138. Genomic Resources for the Study of Cell Wall Biosynthesis in Grasses

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Project Goals: To create genomic resources to identify genes predicted to control grass cell wall biosynthesis and modification in grasses

Due to its large mass, low input requirements and ability to adapt to a wide range of growing conditions, switchgrass is a candidate bioenergy crop. Cost efficient conversion of the lignocellulosic biomass in switchgrass and other grasses into biofuels will require basic knowledge of the genes that control grass cell wall biosynthesis and modification. Our lab is advancing these goals using two different approaches. First, we have identified switchgrass homologs of rice genes known to control biomass and stress-response related traits. We generated a switchgrass BAC library, screened 96,000 BAC clones, and in collaboration with the Joint Genome Institute (JGI), we have sequenced 311 BAC clones, corresponding to 51.7 Mb.

We identified 695 unique switchgrass genes predicted to control cell wall biosynthesis and stress responses. Using microarray and comparative phylogenomic analysis, we established the phylogenetic and functional relationships of the 87 glycosyltransferase 2 (GT2) family genes in rice and switchgrass.

We are also advancing rice genetic resource as an efficient method for identifying agronomically relevant grass genes. We created a collection of 4000 Kitaake rice mutants by fast-neutron mutagenesis. In collaboration with the JGI, we sequenced more than 1000 mutants and have analyzed 41 mutant lines in detail. From this analysis of 41 mutants we identified a total of 2,418 mutations affecting 1,433 unique genes. These mutations include 1,273 single base substitution (SBS), 864 deletions, 145 insertions, 82 inversions, 49 translocations, and 5 tandem duplications Figure 1). One of the mutants, rcs60, shows an altered saccharification profile. An online, user- friendly database, named KitBase (Figure 2) contains sequence and phenotypic data of each mutant has been created. These resources will facilitate studies of grass cell wall biosynthesis and modification.

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