Diversity, evolution, and horizontal gene transfer (HGT) in soda lakes

Holly C. Pinkart[a] and Michael C. Storrie-Lombardi[b]

[a]Central Washington University
400 E. University Way, Ellensburg, WA 98926 USA

[b]Kinohi Institute
530 S. Lake Avenue, #117, Pasadena, California 91101 USA

ABSTRACT

Soap Lake is a hypersaline, alkaline lake in Central Washington State (USA). For the past five years the lake has been the site of an NSF Microbial Observatory project devoted to identifying critical geochemical and microbial characteristics of the monimolimnion sediment and water column, and has demonstrated rich multispecies communities occupy all areas of the lake. Soap Lake and similar soda lakes are subject to repeated transient periods of extreme evaporation characterized by significant repetitive alterations in salinity, pH, and total water volume, yet maintain high genetic and metabolic diversity. It has been argued that this repetitive cycle for salinity, alkalinity, and sulfur concentration has been a major driver for prokaryote evolution and diversity. The rapidity of wet-dry cycling places special demands on genome evolution, requirements that are beyond the relatively conservative eukaryotic evolutionary strategy of serial alteration of existing gene sequences in a relatively stable genome. Although HGT is most likely responsible for adding a significant amount of noise to the genetic record, analysis of HGT activity can also provide us with a much-needed probe for exploration of prokaryotic genome evolution and the origin of diversity. Packaging of genetic information within the protective protein capsid of a bacteriophage would seem preferable to exposing naked DNA to the highly alkaline conditions in the lake. In this study, we present preliminary data demonstrating the presence of a diverse group of phage integrases in Soap Lake. Integrase is the viral enzyme responsible for the insertion of phage DNA into the bacterial host's chromosome. The presence of the integrase sequence in bacterial chromosomes is evidence of lysogeny, and the diversity of integrase sequences reported here suggests a wide variety of temperate phage exist in this system, and are especially active in transition zones.

Keywords: Soda lake, Soap Lake, prokaryotic diversity, genome evolution, horizontal gene transfer, bacteriophage

Reference: Pinkart, H. C. and Storrie-Lombardi, M. C (2007) Diversity, evolution, and horizontal gene ransfer (HGT) in soda lakes. Astrobiology and Planetary Missions X. eds/ R. B. Hoover, G. V. Levin and A. Y. Rozanov. 6694 (34), 1-11.