

detoxification on food. On hazelnuts, with a 1000 W power and 12 min exposure, a reduction in the concentration of total aflatoxins and aflatoxin B₁ of over 70% was obtained. Aflatoxins B₁ and G₁ were more sensitive to plasma treatments compared to aflatoxins B₂ and G₂, respectively. Under plasma treatment, aflatoxin B₁ was more sensitive compared to aflatoxin G₁. 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. Matic¹, A. Garibaldi¹, M.L. Gullino^{1,2}.

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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. Siciliano², A. Garibaldi^{1,2}, M.L. Gullino^{1,2}. ¹AGROINNOVA, Università di Torino, Largo P. Braccini 2, 10095 Grugliasco, Torino, Italy. ²DISAFA, 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. Spanu¹, B. Scherm¹, I. Camboni¹, V. Balmas¹, G. Pani¹, S. Oufensou^{1,2}, N. Macciotta¹, M. Pasquali³, Q. Migheli¹. ¹Dipartimento di Agraria, Università degli Studi di Sassari, Via E. De Nicola 9, I - 07100 Sassari, Italy. ²Laboratoire de Bio-surveillance de l'environnement, Faculté des Sciences de Bizerte, Route de Tunis, 7021 Zarzouna, Université de Carthage. ³DeFENS-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. Stefani¹, V. Catara², E. Emeriau³, R. Koebnik⁴. ¹Università di Modena e Reggio Emilia, Dipartimento di Scienze della Vita, via Amendola 2, 42122 Reggio Emilia (Italy). ²Università di Catania, Dipartimento di Agricoltura, Alimentazione e Ambiente, via S. Sofia 100, 95123 Catania, Italy. ³COST Association, Avenue Louise 149, 1050 Bruxelles, Belgium. ⁴IRD, 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 utmost 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