Coordinated Agricultural Project RiceCAP

- Objective #2 (and partially 1):
- Goals of the PI
  - To identify genes for QTL conditioning sheath blight resistance

Candidate gene approach to durable resistance

- Are defense response genes associated with QTL for disease resistance?
- Are defense response genes better predictors of QTL than random markers?
- Do defense response genes contribute to quantitative disease resistance?
Pathogens and Pests for QTL screens
(inoculations with multiple strains/isolates)

Bacterial blight
Brown Plant Hopper

Blast
Sheath blight

Association of DR genes with rice QTL
Five DR genes associated with blast QTL in SHZ-2 X LTH RI lines

<table>
<thead>
<tr>
<th>DR gene</th>
<th>QTL Chr</th>
<th>% Contribution to DLA variation at location</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chitinase</td>
<td>2</td>
<td>GD-BN 6.7* ( p=0.05 ), IRRI-BN 5.0*, Ca-BN 5.0*</td>
</tr>
<tr>
<td>14-3-3 protein</td>
<td>2</td>
<td>GD-BN 7.1* ( p=0.05 ), IRRI-BN 5.0*, Ca-BN 4.0*</td>
</tr>
<tr>
<td>Dehydrin</td>
<td>7</td>
<td>GD-BN 14.9**** ( p=0.0001 ), IRRI-BN 25.6****, Ca-BN 16.7****</td>
</tr>
<tr>
<td>Oxalate oxidase</td>
<td>8</td>
<td>GD-BN 41.2**** ( p=0.0001 ), IRRI-BN 12.1****, Ca-BN 27.0****</td>
</tr>
<tr>
<td>PR-1</td>
<td>10</td>
<td>GD-BN 13.8**** ( p=0.0001 ), IRRI-BN 10.7****, Ca-BN 16.9****</td>
</tr>
</tbody>
</table>

* \( p=0.05 \), ** \( p=0.01 \), *** \( p=0.001 \), **** \( p=0.0001 \)       
Liu et al., 2004

Location of candidate genes on rice genome physical map confirms genetic mapping

<table>
<thead>
<tr>
<th>Gene description/Accession #</th>
<th>QTL Chr</th>
<th>Chr of contig</th>
<th>Contig ID</th>
<th>Contig location (cM)</th>
<th>Other chrs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chitinase/ X93170</td>
<td>2</td>
<td>2</td>
<td>OJ1124_H01</td>
<td>88.2</td>
<td>4, 3, 8</td>
</tr>
<tr>
<td>14-3-3 protein/ X78671</td>
<td>2</td>
<td>2</td>
<td>OJ1058_F07</td>
<td>93.2</td>
<td>10, 1, 6, 9</td>
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<tr>
<td>Dehydrin/ AF031247-50</td>
<td>7</td>
<td>7</td>
<td>OJ1131_E05*</td>
<td>73.2</td>
<td>***</td>
</tr>
<tr>
<td>Oxalate oxidase/ X93171</td>
<td>8</td>
<td>8</td>
<td>P0610E02 P0461A06</td>
<td>38.5-40.2</td>
<td>4, 2, 48.8</td>
</tr>
<tr>
<td>PR-1/ U8220</td>
<td>10</td>
<td>10</td>
<td>OSJNBa0040 E17 OSJNBa0029 C15</td>
<td>15.2</td>
<td>1, 2, 3, 7</td>
</tr>
</tbody>
</table>

http://www.tigr.org/tdb/e2k1.osa1 
Liu et al., 2004
"Consensus" candidate genes:

- Oxalate
- Oxidase
- Aldose reductase
- NBS-LRR (maize, barley)
- Dihydrofolate reductase-thymidylate synthase
- Peroxidase
- Chitinase
- 14-3-3
- PR1
- Thaumatin
- Catalase
- SOD
- Pal
- Dehydrin
- NBS-LRR (rice, barley)

Rice IR64 x Azucena: blast (Ramalingam et al., 2003)

Wheat: tan spot and/or leaf rust (Faris et al., 1999)

Candidate genes are better predictors of QTL resistance than random SSR markers

- 20 random DR gene probes
- 20 random SSR markers

Liu et al. 2004
**RiceCAP**

- **Experimental approach**
  - To identify candidate defense response genes that may contribute to sheath blight QTL:
    - Selection from studies with Asian rice varieties (Ramalingam et al., 2003; Liu et al., 2004; Wu et al., 2004)
  - To determine if the candidate genes are associated with sheath blight QTL in US rice cultivars
    - In collaboration with mapping groups
  - To demonstrate the candidate genes function in resistance to sheath blight
    - RNAi experiments
    - Possible VIGS experiments
Project Contribution and Integration

• Identification of genes responsible for QTL for disease resistance
• Contribution of markers intimately associated with QTL for breeding program

First Year Benchmarks

• Confirm candidate defense response gene associations with sheath blight QTL
• Develop RNAi constructs for five ‘favorite’ candidates (based on studies with Asian rice)
Personnel Involved

• Graduate student (project covers ¾ of stipend + tuition) or part-time post doc
  – to be identified