

Functional analysis of cell wall related genes in *Sorghum bicolor*

Tong Wei^{1,2*} (tongwei@lbl.gov), Guotian Li^{1,2}, Zhanguo Xin³, Rashmi Jain², Zhangyin Hao¹, Devon Birdseye¹, Dominique Loque¹, Henrik Scheller¹, **Pamela Ronald**^{1,2}

¹ Feedstocks Division, Joint BioEnergy Institute, Lawrence Berkeley National Laboratory, Berkeley, CA; ² Department of Plant Pathology and the Genome Center, University of California Davis, Davis, CA; ³ Plant Stress and Germplasm Development Unit, USDA-ARS, 3810 4th Street, Lubbock, TX

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Project Goals: We are performing a functional genomics study of the cell wall related genes to improve biofuel-related traits in *Sorghum bicolor*.

It is of great importance to study and modify bioenergy crops to reduce the dependence on fossil fuels and release of climate-changing greenhouse gasses. Sorghum is tolerant to drought and grows on marginal lands, which makes it a potential bioenergy crop. To identify the genes involved in cell wall biosynthesis, we searched the sorghum genome and found 570 glycosyltransferase (GT) genes and 377 glycoside hydrolase (GH) genes. More than 60% of these genes have at least one mutant in our sorghum TILLING mutant collection. Here, we exemplified the sorghum functional genomics study by characterizing a sorghum cellulose synthase-like F6 (CslF6) in mixed-linkage β -glucan biosynthesis. Among nine sorghum mutants carrying mutations in CslF6, two lines developed obvious morphological phenotypes, the reduced plant height resembling the rice knockout mutant of *cslf6*. The gene expression assay showed that CslF6 is ubiquitously expressed across different tissue types, with higher expression in stems and young leaves. Further assays demonstrate that the mutants contain less mixed linkage glucan content compared with the wild type BTx623 plants. Our study demonstrates that sorghum CslF6 participates in mixed-linkage β -glucan deposition. The cell wall-related genes we identified here lay the foundation for the future biofuel research in sorghum.

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