Johnson, Ken

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Sent: Monday, August 16, 1999 3:53 PM
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Subject: Quarterly report

Quarterly Project Report

Project Title: Search for Major Genes with Progeny Test Data to Accelerate the Development of Genetically Superior Loblolly Pines".

DOE project #: DE-FC36-99GO10380

1. The status of the technical scope of work:

The research project is progressing well for all three research tasks as proposed.

Task one - Develop Genetic Models and Analytical Methods: One post-doc and one Ph. D. student have been hired to assist PIs to work on this task. Four statistical tests (Bartlett test, Fain test, Log-anova test, and the mixture test) were investigated for detecting major genes that control quantitative traits. Computer simulation data with different degrees of major and poly-gene effects were generated for 6-parent half-diallel progenies. Power and robustness of each statistical test were assessed when the major gene has two alleles, and in the presence of a skewed phenotypic distribution or unbalanced data case. Several diallel progeny test data sets of loblolly pine diallel progeny tests were analyzed with those methods. The results showed that there were detectable major genes for tree height growth in the loblolly pine.

Task two -Molecular Confirmation of Major Gene Segregation: One Ph. D. student has been hired to assist PIs to work on this task. we obtained 260 RAPD markers from one of the 15 crosses from a diallel progeny test data. We also collected 20 -25 samples from each of the remaining 14 crosses in the diallel experiment to validate the quantitative model. DNA samples were isolated with Qiagen Kit. The data were analyzed with PGRI, using simple and multiple regression models. Four markers, M135, M137, M237, and M71, were found having significant association with QTLs controlling the growth rate of loblolly pine. Multiple-gene model analysis showed that over 21% of the within family variation could be explained with the three markers (M137, M237 and M71). M135 was not included due to the close linkage with M137. Both M135 and M137 had almost the same genetic effect. Two putative QTLs could be narrowed to the respond regions shorter than 10 cM when conditional interval mapping was conducted.

Task three - Develop Strategies for Marker-assisted breeding: This task involves in synthesizing the results from task one and two. A general outline has been formulated on how to utilize the pedigree and major gene information for breeding purpose

2. The level of completion (percentage) for each task:

The level of completion for each task is progressed well as scheduled:

Task one - Develop Genetic Models and Analytical Methods: 30%
 Task two -Molecular Confirmation of Major Gene Segregation: 20%
 Task Three - Develop Strategies for Marker-assisted breeding: 10%

3. Significant program/project tests or demonstrations scheduled in the next four months:

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No any program/project tests or demonstrations scheduled in the next four months.

4. Research results and papers presented in conferences:

The PIs, one post-doc and two students have presented the preliminary results to the industry supporters of this research project in two separate meeting. The first meeting was held on May 24 in Raleigh, NC and the second meeting was held on June 15 in Atlanta, GA. One Ph.D. student also presented the preliminary results in a paper to the Southern Forest Tree Improvement Conference on July 12 in New Orleans, LA. Collectively, we have made 13 presentation for different meetings from this research project.

5. Any variances to cost or schedule:

The hiring the post-doc I was delayed because of the delay in the DOE funding. We have not be able to hire Post-doc II for the task of molecular confirmation and hope to hire somebody in the next month or so. However, we will make efforts to meet the original schedule referring to each task.

Please let me know if you have questions about the details. Thanks.

Bailian Li
Project PI