



*The poplar genome sequence provides  
new opportunities for research in The Schatz Center.*

## ***The Louis W. Schatz Center for Tree Molecular Genetics***

***Pennsylvania State University***

### **Progress Report**

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This report covers activities in *The Louis W. Schatz Center for Tree Molecular Genetics* at Pennsylvania State University for the period of January 1 to December 31, 2006. The major event this year for the Schatz Center was our **move to the new School of Forest Resources building** in May.



### Schatz Tree Genetics Research Center

A gift from Louis W. Schatz (SFR '34) and his family in appreciation of his Penn State education and continued personal ties with our University.

The Schatz Center facilities are a show case for advanced research in the new Forest Resources Building. The Schatz Center labs are fully occupied and abuzz with the research activities of undergraduate, graduate and post-doctoral students, as well as visiting scientists. The new facilities mark a new dawn for Schatz Center at the same time that the first complete genome sequence for a tree (poplar) has heralded a new world of opportunities for research in tree genetics. With this third and final move, the Schatz Center finally enjoys a permanent home. For the first time since its inception in 1998, the Schatz Center is now embedded among other forestry, wildlife, and wood products faculty within the School of Forest Resources. This close proximity to colleagues has already led to new research collaborations and new training opportunities for our students, some of which are explained below.

#### *Research Projects in the Schatz Center*

##### Poplar Genomics

The greatest advance in tree genetics to yet occur was the announcement of completion of sequencing of the poplar genome in late 2004. The Schatz Center Director played a key role in getting this very large effort underway, and is an author on

the paper that reports and describes the poplar genome in the prestigious journal *Science* (Tuskan, G.A., et al. "The Genome of Western Black Cottonwood, *Populus trichocarpa* (Torr. & Gray ex Brayshaw)" *Science* vol 313 pages 1596-1604. Sept 15, 2006). The genome of *Populus trichocarpa* is approximately 480 million base pairs contained in 19 chromosomes. In the genome sequence, a total of 58,036 genes were detected. Thus far, researchers have found that virtually all of the genes in the poplar genome are active, although at different times during the year or during tree development. The specific functions of most of the genes are not known, however. Nor do we know how the genes interact to accomplish growth and survival of poplar trees. For the first time, however, such questions can be addressed and genetic tools developed to enhance sustainable production in trees. The Schatz Center is already involved in research that taps the potential of the poplar genome, and we plan to continue to lead this area of research in the future.

*Functional Genomics of Flowering in the Woody Perennial Populus* – This project involves collaboration among four universities to discover the genes regulating the transition from vegetative growth to reproductive bud formation and flowering in poplar. This major project which started in October, 2005, is funded at \$1.7 Million for three years by the National Science Foundation's Plant Genome Research Program. We are studying the regulation of vegetative versus reproductive growth in hybrid poplar by examining the function of key genes that are known to control the shift from leaf buds to floral buds in other model plants. The poplar genome allows us to determine what other genes are involved, and which genes control the expression of other genes in the developmental pathway for hardwood trees. The Schatz Center is specifically determining the tissue-specificity and levels of expression of these genes in both wild type trees and transgenic trees in which the activity of floral genes have been modified. To date we have identified 131 genes involved in the shift to flower bud formation. We will study this set of genes in more detail over the next two years.

### ***Other Activities in The Schatz Center in 2005***

*Genomic Tool Development for the Fagaceae* - We are participating in a major new project which began on September 1, 2006, with \$2.8 Million funding from the National Science Foundation. In this project we are developing DNA sequence databases for genes that are expressed in key North American tree species in the Beech family (the Fagaceae). Work on the project began by students and staff in the Schatz Center collecting tissue samples from American chestnut, Chinese chestnut, northern red oak, white oak, and American beech trees. Stem samples were also collected from American and Chinese chestnut trees inoculated with the blight fungus. RNA (gene transcripts) was prepared from the tissue samples and converted into DNA copies for sequencing. The Schatz Center completed sequencing of the transcripts of genes expressed in the cankers of infected chestnut trees. We are now analyzing the gene sequence data to identify differences among blight-susceptible and -tolerant trees. Over the next year we will sequence the gene transcripts from the remaining samples. Mapping of the resistance genes in chestnut will be conducted later in the project. Restoration of American chestnut to our forests was a project that Dr. Schatz' was personally interested in. So it is gratifying for us to be able to participate in this important new project targeted at disease resistance in chestnut and related species.

We have recently completed two other large multi-institution research projects supported by the National Science Foundation. In the *BAC Resources for Plant Biology* project we constructed libraries covering all of the genes in several taxonomically important green plant species, including yellow poplar (*Liriodendron tulipifera*). We obtained clones from the yellow-poplar library with complete genes for wood biosynthesis, flower growth, and biomass accumulation. In the recently completed *Floral Genome Project*, we developed new gene sequence databases for 15 plant species, including yellow-poplar and several other woody plants. Genes that regulate flower development were isolated from these libraries and compared among species.

The **Genome Sequencing Facility** developed at Penn State in 2005 through the efforts of the Schatz Center Director, John Carlson, and colleagues, is now in full production capacity. The facility has permitted many new large-scale sequencing projects to be initiated across the university. Our GS20 Genome Sequencer will be upgraded in early 2007 to the new **GS100 model** which will have the capacity to produce a minimum of 100 Million bases of DNA per experiment. The upgrade (paid for from university funds) will now permit us to determine the complete genome sequences of plants and fungi in addition to bacteria. Thus we should now be able to find important genes in trees in just a few experiments, rather than years of labor.

The Schatz Center is engaged in several research projects using the new genome sequencing technology. Dr. Carlson is collaborating with entomologists and microbiologists at Penn to discover the microbes in the digestive track that permit the invasive insect pest of *Asian Longhorned Beetle* (ALB) to kill trees by eating the wood in standing trees. Our GS20 data shows that many of the microbial species have not been previously studied. Because it is so rare for an insect to be able to digest all of the components of healthy wood (most termites only infest rotting wood), the microbial enzymes in the ALB could be of great interest in Bioenergy applications, such as conversion of wood to ethanol. For this reason, the US Department of Energy has recently agreed to finish DNA sequencing of the ALB gut microbial community in the genome center for us. Over the next year we will assist the DOE to get the sequences, we will then analyze for wood digesting enzyme genes. The DNA sequencing that we will do for the new *Genomic Tool Development for the Fagaceae* project described above will also be done using our new genome sequencing facility. The first experiment that we conducted using the GS20 sequencer resulted in sequences for several thousand genes that American chestnut expresses in its stems soon after it is infected with the killer chestnut blight fungus. Many of these genes are known to be disease response genes in other plant species. Many other genes are of unknown function. We are now comparing these American chestnut genes to new DNA sequence data that we just obtained from blight-resistant Chinese chestnut stems after inoculation with the fungal pathogen. We hope that this comparison will yield some clues about why Chinese chestnut has blight-resistance and American chestnut does not.

*Schatz Post-Doctoral Fellowships in Tree Genetic Engineering* – Schatz post-doctoral fellows **Dr. Haiying Liang** and **Dr. Abdoulaye Traore** were both recently successful at obtaining permanent positions with excellent opportunities 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. We are pleased that Haiying and Abdoulaye have joined all of the former Schatz post-doctoral fellows in moving directly from the opportunity provided to them in the Schatz Center to launch their own research careers, and in so doing to further establish the reputation of the Schatz Center.

Our current post-doctoral fellows **Teodora Best and Chris Frost** have strong research programs underway. Both have been in the Schatz Center now for one year, and in that time have set up interesting research systems that permit us to examine the genetic response of trees to the damaging effects of air pollution (ozone) and exotic insect pests (gypsy moth).

*The Schatz Awards for Undergraduate Research* are being availed by several students at the University Park campus who are conducting research under the supervision of the Center Director and staff of the Schatz Center. This year we have 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 (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 through 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 first use of the funds will be to purchase a new school bus for student field trips.

*The Schatz Tree Genetics Colloquium at Mont Alto:* Dr. Beth Brantley at Mont Alto and Dr. Carlson at University Park are planning the first colloquium to be held at Mont Alto on Monday April 30, 2007, to follow the School of Forest Resources Centennial celebrations on April 28 and 29, 2007. The colloquium will include presentations covering research activities underway in the Schatz Center along with invited talks on other topics of interest to the Schatz Center.

*The Schatz Student Field Trip Funds* – sufficient funds have accrued in the Schatz Student Travel Endowment to support a trip to California in May of 2007 to once again visit Gordon Schatz and the Humboldt State University. Dr. Carlson will be accompanied by a graduate student from the Schatz Center and several students from the Penn State Forestry Honor Society.

*The Louis and Merry Schatz Faculty Travel Fund* was used in 2006 to support travel by the Center Director, Dr. Carlson, to the Plant and Animal Genome Conference in San Diego, and to assist Schatz Center faculty member Dr. Marc Abrams travel to an international conference in Beijing, China, on the use of tree ring measurements in forest ecology and forest regeneration research.

#### **PUBLICATIONS FROM THE SCHATZ CENTER, in 2006:**

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

Gilbert, M.T., Binladen, J., Miller, W., Wiuf, C., Willerslev, E., Poinar, H., **Carlson, J.E.**, Leebens-Mack, J., Schuster, S. 2006. Recharacterization of ancient DNA miscoding lesions: Insights in the era of sequencing-by-synthesis. *Nucleic Acids Research*, Published on-line August 18, 2006. 8 pages.

Swanson, J-D, **Carlson, J.E.**, Guiltinan, M.J. 2006. Use of image analysis software as a tool to visualize non-radioactive signals in plant in situ analysis. *Plant Molecular Biology Reporter*, 24(1): 105a-105e.

Tuskan, G.A., et al. 2006. The Genome of Western Black Cottonwood, *Populus trichocarpa* (Torr. & Gray ex Brayshaw). *Science* 313: 1596-1604. (Sept 15, 2006).

**Carlson, J.E.**, Leebens-Mack, J.H., Wall, P.K., Zahn, L.M., Mueller, L.A., Landherr, L.L., Hu, Y., Ilut, D.C., Arrington, J.M., Choirean, S., Becker, A., Field, D., Tanksley, S.D., Ma, H., dePamphilis, C.W. 2006. EST database for early flower development in California poppy (*Eschscholzia californica* Cham., Papaveraceae) tags over 6000 genes from a basal eudicot. *Plant Molecular Biology*, 62: 351-369.

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.

**Carlson, J.E., Traore, A.**, Agrama, H.A., Krutovsky, K.V. 2006. Douglas-fir. In: *Genome Mapping & Molecular Breeding in Plants Vol. 7*, (Ed, C. Kole), Springer Heidelberg, Berlin, New York, Tokyo, In Press.

**Liang, H.**, Fang, EG, Tomkins, JP, Luo, M, Kudrna, D, Arumuganathan, K, Zhao, S, Schlarbaum, SE, Banks, JA, dePamphilis, CW, Mandoli, DF, Wing, RA and **Carlson, JE.** Development of a BAC library resource for yellow poplar (*Liriodendron tulipifera*) and the identification of genomic regions associated with flower development and lignin biosynthesis. *Tree Genetics and Genomes*, In press (Accepted August 28, 2006).

Kremer A, Casasoli M, Barreneche T, Bodénès C, Sisco P, Kubisiak T, Scalfi 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, (Ed, C. Kole), Springer Heidelberg, Berlin, New York, Tokyo, In Press.

**Steiner, K. C.** and **J. E. Carlson**, 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:**

Wall, P.K., Leebens-Mack, J.H., Albert, V., **Carlson, J.E.**, Field, D., Altman, N., Ma, H., dePamphilis, C.W. *Populus* Genome Aids Identification of Gene Families across the Angiosperms. Submitted to The Plant Journal.

Michael A. Steele, **John E. Carlson**, Peter D. Smallwood, Amy B. McEuen, Thomas A. Contreras, and William B. Terzaghi. Linking seed and seedling shadows: A case study in the oaks (*Quercus*). Chapter In: "Frugivory and Seed Dispersal." David Westcott, ed. CABI International, publisher. Submitted.

Steele, M.A., Smallwood, P.D., Terzaghi, W.B., **Carlson, J.E.**, Contreras, T., and McEuen, A. Oak dispersal syndromes: do red oaks and white oaks exhibit different dispersal strategies? U.S. Forest Service technical publication. Submitted.

**Abdelali Barakat**, Kerr Wall, Jim Leebens-Mack, **John Carlson** and Claude dePamphilis, 2006, Large-scale identification of microRNAs from a basal eudicot (*Eschscholzia californica*). Submitted to The Plant Journal November 2, 2006.