

# Plant Pathology Seminar Series

## “MAPPING HIGH-TEMPERATURE ADULT-PLANT RESISTANCE TO STRIPE RUST IN SPRING WHEAT AND CHARACTERIZATION OF THEIR INTERACTION ON A MOLECULAR LEVEL”

**Taras Nazarov**

Bread wheat is one of the most important food crops on the global scale. Stripe rust of wheat, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*) became the largest biotic stress factor in the 21st century, limiting wheat production worldwide. New races of the pathogen are more aggressive and able to overcome the defense of previously resistant cultivars. Despite the efficiency of fungicide treatments, genetic resistance is considered to be the most economical and environmentally friendly way to control the disease. Among different types of resistance to stripe rust, high-temperature adult-plant resistance (HTAP) recommended itself as durable and non race-specific. Search for the genes with high levels of HTAP resistance is a major goal for wheat improvement in the last decades.

Here we report the discovery of precise molecular marker for HTAP resistance locus in wheat cultivar Louise. Using Louise x Penawawa mapping population, coupled with data from survey sequences of wheat genome, linkage mapping and synteny analysis, we developed expressed, cleaved amplified polymorphic sequence (CAPS) marker LPHTAP2B on the short arm of wheat chromosome 2B. It perfectly segregates with the resistant phenotype and explains 62% of phenotypic variance based on disease severity, and 58% based on infection type.

Despite recent progress in molecular genetics technologies, still little is known about the interaction between *Pst* and wheat on the gene expression level. Here we present analysis of the molecular interaction between stripe rust race PST-100 and spring wheat in resistant and susceptible host background, using next generation transcriptomics. Resistant host stimulated significantly greater number of overexpressed, putative genes, as well as induced their higher fold change. Stress related pathways, including MAPK, oxidation-reduction, osmotic stress and stress granule formation, were, almost exclusively, upregulated in resistant host background, suggesting the requirement of the resistance-coping mechanism facilitation by fungus. Furthermore, susceptible host background allowed for broad overrepresentation of the nutrient uptake pathways. This is the first study, focused on the stripe rust - wheat interaction, on the whole transcriptome level, from the rust side. It lays a foundation for better understanding of the resistant/susceptible host versus pathogenic fungus interaction in a broader sense.

2:10 pm | Friday, April 7, 2017 | Johnson Hall 343

*PhD Exit Seminar*



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