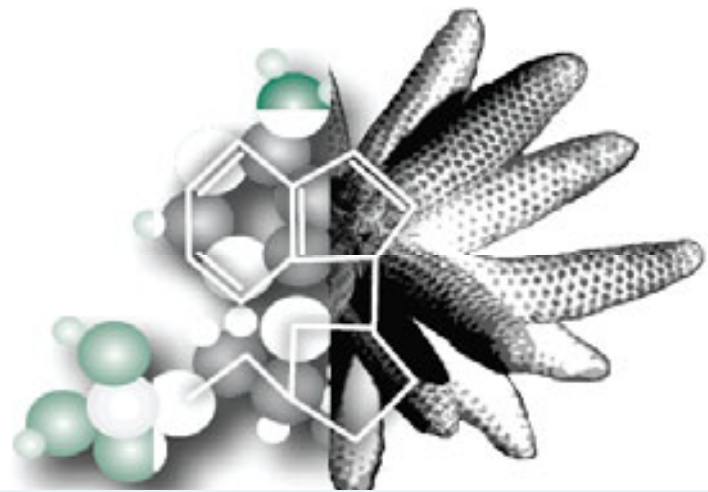


Pine Genome Initiative



Pine Genome Research: A Status Report

University of Georgia

Jeffrey F.D. Dean ~ December 6, 2007

Organized Research Community

HOME SCIENCE PLAN TREEGENES NEWS CONTACT CONIFER GENOME PROJECT

ABOUT THE CONIFER GENOME PROJECT

The Conifer Genome Project (CGP) is a federation of United States conifer genome researchers. The goal of the CGP is to advance conifer genome research through collaborative and integrated study. The CGP has developed a [Five Year Strategic Science Plan](#). The CGP executive committee will organize a meeting open to all conifer genome researchers in late 2006 or early 2007. Please contact any of the executive committee members with your comments and suggestions for advancing conifer genome sciences in the US.

David Neale
Dept. Plant Sciences
University of California, Davis

RESEARCH

- [Loblolly Pine Genome Project](#)
[Accelerating Pine Genomics - HGL](#)
[ACERT](#)
[ACERT2](#)
[Genomics of Wood Formation \(JWU\)](#)
[Loblolly Pine Endicovenense](#)
[Loblolly Pine, Red Genomes](#)
- [Douglas-fir Genome Project](#)
[ACERT](#)
[Aspen2002](#)
- [White Pine Genome Project](#)
[WPGP](#)

Conifer Genome Project - CGP
WebSite

EVENTS

- June 3-8, 2007
[Tree Biotechnology 2007](#)
Florida Delapala, Azores, Portugal
- June 19-22, 2007
[Western Forest Genetics Association \(WFGA\) Meeting](#)
Galveston, Texas

EXECUTIVE COMMITTEE

- [David Neale](#)
University of California, Davis
- [Jeffrey Dean](#)
University of Georgia
- [Glenn Howe](#)
Oregon State University
- [Hubert Grubb](#)
University of Maine

LINKS

- [Pine Genome Initiative](#)
- [Tutorials](#)
- [Conifer Genome Network](#)

A network of U.S. researchers working to characterize a complete conifer genome sequence.

www.pinegenome.org/cgp



International Collaboration

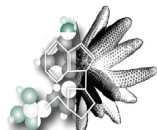


And an international network of researchers has organized to characterize a complete conifer genome sequence.

www.pinegenome.org



Recently Developed Pine Genome Resources



A Pine BAC Resource

- **Approximately 1 million BAC clones representing 6X genome coverage.**
- **Needs to be increased to 15-20X coverage.**

The screenshot shows the MGEL website with a navigation bar (ABOUT, RESEARCH, PUBLICATIONS, EDUCATION, OUTREACH, LINKS, HOME) and a search box. The main heading is "ACCELERATING PINE GENOMICS". Below it is a paragraph about the importance of southern yellow pines and the challenges of pine genomics. A small image of a pine tree is visible. The text continues with a list of goals for the MGEL's Pine Research project, including identifying genes for growth, disease resistance, and wood quality. It also lists several refereed publications and other major research projects.

MGEL's Pine Research

In 2004, a group of scientists lead by MGEL's David G. Peterson were awarded a grant from the **National Science Foundation's Plant Genome Research Program (PGRP)** to generate important molecular and cytogenetic resources for loblolly pine and utilize these resources to provide insight into the structure and evolution of the pine genome. The resulting multi-institutional project, **MS1-0421757**, has come to be known as the **Accelerating Pine Genomics** project or **APG** for short. The information generated in APG studies and the molecular resources themselves are providing the foundation for physical mapping and sequencing of the pine genome. Such molecular genetic information is critical if we are to protect pines and other forest trees from introduced pests and pathogens and develop of plantation pines for renewable raw materials/bioenergy production. See the **Accelerating Pine Genomics** website for details.

Referenced Publications or Book Chapters (to date) with MGEL Personnel as Authors

Lamoreaux et al. 2005, Beaga et al. 2006, Phelan et al. 2007, Daniels et al. 2007, and Chaveslaro et al. 2007.

Other Major Research Projects: Genetics of AspenGalls Resistance | Sequencing the Genome of the Redfirem Heterocyst | Engaging the Genome Sequence of Sorghum | Eukaryote Comparative Genomics | Cotton Genomics Resource Development

Mississippi State University | MAFFES | College of Agricultural, Forest & Life Sciences | DEPARTMENT OF PLANT & SOIL SCIENCES | apg

About Us | Research | Publications | News | Outreach | Outreach | Contact | Outreach | Home

MGEL © 2005. Web design by Foster B. Peterson. Last updated 11-Oct-2007.

www.mgel.msstate.edu/apg.htm

Pine Genome Initiative

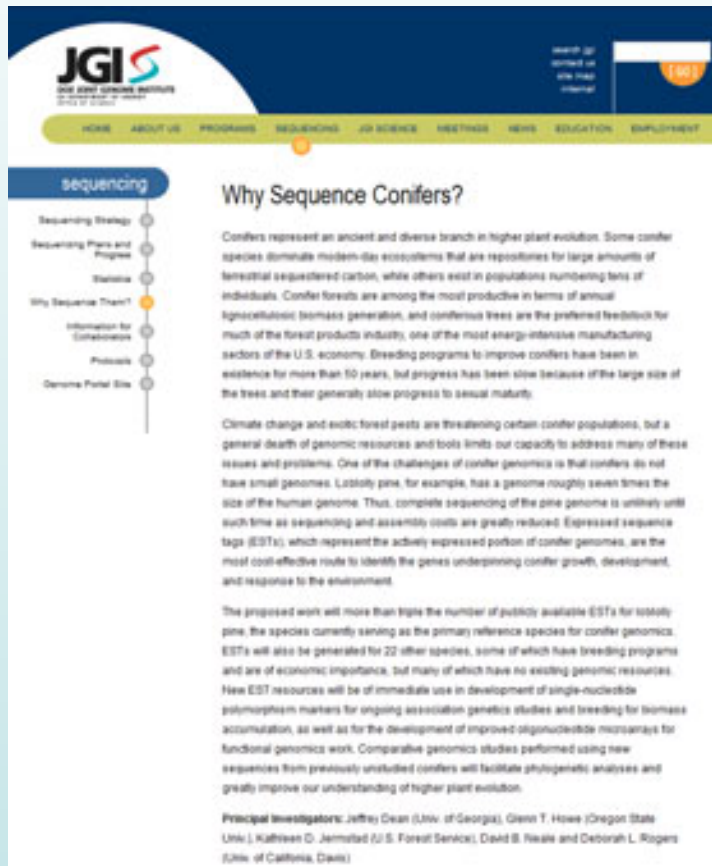


Why Pine, Why Now

www.pinegenomeinitiative.org
Institute of Forest Biotechnology

Slide 5

An Expanded EST Resource



The screenshot shows the JGI website with a navigation menu at the top. The main content area is titled 'sequencing' and 'Why Sequence Conifers?'. It contains several paragraphs of text discussing the importance of conifer genomes, the challenges of sequencing large genomes like pine, and the benefits of ESTs. A sidebar on the left lists various sequencing-related topics.

JGI
Joint Genome Institute
DOE and U.S. Department of Energy

HOME ABOUT US PROGRAMS SEQUENCING JOE SCIENCE MEETINGS NEWS EDUCATION EMPLOYMENT

sequencing

- Sequencing Strategy
- Sequencing Plans and Progress
- Statistics
- Why Sequence Them?
- Information for Collaboration
- Protocols
- Genome Portal Site

Why Sequence Conifers?

Conifers represent an ancient and diverse branch in higher plant evolution. Some conifer species dominate modern-day ecosystems that are repositories for large amounts of terrestrial sequestered carbon, while others exist in populations numbering tens of individuals. Conifer forests are among the most productive in terms of annual lignocellulosic biomass generation, and coniferous trees are the preferred feedstock for much of the forest products industry, one of the most energy-intensive manufacturing sectors of the U.S. economy. Breeding programs to improve conifers have been in existence for more than 10 years, but progress has been slow because of the large size of the trees and their generally slow progress to sexual maturity.

Climate change and exotic forest pests are threatening certain conifer populations, but a general dearth of genomic resources and tools limits our capacity to address many of these issues and problems. One of the challenges of conifer genomics is that conifers do not have small genomes. Loblolly pine, for example, has a genome roughly seven times the size of the human genome. Thus, complete sequencing of the pine genome is unlikely until such time as sequencing and assembly costs are greatly reduced. Expressed sequence tags (ESTs), which represent the actively expressed portion of conifer genomes, are the most cost-effective route to identify the genes underpinning conifer growth, development, and response to the environment.

The proposed work will more than triple the number of publicly available ESTs for loblolly pine, the species currently serving as the primary reference species for conifer genomics. ESTs will also be generated for 22 other species, some of which have breeding programs and are of economic importance, but many of which have no existing genomic resources. New EST resources will be of immediate use in development of single-nucleotide polymorphism markers for ongoing association genetics studies and breeding for biomass accumulation, as well as for the development of improved oligonucleotide microarrays for functional genomics work. Comparative genomics studies performed using new sequences from previously unutilized conifers will facilitate phylogenetic analyses and greatly improve our understanding of higher plant evolution.

Principal Investigators: Jeffrey Dean (Univ. of Georgia), Glenn T. Howe (Oregon State Univ.), Kathleen D. Jermoloff (U.S. Forest Service), David B. Reade and Deborah L. Rogers (Univ. of California, Davis)

<http://jgi.doe.gov/sequencing/why/CSP2008/conifers.html>

- **Public domain EST collection is ~350,000 sequences.**

- ~30K unique
- Significant NSF investment

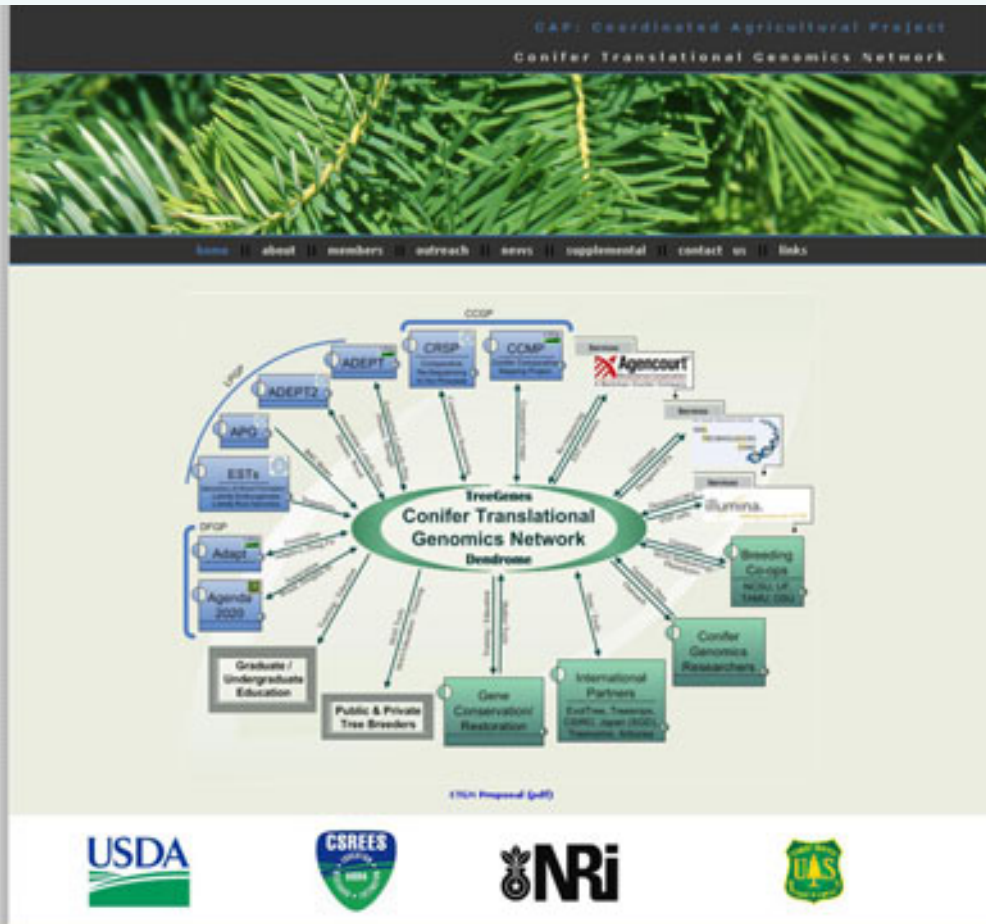
- **JGI will add 500,000 pine ESTs over 2 years.**

- Several million 454 sequencer reads for pine and other conifers

- **Will 454 yield a virtual transcriptome of full-length cDNAs?**



Advanced Molecular Breeding

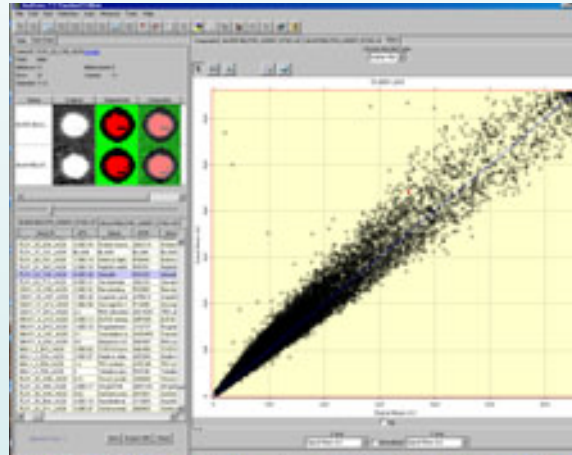
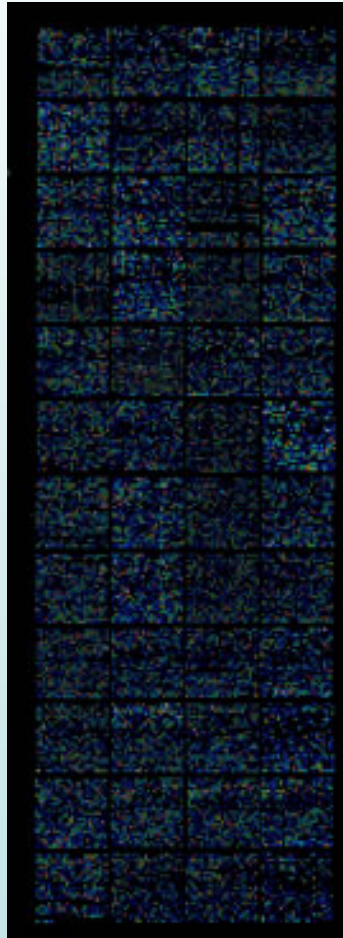


- Deployment of proven SNP markers on a high-throughput platform for conifer tree improvement cooperatives.
- Culmination of several projects funded by USDA, NSF and USFS.
- Substantial private investment through the tree improvement co-ops.

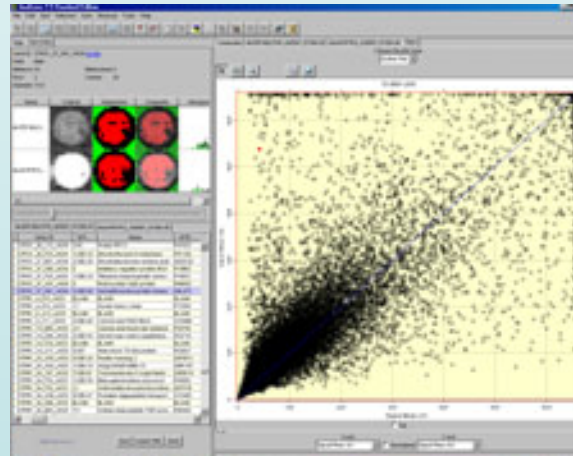
<http://www.pinegenome.org/ctgn/>



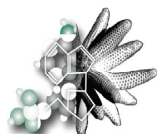
Pine cDNA Microarray (v.2.0)



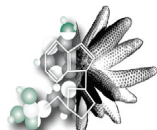
**Needle
v.
Needle**



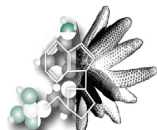
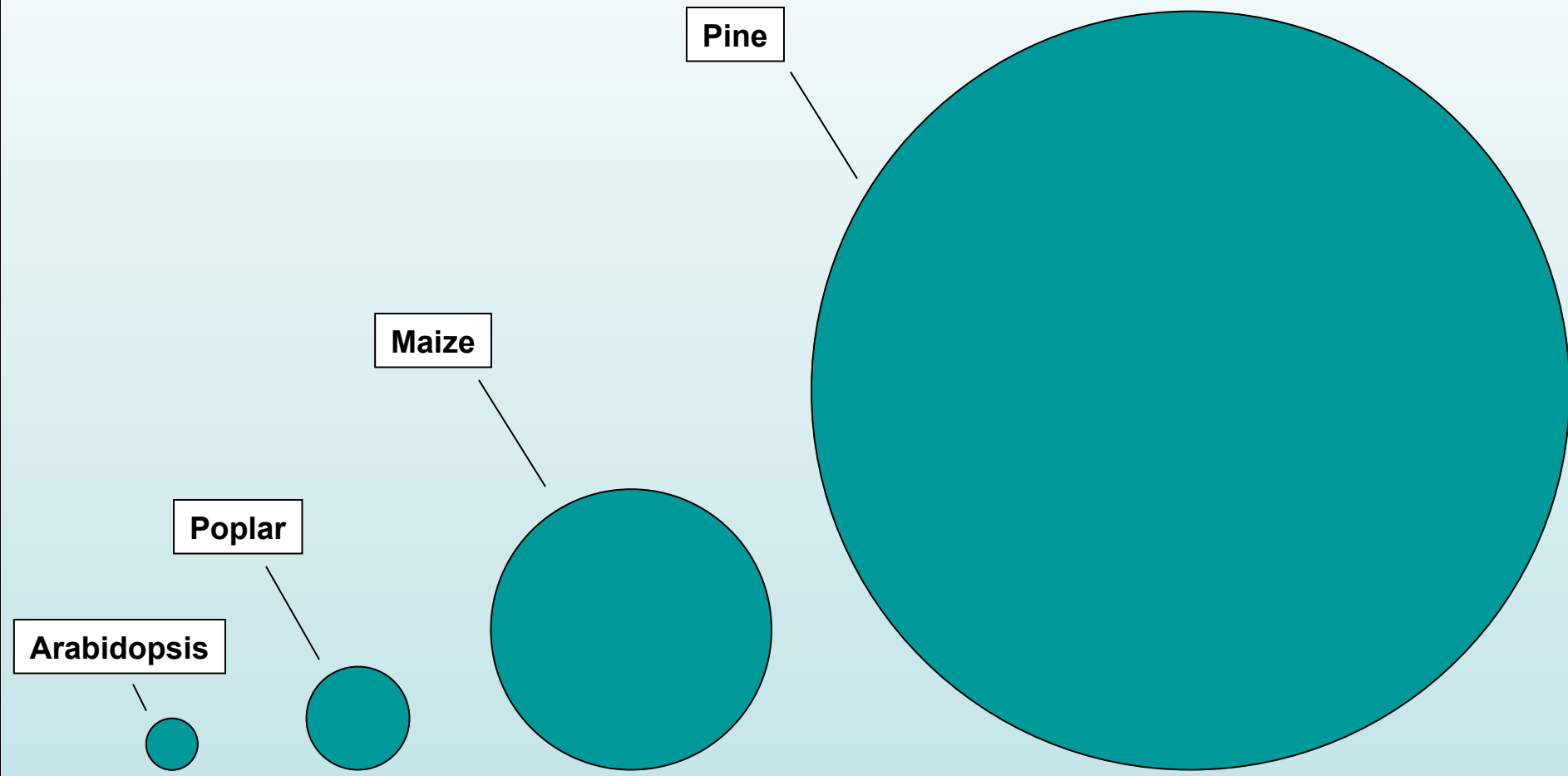
**Needle
v.
Stem**



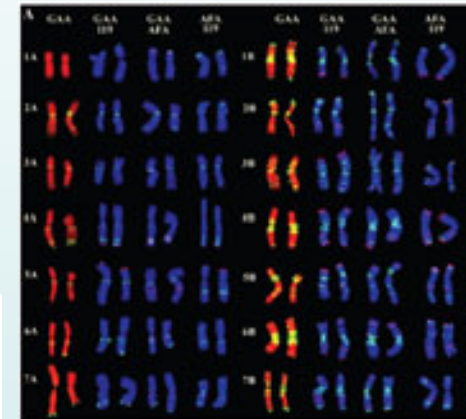
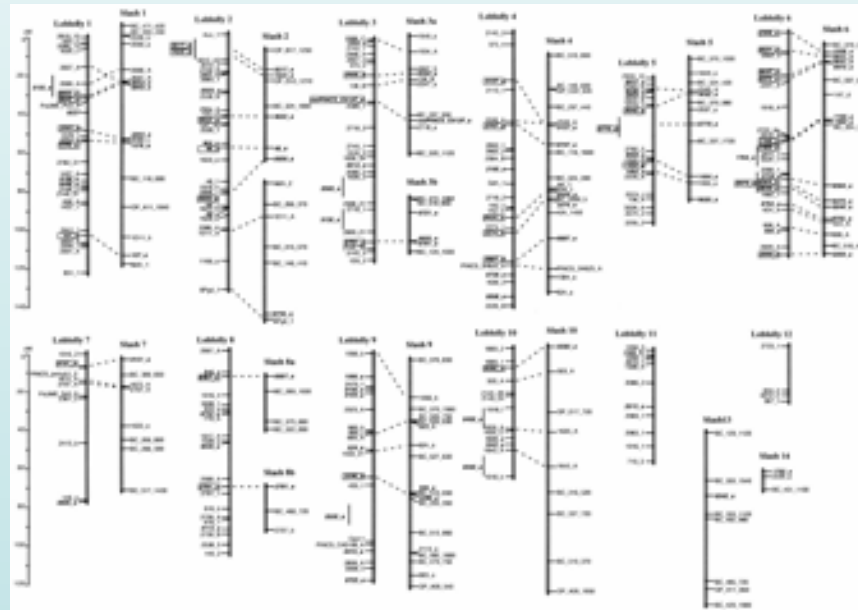
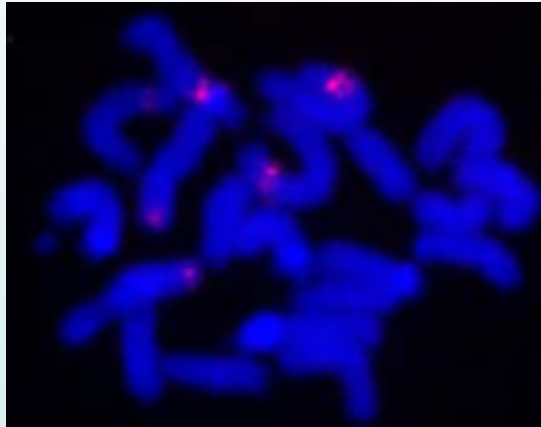
A Selection of Near-Term Issues



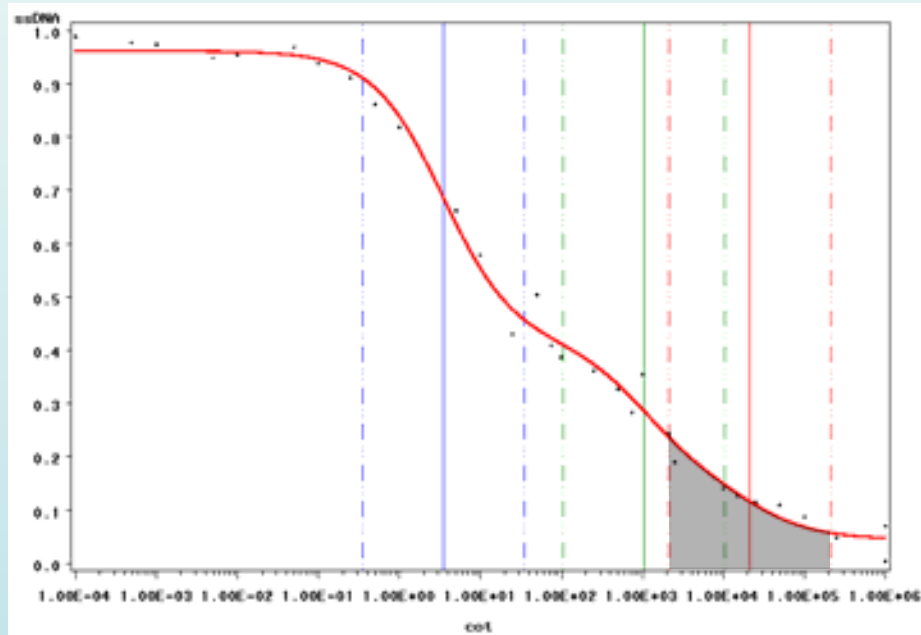
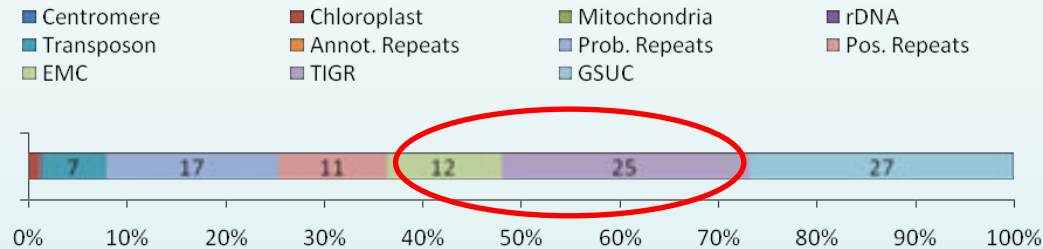
How Best to Subdivide the Work?



How do the Physical and Genetic Maps Align?



How Complex are the Gene Families?

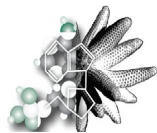


- **37% of random genomic DNA reads show primary homology to ESTs**
 - Ave repetitiveness 7X
- **10-12% of the genome looks unique**
 - Little homology to ESTs

Slide courtesy of D. Peterson, Miss. St.



Why Conifer Genomes Need Attention



Conifer Economics

- U.S. forest products industry
 - 7% of all manufacturing
 - 47% of raw materials production
 - Annual sales of \$230 billion
- Conifer trees
 - 65% of harvested trees in U.S. are conifers
 - 56% of these are southern pines
 - Loblolly pine alone provides 16% of **global** wood production
 - **Pine \$\$\$ = Maize \$\$\$**

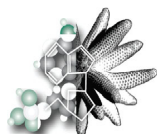


Commercial Competition

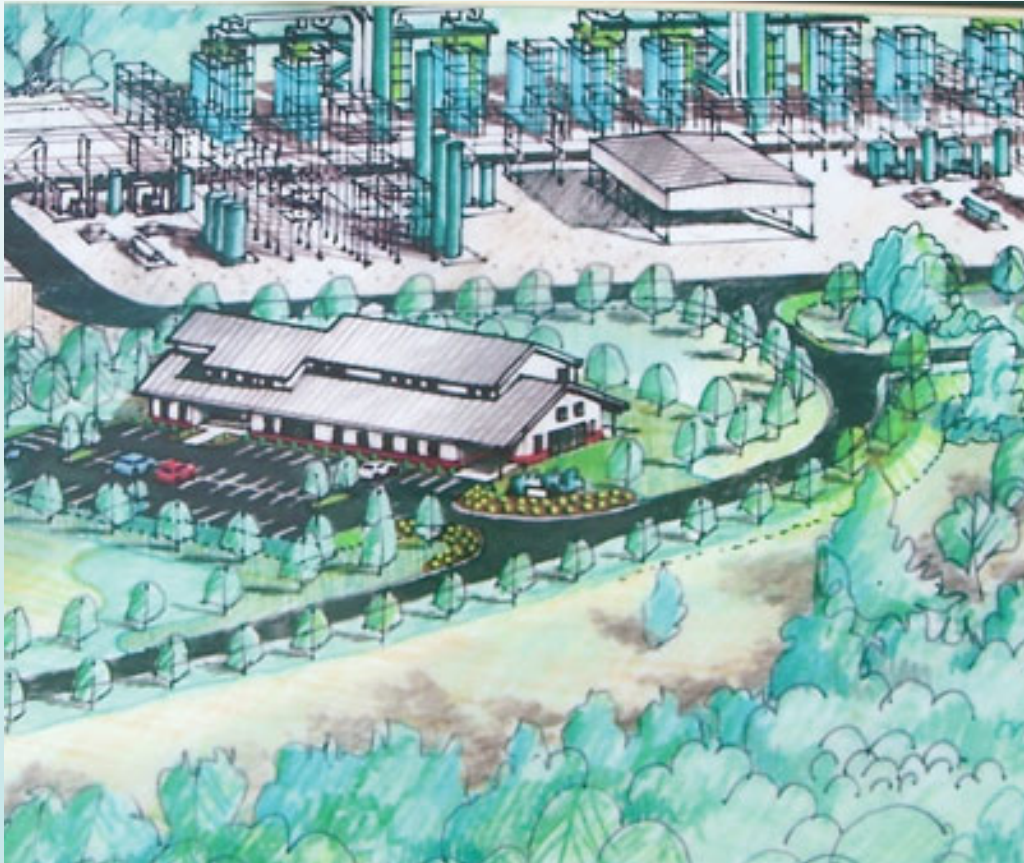
Ex: Loblolly Pine Production in Uruguay



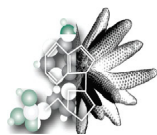
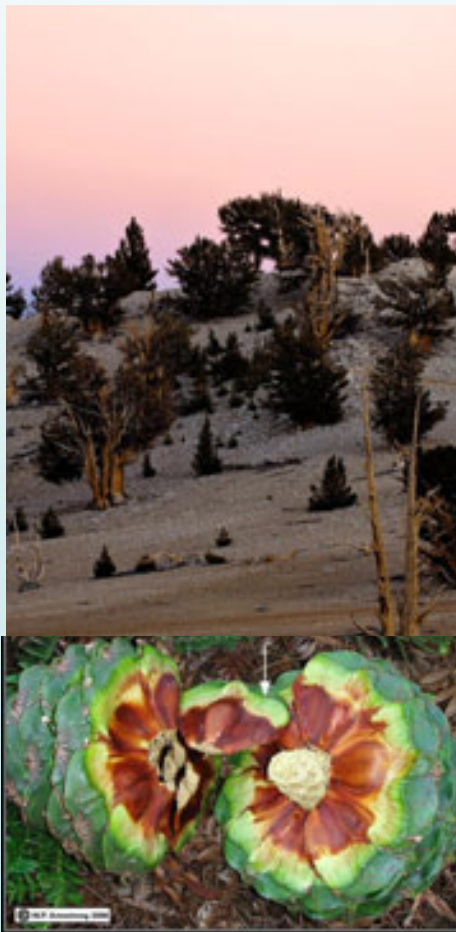
Rural Development



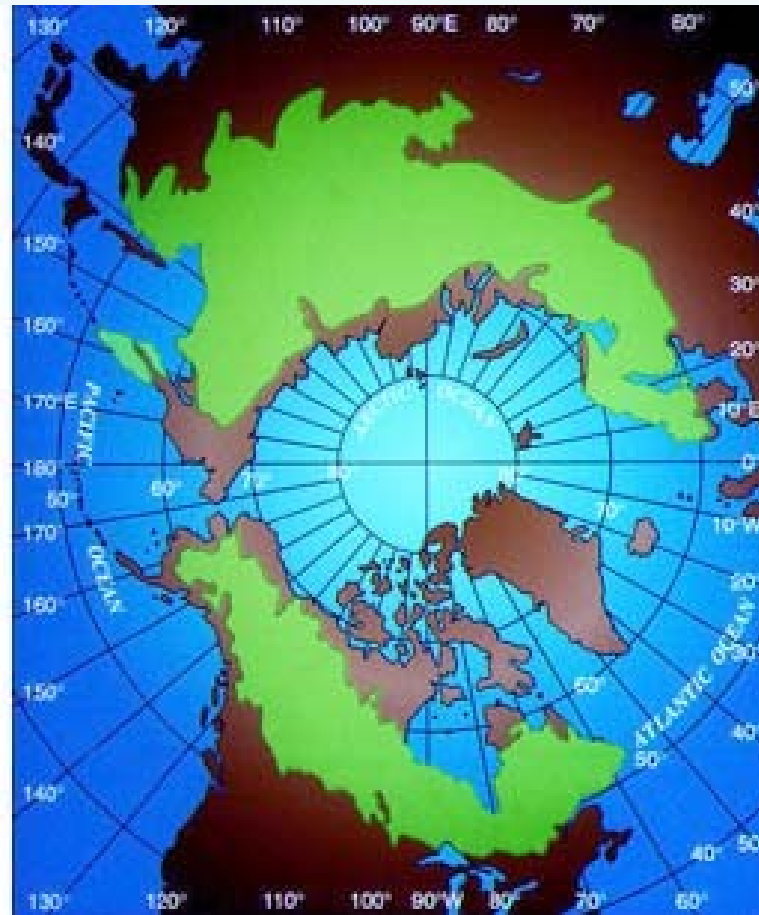
Biofuels from Forest Residues



Diverse & Ancient Species



Environmental Protection



Boreal forests represent ca. 1/3 of the world's forested lands



Disease and Pest Threats

**White Pine
Blister Rust**



Pitch Canker



**Sirex
Woodwasp**



**Hemlock
Wooly
Adelgid**



Genomic Data is Restructuring Plant Evolutionary Relationships

