Network analysis reveals statistical associations between cyanophage host genes and cyanobacterial ecotypes across ocean basins

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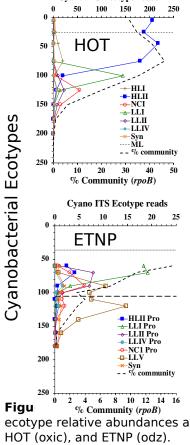
Introduction

• Cyanophage harbor genes for host functions (Breitbart 2012).
  - Eg. Photosystem B (psb), D/RNA binding (pur)
• Different ecotypes of prochlorococcus are adapted to different conditions (Johnson et al. 2006).
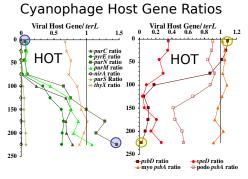Do cyanophage express different genes when infecting with different ecotypes?

Methods

• Cyanophage host genes and cyanobacterial ecotype abundances were obtained from publicly available metagenome libraries (Figure 1).
• Viral host genes were identified by placing sequences on phylogenetic trees.
• Associations were identified between each viral gene and all cyanobacterial ecotypes + environmental and location parameters
  - With many individual Lasso regressions
  - Each lasso has the same manually selected penalty coefficient (lambda = 0.2).

Results

Figu ecotype relative abundances at HOT (oxic), and ETNP (odz). Grey dotted line base of mixed layer. Black dashed line top of anoxic zone (< 0.8 µM [O_2]).
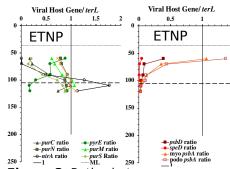

Figure 3. Ratios between cyanophage genes coding for different host functions and the cyanophage terL core gene. Higher values indicate greater expression of these genes by cyanobacterial viral
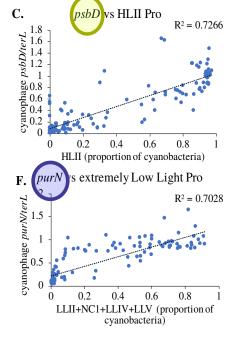
Example Correlations

Figure 4. Example correlations between host gene ratios and cyanobacterial ecotype abundance. Data are from all stations in Figure 1, not just those shown in Figure 2.

Discussion

• We have a system for identifying putative assocations between host gene abundance and cyanobacterial ecotypes.
• It appears that there are different cyanophage ecotypes that associate with different cyanobacterial ecotypes.
• These ecotypes appear to use different genes to adapt to the different cyanobacterial

Acknowledgements

References

• Biller SJ et al. Marine microbial metagenomes sampled across space and time. Sci Data. 2018.
• Breitbart M. Marine Viruses: Truth or Dare. An. Rev. of Mar. Sci. 2012
• Fuchsman CA et al. Niche Partitioning of the N Cycling Microbial Community of an Offshore Oxygen Deficient Zone. F. in Micro. 2017.
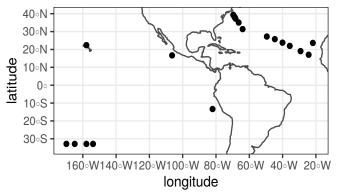• Johnson et al. Niche Partitioning Among

Figure 1. Geographic locations from which samples are collected. Samples were from geotraces cruises GA03 (North Atlantic, East Coast North Atlantic, West Coast North Atlantic) and GP13 (South Pacific) (Biller et al. 2018); from the Hawaii Ocean Time-series (year 2015; Luo et al 2020). ETNP is Fuchsman et al 2017. ETSP is Fuchsman et al (in revision).
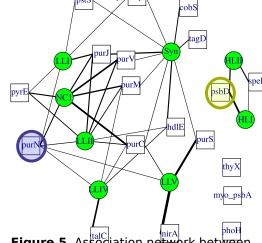

Figure 5. Association network between cyanobacterial ecotypes and host gene ratios. Edge widths are associated with lasso coefficient scores and indicate stronger associations.