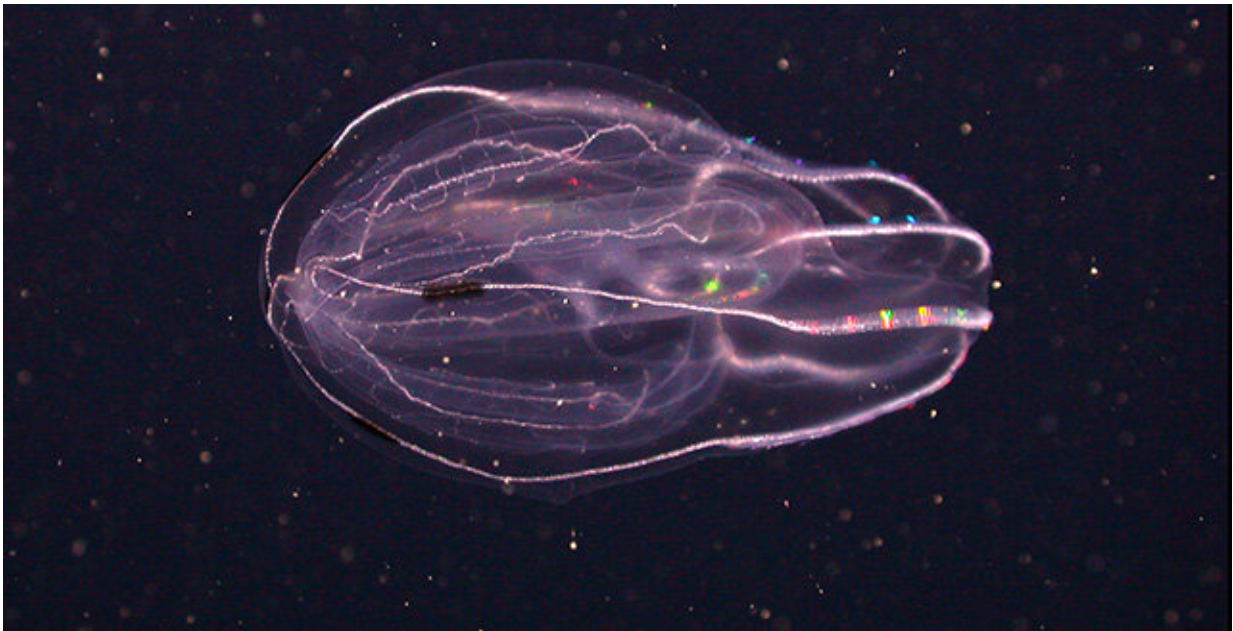


How comb jellies adapted to life in the deep sea

July 4 2019, by Kim Fulton-Bennett



This ctenophore in the genus *Bolinopsis* was photographed almost 1,000 meters (3,300 feet) below the surface of Monterey Bay. Other members of this genus live near the sea surface. Credit: © 2006 MBARI

Washed up on a beach, a comb jelly or ctenophore (pronounced "teen-oh-four") might look like a little transparent grape. But ctenophores are extremely diverse, living from the equator to the poles and from the ocean surface to more than 7,000 meters, or more than four miles, down. MBARI researchers and their collaborators are developing computer

models that compare the genetic material of many species of ctenophores to learn how their body chemistry has evolved to life in different environments.

Jacob Winnikoff, a University of California, Santa Cruz, graduate student in Steve Haddock's lab, recently published a paper about this research in the journal *Integrative and Comparative Biology*.

Winnikoff's coauthors on this paper were Haddock and collaborators Warren Francis at the University of Southern Denmark and Erik Thuesen at The Evergreen State College. The study was part of the DEEPC (Diversity, Ecology, and EcoPhysiology of Ctenophores) project—a National Science Foundation-supported collaboration to study ctenophore evolution.

Winnikoff and his coauthors studied 34 different species of ctenophores living at different water temperatures and depths. Their samples came mostly from MBARI cruises in Monterey Bay (cool, shallow water and cold, deep water), and Hawaii (warm, shallow water). A few were collected by friends traveling to Greenland and Norway (cold, shallow water).

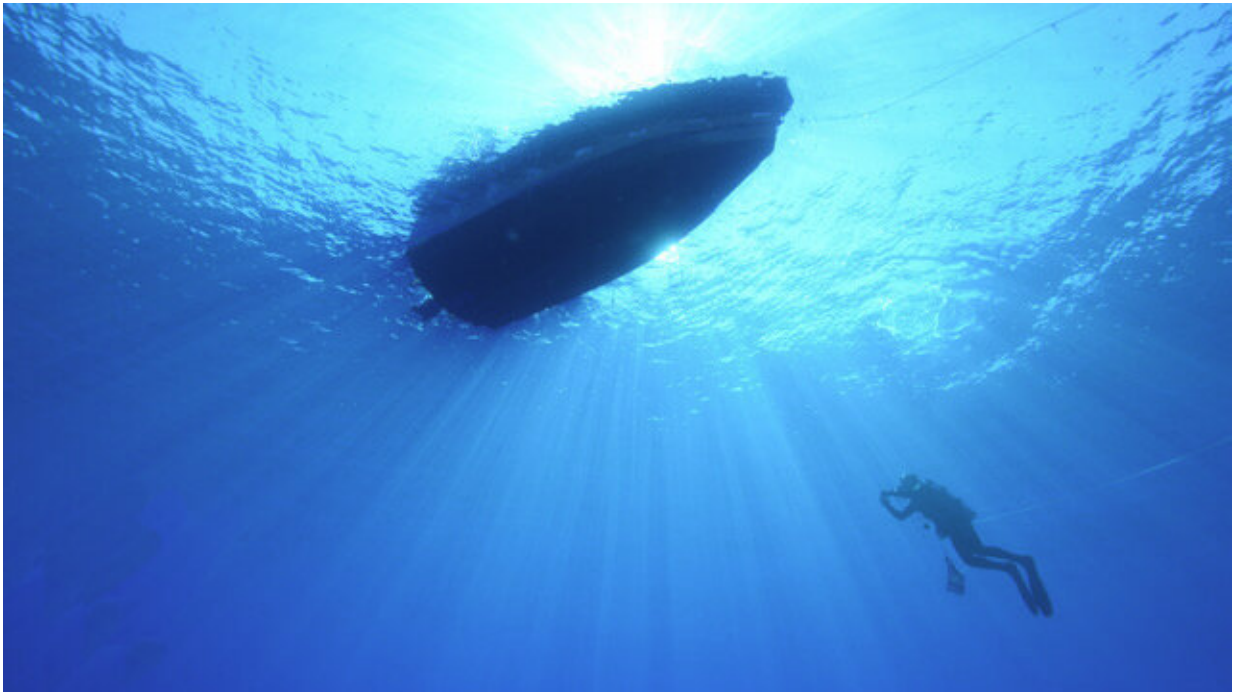
To compare these animals, Winnikoff and his coauthors looked at four key enzymes in the ctenophores' bodies. As Winnikoff explained, "Enzymes are like tiny molecular machines that convert one chemical into another. Many essential biological processes, like turning food into energy, involve 'assembly lines' made up of a series of different enzymes. One of our main goals is to figure out how certain [key enzymes](#) might behave under different temperatures and pressures."

"If you think of enzymes as little machines," Winnikoff continued, "then you could say we were focused on the individual parts that make up these machines, which are called [amino acids](#). More specifically, we were trying to figure out which amino acids are critical for life in the

low temperatures and high pressures of the deep sea."

However, it is extremely difficult to study enzymes inside of a living animal. For this reason, Winnikoff and his colleagues studied the ctenophores' enzymes by looking at their transcriptomes. "A transcriptome is the collection of blueprints that an organism uses to construct its molecular machines," Winnikoff explained.

Just as a blueprint might show all the parts in a particular machine, so the transcriptome includes genetic material that the organism uses to arrange each amino acid in an [enzyme](#). However, unlike a blueprint, the transcriptome does not tell scientists exactly how these parts fit together, nor what each part does.



Some of the ctenophores used in this study were collected during blue-water SCUBA dives near Hawaii. Credit: Steve Haddock © 2018 MBARI

Figuring out the function of each part (amino acid) is a huge challenge. Historically, trained scientists have manually looked through lists of sequences of amino acids and searched for patterns—for example, similarities between animals that live at similar depths.

As part of this research, Winnikoff developed [computer software](#) that attempts to do this automatically—finding patterns in the transcriptomes of ctenophores living at different water temperatures and depths. "This software helps us make educated guesses as to which of an enzyme's parts might be critical to making it work in each animal's normal habitat," Winnikoff explained.

"We were trying to answer questions like, 'Do distantly related ctenophores living in the same environment have the same genetic adaptations, and if so, what are they?'"

In fact, Winnikoff's software did a reasonable job at "predicting" which amino acids were likely to be related to differences in temperature and pressure. "Just getting plausible results is a big milestone," Winnikoff said, "even though the software remains a work in progress."

Winnikoff's model suggested that between five and 15 percent of the amino acids in each enzyme were critical for adaptation to different temperatures and pressures. It also suggested where within each enzyme these amino acids were most likely to be found.

But the model's predictions of critical amino acids are not the same as direct evidence. "This model really looks at correlations between each animal's transcriptome and its habitat," Winnikoff pointed out. "It doesn't prove that these amino acids are actually the ones conveying special properties.

"Eventually, with predictions that are reliable and consistent, we'll be

able to do lab tests to find out if these predictions are true," he said.

"First we'll need to create enzymes in which the critical amino acids are modified or missing. For example, we could modify the amino [acid](#) sequence from a shallow species by adding particular "deep" amino acids. Then we would use bacteria or yeast to produce large amounts of these experimental enzymes. Finally, in the lab, we can test how well the experimental enzymes perform at different pressures and temperatures.

"If our lab results show that the model predictions are correct, this would be really exciting," Winnikoff said. "We have lots of amazing data from next-generation DNA sequencing, but there isn't a lot of software to analyze and compare these data across diverse species. If we can reliably predict critical amino acids, we could use our model to make predictions about how other living things—not just ctenophores—adapt to their environment. In theory, we could even bio-engineer custom enzymes to work under extreme temperatures and pressures—something that would be very useful in an industrial setting."

More information: J R Winnikoff et al. Combing Transcriptomes for Secrets of Deep-Sea Survival: Environmental Diversity Drives Patterns of Protein Evolution, *Integrative and Comparative Biology* (2019). [DOI: 10.1093/icb/icz063](https://doi.org/10.1093/icb/icz063)

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