Cotton Statement of Work for the National Predictive Modeling Tool Initiative (NPMTI)

**Establishing the infrastructure to develop prediction tools for diseases and mycotoxins affecting cotton to better inform management decisions**

**Background:** Plant pathogens pose an economic threat to cotton production. Both soil-borne and foliar pathogens, which can be moved regionally by wind, water, animals, or equipment, require community efforts to alert growers to potential threats and minimize control cost, yield, and quality losses. Predictive tools can provide growers with useful information, encouraging them to utilize an integrated approach to manage cotton diseases. Tools to forecast disease incidence and severity will allow growers to take timely preventative actions such as more favorable planting dates, selection of disease resistant cotton varieties, applications of effective fungicides at the proper time, more efficient use of plant growth regulators, more efficient irrigation management, targeted crop rotations, and tillage.

U.S. cotton is spread across 18 southern states in many different environments. Some diseases are more problematic than others, depending on location and weather patterns. The NPMTI is foundational for leveraging molecular diagnostic tools with modern modeling efforts to create decision support tools for integrated management of cotton diseases wherever cotton may be grown. Specifically, this project deals with economically important diseases such as target spot, areolate mildew, Alternaria leaf spot, Aspergillus boll rot, and the seedling disease complex. Adapting these tools for key cotton diseases will better inform growers and encourage them to adopt an integrated approach to disease management. When completed, these tools will offer decision support at varying temporal and spatial scales and will be used at different points along the spectrum of crop disease surveillance, from pre-plant to early detection.

**Progress:** The CottonResearch Area of the NPMTI has successfully deployed spore traps in eleven states for three growing seasons, 2021 – 2023. These spore traps were used to collect spores of the fungi that cause target spot, areolate mildew, and Alternaria leaf spot. Molecular tools were used to quantify the spores collected over time and relate these quantities to disease incidence and severity by collection location. Additionally, data from current trials of the National Cotton Seed Treatment program and historical data from this program from as far back as 1993 have been used to determine regional pathogen abundance and the soil and weather properties that link pathogen abundance with seedling disease occurrence. Molecular tools identify the pathogen communities associated with the soil, and diseased cotton seedlings have been sequenced for the 2022 and 2023 growing seasons. Historical seed treatment trial data has been used to predict seedling disease occurrence.

**Statement of Work for 2024.** Develop and demonstrate community-wide tools for cotton pathogen prediction and management

**Objective 1.** Create DNA detection tools for cotton pathogens.

1. Field collection of fresh areolate mildew samples by cooperating universities in the southern US
2. Dr. Alejandro Rojas’s lab at Michigan State University will develop and validate quantitative probes for the fungus that causes areolate mildew in the US.

**Objective 2.** To monitor foliar diseases in cotton fields using airborne spore sampling of fungal cotton pathogens.

1. Small plot replicated trials with sampling of airborne spores to build and validate pathogen models.
   1. Eleven trial locations will be initiated across the cotton belt (Auburn University, Clemson University, University of Arkansas, University of Florida, University of Georgia, Louisiana State University, University of Missouri, Mississippi State University, University of Tulsa, University of Tennessee, and Texas A&M University).
   2. Each trial will be arranged in a randomized complete block design with two cotton varieties per trial both known to be susceptible to target spot, areolate mildew or both diseases. Besides variety, a second treatment will be each variety either treated with a single fungicide application or not treated with fungicide. All treatments will be replicated three times.
   3. Yield will be collected for each plot at each trial location.
   4. Weather data will be captured daily at each trial location.
   5. Trails will be rated for the presence of foliar diseases in each plot weekly. Cooperators will also collect limited crop phenology (plant height, 1st flower, 1st open boll).
   6. A spore trap will be placed adjacent to each trial location. Slides from spore traps will be collected and replaced weekly at each trial location. Spore traps will be deployed mid-June at most locations and until approximately two weeks after harvesting of the trial.
2. Commercial field locations with sampling of airborne spores to build and validate pathogen models.
   1. Two commercial cotton fields will be chosen in each cooperating state. At each field location, two spore traps, one at each of two opposing field corners will be placed mid-June and retrieved approximately two weeks after harvest.
   2. Field data will be collected for each location: coordinates of field center and each spore trap, planting date, variety, row spacing, first bloom date, fungicide application(s) by grower (product/rate/date), defoliation date, harvest date, and yield data (from yield monitor or field ticket).
   3. Foliar disease ratings will be done on five fixed points approximately 150 ft from each air sampler in a linear orientation within a row (30 ft apart). Plots will be rated for diseases weekly and slides from spore traps replaced each time the fields are rated for disease.

**Objective 3.** To create cotton epidemiological models for target spot, areolate mildew, and seedling diseases to predict pathogen populations, disease progression, and their impact on the cotton crop.