

Co-evolution of cyanophage and cyanobacteria in Antarctic lakes: Adaptive responses to high UV flux and global warming

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ABSTRACT

Rapid adaptation to acute environmental change demands co-evolution of indigenous viral populations and their hosts. Horizontal gene transfer (HGT) is a highly efficient adaptive mechanism, but a difficult phenomena to detect. The mosaic nature of bacteriophage genomes resulting from HGT has generally been explored using phylogenetic analysis of coding regions [1, 2]. Focusing on the proteome certainly provides one window into the origin and evolution of genome information storage. However, the original fitness function for a nucleotide polymer would arise from a more primal survival imperative predating the appearance of a coding function. Multivariate analysis of a genome information storage metric (lossless compression [4, 5]), nucleotide distributions, and distributions of the three major physiochemical characteristics of the polymer (triple:double bonding [G+C], purine:pyrimidine [G+A], and keto:amine [G+T] fractions) produces a metric to detect and characterize mosaicism in both coding and non-coding regions of a genome. We discuss possibilities and limitations of using these techniques to investigate HGT and the origins and evolution of genome complexity. Analysis of available virus (n=2374) and bacteriophage genomes (n=417) indicates these probes can perform whole-genome taxonomy tasks or sliding window searches for evidence of HGT in a single genome. HGT responses may serve as a canary or bell-weather for global environmental change. We discuss one area of application of considerable interest to our institute: the response of cyanophage and their cyanobacteria hosts to variations in ultraviolet solar flux in geographically isolated Antarctic lakes.

Keywords: Origin and evolution of life, viruses, bacteriophage, horizontal gene transfer, Antarctica, global warming, genome information storage

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