

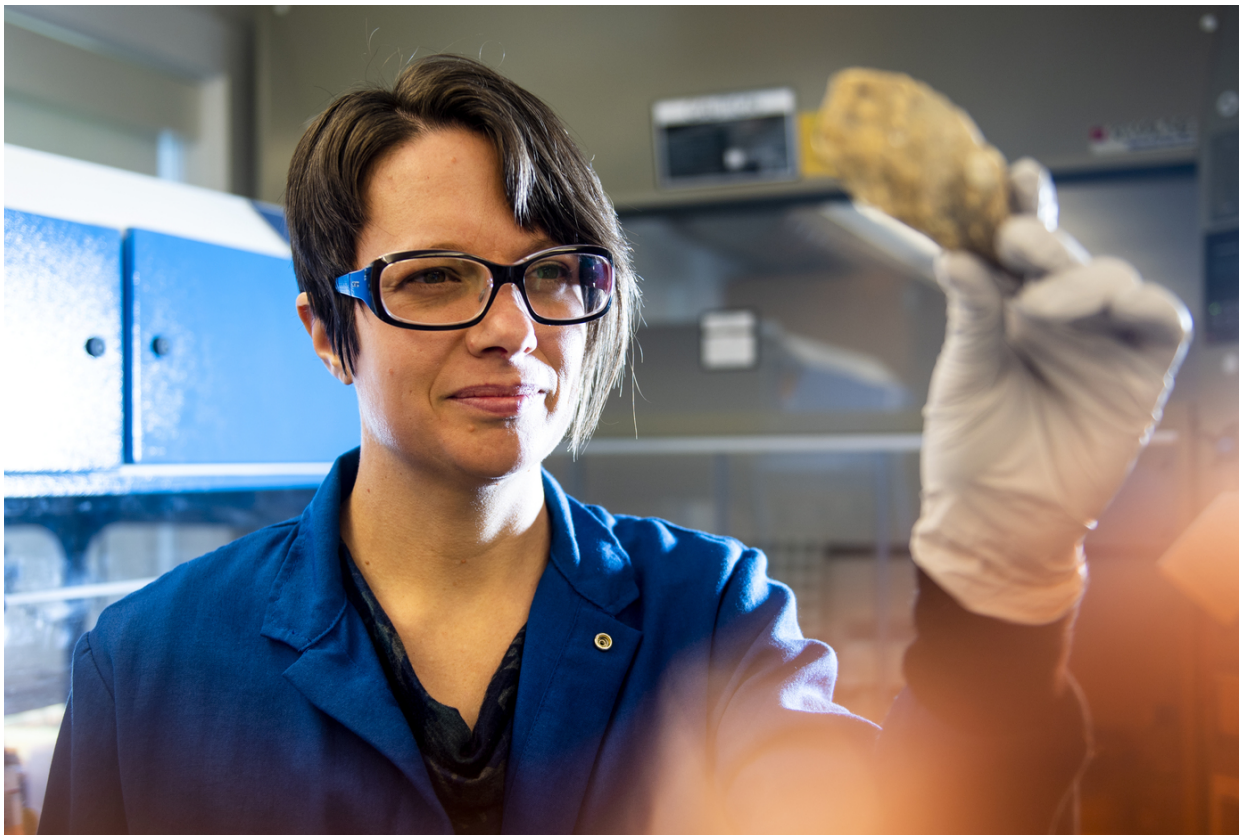
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News

The Lotterhos Lab is predicting species' biodiversity, starting with oysters.

BY KIRAN JOHNSON



Katie Lotterhos, associate professor in marine and environmental Sciences, poses for a portrait in Nahant on Sept. 19, 2019. Photo by Ruby Wallau/Northeastern University

Climate change is altering ecosystems, and organisms will have to adapt. Temperature-sensitive species, like cod and pollock, are shifting their habitats to colder waters. Other species have changed their behaviors, like humpback and fin whales, which have adjusted their feeding patterns because of diminished food supplies. And some species are quite literally adapting, in the evolutionary sense: among them, oysters.

Katie Lotterhos, a Northeastern University associate professor who conducts research at the Northeastern University Marine Science Center's Lotterhos Lab, is a genomic forecaster. Her team uses simulations to pair different combinations of oysters' genetics with various environmental conditions in hopes of predicting how they will adapt to climate change.

"My work thinks about how species have evolved and adapted to the climate in the past and how that evolution either sets them up for success or to be less successful under future climate," says Lotterhos.

She's challenging the traditional models used by evolutionary biologists to predict how organisms adapt to their environment on the genetic level. A common methodology is genotype-environment association (GEA). As an aspect of an environment — like temperature or salinity in the ocean — changes throughout the environment, GEA assumes that the frequency of a single gene responsible for an organism's ability to tolerate that aspect of the environment will rise or fall within the population accordingly. But Lotterhos' lab has found that there's more going on. According to her research, multiple genes can be responsible for a single trait, and inversely, one gene can affect multiple traits. This means that organisms don't adapt to each of the changing factors in their environment independently.

She has also found that GEA is not the best methodology for the era of climate change, because multiple environmental factors are increasingly changing across different geographic spaces. This means organisms have to adapt to more than one changing condition at once. Better methodology could help scientists predict how climate change will affect ecosystems around the world — and how oysters, or any species, can survive a new climate reality.

Oysters, a case study

In the Chesapeake Bay, salinity gradually increases from the inner bay to the outer bay. Along the bay, oysters have adapted to this range of salinity levels. Those in the saltier outer bay don't survive as well in the lower-salinity inner bay because they are adapted to higher-salinity conditions. The reverse applies to oysters on the inner bay.

Salinity tolerance is a trait — like an organism's color or heat tolerance — and whether an oyster has this trait or not is determined by their genes. According to the traditional GEA model, as a scientist gathers data from the inner bay to the saltier outer bay, they should find a higher and higher frequency of oysters with the gene for salinity tolerance. In science jargon, how the frequency of the gene changes across a geographical range is called a “cline.”

But Lotterhos's simulations found something far more complex.

In her 2023 [study](#), published in the Proceedings of the National Academy of Sciences, Lotterhos used simulations to predict the impact of salinity changes on an oyster population living in an estuary. The modeled environment had outer coast sites and inner estuary sites, and the model showed how the frequency of genes appearing in the oysters adapted over time.

“I didn't find the patterns that you might expect, where every [population] had the same genetic way of adapting to a low salinity environment,” she says. Multiple different genes could be responsible for the low salinity tolerance trait.

It turns out that within the oyster genome, which is the full set of its genes, many genes can contribute to something like low salinity tolerance — including genes that also focus on other physical traits.

When many different genes underlie the traits related to salinity tolerance, different patterns of the frequency of genes “go up and down” in oysters that are all living along the same temperature gradient.

“You can get these very complicated patterns of adaptation when the genetic basis of the trait is complex,” says Lotterhos.

The process is complex enough when looking at one environmental factor, such as temperature, but climate change is affecting many factors all at once. Lotterhos explains that “along a temperature gradient,” like the one found in the Chesapeake Bay, “you may have differences in salinity or disease pressure.” Because of this, organisms have to adapt to multiple changing conditions at a time. This idea was central to the study.

The Lotterhos Lab used various simulations to understand the patterns of evolution that occur in changing environments. In another one of the study's simulations, Lotterhos watched how trees adapt to six environments at once. The varying environments were characterized by spatial variation in temperature, moisture level and elevation.

“We basically plug in things like the size of the genome and the mutation rate and the carrying capacity,” which refers to how many individuals an environment can support, she says.

Then, Lotterhos watches as evolution happens — on her computer. What comes out of the simulation are the whole genomes of these individuals. They can then look at how the population at one location with a certain set of environmental parameters compares to the population at a different location with a different environment.

She says that the main finding of the study is that the patterns found at the trait level in an environment — for example, a pattern of increasing salinity tolerance — don’t necessarily have to match the patterns seen at the genetic level.

“GEA methods assume that there’s this simple linear pattern” between a gene and an environment, Lotterhos explains. But GEA is limited because these associations don’t always evolve as obvious patterns, she says. Lotterhos’ lab is developing new methods that are needed to discern the patterns that GEA can’t.

“An area that a lot of climate scientists have called for to be incorporated into these models is genetic diversity within species,” Lotterhos adds. So, she has taken on the task. This is an emerging field called “genomic forecasting.”

Lotterhos hopes that these forecasting models will eventually be applied to restoration and management scenarios to understand what genotypes of a species should be put in a certain location and will be best suited for future changes in climate that occur there.

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