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Title: "A Study of the Microbial Diversity in the North Arm of Great Salt Lake"

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ABSTRACT

A STUDY OF THE MICROBIAL DIVERSITY IN THE NORTH ARM OF GREAT SALT LAKE

Numerous investigations on hypersaline environments have suggested that the microbial community in such environments is highly diverse and dynamic. Great Salt Lake, Utah, is a unique and complex hypersaline environment with many microenvironments such as petroleum seeps and thermal springs. Very little is known about the microbial community of Great Salt Lake (GSL) and its interactions. Culture dependent and independent techniques were employed to study the microbial diversity of Great Salt Lake. Whole community DNA was extracted from GSL water and the 16S rRNA gene was amplified by polymerase chain reaction using bacterial universal primers and archaeal primers. The temporal microbial diversity was determined over the period of four years. In addition, aerobic bacteria of the lake were isolated and characterized. One isolate NA6-27 was selected because it could grow over wide range of temperature and salinity and it was identified as a species of *Haloarcula*.

The microbial community of this lake faces fluctuations in salinity and temperature. The need to cope with the fluctuating temperatures as well as salinities represents a challenge for the microbial community. The microorganisms must adapt to such environmental stresses. This is accomplished by the up or down regulation of important genes. RNA arbitrarily primed polymerase chain reaction (RAP-PCR), which is an inexpensive but sensitive method for studying the differential gene expression, was applied to study the response of a GSL isolate *Haloarcula species* strain NA6-27 to these environmental stresses. Total RNA was extracted from NA6-27, which was grown over different temperatures and salinities. RAP-PCR was performed to identify the differentially expressed genes at different temperatures and salinities. A total of eleven genes were found to be regulated which were related to signal transduction, energy production, transport and translation of stress proteins. Subsequently they were validated using real time PCR.