A Systems Biology, Whole-genome Association Analysis of the Molecular Regulation of Biomass Growth and Composition in *Populus deltoides*

Leandro Gomide Neves[1]* (gomide@ufl.edu), **Matias Kirst**[1,2]

[1]Plant Molecular and Cellular Biology Graduate Program; [2]School of Forest Resources and Conservation, University of Florida, Gainesville, FL

Project Goals: Poplars are the principal short rotation woody crop species for providing clean, renewable and sustainable fuels in North America. Poplars are fast growing, have a perennial growth habit and wide natural distribution that supports its implementation in a broad range of environments. While poplars provide the benefits of ideal bioenergy crop, the genes that regulate biomass productivity and composition are largely unknown, despite their critical relevance for efficient conversion to biofuels. Association genetics has become the primary approach for identification of genes that regulate such complex traits because it permits capturing a broad allelic range at high-resolution. Poplars are particularly suited to unveil the molecular basis of biomass productivity and composition using an association genetics approach because of low domestication, large open-pollinated native populations, and high levels of genetic and phenotypic variation. However, with few exceptions, association genetic studies in poplar and other plant species have been hampered by limited gene and polymorphism coverage.

In this project we are genotyping a large genetically unstructured population of *Populus deltoides*, one of the most widely distributed short-rotation woody crop in North America, using a combination of sequence capture and high-throughput genotyping. In parallel, the population is being phenotyped for biomass productivity and quality traits, for future discovery of marker trait associations. The overall goal is to identify the polymorphisms that accounts for differences in biomass productivity and lignocellulose composition in this species, that can be utilized for genetic improvement through transgenics or marker assisted breeding. Our specific project goals and progress towards their completion is described below:

Initially, a sequence-capture platform based on ultra-long RNA oligonucleotides has been developed based on a reference sequence of *P. trichocarpa* and a partial sequence of *P. deltoides*. The oligonucleotide library has been designed to capture sequences from over 22,000 genes. In total we have designed 220,000 probes that target coding as well as regulatory (promoter and UTR) regions of selected genes, and optimized sequence-capture procedures to multiplex 5 genotypes in each hybridization.

The second objective of this project is to sequence-capture target coding and regulatory sequences in a *P. deltoides* association population of 500 individuals. This population is composed of first generation collections made in the south and southeastern U.S. in the last two decades, and is expected to represents the genetic diversity of *P. deltoides* that exists in breeding programs. This work is currently in progress. We have also propagated the populations for trails in greenhouse and field. Greenhouse trials have been completed during the summer of 2011, when biomass data from above and below ground plant compartments were collected, as well as weekly growth data. Two field trials, in Florida and South Carolina, are being installed in the winter of 2011-2012. Initial biomass data collected from the greenhouse trials will be presented.

During the next year we anticipate the completion of sequencing and polymorphisms detection, to begin the analysis of association between markers and traits. In addition, we are exploring the possibility of using the sequence capture data to uncover gene copy number variation (CNV) in the population of *P. deltoides*. If the presence of variation in copy number becomes evident, we will assess possible associations with trait phenotypes.