Exploring Deployment Options for Short Rotation Woody Cropping Systems

Marilyn A. Buford

&

Carlos Rodriguez-Franco

US Forest Service Research & Development

October 19, 2010

Short Rotation Woody Crops Operations Working Group

Considerations

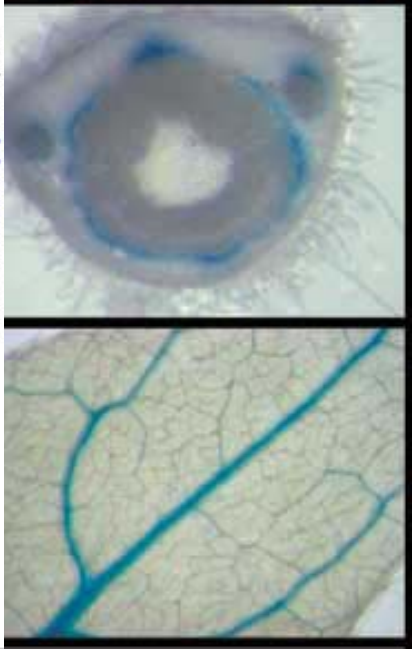
- Crop options
- Conversion Technology
- Demand
- Investment climate
- Policy
- Deployment

Crop Options Components

- Genetics
- Management systems
- Harvest & Transport
- Sustainability

Genetics

- Traditional tree breeding
  - Poplar
  - Willow
  - Loblolly pine
  - Eucalypts
- Genome sequencing and mapping
- Screening
  - Wood formation
  - Crown architecture
- Potential
  - Enhanced breeding, testing and selection
  - Infrastructure for breeding traits and adaptability
  - Enhanced yield, specific stress tolerance, fertility control, eliminating undesirable crop characteristics



RESEARCH ARTICLES

The Genome of Black Cottonwood, *Populus trichocarpa* (Torr. & Gray)

G. A. Tuskan,[1,2]* S. DiFazio,[1,4]† S. Jansson,[5]† J. Bohlmann,[6]† I. Grigoriev,[7]† U. Hellsten,[7]† N. Putnam,[8]† S. Ralph,[6]† S. Rombauts,[10]† A. Salamov,[7]† J. Schein,[11]† L. Sterck,[12]† A. Aerts,[7] R. R. Bhalerao,[5] R. P. Bhalerao,[12] D. Blaudez,[13] W. Boerjan,[10] A. Brun,[13] A. Brunner,[14] V. Busov,[15] M. Campbell,[16] J. Carlson,[17] M. Chalot,[13] J. Chapman,[7] G.-L. Chen,[2] D. Cooper,[4] P. M. Coutinho,[19] J. Couturier,[13] S. Covert,[20] Q. Cronk,[2] R. Cunningham,[1] J. Davis,[21] S. Degroeve,[10] A. Déjardin,[13] C. dePamphilis,[16‡] J. Detter,[7] B. Dirks,[14] I. Dubchak,[7,22] S. Duplessis,[12] J. Ehlting,[6] B. Ellis,[8] K. Gendler,[20] D. Goodstein,[7] M. Gribskov,[23] J. Grimwood,[24] A. Groover,[25] L. Gunter,[1] B. Hamberger,[2] B. Heinze,[26] Y. Helariutta,[12,13,27] B. Henrissat,[28] D. Holligan,[21] R. Holt,[11] W. Huang,[2] N. Islam-Faridi,[14] S. Jones,[11] M. Jones-Rhoades,[15] R. Jorgensen,[24] C. Joshi,[15] J. Kangasjärvi,[12] J. Karlsson,[5] C. Kelleher,[6] R. Kirkpatrick,[11] M. Kirst,[22] A. Kohler,[13] U. Kalluri,[1] F. Larimer,[1] J. Leebens-Mack,[21] J.-C. Leplé,[13] P. Locascio,[2] Y. Lou,[4] S. Lucas,[7] F. Martin,[13] B. Montanini,[13] C. Napoli,[24] D. R. Nelson,[29] C. Nelson,[17] K. Nieminen,[12] O. Nilsson,[12] V. Pereda,[12] G. Peter,[22] R. Philippe,[6] G. Pilate,[13] A. Poliakov,[23] J. Razumovskaya,[7] P. Richardson,[7] C. Rinaldi,[13] K. Ritland,[4] P. Rouzé,[30] D. Ryaboy,[20] J. Schmutz,[24] J. Schrader,[26] B. Segerman,[5] H. Shin,[11] A. Siddiqui,[11] F. Sterky,[10] A. Terry,[7] C.-J. Tsai,[15] E. Uberbacher,[2] P. Unneberg,[19] J. Vahala,[12] K. Wall,[16] S. Wessler,[25] G. Yang,[25] T. Yin,[4] C. Douglas,[1]‡ M. Marra,[11]‡ G. Sandberg,[12]‡ Y. Van de Peer,[10]‡ D. Rokhsar[7,24]‡

[1]Environmental Sciences Division, [2]Life Sciences Division, Oak Ridge National Laboratory, Oak Ridge, TN 37831, USA. [3]Plant Sciences Department, University of Tennessee, TN 37996, USA. [4]Department of Biology, West Virginia University, Morgantown, WV 26506, USA. [5]Umeå Plant Science Centre, Department of Plant Physiology, Umeå University, SE-901 87, Umeå, Sweden. [6]Michael Smith Laboratories, [7]Department of Botany, [8]Department of Forest Sciences, University of British Columbia, Vancouver, BC V6T 1Z4, Canada. [9]U.S. Department of Energy Joint Genome Institute, Walnut Creek, CA 94598, USA. [10]Department of Plant Systems Biology, Flanders Interuniversity Institute for Biotechnology (VIB), Ghent University, B-9052 Ghent, Belgium. [11]Genome Sciences Centre, 100-570 West 7th Avenue, Vancouver, BC V5Z 4S6, Canada. [12]Umeå Plant Science Centre, Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Sciences, SE-901 83 Umeå, Sweden. [13]Eco-Microbe Interactions Unit, Institut National de la Recherche Agronomique (INRA)–Université Henri Poincaré, INRA-Nancy 54280 Champenoux, France. [14]Department of Forestry, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061, USA. [15]Biotechnology Research Center, School of Forest Resources and Environmental Science, Michigan Technological University, Houghton, MI 49931, USA. [16]Department of Cell and Systems Biology, University of Toronto, 25 Willcocks Street, Toronto, Ontario, M5S 3B2 Canada. [17]School of Forest Resources and Huck Institutes of the Life Sciences, [18]Department of Biology, Institute of Molecular Evolutionary Genetics, and Huck Institutes of Life Sciences, The Pennsylvania State University, University Park, PA 16802, USA. [19]Architecture et Fonction des Macromolécules Biologiques, UMR6098, CNRS and Universities of Aix-Marseille I and II, case 932, 163 avenue de Luminy, 13288 Marseille, France. [20]Warnell School of Forest Resources, [21]Department of Plant Biology, University of Georgia, Athens, GA 30602, USA. [22]School of Forest Resources and Conservation, Genetics Institute, and Plant Molecular and Cellular Biology Program, University of Florida, Gainesville, FL 32611, USA. [23]INRA-Orléans, Unit of Forest Improvement, Genetics and Physiology, 45166 Olivet Cedex, France. [24]Center for Integrative Genomics, University of California, Berkeley, CA 94720, USA. [25]Genomics Division, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA. [26]Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA. [27]Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA. [28]The Stanford Human Genome Center and the Department of Genetics, Stanford University School of Medicine, Palo Alto, CA 94305, USA. [29]Institute of Forest Genetics, United States Department of Agriculture, Forest Service, Davis, CA 95616, USA. [30]Federal Research Centre for Forests, Hauptstrasse 7, A-1140 Vienna, Austria. [31]Plant Molecular Biology Laboratory, Institute of Biotechnology, [32]Department of Biological and Environmental Sciences, University of Helsinki, FI-00014 Helsinki, Finland. [33]Department of Biology, 20014, University of Turku, FI-20014 Turku, Finland. [34]Southern Institute of Forest Genetics, United States Department of Agriculture, Forest Service and Department of Forest Science, Texas A&M University, College Station, TX 77843, USA. [35]Whitehead Institute for Biomedical Research and Department of Biology, Massachusetts Institute of Technology, Cambridge, MA 02142, USA. [36]Department of Molecular Sciences and Center of Excellence in Genomics and Bioinformatics, University of Tennessee, Memphis, TN 38163, USA. [37]Southern Institute of Forest Genetics, United States Department of Agriculture, Forest Service, Saucier, MS 39574, USA. [38]Developmental Genetics, University of Tübingen, D-72076 Tübingen, Germany. [39]Department of Biotechnology, KTH, Albanova University Center, SE-106 91 Stockholm, Sweden.

*To whom correspondence should be addressed. E-mail: gtj@ornl.gov

†These authors contributed equally to this work as second authors.

‡These authors contributed equally to this work as senior authors.

We report the draft genome of the black cottonwood tree, *Populus trichocarpa*. Integration of shotgun sequence assembly with genetic mapping enabled chromosome-scale reconstruction of the genome. More than 45,000 putative protein-coding genes were identified. Analysis of the assembled genome revealed a whole-genome duplication event; about 8000 pairs of duplicated genes from that event survived in the *Populus* genome. A second, older duplication event is indistinguishably coincident with the divergence of the *Populus* and *Arabidopsis* lineages. Nucleotide substitution, tandem gene duplication, and gross chromosomal rearrangement appear to proceed substantially more slowly in *Populus* than in *Arabidopsis*. *Populus* has more protein-coding genes than *Arabidopsis*, ranging on average from 1.4 to 1.6 putative *Populus* homologs for each *Arabidopsis* gene. However, the relative frequency of protein domains in the two genomes is similar. Overrepresented exceptions in *Populus* include genes associated with lignocellulosic wall biosynthesis, meristem development, disease resistance, and metabolite transport.

Forests cover 30% (about 3.8 billion ha) of Earth's terrestrial surface, harbor substantial biodiversity, and provide humanity with benefits such as clean air and water, lumber, fiber, and fuels. Worldwide, one-quarter of all industrial feedstocks have their origins in forest-based resources (*1*). Large and long-lived forest trees grow in extensive wild populations across continents, and they have evolved under selective pressures unlike those of annual herbaceous plants. Their growth and development involves extensive secondary growth, coordinated signaling and distribution of water and nutrients over great distances, and strategic storage and redistribution of metabolites in concordance with interannual climatic cycles. Their need to survive and thrive in fixed locations over centuries under continually changing physical and biotic stresses also sets them apart from short-lived plants. Many of the features that distinguish trees from other organisms, especially their large sizes and long-generation times, present challenges to the study of the cellular and molecular mechanisms that underlie their unique biology. To enable and facilitate such investigations in a relatively well-studied model tree, we describe here the draft genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray), and compare it to other sequenced plant genomes.

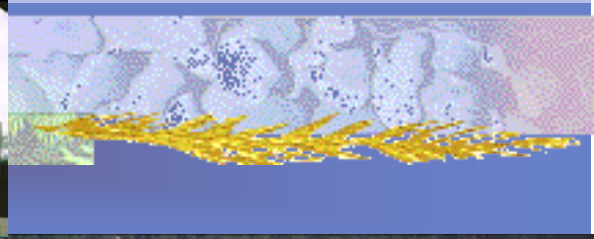
P. trichocarpa was selected as the model forest species for genome sequencing not only because of its modest genome size but also because of its rapid growth, relative ease of experimental manipulation, and range of available genetic tools (*2*, *3*). The genus is phenotypically diverse, and interspecific hybrids facilitate the genetic mapping of economically important traits related to growth rate, stature, wood properties, and paper quality. Dozens of quantitative trait loci have already been mapped (*4*), and methods of genetic transformation have been developed (*5*). Under appropriate conditions, *Populus* can reach reproductive maturity in as few as 4 to 6 years, permitting selective breeding for large-scale sustainable plantation forestry. Finally, rapid growth of trees coupled with thermochemical or biochemical conversion of the lignocellulosic portion of the plant has the potential to provide a renewable energy resource with a concomitant reduction of greenhouse gases (*6*–*8*).

Sequencing and Assembly

A single female genotype, "Nisqually 1," was selected and used in a whole-genome shotgun

Management Systems

- Regeneration options
- Density relationships
- Nutrient and water use efficiency
- Product optimization
- Functional optimization




05/19/2003

Harvest and Transport

- Energy-efficient technologies
- Light-on-the-land technologies
- Multiple systems
- Reduced costs


05/20/2003


05/19/2003

Sustainability

- Productivity
- Soil and water quality
- Habitat
- Landscape function

Photo: Jake Eaton, Potlatch Corporation

Bird Diversity in Willow

Cornell Lab of Ornithology

Conversion Technologies

- Biochemical - Biomass is broken down to sugars using either enzymatic or chemical processes and then converted to ethanol via fermentation.
- Thermochemical - Biomass is broken down to intermediates using heat and upgraded to fuels using a combination of heat and pressure in the presence of catalysts.

Biochemical Conversion

- Breaks down the cell wall through enzymes or acid to extract sugars
- Sugars converted to biofuels using microorganisms.
- Need to match biomass characteristics and processes
- Reduce processing and capital cost and improving the efficiency

Thermochemical Conversion

- Heat and pressure-based conversion of various biomass feedstocks to alcohol and hydrocarbon fuels, chemicals, and power
- Feedstocks for thermochemical processes have little to no restrictions on physical or chemical properties.
- Moisture and particle size are specified for the respective conversion processes

Demand Components

- Ethanol vs. Drop-in fuels
- Engine specifications
- Fuel distribution systems
- Price differential
- Kick-starting demand
- Policy relationships

Investment Climate

- Is there money available? and at what cost?
- Risk
  - Conversion technologies
  - Supply issues
  - Overall economic health
  - Subsidies?

Policy Components

- U.S. energy policy
- U.S. agriculture policy
- U.S. environmental policy

- Affect:
  - Supply
  - Demand
  - And all options in between

EISA 2007 (RFS2)

- Renewable Biomass Definition:
  - Planted crops and crop residue harvested from agricultural land cleared or cultivated at any time prior to the enactment of this sentence that is either actively managed or fallow, and nonforested.
  - Planted trees and tree residue from actively managed tree plantations on non-federal land cleared at any time prior to enactment of this sentence…

Farm Bill 2008

- BCAP*
  - Eligible material: renewable biomass that is eligible for the matching payment component of BCAP
  - Eligible crop: renewable biomass that may be eligible for the establishment and annual payments component of BCAP

* Draft rule 2/8/10

BCAP Renewable Biomass Definition

- Any organic matter that is available on a renewable or recurring basis from non-Federal land or land belonging to an Indian or Indian Tribe…
- Materials, pre-commercial thinnings, or invasive species from NFS or BLM land
  - Risk reduction/health improvement
  - No other value

BCAP Final Rule

- Due any day, perhaps any hour

Policy Components

- Linked
- Apparently not integrated

Deployment

- Pulp-mill model
  - Biorefinery/CHP facility
    - Lands owned/leased for direct supply
    - Landowner contracts
    - Purchase wood on open market
- Open/spot market
- Landowner cooperatives

Deployment

- Variations on a theme
- Determined by
  - Policy
  - Demand (effective conversion/use options)
  - Transport and distribution options
  - Infrastructure (local, regional, and national scale)

Thank you