

# The poplar genome project

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# What makes trees so interesting?

- Forest trees contain most of the Earth's terrestrial biomass.
- Forest trees dominate the most productive terrestrial ecosystems.
- Wood is a vital raw material for industry.



# *Populus*

- ‘The people’s tree’
- ~30 species of poplars, cottonwoods, and aspen worldwide
- Family Salicaceae, which includes willows (*Salix*) and *Populus*



# The biology of *Populus*

- Hybrid poplars are the fastest-growing trees in the temperate zone
- Most species and hybrids can be propagated from cuttings (clones)
- Controlled pollination is easy; poplars are prolific



# *Populus* plantations

- Since 1978 DOE has supported basic and applied research to develop hybrid poplar as a biomass feedstock for renewable energy



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# Why sequence the *Populus* genome?

- ***Populus* is relevant to key DOE missions**
- ***Populus* is well suited for structural genomics**
- **Functional genomics is far more powerful in *Populus* than in any other forest tree**
- **A worldwide poplar research community is ready to make immediate use of the sequence**
- **The DOE's Joint Genome Institute has the capability to sequence and assemble large, complex genomes**

# *Populus* is relevant to key DOE missions

- Renewable energy
- Carbon sequestration
- Bioremediation



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# *Populus* is well suited for structural genomics

- Relatively small genome of 550Mbp (5X *Arabidopsis*, similar to rice, 40X smaller than pine)
- 100K ESTs to be released  
<http://www.biochem.kth.se/PopulusDB/>
- Genetic linkage maps based on large progeny sets (0.05cM resolution in some cases)
- 10X BAC library of a single *P. balsamifera* (*trichocarpa*) clone 'Nisqually-1'
- Closely related to *Arabidopsis*
- JGI to produce 3X shotgun in FY02; 3X shotgun or minimum BAC tiling path in FY03

**The *Populus* genome sequence will overcome many of the limitations inherent in forest tree genetics**

- **Long generation interval**
- **Outcrossing mating system**
- **Lack of inbred lines**
- **Lack of efficient mutagenesis**

# What do we need to study in trees that can't be done in *Arabidopsis*?

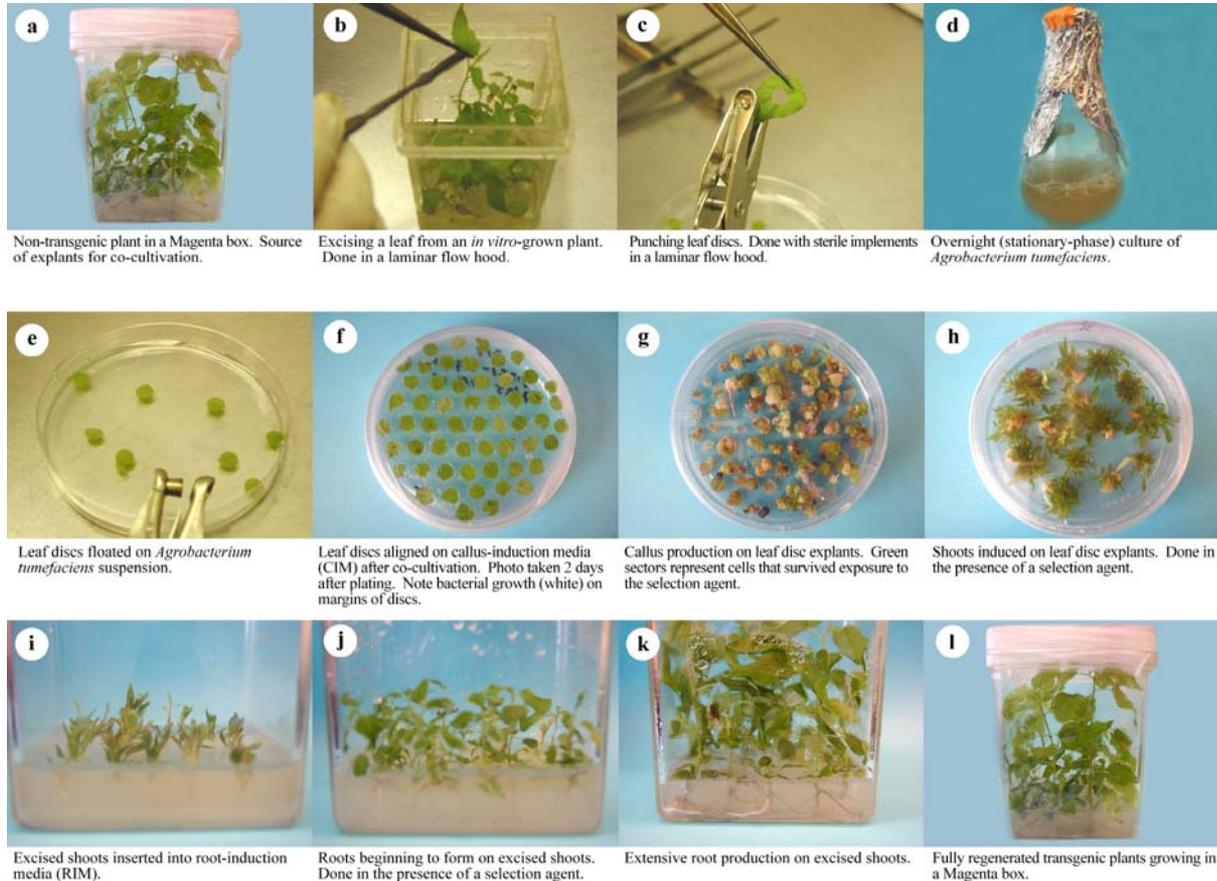
- **Extensive wood formation**
- **Juvenile-mature transition**
- **Crown architecture**
- **Vegetative dormancy**
- **Complex ecology and perennial life history**
- **Practical applications to biomass production**



# What will we do with a genome sequence from *Populus*?

- **Functional genomics**
- **Large-scale analysis of population genetics, adaptation, and hybridization**
- **Comparative genomics**
- **Genome evolution**

# Functional genomics is more powerful in *Populus* than in any other forest tree



Steve Strauss and Rick Meilan, [Tree Genetic Engineering Research Cooperative](#)

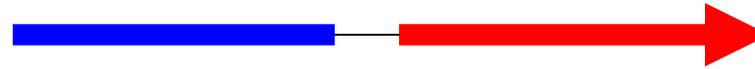
# Transgenesis will do for trees what mutagenesis did for *Arabidopsis*

- Use gene identity (known from DNA sequence) to determine gene function *in vivo*
- Comprehensive, unbiased testing of EVERY ONE of the 25K (50K?) *Populus* genes and gene families
- Rational, predictable modification of tree growth, development, and biochemistry

# Transgenesis will do for trees what mutagenesis did for *Arabidopsis*

- Knock-out of individual genes or whole gene families by RNAi to ascertain gene function
- ‘Knock-in’ or up-regulated or ectopic expression
- Activation tagging to produce dominant gain-of-function phenotypes
- Gene/promoter/enhancer traps to discover genes involved in tree growth and development
- ***TIE GENE IDENTITY TO PHENOTYPE***

# Activation tagging of genes

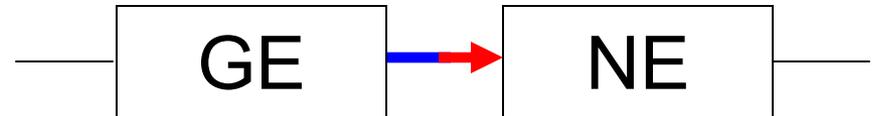


**BAR**  
herbicide  
resistance

**CaMV  
35S**  
strong  
promoter



- ‘Activation tag’ T-DNA can produce dominant overexpressing mutation when inserted upstream of a gene



- ‘Activation tag’ T-DNA can produce recessive knockout mutation when inserted into a gene

# Gene trapping in transgenic *Populus*

- Gene traps to discover genes involved in tree growth and development



Photo courtesy of Andrew Groover, Institute of Forest Genetics

# Traits being genetically engineered in forest trees

- Herbicide resistance (weed control)
- Insect resistance (leaf beetle, budworm)



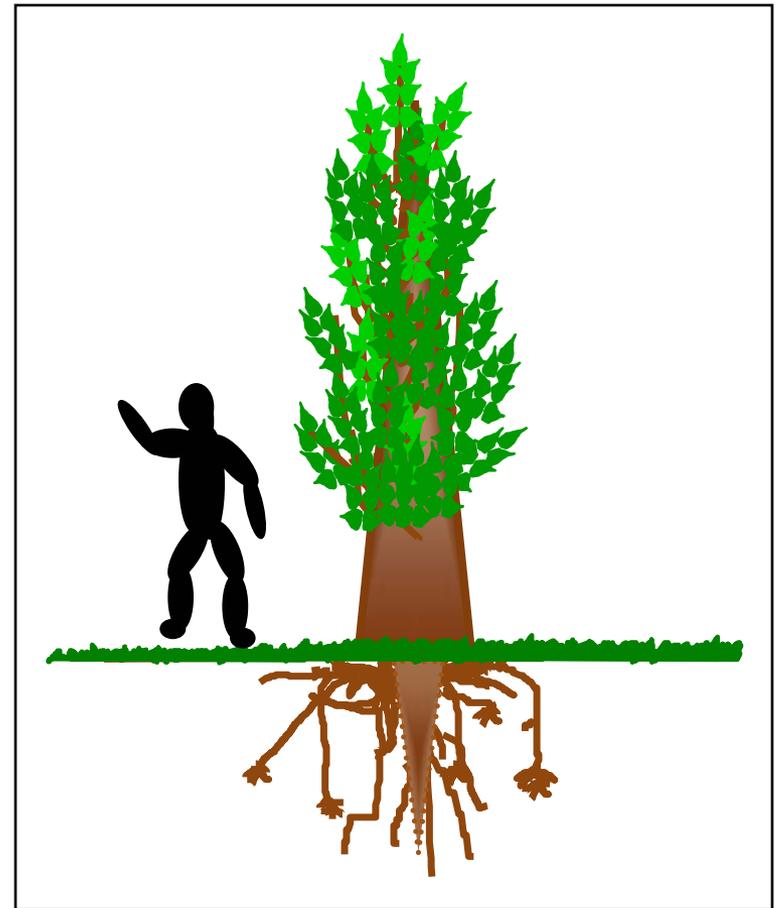
Steve Strauss and Rick Meilan, [Tree Genetic Engineering Research Cooperative](#)

# Traits of the future

- Growth/yield (wood, fiber, renewable energy)
- Wood quality (strength, stiffness, straightness, few knots)
- Disease resistance
- Tolerance of cold, drought, salt
- Novel photosynthetic pathways
- Self-pulping wood
- 'Farm'aceuticals
- Industrial chemical feedstocks (bio-based economy)
- DOMESTICATION

# Domesticated *Populus* attributes

- High growth rate
- Strong apical control; narrow, confined crown; minimal branching
- Maximum light interception in crown
- Non-competitive even at close spacing
- Reduced height growth
- Less extensive root system
- Greater carbon allocation to stem



# **A worldwide poplar research community is contributing to the sequencing effort!**

- Sweden: 100K ESTs, unigene microarrays, metabolic profiling
- Canada: physical mapping of the *Populus* genome
- EU: QTL mapping of physiological traits

# Poplar Genome Steering Committee

|                             |  |
|-----------------------------|--|
| <b>Toby Bradshaw, Chair</b> | <b>Univ. Washington</b>                |
| <b>Steve Strauss</b>        | <b>Oregon State Univ.</b>              |
| <b>Jerry Tuskan</b>         | <b>ORNL</b>                            |
| <b>Dan Rokhsar</b>          | <b>JGI</b>                             |
| <b>Bill Beavis</b>          | <b>Natl. Ctr. For Genome Resources</b> |
| <b>John Carlson</b>         | <b>Penn State Univ.</b>                |
| <b>Brian Johnson</b>        | <b>English Nature</b>                  |
| <b>Rob Martienssen</b>      | <b>Cold Spring Harbor Labs</b>         |
| <b>Göran Sandberg</b>       | <b>Swedish Agricultural Univ.</b>      |
| <b>Chung-Jui Tsai</b>       | <b>Michigan Tech Univ.</b>             |
| <b>Bill Young</b>           | <b>Northern Arizona Univ.</b>          |

# Urgent research needs for *Populus* in the post-sequence era

- **Consolidation of genetic, physical, and sequence maps of the genome**
- **Development of a full suite of genome analysis tools (e.g., microarrays, SNPs)**
- **Funding for high-throughput transgenesis to produce a very large collection ( $N \geq 25,000$ ) of knock-out and knock-in (KOKI) mutants**
- **Secure field sites for large-scale screening/testing of KOKI transgenic trees, accessible to researchers worldwide**
- **Fast, non-destructive phenotyping of important traits in KOKI mutants**

The *Populus* genome sequence will revolutionize forest tree biology

