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## Recent Work

### Title

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## Analysis of Putative Feruloyltransferase Transcript Levels and Cell Wall Composition During Rice Development

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Identification of genes encoding cell wall modifying enzymes has applications in human and animal nutrition, plant defense against pathogens, and biofuel production efficiency. For plants with type II cell walls, such as rice and other grasses, glucuranoarabinoxylans (GAX) are a major component of the hemicellulose found in both primary and secondary walls. Ferulic acid, a phenolic compound, is added to the O-5 of arabinosyl units of GAX. Ferulic acid residues can covalently crosslink arabinosyl residues through dimer formation, or serve as attachment points between GAX chains and lignin, providing rigidity to the cell wall matrix. Therefore, reducing the ferulic acid content of Type II cell walls may improve feedstock deconstruction for production of lignocellulosic biofuels. The genes that encode feruloyltransferases (FTs) have not yet been identified. However, Mitchell and colleagues (Plant Physiology 2007) have recently predicted that FTs may be encoded by a clade of genes from the CoA acyl transferase superfamily based on their greater EST abundance in grasses compared with dicots. Ratios of cell wall components, including GAX and ferulic acid, are dynamic, adjusting to allow for elongation while plants are young, and rigidity, as they mature. To correlate cell wall composition and gene expression during rice development, we have collected RNA and cell wall samples from various rice tissues throughout development. We are conducting quantitative RT-PCR to amplify transcripts from the putative FT genes identified by Mitchell et al. Cell wall sugar and phenolic composition will be examined by HPLC analysis. This study will determine how rice cell wall composition shifts to accommodate the changing needs of the plant, providing valuable data for further rice genomics analyses and evidence to test the hypothesis of Mitchell et al. regarding the putative FTs. Genes from the 20member gene family that show correlation with ferulic acid accumulation will be targeted for functional studies toward improving the deconstruct-ability of grass cell walls for biofuels.