

Baker

Marine Microbiology

Marine microbes include a very broad spectrum of microscopic organisms (microalgae, bacteria, archaea, protozoa, fungi and viruses). They are ubiquitous, inhabiting every niche on earth and together account for more than 90 percent of biomass in world oceans. Microbes are the first link in the food chain, and as such they control the flow of energy, nutrients and the recycling of elements and organic matter. With so many species yet to be discovered, we know very little about the incredible diversity of bacteria and archaea on the planet and even less about their physiology and ecological roles. Dr. Baker uses leading-edge genomic (DNA) methods to uncover the diversity of marine microorganisms, their unique physiology, and their roles in the ecology of our estuaries and oceans.

RESEARCH

- Resolving the metabolisms of microbes involved in petroleum degradation in the Gulf of Mexico
- Characterizing the diversity and physiology microbes involved in the cycling of nutrients, elements and organic matter in the deep sea and sediments
- Understanding how microbial nutrient cycling in the northern Gulf of Mexico is effected by (hypoxia) the dead zone
- Development of computer methods for analysis of DNA sequencing data from natural microbial communities

RESEARCH ACCOMPLISHMENTS

- Recently Brett has been leading a study that has reconstructed over 150 genomes of uncultured microorganisms involved in organic matter degradation, and the cycling of nutrients in estuary sediments.
- Studies involving the genomic (DNA) sequencing from the environment have resulted in the discovery of new kingdoms of microbial life that are involved in globally important processes.

HIGHLIGHTED COLLABORATIONS

- Collaborations with microbial ecologists at Universities of North Carolina and Delaware, Louisiana State University, bioinformaticians at Univ. of Colorado, Denver, and geochemists at Woods Hole Oceanographic Institute

HIGHLIGHTED PRESENTATIONS

- “*Genomic characterization of iron cycling in estuary sediments*” Invited speaker American Chemical Society, 2015, Denver, Colorado
- “*Resolving metabolic pathway and microorganisms involved in coastal petroleum degradation using high-resolution community omics approaches*” Gulf of Mexico Science Conference, 2015, Houston, Texas

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Mapping the flow of carbon and energy within microbial communities

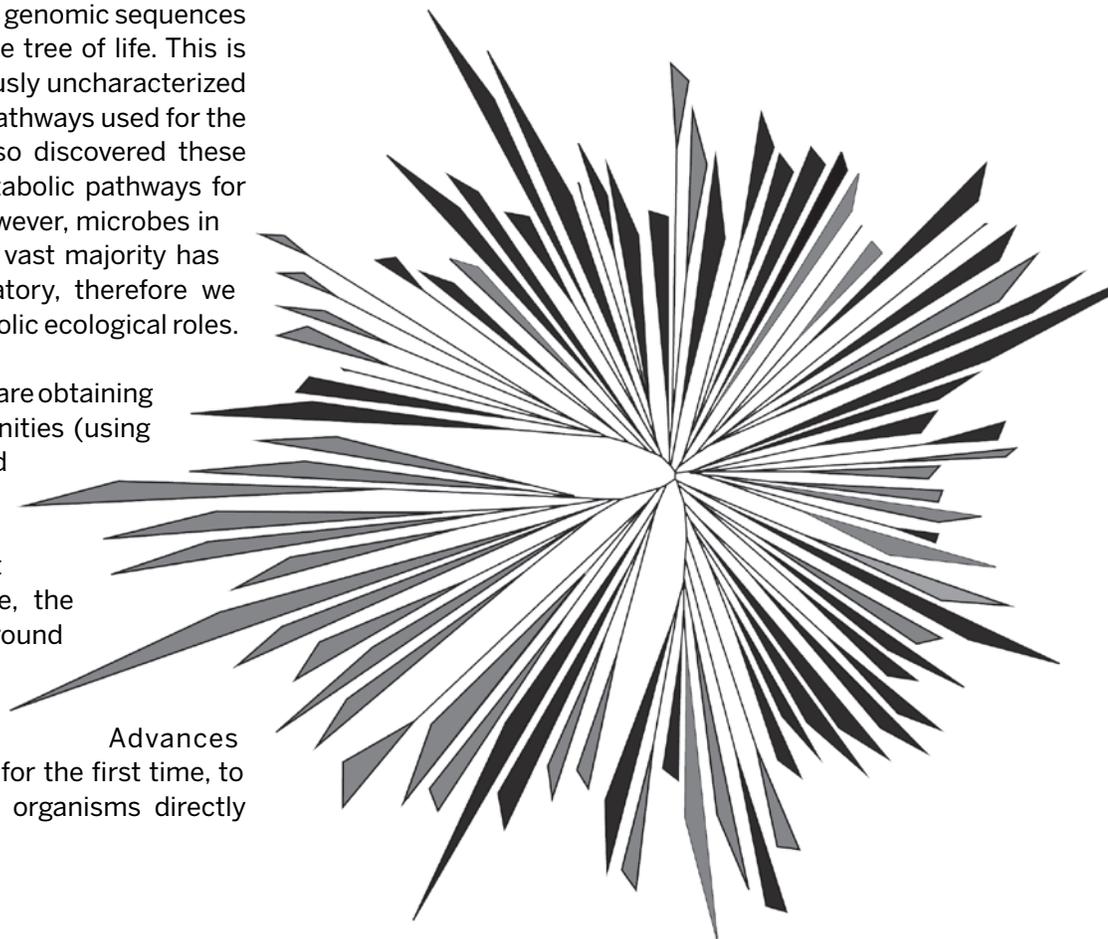
Reconstructing the genomes of microbes on the ocean floor to understand who is doing what and how they drive important chemical processes

WHY Organic matter is deposited on the ocean floor from the overlying water column and is the largest reservoir of organic carbon on the planet. The result is a net sink of atmospheric CO₂ (an abundant greenhouse gas) to the oceans = carbon sequestration. Microorganisms there derive energy by changing the chemistry of sediments. These small organisms are the last living filter of carbon before permanent burial. However, due to the staggering diversity of microbes we know very little about the ecology of these environments.

WHAT do we know about it, and what are the remaining big questions? We have decoded the genomic sequences of dozens of new branches on the tree of life. This is revealing that many of the previously uncharacterized lineages have unique metabolic pathways used for the recycling of carbon. We have also discovered these organisms have several new metabolic pathways for nutrient and element cycling. However, microbes in the oceans are complex and the vast majority has not been cultured in the laboratory, therefore we know very little about their metabolic ecological roles.

FILLING THE KNOWLEDGE GAP We are obtaining genomes from microbial communities (using similar techniques to those used in sequencing the human genome) from a variety of locations; estuaries on the coast of North Carolina and Delaware, the Gulf of Mexico dead zone, around underwater volcanoes in the Gulf of California, and deep below the Pacific ocean floor. Advances in technologies have enabled us, for the first time, to obtain hundreds of genomes of organisms directly from these environments.

IMPACT All of these genomes sequenced belong to organisms that have not been grown in the laboratory and many of them belong to entirely new kingdoms of life that are present throughout the world. Therefore, by looking at the genes they contain we are able to understand, for the first time, their physiologies and what important ecological and chemical processes they are involved in. By doing this for many organisms from the environment we are able to create the first realistic map of the flow of carbon and energy through marine communities. This will also have broad impacts on our understanding of the evolution of life on earth.





Dead Zone impacts on microbes

Understanding how the Dead Zone effects and impacts to the base of the food chain

WHY The northern Gulf of Mexico receives waters that contain high levels of fertilizers from agriculture. These fertilizers can inadvertently feed algae in the water and create a “bloom” of algae that depletes the amount of oxygen in water. When oxygen reaches low levels it can cause kill fish and disrupt the entire ecosystem. Microbes play a very important role and could be part of the solution to this problem. Microbes in the Gulf of Mexico mediate a variety of crucial chemical processes, such nutrient cycling. There is little known about their role in the ‘Dead Zone’ and we are interested in understanding how these microbial communities respond to the dead zone and low oxygen environments.

HOW We are comparing the genomes and gene activity of hundreds of microbes throughout the Dead Zone and comparing them to those from surrounding waters. This provides genetic-level understanding on how these communities are responding to oxygen depletion in the Gulf of Mexico.

IMPACT Ultimately, we will have a full understanding of all the key microbial players, which are the base of the food chain, in the Gulf of Mexico. This will enable us to assess the impacts of the Dead Zone and how its expansion will impact the gulf in the future.

