

Researchers use DNA in seawater to monitor scallop reproduction

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Credit: University of Maine

Researchers from the University of Maine and Bigelow Laboratory for Ocean Sciences have developed a method for studying the timing of scallop spawning by analyzing the environmental DNA found in water samples.

The newly published study provides a tool for managing wild and farmed

shellfish populations, and it demonstrates the promise of emerging eDNA approaches for monitoring the presence and activities of all marine life.

"Knowing when and where [marine organisms](#) spawn is important to understanding their population growth and lifecycle. Usually, monitoring spawning events in [marine invertebrates](#), including sea scallops, can be a difficult task, so being able to track these events by sampling seawater could be hugely beneficial for marine species management and conservation practices," says lead author Skylar Bayer, a UMaine graduate who is now a postdoctoral research associate at NOAA's Northeast Fisheries Science Center's Milford Laboratory in Connecticut.

Many marine organisms are broadcast spawners, meaning that to reproduce, they release tiny reproductive cells, sperm and eggs, or gametes, into the water. Detection in real time of these releases, or spawning events, is difficult, and it is nearly impossible to trace the gametes in [water samples](#) back to the species that released them using traditional microscopy methods, according to the researchers.

The DNA-based quantitative polymerase chain reaction (PCR) approaches used in the project avoided the historical hurdles by analyzing seawater samples for segments of DNA specific to the Atlantic sea scallop, *Placopecten magellanicus*. This allowed the researchers to acquire data about the presence and magnitude of spawning events.

"Quantitative PCR is an incredibly sensitive method that lets us detect specific organisms, even when there might be just a few copies of their genes in a water sample," says Pete Countway, a senior research scientist at Bigelow Laboratory and a co-author of the study. "It's very exciting because this same approach could be applied to virtually any broadcast spawner."

Countway specializes in using molecular and genomic techniques to study the ecology of microscopic marine life, and the project applied those methods from microbiology to larger, commercially valuable species.

The work built on two decades of research into the reproductive ecology of broadcast spawners by co-author Rick Wahle, a research professor in the School of Marine Sciences and director of the Lobster Institute at UMaine.

"This project is a first; it now demonstrates the possibility of understanding spawning events in populations of broadcast spawners—including clams, corals and codfish—in nearly real time, a task that has historically taken weeks to assess with great effort, and only in hindsight," Wahle says.

"Developing an eDNA toolkit to quantify broadcast spawning events of the sea scallop *Placopecten magellanicus*: moving beyond fertilization assays" was published in the journal *Marine Ecology Progress Series (MEPS)*.

More information: SR Bayer et al. Developing an eDNA toolkit to quantify broadcast spawning events of the sea scallop *Placopecten magellanicus*: moving beyond fertilization assays, *Marine Ecology Progress Series* (2019). [DOI: 10.3354/meps12991](https://doi.org/10.3354/meps12991)

Provided by University of Maine

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