

215. *Streptomyces* isolated from herbivorous insects reveal phylogenetically-linked mechanisms for the degradation of lignocellulose

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Project Goals: Identify plant biomass-degrading enzymes from highly cellulolytic *Streptomyces*.

Free-living Actinobacteria in the genus *Streptomyces* are well known for degrading plant biomass in the soil. More recently, *Streptomyces* have been found associated with insect herbivores. Despite *Streptomyces*' predicted contributions to carbon cycling in nature the extent of their biomass degrading ability and the enzymatic mechanism of this activity remain largely unknown. Here, we comparatively analyze strains across the *Streptomyces* genus including free-living soil isolates and strains from insect herbivores. While few soil-isolated *Streptomyces* grow on pure cellulose, two clades of insect-associated *Streptomyces* are enriched in cellulolytic activity. Biochemical analysis of secreted enzymes demonstrates significant differences in substrate specificity between cellulolytic strains. Furthermore, phylogenetic and genomic analyses identify key differences between in carbohydrate active enzyme composition between cellulolytic and non-cellulolytic strains. Genome-wide transcriptomic analyses reveal a highly conserved core set of enzymes used to deconstruct plant biomass as well as strain specific gene expression. Finally, we show that targeted-gene deletion of a global cellulose regulator results in constitutive expression of cellulolytic genes. Together, these data identify phylogenetically related clusters of *Streptomyces* with high biomass degrading activity and increase our understanding of how bacteria deconstruct lignocellulosic biomass in insect herbivore systems.

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