

The Louis W. Schatz Center for Tree Molecular Genetics

Pennsylvania State University

Progress Report

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Prepared by:
John E. Carlson, Ph.D.
Director, The Schatz Center for Tree Molecular Genetics
Professor of Molecular Genetics
School of Forest Resources
Pennsylvania State University
814-863-9164; jec16@psu.edu

<http://schatz.cas.psu.edu/>



This report covers activities in *The Louis W. Schatz Center for Tree Molecular Genetics* at Pennsylvania State University for the 2006 - 2007 fiscal year ending June 30, 2007. The major event this year for the Schatz Center was the first Schatz Tree Genetics Colloquium held on the Mont Alto campus.

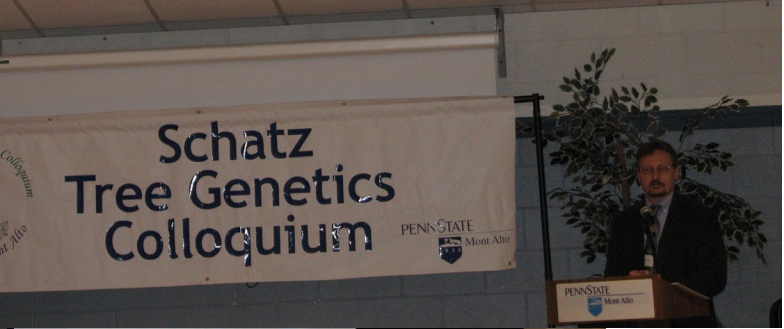
The Schatz Tree Genetics Colloquium

The first Schatz Tree Genetics Colloquium was held at the Penn State University's Mont Alto campus on April 30, 2007. The meeting was attended by over 60 geneticists and alumni who enjoyed the spring weather and the beautiful surroundings of the Mont Alto campus as well as an impressive array of talks about the latest research in tree genetics. The Mont Alto campus organizers for the Schatz Colloquium, Dr. Beth Brantley, Instructor of Forest Technology, and Deb Creager, Alumni Relations Coordinator, made all of the speakers and attendees feel at home with campus tours, a delectable informal barbecue the evening before the meeting, and an impressive banquet at the end. Speakers at the Schatz Colloquium covered a wide range of topics including a massive traditional hardwood tree improvement led by Dr. Scott Schlarbaum at the University of Tennessee who reported recent success in identifying the Butternut trees resistant to the deadly epidemic of canker disease, an historical perspective on tree genetics with hardwoods by Dr. Kim Steiner, Professor of Forest Biology at Penn State, the application of genomics to the analysis of hybrid tree zones in nature by Dr. Steve DiFazio of West Virginia University, the genetics of carbon sequestration and reproduction in poplar by Dr. Amy Brunner of Virginia Polytechnic University, genetic mapping in Northern Red Oak by Dr. Jeanne Romero-Severson of Notre Dame University, breeding for disease resistance in American Beech by Dr. Jennifer Koch of the USDA Forest Service, and breeding for blight resistance in American chestnut by Dr. Fred Hebard of the American Chestnut Foundation. Dr. Carlson's collaborators also presented a series of talks covering all aspects of our research on oaks, beech and chestnut in the *Fagaceae Genomics Project*, including the generation of new mapping populations for American chestnut and Chinese chestnut, the development of new genetic maps and DNA markers for chestnut, high throughput DNA sequencing and DNA library construction, bioinformatic analysis of DNA sequence data, and our Genomic Tool Development for the Fagaceae project website (www.Fagaceae.org).

Students from both the University Park and Mont Alto campuses also gave presentations about their forest management and genetics research projects. The students put a lot of effort into their excellent posters and displays. This provided an opportunity for our students to meet practicing and retired forest management and forest genetics attending the colloquium, from which they learned much more about their own future prospects and professional opportunities.

We appreciate the opportunity that the endowment for the Schatz Tree Genetics Colloquium provides for us to raise the visibility of the Schatz Center for Tree Molecular Genetics and to share our research results and future plans with both the greater scientific community and our alumni. The colloquium was a success and we look forward to many more in the future.

Photos from the first Schatz Tree Genetics Colloquium, April 30, 2007



Current Research Projects in the Schatz Center:

Functional Genomics of Flowering in the Woody Perennial Populus

We are collaborating with research groups at Mississippi State, Virginia Tech, Alabama universities to discover the genes responsible for the vegetative growth versus flowering phases in poplar. This major project is funded at \$1.7 Million for three years by the National Science Foundation's Plant Genome Research Program. The poplar genome sequence allows us to determine all of the genes that are involved, and how genetic mechanisms are fine-tuned in hardwood trees. During the first two years of the project we identified over 130 genes involved in the shift from growth to flower formation in poplar trees, some of which are known to determine whether leaf or floral buds form in other plants. Over the next year we will study the specific functions of these genes.

Genomic Tool Development for the Fagaceae

The Schatz Center plays a key role in this major research project which is funded at \$2.8 Million by the National Science Foundation. The Schatz Center is developing the DNA sequence databases, on which the entire project is based, for key beech family tree species including American chestnut, Chinese chestnut, northern red oak, white oak, and American beech. During the first year of this project, the Schatz Center produced over 230 million bases of sequence for actively expressed genes in these species. We will produce app 470 million bases of new DNA sequence in total, which is over 60 times the amount of sequence data currently available in the public DNA sequence databases for all beech family tree species worldwide. We are analyzing the data to identify genes and their possible functions in susceptibility or tolerance to the chestnut blight and other tree diseases. Restoration of American chestnut was one of examples of biotechnology research that Dr. Schatz was most interested in. So we are very pleased that the Schatz Center is playing a lead role in this important project.

Development of Tree Crops for Biomass Energy and Carbon Sequestration

The objective of this project is to improve our capacity to produce tree bioenergy crops in PA with biomass yields that are sufficient to be economically viable, in a manner that is sustainable and environmentally sound. Bioenergy production is not economically feasible without reliable, local production of biomass. Trees are the most appropriate source of biomass for energy production in PA. PA provides an excellent environment for growing trees and the net energy yields in BTUs and gallons/acre of ethanol are equal to or greater from trees than from other plant biomass sources grown locally. Fast-growing trees sequester large amounts of carbon from the atmosphere during their growth and can contribute a net reduction in atmospheric carbon, to help offset greenhouse gas effects, even when used as fuel. Bioenergy trees are suitable for multi-cropping in agroforestry applications. Trees also provide environmental benefits such as protection of riparian areas, reduction in soil erosion, and creation of habitat for wildlife. Furthermore, trees will often grow in nutrient poor and even industrially contaminated sites, such as surface mines, on which other plants cannot survive. This project involves 1) establishing field trials to identify the tree species and cropping systems that produce the highest biomass yields; 2) identifying genotypes with the best lignocellulose quality for bioenergy; 3) developing economic models based on the field

data. We plan to test several fast growing hardwoods including hybrid poplar, sycamore, yellow-poplar, willow, and American chestnut.

Molecular Tools to Improve Stress Tolerance in Tree Biomass Plantations

Trees grown at high density in energy plantations are susceptible to biotic stresses such as herbivores, and abiotic stresses such as air pollution, which can reduce biomass accumulation. We are investigating how hybrid poplar shifts biomass allocation upon attack insects and when ozone induces early senescence. Tree leaves produce a complex mixture of enzymes and chemicals to protect the tree in response to insect and ozone damage. Our current research with hybrid poplar is aimed at understanding 1) the role airborne chemical signals in defense against biotic and abiotic stresses; 2) the genes which are responsible for protecting poplar from biotic and abiotic stresses; 3) the extent of biomass loss or re-allocation caused by biotic and abiotic stresses; and 4) the genetic basis of differences among genotypes of trees in susceptibility to ozone and herbivore damage. These studies will lead to molecular genetic tools for protecting and improving hybrid poplar and other trees grown in biomass energy plantations.

Novel approach to facilitate lignocellulose conversion to ethanol by introducing a tyrosine rich peptide gene into poplar cell walls.

Lignocellulosic material (including wood) is one of the most predominant natural compounds in the world, but will remain largely underutilized for liquid fuel production until better lignin extraction processes are available. The lignin component of wood interferes with biomass conversion to fuels by limiting access of enzymes to cellulose in the wood. Biotechnology efforts to facilitate lignin removal from lignocellulosic biomass have previously taken the approach of altering or reducing lignin content. We have been active in that research approach. However, altering lignin content can also lead to undesirable phenotypes, such as enhanced susceptibility to insects and diseases. A new approach we are pursuing with the Biochemistry Dept. at PSU is to introduce proteins that will cross-link with lignin, which should make the cellulosic components more easily accessed for ethanol production, while not compromising tree health.

Looking inside wood-eating beetles to discover genes for new enzymes to convert wood into energy

The enzymes that are used in industrial processes to degrade lignin in lignocellulosic material during ethanol production have been isolated from a limited number of fungi and bacteria that decay wood on the forest floor. Very little is known however about the microbes and their associated enzymes inside wood-eating insects that help them convert wood into energy. We have recently shown that the Asian Longhorned Beetle (ALB), which kills trees by eating them from the inside out, is able to quickly degrade lignin in wood as well as cellulose. Thus ALB is an attractive system in which to "prospect" for novel ligno-cellulose digesting enzymes. We have a multi-disciplinary collaboration underway with faculty and students in entomology, plant pathology, and biochemistry to define the microbe species in the digestive track of ALB and their

associated enzymes involved in digestion of wood by ALB larvae. This project is primarily supported by the US Department of Energy.

Micropropagation of Christmas Trees – from lab to field

In vitro cloning by micropropagation can lead to reduced losses in Christmas tree farms. The faithful reproduction of the genotypes best suited to growing in tree farms is possible by eliminating plant-to-plant variation in growth, form, and resistance to pests and diseases. This year we started a new three year project to improve and extend our protocols for true-to-type cloning of the best genotypes of Douglas-fir Christmas trees. We started large scale experiments to establish efficient rooting of micropropagated shoots and to identify the best field sites for testing the clones that we produce from tissue culture by micropropagation. We are also extending our micropropagation system that we developed for Douglas-fir buds from mature trees for use with juvenile trees as well, and to expand the use of our system for *in vitro* selection of enhanced desiccation tolerance from Douglas-fir to Concolor-fir Christmas tree genotypes. This work is primarily supported by the PA Department of Agriculture.

Other Activities in The Schatz Center

Schatz Post-Doctoral Fellowships in Tree Genetic Engineering – Schatz post-doctoral fellows **Dr. Haiying Liang** and **Dr. Abdoulaye Traore** moved to permanent positions in the Fall of 2006 to start their own research programs. Dr. Liang is now an Assistant Professor of Genetics at Clemson University and Dr. Traore is a Senior Scientist with the Masterfoods Company. Our current post-doctoral fellows **Teodora Best** and **Chris Frost** have strong research programs underway on the genetic responses of trees to the damaging effects of air pollution (ozone) and exotic insect pests (gypsy moth).

The Schatz Awards for Undergraduate Research are supporting several students to conduct research in the Schatz Center. This year we had three undergraduate students from the Biochemistry and Molecular Biology Department who are conducting research in the Schatz Center on a wide range of projects including the construction of genetic linkage maps for black cherry and white oak (Joe Flores-Toro), the selection of drought-tolerance in Douglas-fir using tissue cultures (Toby Powell), and the identification of genes responsible for volatile chemicals released from poplar trees when leaves are chewed by caterpillars (Laura Kropp).

Schatz Center Endowment for Library Collections:

The Schatz library fund continues to provide both print and electronic subscriptions of the publications “Canadian Journal of Forest Research”, “Genome”, and others, for Penn State though the university’s main library to important.

The Louis W. Schatz Support Fund for Forestry at Mont Alto continues to be used to enrich the student experience in the Forest Technology Program at the Penn State Mont Alto campus.

The Schatz Student Field Trip Funds – Due to health issues, director Dr. Carlson, was not able to lead student trips the past two years. However plans will be developed in the 2007-08 academic year for a trip to California to visit Gordon Schatz and the Humboldt State University, using the Schatz Student Travel Endowment.

The Louis and Merry Schatz Faculty Travel Fund supported travel this past year by the Center Director, Dr. Carlson, to the Plant and Animal Genome Conference in San Diego, and to attend an international conference on poplar genetics held in Nanjing, China. During the trip to China, Dr. Carlson was also hosted by tree geneticists at the Beijing Forestry University where collaborative research projects were planned. The Schatz Center also supported travel by faculty member Marc Abrams who attended an international conference in Beijing, China, on tree ring analysis in forest ecology and forest regeneration research. In the coming year, the *Schatz Faculty Travel Fund*

Publications from The Schatz Center, 2006 - 2007:

Barakat, Abdelali; Wall, Kerr; Leebens-Mack, Jim; Wang, Yunjiao; **Carlson, John**; dePamphilis, Claude. 2007. Large-scale identification of microRNAs from a basal eudicot (*Eschscholzia californica*) and conservation in flowering plants. *The Plant Journal*, published on line July 17, 2007.

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Gilbert MTP, Binladen J, Miller W, Wiuf C, Willerslev E, Poinar H, **Carlson JE**, Leebens-Mack JH, Schuster S. 2007. Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. *Nucleic Acids Research* 35:1-10.

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Cai, Z., Penafior, C., Kuehl, J.V., Leebens-Mack, J., **Carlson, J.**, dePamphilis, C.W., Boore, J.L., Jansen, R.K. 2006. Complete chloroplast genome sequences of *Drimys*, *Liriodendron*, and *Piper*: Implications for the phylogeny of magnoliids and the evolution of GC content. *BMC Evolutionary Biology* 6:77 (Oct 4, 2006) 20 pages

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Cui, L., Wall, P.K., Leebens-Mack, J.H., Lindsay, B.G., Soltis, D., Doyle, J.J., Soltis, P., **Carlson, J.E.**, Arumuganathan, K., Barakat, A., Albert, V., Ma, H., dePamphilis, C.W. 2006. Widespread genome duplications throughout the history of flowering plants. *Genome Research* 16: 738 - 749.

Books

Carlson JE, Traore A, Agrama HA, Krutovsky KV. 2006. Douglas-fir. **In:** *Genome Mapping & Molecular Breeding in Plants Vol. 7 - Forest Trees*, (Ed, C. Kole), Springer Heidelberg, Berlin, New York, Tokyo, pp 199 - 210.

Steele MA, **Carlson JE**, Smallwood PD, McEuen AB, Contreras TA, Terzaghi, B. 2007. Linking seed and seedling shadows: A case study in the oaks (*Quercus*). **In:** "Seed Dispersal - Theory and its Application in a Changing World." (Ed., David Westcott), CABI International, pp. 322 - 339.

Kremer A, Casasoli M, Barreneche T, Bodénès C, Sisco P, Kubisiak T, Scafì M, Leonardi S, Bakker EG, Buiteveld J, Romero-Severson J, Arumuganathan K, Derory J, Scotti-Saintagne C, Roussel G, Bertocchi ME, Lexer C, Porth I, Hebard F, Clark C, **Carlson J**, Plomion C, Koelewijn HP, Villani F. 2006. Comparative Genetic Mapping in Fagaceae. **In:** *Genome Mapping & Molecular Breeding in Plants Vol. 7 - Forest Trees*, (Ed, C. Kole), Springer Heidelberg, Berlin, New York, Tokyo, pp. 161 - 187.

Steiner KC, **Carlson JE**, editors. 2006. Restoration of American chestnut to forest lands. Proceedings of a Conference held 4-6 May 2004, Asheville, North Carolina USA. School of Forest Resources, The Pennsylvania State University, University Park, Pennsylvania. 230 pp.

Manuscripts Submitted:

Abdelali Barakat, Kerr P Wall, Scott Diloretto, Claude W dePamphilis and **John E Carlson**. Conservation and divergence of microRNAs in *Populus*. Submitted to *BMC Genomics* May 31, 2007 (MS ID # 2005223077146355); revision submitted Aug 21, 2007.

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Haiying Liang, **John E. Carlson**, James H. Leebens-Mack, P. Kerr Wall, Lukas A. Mueller, Matyas Buzgo, Lena L. Landherr, Yi Hu, D. Scott DiLoreto, Daniel C. Ilut, Dawn Field, Steven D. Tanksley, Hong Ma, Claude W. dePamphilis. An EST Database for *Liriodendron tulipifera* L. floral buds: the first EST resource for functional and comparative genomics in *Liriodendron*. Submitted Sept.6, 2007 to *Tree Genetics and Genomes*.

Patent applications

Tien M, **Carlson JE**, Liang H. 2007. A Novel Method to Enhance the Degradation of Lignocellulosic Material for Alternative Fuel Productions" PSU Invention Disclosure No. 2007-3311, Disclosed May 30, 2007.