Controlled Phenotyping Method Study and Genotyping a TIL Population

Yulin Jia and Shannon Pinson

Coordinated Agricultural Project RiceCAP

• Objective #1.3.2 and 1.3.9
  – Development of a sheath blight greenhouse screening method
  – Development of a population /genetic analysis SB4, Teqing-into-Lemont introgression lines (TILs)

Goals: USDA-ARS, DB NRRC, Stuttgart
  – Coordinate the evaluation of existing sheath blight screening methods
  – Lead the genotyping of TIL population
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- Experimental approach (cont.)
  1) Evaluate the existing sheath blight screening methods-Soft drink bottle, mist chamber and detached leaf

Update:
- Detached leaf and mist chamber are in progress
- Coke bottle-completed two independent experiments

<table>
<thead>
<tr>
<th>Variety</th>
<th>RR0140</th>
<th>Rank</th>
<th>RR0321</th>
<th>Rank</th>
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<td>#3</td>
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<td>66.1</td>
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<td>Jasm. 85</td>
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RR0140 (slow growing) = mean of two expt.
RR0321(fast growing)= one expt.
Teqing-into-Lemont Introgression lines = SB4

Overview: TILs look good, in general. Phenotypically MUCH less variable the L/T RILs Lemont genetic background is quite evident

BUT NOT PERFECT
Discovery of the Problem (Shannon Pinson): 50% Teqing allele were detected in 2 of 11 markers….
• One SSR in Chromosome 1 and one SSR in chromosome 2
• Some TIL lines are still segregating phenotypically in 2004

Genotyping 57 BC3F2 Introgression Lines
Unique QTL for sheath blight resistance, independent of height and flowering loci found using Lemont/Teqing (SB4) wide cross

Range and Avg SB ratings 2004 in LA, BmtTX and AlvnTX

note: avg HD of R and S were both = 98 Dy to HD, ht avgs were different with R > S even so, some “good height” TILs with >R than LMNT were found

| TIL: 541 | 79 cm |
| TIL: 615 | 93 cm |
| TIL: 642 | 95 cm |
| TIL: 468 | 95 cm |
| TIL: 455 | 95 cm |
| LMNT | 94 cm |
| SABR | 95 cm |
| EARL | not semidwarf |
| KBNT | not semidwarf |
| TQNG | 111 cm |
Avg and Range of SB ratings 2004 in LA, BmtTX and AlvnTX

LMNT SABR EARL KBNT TQNG

1 2 3 4 5 6 7 8 9

SBR QTL LOD peak +/− 1 LOD

Chromosomes: Chr 1 Chr 3 Chr 4 Chr 7 Chr 8 Chr 12

Gaps easily filled by running more markers
Monomorphic regions needing ‘new markers’
Bob’s parental-line work has dev’d some!
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• Experimental approach (cont.)
  2) Genotyping the TIL population
     – Genotype background of 96 key lines with total of 150 markers – to ID “best, cleanest parents” for fine-mapping work.

Update, 93 key lines were selected by Dr. Pinson
     – Genotyped 133 SSR (115AR, 18 in TX), 33 monomorphic
     – 15 Key lines were identified to contain 1 to 4 of 18 known QTLs

Project Contribution and Integration

• Identified greenhouse phenotyping method would accelerate breeding, mapping populations, mutants and functional genomics of overall objectives

• The SSR data would confirm previously reported SBR-QTLs
• Facilitate the clean up of the TIL population for fine mapping-SBR-genes

• High density of SSR markers will allow the development of TILs to be a functional genetic tool, an important goal of CAP
First Year Benchmarks

– Complete the evaluation of sheath blight screening methods- Still going
– Complete the genotyping Key TILs for identifying the top 20 TIL lines for backcrossing- Done

Personnel Involved

• Yulin Jia and Shannon Pinson: USDA-ARS
  – UA two hourly employees and a Postdoc associate (two months of Lieceng Zhu’s time)

• USDA ARS DB NRRC One technician from Molecular Plant Pathology Group and one supporting staff scientist (15% of Melissa Jia’s time)
Plan of work for Year 2

• Continue the coordinated sheath blight greenhouse screening method study
• Lead genotyping the rest of TILs (170 lines)
• Map the identified candidates genes from Jasmine 85 by SAGE and Microarray using RIL population of Lemont and Jasmine 85 that is under development and also using improved TIL population