

## **Deciphering Controls on Plant Decomposition in Arctic Ecosystems: Identifying Unknown Microbial Condensed Tannin Degradation Pathways**

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**Abstract:** Climate change in the Arctic is progressing rapidly, and much of the focus, thus far, has been on permafrost thaw and the rapid mineralization of soil organic carbon (C) by soil microorganisms. However, climate change is also increasing the abundance of woody deciduous shrubs in the Arctic, altering the vegetative biochemical landscape, which could profoundly impact the entire regional foodweb inclusive of terrestrial and digestive microbial communities. The quantity and quality of the carbon in these plants is a response to climatic factors, resulting in higher amounts of condensed tannins (CT) and other phenolic molecules. Condensed tannins have been reported to inhibit microbial carbon degradation by impacting microbes directly, inactivating microbial carbon degrading enzymes, or binding to nitrogen (N) and limiting available nutrients. Thus, the increase in vegetative CT in Arctic ecosystems has implications for C transformations at all trophic levels: from herbivores dependent on these plants for survival to the soil microbes responsible for degrading leaf litter. Here, we examine the response of microbial communities from arctic ruminants and soil to increased CT isolated from native Alaskan plants.

The goals of the proposal are three-fold: 1) expand CT NMR and mass spectral databases at EMSL so these compounds can be profiled across ecosystems 2) identify unknown enzymes and chemical intermediates involved in CT biodegradation 3) determine the impact of CT on soil and rumen microbial communities. Currently there is very little known about the capacity for microbial CT degradation. First we will chemically degrade a model CT and an environmentally relevant CT isolated from Alaskan willows to build a library of potential biodegradation products and structurally identify parent compounds. We will then use the combined capabilities of JGI and EMSL, along with resources in our own laboratories, to identify microbial enzymes and metabolites involved in CT degradation using a pure culture model organism. We propose to grow this organism with a chemically characterized CT and use metagenomic and metaproteomic analyses to determine genome-encoded, metabolic pathways active during CT degradation. We will assess the products of microbial metabolism using the CT-related compounds database created in (1). The results of this experiment will be the first to link the enzymes, metabolites and degradation products to recreate a model CT degradation pathway. We will then expand to test relevant arctic microbial communities for the capacity to respire or ferment CT. Here we will incubate rumen and soil microbial communities with Alaskan willow CT under different conditions and assess the impact of CT on microbial community structure and function. The results of this experiment will identify the capacity for CT to inhibit microbial carbon degradation, uncover potential CT resistant organisms and mechanisms of resistance, and provide insight into how increasing CT may impact carbon cycling in arctic ecosystems. This proposal combines expertise in meta-omics, microbial metabolism, CT biochemistry, soil microbiology, and Arctic ecology to address current knowledge gaps critical to examining plant and microbial interactions under changing climate scenarios.