

same isolates after acquiring resistance were identified and further analyzed. The second objective was to investigate if there is a regulatory epigenetic process, such as small non-coding RNAs or chromatin remodeling, mediating this mechanism. This study will narrow-down all possible hypotheses and generate new questions that might contribute to the comprehension of epigenetic and molecular processes of this pathogen.

Catch my drift? Inoculum detection as a decision aid for agricultural systems

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Regional spread of diseases has been traditionally monitored by and communicated between growers, and continues to be monitored by extension specialists, crop consultants, and through formal, nationwide scouting programs. As technology continues to improve and become accessible, so too does our ability to sample for and detect airborne pathogens. Airborne inoculum sampling is now being commercially used to initiate and time fungicide applications in grape powdery mildew management in the Western United States, and similar methods have been developed for diseases in other crops. In addition to using inoculum detection for fungicide applications, inoculum sampling methods can be used to develop more accurate epidemiological models, to rapidly sample for pesticide-resistant pathogen populations, or assess mycotoxin production potential of airborne inoculum. These tools are shifting crop management to targeted approaches that improve disease management and reduce costs to producers.

Central role of dsRNA in the elicitation of antiviral defenses in plants

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Plant viruses rely on macromolecular assembly and transport pathways for replication and for targeting the plasmodesmata (PD) for cell-to-cell movement. Our team investigates these processes in the context of plant defence responses and is interested to identify mechanisms leading to disease. We showed that mutants affected in the pathogen-recognition receptor (PRR) co-receptor kinase BAK1/SERK3 exhibit increased susceptibility to different RNA viruses, thus indicating a role of pattern-triggered immunity (PTI) in antiviral defense. Interestingly, Arabidopsis plants responded to crude extracts from virus-infected plants, but not to purified virions, showing that the molecules that elicit the antiviral PTI response are produced by the infected cell. Infection by RNA viruses is generally associated with the occurrence of double-stranded (ds)RNAs. Accordingly, we found that PTI is elicited by dsRNA. The application of dsRNAs and the synthetic dsRNA analog poly(I:C) to Arabidopsis plants induces typical PTI responses, including the activation of MPK6 and MPK3, ethylene synthesis and defense gene expression. Moreover, poly(I:C) treatment induces seedling growth inhibition, a phenotype associated with the activation of plant immunity. Consistent with the hypothesis that dsRNAs are perceived as viral pathogen-associated molecular patterns (PAMPs) in plants, dsRNA treatment can protect plants against virus infection. The PTI responses were not impaired in plants lacking dicer-like (DCL) proteins indicating that DCLs do not serve as the dsRNA receptors leading to PTI. The dsRNA receptors involved in the triggering of PTI as well as the downstream mechanisms that restrict virus infection may be identified by future studies.

Metagenomic analysis of the aerial mycobiome of rice paddies

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Airborne microbiome represent a new fascinating topic that has been understudied in comparison with the microbiota present in other environments. Only a small fraction of the organisms in the atmosphere can be studied using traditional culture-based methods. In this study, the aerial composition of fungi in a rice paddy has been examined along the crop production cycle (from June to September) using a targeted DNA-based method (qPCR) to target *Magnaporthe oryzae* and *Cochliobolus miyabeanus* and by high throughput sequencing (HTS) targeting the ITS region. Alpha diversity analysis at the beginning of the trial (June) showed a higher level of complexity than at the end of the trial as well as a higher number of operational taxonomic units (OTUs) that decreased over time. The main taxa identified by HTS where the relative abundance drove the cluster separation as a function of the time and temperature were *Alternaria*, *Magnaporthe*, *Cochliobolus*, *Aspergillus*, *Penicillium* and *Myrothecium*. In parallel, oligotyping analysis on the main OTUs was performed to obtain a sub-OTU identification. The results revealed the presence of several characteristic oligotypes associated with meteorological conditions. In addition, a selective pressure in function of temperature on the air mycobiota composition was clearly evidenced. Indeed, changes in temperature level can drastically affect the mycobiota community structure, with a possible impact on the disease development in rice.

Spatial and compositional diversity in the microbiota of harvested fruits: What can it tell us about biological control of postharvest diseases

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Accumulating evidence indicates that the composition of the microbiota inhabiting an organism (both endo- and epiphytically) can have a profound effect on host physiology and defense responses. The role of the microbiota in plant health and physiology, however, is poorly understood, and few studies have focused on temperate fruit trees. A global effort is underway to characterize the endophytic and epiphytic microbiome of apple fruit with the goal of developing a microbial consortium for the management of a wide range of postharvest diseases, and potentially physiological disorders. Spatial studies of the microbiota of apple peel, calyx-end, stem-end, and wounds tissues have revealed distinct compositional differences, as well as differences between organic and conventional management systems. Other studies have indicated a distinct genotype effect on defining the endophytic microbiota in apple shoots. These data suggest that apple pedigree influences the composition of the endophytic microbiota and that the host and microbiome have co-evolved to some extent, as suggested in the holobiont concept. The effect of postharvest processes, such as waxing and storage, on the apple fruit microbiome will be presented, as well as a global analysis of the apple fruit microbiome. The implications of greater knowledge of the apple microbiome on disease and cultural management strategies, cultivar breeding, and abiotic stress resistance, will be discussed.

Ecology and evolution of oomycete communities in response to soybean seed treatments

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Soil conservation efforts combined with earlier planting dates has led to increased crop residue and cooler soil at planting. This exposes seeds and developing seedlings to adverse conditions for extended periods of time. To gain a better understanding of soybean seed treatments as oomycete community filters, culture based techniques, evolutionary analysis and genetics are utilized. A high-throughput assay was developed and applied to evaluate the fungicide sensitivity of 81 oomycete species across ten clades to ethaboxam and mefenoxam. Species within three separate *Pythium* clades all had reduced sensitivity to ethaboxam, suggesting that reduced sensitivity to ethaboxam is inherent and possibly related phylogenetically. Therefore,