



Conference Abstract

Improving our Understanding of Environmental Stress Impacts and Responses of the Microbiome

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Abstract

Over the course of this century, it will be important to identify cost effective/low maintenance solutions for treating contaminants in receiving watersheds. Adopting these strategies will involve a better understanding of what defines a “natural” environment compared to these contaminated sites. Traditional geochemical testing and standard microbial community analyses (e.g., DNA profiling) or using isolates can be limited with respect to their ability to infer real-time, active processes of bacterial communities. In recent years the application of genomics to identify the microbial microbiome in anthropogenic stressed conditions has advanced considerably. In many cases, the activity of microorganisms will directly impact the chemical conditions in both surface and subsurface water column and contaminated sediment environments controlling the fate of nutrients and contaminants alike. Questions arise such as:

1. What are the baselines or reference systems that can be used?
2. What indices can be used to study the long-term and short-term controls on the mobility, cycling, and bioavailability of toxic metals and organic contaminants?

In many cases the balance of chemical oxidizing and reducing components in water will control the development of chemical and nutrient gradients observed in either natural and/or applied systems (e.g., constructed wetlands or bioreactors). In these cases, biogeochemical systems will determine the direction and onset of specific metabolic pathways as defined by their favorable thermodynamic outcome, an issue for

most bioremediators (i.e., microorganisms). Also, the degree of chemical alteration (toxicity or degradation products) can be directly linked to the proportion of their biological activity.

In this presentation, contrasting case studies highlighting natural (baseline) and anthropogenically impacted landscapes will be discussed. The focus will be on identifying and linking physicochemical processes to microbial community function using emerging omics for geochemical applications and ascertaining novel contaminant bioindicators.

Keywords

Omics, transcriptomics, microbial function , Gradients of environmental stress, geomicrobiology, nitrogen metabolism, degradation genes

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Conflicts of interest

The authors have declared that no competing interests exist.