Five trees per experimental plot were chosen in each of seven commercial peach orchards located in Catalonia, NE Spain. Disease monitoring was carried out from March to summer (June-July) 2013 to 2015, by recording the incidence and severity of the disease on fruits. An automatic weather station was located in each plot to record the main environmental data. Accumulated degree-days (ADD) from the blossom biofix were calculated for each orchard. Observations indicated that primary infections were detected at 242.0 ± 13.1 ADD, while last infections were at 483.5 ± 42.2 ADD (mean ± standard error, n = 15). Disease progress followed a clear sigmoidal trend, and Beta-regression equations between disease incidence on fruits and ADD were successfully fitted using Bayesian inference with Integrated Nested Laplace Approximation. The model showed good performance when validated against independent data. This preliminary research is a first step towards a decision support system based on epidemiological modelling for the integrated management of peach powdery mildew in Catalonia.

Huanglongbing epidemiology in Brazilian orchards. K. PAZOLINI, J.H. ARRUDA, G.A. CHINELATO, A. BERGAMIN FILHO, J. BELASQUE JUNIOR. *Luiz de Queiroz College of Agriculture, University of São Paulo, Av. Pádua Dias, 11 – Piracicaba, Brazil. E-mail: pazolinikelly@gmail.com*

Huanglongbing (HLB) (caused by 'Candidatus liberibacter spp.') is the main citrus disease worldwide. There are still no viable curative measures or varieties with genetic resistance to HLB. Recommended disease management is the use of healthy seedlings, eradication of symptomatic trees and chemical control of the vector, *Diaphorina citri*. Our aim was to understand the temporal and spatial progress of HLB in an area, with strict management of disease in Brazilian orchards. Temporal (logistic and Gompertz) and spatial (exponential and power law) models were tested, by non-linear regression to orchard data (177 plots for temporal, 12 plots for spatial analyses),

on a single farm in São Paulo state. The management of HLB in this property was carried out with four or more inspections per year, for eradication of symptomatic trees and weekly or biweekly sprays with insecticides for vector control. For temporal analyses, the logistic model was adjusted ($P < 0.05$) to 115 of the 177 plots studied (progress rates of 0.2 to 1.5), while the Gompertz model was adjusted to only 29 plots (progress rates from 0.2 to 0.5). For spatial analysis, both models presented a good fit to the 12 plots studied. However, the model inverse power law presented the best residual pattern and greater R^2 (0.91) than the exponential model ($R^2 = 0.88$). The progress of HLB with time was best described by the logistic, and in space by the inverse power model.

Microbiomes and their roles in plant health

New *Pseudomonas* strains from olive rhizospheres as effective biocontrol agents against *Verticillium dahliae*. C. GÓMEZ-LAMA CABANÁS[1], G. LEGARDA[2], D. RUANO-ROSA[1], P. PIZARRO-TOBÍAS[3], A. VALVERDE CORREDOR[1], J.L. NIQUI[3], J.C. TRIVIÑO[2], A. ROCA[3], J. MERCADO-BLANCO[1]. *[1]Department of Crop Protection, Institute for Sustainable Agriculture (CSIC), Avenida Menéndez Pidal s/n Campus 'Alameda del Obispo', 14004 Córdoba, Spain. [2]Bioinformatics Department, Sistemas Genómicos Ltd, Valencia, Spain. [3]Bio-Ilíberis Research and Development SL, Granada, Spain. E-mail: cgomezlama@gmail.com*

Previous studies have demonstrated that rhizospheres of nursery-produced olive (*Olea europaea* L.) plants are sources of bacteria with potential as biological control agents (BCA) of Verticillium wilt of olive (VWO), caused by *Verticillium dahliae.* A collection of 189 bacterial isolates from healthy olive (cv. Picual) plants was generated, based on different morphological and biochemical characteristics and *in vitro* antagonistic activity against several olive pathogens. Three strains (PIC25, PIC105 and PICF141) showing the greatest potential as BCAs, particularly against *V. dahliae*, were eventually selected. These were further tested for nutritional requirements and chemical sensitivities. Their effectiveness against VWO

caused by the defoliating pathotype of *V. dahliae* was also demonstrated. Genotypic and phenotypic traits traditionally associated with plant growth promotion and/or biocontrol abilities were evaluated (e.g. phytase, xylanase, and glucanase activities, and siderophore and HCN production). Phylogenetic analysis revealed that the strains belonged to the *Pseudomonas* genus. Strain PICF141 was affiliated to the 'P. mandelii subgroup', with *P. lini* as the closest species. Strains PIC25 and PIC105 were affiliated to the 'P. aeruginosa group', *P. indica* being the closest species. Strain PIC105 was identified as *P. indica*, this being the first reort of the species as a potential BCA. Sequencing and *in silico* analyses of the genomes of these strains enabled the identification of traits involved in plant-bacteria interactions. Seed adhesion and root colonization abilities of the novel BCA were also assessed, providing valuable information for the development of future bioformulations based on these rhizobacteria.

New bacterial antagonists for the biocontrol of fire blight caused by *Erwinia amylovora*.
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The biocontrol effectiveness of antagonistic bacteria against fire blight (caused by *Erwinia amylovora*) was evaluated under *in vitro* and field conditions. Among 61 bacteria isolated from soil and flowers of fire blight host plants from different Moroccan areas, 20 isolates showed antagonistic activity against the pathogen during agar-diffusion-tests, attached blossoms assays and in a bioassay on immature pear fruits. Effective isolates were identified using biochemical tests and 16S rDNA gene sequencing. These isolates

were grouped into the following genera: *Alcaligenes* (ACBC1), *Bacillus* (CPa12, CPa2, HF6, JB2, LMR2, SF14, SF16, SP10, SP13, SP18), *Brevibacterium* (SF3, SF4, SF7, SF15), *Pantoea* (ACBC2, ACBP1, ACBP2), *Pseudomonas* (SP9), *and Serratia* (HC4). The isolates were reported in the NCBI nucleotide sequence database (GenBank) under the accession numbers from KY357285 to KY357304. In a field assay with susceptible apple varieties, spray treatments were carried out with different bacterial antagonists. Their efficacies were evaluated 15 d post-inoculation on blossoms, and ranged from 55 to 95% for 11 strains. Most strains gave efficacies that were better than that obtained with commercial bacterial strains P10c (66%) and QST713 (63%). The strains showed no pathogenicity towards plant tissue (pear fruitlets, pear and apple blossoms, and tobacco leaves), and are, therefore, considered as potential candidates to as microbial biocontrol formulations for fire blight control.

Qualitative and quantitative impacts of *Bactrocera oleae* on the fungal microbiota of ripe olive drupes.
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The olive fly, *Bactrocera oleae,* is a major key pest of olive drupes, greatly affecting quality and quantity of olive oil production. Fungus species associated with olive drupes can also have important impacts on olive production. However, little is currently known about the interaction between olive fly and fungi. Ripe olive drupes of three olive varieties, either with or without olive fly infestations, were collected in southern Italy. These were pitted and total DNA was extracted and analyzed using real-time quantitative PCR (qPCR) and metabarcoding based on Illumina MiSeq sequencing. Both analyses were performed using fungal universal primers targeting the ITS2 region of the rDNA. QPCR analyses enabled the quantification of the total fungal DNA, and revealed