Microbial Biosignatures of Geospatial Location in Ship Microbiomes.

Microbe are ubiquitous in the world’s oceans and important players in biogeochemical cycling. Distinct environmental conditions in the oceans are known to select for different microbial populations in specific locations. Ships transit the world’s oceans on daily basis. Microbes colonize ships and can be carried with them from one port to another. In this project, we are seeking to understand the ability of microbes to colonize vessels and be transported by them on voyages. Samples were collected from 20 ports around the world in order to identify key microbial features that distinguish one location from another. This was accomplished through combining high resolution microbial community analysis using next-generation sequencing with machine learning. Additionally, the microbial community present on ships surfaces and in bilge water was analyzed. We constructed machine learning models that accurately classify the location of sample collection from the microbial community composition alone. This suggests that there are sufficient differences in the microbial community between locations that can be used differentiate geospatial locations. Our work has also shown that the microbiome of a ship is mostly distinct from the water, but a substantial portion of the boat microbial community is derived from port water microbes. Recent work has sought to characterize the rate of change in boat microbiomes during voyages to better understand the rates of colonization of ship surfaces during transits. This work will help clarify the potential for ships to serve as conduits for bacterial dispersal in the oceans.