Title: Nutrient Limitation Drives Dynamics of Host-virus Interactions

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Project Goals:

The overarching goal of this project is to establish ecological paradigms for how viruses alter soil microbiomes and nutrient cycles by developing foundational (eco)systems biology approaches for soil viruses. Here, we used a multi-omics approach to investigate phage-specific metabolic reprogramming in virus-infected cells (virocells) to build critically needed model systems and in-silico resources and tools extending to new soil model phage-host systems. Together, these efforts will establish a foundational ecological understanding for the soil microbiome while also developing essential tools and resources for transformative soil viral ecology advances. The development and application of –omics approaches will further help investigate microbial community processes involved in biogeochemical nutrient cycling in terrestrial ecosystems.

Abstract:

Viruses utilize infection to control bacteria that perform vital planetary functions by changing them into new entities called virocells that are reprogrammed to obtain energy and resources differently from uninfected cells[1]. Since microbial metabolic outputs dictate ecosystem-level biogeochemical processes, and virocells are fundamentally reprogrammed metabolically, their interaction with the surrounding environment is expected to be different. Here we used a known, ecologically relevant bacterium (*Pseudoalateromonas*) and two unrelated infecting phages (HP1, a podophage, 45.06 Kbp dsDNA, and HS2, a siphophage, 37.72 Kbp dsDNA)[2] under phosphorus (P) rich and poor conditions to see whether infection dynamics are the same or different under the different nutrient types and to develop foundational approaches to studying soil viruses. Using an integrated multi-omics approach, we found that under nutrient-rich conditions, differences in the phage mechanism of action were driven by the metabolic reprogramming of the host, resulting in two different virocells with different energy and resource acquisition strategies[3]. In contrast, under nutrient limitation, we found that the environment quite strongly drove the metabolic reprogramming of the host, where the common strategy across different phages was survival under stress. These findings contribute to a better biological knowledge of phage-host interactions and the effects of nutrient constraints on their dynamics, shedding light on the environment-specific impacts on virocells that could significantly affect the metabolic reprogramming of the host and thus reshape the biogeochemical cycles in various ecosystems. Our research reveals significant insights into phage-host interactions and offers methods for new soil model phage-host systems.

References/Publications

1. Correa, A. M., Howard-Varona, C., Coy, S. R., Buchan, A., Sullivan, M. B., & Weitz, J. S. (2021). Revisiting the rules of life for viruses of microorganisms. Nature Reviews Microbiology, 1-13.
2. Duhaime, M. B., Solonenko, N., Roux, S., Verberkmoes, N. C., Wichels, A., & Sullivan, M. B. (2017). Comparative omics and trait analyses of marine Pseudoalteromonas phages advance the phage OTU concept. *Frontiers in microbiology*, *8*, 1241.

3. Howard-Varona, C., Lindback, M. M., Bastien, G. E., Solonenko, N., Zayed, A. A., Jang, H., ... & Duhaime, M. B. (2020). Phage-specific metabolic reprogramming of virocells. *The ISME journal*, *14*(4), 881-895.

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