

Abstract

Coral reefs are declining globally. Degraded reefs are often overgrown by bacteria. However, the role of viruses that infect these bacteria, and particularly their metabolic effects, are poorly understood. To address this, we analyzed the frequency of central carbon metabolism genes in viral communities from healthy through degraded reefs, finding that viral metabolism shifts from Pentose Phosphate Pathway and reductive Tricarboxylic Acid Cycle on lytic dominated reefs to Entner-Doudoroff glycolysis on temperate, degraded reefs. We then constructed a compartment model to assess the ecosystem impacts of this metabolic switch. Our model suggests that lytic viral metabolism may lead to further viral production on healthy reefs while temperate viral metabolism might lead to further bacterial overgrowth of degraded systems. Altogether, this implicates viral metabolism in feedback loops that likely enhance ecosystem resilience on healthy reefs and exacerbate the decline of degraded coral reefs.

Background:

The dissolved organic carbon, disease, algae, and microbes (DDAM) positive feedback loop shows the interactions on a reef ecosystem that lead to coral death.¹

Bacteriophages can be either lytic or temperate. Lytic viruses infect bacterial hosts, replicate, and kill host cells via lysis. Temperate viruses non-lethally infect bacterial hosts and insert their genetic information into the bacterial genome.

Healthy reefs are characterized by high coral cover, low microbial biomass, and lytic viral communities.²

Degraded reefs are characterized by high algal cover, large microbial biomass, and temperate viral communities.²

Big questions:

- How does viral metabolism change between lytic and temperate communities?
- What role do viruses and their metabolism play in the structuring of a reef ecosystem and how do they contribute to coral health and degradation?

Methods:

Viral metagenomes were purified and processed from seawater samples collected from 17 coral reefs in the Pacific Ocean. They were then annotated by BLAST against the SEED database on MG-RAST. The correlation between the frequency of genes in a given function and viral community temperateness were assessed using Spearman's Rho.

Using Spyder, we implemented a simple compartment model that incorporates algal (A), coral (C), bacterial (B), and viral (V) pools. The model allowed us to assess the relative impact of changing the rates of (i) coral-algal inhibition, (a) algal-mediated DOC supply to bacteria, (m) bacterial anabolic metabolism, (d) bacterial-mediate coral disease, (k) viral lysis of bacteria, (l) lytic viral metabolism, and (t) temperate viral metabolism. Thick lines indicate a rate of 0.5 while thin lines indicate a rate of 0.1. The equations used when constructing the ecosystem compartment model include:

$$B_{temp} = a * A + m * A \quad V = k * B + l * B$$

$$B = B_{temp} + t * B - k * V \quad C = C_i - d * B \quad A = 1 - i * C$$

Conclusions:

- Temperate viruses are more cell like (Figure 1)
- Entner - Doudoroff glycolysis is enriched in temperate communities and associated with enhanced host biomass (Figure 2)
- Lytic viruses are focused on ATP generation for viral replication (Figure 3)
- On degraded reefs temperate viral metabolism enhances bacterial growth which causes coral death and leads to ecosystem degradation (Figure 4)
- Lytic viruses act as a resilience mechanism against bacterial growth on healthy reefs (Figure 4)

References:

- ¹ Nelson, H.R., Altieri, A.H. Oxygen: the universal currency on coral reefs. *Coral Reefs* 38, 177–198 (2019).
² Knowles, B., Silveira, C., Bailey, B. et al. Lytic to temperate switching of viral communities. *Nature* 531, 466–470 (2016).

Acknowledgements:

The authors would like to thank NSF for awarding a Hopeful Monsters stipend as well as Big Summer, Alex Hoffmann, and Caroline Baron.

Results:

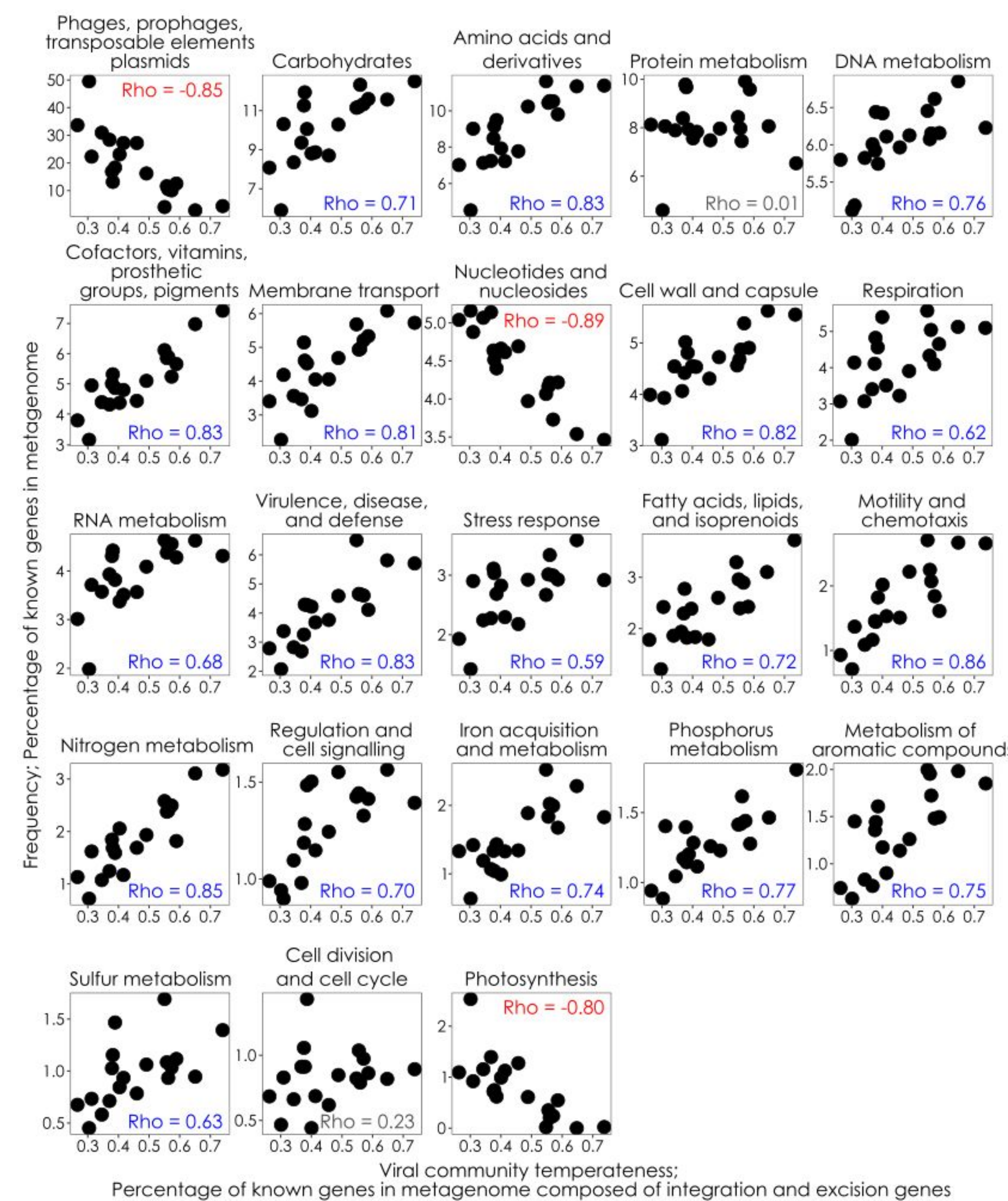


Figure 1. Correlation between temperateness and gene frequency grouped by broad metabolic category

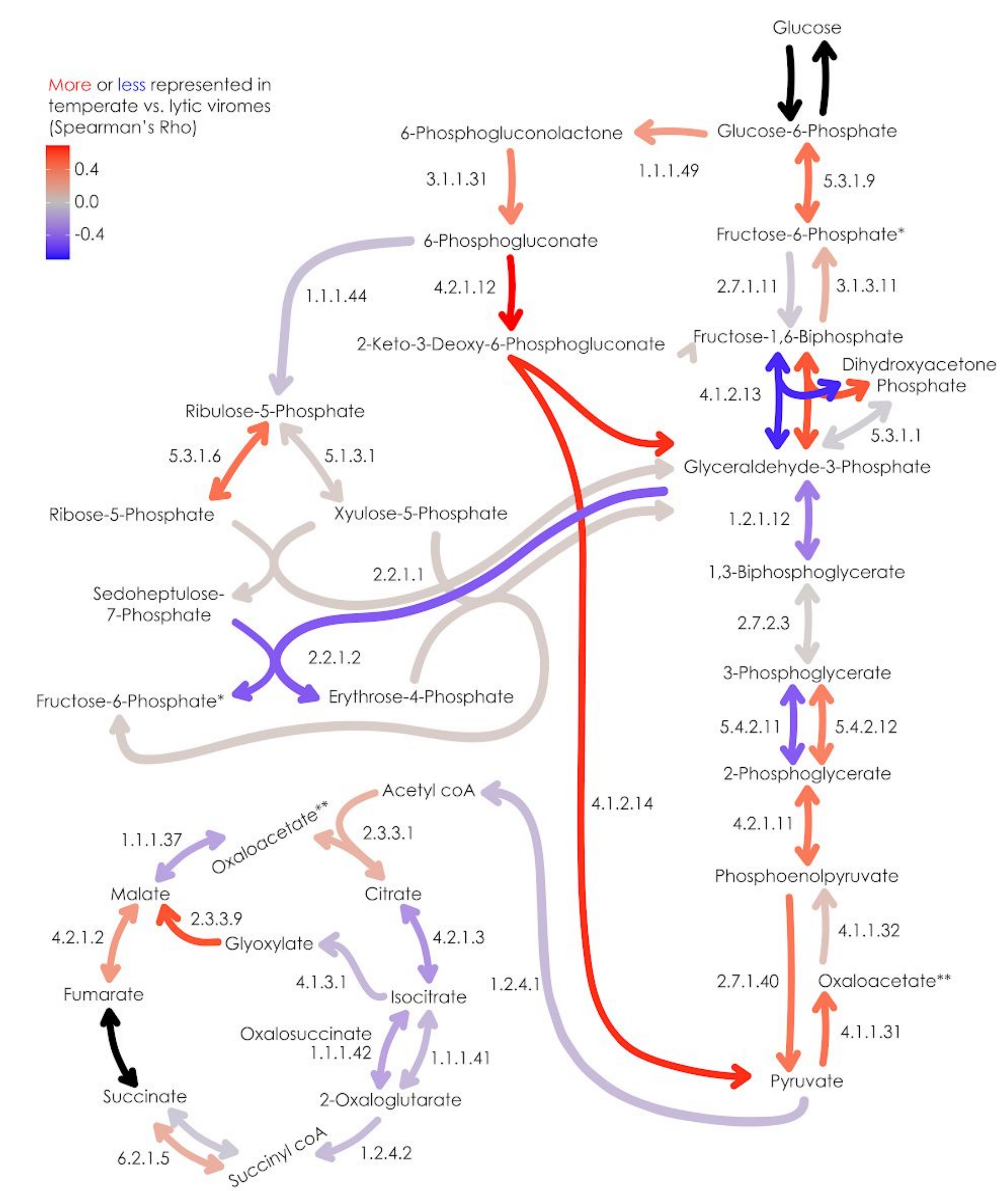
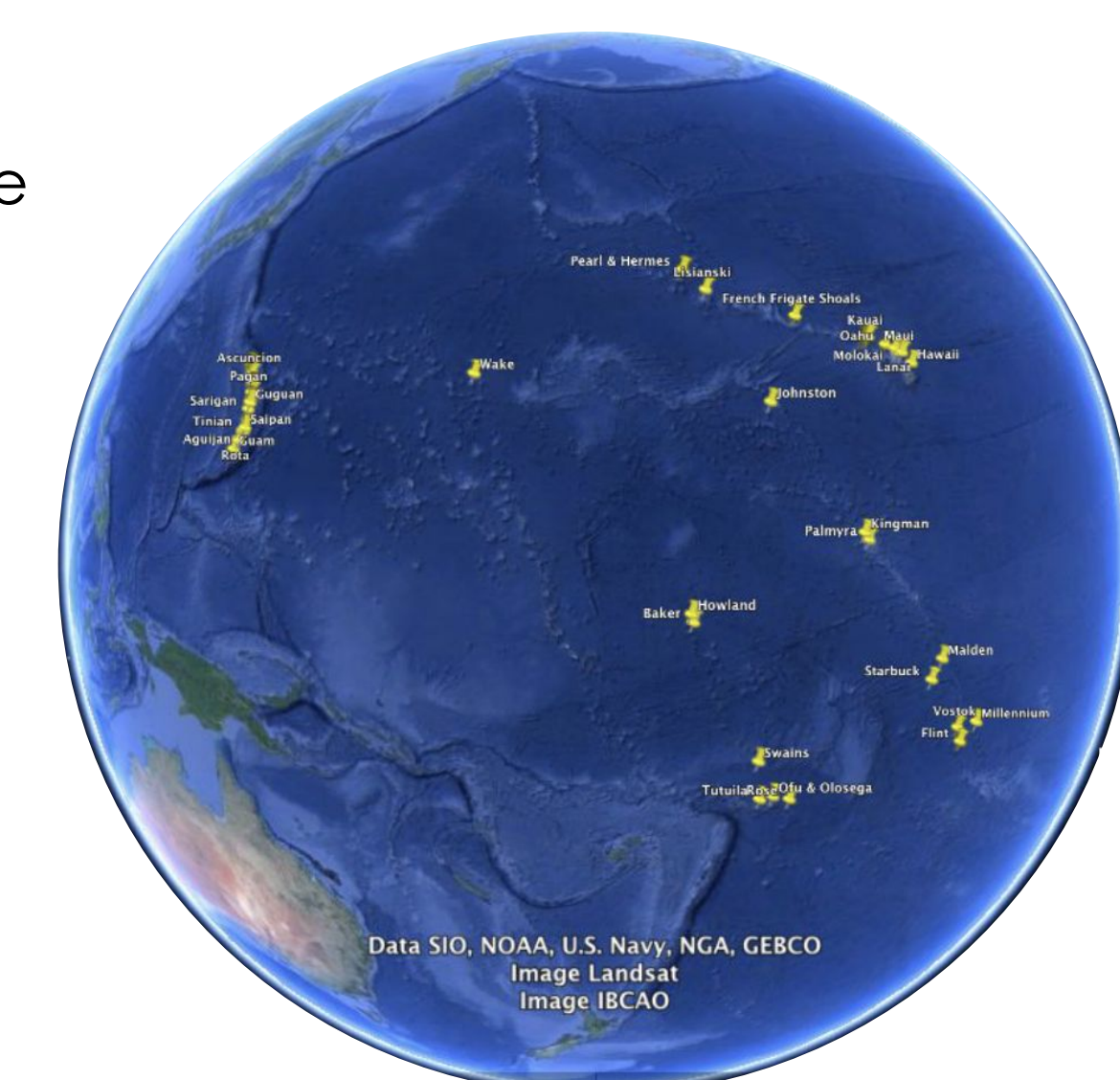
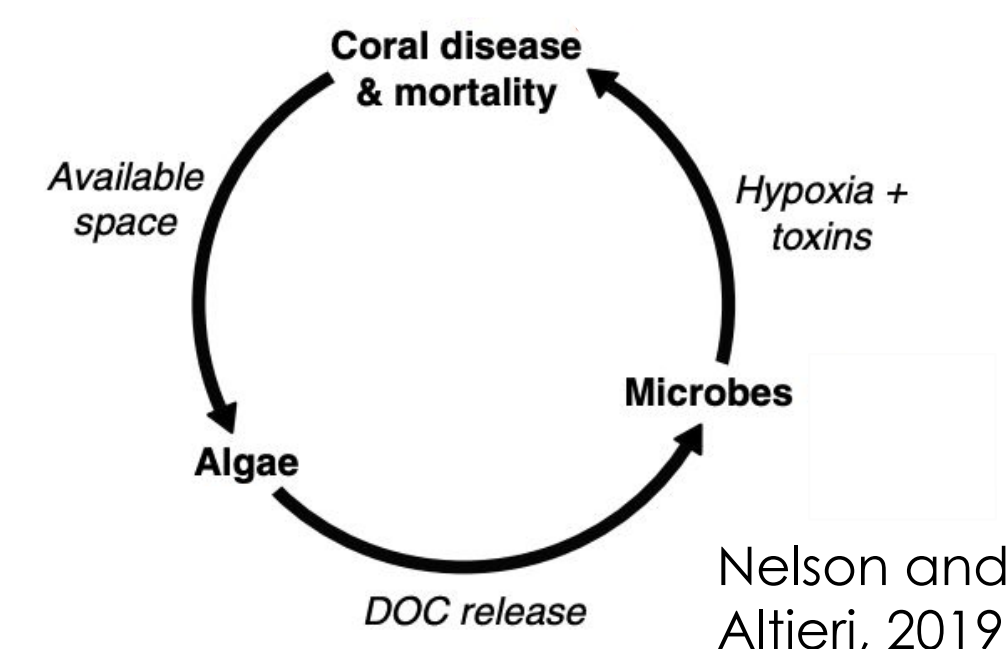


Figure 2. Change in frequency of central carbon metabolism genes across the lytic to temperate community spectrum



DDAM Feedback Loop



Map of Sampling Locations

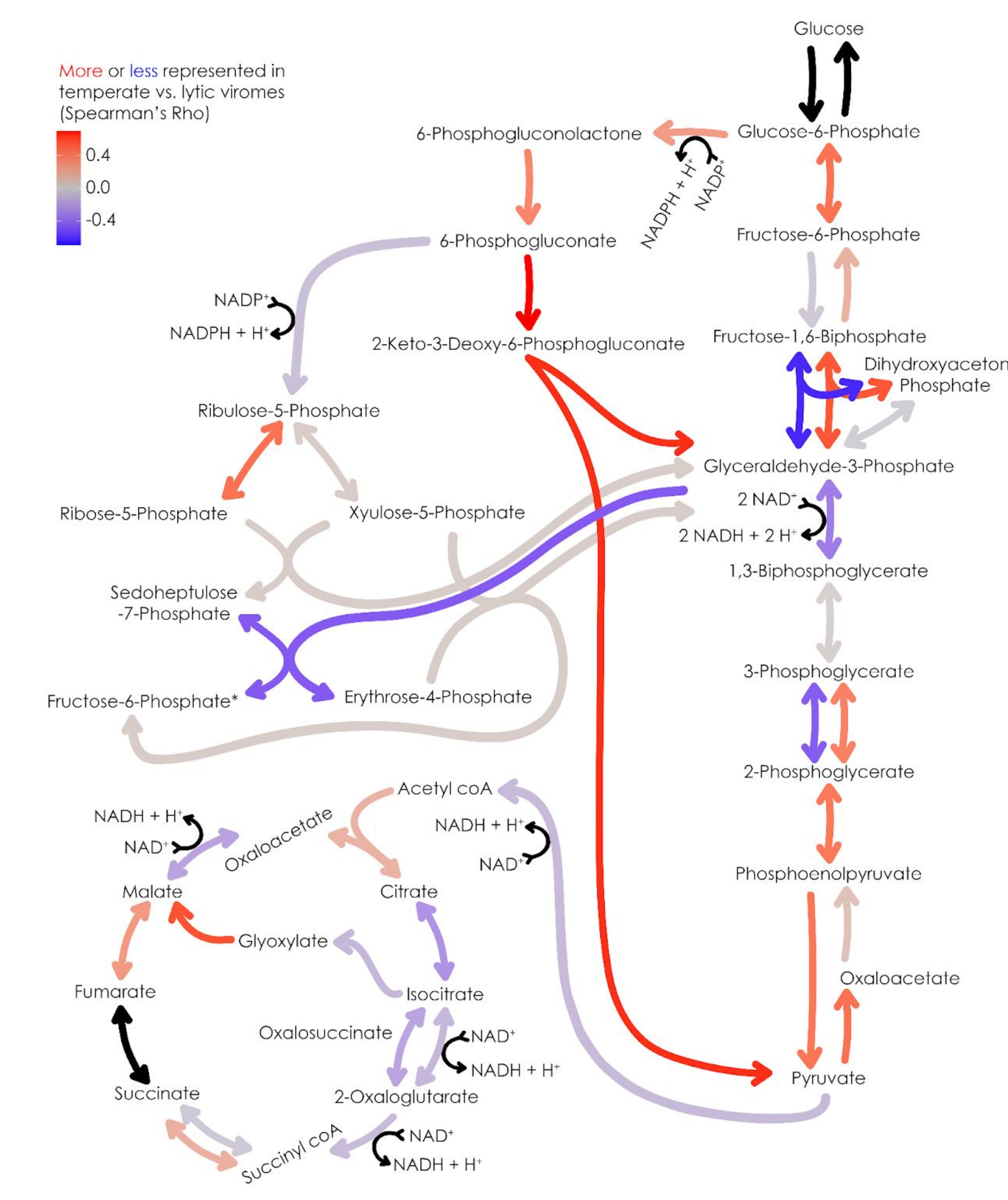


Figure 3. Changes in redox gene frequency in central carbon metabolism pathways across the lytic to temperate viral community spectrum

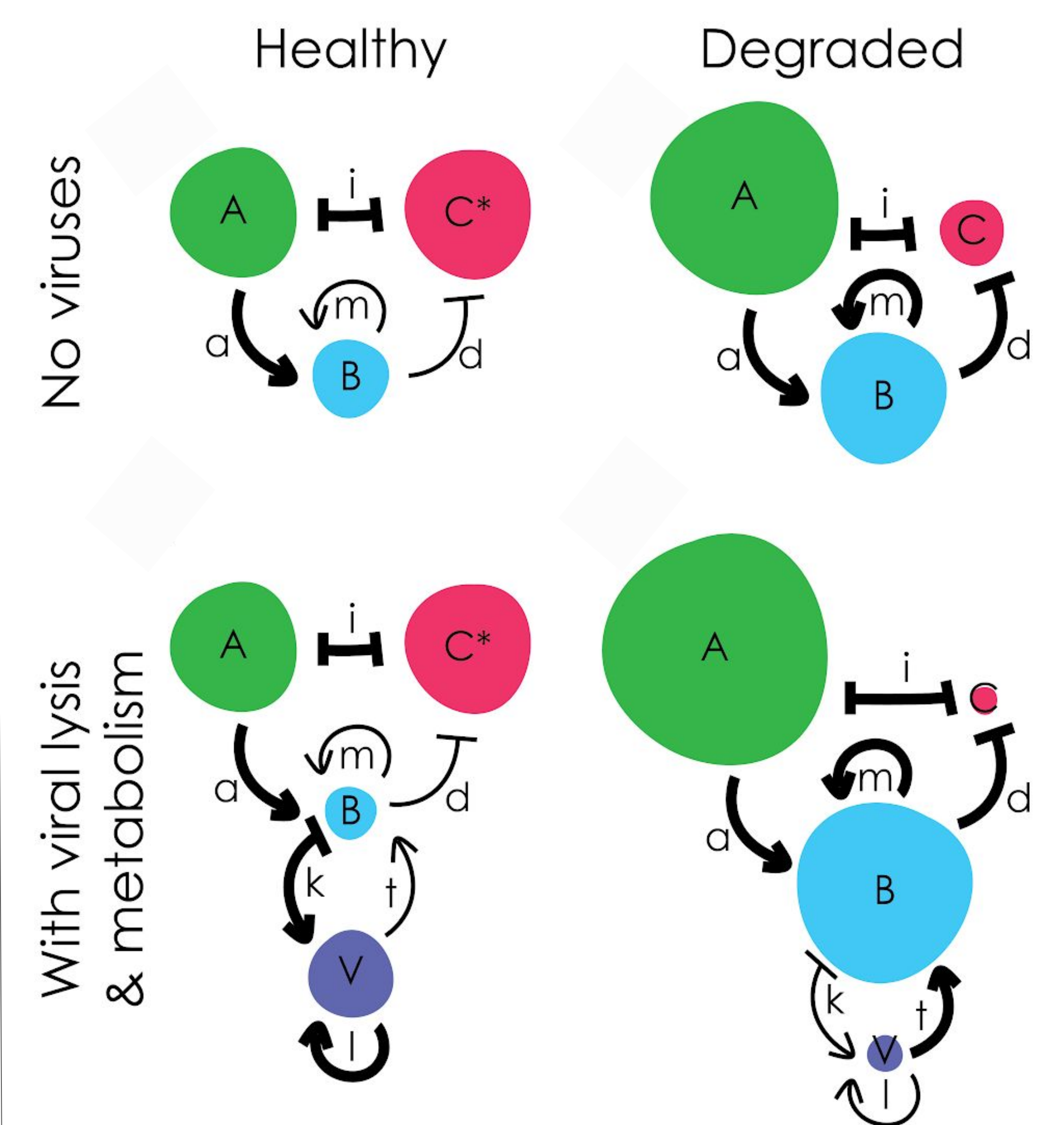


Figure 4. Ecosystem compartment model incorporating viral metabolic effects on resilience of healthy coral reefs and exacerbation of reef degradation