

**Project No. and Title:** NCCC307 Biochemistry and Genetics of Plant-Fungal Interactions

**Period Covered:** 3/14/2019 to 10/9/2020

**Date of This Report:** 10/28/2020

**Annual Meeting Date:** 10/9/2020. Virtual workshop via Zoom

**Participants:**

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**Adopted Agenda: Brief Summary of Minutes of Meeting:** October 9, 2020, Zoom

4:00 – 4:15 pm – Roll call

4:15 – 4:30 pm - Welcome to NCCC307. Future directions and workshop plans by Co-Chairs, by Jenny Lorang and Daren Brown

4:30 – 4:45 pm – Kamaldeep Bansal: Cytology and gene expression in *Monilinia vaccinacorymbosi*.

4:45 – 5:00 pm – Rebecca Shay: Biofilm formation in *Fusarium graminearum*

5:00 – 5:15 pm – How is Covid-19 affecting your research?

5:15 – 5:30 pm – Pei-Ling Yu: The early phase of *Sclerotinia* infection

5:30 – 5:45 pm – Lightning talks:

Zhaohui Liu: Wheat tan spot

Patricia Santos: Polyacetylenes and Carrots

Jessica Lohmar: *Fusarium verticillioides* Spore killer

Dr. Liu described new virulence genes in the wheat tan spot fungus *Pyrenophora tritici-repentis* that follow the inverse gene-for-gene fungal/plant model. Dr. Santos described a resistance mechanism in carrots to fungi involving polyacetylenes. Dr. Lohmar described a gene in *Fusarium verticillioides* that codes for a meiotic drive element involved in spore killing. Discussion were lively and far exceeded the allotted time.

5:45 – Open panel discussion, questions, and closing remarks.

## Meeting Abstracts

Cytology and gene expression in *Monilinia vaccinii-corymbosi*

Kamaldeep Bansal and Jeffrey Rollins, University of Florida, Gainesville, FL

*Monilinia vaccinii-corymbosi*, a hemi-biotrophic member of Sclerotiniaceae, causes mummy berry disease on blueberries. Fruit infection is highly specific as conidial germ tubes enter the host through the gynoecial pathway, mimicking a pollen tube. To understand the evolution of this intricate host specificity within closely related Sclerotiniaceae members, we performed comparative genomics, infection transcriptomics and infection cytology. Comparative genomics revealed the presence of two lineage-specific, expanded gene families. Transcriptomic analysis has demonstrated that significant numbers of both family members are specifically expressed during different stages of floral infection. Cytological examination with GFP-fusions has provided new insight into the pathway of gynoecial infection.

Biofilm formation in the filamentous fungal plant pathogen *Fusarium graminearum*

Rebecca Shay and Frances Trail, Michigan State University, East Lansing, MI

Biofilms are microbial structures that protect cells safe from external stresses. Although biofilms are well studied in bacterial systems, few studies involved filamentous fungi. *Fusarium graminearum* is a filamentous fungal pathogen that causes Fusarium Head Blight in cereal crops, which can result in devastating crop losses. We are characterizing the formation of biofilms in *F. graminearum in vitro*, where we have observed an altered hyphal morphology, with predominantly short, bulbous hyphae under some conditions. We have mapped the full development of *F. graminearum* biofilms *in vitro* from the initial adhesion, to identification of components of the extracellular matrix, to dispersal of propagules and senescence of biofilms, and are investigating the conditions that promote biofilm formation. From this work, we will determine a role for biofilms in pathogenicity to provide new targets for disease control.

## The early phase of *Sclerotinia* infection

Pei-Ling Yu and Jeffrey A. Rollins, University of Florida, Gainesville, FL

To test a two-phase infection model for *Sclerotinia sclerotiorum*, we performed comparative transcriptome analysis from wild type (WT)- and  $\Delta$ ss-oah1 mutants-infected *Arabidopsis thaliana*. Spatial clustering of transcript profiles demonstrated that while  $\Delta$ ss-oah1 mutant stage II shared a common transcript pattern with WT stage II, the  $\Delta$ ss-oah1 mutants shifted to a unique stage thereafter. Pathway enrichment analysis highlighted an upregulation of the autophagy pathway at stage III of the  $\Delta$ ss-oah1 mutant compared to WT. In fungi, autophagy is regulated by cyclic AMP (cAMP) dependent protein kinase A pathway. Two genes, encoding a catalytic subunit (pka2) and a regulatory subunit (pkaR) of protein kinase A (PKA), were disrupted using CRISPR-Cas9 and functionally characterized.

## Accomplishments:

NCCC307 committee members contributed knowledge of biochemistry and genetics of plant fungal interactions over the past year and a half by: 1) providing genome resources of pathogens of wheat and maize, 2) uncovering plant genes coopted by fungi during growth, 3) characterizing new and emerging fungal pathogens; 4) identifying new fungal secondary metabolites that could play important signaling roles during fungal/plant interactions and 5) identifying new plant and fungal disease resistance genes. These efforts have produced more than 85 peer-reviewed journal publications from March 2019 through October 2020 reporting period (Appendix).

## Impacts:

The publications by NCCC307 participants has provided knowledge on new and emerging fungal pathogens and how these fungi and others maintain or advance growth in planta using a variety of strategies including secondary metabolism, the manipulation of plant resources and genes, and co-infecting with bacteria. Additional work has advanced our knowledge of host plants including genome sequences and genome-wide association mapping of resistance. The discussions initiated between among participants during and after our meeting has fostered the sharing of ideas and biochemical and genetic data which has contributed to these publications as well as precipitated new research directions. Thus, the results benefit academic, government, and private-sector organizations that assess the risks that fungi pose to human and animal health. This research will be of use to plant pathologists, plant breeders, and other scientists involved in the identification of fungal species responsible for mycotoxin contamination problems and the development of new strategies to limit mycotoxin contamination in crop plants and thereby ensure food and feed safety.