

Patterns and processes of aquatic microbial communities across space and time

Hugo Sarmiento ¹

¹*Universidade Federal de São Carlos*

Microbes are the engines of the Earth. In aquatic environments, they regulate nutrient cycling, mediate energy flow, and are key to ecological resilience. Despite their key role, the ecological and environmental factors that shape microbial diversity, composition, and function across spatial and temporal dimensions remain at the forefront of research. From freshwater systems to coastal areas and the open ocean, aquatic microbes inhabit dynamic habitats structured by gradients in light, temperature, nutrients, and physical connectivity. Unlike terrestrial ecosystems, aquatic environments are in constant motion, with water masses, currents, and mixing processes continuously redistributing organisms and resources. This inherent fluidity has profound implications for microbial ecology, influencing dispersal, connectivity, and the scale at which environmental selection operates, which makes prediction and modeling challenging. This presentation examines how ecological processes (selection, dispersal, drift and speciation) interact with spatial (horizontal and vertical) and temporal (seasonal and interannual) variability to structure microbial communities. Insights from global surveys highlight consistent biogeographic patterns, including latitudinal diversity gradients and vertical stratification, while long-term time-series emphasize the influence of seasonality, climate variability, and energy flux on microbial dynamics. Drawing from recent findings in both marine and freshwater systems, this talk emphasizes the importance of integrating broad-scale spatial observations with high-resolution temporal data to advance understanding of aquatic microbial ecology. The urgent need to expand monitoring with standardized protocols in underrepresented regions and timeframes will also be discussed, with emphasis on ethical collaboration and capacity building to improve our understanding of how aquatic microbial communities respond to environmental change in a rapidly changing world.

How can microbial traits help understand and predict ecosystem functions?

Elena Litchman ¹

¹*Michigan State University*

Understanding how microbial communities and ecosystems will function in the future is a question of both fundamental and applied importance. Major ecosystem functions, such as productivity, biogeochemical cycling, carbon sequestration and their resilience to perturbations depend on the performance of diverse microbes that respond differently to environmental conditions. Predicting how microbial community composition drives ecosystem functions requires a mechanistic approach that allows to incorporate biodiversity and can be scaled up. Here I discuss how functional traits can provide such a mechanistic foundation to help tackle fundamental and applied problems. I will provide examples of using traits to answer key questions in microbial ecology and ecosystem functioning. I will show how the diversity in phytoplankton thermal performance curves can help maintain productivity under temperature fluctuations and how comparing traits of harmful algal bloom (HAB)-producing species

to other phytoplankton and to environmental conditions may help predict HAB occurrence. Finally, I will outline some challenges and future directions of using trait-based approaches in microbial ecology.

Ordering microbial diversity into ecologically cohesive units

Martin Polz ¹

¹*University of Vienna*

Microbial diversity is vast and ordering it into units of diversity that reflect cohesive ecology remains challenging. Theory predicts that the balance of gene flow and selection is key in determining one of two evolutionary paths towards creating units of genetic similarity, and of phenotype and ecological function. First, if recombination is frequent and selection moderate, ecologically adaptive mutations or genes can spread in niche-specific manner within populations independently of their original genomic background (gene-specific sweeps). In fact, these gene-specific sweeps may serve to predict recent adaptations that differentiate populations from their next of kin, an approach we have previously termed “reverse ecology”. Second, if the effect of recombination is smaller than selection, genome-wide selective sweeps should occur creating a genomically homogeneous population. We will show that both paths towards creating adaptive populations are realized in diverse microbial communities and we will end with a discussion of how such ecological population structure relates to common sequence similarity cutoffs frequently used to delineate species and populations.

The role of behaviour in inter-microbial relationships in the pelagic ocean

Justin Seymour ¹

¹*University of Technology Sydney*

Rather than solo travellers on the ocean’s currents, planktonic marine microbes are embedded within intricate ecological networks, whereby complex inter-species relationships can often be just as important as abiotic environmental drivers in governing microbial community composition and function. Arguably among the most important of these inter-microbial interactions are those involving phytoplankton and bacteria. These relationships can be symbiotic in nature, and often involve reciprocal exchanges of metabolites, resulting in mutual growth enhancement and sometimes ecosystem-wide biogeochemical outcomes. The physical nature of the pelagic realm, along with the specificity of chemical exchanges involved in these interactions, often means that close proximity of partner organisms will be crucial for phytoplankton-bacterial symbioses. Therefore, microbial behaviours including motility and chemotaxis will potentially be key for the establishment and maintenance of relationships. In my talk I will synthesize results derived from laboratory-based experimentation and in situ behavioural assays, which have provided a view into the intricate social lives of planktonic marine microbes. These studies have revealed the importance of specific chemical currencies, unique behavioural strategies and metabolic co-dependencies in