**Active site and laminarin hydrolysate in glycosidase hydrolase family 55 (GH55)**

Microbial communities that have symbiotic relationships with biomass insects are now recognized to be a relevant source of microbes with diverse metabolic and biosynthetic capabilities that could be used in improving the enzymatic deconstruction of biomass materials for biofuel production. Recently, a highly cellulolytic and hemicellulolytic Actinomycete, *Streptomyces* sp. SirexAA-E (SirexAA-E), was isolated, and genomic, transcriptomic and biochemical studies have shown that this microbe secretes an array of glycoside hydrolases (GHs) and oxidative enzymes. The gene SACTE\_4363, encoding a GH family 55 protein described hereafter as SacteLam55A, was of interest because it was upregulated and secreted into the medium when SirexAA‑E was grown on cellobiose, xylan, and various pretreated switchgrass samples, but was not detected in the secreted proteome when SirexAA-E was grown on glucose. Researchers in the DOE’s Great Lakes Bioenergy Research Center used a combination of gene synthesis, cell-free protein translation, catalytic assays and X-ray crystallography to provide a correlated biochemical and structural characterization of the GH55 family. This was done in collaboration with JGI and data collected at the DOE Argonne National Laboratory. High resolution crystal structures with substrates bound and ensemble refinement suggest a simple new mechanism for promoting processive reactivity. By doing this, researchers were able to find a new way to annotate bioenergy phylogenetic space. The relevance of this work is that the natural enzymes screened displayed a broad range of catalytic rates and pH and temperature optima.

**References:** Bianchetti CM, Takasuka TE, Deutsch S, Udell HS, Yik EJ, Bergeman LF, Fox BG. “Active Site and Laminarin Binding in Glycoside Hydrolase Family 55”. Journal of Biological Chemistry (2015). 290 (19):11819.

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