

# CTGN Newsletter

## Conifer Translational Genomics Network

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Coordinated Agricultural Project  
Conifer Translational Genomics Network

### ! CTGN Website has a New Look and New Content

The CTGN website (<http://dendrome.ucdavis.edu/ctgn>) has undergone a notable format change and acquired considerable content. We encourage you to take some time to browse. The CTGN CAP is thoroughly described in the material found at the **Home**, **Description**, and **Organization** links while details on the CTGN team, including quick email access, may be found at the **People** link.

The **Education and Extension** link provides easy access to a broad spectrum of information, in-

cluding announcements for Project-supported internships, our second annual Shortcourse on Genomics In Tree Breeding and Forest Ecosystems, and an international Symposium on Genomics in Tree Breeding that we will host in June of 2011. Access to teaching materials used in the 2009 Shortcourse and a graduate-level course offered at one of our participating institutions is also provided. Finally, we have enumerated all outreach presentations made by Project staff and provided detailed,

professional evaluation reports on all our major education and extension activities.

Readers may find all past Project progress reports and newsletters located at the **Reports** link and may quickly browse for fact sheets and past literature reviews at the **Resources** link.

### ! CTGN Science Progress

**Cooperative Forest Genetics Research Program (CFGRP), University of Florida (Dr. Dudley Huber—Co-PD)**

The CFGRP works primarily with slash pine (*Pinus elliottii*), secondarily with loblolly pine (*P. taeda*), and recently, has developed a hybridization program between the two species. We are using SNP markers developed in the CTGN project for an array of applications in our tree improvement program.

For instance, in our species hybridization and introgression program, markers will be used for foreground and background selection to signifi-

cantly speed up the process. Additionally, markers are finding application here for identifying genes/alleles from parental species that are controlling QTLs. Using genotypes for 261 individuals in a BC1 (pseudo-backcross) population, preliminary analyses were performed on 980 SNP loci whose alleles were segregating approximately 1:1. First the 980 loci were mapped and a scaffold of 180 loci selected and used in QTL searches. Among 1st year traits, QTLs were found for total height and basal diameter. More refined analyses await genotypes for a larger number of individuals. In addition to these traits we have measured tip moth incidence, vegetative phenology (bud burst, bud set), and crown and foliar characteristics, all traits that are of economic or adaptational significance. A paper was submitted for publication from

the analysis of 1st growing season traits, part of the MS thesis of **Patricio Muñoz**, a student supported by this project.

(continued on page 2)

### ? What is the CTGN?

The Conifer Translational Genomics Network Coordinated Agricultural Project (CTGN CAP) is an integrated research, education, and extension project aimed at maintaining or restoring healthy forests and ecosystems. It is a multi-state, multi-institution project, funded by USDA/NIFA/AFRI and the USDA Forest Service. The primary CTGN goal is to deliver genomics-assisted breeding capability to America's conifer tree breeders by linking laboratory and field research with a comprehensive education and extension program that seeks to provide widespread training for post-doctoral researchers, graduate and undergraduate students, tree breeders, managers, stakeholders, and the general public (see chart, page 4).

\* In this issue, we present brief reviews of the scientific progress made by our collaborating institutions, describe our recent CTGN website overhaul, introduce a project flow-chart that shows which CTGN unit handles specific tasks, and announce upcoming extension and education activities. The issue also features a literature review and a focus on the second of our institutional partners, the Western Gulf Forest Tree Improvement Program, along with an events calendar and interesting forest facts. We hope you enjoy the material and welcome your thoughts on what you might like to see delivered in future issues.

Nicholas Wheeler, Leader  
CTGN Extension and Education Teams

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<http://dendrome.ucdavis.edu/ctgn>

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02.2010

## CTGN Science Progress (continued)

**Industry Cooperative Tree Improvement Program (ICTIP) at North Carolina State University (Dr. Steve McKeand, Dr. Fikret Isik, and Dr. Ross Whetten—Co-PDs)**

ICTIP is engaged in several aspects of the CTGN project including 1) the validation of previously discovered SNPs by trait associations in operational tree improvement populations, 2) the development and evaluation of new methods incorporating marker-assisted selection into conifer tree breeding programs, and 3) the development and delivery of education and extension programs for students and cooperative members.

**Validation:** DNA sampling and SNP genotyping for the last 192 individuals (superior clones from a number of elite populations) will be completed by March 2010 which will allow **Jaime Zapata**, a PhD student supported by the CTGN at NC State, to finish statistical analysis of marker-phenotype validation. Jaime has been analyzing SNP marker data using TASSEL and ASReml software. Early results are very encouraging. An index to predict sawtimber potential for loblolly pine parents was recently developed. The index value was generated using BLUP breeding values for over 2000 progeny-tested parents; this method removes the environmental effects from field trials and is based on many progeny per parent. Approximately 220 parents had 4800 SNP genotypes available for association testing, which was performed in TASSEL using the parental index value for predicted sawtimber value as the phenotype. Results show 69 SNPs were significantly associated with predicted sawtimber value at the  $p < 0.01$  level prior to multiple testing correction. R-square values from the association tests were as high as 0.12 for the most significant SNPs. In addition, six field trials from elite clonally replicated test populations have been planted. This population consists of progeny from parents that have been genotyped through the CTGN. This population will provide a recruitment population from which selections can be made using a combination of phenotypic data and marker-trait associations with an operational population.

**Modeling marker applications:** The NCSU team has been working on several analytical tools to incorporate SNP markers in estimations of breeding values using routine BLUP analyses. Protocols have been developed for TASSEL, ASReml, and SAS software for processing large numbers of SNP markers using linear mixed models. The mixed models validate the association of SNP markers with the phenotypes (growth) while taking into account the population structure (relatedness in the data) and correcting for common and specific environmental variation. F-test probability values of markers are corrected for false discovery rates (q-values) and the significant markers are treated as random effects in mixed models to evaluate

their efficiency in improving average prediction error of estimated breeding values. We have also made progress on a simulation project. The objective is to understand the effect of population parameters (heritability, effective population size, number of markers in LD with the trait loci) on the accuracy of breeding value estimates, in simulated forest tree breeding populations. Ross Whetten wrote simulator software in R to create mating populations with different levels of heritability and differing numbers of QTLs in LD with SNP markers. The simulator software is being used to test alternative strategies for application of marker-trait associations in forward selection.

**The Pacific Northwest Tree Improvement Research Cooperative (PNWTIRC) and the Northwest Tree Improvement Cooperative at Oregon State Univ (NWTIC) (Dr. Glenn Howe – Co-PD)**

Douglas-fir genomic resources are inferior relative to the SNP resources and association databases in loblolly pine. Consequently, we are using transcriptome sequencing (454 and Illumina Genome Analyzer) to dramatically increase the number of SNP markers in Douglas-fir. RNAs isolated from a diverse array of genotypes, tissues, developmental stages, and environmental conditions are being used for sequencing, in a DOE Joint Genome Institute (JGI) project, and SNP discovery. JGI completed the construction of the normalized cDNA library, and we expect to receive 454 sequence by February 2010 (~1 million reads of 400 to 450 nts each). We are sequencing other Douglas-fir samples using Illumina sequencing (60 to 80 nt single-end reads), in collaboration with Richard Cronn (USFS). Samples for both sequencing projects were chosen to find SNPs in a diverse set of genes, while also testing library construction, multiplexing, and variability among technical and biological replications. The resulting SNPs from these projects will be used to design new SNP chips for Douglas-fir.

**Genetic Stock Centers (Dr. Dana Nelson and Dr. Brad St. Clair—Co-PDs)**

The United States Forest Service has committed to developing an international Genetic Stock Center as part of its role in the Conifer Translational Genomics Network. The primary goal of the stock center is to archive, curate, and make available to researchers valuable genetic material. The Forest Service is an important partner in this effort due to their commitment to long-term research.

There are three components to the stock center at this time: (1) a loblolly pine clonal archive at the Southern Institute of Forest Genetics, Southern Research Station near Saucier, Mississippi, (2) a Douglas-fir clonal archive at the Pacific North-

west Research Station near Corvallis, Oregon, and (3) DNA stored in  $-80^{\circ}\text{C}$  freezers at UC Davis. The archives of loblolly pine and Douglas-fir are genotypes from genetic mapping and association mapping populations from earlier studies. Approximately 2,000 clones are being propagated as grafts and rooted cuttings to be maintained by the Forest Service at those two field sites. The molecular biology resources include cDNA libraries and clones, BAC libraries and clones, mapping and association population DNAs, and PCR primer sets from earlier research. Dendrome and TreeGenes will be further developed to serve as the web resource and database components of the genetic stock center, to be maintained by CTGN staff at UC Davis.

Funding from the USDA for this project is making it possible to establish the field archives, set up the databases, and build a system for public distribution for these valuable genetic resources. Although the initial emphasis is on Douglas-fir and loblolly pine genotypes, our vision includes other conifers and perhaps also broad-leaved species. Our long-term goal is the complete integration and curation of the biological and information resources for forest tree genomics.



## ! TAMU—Western Gulf Forest Tree Improvement Program

The Western Gulf Forest Tree Improvement Program (WGFTIP) is one of three tree genetics cooperatives hosted by the Texas Forest Service. The pine program started in 1951 and was the first collaborative effort to improve forest trees for commercial use in the United States. From its inception, the program involved state forestry agencies, the Texas A&M University, and forest industries. WGFTIP focuses on loblolly pine (*Pinus taeda*) which accounts for over 90 percent of our seed production, but we also run smaller programs for slash pine (*P. elliottii*), shortleaf pine (*P. echinata*), longleaf pine (*P. palustris*), and Virginia pine (*P. virginiana*). Similar programs were later started for hardwoods and urban trees.

The WGFTIP was organized in its current structure in 1969. At that time, all active members were either forest industries planting trees on their own land or state forestry agencies supplying seedlings to the public. WGFTIP continues to support reforestation in the states of Arkansas, Louisiana, Mississippi, Oklahoma, and Texas. The current membership, however, is much more diverse than the founders could have ever foreseen. The thirteen members that support the active breeding program still include integrated forest industries that own both forest land and mills along with state forestry agencies. The program is also supported by a wide variety of organizations united by a common interest in forest genetics. This includes Timber Investment Management Organizations (TIMOs) and Real Estate Investment Trusts (REITs) that typically manage timberland as part of investment portfolios. These organizations are primary wholesalers of wood and are motivated to improve forest productivity to lower production costs. Others are seed companies that operate commercial nurseries marketing genetically improved seedlings. Finally, we have support from

### WGFTIP Mission Statement

*The objective of the WGFTIP is to provide sustained and coordinated leadership and technical assistance in the selection, propagation, and genetic testing of desirable clonal lines of southern pine and hardwood species. Further objectives are to promote cooperation in the area of forest genetics through the exchange of information, data, assistance, and plant materials between and among members, as well as the promotion of pertinent research.*

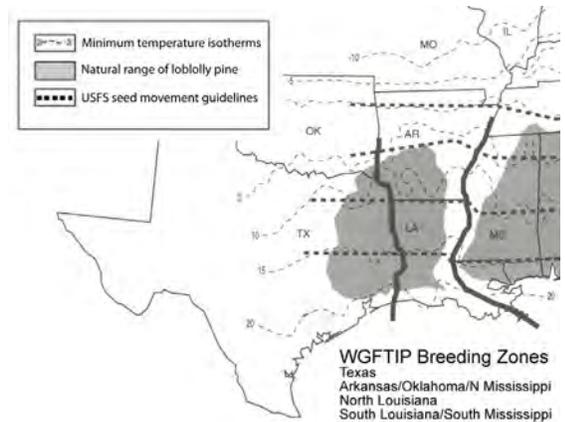
biotech companies that view genetic improvement as a foundation for new product innovation. Currently this includes both full-sib family forestry and clonal lines.

The WGFTIP staff headquartered in College Station includes Dr. **Tom Byram**, Dr. **Fred Raley**, **Marvin Lopez**, and **Joe Hernandez** with clerical support provided by **Penny Sowell**. Our interests are in applied tree breeding and deployment practices. The Texas Forest Service supplies field support to the program through the services of **I.N. Brown** and **Walter Burks** at the Magnolia Springs Seed Orchard and **Gerald Lively** and **Scott Taylor** stationed at the Arthur Temple Sr. Research Center in East Texas. Key collaborators on the CTGN project include Dr. **Konstantin Krutovskiy**, a population geneticist in the TAMU Department of Ecosystem Science and Management, and two of his students, **Tomasz Koralewski** (receiving support from CTGN) and **Vikram Chhatre**.

The ultimate objective of the CTGN is to apply molecular markers to forest trees for selection and breeding. The WGFTIP also anticipates using the data generated by the CTGN to better characterize the structure of its current breeding populations with an eye to improving both effectiveness and efficiency.

### \* Key innovations and adoptions

- 1) Sub-lined breeding populations for management of inbreeding.
- 2) Advancing-front seed orchards for rapid capture of genetic gain in the deployment population.
- 3) Complementary breeding and field testing protocols.
- 4) Clonal (S.E.) evaluation of selections in a wood quality elite breeding program.



WGFTIP staff headquartered at College Station (left to right): Joe Hernandez, Larry Miller (ret.), Penny Sowell, Fred Raley, and Tom Byram.



**\* From the Literature**

New or recent publications relevant to the science concepts of the CTGN CAP...

**Genomic selection in dairy cattle: Progress and challenges**

Hayes, B.J., P.J. Bowman, A.J. Chamberlain, and M.E. Goddard. 2009. *J. Dairy Sci.* **92**:433-443. doi:10.3168/jds.2008-1646

Genomic selection has revolutionized cattle breeding during the last several years. This article nicely summarizes the short history of genomic selection, its current applications in various countries, and some challenges. For tree breeders, it is time again to look at animal breeders to see if we can adopt their applications for use in tree improvement.

The authors link the genomic selection revolution with two developments: (1) sequencing of the bovine genome accompanied by discovery of thousands of SNP markers and inexpensive genotyping platforms and (2) the demonstration by Meuwissen et al. (2001) showing that breeding values can be predicted very accurately using markers alone.

The authors describe genomic selection in two steps: First, the effect of a small chromosome segment or SNP marker is estimated in a reference or training population using a linear mixed model. Significant SNPs from the first model are then fitted simultaneously in a second linear mixed model to obtain predictions for each SNP. In the subse-

quent generation, the progeny are genotyped and only marker information is used to estimate breeding values without progeny testing.

The authors summarize the application of genomic selection in dairy cattle breeding around the world and compare the results. A common finding in the United States, New Zealand, and Australia was that a straightforward BLUP method for estimating marker effects gave reliabilities of genomic-estimated breeding values almost as high as more complex methods, such as Bayesian methods.

The criterion for successful genomic selection is measured by the accuracy of breeding values. The authors discuss the parameters that affect the accuracy of genomic selection. The parameters are linkage disequilibrium, population size, heritability, and the distribution of QTL effects. The authors conclude that for successful genomic selection, single markers must be in sufficient LD with the QTL. For forest trees, this suggests that a large number of markers is required because the genome size of trees is large and LD decays rapidly. The authors suggest that there should be a large number of animals with phenotypic records to estimate the effects of SNPs. Another important parameter is heritability. A high heritability requires fewer phenotypic records. Finally, if there are many QTLs of small effects, a large number of phenotypic records

will be required to estimate marker effects accurately.

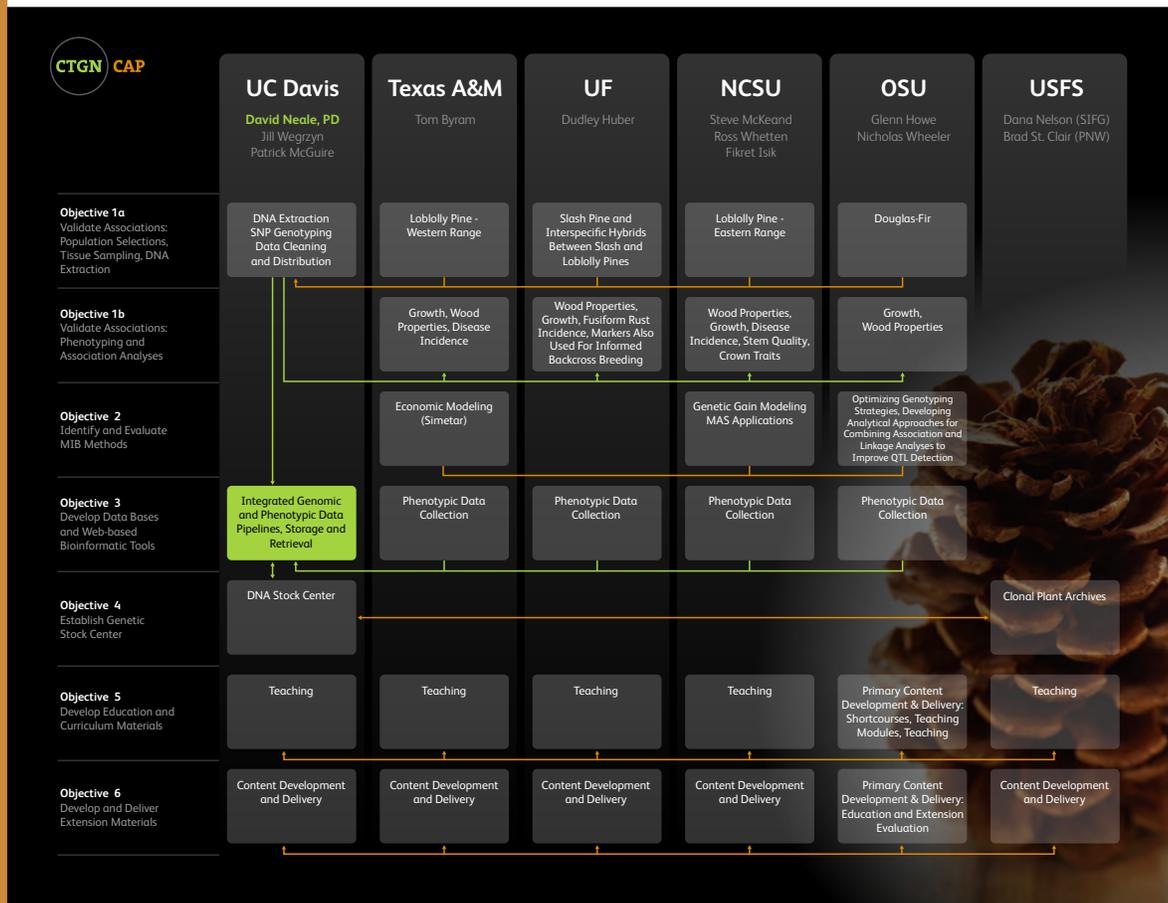
The implications of genomic selection summarized by the authors are profound. According to some estimates, using genomic selection, progeny testing can be avoided in cattle breeding which saves up to 92% of the cost of testing. The increase in reliability is sufficiently high such that at least two dairy breeding companies are already marketing bulls for commercial use based only on their genomic estimated breeding values at two years of age. The authors predict that the genomic-selection strategy should at least double the rate of genetic gain in the dairy industry, mainly by reducing breeding cycles and eliminating progeny testing.

The major challenges with genomic selection and its implementation are (i) increasing the accuracy of genomic selection, (ii) integrating genomic information into national and international genetic evaluations, and (iii) managing long-term genetic gain.

If genomic selection works for forest trees, it will surely revolutionize tree breeding. The impact on tree breeding would be much larger than for any other crop and animal species because forest trees have a longer cycle of breeding.

*Reviewed by Fikret Isik.*

*Cited reference:*  
Meuwissen, T.H.E., B.J. Hayes, and M.E. Goddard. 2001. Prediction of total genetic value using genome wide dense marker maps. *Genetics* **157**:1819-1829.



**CTGN CAP organization chart.** Columns represent the collaborating units and rows depict specific components of the Project objectives. Colored lines represent the flow of activities and information.

## ! CTGN Education and Extension

The Extension and Education elements of the CTGN Project are managed by Dr. **Nicholas Wheeler** at Oregon State University. He may be reached by email ([wheeleni@onid.orst.edu](mailto:wheeleni@onid.orst.edu)) or phone: 360-278-3535 (office) or 360-701-4886 (cell).

### “Genomics in Tree Breeding and Forest Ecosystems”—June 21–25, 2010

A five-day shortcourse designed to provide a complete introduction and review of genomics applications for graduate students and practicing professional tree breeders and genetic resource managers will be offered on the Oregon State University campus in Corvallis, OR. Details on the shortcourse, with directions for application, may be found at our Project website (<http://dendrome.ucdavis.edu/ctgn/educationextension/shortcourse.php>).

### “Genomics for Applied Tree Breeding and Ecosystem Management – With Application to Gene Conservation and Climate Change”—July 13–14, 2010

The one- to two-day workshop will focus primarily on the application of genomics in the characterization and management of natural populations, though there will be an applied breeding element. The workshop will be hosted by the USDA Forest Service’s Dorena Genetic Resource Center in Cottage Grove, Oregon. It will deliver information for geneticists and natural resource managers from regional Federal Agencies who might not otherwise be able to attend the full five-day shortcourse in June (described above). The workshop announcement may be viewed at [http://dendrome.ucdavis.edu/ctgn/files/2010Workshop\\_OR.pdf](http://dendrome.ucdavis.edu/ctgn/files/2010Workshop_OR.pdf). All inquiries regarding this workshop should be directed to Dr. **Richard Sniezko** ([rsniezko@fs.fed.us](mailto:rsniezko@fs.fed.us)).

### “Genomics-Based Breeding in Forest Trees”—June 22–24, 2011

This international symposium will focus on the application of markers in tree breeding. We anticipate having a limited number of invited speakers representing applications of genomics in crops and livestock as well. Those interested in receiving email announcements and notifications for the Symposium should contact **Patrick McGuire** ([pemcguire@ucdavis.edu](mailto:pemcguire@ucdavis.edu)) with their contact information. Updates on Symposium progress will be posted at our Project website: <http://dendrome.ucdavis.edu/ctgn/educationextension/symposium.php>.

### Presentations/Posters

\* Andrew J. Eckert, Jill L. Wegrzyn, Jennifer M. Lee, John D. Liechty, Kristian Stevens, Kathleen D. Jermstad, Betty Woolf, Wei Tao, C. Dana Nelson, Santiago C. Gonzalez-Martinez, Charles H. Langlely, and David B. Neale. 2010. Patterns of nucleotide diversity and associations to environ-

mental heterogeneity across the functional gene space of loblolly pine (*Pinus taeda*). Plant and Animal Genome XVIII, Forestry Workshop.

- \* Jill L. Wegrzyn, Ben Figueroa, Minyoung Choi, John D. Liechty, Andrew J. Eckert, and David B. Neale. 2010. Bioinformatic Solutions for data storage, analysis, and interpretation in forest genomics: Overview of the tools and resources from the Dendrome Project. Plant and Animal Genome XVIII, Forestry Workshop.
- \* Fikret Isik and Ross Whetten. 2010. Effects of marker numbers and population parameters on the accuracy of predicted breeding values in forest trees. Plant and Animal Genome XVIII, Forestry Workshop.
- \* Ross Whetten. 2009. Conifer Translational Genomics Network (CTGN). Using markers in tree breeding. A presentation given to the NC State University Cooperative Tree Improvement Program Contact Meeting, Dec. 3–5, 2009. Tuscaloosa AL.
- \* Anna Stambolia-Kovach, Jill L. Wegrzyn, Genis Parra, Carson Holt, James Hartigan, Charles M.

Nicolet, George E. Bruening, Michela Troggio, Carol Loopstra, Mark Yandell, Ian Korf, Charles H. Langlely, and David B. Neale. 2010. Whole genome shotgun and BAC sequences in loblolly pine (*Pinus taeda* L.): The majority of the 22-Gb genome appears to be highly diverged and nested repetitive elements. Plant and Animal Genome XVIII, Forestry Workshop.

### Curriculum development

**Fikret Isik** (NCSU) taught a graduate course called Quantitative Forest Genetics at NCSU in which genomics-based selection using mixed models was incorporated. Graduate students working with the NCSU Tree Improved Cooperative attended the course and learned the theory and application of mixed models for genomics-based selection and creating kinship matrices from markers.

**David Neale** (UC Davis) will be teaching a molecular breeding course (Genetics Graduate Group GGG 298) at UC Davis this spring quarter. A syllabus will be posted at the CTGN website in the near future.

SHORTCOURSE
OFFERED BY **CTGN** CAP

GENOMICS  
IN TREE BREEDING  
AND FOREST  
ECOSYSTEMS

June 21–25, 2010  
Oregon State University  
Corvallis, OR

Shortcourse Fee: \$250  
(covers housing, meals, and  
course supplies)

Application Deadline:  
April 1, 2010

**A shortcourse on genomics-based strategies for plant breeding and gene-resource management, with examples from forest trees, food crops, livestock, and humans.**

**Overview**  
The Conifer Translational Genomics Network Coordinated Agricultural Project will offer an intensive, five-day shortcourse on genomics in plant breeding and gene-resource management. The course, organized in module format, will provide detailed overviews of genomics-based breeding strategies (e.g., MAS / MAB) and gene-resource management through lectures and interactive learning (computer exercises). Modules will address such topics as population and quantitative genetics; molecular population genomics; genetic, QTL, and association mapping; genomics-assisted breeding; and genomic applications in gene-resource and ecosystem management.

**Target Audience**  
Graduate students, post-doctoral scientists, breeders, and gene-resource managers are invited to register for the course. In special circumstances, advanced undergraduate students will be considered. Professional and university course credit may be offered. There are no formal prerequisites, but prospective participants should have general familiarity with topics such as population and evolutionary genetics, molecular and quantitative genetics, genealogy, or plant breeding.

**Sponsored by**








**Application Information:**  
<http://dendrome.ucdavis.edu/ctgn>

**Project personnel**

University of California, Davis

**David Neale**, Project Director, team leader for Obj. 1

**Jill Wegrzyn**, Co-PD, team leader for Obj. 3

**Patrick McGuire**, Co-PD, Project Coordinator, team leader for Obj. 4

University of Florida

**Dudley Huber**, Co-PD, team leader for all breeding, testing, phenotyping, and association testing in slash pine at Florida (Obj. 1.4)

North Carolina State University

**Steve McKeand**, co-PD, team leader for breeding/testing, phenotyping, and association testing in loblolly pine in the eastern range of the species (Obj. 1.2)

**Fikret Isik**, Co-PD contributing to methods development: MAS/MAB applications (Obj. 2)

**Ross Whetten**, Co-PD contributing to association testing and evaluation (Obj. 1.2)

Texas A&M University

**Tom Byram**, Co-PD, co-team leader with Wheeler for methods development: MAS/MAB applications (Obj. 2)

Oregon State University

**Glenn Howe**, Co-PD, team leader for phenotyping and association testing in Douglas-fir (Obj. 1.5)

**Nicholas Wheeler**, Co-PD, co-team leader with Byram for methods development: MAS/MAB applications (Obj. 2) and team leader for curriculum development (Obj. 5) and curriculum delivery (Obj. 6)

United States Forest Service, Southern Institute of Forest Genetics

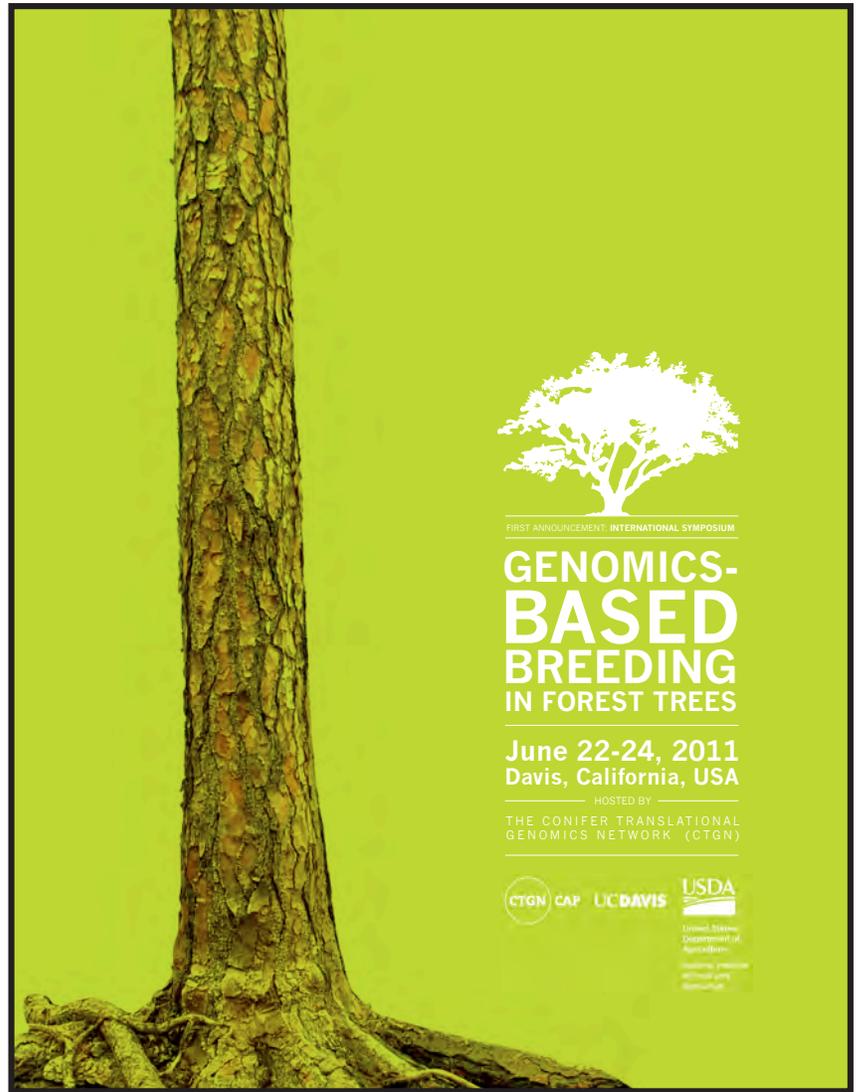
**Dana Nelson**, Co-PD, contributing to the development of the Genetic Stock Center (Obj. 4)

United States Forest Service, Pacific Northwest Research Station

**Brad St. Clair**, Co-PD, contributing to the development of the Genetic Stock Center (Obj. 4)

Cedar Lake Research Group, LLC  
Portland OR

**Michael Coe**, Education/Extension  
Evaluation Manager



FIRST ANNOUNCEMENT: INTERNATIONAL SYMPOSIUM

**GENOMICS-BASED BREEDING IN FOREST TREES**

June 22-24, 2011  
Davis, California, USA

HOSTED BY  
THE CONIFER TRANSLATIONAL GENOMICS NETWORK (CTGN)



**Tree Facts**

*Historical trends indicate that the standing inventory (the volume of growing stock) of hardwood and softwood tree species in US forests grew by 49 percent between 1953 and 2006. Interestingly, the number of acres of forestland in the USA has remained essentially the same during the past century. The USA, with 8 percent of the world's primary forest, ranks fourth on the list of most forest-rich countries, following the Russian Federation, Brazil, and Canada. On average, 11 percent of the world's forestland benefits from some type of conservation effort. In the USA, 20 percent is protected by conservation initiatives. (From: The State of America's Forests, Society of American Foresters, <http://www.eforester.org/publications/americanforests/StateOfAmericasForests.pdf>).*

**CALENDAR**

- June 17–18, 2010.** CTGN CAP Annual Meeting. Oregon State University, Corvallis OR USA.
- June 21–25, 2010.** CTGN CAP Short Course. Oregon State University, Corvallis OR USA.
- September 20–25, 2010.** Fifth International Poplar Symposium (IPS-V). Orvieto, Italy. (<http://www.sisef.it/IPS-V/>)
- June 22–24, 2011.** International Symposium—Genomics-Based Breeding in Forest Trees. University of California, Davis CA USA.
- June 26–July 1, 2011.** International Conference—Tree Biotechnology 2011: From Genomes to Integration and Delivery. Porto Segura, Bahia, Brazil. Contact: **Dario Gratapaglia** ([dario@cenargen.embrapa.br](mailto:dario@cenargen.embrapa.br)).

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United States  
Department of  
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Agriculture