

canopy vigour, and escaping detrimental stress conditions may play a crucial role in the containment of the disorder. Tools for IBS prevention include the varietal choice addressed towards non-sensitive genotypes, the modulation of the external inputs for a more balanced plant development, the anticipation of sowing and maturation or haulm killing practices.

Sequencing of avirulent strains of *Fusarium fujikuroi* contributes to clarify the pathogenicity mechanism on rice

E. Piombo^{1,2}, M. Rosati², M.L. Gullino^{1,2}, D. Spadaro^{1,2}

¹AGROINNOVA – Centre of Competence for the Innovation in the Agro-environmental Sector; University of Turin, Largo Braccini 2, 10095 Grugliasco, TO, Italy; ²Department of Agricultural, Forestry and Food Sciences (DISAFA), University of Turin, Largo Braccini 2, 10095 Grugliasco, TO, Italy. E-mail: davide.spadaro@unito.it

Bakanae, caused by *Fusarium fujikuroi*, is one of the most important diseases of rice. Crop losses are largely depending on climate and rice cultivars, varying from 3% to 75%. The most common symptoms are abnormal height, thin leaves and empty grains, but some strains have been known to induce stunting and withering instead. The induction of elongation has been linked to the production of gibberellins, but the mechanisms of pathogenicity by *F. fujikuroi* are unclear. Despite the high number of *F. fujikuroi* strains deposited in online databases, no genome of proven avirulent strains is available, and no comparative genomics study between virulent and avirulent isolates has been ever conducted. Through pathogenicity trials, we confirm the avirulence of *F. fujikuroi* strain SG4, and the low virulence of strain C2S. Their genomes were sequenced by Illumina MiSeq, and compared to the genome of the virulent strain I1.3. Two methods are used to compare the genomes: gene prediction and SNP calling. Gene prediction is conducted with MAKER, finding 13,527, 14,795 and 14,534 genes for I1.3, SG4 and C2S, respectively. SNP calling is performed using the genome of *F. fujikuroi* strain IMI 58289 as reference. Genes present in I1.3 and not in SG4, as well as genes with putatively impactful polymorphisms in SG4 and not in I1.3, are identified and analysed, producing a set of 13 genes putatively related to pathogenicity in *F. fujikuroi*, many of which are related to plant cell wall degradation.

Search for resistance response to *Zymoseptoria tritici* in wheat landrace from world different areas

S. Pipponzi¹, J. Novi¹, T.C. Marcel², S. Gelisse², M. Maccaferri¹, A. Prodi¹

¹Department of Agricultural Science DISTAL, Alma Mater Studiorum University of Bologna, Viale G. Fanin, 44-46, 40127, Bologna, Italy; ²UMR BIOGER, INRA, AgroParisTech, Université Paris-Saclay, 78850 Thiverval-Grignon, France. E-mail: antonio.prodi@unibo.it

Zymoseptoria tritici is a wheat foliar pathogen causing *Septoria tritici* blotch (STB), the most damaging disease of wheat in Europe, causing yield losses of up to 50%. During the cropping season, *Z. tritici* disseminates over short distances by producing pycnidiospores generated by asexual reproduction. A collection of 175 landraces of *Triticum durum* was gathered from 32 states worldwide. This set was infected with four Mediterranean strains of the fungus isolated from *T. durum* (two of them were isolated in Italy, one in France and one in Tunisia), with the aim of identify some resistant genotypes. The inoculum was spread on the leaf surface and plants were kept at a temperature of 18–20°C and 80% of

humidity. Symptoms evaluation was performed after 20 and 26 days based on the necrotic and sporulating leaf area extension. Consequently, AUDPC values were obtained. A 90K SNP array was performed on the genotypes. Based on the similarity, the accessions were divided into six groups. To each group correspond one well defined geographical area. Taking into account the extension of the sporulating leaf area, it was established that about 10% of the seedling genotypes were resistant to three or four different *Z. tritici* strains. AUDPC values and the groups obtained with a 90KSNP array, the accessions from Greece and Crete. Instead, considering the appear to be the most resistant to all the four *Z. tritici* stains used in the trials.

Production of beneficial microbes with improved properties

A. Pironti¹, R. Marra¹, A. Staropoli^{1,2}, G. Manganiello¹, N. Lombardi¹, F. Vinale^{1,2}, S.L. Woo^{2,3}, M. Lorito^{1,2}

¹University of Naples Federico II, Department of Agricultural Sciences, Via Università 100, 80055 Portici (NA), Italy; ²National Research Council, Institute for Sustainable Plant Protection, Via Università 133, 80055 Portici (NA), Italy; ³University of Naples Federico II, Department of Pharmacy, Via D. Montesano 49, 80131 Naples, Italy. E-mail: angela.pironti@unina.it

The efficient use of biocontrol agents (BCA) and the development of protocols to produce active propagules are fundamental aspects in the establishment of a biological control program. New BCAs may be obtained from suppressive soils or using genetic manipulation techniques, such as transformation, mutagenesis or protoplast fusion (PF). Numerous studies used PF to make intra- and inter-species crosses of *Trichoderma* fungi. In this work we used PF to produce *Trichoderma* hybrids with improved efficacy compared to parental strains in terms of biocontrol ability, production of bioactive metabolites and/or promotion of plant growth. The progeny obtained by recombinant fusion between two *Trichoderma* strains (*T. harzianum* strain M10, *T. virens* strain GV41) was screened by testing biocontrol activity against pathogenic fungi (*Rhizoctonia solani*, *Botrytis cinerea*) and plant growth promotion ability. About 80% of tomato plants treated with the hybrid mixture was not affected by *R. solani* and increased root length compared to control and parentals. Fifty monospore cultures were isolated from the rhizosphere of tomato plants treated with *Trichoderma* hybrid mixture and new strains named A5 and A3 were selected. Metabolomic analysis of hybrids detected compounds that were not found in parental strains liquid cultures. Further characterization of fungal hybrids is in progress.

Isolation, molecular characterization and aflatoxigenic potential of *Aspergillus flavus* strains isolated from corn conserved as silage

S. Prencipe^{1,2}, G.R. Meloni^{1,2}, F. Ferrero¹, G. Borreani¹, M.L. Gullino^{1,2}, D. Spadaro^{1,2}

¹DISAFA - Dipartimento di Scienze Agrarie, Forestali ed Alimentari, Università degli Studi di Torino, Grugliasco (TO), Italy; ²Centro di competenza per l'Innovazione in campo agroambientale (AGROINNOVA), Università degli Studi di Torino, Grugliasco (TO), Italy. E-mail: davide.spadaro@unito.it

The presence of *A. flavus* and aflatoxins (AFs) in corn silage could constitute a problem for human and animal safety. During 2016–2018 an extensive sampling of *Aspergillus* Section *Flavi* from the field, at silos