194. Accelerated Development of Optimal Feedstock for Bioenergy Using Genome-Wide Selection

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Project Goals: Our overall goals are to hyper-accelerate pine breeding, to generate cultivars of loblolly and slash pine tailored to produce high energy yields, that are ready for deployment within the duration of this project. To achieve these goals we are using genome-wide selection prediction models to identify and generate crosses designed to support the short-term needs of the bioenergy industry. Genome-wide selection prediction models were previously developed for this population, which has been grown at multiple sites, and was phenotyped for growth, disease resistance and juvenile wood composition traits (lignin, cellulose, and terpene content). In parallel, we are also genotyping and phenotyping advanced breeding populations of loblolly and slash pine that encompass a broader genetic diversity of each species. For these populations, genome-wide selection prediction models will be generated for growth traits, wood chemistry and terpene flow. These genetically diverse populations will serve as the foundation for the next generation of advanced pine feedstocks for the bioenergy, biofuels and renewable chemicals industries.

Southern pines, such as Pinus taeda (loblolly pine) and Pinus elliottii (slash pine), are a proven sustainable source of renewable biomass for bioenergy and renewable chemicals. The S.E. forest industry produces ~18% of the global supply of industrial roundwood, 25% of the global pulp supply and 40% of the global pine chemical supply. This industry also generates 77% of all industrial biomass energy in the U.S. by burning wood waste and lignin at high thermal efficiencies with combined gas cycle turbines. The 93 million hectares of standing pines in the S.E. include 15.6 million hectares of genetically improved plantations; all grow with low water, fertilizer and herbicide inputs on land that is largely not suitable for cultivation of food crops. This large extant southern pine resource, with its well established supply chain and predictable year round supply is a promising source of bioenergy. To sustainably meet this potential it will be necessary to develop pine trees that produce higher energy and renewable chemical yields per acre, per year. Because of the wide natural genetic variation in southern pine growth rates and wood properties, traditional breeding can achieve this potential. However, breeding of pines is a long and complex process, due to the fact that each breeding cycle takes several decades and large field trails. Thus, current traditional breeding practices are too costly and slow to rapidly develop pines to reach the productivity required.

We recently demonstrated the potential that genome-wide selection, based on molecular markers, has to more than double genetic gains in tree breeding. These gains are achieved using prediction models for (i) early genotypic selection of elite individuals, leading to a dramatic reduction in the length of the breeding cycle; and for (ii) selecting crosses that generate optimal allelic combinations in the progeny, reducing the complexity and costs of breeding programs.

The first objective of this project is to use genome-wide selection to rapidly develop highly productive loblolly pine families and cultivars, to support the short term needs of the bioenergy industry, including disease-resistant, fast growing germplasm with high cellulose, high lignin or high terpene content. We previously phenotyped and genotyped the loblolly pine reference breeding population CCLONES, which has been grown on sites spanning the main breeding zones. This population has been phenotyped for biomass growth, wood composition and disease resistance traits. In this project, the phenotypic and

genotypic data was used to develop advanced models that include additive and dominance effects, which improves prediction accuracies significantly compared to traditional methods. These improved methods have now been used for mate-pair allocation, to identify the crosses predicted to generate the highest yielding families. In the remaining ~ 3 years of this project, the best crosses will be made and progeny screened to identify elite individuals for bioenergy and biofuel production.

The first aim we will apply advanced GWS prediction models for mate-pair allocation and early identification of elite individuals to an existing population, creating a resource for immediate development of highly productive loblolly pine families and cultivars for bioenergy. However, CCLONES has limited genetic diversity, includes only one of the two pine species (loblolly and slash pine) widely planted in the S.E. U.S., and has a relatively small size. To address these limitations and create a resource for long-term improvement of southern pines for bioenergy, in our second objective we are genotyping and phenotyping large, genetically diverse breeding populations of loblolly and slash pine. Those populations comprise the most advanced third generation genetic material from the Cooperative Forest Genetics Research Program (CFGRP) at UF. For slash pine, these large populations have already been established in field sites. For loblolly pine, field trials will be planted in the winter 2014-2015. DNA has already been extracted from these populations, and genotyping and phenotyping will be completed over the next 24 months. As part of the in-kind support provided by members of the CFGRP, measurements of growth for both loblolly and slash pine will proceed beyond the duration of this project, until the trials reach 12 years of age.

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