Objective 1; Molecular Marker Support
Project Contribution and Integration

• Assist Molecular Breeding Team by marker identification

• Assist Gene Function team by candidate gene prediction

Hulbert
Fjellstrom
Leong
Nguyen

Personnel Involved

• PI’s Clare Nelson & Scot Hulbert
• Post Doc
• Graduate Student
Project Contribution and Integration

• Construct database & website
  Data presentation & interpretation to group/public

• Assist QTL mapping analyses

• Marker generation in specific genomic areas

• Candidate gene prediction/mapping (informatics)
  Informatics of sequence in QTL intervals

Informatics example: NBS-LRR genes

<table>
<thead>
<tr>
<th>Class</th>
<th>Description</th>
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<tbody>
<tr>
<td>2</td>
<td>nT-NBS-LRR</td>
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<tr>
<td>3</td>
<td>divergent nT &amp; NBS</td>
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<tr>
<td>4</td>
<td>nT-partial NBS - L-rich</td>
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<tr>
<td>5</td>
<td>partial NBS - LRR</td>
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<tr>
<td>6</td>
<td>S-rich – divergent TIR &amp; NBS</td>
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<tr>
<td>7</td>
<td>Pseudogenes</td>
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First Year Benchmarks

• Create database and web site (1st priority)
• Examine genomic/genetic information to identify candidate genes
• Begin annotating sheath blight QTL regions