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The Utilization of Arabidopsis Genetic Variants to Understand Cell Wall Structure and Biosynthesis

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The process of plant cell wall biosynthesis involves a complex series of biochemical processes involving many hundreds of proteins. Determining the function of a specific gene through functional genomics techniques have proved problematic due to genetic redundancies and undetectable changes. Common techniques have used mutant collections in forward genetic screens or reverse genetics to directly target and disrupt genes of interest. Since such techniques are heavily reliant on some phenotypic discrimination to assess gene function, the absence of a measureable difference often results in little useful information. Furthermore the complete absence of many genes produced by such techniques results in a lethal phenotype as the gene is absolutely required for normal function of the plant. A more subtle approach utilizes genetic differences in naturally occurring variants to provide important information about gene function and genetic diversity. In collaboration with the Joint Genome Institute we have sequenced two Arabidopsis accessions (Bay-0 and Sha-0) that have previously been shown to have measureable differences in Ara-Rha ratios in cell wall extracts. This genetic information and the utilization of recombinant inbred lines (RIL's) will be used to map QTL's identified in these and other Arabidopsis accessions to identify loci that contribute to functional differences in plant cell walls.

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