The co-evolution of Fe-,Ti-oxides and other microbially induced mineral precipitates during the diagenesis of sandy sediments

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Ilmenite ($FeTiO_3$) and related Fe-,Ti-oxides are ubiquitous components of modern beach sands and are often associated with "fossil" microstructures in ancient sedimentary rocks [1,2]. The mineral composition of the ancient sedimentary rocks we see today, however, differs from what was originally formed in the sediments billions of years ago. This change in composition is usually attributed to long, complicated histories and atmospheric influences, while the contribution of microbes is not typically considered. Here the goal is to understand the co-evolutionary path of microbes and minerals in sandy, shallow sub-aquatic environments under early diagenetic conditions. Laboratory experiments were done to document the precipitation of minerals on cyanobacterial cellular material as well as the phase changes in natural ilmenites to determine if microbes passively influence mineral phase pathways. The precipitates, ilmenite grains, and fossilized cells were analyzed using scanning electron microscopy (SEM), x-ray diffraction (XRD), and micro Raman spectroscopy. The results show that microbial fossilization occurs and a variety of mineral phases precipitate under early diagenetic conditions ($T<70°C$) in wet, sandy environments. The minerals that form in the presence of microbes differ in crystal habit and chemical composition from those without microbes. This study aids in understanding the microbial role in diagenesis and helps redefine geochemical biosignatures that can be used for the detection of ancient microbial life in sedimentary rocks on Earth as well as for future planetary life exploration missions.

[1] Morad & Aldahan (1982) *Journal of Sedimentary Petrology,* **52,** 1295-1305. [2] Bower (2011) *Journal of Raman Spectroscopy,* **42** **(8)**, 1626-1633.

Using Genomics to Reveal the Secrets Underlying the Ecological Success of Marine Diatoms

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Diatoms are thought to be the most successful group of eukaryotic phytoplankton in the modern ocean. Recently completed whole genome sequences from two species, *Thalassiosira pseudonana* and *Phaeodactylum tricornutum*, have revealed a wealth of information about the evolutionary origins and metabolic adaptations that may have led to their ecological success. A major finding is that they have acquired genes both from their endosymbiotic ancestors and by horizontal gene transfer from marine bacteria. This unique melting pot of genes encodes novel capacities for metabolic management, for example allowing the integration of a urea cycle into a photosynthetic cell. Our studies focus on *P. tricornutum* and exploit the availability of techniques for reverse genetics, digital gene expression profiling, genome and epigenome maps, ecotypes with differential capacities to adapt to different conditions, and distinct morphotypes that can be induced to change shape in response to ecologically relevant stimuli. Using these resources we explore both the physiological functions of diatom gene products and the evolutionary mechanisms that have led to diatom success in contemporary oceans.

A next objective is to explore the functional roles of diatom biodiversity in the world's oceans. With biology becoming quantitative, systems level studies can now be performed at spatial scales ranging from molecules to ecosystems. Biological data generated consistently across scales can be integrated with physico-chemical contextual data for a truly holistic approach. While the marine planktonic ecosystems that diatoms inhabit comprise the base of the ocean food web, and are crucial in the regulation of Earth's biogeochemical cycles and climate, their organization, evolution and dynamics remain poorly understood. The *Tara* Oceans expedition was launched in September 2009 for a 3-year study of the global ocean ecosystem aboard the schooner *Tara*. A unique sampling programme encompassing optical and genomic methods to describe viruses, bacteria, archaea, protists and metazoans in their physico-chemical environment has been implemented. The project aims to generate systematic, open access datasets usable for probing the morphological and molecular makeup, diversity, evolution, ecology and global impacts of plankton on the Earth system, as well as to explore and exploit their biotechnological potential.

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