Sequencing the *Populus* Genome: A Model Organism for Bioenergy and Carbon Sequestration Research

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Sponsor: DOE Office of Science, Biological & Environmental Research

- **Many of the features that distinguish trees from other organisms, especially their size and long generation times, present formidable challenges to the study of the cellular and molecular mechanisms that underlie their unique biology.**
- **Sequencing a model woody perennial would provide an unprecedented opportunity to explore this unique biology at a fundamental scale.**
- **ORNL and DOE scientists recently reported that they had successfully sequenced the first tree genome – *Populus*.**
- **This information will greatly improve our ability to: 1) use trees as a renewable source of energy, 2) enhance carbon storage in managed tree plantations and 3) understand mechanistic ecosystem responses to global climate change.**

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In summary, 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.

Tuskan G.A. *et al*. 2006. The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). Science 313:1596-1603.


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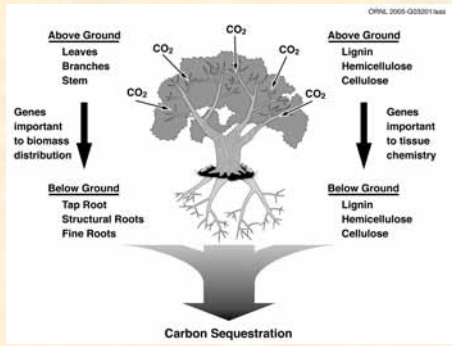
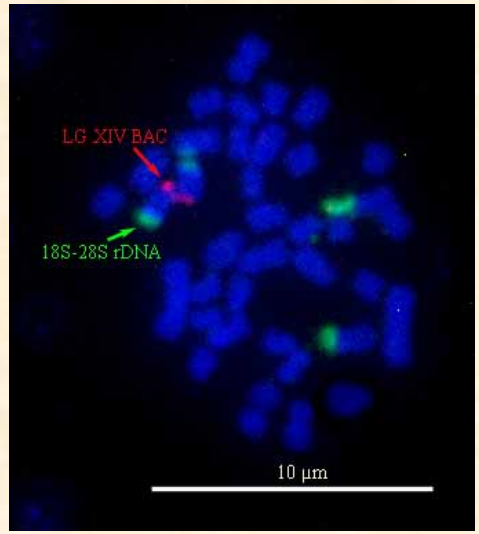
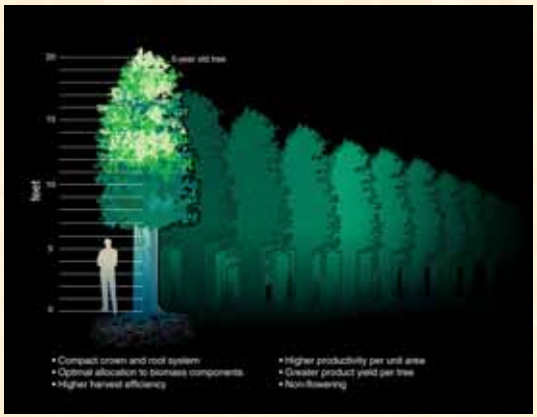
AAAS


ORNL 2005-G03201/aas
Above Ground
Leaves
Branches
Stem
CO_2
CO_2
CO_2
CO_2
CO_2
Above Ground
Lignin
Hemicellulose
Cellulose
Genes important to biomass distribution
Genes important to tissue chemistry
Below Ground
Tap Root
Structural Roots
Fine Roots
Below Ground
Lignin
Hemicellulose
Cellulose
Carbon Sequestration


LG XIV BAC
18S-28S rDNA
10 µm


• Compact crown and root system
• Optimal allocation to biomass components
• Higher harvest efficiency
• Higher productivity per unit area
• Greater product yield per tree
• Non-flowering