Coordinated Agricultural Project
RICECAP

• Objective #2:
• Goals of the PI
  - Validate the function of candidate genes associated with sheath blight resistance and milling quality.

RICECAP

• Experimental approach
  – Identify candidate genes associated with sheath blight resistance and milling quality based on literature searches, gene expression, pathway analysis, and QTL mapping data from Objective 1.
  – Select 15 candidate genes for functional validation via RNAi and transgene overexpression.
  – Generate 15 independent transgenic lines for each overexpression and RNAi constructs.
  – Evaluated transgenic progeny for sheath blight resistance and milling quality in collaboration with mapping groups.
Sheath Blight Resistance:

- No known major resistance genes
- only quantitative difference among various cultivars

Nipponbare  
Jasmine 85

Four days post inoculation with *R. solani* isolate RR0107

Selection of Candidate Genes

- Literature Search
- QTL and association Mapping (Objective 1)
- Gene expression profiling
- Proteomic analysis
- Defense pathway analysis
A Simplified Model for Signal Transduction in Plant Defense Responses

Pathogen

Cell wall

Plasma membrane

Elicitor

Receptor

Protein phosphorylation

Ion fluxes

O2

SOD

H2O2

Direct antimicrobial effects, lignification, crosslinking of cell wall proteins

NADPH oxidase

Signal Interaction & Amplification

Activation of transcription factors

Alteration of redox status

Protein phosphorylation

H2O2

NO

C2H4

SA

JA

ABA

HR

SAR

RiceCAP

Determination of Specific Defense Pathways Important for Sheath Blight Resistance

- Effect of exogenous salicylic acid, jasmonic acid, ethylene and abscisic acid on sheath blight resistance.

- Effect of endogenous SA, JA, ET and ABA signaling on sheath blight resistance.

Example: JA insensitive coil lines

RiceCAP
Suppression of Rice COI1 Expression in Transgenic Lines via RNA Interference

Transgenic Analysis

(T2 lines inoculated with R. solani)
Quantification of *R. solani* Growth in Rice Leaves by Real-time PCR

Project Contribution and Integration

- Identify candidate genes associated with sheath blight resistance and milling quality based on literature searches, gene expression, pathway analysis and QTL mapping data from Objective 1.
- Validate the function of candidate genes in sheath blight resistance and milling quality
First Year Benchmarks

• Develop real-time PCR assay for quantification of *R. solani* growth in rice
• Determine the effect of exogenous SA, JA, ET and ABA treatment on sheath blight resistance
• Determine the role of endogenous SA, JA and ET signaling on sheath blight resistance
• Develop RNAi and overexpression constructs for five candidate genes

Personnel Involved

• One postdoc (67% funding for year 1)
  Dr. Ronald J. Sayler