Molecular Effort

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

**RiceCAP**

- 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.
    Select the best 20 lines for Texas-ARS backcrossing into Lemont – for fine mapping efforts
RiceCAP

• Experimental approach (cont.)
  2) Genotyping TIL populations
     – Genotype remaining 170 TIL lines with 150 SSR markers
     – Implementation of recommendations by Boards
• Developing RILs of Lemont and Jasmine 85
• Verification of DNA Microarray data using a total of three biological replications

Project Contribution and Integration

• 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
• New sheath blight population-RIL of Lemont X Jasmine 85 would facilitate integration of molecular data from SAGE and DNA microarray.
Results

269 TILs-106 SSRs

Rate of successful marker amplification for each TIL:
62.7% - 100.0%

Out of 269 TILs:

19 (7.1%) TILs are heterozygous at ≥5 loci

30 (11.1%) TILs had non-parental alleles at ≥5 loci

Data were analyzed using JoinMap 3.0

Results

Among 269 TILs:

6.3% 17/269 TILs: skewed towards TQNG
Percentage of TQNG allele* ≥ 66.3%

7.8% 21/269 TILs: NOT skewed towards TQNG & LMNT
Percentage of TQNG allele = 36.6% – 64.6%

85.9% 231/269 TILs: skewed towards Lemont
Percentage of TQNG allele ≤ 34.3%

* Percentage of TQNG allele (%) = TQNG allele/(TQNG allele + LMNT allele)X100, data were analyzed by JoinMap 3.0.
Rice Responses to *R. solani*

Suppression began at 6 h, and induction began at 10 h and 16 h

QRT PCR Confirmation

**Relative Expression of Putative Defense Genes**
(Real-Time PCR Analysis)

- Housekeeping gene
- Gene 1
- Gene 2
- Gene 3
Conclusions

• Shannon Pinson selected 15 Best TILs;
• 150 TILs can be advanced to be an important functional genomic tool;
• Real time PCR is useful to test differential expressed genes at sheath blight QTLs.

Personnel Involved

• Yulin Jia: USDA-ARS, Stuttgart, AR
• Shannon Pinson, USDA-ARS, Beaumont, TX
  – Postdoctoral researcher (Guangjie Liu, 100%)
    • Evaluation of sheath blight screening method
    • Leading SB4 introgression genotyping
    • Developing RILs of Lemont X Jasmine 85

• USDA ARS DB NRRC One technician Knstantin Gubrij, from Molecular Plant Pathology Group and one supporting staff scientist (5%, Melissa Jia)

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