

## 216. Highly Cellulolytic Microbial Communities Enriched from Leaf-Cutter Ant Refuse Dumps

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<http://currielab.wisc.edu/antcam>

**Project Goals: This project aims to understand how cellulose is degraded by a community of microbes to inform on soil carbon cycling and on mechanisms of biomass degradation for biofuel production.**

Microbial degradation of cellulose is a key driver of the global carbon cycle, but little is known about the role of communities in this process. Here, we study the leaf-cutter ant refuse dump as a model system to explore biomass degradation by a community of microbes using culture-dependent and -independent techniques. Leaf-cutter ants are the dominant herbivore in New World tropical ecosystems. However, harvested leaves are not used by the ants as a primary food source, but rather as nutrients for a fungal cultivar that partially degrades the leaf material and provides energy to the colony. Non-digested leaf material, which is enriched in recalcitrant plant polymers such as cellulose and lignin, is moved to refuse dumps. Previous culture-independent work showed these nutrient-rich refuse dumps contain a diverse microbial community enriched in biomass-degrading enzymes. Here, we show that microbial communities in refuse dumps are highly capable at deconstructing cellulose; in ten days, the most highly cellulolytic communities degrade the same amount of cellulose as *Trichoderma reesei* RUT-C30, a fungus used in the biofuels industry. Our analysis of 16S pyrotag sequencing reveals that cellulose-enriched communities are dominated by Bacteroidetes and Proteobacteria. Additionally, specific operational taxonomic units (OTUs), including *Diaphrobacter* and *Chryseobacterium*, are significantly more abundant in highly cellulolytic communities than in non-cellulolytic communities, while Microbacteriaceae are significantly less abundant. However, there were few OTUs present that are known to degrade cellulose, even in highly cellulolytic samples, suggesting that cellulose degradation may be performed by previously unappreciated cellulolytic organisms or microbial consortia. We expanded on this work with long-term enrichments of highly cellulolytic communities. Characterization of these communities using metagenomic and metatranscriptomic analyses and culture-based experiments is currently underway. The results of this research are important for understanding community-based cellulose degradation in a biomass-enriched environment and for providing insights to improve cellulosic biofuel production.

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