

incidence and severity of the disease, accumulated loss of fresh mass, firmness, soluble solids content, titratable acidity and ascorbic acid were evaluated. The pressures of 600 and 800 kPa reduced the incidence of the disease by 25% in relation to the control, highlighting the treatments of 600 and 800 kPa that also presented the lowest severity of the disease. There was a tendency to increase ascorbic acid content with increasing applied pressure, signaling the induction of defense compounds in tomatoes.

This work was supported by the São Paulo Research Foundation (FAPESP) (grant 2018/05465-5).

Genome and transcriptome of two strains of *Metschnikowia fructicola* provide new insight on the biocontrol mechanisms against postharvest diseases

E. Piombo¹, N. Sela², M. Wisniewski³, M. Hoffmann⁴, M.L. Gullino^{1,5}, M.W. Allard⁴, E. Levin⁶, D. Spadaro¹, S. Drobny⁶

¹Department of Agricultural, Forestry and Food Sciences (DISAFA), University of Torino, 10095 Grugliasco (TO), Italy; ²Dept. Plant Pathology and Weed Research, ARO, The Volcani Center, Rishon Le-Zion, 7505101, Israel; ³United States Department of Agriculture, Agricultural Research Service (USDA-ARS), Kermersville, WV 254430, USA; ⁴United States Food and Drug Administration (FDA), Division of Microbiology, Office of Regulatory Science, College Park, MD 20740, USA; ⁵Centre for Agro-Environmental Innovation (AGROINNOVA), University of Torino, 10095 Grugliasco (TO), Italy; ⁶Department of Postharvest Science, ARO, the Volcani Center, P. O. Box 15159, Rishon Le-Zion, 7505101, Israel. E-mail: edoardo.piombo@unito.it

The yeast *Metschnikowia fructicola*, the base of a commercial biofungicide, is an efficient biological control agent of postharvest diseases of fruits and vegetables. Several mechanisms of action are exploited by *M. fructicola* to inhibit postharvest pathogens, including the release of iron-binding compounds, the induction of defense signaling genes, the production of cell wall degrading enzymes and high amounts of superoxide anions. The whole genome sequence of two strains of *M. fructicola* was sequenced by PacBio and Illumina sequencing, enabling to obtain a high-quality draft genome of 93 contigs, consisting of approximately 26 Mb. 564,302 homologous single nucleotide polymorphisms (SNPs) were detected by comparing the genomes by SNP calling, suggesting a high intraspecific variability. The genome is exceptionally large when compared with those of closely related organisms, and the most probable cause of this size is a recent whole genome duplication event, especially considering the high rate of homology found among the genes predicted in *M. fructicola* (5,132 out of 8,629 genes have a homolog). The genome was also searched for the CAZyme genes, and 1,145 such putative genes, an exceptionally high number, were identified. A transcriptomic analysis of *M. fructicola* placed in contact with either grapefruit peel tissue or *Penicillium digitatum* revealed a high level of CAZyme genes expression when the yeast was placed in wounded fruit tissue. This assembly represents an extraordinary resource for researchers studying *M. fructicola*, making them able to pursue comparative genomics studies aimed at explaining the biological control activity and the extreme variability of this yeast.

New insights into the infection process of *Fusarium fujikuroi* in rice using a GFP expressing isolate

E. Piombo^{1,2}, L. Campos³, D. Spadaro^{1,2}, M.L. Gullino^{1,2}, B. San Segundo de los Mozos³, A. Infantino⁴, M. Aragona⁴

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; ³Centre for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB Edifici CRAG, Campus UAB, Bellaterra (Cerdanyola del Vallès), 08193 Barcelona, Spain; ⁴Council for Agricultural Research and Economics (CREA), Research Centre for Plant Pathology and Certification, Via Bertero 22, 00156 Rome, Italy. E-mail: maria.aragona@crea.gov.it

Fusarium fujikuroi (teleomorph: *Gibberella fujikuroi*) is the main seed-borne pathogen of rice, causal agent of Bakanae, a disease that in the last years has become of increasing economical concern in many Italian rice-growing areas. A virulent *F. fujikuroi* isolate was tagged with the green fluorescent protein (GFP) gene, using *Agrobacterium tumefaciens*-mediated transformation, and the virulence of the GFP isolate has been confirmed. By using the GFP isolate, fungal development during the *F. fujikuroi*/rice interaction was analysed by LASER scanning confocal microscopy (LSCM). The infection of rice roots was investigated from 24 h to 12 days post-inoculation both in resistant and susceptible cultivars. Roots of resistant genotype seem to trigger a hypersensitive response at the infection site and LSCM analysis of root sections allowed the visualisation of fungal growth within host tissues. Gene expression analysis of genes involved in pathogenesis and hypersensitive response is currently under way, by qPCR on the *F. fujikuroi*-infected rice roots. Analysed genes include chitinases, peroxidases and genes involved in gibberellin synthesis. The knowledge of plant infection and colonization mechanisms, together with the host response, will provide useful information for developing better control strategies of the pathogen and for improving breeding programmes for bakanae resistance.

Molecular identification and characterization of phytoplasmas infecting tomato in Oltrepò pavese (northern Italy)

F. Quaglino, C. Comaschi, P. Casati, A. Passera, P.A. Bianco

Department of Agricultural and Environmental Sciences - Production, Landscape, Agroenergy, Università degli Studi di Milano, Milan, Italy. E-mail: fabio.quaglino@unimi.it

Tomato is affected by economically important phytoplasma diseases, such as stolbur, tomato big bud, tomato yellows, tomato witches'-broom, tomato little leaf, and hoja de perejil. Such diseases, characterized by different geographic distribution patterns, have been associated with eight distinct '*Candidatus* Phytoplasma' species in at least 30 countries throughout the world. In Italy, phytoplasma diseases of tomato were associated with infections by '*Ca. Phytoplasma solani*', '*Ca. Phytoplasma asteris*' and phytoplasmas of taxonomic groups 16SrIII and 16SrV. The present work aimed to investigate the aetiology of a disease affecting tomato in Oltrepò pavese (Lombardy, North Italy). During field surveys, carried out in a tomato plantation in August 2015, symptoms typically associated with phytoplasma infection (leaf purpling, witches'-broom, flower and fruit alterations, and stunting) were observed on tomato