

Physiological and Molecular-Genetic Characterization of Basal Resistance in Sorghum

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<https://sites.google.com/a/ncsu.edu/maize-disease/home>

Project Goals: Short statement of goals. (Limit to 1000 characters)

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 and seeks to:

- *Develop robust assays to measure the MAMP response and disease resistance in sorghum.*
- *Screen a set of diverse sorghum germplasm for variation in the MAMP response and disease resistance.*
- *Identify genes differentially regulated during the MAMP response in high and low responding sorghum genotypes.*
- *Assess the effect of MTI on disease progression in sorghum*
- *Identify loci associated with variation in disease resistance and the MAMP response.*

We are making extensive use of available resources for sorghum genomics and quantitative genetics; such as, the genome sequence and various sorghum mapping populations. Over the first year of the project we have made significant progress:

- We obtained four mapping populations and associated genotypic data from collaborators, increased seed and performed a disease trial using the pathogen *Bipolaris sorghicola*, causal agent of target leaf spot.
- We developed a protocol for assessing the response of sorghum to MAMPs by detecting the production of reactive oxygen species (ROS).
- We assessed a set of parental lines for the MAMP response, and for resistance to one bacterial pathogen (*Herbaspirillum rubrisubalbicans*, causal agent of mottled stripe disease) and to three fungal pathogens (*Bipolaris sorghicola*, *Exserohilum turcicum* and *Colletotrichum sublineolum*-causal agents, respectively, of target leaf spot, northern leaf blight and sorghum anthracnose). We identified significant line-to-line variation for each of these traits
- We identified quantitative trait loci (QTL) on chromosomes 4, 6 and 7 associated with variation in response to the MAMP flg22 (an epitope of flagellin) and QTL on chromosomes 6 and 7 for variation in the response to the MAMP chitin. The QTLs on chromosome 6 for the flg22 and chitin responses are at the same position in the genome.
- Using data from a single environment, we tentatively identified one QTL on chromosome 7 associated with variation in target leaf spot resistance. This QTL overlaps with a QTL associated with the flg22 response.
- We identified QTL on chromosomes 7 and 10 associated with resistance to *H. rubrisubalbicans*.
- We have shown that eliciting the MAMP response increases resistance to *H. rubrisubalbicans* in sorghum.

We are currently working on several sub-projects:

- We are assessing an 800-line sorghum association population for response to flg22 and for resistance to Target leaf spot.
- We have cloned the closest homolog in sorghum to OsFls2, the rice flg22 receptor. We are assessing its function to determine whether it is a Flg22 receptor as well
- We have made proteinaceous and non-proteinaceous extracts from *B. sorghicola* and we are assessing their effectiveness as elicitors of the MAMP response.
- We are characterizing the MAMP response at the transcriptional level. We are comparing the response elicited in several different lines and by several different MAMPs.

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

Funding statement.

This work is funded by DOE grant #DE-SC0014116 “Physiological and Molecular-Genetic Characterization of Basal Resistance in Sorghum”