

Anticipating and understanding new *Xylella fastidiosa* epidemics across European landscapes; insights from remote sensing and network analysis

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Europe's major *X. fastidiosa* outbreaks have progressed steadily in the past years as data on the bacterial strains causing them, and on the host range and vectors of the pathogen in various regions, became available. The initial uncertainty around these critical epidemiological aspects of the *X. fastidiosa* invasions hampered estimates of their rate and reach should eradication or containment efforts fail. We explored whether network analysis could help circumvent known knowledge gaps in *X. fastidiosa* epidemiology; Relying only on distribution maps of a known host plant (>60 000 olive groves), and the dispersal abilities of a putative vector, we gained network-based insights into the effort required for eradication or containment of the pathogen in southern Italy, and into opportunities to optimize pest management efforts at the landscapes scale. Early detection of new foci play a critical role in ensuring such efforts are efficient. Hyperspectral and thermal remote sensing, at spatial resolutions fine enough to delineate tree crowns, provide estimates of several plant functional traits in individual trees. After coordinated aircraft and field campaigns, we found that based on these traits, olive trees with *X. fastidiosa* infection symptoms can be detected and mapped with >80% accuracy. Furthermore, we found strong evidence that they, in some cases, allow the identification of *X. fastidiosa* affected trees weeks to months before they developed visible symptoms.

Analyzing the expression of *Candidatus Liberibacter solanacearum* effectors in insect and plant hosts

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Candidatus Liberibacter solanacearum (Lso), the causal agent of Zebra Chip disease, is an emerging pathogen causing significant crop losses in Solanaceous plants. There are no commercial cultivars with resistance to Zebra Chip, making disease management difficult. Lso haplotypes A and B are transmitted by the psyllid vector *Bactericera cockerelli* and infect the phloem of tomato and potato. Many bacterial pathogens secrete effectors to manipulate and establish in their hosts. Genome analyses revealed the presence of the SEC secretion system in Lso. We utilized available genome sequences to predict conserved SEC-dependent effectors from haplotype A (R1, Lso-NZ1, HenneA), haplotype B (CLso-Z1), and haplotype C (FIN111, FIN114). Effectors were predicted according to the presence of the secretory signal peptide using SignalP 3.0 and 4.0, proteins smaller than 25 KDa without a transmembrane domain were selected and manually verified. We identified a suite of core effectors present in haplotypes infecting tomato and potato. The expression of core Lso effectors was analyzed in plant and insect hosts by qPCR, identifying those that are preferentially expressed in either organism. Lso effector expression patterns could be used to predict the role of individual proteins in colonizing the insect vector and plant host. A greater understanding of how phloem-limited bacterial pathogens interact with their hosts can ultimately be used to develop targeted disease control strategies.

Dream big: Solid state/LED lighting will allow you to affect pathogen biology in ways that you never could before

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Plants and pathogens coevolved over millions of years in an environment of 24 hr cycles of natural sunlight during day, and near-complete darkness at night. By comparison, horticultural uses of electric lighting span a mere instant of evolutionary time: less than 100 yr. High Pressure Sodium (HPS) represents the most common electric lighting source used for enhanced plant growth today, but Light Emitting Diode (LED) technologies have been developed to the point where they are durable and energy efficient, albeit at a 2- to 6-fold higher purchase price. An under-exploited benefit of LEDs is their ability to be precisely controlled in terms of spectrum, amount, duration, timing, and distribution for the purpose of suppressing plant pathogens, while still providing enhanced plant growth. LEDs make possible the strategic control of the lighting environment to attack photoregulatory pathways of pathogens, and thereby disrupt pathogenesis. A number of examples will be presented, encompassing suppression of downy mildews, disruption of circadian rhythms, stimulation of inoculum release during environmentally unfavorable periods, effects of selected wavelengths on the sporulation process, and potential effects of counter-phasing of different spectra. The unique physical and electromechanical attributes of LED systems as they relate to these potential uses, their limitations, and directions for future research will be discussed.

An effector from the Huanglongbing-associated bacterium targets a specific family of proteases in citrus

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The citrus industry continues to be threatened by Huanglongbing (HLB) disease. All citrus cultivars can be affected by the HLB-associated bacterium, *Candidatus Liberibacter asiaticus* (CLAs), and effective management strategies are still needed. Insect-transmitted and phloem-colonizing pathogens, like CLAs, utilize the general Sec secretion system to deliver virulence proteins into the host. These proteins can aid infection by manipulating plant physiology and subverting host immunity, thereby promoting bacterial colonization and disease progression. We investigated the virulence function of a CLAs effector, Sec-delivered effector 1 (SDE1), which is conserved among all CLAs isolates. SDE1 has ~10-folds higher expression in plant hosts compared to the insect vector, implicating a possible role in HLB progression. Using yeast two-hybrid screening, we found that SDE1 directly interacts with several members belonging to a specific family of proteases, known as papain-like cysteine proteases (PLCPs). PLCPs in other pathosystems have been shown to contribute to plant defense against pathogens including bacteria, fungi and *Phytophthora*. Interestingly, all these different pathogens produce effectors to inhibit PLCP activity and promote infection. We found that SDE1 also inhibits the protease activity of PLCPs *in vitro* and in citrus. Using a surrogate system, we further showed that SDE1 can promote bacterial infection. These findings support a model that SDE1 acts as a PLCP inhibitor in order to suppress immune response in citrus and promote CLAs infection. We will discuss ongoing progress on the characterization of SDE1 and the potential of exploiting SDE1-PLCP interaction for the development of HLB management.

Grapevine and Fungal Trunk Pathogens Interactions and the Global Impacts of Climatic Events

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Grapevine trunk diseases (GTDs) represent one of the most important problems for viticulture worldwide. Characterizing the impact of GTDs on grapevine physiology is a key step to understanding the mechanisms that lead to disease development and symptoms expression, which will assist in the development of effective control strategies against GTDs. For GTD-affected vines, carbon metabolism seems to be strongly altered associated with an