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

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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-seqeuencing 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.

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