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Genome-wide signature of adaptation in a recently introduced pathogen

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First detection and pathogenicity of *Rhizoctinia solani* AG-1 IA on peanut in Arkansas

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In 2012, symptoms typical of Aerial blight were observed on peanut in a field in Arkansas. Leaves in the lower canopy had water soaked, grayish green lesions or tan to brown lesions. Localized mats of leaves and mycelium collected on stems and threads of hyphae spread along stems to adjacent leaves. Dark brown sclerotia (1.5 - 4 mm) were attached to the surface of infected peanut tissue. Isolations from surface-disinfected leaves consistently yielded light brown to brown colonies with sclerotia typical of *Rhizoctonia solani* AG-1 IA. The fungus was identified to be *R. solani* AG-1 IA based on hyphal anastomosis group reactions. Koch's postulate was successfully completed in a greenhouse experiment on five peanut cultivars. Only leaves, petioles, and were infected whereas stems were visually non-affected. In a detached leaflet assay, larger ($P = 0.05$) brown lesions developed on cv. Flavor Runner 458 than GA09B, FL07, FloRun107, and Red River Runner. Although *R. solani* AG-1 IA is an important pathogen on rice and soybean in the state, to our knowledge this is the first report of Aerial blight of peanut in Arkansas. Currently, there is a renewed interest in peanut production in the state and production practices include irrigation and various rotation schemes with soybean and less frequently rice, which can potentially increase inoculum for the subsequent crop. Thus, this may be an important disease of peanut in Arkansas.

Controlling soilborne pathogens using *Trichoderma*: The Integrated Pest Management Innovation Lab's work in Bangladesh, India, and Indonesia

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Microbial biopesticides are used for the biological control of insect pests, plant pathogens, and weeds. One such bioagent, *Trichoderma*, a naturally occurring fungus in agricultural and forest soils, is used by biological control programs in seed treatments, in foliar sprays, in compost, and as tricholeachates. This inexpensive, environmentally-friendly bioagent and its common species *T. harzianum* and *T. viridae* have been promoted by the Integrated Pest Management Innovation Lab (IPM IL) as part of its IPM packages to control diseases in cucurbits, cabbage, eggplant, onion, and tomato in Bangladesh, India, and Indonesia. *Trichoderma* offers an alternative to expensive and often toxic pesticides, and farmers have seen significant increases in yield and income when using it. Because of this success, the IPM IL is now scaling up *Trichoderma* adoption through collaboration with NGOs, the private sector, and host country institutions in program countries.

IPM Innovation Lab successful delivery of IPM technologies in the developing world: Capacity building through long- and short-term training

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Research and implementation of Integrated Pest Management (IPM) strategies in developing countries is limited by the lack of effective technology dissemination programs, strategies, and infrastructure. The IPM Innovation Lab (IPM IL, formerly the IPM Collaborative Research Support Program or IPM CRSP) has been very successful in delivering tailored, farmer-friendly, cost-effective, environmentally and ecologically sound, and gender-sensitive IPM technologies through long- and short-term capacity building programs. These programs are integral parts of the IPM IL mission and goals. The IPM IL trains local practitioners, project managers, and farmers on how to use and adopt IPM technologies through long-term training such as internships and undergraduate and graduate academic and professional degrees. Short-term training focuses on designing and implementing IPM packages, holistic suites of IPM recommendations for specific crops, in the pre-planning phase, during field implementation, and throughout the dissemination phase of the programs. The IPM IL recognizes the importance of bridging gaps between research scientists, technicians, field agents, extension agents, farmers, and other stakeholders in order to successfully deliver and disseminate IPM packages and promote their adoption.

Genome-wide signature of adaptation in a recently introduced pathogen

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Introduction success of a new plant pathogen involves adaptive processes to its novel habitat. Such local adaptation processes are influenced by the interplay of demographic effects and selective forces. The Eurasian poplar leaf rust *M. larici-populina* is responsible for severe damage in European poplar cultivation. Outbreak of this fungus in North-America was first reported in early 1990. Since then the pathogen appears to have become well established, infecting new host species such as balsam poplars. To obtain a comprehensive picture of the evolutionary changes involved in the adaptation of this rust to its new environment, we sequenced 44 strains from the source and the introduced populations and mapped the reads onto the *M. larici-populina* reference genome. Our objectives were to reconstruct the history of the introduction and then the evolutionary history of alleles under selection. Genome-wide distribution of polymorphisms displayed the signature of a severe founder event into the North-American population. We then developed a model-based approach with a subsample of 22K SNPs to infer the null-demographic parameters. Finally, in a genomic scan of the four largest scaffolds, we found 32 regions having a strong divergence between the two populations. These regions include 14 secreted protein-coding genes that are candidate for adaptation; this hypothesis will be tested by conducting coalescent simulations based on the demographic model previously inferred.

Examination of molecular diversity of the spinach downy mildew pathogen *Peronospora farinosa* f. sp. *spinaciae* with SSRs

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Downy mildew is the most economically important disease of spinach. This disease is caused by the obligate oomycete pathogen *Peronospora farinosa* f. sp. *spinaciae* (*Pfs*). More than ten new races and multiple novel strains of *Pfs* have been identified during the last two decades. Examination of the molecular diversity among these races or isolates of *Pfs* may provide insights as to the evolution and molecular identification of the pathogen. Based on the genome sequence of *Pfs* isolate UA0510C sequenced with Illumina technology, 48 pairs of SSR primers were designed from sequences confirmed as oomycete sequences in Genbank. These primers were tested on 6 *Pfs* races (Race 6, 10, 11, 12, 13 and 14), 3 novel strains (UA4711, UA1012B and UA1312) and three other oomycete pathogens, including the spinach white rust pathogen *Albugo occidentalis* (*Ao*), the Swiss chard downy mildew pathogen *Peronospora farinosa* f. sp. *betae* (*Pfb*), and the quinoa downy mildew pathogen *Peronospora variabilis* (*Pv*). All 48 primers could amplify fragments from *Pfs*. Four primers could amplify the DNA from the other three pathogens, and a few primers could amplify DNA from *Pfb* and/or *Ao*. The majority of the primers were *Pfs* specific. Thirty-two of the 48 pairs of primers were polymorphic among the *Pfs* isolates tested. Heterozygous alleles were observed in some isolates when amplified with a few primers. A robust molecular marker system is being developed for *Pfs*.

A novel recombinant of *Bean common mosaic virus*

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Bean common mosaic virus (BCMV) exists as a complex of strains distinguished based on reactions towards seven resistance genes known in common beans; at least seven BCMV pathotypes have been identified. In order to understand the genetic determinants of pathogenicity for BCMV, the whole genome was cloned and sequenced for the BCMV strain US10 which belongs to pathotype VII. This sequence was compared to a recently characterized isolate of BCMV, RU1-OR, which also displays the same pathotype VII. Inspection of the nucleotide sequences for BCMV RU1-OR and US10, and two closely related sequences BCMV RU1-D and RU1-W (both pathotype VI) revealed that BCMV RU1 isolates originated through a series of recombination events between US10 and a yet unknown parental genome, resulting in changes in virus pathology. The data obtained suggest that a fragment of the US10 genome in the P1 region may be involved in its ability to overcome the BCMV resistance in beans conferred by the *bc-2²* gene.

QTL mapping of resistance to stripe rust in spring wheat PI 182103

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Wheat stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is an important wheat disease worldwide. Seeking new genes is essential for developing wheat cultivars resistant to the disease. PI 182103, a spring wheat originally from Pakistan, showed high stripe rust resistance for many years in the field