

CTGN Newsletter

Conifer Translational Genomics Network

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Coordinated Agricultural Project
Conifer Translational Genomics Network

? 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 by bringing genomic-assisted breeding to applications in the United States. It is a multi-state, multi-institution project, funded by the USDA National Institute for Food and Agriculture (NIFA, formerly CSREES) and the USDA Forest Service. (In its first two years, the Project was funded by the CSREES National Research Initiative. Following reorganization at USDA, the third and fourth years are being funded by the Agriculture and Food Research Initiative—AFRI).

The primary goal of the CTGN Project is to deliver marker-assisted selection (MAS) and marker-assisted breeding (MAB) to America's tree breeding cooperatives which provide over 1.3 billion seedlings annually in the United States. We are leveraging over 50 years of tree breeding experience and population development from the cooperatives with the results from 15 years of experience in the molecular dissection of complex traits to further develop MAS/MAB tools that accelerate the rate of tree breeding. These 15 years of research represent a remarkable convergence of public funding and multi-institution, multi-investigator collaborations. Investments in conifer genetics were made by the major US public funding sources for plant genomics research, the USDA CSREES and the US National Science Foundation Plant Genome Research Program (NSF PGRP). Building on the groundwork of early markers and genetic maps and mapped QTLs, several large-scale projects accelerated the pace of linking traits with markers and optimized the technology platforms for efficient high-throughput use with conifers. The ADEPT Project (Allele Discovery of Economic Pine Traits) was funded by the USDA CSREES Initiative for Future Agriculture and Food Systems (IFAFS) and identified single nucleotide polymorphism (SNP) markers within candidate genes controlling economically important traits in loblolly pine. Similarly, the ADAPT Project (USDA CSREES National Research Initiative funding) generated marker/trait associa-

tions in Douglas fir. The ADEPT2 Project (NSF PGRP funded) further added to the SNP database by taking advantage of high-throughput sequencing technology to resequence amplicons from candidate genes from a range-wide sample of loblolly pine. In these projects the associations made between the markers and the traits were validated in experimental 'discovery' populations created for the purpose of these genomic analyses. Links for further information on these and other stage-setting projects are available from the home page of the CTGN website (<http://dendrome.ucdavis.edu/ctgn>).

We seek to marshal this research experience and expertise and the markers and genomic tools and innovations and apply them to the validation of the markers in operational breeding populations in use by the tree improvement cooperatives (our Objective 1 below). Methods for implementing MAS/MAB to use these validated markers in applied tree breeding programs are being defined and economically evaluated using assumptions derived from study results (our Objective 2). Project outcomes are being delivered directly to breeders and documented in databases (part of Objective 3) maintained on the web at the Dendrome/TreeGenes site (<http://dendrome.ucdavis.edu>). This work adds great value to the validation populations. To improve their long-term security, clonal archives of these populations are being established as a genebank. In addition, the significant molecular biology re-

sources and reagents for conifers developed over the years such as cDNA libraries and clones, BAC libraries and clones, mapping and association population DNAs, and PCR primer sets will be curated along with the clonal archives to form a conifer genetic stock center (our Objective 4). A comprehensive education and outreach program is providing widespread training for school teachers, undergraduate and graduate students, tree breeders, managers, lay-people and other stake-
(continued on p. 2)

* The CTGN CAP kicks off its third year this month by introducing this first issue of our Newsletter. It is intended to provide a wider range of information and materials to a broader audience than did our former means of communication, "The Project Progress Report". The Newsletter will be published on a quarterly basis and will feature Project updates, extension and education materials and activities, a calendar of events, relevant articles and websites of interest, and background information on collaborating labs and organizations. It will be distributed electronically, via email, and posted on our Project website. We welcome suggestions for content of future issues.

In this issue the collaborator focus is on the co-Project Directors from the North Carolina State University Department of Forestry and Environmental Resources and the North Carolina Cooperative Tree Improvement Program (p. 3).

Nicholas Wheeler, Leader
CTGN Extension and Education Teams

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Contents

| | |
|-----------------------------|---|
| Project organization | 2 |
| UC Davis role | 2 |
| Featured cooperator | 3 |
| Current literature | 4 |
| Education & Extension | 5 |
| Research results | 6 |
| Personnel; Calendar | 6 |

Issue: 01

10.2009



? Who is the CTGN?

The CTGN team is distinguished among the crop CAPs in that most team members are involved in both of the two distinct but critical elements of our Project: *providing* the science to validate genetic associations and *directing* the major tree improvement cooperatives that will apply the technology in operational programs. In this sense, we are simultaneously the drivers behind the science, the immediate target of extension, and the platform for delivering education and more distributed extension materials. Team members, listed in the box on page 6, represent five universities, the Texas Forest Service, and the United States Forest Service. We derive guidance and feedback from advisory committees: a Scientific Advisory Board, an Extension Committee, and an Education Committee (see Figure 1). Project evaluation for extension and education activities is provided by an independent evaluator, Dr. Michael Coe of Cedar Lake Research, Inc.

The Project Director and Coordinator coordinate and facilitate all management activities including daily communications, budget and finances, progress reports, annual meetings, and website postings. Team Leaders are responsible for management, evaluation, and monitoring of specific goals and objectives. Project communication takes place by email, individual and conference calls, the tools of the Project website, and annual Project meetings.

? What is the CTGN?

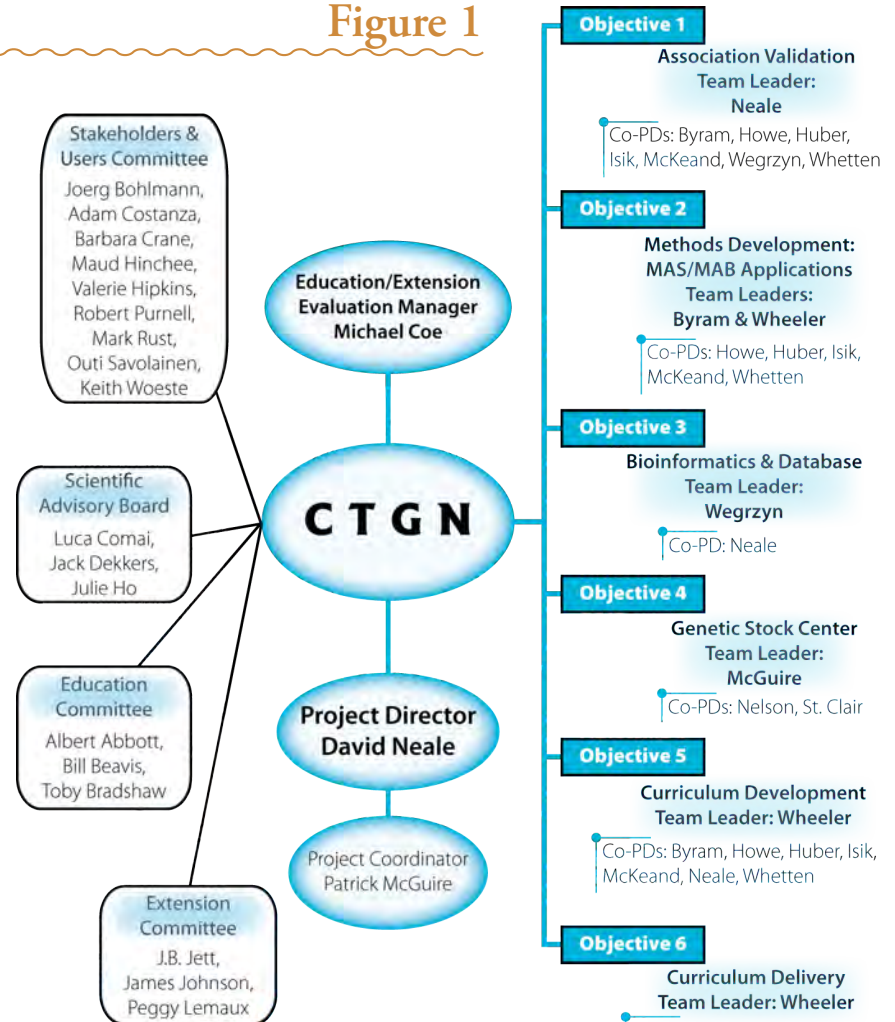
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holders (our Objectives 5 and 6, see page 5 for a progress summary). The CTGN draws from or delivers to virtually all conifer genomics scientists and tree breeders in the United States and this Newsletter is one means of that delivery.

To summarize, the six CTGN objectives are:

1. Validate SNPs by quantitative trait associations discovered under prior USDA and NSF funding in operational tree improvement populations of loblolly pine, slash pine, and Douglas-fir.
2. Develop and economically evaluate new methods incorporating marker-assisted selection into conifer tree breeding programs.
3. Develop databases (TreeGenes) and web-based tools (Dendrome) to facilitate all aspects of the Project.
4. Develop an international conifer genetic stock center.
5. Develop an education plan for undergraduate and graduate curriculum development in genomics-based breeding in forest trees.
6. Develop and deploy an extension curriculum for continuing education in genomics-based breeding for practicing tree breeders and forest tree gene-resource managers.

Figure 1



* CTGN hub: UC Davis

The David Neale lab in the Dept. of Plant Sciences (<http://dendrome.ucdavis.edu/NealeLab/>) serves as the hub for the CTGN Project. The sequencing and genotyping activity (Objective 1), bioinformatics and database activity (Objective 3), and the conifer genetic stock center (Objective 4) are all coordinated from here or actually carried out here. **CTGN Project Director Neale's** primary research interest is in the discovery and understanding of function of genes in forest trees, especially those controlling complex traits, through genetic mapping and genomic science technologies. He serves as team leader for the overall association validation effort (Obj. 1) and, within Obj. 1, he is team leader for the candidate gene SNP-genotyping of the Project's

breeding program trees (Obj. 1.1). **Jill Wegrzyn** (CTGN co-PD) is the bioinformatician responsible for Project data movement, tracking, and display, the Project's website and phone, and the databases TreeGenes and the DiversiTree database and query interface and the team leader for Objective 3. **Patrick McGuire** (CTGN co-PD) serves as CTGN Project Coordinator and team leader for Objective 4. **Katie Tsang** is lab manager, organizing the DNA extraction from samples from all Project collaborators and managing the movement of DNA samples on to the genotyping process. **John Liechty**, **Ben Figueroa**, and **Minyoung Choi** are bioinformatics programmers who contribute to Objective 3.



! NCSU—Cooperative Tree Improvement Program

The Cooperative Tree Improvement Program at North Carolina State University (<http://cnr.ncsu.edu/tip/>) is in its 54th year of operation, and the primary goal of the Cooperative continues to be to enhance the value of southern forest lands by increasing the productivity and quality of forest plantations through intensive breeding and propagation efforts. Most of our work is with loblolly pine (*Pinus taeda* L.), by far the most important commercial timber species in the South, having been planted on over 1 million acres and as many as 2 million acres each year for the past 30+ years. Much of the increased productivity on almost 20 million acres of forest plantations in the South is due to the efforts of the members of the Cooperative.

The Cooperative is supported by forest landowners, timber investment management organizations, real estate investment trusts, forest products companies, consulting firms, propagation companies, nurseries, and state forestry agencies in the southeastern US. There are currently 12 Full Members and 12 Contributing Members of the Cooperative. A complete description of the membership and staff of the Cooperative can be found at <http://cnr.ncsu.edu/tip/people.htm>.

The academic and research leadership for the Cooperative is provided by three faculty members of the Dept. of Forestry and Environmental Resources, North

Carolina State University, a research assistant, and a graduate student. All three faculty members are also co-Project Directors of CTGN CAP. Professor **Steve McKeand** is Director of the Cooperative. He has primary responsibility in the breeding, testing, and selection phases of the Tree Improvement Program. Dr. McKeand's specific research interests include: genetic effects on nutritional and ecophysiological processes in forest trees, genetic and environmental control of wood properties, biotechnology/breeding interface, propagation effects on forest trees, seed orchard management, and genotype by environment interactions.

The two other two faculty members provide leadership with different areas of expertise relevant to the Cooperative's goals: The research interests of Dr. **Fikret Isik** (Research Associate Professor of Quantitative Genetics) include quantitative genetics and forest tree improvement, genetic and epige-

netic basis of disease resistance of forest trees, wood density assessment and genetics, application of molecular markers in tree breeding and selection, and conservation of forest genetic resources. Dr. **Ross Whetten** (Associate Professor) provides a focus on the biochemistry and molecular biology of tree growth and development and the development of technology and its application to practical problems in tree improvement and disease management. Research

assistant **Joshua Steiger**, funded part-time by the CTGN Project, provides support for the field and lab research carried out by the Cooperative. PhD student **Jaime Zapata**, also funded by the CTGN, carries out research on loblolly pine relevant to the CTIP mission and the CTGN Project.



NCSU—Cooperative Tree Improvement Program Staff (left to right): Ross Whetten, Patrick Cumbie, Josh Steiger, Fikret Isik, Tori Batista-Brooks, Jim Grissom, Saul Garcia, J.B. Jett, and Steve McKeand

* Accomplishments

- ✓ \$50 to over \$300 net present value per acre to landowners simply by planting the best genotypes that are currently available from commercial and state forest nurseries.
- ✓ 217 graduate students studied and received masters & PhD degrees with Cooperative faculty.
- ✓ 66 post-docs and visiting scientists from 34 countries from five continents have also studied and conducted research with us.
- ✓ 838 papers, 283 published in refereed journals signify the intellectual contribution of Cooperative students, scientists, staff, and collaborators to forestry, tree improvement, and biological sciences (see http://cnr.ncsu.edu/tip/publications_citations.html for the list).
- ✓ 16,230 controlled crosses among loblolly pine selections have been established in field trials.
- ✓ 1138 tons of improved loblolly pine seed produced by the Cooperative members over the past 40 years—enough seed to plant over 25 billion seedlings.
- ✓ 7511 selections established in Genetic Diversity Archives to conserve the precious loblolly pine genetic resource for future generations of breeders and foresters.
- ✓ 2200 acres of advanced-generation seed orchards, intensively managed to produce genetically improved seeds that will assure a reliable, affordable, and ecologically sustainable supply of wood for decades to come.

* From the literature

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

≡ The genetics of quantitative traits: Challenges and prospects

MacKay, Trudy, Eric Stone, and Julien Ayroles. 2009. *Nature Reviews Genetics* 10:565–577 (August 2009) | doi:10.1038/nrg2612

For those of us seeking to use genomic tools to clarify the genetic basis of quantitative traits, and inform our plant breeding efforts, this article is a must-read. The authors clearly articulate the remarkably complex nature of the relationship between genotypes and phenotypes and posit that the way forward is through “systems genetics”. As the authors point out, despite two decades of intensive efforts at identifying and locating QTL affecting quantitative traits, we have fallen short of explaining genetic variation in terms of underlying genes, effects of segregating alleles in different genetic backgrounds and environments, the molecular basis of functional allelic effects, or the population frequency of causal variants.

The article nicely contrasts the approaches to dissecting complex traits (linkage mapping vs association genetics) in the context of the major components of QTL mapping: detection and localization. The authors conclude that, regardless of approach, what we have learned is that QTL alleles with large effects are rare, most genetic variation for quantitative traits is due to many loci with small to very small effect, and that multiple loci with opposite effects are commonly found in tight linkage. Regarding the molecular basis of quantitative variation, evidence from humans and fruit flies indicates that rare variants and variants with minor allele frequencies less than 5% are frequently associated with variation in quantitative traits.

In detailing challenges to understanding the genetic architecture of complex traits, an excellent treatment is given of context-dependent effects and pleiotropy, issues we typically consider nuisances but are of great importance to our ability to apply what we learn to tree breeding. Context-dependent effects include epistasis (genotype by genotype interactions), genotype by environment, and genotype by sex interactions. The pleiotropy discussion was fascinating. The authors note that genes may have pleiotropic effects, but individual variants likely do not. That is, independent variants (say, SNPs) within a given gene may affect different traits.

The latter half of the paper is an argument for systems genetics or genetical genomics as the way forward in understanding the genetic architecture of complex traits. This basically is a call to large scale use of technologies such as whole-genome transcriptional profiling, proteomics, metabolomics, and organismal phenotypes, all areas now being tested, albeit modestly, by a small cadre of forest geneticists.

As tree breeders what can we take from this paper? First, that we will probably never know everything we want to know about the genetic basis of the traits that interest us, but we probably can know enough to make genetic gains using genomic tools. Secondly, that there is always a need for validation across sites, years, and genetic backgrounds. Finally, more is always better. The more genes/SNPs evaluated, the more likely we are able to explain the variation that interests us.

Reviewed by Nicholas Wheeler

≡ Gene-assisted selection: Applications of association genetics for forest tree breeding

Wilcox PL, CE Echt, and RD Burdon. 2007. p 213–249 in Oraguzie NC, EHA Rikkerink, DE Gardiner, and HN De Silva (eds). *Association mapping in plants*. Springer. New York NY USA.

This comprehensive treatment of association genetics and its potential applications in forest tree breeding provides thorough background on the topic for tree breeders and forest geneticists. The authors use this book chapter to clearly define the distinguishing characteristics of forest trees, relative to other crops. Though now slightly dated, the work summarizes the status of genomic information and what we have learned about linkage disequilibrium and nucleotide diversity in tree species. The paper has a nice section on comparisons between MAS using association versus MAS using linkage mapping (within-family selection).

Wilcox et al. favor the use of the term GAS or gene-assisted selection to describe association genetics in forest trees. Though GAS has yet to find widespread use in the literature, it provides an apt description of how association differs from our earlier linkage mapping approaches to characterizing the genetic basis of complex traits. The paper describes a number of generic benefits to GAS and points out that it has applications across all tree improvement strata. A valuable section of the paper details the basic prerequisites for operational implementation of association genetics in tree breeding which includes, among other things, appropriate populations, efficient phenotypic assays, quantitative capabilities, high throughput genotyping, and good marker selection. Authors point out the need for close communication between tree breeders and the genomic scientists, the meshing of organizational and institutional requirements, and the appropriate allocation of resources to various parties.

The chapter concludes with a description of a number of specific types of applications for associ-

ation genetics in tree breeding, and ultimately the potential limitations and hurdles that must be accommodated or overcome for successful application. This chapter is an important work by accomplished tree breeders and genomics experts and should be read by the tree breeding community.

Reviewed by Nicholas Wheeler.



! CTGN Education and Extension Activities

The Extension and Education elements of the CTGN Project are managed by Dr. Nicholas Wheeler out of Oregon State University. He may be reached by email (wheeleni@onid.orst.edu) or phone: 360-278-3535 (office) or 360-701-4886 (cell). Here we report on some key activities of the past year.

Special topics course

"Association Genetics and Breeding" was presented at Oregon State University (3 quarter credits, winter quarter, 2009; <http://www.cof.orst.edu/cof/fs/clpg/>). Largely organized and taught by PD D. Harry, the course featured guest lecturers from other PDs from this Project and PDs from other CAP projects (the Wheat, Barley, and Solonaceae CAP Projects). The course was attended by 10 graduate students representing Forestry (4), Crop and Soil Science (3), Horticulture (1), and Animal Science (2) and a number of casual faculty. Course structure included 13 lectures (80 minutes), 3 class periods featuring data and software exercises, and 3 class periods for discussion topics.

Our goal is to expand the curriculum developed here for use at the other institutions within our Project. Currently the course is scheduled for delivery in alternate years at Oregon State University, and will be given for the first time at UC Davis this year. Plans are being developed for delivery at NCSU within the next calendar year. We are open to sharing our materials with other institutions and would like to encourage interested faculty to contact us directly if interested.

Short-course

"Genomics in Tree Breeding and Forest Ecosystems" was an intensive five-day short-course held June 15–19, 2009 on the UC Davis campus and, attended by 24 participants, representing seven countries. Participants included nine graduate students/post-doctoral fellows and 15 professionals, nine of whom had PhDs. There were seven tree breeders in the group.

Primary instruction was provided by David Harry and Nick Wheeler, with support from co-PDs F. Isik, R. Whetten, T. Byram, and J. Wegrzyn. Additional assistance came from A. Eckert and V. Hipkins. The short-course consisted of ten modules presented in Powerpoint format (54 to 110 slides in length). Six of the modules featured exercises that extended concepts presented in modules to manipulation of data sets in relevant genomics software applications. Our intent is to deliver this short course in each of the last two years of this Project.

Presentations

In the first two years of the Project, Co-PDs delivered nearly 50 outreach presentations, including invited talks, class lectures, posters, talks to professional societies, conference talks, and so forth, and we have developed and widely circulated a CTGN CAP brochure. We anticipate adding presentations for public access at the Project website. Recent presentations include:

- ✦ "New developments in genetic markers and their applications" Invited talk: Northwest Seed Orchard Managers Meeting, Aurora, Oregon, June 25, 2009. (D. Harry / N. Wheeler)
- ✦ "Marker Informed Breeding in Tree Improvement: How Does That Work?" Volunteer Talk: Western Forest Genetics Association Conference, Aug. 10–13, 2009. (N. Wheeler / T. Byram)
- ✦ "Development and application of genomic-based tools to manage forests in response to climate change" and "Association studies for complex traits in conifers" Two invited talks: Workshop on Opportunities, Challenges, and Limitations of Genomics-Based Technologies in Forest Tree Breeding and Forest Genetics, Oct. 7–9, 2009. Forest Resesarch Institute, Freiburg, Germany. (D. Neale)

Extension plans

Emphasis this coming year will be on broadening our exposure to a wider audience. We will do

this through direct encounters (short-courses, classroom lectures, seminars and Co-op meeting talks (co-op members, co-op directors, and staff)), consultative interactions (meetings with co-op members to advise and assist them with genomic applications (i.e., fingerprinting orchard parents, locating vendors, assisting with contracts, etc)), On-line Resources (putting shortcourse materials on-line so that other institutions can use them to develop their own courses, eXtension commitments), and peer-reviewed papers. Our target is to make at least 15 contacts per year.

Project publications

A series of three papers targeted to providing tree breeders with additional tools for the use and evaluation of marker informed breeding applications are underway. The first, "Marker Informed Breeding (MIB) in Forest Trees: I. Breeding and Selection Applications for Recurrent Selection Programs", is nearing completion. It will provide materials for future extension talks with tree improvement cooperative members. The second paper, based on simulation studies, will inform us on gain expectations and details of how to include markers in kinship matrix calculations and BLUP-derived BV estimates. The final paper will provide a stochastic simulation of the economic risk of marker-informed breeding in forest trees.

Evaluation

Education and Extension activities conducted by CTGN are being evaluated on an ongoing basis by our independent evaluator, Dr. Michael Coe. As part of this study, participants in the 2009 CTGN week-long summer workshop in 'Genomics in Tree Breeding and Forest Ecosystems' answered a questionnaire two months before and again immediately after the course. The survey included questions about participants' academic background and focus; knowledge, skills, and interest in areas related to the use of genetic markers; ability to teach or communicate to others about these topics; and interest and ideas about further work in marker-assisted breeding and related subjects. After the workshop, participants were significantly more confident in their ability to perform key tasks related to the use of genetic markers; their scores on a 12-item efficacy scale were on average more than a standard deviation higher after the course. A similar increase was observed after the course in participants' confidence in their ability to teach or communicate about markers to various kinds of audiences.

Participants also answered a set of feedback questions about the course. Each of the ten course modules was rated for length as well as clarity and effectiveness, with average responses indicating general satisfaction but a need for some modules

(continued on p. 6 at Education &...)



Attendees and instructors of the 2009 short-course, "Genomics in tree breeding and forest ecosystems", held in Davis, June 15–19, 2009

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 and Consulting Group, LLC, Portland OR

Michael Coe, Education/Extension Evaluation Manager

Recent CTGN research landmarks

In the first two years of the CTGN project, the target was to get 10,000 individual trees from the industry validation populations genotyped for the suite of markers that had been selected (a pool of 7600 SNPs). Of the 10,000, 6000 trees are from loblolly populations via the NCSU Cooperative Tree Improvement Program, the University of Florida Cooperative Forest Genetics Research Program (CFGFRP), and the Texas A&M University Western Gulf Forest Tree Improvement Program, 2000 are from slashpine via the University of Florida CFGFRP, and 2,000 are from Douglas-fir populations via the Pacific Northwest Tree Improvement Cooperative and the Northwest Tree Improvement Cooperative.

The cooperatives collected needles and sent them to the high-throughput DNA isolation facility in the Neale Lab at UC Davis (built with CTGN support). DNA samples were sent to Illumina, Inc. in San Diego CA for genotyping with the selected 7600 SNPs from the earlier projects. The high numbers and thus, high

throughput, are needed because MAS/MAB requires a high density of mapped markers in the populations to be successful at tracking changes in breeding programs.

To date, genotyping of the 6000 loblolly pine individuals is complete, the Douglas-fir and slash pine genotyping is well underway. The resulting genotype data are accumulated in a relational database, integrated with the available phenotypic data for these same individuals and made available to Project investigators and the cooperatives for analyses.

Interfaces are now available to permit Project users to upload accessions/IDs and other list formats and retrieve detailed information from the TreeGenes database in return. The data types available for search now include EST, EST contig, amplicon, sequence assembly, and SNP. A search can begin at any of these levels and can yield detailed information on tracefiles, FASTA sequences, SNP scores, annotations, genotypes, and more.

Education &...

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to be lengthened (or for students to do more preparatory work beforehand). Course participants rated the course materials and curriculum highly, and most plan to apply what they learned in further academic or professional work. In addition to structured ratings, participants also provided open-ended feedback to help guide future CTGN educational activities. A detailed report of these findings will be available in January, 2010.

Tree facts

Collectively, timber is among the most highly valued commodities in America. About 1.3 million people are directly employed in the planting, growing, managing, and harvesting of trees and production of wood and paper products in all 50 states. The forest industry ranks among the top ten manufacturing employers in 42 states, with an annual payroll of about \$60 billion. Each person uses wood and paper products equivalent to what can be produced from one 18 inch in diameter 100 foot tree every year. Each year we plant about 1.7 billion trees in the US.

Support for the CTGN CAP comes from the US Department of Agriculture: the AFRI Applied Plant Genomics Coordinated Agricultural Project and the Forest Service.



CALENDAR

November 10–13, 2009. Genomics of Forest and Ecosystem Health in the Fagaceae (Beech family). Research Triangle Park NC. (<http://www.ces.ncsu.edu/nreos/forest/feop/GFEF/>)

January 10, 2010, 8:00am to 6:00pm: Forest Trees Workshop and annual meeting of the International Union of Forestry Research Organization, in conjunction with the XVIII Plant and Animal Genome Conference, January 9-13, 2010, Town and Country Hotel, San Diego CA USA. (<http://www.intl-pag.org/>)

May 26–29, 2010. International Symposium on Biology of Rare and Endemic Plant Species. Muğla, Turkey. (<http://www.metu.edu.tr/~biorare/>)

June 17–18, 2010. CTGN CAP Annual Meeting. Oregon State University

June 21–25, 2010. CTGN CAP Short Course. Oregon State University

September 20–25, 2010. Fifth International Poplar Symposium (IPS-V). Orvieto, Italy. (<http://www.sisef.it/IPS-V/>)