Objective 1 – Identify and use candidate genes and other molecular markers linked to QTL which control milling quality and resistance to sheath blight disease
Overview of Four Year Research Plan

- Objective 2 – Validate the function of candidate genes associated with milling quality and SB resistance

- Objective 3 – Develop technical training programs and resources to ensure implementation of molecular marker and gene validation technologies to solve rice problems
Overview of Four Year Research Plan

- Objective 4 – Provide education opportunities for students and consumers emphasizing the potential of genomic research for improving the abundance and quality of rice

Summary research objectives

- Develop markers associated with genes that control MY and SB
- Validate the function of these candidate genes
- Develop training programs to empower the rice research community to utilize the outcomes of this research and genomics
- Educate consumers and students about the value of genomics research and agriculture
Why Milling Yield and Sheath Blight

Unique QTL for sheath blight resistance, independent of height and flowering loci found using a wide cross
Overview of Molecular Breeding Workplan

- Develop series of segregating genetic populations for mapping
- Develop improved phenotyping methods
- Identify 150-200 uniformly distributed polymorphic markers among parents of crosses
- Conduct MAS training workshop
- Phenotype and genotype first mapping populations
- Identify QTL and chromosomal regions associated with trait
- Provide annual progress reports to review boards and USDA for continued funding and agreement on approach

Populations Selected for Milling Quality

<table>
<thead>
<tr>
<th>Cross</th>
<th>Parents</th>
<th>Parental Diversity</th>
<th>Phenotypic Range</th>
<th>Population Type</th>
<th>Project Year</th>
</tr>
</thead>
<tbody>
<tr>
<td>MY1</td>
<td>Cypress/RT0034</td>
<td>65% 40%</td>
<td>Wide</td>
<td>&gt;15%</td>
<td>Random F12</td>
</tr>
<tr>
<td>MY2</td>
<td>Cypress/LaGrue</td>
<td>65% 55%</td>
<td>Narrow</td>
<td>10%</td>
<td>Random F7</td>
</tr>
<tr>
<td>MY3</td>
<td>L204/01Y110</td>
<td>66% 57%</td>
<td>Very narrow</td>
<td>9%</td>
<td>Random F7</td>
</tr>
</tbody>
</table>
Populations Selected for Sheath Blight

<table>
<thead>
<tr>
<th>Cross</th>
<th>Population</th>
<th>Parental Diversity</th>
<th>Phenotypic Range</th>
<th>Population Type</th>
<th>Project Year</th>
</tr>
</thead>
<tbody>
<tr>
<td>SB1</td>
<td>Rosemont/Pecos</td>
<td>Narrow</td>
<td>5</td>
<td>Random F3</td>
<td>1</td>
</tr>
<tr>
<td>SB2</td>
<td>Cocodrie/010277</td>
<td>Wide</td>
<td>6</td>
<td>DH</td>
<td>2</td>
</tr>
<tr>
<td>SB3</td>
<td>Cocodrie/0066601</td>
<td>Wide</td>
<td>6</td>
<td>DH</td>
<td>3</td>
</tr>
<tr>
<td>SB4</td>
<td>Lemont/TeQing</td>
<td>Very wide</td>
<td>5</td>
<td>TIL</td>
<td>3,4</td>
</tr>
</tbody>
</table>

Milling Yield Project Timeline

2004
- Develop improved protocol for collecting phenotypic data of milling sub-components
- Produce increased seed of MY 1 for multi-loc trials
- Advance MY2 and MY3 via selfing

TX, MO, AR, LA

YR 1
- CAP Funding begins
- Identify polymorphisms in parents, develop markers
- Evaluate 200 progeny MY 1 at two locations in rep. trial
- Genotype 200 progeny
- Data analysis, QTL identification
- Advance MY2 and MY3 via selfing

Hulbert/Nguyen

TX, LA, CA

YR 2
- Identify polymorphisms in parents, develop markers
- Evaluate 200 progeny MY 2 at two locations in rep. trial
- Genotype 200 progeny
- Data analysis, QTL identification

Hulbert/Nguyen

AR, LA, TX, CA

YR 3
- Identify polymorphisms in parents, develop markers
- Evaluate 200 progeny MY 3 at one CA location in rep. trial
- Genotype 200 progeny
- Data analysis, QTL identification

Hulbert/Nguyen

CA

KSU, CA
Sheath Blight Project Timeline

**YR1**
- Develop improved protocol for greenhouse evaluation of SB TX, AR, LA, Col.
- Identify polymorphisms in parents, develop markers Hulbert/Nguyen
- Develop DH populations LA
- Conduct field studies to verify SB res. TILs TX, LA
- Backcross res. TILs with Lemont TX
- Data analysis, QTL identification in SB1 KSU, TX

**YR2**
- Evaluate 200 progeny SB 2 at two locations in rep. trial and GH AR/LA
- Genotype 200 SB2 progeny LA
- Genotype 20 TILs with 100 markers, identify chrom. Regions TX
- Data analysis, QTL identification KSU, LA
- Advance SB3 and TILs via selfing TX, LA

**YR3**
- Identify polymorphisms in parents, develop markers Hulbert/Nguyen
- Evaluate 200 progeny SB 3 at two locations in rep. trial and GH AR/LA
- Genotype 200 SB3 progeny AR
- Data analysis, QTL identification KSU, AR
- Evaluate BC TILs for SB res. And develop fine mapped markers TX

**YR4**
- Evaluate BC TILs for SB res. AR, LA
- Assoc. SB segregation with finely mapped markers TX
- Data analysis, QTL identification KSU, TX

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**Year 1 - Who is doing what in molecular breeding**

- Leong (WI)/Nguyen (MO)
  - SNPs with Chips CPRS, LGRU
- Nelson – KSU
  - Collection of phenotypic and genotypic data and analysis

- Hulbert KSU –
  - Markers in cand. genes

- DBNRRRC
  - Sheath Blight Method
  - SB4 genotyping

- TX
  - Genotyping all parents and MY 1 progeny
  - Genotyping of SB1

- CA MY1 Fissuring Advancing MY3
- AR MY1 Phenotyping
- LA MY1 Phenotyping SB Method Advancing MY2, SB2, SB3
- MY1 Field Backup SB Method Advancing MY2 and SB4

- REPORT RESULTS
Meeting Objectives – MY1

- Finalize field layout – Discussion with statistician
- Discussion of milling yield and subcomponents to measure
- Milling method
- Protocol for phenotyping traits
- Protocol for cultural management
- Weather data
- Timeline

Meeting Objectives – SB method

- Finalize greenhouse and field plans
- Protocol for phenotyping traits
- Protocol for cultural management GH and field
- Weather data
- Timeline
**Status of MY 1 Population**

- 500 F11 progeny grown in 04 TX
- Screened parents with 30+ markers, all but 4 polymorphic – markers no a problem
- Eval. Progeny with 5 markers to remove any outcrosses – about 1/3
- Will identify 300-400 to plant by 3/1
- Will complete fingerprinting of 150 markers on all families by harvest
- Identify 200 to harvest

**Status of milling method**

- Difference in replicates – 1% whole, .5% total
- Among states - 10% difference in whole, and 4% difference in total using the same cleaned seed
- TX and LA usually low, MO usually high
- Field sample variables: drying, threshing, cleaning, storage, milling, seperating
Analysis of previous milling data

- Multi-loc-yr URRN –
  - Reps within a paddy not different
  - Loc more important than year
- Multi-yr LA URRN
  - Reps in same paddy not important
  - YRxGeno = Geno
- Mapping pop
  - Replicates of same field sample not different
  - Repeated checks in same paddy not different
  - Samples in different paddies are different

Scope of trial

- Plant 300-400 lines/parents/repeated checks
- Single row plots
- Two reps, one paddy or each in different paddies
- Plant 3 loc, harvest 2 loc
- Identify 200/400 to harvest using markers
- Plant 1-2 loc in 2006 (may need to modify plans for SB pops)
Cultural management

- Plant late, overseed, thin to uniform stand
- Soil test and fertility plans
- Herbicide plans – Command?
- Insect and disease control – preventative
- Weather data logger

Traits to measure per plot

- Emergence
- Plant stand
- Heading
- Tillers/unit area
- Harvest
- Harvest moisture
- Grain traits
Progress from CPRS/PNDA

- 250 F10 progeny, AFLP analysis
- Heading, grain dimen, milling, grain chem, grain physical (coming)
- Most important factors assoc with milling – green kernels and chalk
- Not important – grain dimension, heading, height, grain chemistry
- QTL for milling on chrom 2, 4, 10
- Mapping other traits also – hd, ht, pub, gd
- Encouraged we will be “successful” in MY1, can verify these findings