Systems-level Discovery and Characterization of Cellulolytic Enzymes from the Wood Wasp Symbiont *Streptomyces*.

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Project Goals: Lignocellulosic biomass degradation is critical to carbon cycling in terrestrial ecosystems, and is of increasing scientific interest. Cellulolytic microbes deconstruct the recalcitrant polymers present in plant biomass into simple sugars. Our goal is to examine and learn cellulolytic capability from one of the highly cellulolytic bacterium isolated from the cellulosic environment, *Streptomyces*, by the systems-level approaches.

Lignocellulose represents the largest reservoir of organic polymers in terrestrial ecosystems. Animals typically gain access to the energy stored in plant biomass through anoxic hydrolysis reactions provided by symbiotic gut microbes. Here we reveal an alternative mechanism, the aerobic deconstruction of hemicellulose and cellulose by *Streptomyces* sp. SirexAA-E (ActE), a bacterium associated with the feeding tunnels of the pinewood-boring wasp *Sirex noctilio*. Genome-wide expression profiling, proteomics, and biochemical assays show that this highly cellulolytic microbe produces an expanded repertoire of hydrolytic and oxidative enzymes with high specific activity for deconstruction of cellulose, mannan, xylan, and biomass. The rapid deconstruction of plant polysaccharides provided by aerobic bacteria that associate with herbivorous insects and propagate externally likely represents a substantial, and previously underappreciated contribution to biomass utilization in natural environments. This work provides the first extensive systems biology characterization of the capabilities of the genus *Streptomyces* in the utilization of a wide variety of polysaccharides relevant to biofuels production.

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