

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 the base of the bolls. 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

Geographic regions:
AS – American Samoa
BL – Brazil
FZ – Florida
GB – Great Britain
GU – Guam
HI – Hawaii
IT – Italy
MY – Malaysia
NL – Netherlands
NZ – New Zealand
JP – Japan
PW – Palau
PH – Philippines
SN – Saipan
TN – Tennessee

Pathogenicity
Profiles:
● Basil
● Bean
● Cowpea
● Cucumber
● Papaya
● Soybean
● Sweet Potato
● Tomato

SN18 Carica papaya
PW37 Carica papaya
GU32 Carica papaya
SN53 Carica papaya
PW93 Carica papaya
PW25 Carica papaya
BZ DOA166 Carica papaya
PW01 Carica papaya
SN02 Carica papaya
FL117 Carica papaya
PW12 Carica papaya
PW17 Carica papaya
PW48 Carica papaya
PW97 Carica papaya
PW27 Carica papaya
PW20 Carica papaya
PW43 Carica papaya
PW04 Carica papaya
FL1757 Oryzomys vulgare
PW87 Cucumis sativus
FL34 Tabebuia pallida
YP24 Cucumis sativus
AS54 Vigna unguiculata
FL37 Ciceronidium paniculatum
GU32 Solanum
AS67 Commelina benghalensis
AS71 Cucurbita pepo
GU1 Ochrosia oppositifolia
PW80 Epicaria repta
PW93 Epicaria repta
PW94 Stachytarpheta jamaicensis
GU1115 Vicia pavlovii
GU11 Ceratium vulgare
GU36 Stachytarpheta jamaicensis
AS71 Oryzomys vulgare
GU25 Buchanania fordiana
MY C3191 Hevea brasiliensis
MY CLN16 Hevea brasiliensis
GU171 Buddia alata
H01 Oomycete basidium
JN C. cinereus AS45 42521
FL51 Vigna unguiculata
YF12 Plectranthus barbatus
JN N48 30205 Sesamum indicum
GU28 Lantana camara
AS58 Cucumis annuum
PW91 Luffa acutangula
BZ JMP219 Glycine max
AS81 Ciceronidium quadriloculare
SN02 Momordica charantia
SN05 Momordica charantia
YP26 Cucumis sativus
GU3 Cucurbita annuum
PW92 Cactanthus roseus
GU12 Cactanthus roseus
AS58 Vigna unguiculata
GU104 Macroplum atropurpureum
GU70 Solanum melongena [p.14
SN59 Lantana camara
FL51 Vaccinium corymbosum
AS49 Solanum lycopersicon
GU114 Teramith labialis
SN69 Pachystachys lutea
YP42 Solanum lycopersicon
AS50 Solanum lycopersicon
SN43 Sainpaulia ionantha
PW99 Momordica charantia
GU79 Acanthus ilicifolius
GU32 Euphorbia heterophylla
GU16 Axytia genetica
AS119 Cucurbita pepo
SN08 Luffa acutangula
AS117 Carica papaya fruit
AS80 Cucumis sativus
GU5 Calotropium mucronatum
GU112 Glycine max
SN48 Coccinia grandis
GU65 Passiflora foetida
GU119 Plectranthus amboinensis
GU109 Bauhinia galepini
GU89 Moringa oleifera
BZ RW3231 Plectranthus barbatus
PW101 Vigna unguiculata
SH45 Axytia genetica
GU99 Sainpaulia ionantha
NL13-3 Sainpaulia ionantha
FL12 Hydrangea macrophylla
JN N48 712045 Solanum melongena
GU44 Jatropha curcas
GU83 Euphorbia heterophylla
AS65 Solanum melongena
GU111 Manihot esculenta
GU98 Spatoloches campanulata
GU120 Plectranthus barbatus
AS92 Cucumis sativus
GU01 Cassia fistula
BZ JMP216a Lantana camara
FL16 Salvia farinosa
FL09 Lantana camara
GU26 Solanum lycopersicon
FL21 Bauhinia galepini
GU101 Euphorbia mili
GU06 Hyptis walteri
PW67 Solanum lycopersicon
SN27 Solanum lycopersicon
SN24 Solanum lycopersicon
GU41 Eugenia unifera
MS31 Solanum lycopersicon
PW69 Chromolaena odorata
GU126 Solanum lycopersicon
GU102 Phaseolus vulgaris
BZ JMP217 Solanum lycopersicon
SN37 Vigna unguiculata
GU107 Mikania micrantha
SN40 Cucumis sativus
PW63 Solanum lycopersicon
GU23 Momordica charantia
GU12 Calotropium mucronatum
SN30 Solanum lycopersicon
GU49 Syzygium jambos
FL122 Solanum lycopersicon
GU136 Ficus benjamina [p.4
NZ C. citrifolia CAB1 211585
NZ C. citrifolia CBS 169.77
NL C. olivaceae CBS 291.74
IT C. proliferata CBS 1122993

PL1
basil
cucumber
cowpea
lineage
rDNA ITS
haplotype TG

PL2
cucumber
sweet potato
lineage
rDNA ITS
haplotype CG

PL3
basil
cucumber
tomato
lineages
rDNA ITS
haplotype CG

PL4
bean
cucumber
sweet potato
tomato
lineage
rDNA ITS
haplotype CA

GB C. amthii CAB 5649b

– 0.0005 substitutions/site

- Dixon et. al (2009) *Phytopathology*

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



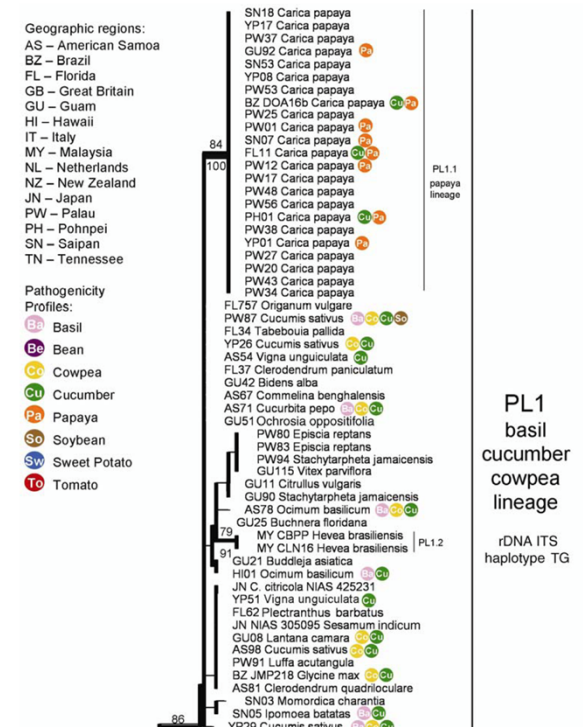
Host range

- 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