Quarterly/Final Progress Report

For: QTL and Candidate Genes for Growth Traits in *Pinus taeda* L.

Covering Entire Granting Period: April 1, 2000 to October 1, 2002

Recipient: Claire G. Williams
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Consortium: International Paper, The Timber Company, Weyerhaeuser, Union Camp Corporation, PE-Celera,

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Project Objective: Develop low-copy microsatellites for *Pinus taeda* L. and conduct a molecular dissection of growth traits.

Summary:

Phase 1: Marker development.

Our enriched-copy libraries for developing microsatellites, made in 1999 prior to the DOE award, were based on isolating the low-copy or undermethylated portion of the *Pinus taeda* genome. These library methods made microsatellite development far more cost-effective. The protocols have been published.

Developed 245 nuclear microsatellite markers and released them to the public domain through 1) a Web site (http://forestry.tamu.edu/genetics), 2) an international workshop sponsored by USDA, NSF and Forest Service grants and 3) a training manual (Auckland et al. 2002 Conifer Microsatellite Handbook, Corporate Press, Raleigh NC 57 p). This effort was also aided by a short-term industrial marker consortium, a USDA-Forest Service Agenda 2020 grant and grant funds from the Texas Higher Education Coordinating Board. This phase of the project was published.

The importance of this microsatellite marker achievement is that other conifer groups worldwide have not been able to get any large number of microsatellite markers. There are three reasons for the lack of microsatellite markers:

1) the public sequences databases, another source of sequences bearing repeat motifs, have many EST sequences from coding regions but this type of pine sequence rarely has any polymorphic microsatellite repeat motifs,

2) the public sequence databases so not have the right knid of sequences for finding polymorphic repeat motifs. There are less than 100 genomic sequences from known, fully characterized