

Discovery of plant glucuronoxylan synthesis gene lays groundwork for improved biofuel processing

Background:

Cellulose, lignin and glucuronoxylan are the principle components of plant secondary wall structure. The synthesis of xylans is poorly understood, thus efforts to improve our understanding will lead to improved strategies to modify secondary cell wall structure.

Approach:

BESC researchers at UGA, Georgia Tech and UCR worked to provide genetic and biochemical evidence that a previously uncharacterized gene plays a major role in cell wall development of *Arabidopsis* plants.

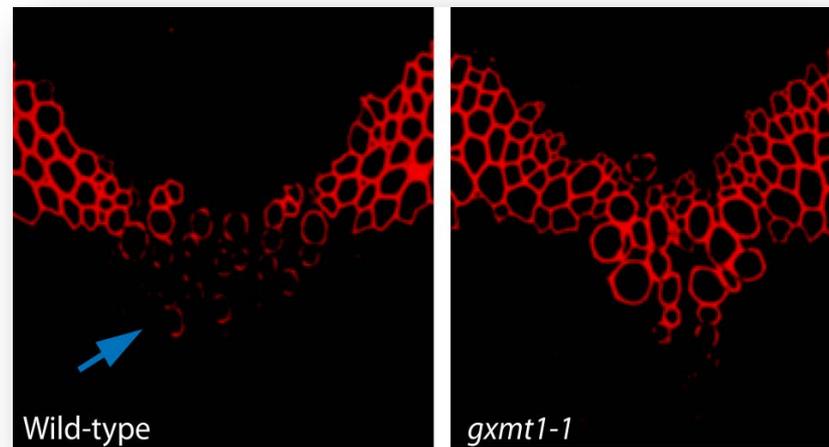
Outcomes:

- The team characterized a methyltransferase (GXMT1) that catalyzes methylation of glucuronic acid residues in glucuronoxylan.
- The gene GXMT1 was previously classified as a domain of unknown function (DUF) 579 protein.
- GXMT1 is responsible for methylation of as much as 75% of the glucuronic acid residues in glucuronoxylan.
- Mutations of GXMT1 result in altered Lignin structure leading from the reduced methylation.

Significance:

The ability to selectively manipulate polysaccharide methylation may provide new opportunities to modulate biopolymer interactions in the plant cell wall of bioenergy crops such as switchgrass.

This work extends the portfolio of BESC structural targets that can be modified either alone or in combination to increase the economic value of lignocellulosic biomass.



- Differences in glucuronoxylan methylation at the single cell level were probed in transverse sections of wild-type and *gxmt1-1* mutant stems using immunofluorescence microscopy.
- The glucuronoxylan in the secondary walls of wild-type vascular xylem (arrow) is highly methylated as it is only weakly labeled.
- In contrast, all secondary walls of *gxmt1-1* stems are strongly labeled by CBM35 indicating that in these tissues the amount of xylan methylation is dramatically reduced.