Project Overview
Analysis of genes affecting plant regeneration and transformation in poplar

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A National Science Foundation funded project

• NSF Plant Genome Research Program (IOS # 1546900)

• All NSF projects require both scientific research and outreach/education efforts

• Leverage the expertise and research discoveries to benefit education and society

• An interdisciplinary, 5 year project
  – Botany, genetics, computer science, statistics, bioinformatics, social science, education
What is genetic engineering?

• Direct modification of DNA
  • Vs. indirect modification in breeding and marker selection

• Asexually modified, usually in somatic cells
  • Then regenerated into whole organisms, most often starting in Petri dishes

• Gene transfer called “transformation”
The same process required for “gene editing”
Regeneration and transformation varies widely among wild cottonwoods.
Project rationale and goals - 1

• Regeneration and transformation (RT) is critical to producing genetically engineered plants for science or application

• The biological controls on RT, and the causes of the great genetic variability in it, are unknown

• If we ID the genes that control RT, we can gain insight into how it works

• If we understand RT better, we can develop better methods for genetic engineering
The project will conduct a genome-wide association study (GWAS) of RT in *Populus* (= cottonwoods, aspens)

- Use of DOE re-sequenced cottonwood collection (~1,000 wild genotypes)
- We add on the RT traits and map the genes

The project has three main activities

1. Develop novel phenomic (= in depth trait analysis) methods based on image analysis
2. Identify genetic elements that control RT by GWAS
3. Develop new social science and education methods for teaching about genetic engineering to high school students and teachers
GWAS is widely used in human genetics to understand diseases, etc.

**Genome-wide Association Study (GWAS)**

- DNA Sequencing
- 3 billion nucleotides (characters)

**Case (with disease)**

GWAS aims to find the associations between genetic variations and observable traits.

**Control (without disease)**

DNA Sequencing
Phenomics: Image acquisition system concept
Phenomics: Machine vision analysis concept
Phenomics: Hyperspectral analysis of transformation with fluorescent marker genes
Pilot study of rootability
Machine vision analysis
Some preliminary gene identifications

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<th>Chromosome</th>
<th>Position</th>
<th>-log10 P-value</th>
<th>Gene</th>
<th>Notes/Description</th>
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Outreach: Genetic aspects of case studies

- Two GMOs under consideration at present
- Herbicide resistant soybean
  - Most widely used GMO, great economic and ecological benefits, and also significant agronomic and ecological problems
  - Great materials and teaching modules available, including diagnostic “GMO dipstick”
- Bruising reduced “Innate Potatoes”
  - Only potato genes modified or introduced
  - Example of response to consumer demand, GMO controversy
  - Clearly visible consumer-friendly trait, no need for dipstick
Soy system well developed, materials available for free or low cost
Innate vs. parent lines after cutting

<1 minute after cutting

1 hour after cutting

2 days after cutting