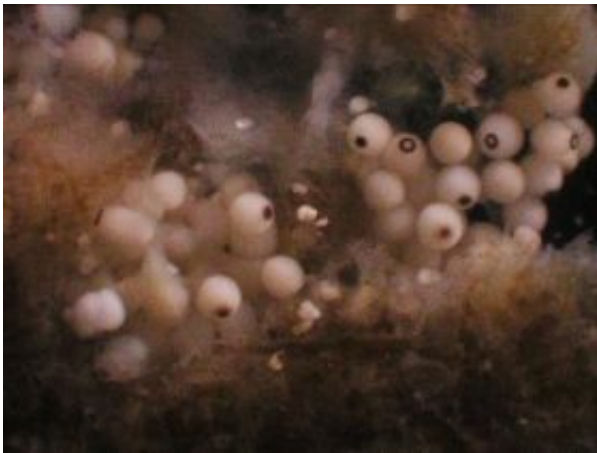


Genomics of large marine animals showcased in the biological bulletin

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The interior of the brood chamber of a sponge, *Amphimedon queenslandica*, showing embryos in the early phases of development. Credit: Bryony Fahey (University of Queensland)

Though the slow moving purple sea urchin may look oblivious, lacking a head, eyes and ears, this prickly creature has an impressive suite of sensory receptors to detect outside signals. And don't overlook this animal's self-defense abilities: it has much more ammunition to activate its innate immune system than humans have. The starlet sea anemone lives in coastal areas that face increasing pollution, and it is better equipped than many land, ocean, and freshwater animals to tolerate environmental stress.

These insights into the biology of marine organisms didn't come from observational studies; they were revealed by deciphering and comparing the animals' genomes. The powerful advantages of using gene catalogs to infer biological function in marine animals are highlighted in a virtual symposium in the June issue of *The Biological Bulletin*, published by the Marine Biological Laboratory (MBL) in Woods Hole, Massachusetts.

Emerging research on the genomic structure of marine organisms is giving scientists new clues as to how certain physiological systems evolved. The genomes of ancient Cnidarians, of which the jellyfish is best known, are being used to discern how cells adhere to form organs and organisms. The genome of *Ridgeia piscesae*, a tubeworm that has co-evolved with bacteria to thrive in the extreme environment of deep-sea hydrothermal vents, is illuminating the molecular underpinnings of symbiosis.

Genetic sequencing, a once-expensive technology, continues to enjoy reductions in cost and increases in speed that allow even smaller laboratories to produce molecular "maps" to study and compare organisms.

"Science runs on three things – very bright ideas, improved technology and the money to do the research," says R. Andrew Cameron of the California Institute of Technology, who organized *The Biological Bulletin* virtual symposium along with Jonathan P. Rast of the University of Toronto. "As genomes become less and less expensive to sequence, then it is easier to justify sequencing more genomes to open new areas of study."

By plugging DNA sequences from a marine organism like the sea urchin into a genetic database, researchers can find similarities between sea urchin genes of an unknown function with, for example, human proteins used for sensing light. Further experiments can then test if the sea urchin

genes are coding for a sensory protein. Comparing the human and the sea urchin genes can also help illuminate how the sensory protein evolved.

"The benefit of having new model systems is that we can ask questions with organisms in which peculiar characteristics of the genome are very important," Cameron says. For example, some of the marine animals featured in this virtual symposium have unexpectedly complicated sensory systems or immune systems that differ greatly from those of the fruit fly or the nematode worm, standard models in genetic studies. "I think there is good justification for these marine metazoan studies in that we will eventually apply this knowledge to the organism we're most interested in – ourselves," he says.

Source: Marine Biological Laboratory

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