

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

Jacob A. Cram, David García-Prieto, Matthew Hayes, Clara Fuchsman



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

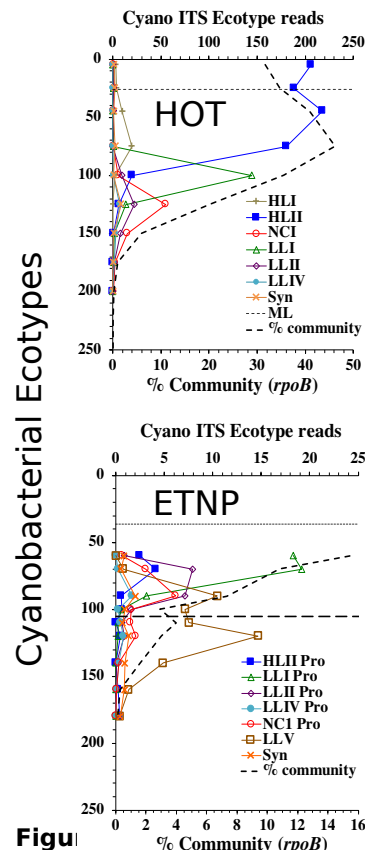


Figure 1. Cyanobacterial ecotype relative abundances at HOT (oxic), and ETNP (od2). Grey dotted line base of mixed layer. Black dashed line top of anoxic zone ($< 0.8 \mu\text{M} [\text{O}_2]$).

Cyanophage Host Gene Ratios

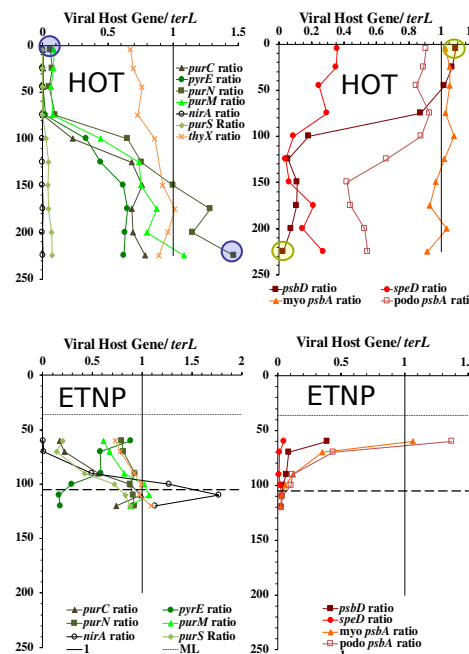


Figure 3. Ratios between cyanophage genes coding for different host functions and the cyanophage *terL* core gene. Higher values indicate greater expression of these genes by cyanobacterial viral

Example Correlations

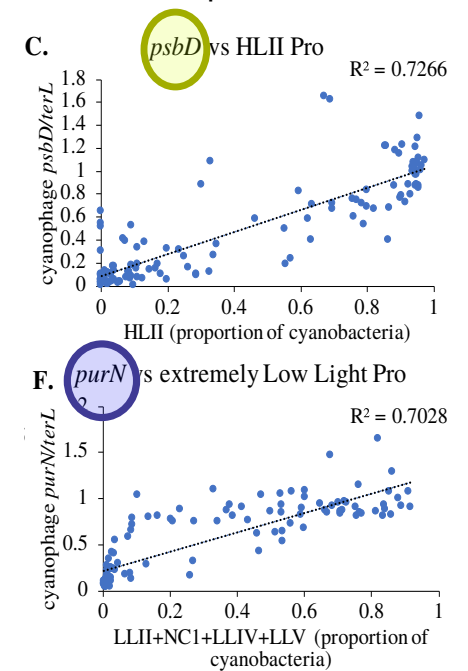


Figure 4. Example correlations between host gene ratios and cyanobacterial ecotype abundance. Data are from all stations in Figure 1, not just those shown in Figure 2.

Discussion

- We have a system for identifying putative associations 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

The authors thank JL Weissman and S Gle for helpful conversations and advice.

References

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

