

A close-up photograph of several white cotton bolls on a branch, set against a clear blue sky. The bolls are fluffy and white, with some brown, dried bracts visible at their base. The text is overlaid on the image.

**Host range, pathogenicity, and genetic  
diversity of *Corynespora cassiicola*  
from cotton**

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*Corynespora cassiicola* is causing numerous emerging diseases, including target spot of cotton

A disease is emerging if

- increase in host range, geographic range, or incidence is observed, or
- new strains evolve

## Causes of disease emergence include...

- Pathogen adaptation
- Pathogen introduction
- Host susceptibility
- Environmental change



Target spot on cotton (photo: Nick McGhee)

Which of these explain emergence of target spot on cotton?

# *Corynespora cassiicola* has a very wide host range

Pathogen of crop plants, ornamentals, and weeds

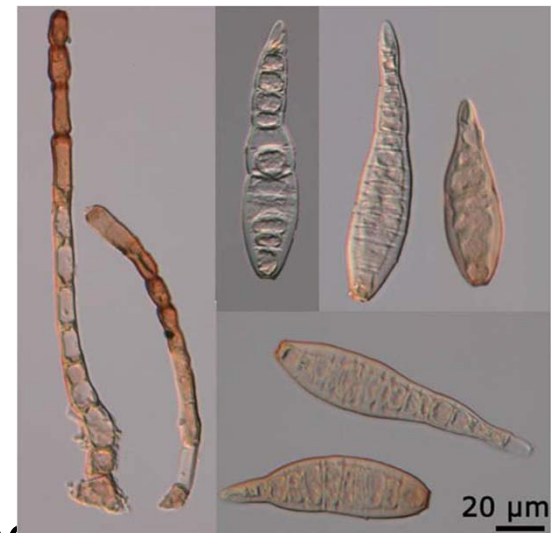
- rubber tree, hydrangea, mandevilla, cassava, lantana, balsam pear, basil, highbush blueberry, papaya, eggplant, azalea, cocoa, sweet potato
- cotton, soybean, tomato, cucumber, cowpea, pepper, bean

Cassiicolin - host selective plant toxin

Endophyte

Saprophyte

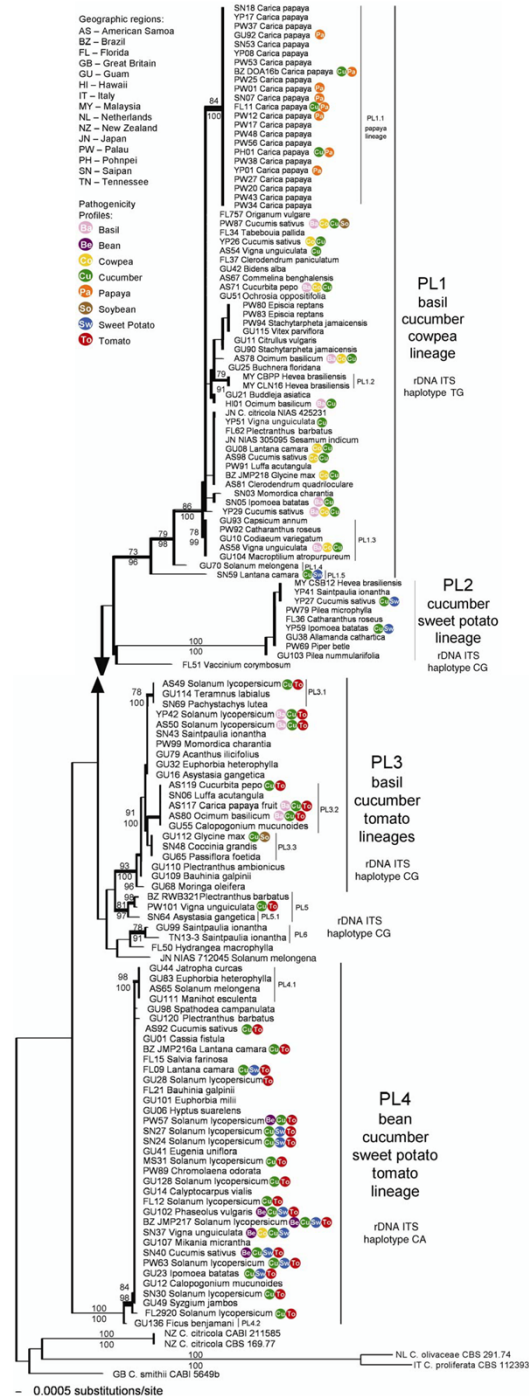
Subcutaneous skin infections, corneal infections



## Population biology of *C. cassiicola*

- Few studies addressing population biology
- Dixon et al. (2009) most comprehensive study to date
- Sequenced 4 genes from 143 isolates from different hosts and geographic locations
- 50 isolates on 8 economically important hosts
  - Basil, bean, papaya, tomato, cowpea, cucumber, soybean, sweet potato

# Host range and phylogenetic diversity



- Phylogenetic lineages
  - wide geographic range
  - wide host range
- Some host specialization
- No cotton isolates, 2 soybean isolates

# Research Objectives

1. Determine the host range of *C. cassiicola* isolates from cotton and pathogenicity of isolates from other hosts in the southeastern USA to cotton
2. Determine the phylogenetic relationship of isolates of *C. cassiicola* from cotton with isolates from other hosts
3. Characterize the genetic diversity of *C. cassiicola* isolates from cotton

# Why is this important?

- Host range
  - Identify alternative hosts of cotton isolates
  - Identify sources of inoculum
  - Determine if different populations exist in SE
- Phylogenetic relationships
  - Determine where it came from
  - Identify other potential hosts
  - Identify if specialization exists
- Diversity of cotton isolates
  - Determine if there are differences in aggressiveness, host range, fungicide resistance
  - Develop a panel for resistance assays, breeding
  - Identify mechanisms of dispersal
  - Understand why it emerged



# Research approach

- Isolate collection
  - Diverse hosts in southeast
  - Diverse geographic locations (SE and worldwide)
  - Focus on cotton and soybean isolates



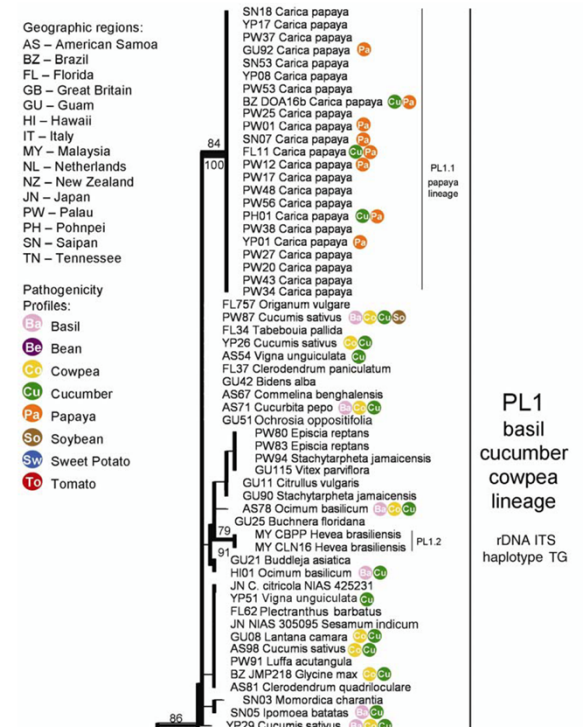
## Host range

- Inoculate cotton seedlings with diverse isolates
  - Resistant and sensitive cotton cultivars
- Inoculate diverse hosts with cotton isolates
  - Soybean, cowpea, cucumber, tomato seedlings
- 40 isolates, 10 each from cotton and soybean
- Evaluate for symptoms



# Phylogenetic relationships

- Cotton isolates (100)
  - Diverse varieties
  - Diverse geographic regions
- Soybean isolates
- Other isolates from southeastern US
- 150 total isolates
- Sequence 4+ genes
- Construct phylogenetic trees
- Lineages to which cotton, soybean and other hosts belong
- Clustering?



# Genetic diversity

- Sequence 6 genes for numerous cotton isolates throughout southeastern US
- Also from other countries where *C. cassiicola* on cotton found

# Summary

- *Corynespora cassiicola* is an emerging disease
- Wide host range with some specialization
- Research on cotton and soybean populations is needed
- Research will provide insight into where it came from, why it is emerging, and diversity of cotton populations
- Knowledge will improve disease management
  - Alternative hosts
  - Sources of inoculum
  - Resistance