

striction enzymes (*AseI* and *HpyCH4V*). In addition, the ITS1 region of 94 isolates was sequenced to substantiate results. Seven previously reported microsatellite markers were used for genotyping all 516 *P. viticola* isolates. Results obtained from CAPS analysis and ITS1 sequencing suggest that the population of *P. viticola* in São Paulo State may be a single cryptic species, *P. viticola* clade *aestivalis*. Twenty-three alleles and 55 multilocus genotypes (MLGs) were observed among the 516 isolates. Half of the MLGs observed were clonal, and four dominant MLGs represented 66% of the observed genotypes. Most populations showed significant linkage disequilibrium, and excess of heterozygosity was verified in many loci. Principal coordinate analysis revealed no clusters among populations. No significant isolation by distance was found, suggesting high levels of gene flow. These results demonstrate that epidemics result from multiple clonal infections caused by a few genotypes, and that asexual reproduction predominates for *P. viticola* in São Paulo, Brazil.

This research was supported by the São Paulo Research Foundation (FAPESP Project 2015/26106-5) and the University of Georgia.

**Development and verification of a dynamic model for predicting olive scab development.** J. ROMERO<sup>1</sup>, L.F. ROCA<sup>1</sup>, C. AGUSTI-BRISACH<sup>1</sup>, E. GONZALEZ-DOMINGUEZ<sup>2</sup>, V. ROSSI<sup>2</sup>, A. TRAPERO<sup>1</sup>. <sup>1</sup>Departamento de Agronomía, Universidad de Córdoba, Campus de Rabanales, Edif. C4, 14071 Córdoba, Spain. <sup>2</sup>Istituto di Entomologia e Patologia vegetale, Università Cattolica S. Cuore, Via E. Parmense 84, 29100 Piacenza, Italy. E-mail: joaquinromrod@gmail.com

Olive scab, caused by *Venturia oleaginea*, is the main olive leaf disease worldwide. Traditionally, chemical control of this disease was based on a fixed schedule of fungicide applications, mainly using copper products. However, integrated pest management (IPM) should be implemented to rationalize fungicide treatments. A mechanistic model to predict risk of infection and olive scab epidemics was developed, according to the system analyses, and implemented in a computerized system. Hourly data of air temperature, rainfall and relative humidity were used to produce daily olive scab predictions as outputs. Simulations are based on sub-processes of conidial

production and dispersal, infection and latent period (i.e., the state variables). Mathematical equations that relate state variables (i.e., the driving variables) were developed using published data on *V. oleaginea*. The model was able to represent the real system, and assisted understanding of olive scab epidemics in four olive-growing areas, traditionally considered as having different favourable conditions for olive scab development. Model outputs for these areas were generated, agreeing with traditional knowledge. Based on the model outputs, different strategies of fungicide treatments can be suggested in each growing area, reducing the amount of fungicide applied. Weaknesses of the model are discussed, and additional research is advisable. However, this model could be useful for implementing an IPM approach. This is the first olive scab model based on the biological knowledge of the disease. Other disease models will soon be added to complete a decision support system for the main aerial diseases in olive groves.

This research was supported by the project “Validación del modelo epidémico Repilos” funded by the Bayer Crop Science. Carlos AGUSTÍ-BRISACH is the holder of a ‘Juan de la Cierva-Formación’ fellowship from MINECO.

**Epidemiology of peach powdery mildew (*Podosphaera pannosa*) in Catalonia, Spain: towards a degree-day model to initiate fungicide spray programmes.** N. MARIMON<sup>1</sup>, J. LUQUE<sup>1</sup>, J. MARTÍNEZ-MINAYA<sup>2</sup>, D. CONESA<sup>2</sup>, A. VICENT<sup>3</sup>. <sup>1</sup>Patologia Vegetal, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Carretera de Cabrils km 2, 08348 Cabrils, Spain. <sup>2</sup>Departament d’Estadística i Investigació Operativa, Universitat de València, 46100 Burjassot, Spain. <sup>3</sup>Centro de Producción Vegetal y Biotecnología, Instituto Valenciano de Investigaciones Agrarias (IVIA), 46113 Moncada, Spain. E-mail: neus.marimon@irta.cat

Powdery mildew of peach (caused by *Podosphaera pannosa*) is a common disease in Spain where these fruit trees are grown. The disease is usually managed by calendar-based fungicide spray programmes, commencing at the petal fall host stage. This study monitored powdery mildew progress in untreated trees, in order to: 1) describe overall disease progress in relation to a degree-day scale starting at 50% blossom; and 2) establish a degree-day threshold for the detection of primary infections and thus initiate a more rational weather-based fungicide programme.

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  $242.0 \pm 13.1$  ADD, while last infections were at  $483.5 \pm 42.2$  ADD (mean  $\pm$  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.

This research was supported by projects RTA2013-00004-C03-00 (INIA, Spain), MTM2016-77501-P (Ministry of Economy and Competitiveness, Spain) and VALi+d ACIF/2016/455 (Generalitat Valenciana), and the European Regional Development Fund (ERDF). The first author was supported by a predoctoral grant by INIA, Spain.

**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.

This research was supported by the projects 2016/01796-1(FAPESP) and 161090/2015-0 (CNPq).

## Microbiomes and their roles in plant health

**New *Pseudomonas* strains from olive rhizospheres as effective biocontrol agents against *Verticillium dahliae*.** C. GÓMEZ-LAMA CABANÁS<sup>1</sup>, G. LEGARDA<sup>2</sup>, D. RUANO-ROSA<sup>1</sup>, P. PIZARRO-TOBIÁS<sup>3</sup>, A. VALVERDE CORREDOR<sup>1</sup>, J.L. NIQUÍ<sup>3</sup>, J.C. TRIVIÑO<sup>2</sup>, A. ROCA<sup>3</sup>, J. MERCADO-BLANCO<sup>1</sup>. <sup>1</sup>Department of Crop Protection, Institute for Sustainable Agriculture (CSIC), Avenida Menéndez Pidal s/n Campus 'Alameda del Obispo', 14004 Córdoba, Spain. <sup>2</sup>Bioinformatics Department, Sistemas Genómicos Ltd, Valencia, Spain. <sup>3</sup>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