

accumulation of *Alternaria* mycotoxins in the kernels. Ninety-two *Alternaria* strains isolated from wheat in Northern Italy were characterized by sequencing portions of the allergen alt1a, glyceraldehyde-3-phosphate dehydrogenase and translation elongation factor 1 $\alpha$  genes, according with a multi-locus gene sequencing approach. The analysis of the combined sequences of the 3 genes resulted in a Maximum Parsimony tree showing 2 well defined groups: *A. infectoria* and *A. alternata*. The *A. infectoria* reference strain clusterized with 8 out of 92 strains tested, while the remaining 84 strains clusterized with *A. alternata*, *A. tenuissima* and *A. arborescens* reference strains. In *A. alternata* group, 4 different clades were defined: Clade A, including 42 strains and both *A. alternata* and *A. tenuissima* reference strains; Clade B including 18 strains and the *A. arborescens* reference strain; Clades C and D, including 12 and 12 strains, respectively. A high level of genetic variability among and within the clades was observed. The capability of the *Alternaria* strains to produce Alternariol (AOH) and Methyl Ether Alternariol (AME) on sterilized rice was evaluated. Eighty-nine strains produced AOH (1-8060  $\mu\text{g/g}$ ), while ninety strains produced AME (1-14340  $\mu\text{g/g}$ ), with a high variability among strains belonging to the same species. On the other hand, a low capability to produce both AOH (mean value 52  $\mu\text{g/g}$ ) and AME (mean value 84  $\mu\text{g/g}$ ), was observed in *A. infectoria* strains.

**64. COMMUNICATING EUROPEAN PROJECTS: A DIFFERENT APPROACH FOR RESEARCH INNOVATION.** A. Masino<sup>1</sup>, A. Bertin<sup>2</sup>, M.L. Gullino<sup>1</sup>. <sup>1</sup>Centro AGROINNOVA, Università di Torino, Italy. <sup>2</sup>SPIN-TO srl, Via Roma 366, Torino, Italy. E-mail: andrea.masino@unito.it

Since 2004 Agroinnova gained a broad expertise in the coordination of complex and multidisciplinary European projects and initiatives in the sustainable agriculture sector. EU projects aim at updating and improving the environmental knowledge of European decision makers and experts, as well as public and students. Moreover, one of the objectives of European Commission Program Horizon 2020 is to bring researchers closer to the public and to increase awareness of research and innovation activities, with a view to supporting the public recognition of researchers. Communication often combines sciences with entertainment, especially when addressing young audience. It can take various forms: educational activities (e.g. summer school and training courses) hands-on experiments and science shows (*European Researchers Night*), debates and conferences (*Raccontare la Salute delle Piante, Incontri Fitoiatrici, Designing the Circular Economy, Open Day*), artistic performance (*EMPHASIS for the Environment*), etc. Agroinnova will focus to keep the following goals in the near future: increasing awareness among the general public of the importance of research and innovation and more favourable general attitude towards its funding; better understanding of the key benefits that research brings to society; reducing in the stereotypes about researchers and their profession. The key to success in communication, as with science and research, is to continue developing skills through focused practice. This extra effort will pay off in the long run.

**65. DEVELOPMENT OF AGROBACTERIUM-MEDIATED TRANSFORMATION OF THE BIOCONTROL AGENT CRYPTOCOCCUS LAURENTII LS28.** C. Miccoli<sup>1</sup>, G. Ianiri, R. Castoria. <sup>1</sup>Università degli Studi del Molise, sede Campobasso, via Francesco De Sanctis, 1 - 86100, Campobasso, Italy. E-mail: castoria@gmail.com

*Penicillium expansum*, the causal agent of blue mold of stored pome fruits, produces patulin, a mycotoxin that contaminates both

fruits attacked by this pathogen and derived products. Infections by *P. expansum* are mainly controlled by using synthetic fungicides, but alternative approaches such as biological and/or integrated control are needed, both for the onset of resistant fungal strains, and the toxicological and environmental risks posed by fungicides. This has recently led EU to require the decrease of chemical input in agriculture (EU Directive 2009/128). Likewise the biocontrol agent (BCA) *Rhodosporidium kratochvilovae* LS11, *Cryptococcus laurentii* LS28 is capable of reducing the incidence of blue mold and to detoxify PAT to less toxic compounds (ascladiol and deoxyapatulinic acid). With the aim of preparing tools to study the mechanisms of action of LS28 at a molecular level, random mutagenesis based on *Agrobacterium tumefaciens*-mediated transformation (AMT) has been developed for this BCA. Different selective markers (auxotrophy for Uracil and resistance to antibiotics) were assessed and Hygromycin-resistant transformants, which harbor *hygR* gene (Hygromycin B Phosphotransferase), were successfully selected. Molecular characterization of these transformants is being carried out. Furthermore, screening of transformants is also in progress for identification of phenotypes of interest through incubation with patulin and with different stressors that are known to affect biocontrol activity of LS28.

**66. CHARACTERIZATION OF ALIVE FUNGAL POPULATION IN WHEAT FLOUR.** S.A. Minutillo, D. Ruano-Rosa, F. Garganese, M.G. Li Destri Nicosia, G.E. Agosteo, L. Schena. Università Mediterranea, Dipartimento di Agraria, località Feo di Vito, 89122 Reggio Calabria, Italy. E-Mail: serena.minutillo@unirc.it

Mycotoxigenic fungi constitute a threat for humans but little is known about their presence in flour, raw material of baked goods. The aim of this work was the characterization of fungal population in wheat flour samples (types "0", "00" and wholemeal) from four mills and one shopping centre (commercial flours). The extent of fungal contamination (expressed in CFU/g of flour) was determined using a conventional plating method and potato dextrose agar as culturing medium. Single representative colonies were identified according to morphological features and by sequencing the ITS regions of the rDNA. Wholemeal flours were found the most contaminated (653-1840 CFU/g) while type "0", on average, showed the lowest values (54-87 CFU/g). Intermediate values were observed for type "00" (87-247 CFU/g). Within each typology, except for the wholemeal one, commercial flours presented values of contamination lower than mill flours. *Penicillium* spp. was the most frequent genus (in all samples) and was particularly abundant in wholemeal flours with 593-1840 CFU/g. *Cladosporium* spp. and *Aspergillus* spp. were found in types "0" and "00" (7-33 and 7-20 CFU/g respectively) but not in wholemeal. The genus *Alternaria* was isolated from all sample (7-47 CFU/g), while *Fusarium* spp. was found in a single sample of type "00" and with a low concentration (7 CFU/g). Other non-identified fungi accounted for an average of 7-73 CFU/g. Data of the present study highlights an abundant presence of alive fungal propagules in wheat flour and a relevant potential threat for consumers since most detected genera are potential mycotoxin producers.

**67. STORAGE UNDER N2 CONTROLLED ATMOSPHERE REDUCES CEREALS GRAIN QUALITY AND QUANTITY LOSSES.** L. Moncini<sup>1</sup>, S. Sarrocco<sup>2</sup>, G. Pachetti<sup>1</sup>, G. Vannacci<sup>2</sup>. <sup>1</sup>Centro Ricerche Strumenti Biotecnici nel settore Agricolo-forestale (CRISBA), c/o ISIS "Leopoldo II di Lorena" Cittadella dello Studente, 58100, Grosseto, Italy. <sup>2</sup>Università degli Studi di Pisa - Dipartimento di Scienze Agrarie, Alimentari e Agro-Ambientali, Plant Pathology