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