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Baseline microbial characterizations of an imperiled aquatic diversity hotspot: Ash Meadows National Wildlife Refuge

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Abstract  
Located in the discharge zone of the Death Valley Flow System, Ash Meadows National Wildlife Refuge is a spring-fed desert oasis and biodiversity hotspot about 90 miles northwest of Las Vegas. These critical wetlands are potentially threatened by groundwater pumping, exotic species invasions, and climate change. Although a major component of the lower food web, very little is known about the microbial makeup of this ecosystem. As a first step towards understanding the microbial and biogeochemical aspects of this system, a detailed molecular-based characterization of microbial communities, baseline chemistry, and physical characteristics of various springs of Ash Meadows will be conducted over the summer of 2009. Specifically, springs will be compared using DNA extraction followed by PCR amplification of the 16s rRNA gene, DNA fingerprinting, cultivation, and flow cytometric cell counting.
Baseline Microbial Characterizations of an Imperiled Aquatic Diversity Hotspot: Ash Meadows National Wildlife Refuge

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Abstract

Located in the discharge zone of the Death Valley Regional Flow System (D-V), Ash Meadows National Wildlife Refuge (AMNWR) is a spring-fed desert oasis about 100 miles northwest of Las Vegas. These critical wetlands are in constant threat from human water pumping and natural climate change. Although a major component of the broader flood way, very little is known about the microbial evolution of this system. Here we propose to develop a detailed microbial-level characterization of microbial communities at the various springs of Ash Meadows to obtain a basis for understanding future climate change impacts and climate change water allocation.

Freshwater and aquatic ecosystems are facing increasing anthropogenic pressures worldwide, especially in arid regions where we are losing unique aquatic habitats without even knowing the nature and extent of their biodiversity (3). Ash Meadows provides a unique example of desert wetlands that are now extremely uncommon in the southwestern United States (10). Ash Meadows National Wildlife Refuge contains over 100 plant and animal species that are classified as state-protected, sensitive, or priority species (11). It also supports 35 eukaryotic species, twelve of which are currently listed as threatened or endangered. In addition to natural threats, DeSouza et al. (3) reported that 18.7% percent of the biological yield of this system is already allocated to and/or taken by other entities (e.g., DRI) and hope to obtain additional water rights. This paper highlights several research models, all predicting that the system's trajectories will have an adverse affect on all the ecosystems supported by the groundwater. Despite the importance of this site to wildlife, only minimal microbial biodiversity and biogeochemical characterization has been performed to date (8). Thus, to better understand the organisms and processes of the oasis of the Ash Meadows Wetland, we propose to develop a detailed microbial-level characterization of aquatic microbial communities.

Objectives

- Determine if microbial communities and aquatic chemistry emanating from spring thaws is similar and resemble that nearly every day.
- Verify the hypothesis that photosynthetic microorganisms (e.g., cyanobacteria) will be found in the water due to specific community selection driven by irradiation.
- Begin to develop a baseline dataset for Ash Meadows at aquatic chemistry, and physical measurements.
- Attempt to identify the factors that control microbial growth in Ash Meadows springs.

Methods

Samples were taken June 6, 2009 as well as July 2, 2009. New DNA samples were collected using a Skalar microportable peristaltic pump and 2.2µm membranes filters (polycarbonate, Pall). These samples were then stored at -80°C. Samples from spring thaws were obtained by inserting a tube into a peristaltic pump with a 4µm hydro-pore size filter. Aquatic diversity measurements (nutrients, major, and other dissolved gases) were performed at the DRI water laboratory in Reno, NV. Physical measurements: temperature, DO, conductivity, turbidity were made using YSI multimeters available in the Mesquite. Cells were determined for all samples using an Advanced Analytical LabPro 3000 flow cytometer. DNA was extracted from the filters and used to determine bacterial diversity (Prokaryote bDNA extraction kit, MoBio) and 16S rRNA genes obtained by PCR amplification and cloning (Taq polymerase). The diversity of the bacterial communities in the Ash Meadows springs was characterized either with the probes Crystal Spring and Big Sprin (Figures 5, 6) using the basis of the DRI, Southern Nevada, and Big Springs. More diverse source water

Results

- Phylogenetic analysis of the clone libraries suggests that community structure changes from a spring's source to its downstream waters (Figure 3).

Future Work

- Conduct further phycological analysis of clone libraries.
- Generate downstream samples from other springs at Ash Meadows.
- Combined analysis of T-RFLP data to further elucidate community structure.
- Collaborate with DRI colleagues on developing community-wide approaches.
- Perform colony Phyc and phylogenetic analysis on spring derived isolates.
- Cultures have been isolated from samples.

References


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