

Comparing deep-sea sponges of the species *Geodia barretti* from different locations in the North Atlantic

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The study of genetic and geographic structures of populations for poorly studied species is not exactly straightforward. It is difficult to accurately compare populations of a species from which no genetic data is available.

So, is there a way of comparing populations of such as species?

There is one possibility, which is by using genetic markers called “Exon-Primed Intron-Crossing” (EPIC) markers. These markers, which are first designed for well-studied species, find a specific piece of DNA that all individuals of a species have. So, by using the markers we can, for example, take the same DNA fragment from several individuals that come from different locations. Then we translate the DNA fragments of these individuals and look at how different they are. This can give us a lot of information about the relationships within and between the populations of a species, as well as its history.

Since a lot of genetic information is conserved across different species, we can test these markers on a species that we barely know, and the probability of finding a corresponding DNA fragment can still be quite high.

EPIC markers could be very useful for different studies but they haven’t been extensively used since they are relatively new. In this project, the markers were tested on samples of the deep-sea sponge *Geodia barretti*. The sponges that were used came from different locations; from the Mediterranean Sea, to the coast of Norway, and all the way to the other side of the Atlantic, by the Eastern coast of Canada.

The markers were successful because we were able to compare DNA segments for most of the sponge samples, and we found that, genetically, there are some differences among the sponges. EPIC markers are potentially useful for more sponge population studies, as well as for other marine invertebrates that are not well known.

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