Identification and Characterization of Host-Resistance Genes and Mechanisms to Sorghum Anthracnose Disease

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Background

- Sorghum anthracnose is a devastating disease
- Cultivar resistance – effective and viable
- Appropriate use of resistance genes
- Studies of mapping resistance loci – widely undertaken
Knowledge gaps

• Gene identification and characterization

• Molecular mechanisms of pathogen-recognition and resistance-responses

• Potential tradeoffs of the disease resistances
Objectives

• To identify and characterize genes that confer resistance

• To study the underlying molecular mechanisms

• To study potential tradeoffs of the resistance response
Sorghum genotypes were evaluated
Evaluation of sorghum genotypes identified resistant genotypes

<table>
<thead>
<tr>
<th>Strains of</th>
<th>Genotypes of sorghum</th>
<th>R 3</th>
<th>R 4</th>
<th>R 5</th>
<th>R 6</th>
</tr>
</thead>
<tbody>
<tr>
<td>C. sublineol</td>
<td></td>
<td>S</td>
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<tr>
<td>C. sublineol</td>
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</tbody>
</table>

Pathogen growth (qPCR)

Quantification of Pathogen growth (qPCR)

Host-pathogen combination
Genetic analysis suggested monogenic and dominant resistance

Parent 1

Susceptible

Parent 2

Resistant

F1

Resistant

F2

601 Resistant: 196 susceptible

(Fits to 3:1, $X^2 = 0.071$)
“BSA-seq” at F2 was used to identify the resistance locus

Takagi H. et al., The Plant J.(2013) 74, 174–183
“BSA-seq” mapping the resistance locus
Initial attempt to estimate & narrow-down # candidate genes

1\textsuperscript{st}: Average SNP frequency .............. 114 genes (sliding window)

2\textsuperscript{nd}: Gene annotation information.......... 23 genes

3\textsuperscript{th}: SNP, indel & codon information ..... 6 genes
Fine mapping narrowed the candidate locus

Based on 72 Susceptible F2 progenies

<table>
<thead>
<tr>
<th>Genotype</th>
<th>m1</th>
<th>m2</th>
<th>m3</th>
<th>m4</th>
<th>m5</th>
<th>m6</th>
<th>m7</th>
<th>m8</th>
<th>m9</th>
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<tbody>
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<td>37</td>
<td>43</td>
<td>62</td>
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<td>25</td>
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<td>7</td>
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<td>RR</td>
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<td>8</td>
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<td>1</td>
<td>0</td>
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<td>0</td>
<td>0</td>
<td>3</td>
</tr>
</tbody>
</table>

Markers within the candidate locus

3mbp

120kb
Candidate genes identified

Candidate genes

| NLR1 | IncRNA | NLR2 |
Gene expression suggested a more likely candidate gene

<table>
<thead>
<tr>
<th>parents</th>
<th>The candidate genes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>NLR1</td>
</tr>
<tr>
<td>Susceptible</td>
<td>✓</td>
</tr>
<tr>
<td>Resistant</td>
<td>✓</td>
</tr>
</tbody>
</table>

cDNA (parental & F2 of NLR2)
The sequence is highly polymorphic between parental lines

Predicted structure of the gene

- NLR1
- IncRNA
- NLR2

1 kb deletion

7.3 kb deletion

5.4 kb deletion

R parent

S parent

BTX623 (S)
Ongoing & future studies

- Characterization and validation
- Biology of the resistance response
- Gene regulatory network
- Potential resistance tradeoffs
Acknowledgment

• Dr T. Mengiste

• Dr G. Ejeta

• Postdocs and graduate researchers
Thanks