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Conference Details

Communication Type:Poster but probably talk
Total Expense (USD):$955 plus flight ($600)
Date: March 14-19, 2017
Location:Pacific Grove, CA

Conference Title: 29th Fungal Genetics Conference
Communication Title: Evolution of Plant Penetration by Fungal Pathogens

ABSTRACT

Attendance to the meeting International 29th Fungal Genetics Conference 2017 organized by the Genetics Society of America in March 14-19th 2017, Pacific Grove, California.

My research is focused on developing a better understanding of the spore germination process in five fungal plant pathogens. Fungal pathogens are highly relevant in the US agriculture system, since they cause billions of dollars in losses annually and are responsible for the majority of plant diseases. Although spore germination is the first step in most fungal diseases, and highly vulnerable to attack by antifungal agents, the genetics of spore germination has never been comparatively explored across multiple fungal species. My overarching goal is to determine how the gene expression patterns in fungal pathogens have changed during evolution. This research will advance the knowledge in the area of fungal diseases necessary for developing new antifungals. Our experiments focus in five important fungal plant pathogens and one non-pathogen species, to yield genetic differences in spore germination and host penetration processes. To identify infection-specific genes we will compare the gene expression patterns from fungal plant pathogens versus non-pathogen species. In addition, we will compare the evolutionary changes in gene expression among different fungal penetration types to identify genes that have substantially higher expression in one lineage versus others. Employing this comparative approach, we will be able to distinguish components of spore germination that are conserved and therefore may be targeted to control disease initiation across a variety of fungi.

Transcriptomic and functional experiments included in my research project are integrated in Dr. Frances Trail's laboratory's goals. Our objectives aim to achieve two major outcomes: identify fungal genes and processes essential to initial infection by spores and to gain knowledge about the asexual process of spore germination versus sexual reproduction, which is much more studied so far.

The selected fungi for these studies are: *Fusarium graminearum*, which causes head blight in wheat and barley; *Magnaporthe oryzae*, which causes rice blast; *Colletotrichum graminicola*, which causes anthracnose in maize; *Venturia inaequalis*, which causes apple scab in trees; Verticillium dahlia, which causes Verticillium wilt on over 400 plant species and *Neurospora crssa,* which is a saprotroph fungus that will be used as a model organism for comparison.

Application must not exceed two pages and must be submitted as a pdf file to msu.pda@gmail.com
More details can be found at https://msupda.wordpress.com/
Applications that do not respect these criteria will not be considered for the MSU PDA travel award.

Fungal spores are responsible for initiation and propagation of the majority of biotic plant diseases. Once spores develop into fungal hyphae and infiltrate host tissue, fungi are much harder to eliminate. The commonalities and differences of gene expression patterns across the chosen fungi present a tremendous opportunity for understanding this process as a whole. To discover effective disease prevention and treatment options, it is imperative to identify components of the transcriptional program underlying fungal asexual spore germination. The expected results will provide insights on genes that undergo transcriptional shifts during the spore germination process, as well as those that are unique to infective germination, and those that are unique to specific fungi.

COMMUNICATION OUTCOMES

The techniques involved in this work include novel RNA-seq (ribonucleacid acid sequencing) of four different stages of the germination process in two different conditions (on hosts and on growth media). This new approach will provide an unprecedented large amount of data to compare between lineages and conditions. These data will be available to the scientific community for further studies. Also, further analysis of the most interesting genes will increase our knowledge in the asexual spore germination of some of the most important fungal plant pathogens and will provide new information on potential fungicide targets, with implications for a variety of plant diseases.

For the purpose of exchanging ideas and increasing networking, specialists in the fungal field meet every 2 years for an International Conference that has proved deeply efficient in the transfer of new discoveries and techniques and generating fruitful collaborations. I aim to engage research fellows in a new debate about how to address our efforts in developing new targeted compounds to control fungal diseases. Moreover, I hope to interact in person with colleagues from different expertise areas within fungal biology, and improve my skills in communicating my research as well as establish new collaborations. Also, I will attend to two different workshops: The *Fusarium* Workshop and How To Get Published Workshop. The first one interests me greatly since my research group works with *Fusarium graminearum,* while the second one will give me new tools to be more competitive in publishing, as well as being in contact with *GENETICS* and *G3* journal editors.

Finally, Dr. Frances Trail's lab is setting up a professional twitter account to be able to make science accessible to general audience. We will tweet all the activities that we do along the year, including meetings. I also aim to approach my research to a wider public so in the course of this meeting I plan to connect and share experiences with researchers in my field being active in social media such as Twitter, Facebook.