Effect of Transgenic Cotton Plants Transformed with Antimicrobial Synthetic peptide D4E1 on Cotton Seedling Disease and Soil Microbial Diversity

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- USDA estimates the global cotton crop amount to be approximately 120.3 million bales in 2007.
- USDA projects a '08-09 US cotton crop of 13.77 million bales.
- An average of 2.85% of cotton crop is lost annually as a result of infection of cotton seedling disease
  - translates to over 150 million dollars a year.
- In Alabama specifically, seedling disease is responsible for losses ranging from 3 to 11 percent annually.

Alabama Cooperative Extension Office ANR-1011April 1998. William S. Gazaway (National Cotton Council of America)





# **Current Management Methods**

- Managed by various farm practices
  - Crop Rotation
  - Preparation and Drainage of seedbed
  - Avoid Mechanical Injury
  - Application of Fungicides
- Ineffective
  - No one treatment addresses all pathogens in complex
- <u>No known lines of cotton are resistant to cotton</u> seedling disease

### Synthetic Antimicrobial Peptides as a Control Method for Phytopathogens

- Jaynes et al. (1993) introduced a gene encoding a designed synthetic peptide in tobacco.
  - Showed resistance to bacterial wilt
- Transgenic potato plants expressing an alfalfa defensin gene, *alfAFP*

 showed increased field resistance to *Verticillium dahliae* (Arce 1999).

- Expression of the *attacin* gene from the giant silk moth, *Hyalophora cecropia* 
  - demonstrated improved bacterial resistance in transgenic potato and pear, respectively



- More target specificity
- Increased efficacy at lower concentrations.
- Rapid biocontrol ability against a wide range of fungal and bacterial pathogens at low concentrations

• Non-toxic to mammalian and animal cells.







# Details about D4E1 Construct

• Construct: pBI121

- Mode of transformation
  disarmed Agrobacterium tumafaciens
- Promoter: 35S 5'
  - cauliflower mosaic virus- (double promoter)
- Terminator:
  - nopaline synthase (nos) 3' from Agrobacterium tumafaciens T-DNA

Selectable Marker

– Kanomycin Resistance



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# Overview of Field Experiment and Layout

# Lines

### Three lines (Coker 312):

- C357(line 1)- two integration sites
- C358 (line 2) –three integration sites
- C373 (line 3) one integration site
- Control with a GUS reporter gene.
- All 4 sets of seeds were transformed and provided by USDA ARS division, New Orleans, LA.

Rajasekaran, K, Cary, J.W., Jaynes J.E., and Cleveland, T.E. (2005) .Plant Biotechnology Journal 3 (6), 545–554





# Collection and Scoring of Seeding

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Scoring system was then applied to each cotton seedling that was planted in an effort to quantify the emergence of potential disease symptoms.

- 1 2 plant germinated at time of observation
- 2 1 plants germinated at time of observation
- 3 No germination
- 4 Germinating (emerging from soil, but not fully emerged)
- 5 Both Plants weak
- 6 1 plant strong/1 plant weak
- 7 1 plant germinated but weak
- 8 1 plant germinated but died
  - 2 plants germinated but died

## Examples of Diseased Seedlings



# Discussion

- Preliminary Results indicated that in both trial 1 and 2 showed the three D4E1 lines showed fewer disease symptoms than the control.
- Further evaluation of transgenic lines will be conducted.
- Comparison of the evaluation rubrics.
  - Greenhouse experiment
  - Replication of field trial

# **Overall Objectives and Next Steps**

- 1. Evaluate the effect that *D4E1* will have on cotton seedling disease.
  - Begin Greenhouse Experiment (November)
- 2. Determine whether *D4E1* transgenic cotton plants develop on a comparable level as non-transgenic varieties.
  - Continue cotton plant characterization

# Next Steps cont.

- 3. Evaluate whether effect D4E1 transgenic crop expressing a synthetic antimicrobial peptide have any effect the soil microbial community
  - Analysis of Soil Samples- DNA Extraction, PCR amplification, and DGGE

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