RICE. L. Sella[1], A. Quarantin[1], F. Favaron[1], L.T. Đô[2], V.V. Van[3], N.M. Hung[2]. *[1]University of Padova, Department of Land, Environment, Agriculture and Forestry, Viale dell'Università 16, 35020, Legnaro (PD), Italy. [2]Duy Tan University, K7/25 Quang Trung, Da Nang, Vietnam. [3]Nguyen Tat Thanh University, 298-300A Nguyen Tat Thanh Street, District 4, Ho Chi Minh City, Vietnam. E-mail: luca.sella@unipd.it; lethdo@hotmail.com*

In 2030, the global rice production is expected to increase to meet the demand of the growing world population. However, rice is severely affected by the blast disease caused by the fungus *Magnaporthe oryzae*, which can reduce by 10-30% the total annual rice production. In the early stages of the infection process, *M. oryzae* forms an appressorium to assist its penetration into plant tissue and expresses many polysaccharide and lignin-degrading enzymes. Among these, polysaccharide monooxygenases (PMOs) degrade their substrates by an oxidative mechanism and could be important virulence factors for the fungus. The first objective of the project, which is part of the Scientific and Technological Cooperation Agreement between the Italian Ministry of Foreign Affairs and International Cooperation and the Department of International Cooperation of the Ministry of Science and Technology of Vietnam, is to identify the role played by *M. oryzae* PMOs and related enzymes during pathogenesis, with the final aim to develop new methods to control rice blast disease. Candidate *M. oryzae* genes encoding PMOs and related enzymes have been identified by an *in silico* analysis of the fungal genome and their expression during the infection process, and particularly during appressorium formation, has been characterized by transcriptomic analysis. Knock-out mutants of the most expressed genes will be generated and their virulence evaluated on rice plants. The role played by the target enzymes on appressorium formation will also be evaluated.

EVALUATION OF BARLEY ENTRIES DEVELOPED FOR ORGANIC OR LOW INPUT AGRICULTURE FOR THEIR SUSCEPTIBILITY TO *FUSARIUM* HEAD BLIGHT INFECTIONS AND MYCOTOXIN ACCUMULATION. M.T. Senatore[1], G. Beccari[1], F. Coccia[1], L. Raggi[1], U. Bonciarelli[1], F. Tini[1], M. Sulyok[2], M. Guiducci[1], V. Negri[1], L. Covarelli[1]. *[1]Department of Agricultural, Food and Environmental Sciences, University of Perugia, Borgo XX Giugno 74, 06121 Perugia, Italy. [2]Department of Agrobiotechnology (IFA-Tulln), University of Natural Resources and Life Sciences, Vienna, Konrad Lorenzstr. 20, 3430 Tulln, Austria. E-mail: lorenzo.covarelli@unipg.it*

The aim of the present study was to evaluate the response to *Fusarium* Head Blight (FHB) infections and mycotoxin accumulation of nine different barley entries: i) five pure lines (namely SOL 1, SOL 2, SOL 7, SOL 30 and SOL 57, respectively), ii) one Composite Cross Population (CCP) (namely AUT DBA) and iii) one line mixture (namely *mix48*) all developed for organic or low input agriculture using an Evolutionary Breeding approach, and iv) two commercial varieties used as controls (Quench, Rattan). The evaluation was conducted in an experimental field plot trial under both artificial inoculation, with a mixture of four *Fusarium* species (*F. graminearum*, *F. culmorum*, *F. avenaceum* and *F. poae*), and natural inoculum conditions. FHB was evaluated by isolation and identification of the different *Fusarium* species infecting the grains, fungal biomass quantification of the four artificially inoculated *Fusarium* species by q-PCR and fungal secondary metabolites quantification in the grains by LC-MS/MS. Under natural infection conditions the fungal complex associated with FHB was predominantly composed of *F. tricinctum*, while *F. culmorum* was the most isolated species under artificial inoculation conditions. Quantitative PCR and LC-MS/MS analyses highlighted differences between the tested barley entries. For example, the lowest levels were detected in the commercial varieties Quench and Rattan, probably because of their late cycle with respect to the others. However, some lines such as SOL 57, SOL 1 and the mixture *mix48* proved to be in some instances not significantly different from Quench variety.

EFFICACY OF *BACILLUS* spp. IN THE CONTROL OF *ASPERGILLUS PARASITICUS* AND AFLATOXINS ON PISTACHIO. F. Siahmoshteh[1], I. Siciliano[2], M. Razzaghi-Abyaneh[3], M.L. Gullino[2,4], D. Spadaro[2,4]. *[1]Department of Food Science and Technology, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran. [2]DISAFA - Dipartimento di Scienze Agrarie, Forestali ed Alimentari, Università degli Studi di Torino, Grugliasco (TO), Italy. [3]Department of Mycology, Pasteur Institute of Iran, Tehran 13164, Iran. [4]Centro di competenza per l'Innovazione in campo agro-ambientale (AGROINNOVA), Università degli Studi di Torino, Grugliasco (TO), Italy. E-mail: davide.spadaro@unito.it*

Pistachio (*Pistacia vera*) has important economic, nutritional and health aspects but it can be contaminated by aflatoxigenic fungi in the field and during storage. Biological control could be considered as an alternative to chemical treatment. Two *Bacillus* spp. were tested *in vitro*, and both strains were able to reduce the mycelial growth and they were able to degrade aflatoxins (AFB1, AFb2, AFG1, and AFG2) during the first three days after inoculation. The cultivar of pistachio 'Ahmad-Aghaei' was the most susceptible to fungal colonization among the four main Iranian cultivars, and was used in this study. *Aspergillus parasiticus* was able to grow and produce aflatoxins on pistachios, but at longer inoculation periods a natural decrease of aflatoxins was registered. The highest reduction for AFB_1 was recorded at eight days after inoculation for both strains (54.9% and 52.5%), anyway both antagonists were able to reduce the fungal incidence and the number of spores on pistachio with a stronger effect during the first five days after inoculation. Both bacterial strains showed good antifungal activity and aflatoxin reduction on pistachio kernels. Altogether, these results indicate that *Bacillus* species could be considered as potential biocontrol agents to reduce the growth of mycotoxigenic fungi and the subsequent aflatoxin contamination of nuts in practice.

ROASTING AND COLD ATMOSPHERIC PLASMA ARE EFFICIENT METHODS FOR AFLATOXIN DECONTAMINATION ON HAZELNUTS. I. Siciliano[1], D. Spadaro[1,2], M.L. Gullino[1,2]. *[1]Università degli Studi di Torino, Centro AGROINNOVA, Largo Braccini 2, 10095 Grugliasco (TO), Italy. [2]Università degli Studi di Torino, DISAFA, Largo Braccini 2, 10095 Grugliasco (TO), Italy. E-mail: ilenia.siciliano@unito.it*

Aflatoxins, produced by *Aspergillus flavus* and *A. parasiticus* are a group of secondary metabolites dangerous to humans and animals that can contaminate different foodstuffs, such as nuts. Food processes, including roasting, may have different effects on mycotoxins, and high temperatures have proven to be very effective in the reduction of mycotoxins. Traditional static hot air roasting and infra-red rays roasting were applied and compared for the detoxification of hazelnuts from aflatoxins. At the temperature of 140°C for 40 min of exposure, detoxification was effective for both roasting techniques, residual aflatoxins were lower than 5%. After roasting, the perisperm was detached from the nuts, residual aflatoxins in the perisperm ranged from 80 up to 100%. Cold atmospheric pressure plasma also has the potential to be a promising method for aflatoxin

detoxification on food. On hazelnuts, with a 1000 W power and 12 min exposure, a reduction in the concentration of total aflatoxins and aflatoxin B_1 of over 70% was obtained. Aflatoxins B_1 and G_1 were more sensitive to plasma treatments compared to aflatoxins B_2 and G_2, respectively. Under plasma treatment, aflatoxin B_1 was more sensitive compared to aflatoxin G_1. The synergistic use of these two treatments along the hazelnut production chain could reduce the health risks associated with the presence of aflatoxins.

DIFFUSION OF BAKANAE DISEASE WITHIN THE RICE FIELD. D. Spadaro[1,2], S. Matić[1], A. Garibaldi[1], M.L. Gullino[1,2]. *[1]Università degli Studi di Torino, Centro AGROINNOVA, Largo Braccini 2, 10095 Grugliasco (TO), Italy. [2]Università degli Studi di Torino, DISAFA, Largo Braccini 2, 10095 Grugliasco (TO), Italy. E-mail: davide.spadaro@unito.it*

Bakanae is a monocyclic disease caused by *Fusarium fujikuroi*. The fungus is easily spread by conidia from the infected plants by wind and water. This study has been carried out to confirm the involvement of the wind in the conidial spread and in Bakanae diffusion in the rice field. A seven-day spore trap was located in the center of a rice field (Vercelli, Northern Italy), sown with local rice lines in order to capture air-borne particles. The rice lines were surrounded by a susceptible rice cultivar, 'Galileo', highly infected with *F. fujikuroi*. Spore monitoring was performed from flowering until harvest on a daily basis. There was no uniform trend in conidial transmission of *F. fujikuroi* during the monitored period by the microscopic observations of the tape, but there was an increase during the flowering and late maturation stage. A slight increase in diffusion of conidia was found at the milky stage of grain maturation, too. A higher occurrence of winds and rains was also registered at flowering and at the end of maturation, compared to the other periods of the monitoring and the previous cultivation seasons, which suggests that wind and rain might participate in conidial transmission of *F. fujikuroi*. In conclusion, the results obtained show that aerial conidial diffusion of *F. fujikuroi* happens, as a consequence of the spread of conidia from the severely infected rice cultivar.

MYCOTOXIGENIC FUNGI AND MYCOTOXINS IN CHESTNUTS AND DERIVATIVES. D. Spadaro[1,2], S. Prencipe[1,2], I. Siciliano[2], A. Garibaldi[1,2], M.L. Gullino[1,2]. *[1]AGROINNOVA, Università di Torino, Largo P. Braccini 2, 10095 Grugliasco, Torino, Italy. [2]DISAFA, Università di Torino, Largo P. Braccini 2, 10095 Grugliasco, Torino, Italy. E-mail: davide.spadaro@unito.it*

Italy is the first chestnut producing country in Europe. Almost 20% of the total production is devoted to industrial processing, including chestnut flour, dried chestnuts and marrons glacés. In postharvest, chestnuts and derivate products can be affected by parasitic fungi, including species of *Penicillium*, agents of green mould, and some species of *Aspergillus*, able to produce mycotoxins, among the others aflatoxins and ochratoxin A. European Commission Regulation 165/2010 establishes the maximum thresholds for aflatoxins in nuts, including chestnuts. Nowadays, the levels of other mycotoxins are not regulated in chestnuts. Aflatoxins are produced by *A. parasiticus* and *A. flavus*. Among the *Penicillium* spp., *P. crustosum* is able to produce ochratoxin A, penitrem A and roquefortine C, *P. expansum* can produce roquefortine C and patulin, while *P. bialowiezense* is able to produce mycophenolic acid. Prevention of contamination by mycotoxigenic fungi represents the most rational and economic strategy to reduce the mycotoxin risk. When prevention is not effective, mycotoxin detoxification can be an alternative to be developed for the chestnut chain.

***FcRav2*, A GENE WITH ROGDI DOMAIN INVOLVED IN FUSARIUM HEAD BLIGHT AND CROWN ROT ON DURUM WHEAT CAUSED BY *FUSARIUM CULMORUM*. F. Spanu[1], B. Scherm[1], I. Camboni[1], V. Balmas[1], G. Pani[1], S. Oufensou[1,2], N. Macciotta[1], M. Pasquali[3], Q. Migheli[1].** *[1]Dipartimento di Agraria, Università degli Studi di Sassari, Via E. De Nicola 9, I - 07100 Sassari, Italy. [2]Laboratoire de Bio-surveillance de l'environnement, Faculté des Sciences de Bizerte, Route de Tunis, 7021 Zarzouna, Université de Carthage. [3]DeFENS-Department of Food Environmental and Nutritional Sciences, Università degli Studi di Milano, Via Celoria 2, 20133 Milano, Italy. E-mail: soufensou@uniss.it*

Fusarium culmorum is a soil-borne fungal pathogen able to cause foot and root rot and Fusarium head blight on small grain cereals, particularly on wheat and barley. It causes significant yield and quality loss and results in the contamination of kernels with type B trichothecene mycotoxins. Knowledge on pathogenicity factors of this fungus is still limited. A transposon tagging approach based on the *mimp1/impala* double component system has allowed us to select a mutant altered in multiple metabolic and morphological processes, trichothecene production and virulence. The flanking regions of *mimp1* were used to seek homologies in the *F. culmorum* genome and revealed that *mimp1* had reinserted within the last exon of a gene encoding a hypothetical protein of 318 amino acids which contains a ROGDI like leucine zipper domain, supposedly playing a protein-protein interaction or a regulatory role. By functional complementation and bioinformatic analysis we characterized the gene as yeast *Rav2* homologue, acknowledging the high level of divergence in multicellular fungi. Deletion of *FcRav2* or its orthologous gene in *F. graminearum* highlighted its ability to influence a number of functions including virulence, trichothecene type B biosynthesis, resistance to azoles and resistance to osmotic and oxidative stress. Our results indicate that the FcRav2 protein (and possibly the RAVE complex on the whole) may become a suitable target for new antifungal drug development or plant-mediated resistance response also in filamentous fungi of agricultural interest.

EU-COST ACTION CA16107 - EUROXANTH: INTEGRATING SCIENCE ON *XANTHOMONADACEAE* FOR INTEGRATED PLANT DISEASE MANAGEMENT IN EUROPE. E. Stefani[1], V. Catara[2], E. Emeriau[3], R. Koebnik[4]. *[1]Università di Modena e Reggio Emilia, Dipartimento di Scienze della Vita, via Amendola 2, 42122 Reggio Emilia (Italy). [2]Università di Catania, Dipartimento di Agricoltura, Alimentazione e Ambiente, via S. Sofia 100, 95123 Catania, Italy. [3]COST Association, Avenue Louise 149, 1050 Bruxelles, Belgium. [4]IRD, Cirad, Université Montpellier, UMR IPME, 911 Avenue Agropolis, 34394 Montpellier, France. E-mail: emilio.stefani@unimore.it*

Bacteria of the family *Xanthomonadaceae*, including species of *Xanthomonas* and *Xylella fastidiosa*, are devastating plant pathogens. Many are quarantine organisms in the EU and their study is of uttermost importance. These pathogens infect all kinds of crop plants. The COST Action CA16107 "EuroXanth" aims at creating an interdisciplinary network in order to develop strategies for sustainably protecting plants and prevent yield losses. COST (European Cooperation in Science and Technology) is a funding agency for research and innovation networks. COST Actions help connect research initiatives and enable scientists to grow and share ideas with their peers. Specifically, this COST Action addresses key aspects of the pathogen-vector-host interactions, from the cellular to the population level. A better insight into population structures and virulence mechanisms of the pathogens, together with the exploration of the molecular mechanisms underlying disease resistance, will enable development of durably resistant plant cultivars and exploitation of bio-control schemes tailored to population