Lawrence Berkeley National Laboratory

Recent Work

Title
Exploiting Natural Variation in Arabidopsis thaliana to Understand Cell Wall Biosynthesis and Composition

Permalink
https://escholarship.org/uc/item/7xs5m2m6

Authors
Christiansen, Katy M.
Smith, A. Michelle
Loque, Dominique
et al.

Publication Date
2009-12-10
Exploiting Natural Variation in *Arabidopsis thaliana* to Understand Cell Wall Biosynthesis and Composition

Katy M. Christiansen*, A. Michelle Smith, Dominique Loque, and Joshua L. Heazlewood

Presenting author: *Katy M. Christiansen – KMChristiansen@lbl.gov

Joint BioEnergy Institute, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA.

Genetic variation in different accessions of *Arabidopsis thaliana* has occurred through thousands of years of geographic spread and adaptation. As a result of this diversity, disparate accessions have phenotypic differences that can be used to identify genes that contribute to the biosynthesis and composition of cell walls. Forward and reverse genetic screens to identify single mutants often prove difficult for detection of genetic differences that may lead to more subtle phenotypes. Exploiting the inherent genetic variation in *Arabidopsis* accessions through quantitative trait analysis will allow for the detection of variation in cell wall biosynthesis and composition. We selected two methods for screening parental accessions: measuring monosaccharide composition by HPAEC and structural changes by Near Infrared (NIR) spectroscopy. From these analyses, we selected Ri-0 as the most different accession from the reference accession Col-0. Recombinant inbred lines (RILs) derived from Col-0 and Ri-0 parents were used to determine quantitative trait loci (QTL) that contribute to the differences observed in monosaccharide and pectin content and NIR spectroscopy. Two putative candidate genes encoding enzymes involved in nucleotide sugar conversion have been identified. We are currently determining differences between the parental versions of the genes and how any differences contribute to the observed phenotypes. Additionally, we have re-sequenced two *Arabidopsis* accessions, Bay-0 and Shahdara, in collaboration with the Joint Genome Institute. This effort has resulted in a collection of SNPs between these accessions and the reference *Arabidopsis* accession, Col-0. Re-sequencing efforts are being expanded to other accessions, beginning with Ri-0. Information obtained from resequencing will aid in QTL analysis and be of service to the general *Arabidopsis* community.

This work was part of the DOE Joint BioEnergy Institute (http://www.jbei.org) supported by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research, through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U.S. Department of Energy.
DISCLAIMER

This document was prepared as an account of work sponsored by the United States Government. While this document is believed to contain correct information, neither the United States Government nor any agency thereof, nor the Regents of the University of California, nor any of their employees, makes any warranty, express or implied, or assumes any legal responsibility for the accuracy, completeness, or usefulness of any information, apparatus, product, or process disclosed, or represents that its use would not infringe privately owned rights. Reference herein to any specific commercial product, process, or service by its trade name, trademark, manufacturer, or otherwise, does not necessarily constitute or imply its endorsement, recommendation, or favoring by the United States Government or any agency thereof, or the Regents of the University of California. The views and opinions of authors expressed herein do not necessarily state or reflect those of the United States Government or any agency thereof or the Regents of the University of California.