

Metabolic adaptation of *C. thermocellum* to growth inhibitors released during deconstruction of switchgrass

Background

- It is important to understand the metabolism of *C. thermocellum* metabolism when growing on complex lignocellulosic substrates to better identify any potential industrial bottlenecks that could undermine efficient biofuel production.

Approach

- An integrated omics approach was conducted to examine the temporal molecular changes of *C. thermocellum* grown on switchgrass to assess the metabolic and protein changes that occur during the conversion of plant biomass to ethanol.

Outcomes

- The most striking feature of the metabolome was the observed accumulation of long-chain branched fatty acids over time, implying an adaptive restructuring of *C. thermocellum*'s cellular membrane in response to the gradual accumulation of lignocellulose-derived inhibitory compounds.
- Proteomic analysis revealed time-dependent increases in enzymes involved in the interconversion of branched amino acids valine, leucine, and isoleucine to iso- and anteiso-fatty acid precursors.
- Additionally, *C. thermocellum* appears to shift glycolytic intermediates to alternate pathways to modulate overall carbon flux in response to C5 sugar metabolites that increase during lignocellulose deconstruction.

Significance

- Integrated omics data of microbial growth on complex lignocellulosic biomass over time provided a detailed view of the molecular machinery (metabolites and enzymes) that reveals temporal adaptation to a complex, lignocellulose substrate – information that is critical for engineering *C. thermocellum*'s industrial efficacy.

