

Utility of a *Sorghum bicolor* RNA atlas for improving energy sorghum stem composition

Brian McKinley, Bill Rooney, Jeremy Schmutz, Curt Wilkerson, John Ralph and John Mullet

Photoperiod sensitive energy sorghum hybrids accumulate ~20-40 Mg of dry biomass per hectare during ~200 day growing seasons. Approximately 80% of energy sorghum's harvestable biomass is located in plant stems that are 4-5 meters in length and ~20-40 mm in diameter. The composition of sorghum stems has been characterized by NIR, HPLC, and NMR at different stages of plant development, at various times during the growing season, and in well watered and water-limited environments. The analysis showed a wide range of stem biomass composition, variation in the ratio of cell wall to non-structural carbohydrates, and dynamic changes in composition during development. Sorghum stems accumulate sucrose, glucose, fructose, starch, and mixed linkage glucans that can be efficiently converted to a wide range of biofuels and bio-products at low cost. Stem structural carbohydrates, especially from *bmr*-genotypes with modified lignin chemistry, can also be converted to products following pretreatments. Further improvement in energy sorghum stem composition through pathway engineering requires in depth knowledge of target genes, pathways, and their regulation. To obtain this information, an RNA Atlas of gene expression profiles from sorghum tissues and developmental states was collected in part through a JGI Community Sequencing Project. Results from transcriptome analysis of sorghum stems enabled the identification of >200 genes involved in cell wall biosynthesis, and key genes/pathways that regulate the accumulation of sucrose in sorghum stems. The database is being used to identify promoters for engineering stem composition in a tissue specific manner at optimal times during sorghum development.