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

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A National Science Foundation funded project

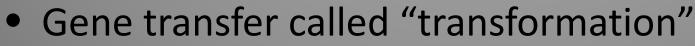
• NSF Plant Genome Research Program (IOS # 1546900)

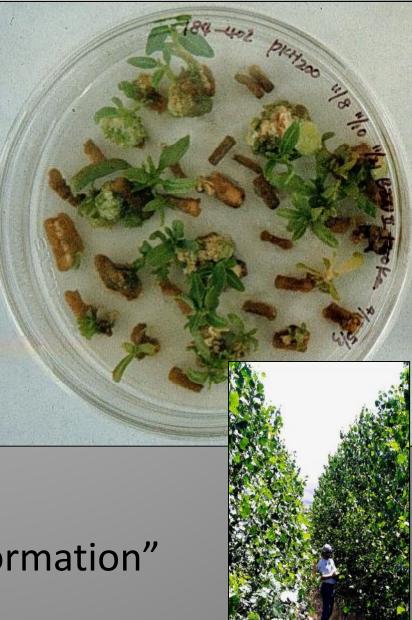


- All NSF projects require both scientific research and outreach/education efforts
- Leverage the expertise and research discoveries to benefit education and society
- An interdisciplinary, 5 year project
 - Botany, genetics, computer science, statistics, bioinformatics, social science, education

What is genetic engineering?

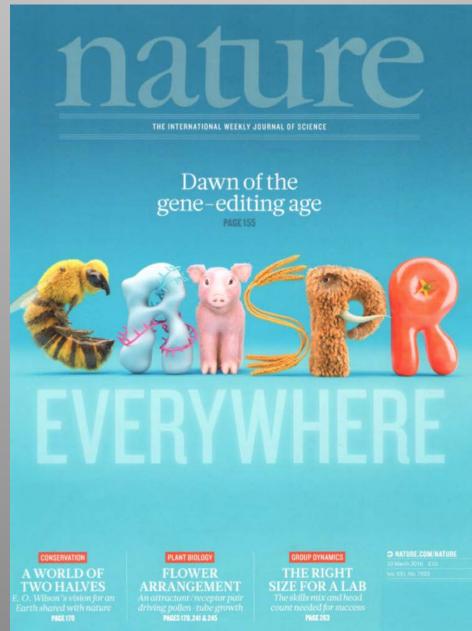
- Direct modification of DNA
 - Vs. indirect modification in breeding and marker selection
- Asexually modified, usually in somatic cells
 - Then <u>regenerated</u> into whole organisms, most often starting in Petri dishes





The same process required for "gene

editing"



Regeneration and transformation varies widely among wild cottonwoods



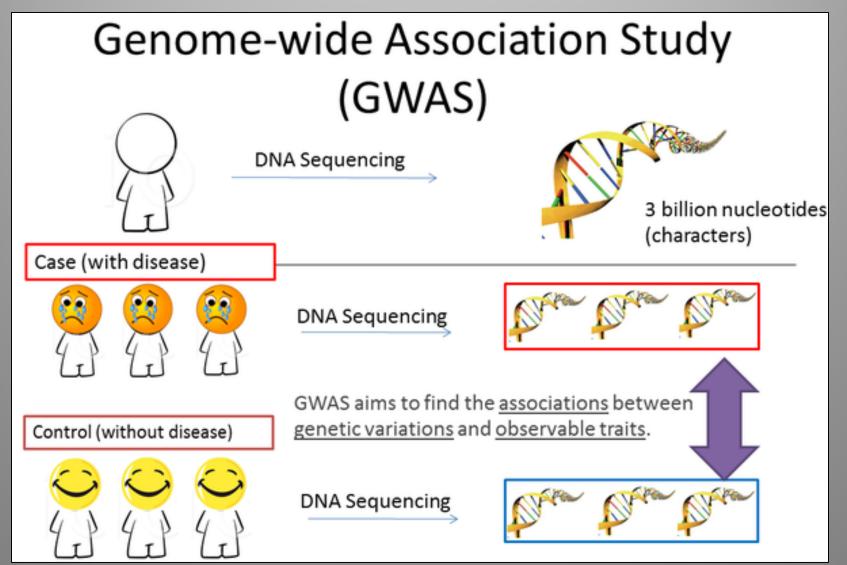
Project rationale and goals - 1

- 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

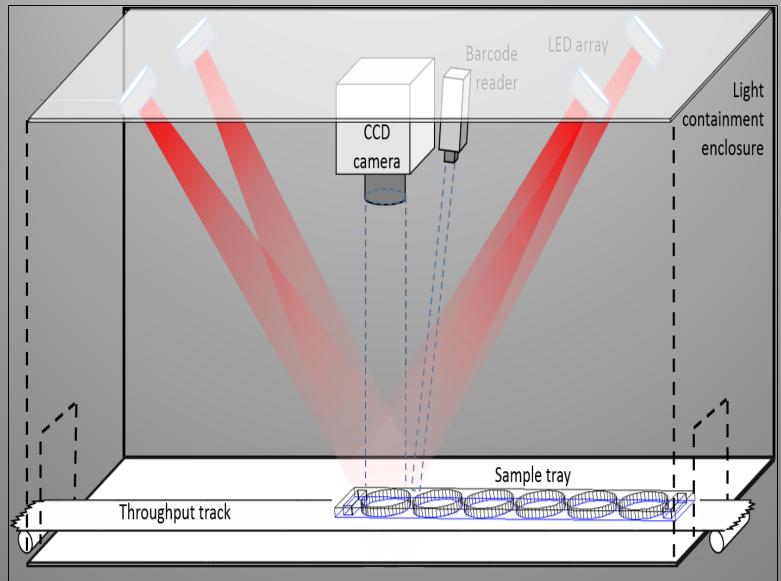
Project rationale and goals - 2

- 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

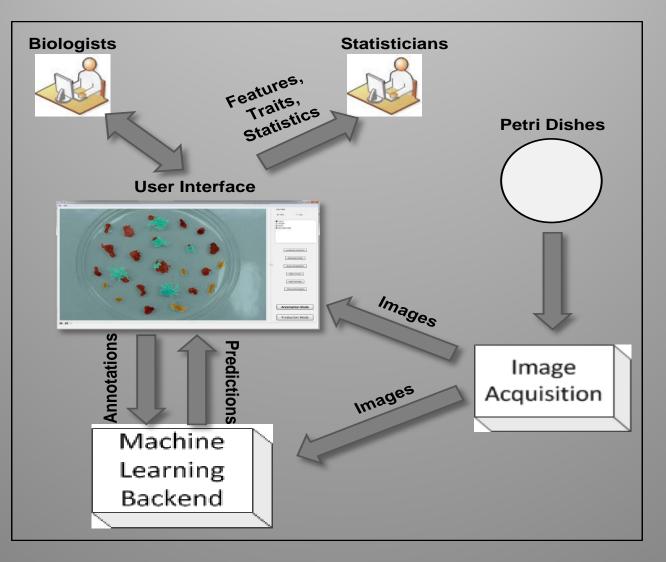
GWAS is widely used in human genetics to understand diseases, etc



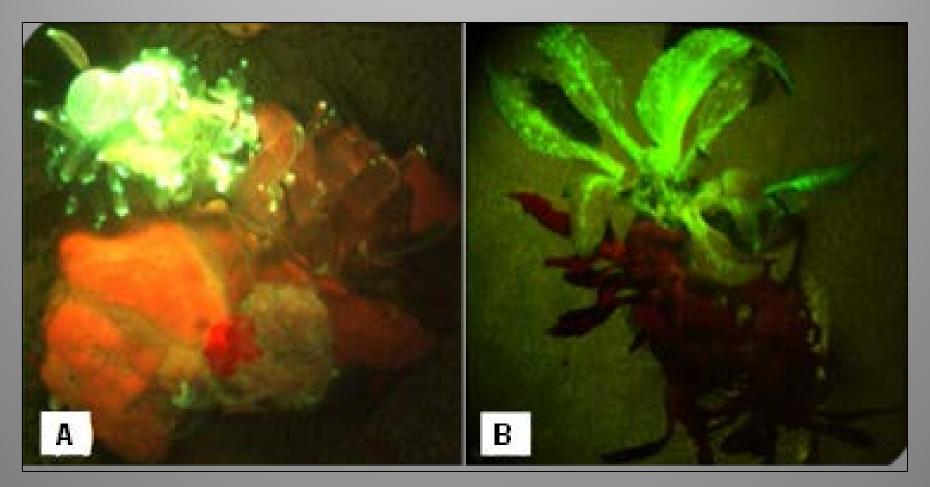
Phenomics: Image acquisition system concept



Phenomics: Machine vision analysis concept



Phenomics: Hyperspectral analysis of transformation with fluorescent marker genes



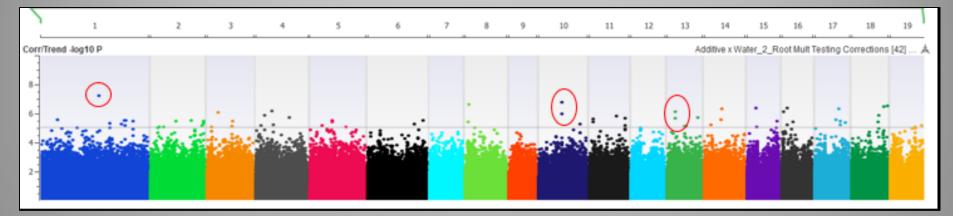
Pilot study of rootability



Machine vision analysis



Some preliminary gene identifications

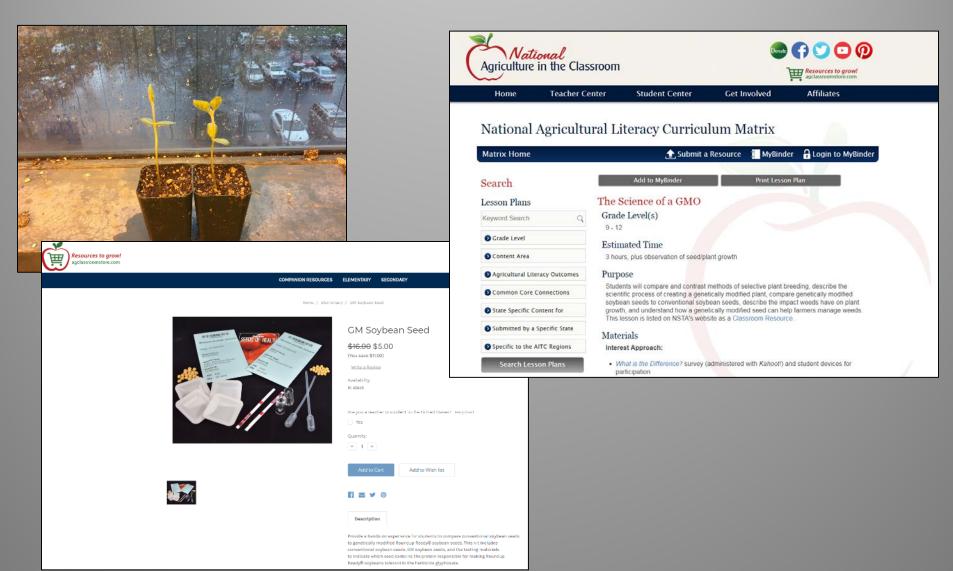


Chromosome	Position	-log10 P-value	Gene	Notes/Description
1	27299510	7.20	Potri.001G264500.1	SNP in gene, UBX domain, Arabidopsis homolog PUX1 gene, loss of which is known for accelerated growth of roots
10	10735457	5.94	Potri.010G081300.1	Protein Argonaute 10, known for small RNA-directed gene slicing, expressed in roots
10	10808758	6.71	Potri.010G081900.1	Expression in roots, Arabidopsis homolog dyggve-melchior-clausen syndrome protein
13	3730879	6.09	Potri.013G051100.2	SNPs very close, both hit in gene. Zinc
13	3730867	5.61		finger FYVE domain containing protein, high expression in root tips

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

2 days after cutting



1 hour after cutting

