

Sequencing the Waterworld

The dynamic oceanic habitat presents a range of challenges to the denizens of the deep. Recent technological advances, particularly the ability to sequence single organisms, provide an inside look at these communities, revealing the ways species adapt to their surroundings and how the aqueous environment drives unexpected solutions for its distinct conditions.



Sampling the deep blue sea: instruments descend into ocean waters. Figure courtesy of A. Thompson.

A Global Collective, Riding the Waves

Prochlorococcus, the smallest and most abundant known photosynthetic organism, is a marine cyanobacterium responsible for a sizable portion of global photosynthesis. What it lacks in size, it compensates by number; *Prochlorococcus* live in vast regions of Earth's tropical and subtropical oceans, displaying intricate geographic patterns and phenotypic diversity to match, consigning them into specific ecotypes or clades. Kashtan et al. (2014) now took a closer look at this oceanic collective by sequencing single cells of coexisting wild *Prochlorococcus* and find extraordinary cell-to-cell genomic diversity within clades. Indeed, each clade contains many subpopulations of cells with distinct genomic combinations attached to a conserved "core" genotype. The advantage of such a flexible genetic population comes to the fore during different seasons when genotypes conferring selective advantages to specific environmental conditions become more abundant, allowing rapid adaptation to change. Interestingly, each clade has its own set of core alleles and flexible gene content, suggesting that they originally segregated a few million years ago. Thus, genetic microdiversity within a species provides a unique adaptive mechanism allowing a rapid response to environmental challenges.

Kashtan, N., et al. (2014). *Science* 344, 416–420.

At the Hearth of a Mineral-Fueled War

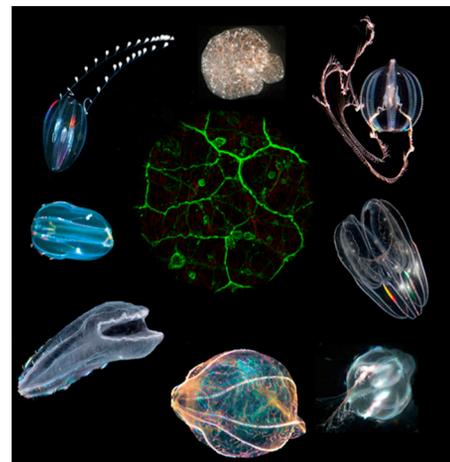
Deep-water hydrothermal vents create a hot, mineral-rich world teeming with bacterial life adapted to using inorganic compounds as energy sources. Viruses are also ubiquitous at these underwater hot springs, although little is known about their biology. A study of viral genomes by Anantharaman et al. (2014) now uncovers an unusual strategy by which viruses apparently infect hot-spring bacteria growing on sulphur. The researchers identified a set of new viruses that carry genes coding for sulphur oxidation, with the potential to confer the ability to supplement bacterial pathways upon infection. Such "auxiliary" genes provided by the virus may enhance sulphur oxidation in the host, effectively promoting the process by which bacteria extract energy from sulphur and ensuring abundant production of viruses. Through this manipulation of chemosynthetic pathways, alternative energy sources can be tapped during host infection.

Anantharaman, K., et al. (2014). *Science* 344, 757–760.

Starting All Over

Comb jellies, also known as ctenophores, are planktonic predators with sophisticated behaviors that are made possible by complex and well-developed nervous and muscular systems. Arguably one of the evolutionarily earliest branches of animals with such features, analysis of comb jellies may yield precious insights into the origins of neural circuits. With that in mind, Moroz et al. (2014) delved into characterization of the genome of the ctenophore Pacific sea gooseberry and phylogeny of ten other ctenophores. Their analysis reveals a unique genome that lacks scores of genes considered essential for development, nervous system, and immune function. Expression, metabolomic, and functional analyses further confirms these findings, showing that, despite its robustness, the ctenophore nervous system makes do with a very distinct repertoire of neuromodulators remarkably different from those in other animals, paralleled by developing a great diversity of electrical synapses. Based on these findings, the authors postulate that ctenophores underwent a separate evolutionary process in which many of the physiological systems have been developed through innovation, possibly providing an extreme example of convergent evolution.

Moroz, L.L., et al. (2014). *Nature* 510, 109–114.



The diversity of ctenophores and their nervous systems. Figure courtesy of L.L. Moroz, G. Pauley, M. Citarella, and T. Norekian.



Marine sponge *Theonella swinhoei*. Image courtesy of Yoichi Nakao.

Deep-Sea Factories

Bacteria are often studied for their ability to synthesize biomedically important natural compounds; however, only a limited number of such “metabolically talented” taxa have so far been characterized. Marine sponges form one of the richest microbial habitats, hosting diverse symbiotic bacterial phylotypes that are a source of hundreds of distinct metabolites, some of which are already used for medical purposes. Previous attempts to characterize bacteria hosted by the sponges and producing these compounds have been hampered by the limited ability to distinguish their taxonomic features. However, a recent study by Wilson et al. (2014), using single-cell sequencing analysis to detect metabolic genes carried by bacteria, shows that a chemically rich and phylogenetically unusual group of bacteria manufactures these bioactive substances. This inroad into characterizing an uncultivated prokaryote strain provides an avenue to move from laborious isolation of metabolites from sponges to heterologous expression of bacterial genes or the development of cultivation methods for symbionts.

Wilson, M.C., et al. (2014). *Nature* 507, 58–62.

Bacterial Feng Shui

Marine tubeworms *Hydroides elegans* are a sessile species whose survival depends on the ability to settle in the right habitat. Tubeworms start off as free-swimming larvae that metamorphose upon contact with surface-bound bacteria. There is ample interest in understanding the process by which tubeworms settle; in addition to the unusual role of bacteria in inducing a developmental switch, their widespread mineralized tubes create a costly problem for the shipping industry. Shikuma et al. (2014) describe the unusual molecular mechanism mediating tubeworm-bacterial interaction by investigating bacterial genes that are necessary for tubeworm metamorphosis. The authors found a set of genes that produce a structure similar to the tail of bacteriophage viruses and showed that this syringe-like structure is indeed necessary for larval metamorphosis. Although such structures were previously described in bacteria, they were primarily considered defense mechanisms against other bacteria or even larger species. Using electron cryotomography, the authors also studied the details of these phage tail-like arrays, showing their contractile properties. Thus, the study uncovers an unprecedented mechanism by which bacteria can trigger developmental processes, reflecting more broadly on the role of external cues in such functions.

Shikuma, N.J., et al. (2014). *Science* 343, 529–533.



Hydroides elegans in its calcified tube with the extended tentacular plume. Figure courtesy of B. Nedved.

Mirna Kvajo