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Wild cottonwoods show extraordinary variation in regeneration responses. Shown are genetic differences in response to standard shoot regeneration and rooting treatments. We will develop imaging, computation, and GWAS methods for identification of associated genes.

Project Objectives

Regeneration of differentiated organisms from single cells is a critical need for functional genomics and for the production of genetically engineered organisms. The project will conduct a genome-wide investigation of the genes that control regenerability and transformation (RT) in *Populus*, which is one of the best studied crop species with respect to these traits. Extensive genomic resources for *Populus* will be leveraged, including rich transcriptome databases, a high-quality reference genome, and a fully resequenced genome-wide association study (GWAS) population of 1,084 undomesticated genotypes with extremely low levels of linkage disequilibrium. The project will identify genetic elements that control RT, develop novel phenomic methods based on image analysis, and develop new social science and education methods for teaching about genetic engineering to diverse high school students and teachers.

Participants				
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Background

To engineer plants effectively, genes must be first inserted into DNA and then plants containing the new DNA must be grown to maturity. For many plants, these steps are challenges that must be overcome so that scientists can study gene function and can engineer crops for genetic improvements. This project uses advanced DNA sequence databases, imaging, and computational methods to map the genes that control the processes of regeneration and transformation needed for genetic engineering. The project develops new and more efficient image acquisition and analysis software that will enable scientists in many fields to study plant regeneration and related processes more rapidly and precisely. At the same time, the project is developing a program to educate high school teachers and students about the foundation of genetics and genomics as an important step to communicate effectively about genetically engineered crops and food. Educational modules will contribute to teacher curricula in partnership with the Science & Math Investigative Learning Experiences (SMILE) program at Oregon State University as part of an extensive STEM network of high school teachers and students in rural and underserved communities in the Pacific Northwest.

Expected Deliverables

Specific objectives are to (1) explore a variety of RT methods to maximize variation in RT responses; (2) develop new phenomic tools, including an image capture and generalizable machine-vision system, to precisely determine in vitro phenotypes; (3) using GWAS, map sets of alleles that are associated with variation in RT frequency; and (4) study cognitive processes with respect to GE crops, develop case studies and new teaching materials, deliver them to rural and underserved communities in the Pacific Northwest, and through publications, social media, and conferences share the project's insights and teaching modules internationally.

Keywords: *Populus, in vitro,* biotechnology, differentiation, GWAS, phenomics

Project Website