

PineRefSeq

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**Conifer Genomics Workshop
Banbury Center
March 18-21, 2007**

Scientific
Advisory Committee

Tom Byram
David Jaffe
Pankaj Jaiswal
Richard McCombie

Collaborations

Sally Aitken, AdapTree, Canada,
Interior spruce and Lodgepole pine genomics
Rich Cronn, USA, Doug as-fir transcriptome
Pär Ingvarsson, Sweden, Norway spruce genome

Loblolly Pine Genome Project

Dendrome

Project Director
David Neale

Project Coordinator
Patrick McGuire

Training Coordinator
Nicholas Wheeler

Specific Aim 1

High quality reference
genome sequences of
loblolly pine and three
other conifer species

Charles Langley, Pieter de Jong,
Maxim Koriabine, Steven Salzberg,
James Yorke, Aleksey Zimin,
David Neale

Specific Aim 2

Transcriptome sequencing
for gene discovery, reference
building, and aids to genome
assembly

Keithanne Mockaitis, Carol Loopstra

Specific Aim 3

Dendrome and *TreeGenes*
databases: Annotation, data
integration, and distribution

Doreen Main, Jill Wegrzyn,
David Neale





PD David Neale (r), co-PD Jill Wegrzyn (c), and (l to r) John Liechty, Ben Figueroa, and Patrick McGuire UC Davis



The Maryland Genome Assembly Group featuring co-PD Steven Salzberg and Daniela Puiu (Johns Hopkins U) and co-PD Jim Yorke and Aleksey Zimin (U of Maryland)



(l to r) Co-PD Pieter de Jong, Ann Holtz-Morris, Maxim Koriabine, Boudewijn ten Hallers CHORI BAC/PAC



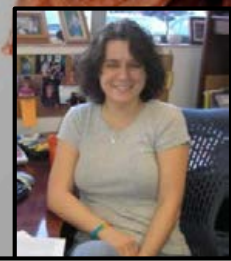
Co-PD Keithanne Mockaitis and Zach Smith Indiana U



Co-PD Chuck Langley (r) and (l to r) Marc Crepeau, Kristian Stevens, and Charis Cardeno UC Davis



Co-PD Carol Loopstra and Jeff Puryear TAMU



Co-PD Dorrie Main WSU

Guiding Principles of the PineRefSeq Project

- **EMPOWERMENT.** Our goal is to develop the technologies, platforms and bioinformatics infrastructures to rapidly and inexpensively sequence large and complex genomes of coniferous forest trees. This will allow the forestry community to begin sequencing the many genomes of economic and ecological importance without a dependence on centralized genome centers.
- **ADAPTIVE.** We recognize the sequencing technologies are developing rapidly and that we must have the expertise and flexibility to rapidly adopt new approaches into our overall sequencing strategy.
- **COMPARATIVE.** We recognize the power of comparative genomics approaches in assembling and annotating genome sequences and will use this approach throughout the project.
- **Open Access.** Unrestricted and rapid release of data.



Loblolly pine (*Pinus taeda*), n=12
 Genome size: 24,000 Mb
 Genotype to sequence: 20-1010
 Mapping population: 6-1030x8-1070 and
 20-1010x11-1060 (1000 F₁ progeny)



Sugar pine (*Pinus lambertiana*), n=12
 Genome size: 33,500 Mb
 Genotype to sequence: 6000
 Mapping population: 5038x5500 (1300 F₁ progeny)



Douglas fir (*Pseudotsuga menziesii*), n=13
 Genome size: 18,700 Mb
 Genotype to sequence: 412-2
 Mapping population: 412-2x013-1 (500 F₁ progeny)



Norway spruce (*Picea abies*), n = 12
 Genome size: 18,200 Mb
 Spruce Genome Project
<http://www.upsc.se/Networks/Networks/sprucegenome.html>



20-1010





