

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

**Period Covered:** 10/10/2020 to 3/16/2022

**Date of Report:** 9/9/2022

**Annual Meeting Date:** 3/16/2022. Held as workshop concurrent with Fungal Genetics Meetings in Asilomar, CA

**Participants:**

Lorang, Jennifer (lorangj@science.oregonstate.edu) - Oregon State University; Brown, Daren (daren.brown@ars.usda.gov) - USDA-ARS Peoria, Illinois; Friesen, Tim (timothy.friesen@ars.usda.gov) - USDA-ARS Fargo, North Dakota; Liu, Zhaohui (zhliu@ndsu.edu) - North Dakota State University; Shi, Gongjun (gonghun.shi@ndsu.edu) - North Dakota State University; Thomas Baldwin (thomas.t.baldwin@ndsu.edu) - North Dakota State University; Slot, Jason (slot.1@osu.edu) - Ohio State University; Redman, Regina (rsredman@adsymtech.com) - Adaptive Symbiotic Technologies Seattle, WA; Rodriguez, Rusty (rjrodriguez@adsymtech.com) - Adaptive Symbiotic Technologies Seattle, WA; Rollins, Jeff (rollinsj@ufl.edu) - University of Florida; Todd, Richard (rjtodd@ksu.edu) - Kansas State University; Keller, Nancy (npkeller@wisc.edu) - University of Wisconsin; Trail, Frances (trail@msu.edu) - Michigan State University; Wolpert, Thomas (wolpertt@science.oregonstate.edu) - Oregon State University; Ciuffetti, Lynda (ciuffetl@science.oregonstate.edu) - Oregon State University; Dianiris Rosario-Luciano (lucianorosario@wisc.edu) - University of Wisconsin; Mickey Drott (mdrott@wisc.edu) - University of Wisconsin; Yarden, Oded (oded.yarden@huji.ac.il) - The Hebrew University of Jerusalem; Nadal, Marina (marina@bunney.com) - Mycotechnology Inc.; Turgeon, Gillian (bgt1@cornell.edu) - Cornell University; Hunter, Cameron (chunter2@ksu.edu) - Kansas State University; Kubo, Yasuyuki (y\_kubo@kpu.ac.jp) - Kyoto University; Valent, Barbara (bvalent@ksu.edu) - Kansas State University; Xu, Jin-Rong (jinrong@purdue.edu) - Purdue University; Kistler, H. Corby (corby.kistler@usda.gov) - USDA-ARS St. Paul, MN; Steyer, Joel (jsteyer@ksu.edu) - Kansas State University; Josh Konkol (jkonkol@ufl.edu) - University of Florida; Shay, Rebecca (shayrebe@msu.edu) - Michigan State University; Konkel, Zachary (konkel.8@buckeyemail.osu.edu) - Ohio State University.

**NCCC-307 Meeting Minutes - March 16, 2022, Asilomar CA**

**7:00 pm– 7:10 pm** – Beverages, visiting and AV setup

**7:10 pm– 7:20 pm** – Welcome to NCCC-307. Future directions and workshop plans by Co-Chairs, by Jenny Lorang and Daren Brown

**7:20 pm– 7:40 pm** – **Dr. Milton Drott**

**7:40 pm– 8:00 pm** – **Rebecca Shay**

**8:10 pm – 8:45 pm – Lightning talks!**

**Joel Steyer** (PhD student Richard Todd)

**Dianiris Rosario-Luciano** (PhD student with Nancy Keller)

**Zachary Konkel** (PhD student with Jason Slot)

**Josh Konkol** (PhD student with Jeff Rollins)

**8:45 pm** – Open discussion, questions, and closing remarks (but went late as usual!!)

## Abstracts

### **"Computational assessment of secondary metabolite gene clusters in *A. flavus* and *Amanita* spp."**

*Mickey Drott and Nancy P. Keller*

The deadly poisonous *Amanita phalloides* is invading California but whether its toxic secondary metabolites drive the invasion is unknown. We developed a bioinformatic pipeline to automate identification of toxin producing MSDIN genes and probed 88 genomes from California and the native European range, discovering a diverse MSDIN pangenome with both core and accessory elements. Toxin genes are maintained by strong natural selection. Genes are clustered within genomes. The enormous diversity of MSDINs was generated by ancient and independent gene family expansions among genera of Agaricales, and we report the first discovery of an MSDIN in an *Amanita* outside the clade of "lethal Amanitas". The dynamic evolution of MSDINs in both ranges of the fungus underscores their potential role in mediating ecological interactions, and comparisons between *A. phalloides* and other species is reshaping our understanding of the genes' evolutionary history. Our results enable large-scale drug prospecting efforts in a previously-inaccessible class of secondary metabolite and provide a roadmap for approaching other metabolites found in *Basidiomycete* genomes.

### **Formation and genetics of biofilms in *Fusarium graminearum***

*Rebecca Shay and Frances Trail*

Biofilms are known to play important roles in bacterial pathogens of plants and animals where the formations help protect cells from defense responses and antimicrobial treatments. Our studies focus on the economically important plant pathogen *Fusarium graminearum*, a filamentous fungus, which is the primary causal agent of the disease Fusarium head blight. Biofilm formation is initiated *in vitro* with the adhesion of propagules to a surface, followed by growth of the structures and development of an extracellular matrix, then dispersal of propagules and senescence of biofilms. We have documented this formation, along with the serial addition of components of the complex extracellular polymeric matrix around the biofilm. Going forward, we are exploring the underlying genetic components of this process. Through the use of RNA-sequencing, we have profiled the transcriptome of biofilm formation over time. The different stages of biofilm development were compared sequentially for differentially expressed transcripts,

from which a list of candidate genes with a high probability for a role in biofilms have been selected for functional analysis. These genes showed significantly different expression between developmental stages, and the functional annotations are of interest with the stages of development. From this work, we hope to provide new targets for disease control through biofilm formations in *F. graminearum*.

### **Accomplishments:**

NCCC307 committee members collectively increased our understanding of biochemistry and genetics of plant-fungal interactions these past six months by: 1) increasing our understanding of the links between plant and fungal viruses, 2) better understanding the function of secondary metabolites, their synthesis, and their evolutionary history, 3) understanding meiotic drive and RNA editing, 4) understanding where inside a cell secondary metabolites are synthesized, and 5) appreciating how convergent assembly of metabolic modules contributes to fungal adaptation to plant defenses. These efforts have produced more than 105 peer-reviewed journal publications from October 10, 2020, through March 16, 2022 reporting period.

### **Impacts:**

The publications by NCCC307 members describing their research findings have increased understanding of how plant-fungi interactions impact economically important diseases of crops and food production and threats to humans and animals through the consumption of mycotoxin contaminated foods. The exchange of ideas and biochemical and genetic data among members has contributed to these publications and fostered new ideas and research directions. This research will be of use to plant pathologists, plant breeders, and other scientists involved in the development of control strategies aimed at reducing crop diseases and mycotoxin contamination problems caused by fungi. The research will also benefit academic, government, and private-sector organizations that assess the risks that fungi pose to human and animal health.

**Publications: See Appendix.**