PHYSIOLOGICAL AND MOLECULAR-GENETIC CHARACTERIZATION OF BASAL RESISTANCE IN SORGHUM

Jennifer Kimball[1] , Thalita Tuleski[2,3] , Xinye Zhang[1], Yaya Cui[2], Catherine Espinoza[2] , Dongqin Chen[2], Rozalynne Samira[1], Gary Stacey[2] and **Peter Balint-Kurti***[1,4]

[1]North Carolina State University, Raleigh NC,; [2]University of Missouri, Columbia, MO [3]Federal University of Paraná, UFPR, Brazil; [4]US Dept. of Agriculture, Agricultural Research Service, Raleigh, NC, *Presenting author

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PROJECT GOALS

The objectives of the project are the following

- I. *Develop robust assays to measure the microbe-associated molecular pattern (MAMP) response and disease resistance in sorghum.*
- II. *Screen a set of diverse sorghum germplasm for variation in the MAMP response and disease resistance.*
- III. *Identify genes differentially regulated during the MAMP response in high- and low-responding sorghum genotypes.*
- IV. *Assess the effect of MTI on disease progression in sorghum*
- V. *Identify loci associated with variation in disease resistance and the MAMP response. Examine possible correlations between variation in the MAMP response and in disease resistance*

PROJECT SUMMARY

Plants recognize certain conserved microbial molecules (microbe-associated molecular patterns or MAMPs) and mount a basal defense response called MAMP-triggered immunity (MTI) that limits subsequent colonization. In many cases, the basal defense response is believed to be responsible for non-host resistance: the phenomenon whereby most plants are resistant to most microbial pathogens. Furthermore, there is some evidence that the MAMP response may be involved with quantitative disease resistance, resistance which although partial, tends to be extremely durable. While much is known about the MAMP response in model species, this is not the case for crop plants. Furthermore, naturally-occurring variation in the MAMP response within a species and its relationship to quantitative disease resistance is not well understood. This project builds on our work investigating the genetics controlling the Arabidopsis and soybean MAMP response and on characterizing maize quantitative disease resistance.

PROGRESS

Objective I. We have developed robust reactive oxygen species (ROS)-based assays for response to chitin and flagellin (flg22). We have also worked on assays measuring nitric oxide (NO) production in response to these PAMPs though this assay produces a very high background level in non-treated lines.

Objective II. We have measured the responses to chitin and flagellin in more than 500 diverse sorghum lines. We have identified several high responders to both MAMPs.

In roots we have identified an interesting biphasic response with peaks at about 5 minutes and 25 minutes after elicitation. This biphasic response segregates in the population. Our data suggests that the strength of the MAMP response in roots is not correlated with that in leaves.

We have examined the PAMP response over developmental time and have shown that it varies significantly with increased responses occurring about 45 days after planting

Objective III. We have isolated RNA from leaves and roots of 2 lines, Btx623 and SC155-14E, treated with flg22, chitin and water (as a control). We are currently performing RNAseq analysis on these samples. Results will be presented.

Objective IV. We have developed greenhouse disease assays for three fungal diseases (Target leaf spot, northern leaf blight, anthracnose leaf blight) and one bacterial pathogen (*Herbaspirillum rubrisubalbicans*, causal agent of mottled stripe disease). We have shown that elicitation of the PAMP response with either flg22 or chitin can confer resistnace to Herbaspirillum rubrisubalbicans. We have attempted to perform similar experiments with the fungal diseases but have not yet been able to obtain satisfactory data.

Objective V. We have assessed an association mapping population of 500 diverse lines for response to flg22 in two replications and have identified several associated SNPs and candidate genes. Several candidate genes are predicted to be involved in oxidative stress response, heavy metal detoxification and defense response. We have mapped resistance to sorghum target leaf spot in this population in one environment with two replications. We identified several QTL including one QTL that had been previously identified in other studies.

We have assessed the PAMP response and disease resistance of two recombinant inbred population (RIL) populations (BTx623 x SC155, 107 lines and BTx623 x BTx642,130 lines). We assessed them in replicated field trials in 2016 and 2017 for resistance to the pathogen *Bipolaris sorghicola* , the causal agent of target leaf spot and have identified several QTL. We also assessed the Btx623 x SC155 population for response to flg22 and resistance to *H. rubrisubalbicans* and we are currently performing similar assays for the BTx623 x BTx642 population. We have not identified any QTL shared between the disease resistance and PAMP response traits.

Under separate funding we have undertaken a similar project in maize. We anticipate that the results of our sorghum and maize projects will mutually inform the other. We will present the latest data from both these projects in our poster at the PI meeting

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