silenced soybean leaves also produced less ROS after rust inoculation when stained with 3,3'-diaminobenzidine (DAB). These results indicate a direct function of PR10 in conferring ASR resistance possibly through enhancing the production of ROS at the site of rust infection.

Bacillus amyloliquefaciens **strains in the management of** ***Cercospora*** **leafspot of lettuce in Trinidad**

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Lettuce (*Lactuca sativa*) is a vegetable crop that is favoured and highly demanded in many cultures around the world and mostly consumed fresh. It is a short crop, meaning, most varieties are harvested within 4–5 weeks after transplant. According to the United States Department of Agriculture (2016), the value of utilized lettuce in 2016 amounted to near $2 billion in the United States alone, falling second to tomatoes. Within recent times, there has been a growing concern over the use of pesticides and the impact they have on human health and the environment. In Trinidad, the fungal leafspot of lettuce caused by *Cercospora lactucae-sativae* is a growing concern as the disease severely affects the quality and reduces yield of the crop forcing farmers to resort to the only known remedy of chemical treatment. This research explored the potential of growth and biocontrol efficacy of indigenous *Bacillus* strains isolated from rhizosphere soils against leafspot disease. Preliminary research has showed the antagonistic potential of *Bacillus amyloliquefaciens* to inhibit the fungal pathogen by up to 74% *in-vitro* and boost the seedling growth (leaf area) by about 300%. The PCR analysis of antibiotic lipopeptides genes *viz.*, Iturin, Bacillomycin, Bacilysin, Fengycin, Surfactin and Zwittermycin in those *B. amyloliquefaciens* strains were positive. *Bacillus* species which did not show positive for any of the lipopetides resulted in little or no inhibition, indicating that the antibiotic genes contributed significantly to inhibitory properties of the *B. amyloliquefaciens*. Further testing of the antagonistic *B. amyloliquefaciens* strains under protected and field settings is required to understand the biocontrol efficacy against leaf spot disease in lettuce.

Quantitative resistance to bacterial pathogens of rice

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Disease resistance is the foundation for managing many plant diseases, because resistant varieties have the strongest impact with minimal environmental effects or cost. Consequently, sources of broad-spectrum resistance (BSR), or resistance that is effective against multiple and/or diverse pathogens is of particular interest. However, achieving BSR depends on having effective resistance sources to introgress into elite germplasm. Multi-parent Advanced Generation Inter-Cross (MAGIC) populations are powerful tools for identifying resistance because they have high levels of recombination and enhanced resolution relative to biparental populations. We screened an indica rice MAGIC population developed from eight elite founders for BSR to diverse strains of the rice bacterial blight and leaf streak pathogens *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) and *X. o.* pv. *oryzicola* (*Xoc*), respectively. In addition, building on our hypothesis that durable disease resistance is attainable by targeting key microbial virulence factors, we screened for resistance to *Xoo* strains isogenic for the known and common virulence factor TAL7b. A combination of genome-wide association studies and interval mapping analyses revealed a number of loci that conferred BSR to both *Xoo* and *Xoc*, as well as resistance targeted at TAL7b. These BSR QTL are excellent sources for durable, broadly effective resistance in the field.

Identifying molecular components of reduced demethylation inhibitor (DMI) fungicide sensitivity in ***Blumeria graminis*** **f.sp.** ***tritici***

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Blumeria graminis f.sp. *tritici* (Bgt), the causal agent of wheat powdery mildew, occurs annually in states along the eastern seaboard of the United States (US) and infects wheat worldwide. Reduced sensitivity to DMI fungicides has been observed in both European and Australian Bgt populations. The first evaluation of DMI sensitivity in US Bgt populations was conducted with isolates collected from 15 US states. Sensitivity to two DMIs (tebuconazole and prothioconazole) was measured for 380 isolates, with a third DMI (metconazole) measured for 100 isolates. A large range in DMI sensitivity was observed, with a significantly larger reduction in sensitivity observed in eastern US states compared to central Great Plains states. Discovering the molecular drivers of DMI sensitivity in US Bgt populations will assist in addressing fungicide resistance in US wheat production and add to understanding how fungicides influence the global Bgt population. Targeted partial genome sequencing of phenotyped isolates identified genetic components related to the observed differences in DMI sensitivity. Sequencing of the DMI-targeted CYP51 gene revealed a Y136F mutation that significantly correlates with reduced sensitivity to tebuconazole ($P<0.001$, $R^2=0.11$); however, 17 tebuconazole-insensitive isolates lack the mutation and 67 sensitive isolates have Y136F. Future analyses will evaluate more SNPs for DMI sensitivity association and qPCR analysis of CYP51 for expression and copy number.

Can rainfall be a useful predictor of epidemic risk across temporal and spatial scales?

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Plant disease epidemics are largely driven by within-season weather variables when inoculum is not limiting. Commonly, predictors in risk assessment models are based on the interaction of temperature and wetness-related variables, relationships which are determined experimentally. There is an increasing interest in providing within-season or inter-seasonal risk information at the region or continent scale, which commonly use models developed for a smaller scale. Hence, the scale matching dilemma that challenges epidemiologists and meteorologists: upscale models or downscale weather data? Successful applications may be found in both cases, which should be supported by validation datasets whenever possible, to prove the usefulness of the approach. For some diseases, rainfall is key for inoculum dispersal and, in warmer regions (e.g., tropics) where temperature is less limiting for epidemics, rainfall extends wetness periods. The drawbacks of using rainfall at small scales relate to its discrete nature and high spatial variability. However, for pre- or early-season predictions at large spatial scales sources of reasonably accurate rainfall summaries are available and may prove useful. The availability of disease datasets at various scales allows the development and evaluation of new models to be applied at the correct scale. We will showcase examples and discuss the usefulness of rainfall as key variable to predict soybean rust and wheat scab from field to region.

Development of a quantitative PCR-based method for the detection and monitoring azoxystrobin resistance in ***Pyricularia oryzae*** **populations**

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