Microbial Life in the Atacama Desert: Using a Multidiciplinary Approach to Examine the Habitability Potential and Microbial Diversity in a Mars Analog Environment. T. B. Shirey[1] and J. B. Olson[1] The University of Alabama, Department of Biological Sciences, Tuscaloosa, AL 35487.

Introduction: When setting out to explore the potential for life on Mars, it is the biosphere of Earth that is used as a rubric for discovery. Research into habitable conditions for life in the solar system includes studies of analogous environments on Earth with comparable conditions suitable for harboring life. Fortunately, there are select environments on Earth that mimic many of the conditions found on Mars, and although no environment on Earth is perfectly comparable to Mars, we can utilize unique natural analog environments on Earth as alternatives to direct exploration.

One such Mars analog environment is the Atacama Desert, Chile, the environment in which this study was conducted. The Atacama is a narrow stretch of desert in northern Chile spanning over 1000 km, from 18ºS to 27ºS. Over time, the Atacama has been transformed by associated geologic formations and atmospheric conditions into one of the most unique and inhospitable landscapes on the planet. As a result, this desert has served as a Martian analog for several NASA studies [1, 2].

Apart from the apparent geological similarities between the Atacama Desert and Mars, a common attribute shared by both is lack of water availability. The Atacama is an arid to hyper-arid desert and considered the driest region on Earth [3]. The lack of available water in the Atacama creates an intensely inhospitable climate for life to persist. It has been postulated that perhaps in areas of extreme hyperaridity in the Atacama, the dry limit of microbial habitability has been reached [4]. Although the Atacama suffers from an extreme lack of water availability throughout its landscape, a precipitation gradient exists along a latitudinal transect. This gradient produces degrees of "dryness" within the desert that can serve as a backdrop to examine its effects on the microbial communities that exist there.

The primary focus of this study was to examine the distribution and diversity of microbial communities in the Atacama Desert along a latitudinal transect subjected to a measured precipitation gradient. One particular emphasis of this study is to utilize a multifaceted approach, applying both direct and indirect methods of microbiological community characterization, to examine the microbial communities within the desert. Benefits of using a multi-pronged approach become clear when one considers the limitations encountered from any individual method of examination. Moreover, this particular approach uses both traditional microbiological cultivation techniques and contemporary molecular methodologies, which, when combined and examined in context, should generate a clearer picture of the overall microbial community in the Atacama.

Sampling: Soil samples were aseptically collected from six different sites (AT-01, -02, -03, -04, -05, -08) in the Atacama Desert along a 600 km latitudinal transect. Between the six sampling sites, 71 samples of Atacama soils were collected. Soils were collected from 27ºS near the city of La Serena, continuing north to 18ºS. Within this transect is the hyperarid Yungay region, which is known as the driest region of the Atacama. The southernmost sites (AT-01 and AT-02) are characterized as "wetter" environments, while the northern sites (AT-04, 05, and 08) are within the range of extreme hyperaridity. Site AT-03 represents a transitional site between hyperarid and extreme hyperarid.

Methods: Two types of methodologies (direct and indirect) were utilized for this study. Direct methods of microbial characterization included using phospholipid fatty acid (PLFA) analysis for both quantifying microbial biomass and examining community structure, and direct cell counts using DAPI epiflourescence microscopy.

Indirect methods of analysis examined both DNA extracted directly from Atacama soils, and from enrichment cultures cultivated in media with varying nutrient concentrations. A variety of media (both solid and liquid) were specifically developed for this study with compositions ranging from nutrient rich to highly oligotrophic. DNA extracted from both the soil and the enrichment cultures was quantified and used for PCR analysis. Amplified products of the 16S rRNA gene tagged with a fluorescence label were subsequently used for terminal restriction fragment length polymorphism (T-RFLP) analysis to examine the bacterial community composition along the sampling transect.

Results: Although experiments are continuing, data collected thus far indicate an association exists between bacterial habitability and latitude within the interior of the Atacama Desert. This latitudinal correspondence is likely due to the precipitation gradient that exists along the south-north transect.

Extracted DNA per gram of soil was highest at the southernmost latitude (14.1 ng/µl) and lowest in the northern latitudes (2.9 ng/µl). Likewise, based on gel electrophoresis banding intensities, the southern-

most sites yielded the most amplifiable DNA, with amplification decreasing with decreasing latitude. Moreover, with the exception of site AT-01, the liquid cultures produced extractable DNA that was comparable to that taken directly from the soil.

Extracted DNA concentrations corresponded to colony forming unit (CFU) counts of bacteria cultured from the Atacama soils. A range of CFU/g soil was seen along the sampling transect (3.0×10^4 to 0 CFU/g). Like DNA concentrations, total CFU/g was highest in the south and decreased with decreasing latitude. Again, this is attributed to the precipitation gradient along the sampling transect.

Bacterial cultivations on various types of solid media showed a degree of morphological variation that was not entirely unexpected. The solid media used for this study was developed with a range of nutrient and mineral concentrations, that should each select for bacteria with differing growth requirements.

Conclusions: The Atacama Desert is an ideal environment to examine the microbial limits of habitability. This type of study can be beneficial to future search for life missions, as it examines both habitability potential and method efficacy within a natural planetary analog. Although conditions in the Atacama Desert are extreme and inhospitable to life, bacteria, although perhaps existing in a state of dormancy, do exist along many sampled regions of the desert. Within the context of all data collected thus far, CFU counts, PCR amplifiable products and DNA concentrations appear to correlate.

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