Comparative Genomics of Environmental Stress Responses in North American Hardwoods

“The Hardwood Genomics Project”

Third annual project meeting, Sept 13, 2013
Project Investigators

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Mark Coggeshall, University of Missouri
Haiying Liang, Clemson University
Oliver Gailing, Michigan Technological University
Ketia Shumaker, University of West Alabama

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Meg Staton, Bioinformatics, Clemson University
Nick Wheeler, Project manager.

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Ron Sederoff, Steve DiFazio, Dana Nelson, Bert Abbott, Doug Soltis

Comparative Genomics of Hardwood Tree Species
http://www.hardwoodgenomics.org
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<td>Undergrad</td>
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Project Goal

Our primary goal is to develop genomic resources that will facilitate operational responses to anticipated and unforeseen forest health challenges and further research in population, evolutionary and conservations genetics for an array of hardwood species native to eastern North America.

Specifically, we envision that resources developed will identify candidate genes for resistance or tolerance to biotic and abiotic stresses, provide genetic reagents for marker assisted selection and management of genetic diversity (conservation), and allow for enhanced phylogenetic inferences.
Specific Project Objectives

1. Develop deep EST sequence libraries focusing on stress-response
2. Develop BAC libraries for Black Walnut and Northern Red Oak
3. (Develop a gene-space physical map for Northern Red Oak)
4. Identify DNA markers from EST and gDNA sequences
5. Develop framework and high-density genetic linkage maps
6. Identify syntenies among genomes
BASIS OF SPECIES SELECTION:
- Phylogenetic breadth
- Geographic coverage
- Economic importance
- Ecological impacts

Species being studied

- **Liriodendron tulipifera**
  - Model magnoliid
  - Fast growing hardwood

- **Liquidambar styraciflua**
  - Basal Eudicot
  - Fast growing hardwood

- **Gleditsia triacanthos**
  - Widely adapted nitrogen fixer
  - Potential in agroforestry

- **Quercus rubra**
  - Dominant upland species
  - Complementary to European work
  - Fine hardwood

- **Juglans nigra**
  - Cultivars/specialty crop
  - Agroforestry program
  - Fine hardwood

- **Acer saccharum**
  - Shade tolerant
  - Widely adapted

- **Nyssa sylvatica** (Black gum)
  - Basal Asterid
  - Widely distributed and adapted

- **Fraxinus pennsylvanica**
  - Widely adapted; extensively planted
  - Acutely threatened

http://www.hardwoodgenomics.org

Liriodendron tulipifera
Liquidambar styraciflua
Gleditsia triacanthos
Quercus rubra
Juglans nigra
Acer saccharum
Fraxinus pennsylvanica
## Target species and genomic resources underway in this project

<table>
<thead>
<tr>
<th>Order</th>
<th>Species</th>
<th>Populations</th>
<th>Genomic resources</th>
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<tbody>
<tr>
<td></td>
<td></td>
<td>FS/HS</td>
<td>ESTs</td>
</tr>
<tr>
<td>Magnoliales</td>
<td><strong>Yellow-poplar</strong>  <em>Liriodendron tulipifera</em></td>
<td>FS</td>
<td>NSF†</td>
</tr>
<tr>
<td>Proteales</td>
<td><strong>Sweetgum</strong>  <em>Liquidambar styraciflua</em></td>
<td>HS</td>
<td>YES</td>
</tr>
<tr>
<td>Fabales</td>
<td><strong>Honey locust</strong>  <em>Gleditsia triacanthos</em></td>
<td>FS</td>
<td>YES</td>
</tr>
<tr>
<td>Fagales</td>
<td><strong>Black Walnut</strong>  <em>Juglans nigra</em></td>
<td>FS</td>
<td>YES</td>
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<tr>
<td></td>
<td><strong>Northern red oak</strong>  <em>Quercus rubra</em></td>
<td>FS</td>
<td>NSF&amp;</td>
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<tr>
<td>Fagales</td>
<td><strong>Sugar maple</strong>  <em>Acer saccharum</em></td>
<td>HS</td>
<td>YES</td>
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<tr>
<td>Sapindales</td>
<td><strong>Green ash</strong>  <em>Fraxinus pennsylvannica</em></td>
<td>FS</td>
<td>YES</td>
</tr>
<tr>
<td>Lamiales</td>
<td><strong>Black gum</strong>  <em>Nyssa sylvatica</em></td>
<td>HS</td>
<td>YES</td>
</tr>
</tbody>
</table>

### Key:
- **YES** – Activity Funded; **X** – Activity Not Funded; **S** – Effort supplements existing population; **HSC** – Half-sib collections being made, but identification of full-sibs unfunded; **AA** – Some accessions available from unfunded collections; **- NSF** - Resource developed in NSF project “Genomic Tool Development for the Fagaceae” TRPGR: 06055135; **NSF†** - Resource developed in NSF project “Ancestral Angiosperm Genome Project” TRPGR: 0638595; **IRA** – If Resources Allow

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**Comparative Genomics of Hardwood Tree Species**

[http://www.hardwoodgenomics.org](http://www.hardwoodgenomics.org)
Comparative Genomics of Environmental Stress Responses in North American Hardwoods

Project leadership
J.E. Carlson, PI

Scientific Advisory Board
Sederoff, DeFazio, Nelson, Abbott, Soltis

Project time frame: February 1, 2011 to January 31, 2015

Genetic Maps
J Romero-Severson

EST Sequencing
Carlson

Treatments and RNA preps, Liang, Best

EST Bioinformatics, M. Staton

Marker development

Project Manager
Wheeler

Website, M. Staton

Reporting

Annual meetings

Outreach

First Nations Schools
Schlarbaum, JRS

BAC Libraries
Liang

Library construction
CUGI

NSF Plant Genome Research Program

Green ash, JEC

Red Oak, JRS, OG

Black Walnut, JRS

Yellow-poplar, HL

Honeylocust, OG

Mapping populations, SCS, MVC

Summer Research
Shumaker, JEC

Project Organizational Chart

http://www.hardwoodgenomics.org
Changes to original plan

1) Added SSR discovery by genomic DNA sequencing
   • Seedling availability not matching up with plan for ESTs sequencing for 2 species per year
   • SSRs needed in short term for genotyping
   • Rich Cronn agreed to collaborate on gSSR development

2) Tissue sampling for ESTs
   • Some parent trees not cooperating with masting so seedling availability not matching plan for EST development
   • Decided to collect tissues from parent trees for initial ESTs

3) Population development
   • Some shifting in time line of development of seedling populations resulting from masting issues with certain parent trees
   • Prioritization of minor species for resource development
      ➢ No maps for Black gum, sweetgum, sugar maple
      ➢ Linkage Map instead for green ash
      ➢ No physical maps

4) REU Supplement awarded for 2 students to conduct integrated field and lab studies with Scott and Haiying.
• Project management, reporting – John and Nick
• Population development – Mark and Scott
• EST data – Haiying (seedling treatments) and John (sequencing)
• gDNA sequencing with Rich Cronn’s lab
• SSR DNA marker development
  Meg: Bioinformatics
  Oliver: Honeylocust, Sugar maple
  Haiying: Tulip Poplar, Red bay
  Jeanne: Black Walnut, Northern red oak, Green ash
  John: Black gum, Sweetgum , Green ash
• Genetic maps
  Q. rubra - Jeanne and Oliver
  J. nigra - Jeanne
  G. tricanthos - Oliver
  F. pennsylvanica, - John
  L. tulipifera - Haiying
• BAC libraries – Haiying, CUGI
• Bioinformatics - Meg and Charles
• Educational outreach
  ➢ Eastern Band of the Cherokee Tribal Schools - Scott and Jeanne
  ➢ REU - Scott and Haiying
  ➢ Undergraduate summer research program at Penn State – Ketia, Teo