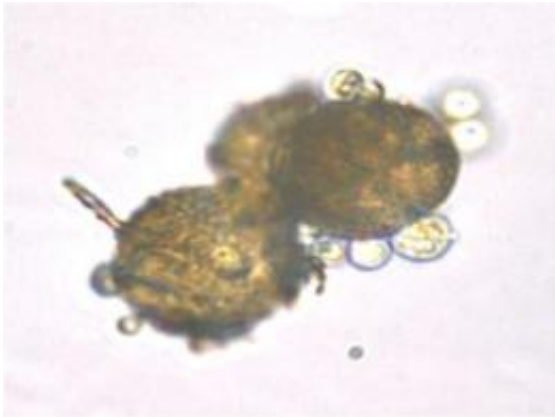


Little-known marine decomposers attract the attention of genome sequencers

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Labyrinthulomycetes from Peconic Bay are shown growing on pollen grains.
Credit: Enixy Collado Mercado, Stony Brook University

The Department of Energy's Joint Genome Institute (JGI) announced today that they will sequence the genomes of four species of labyrinthulomycetes. These little-known marine species were selected for sequencing as the result of a proposal submitted to the competitive JGI Community Sequencing Program by a team of microbiologists led by Dr. Jackie Collier, assistant professor at the School of Marine and Atmospheric Sciences (SoMAS) at Stony Brook University.

"Labyrinthulomycetes are a huge group of organisms that behave ecologically like fungi," said Dr. Collier. "But we know so little about them and there is more diversity among this group than among all the

animals you can think of."

Labyrinthulomycetes are single-celled marine decomposers that eat non-living plant, algal, and animal matter. They are ubiquitous and abundant—particularly on dead vegetation and in salt marshes and mangrove swamps. Although most labyrinthulomycetes species are not pathogens, the organisms responsible for eelgrass wasting disease and QPX disease in hard clams are part of this group.

In some regions, labyrinthulomycetes may be as important as bacteria in degrading organic matter. In coastal systems, the abundance of bacteria is tied to levels of organic matter from marine sources, while the abundance of labyrinthulomycetes is more closely tied to levels of particulate [organic matter](#) from land sources. This suggests that labyrinthulomycetes may play an important role in the marine carbon cycle by breaking down material that is difficult to degrade. Because labyrinthulomycetes—unlike bacteria—make long chain [polyunsaturated fatty acids](#) (PUFAs), they are also thought to improve the nutritional value of poor quality organic detritus.

"The genome sequences will provide a quantum leap in our understanding of the physiological capacity of these organisms," said Dr. Collier. "The genes can tell us which enzymes a species is capable of producing, which in turn tells us what kinds of material they can potentially degrade and what role they play in a marine ecosystem's food web."

In addition, genomic information might suggest ways to exploit labyrinthulomycetes in novel biotechnological applications. Labyrinthulomycetes produce a wide array of enzymes and some species can degrade crude oil. Also, some labyrinthulomycetes are currently cultured for nutritional supplements. If PUFAs derived from labyrinthulomycetes were to replace fish oils and meal used in

aquaculture and animal farming, it would likely reduce the number of fish caught for use as animal feed and have a positive impact on the health of the world's oceans.

Source: Stony Brook University ([news](#) : [web](#))

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