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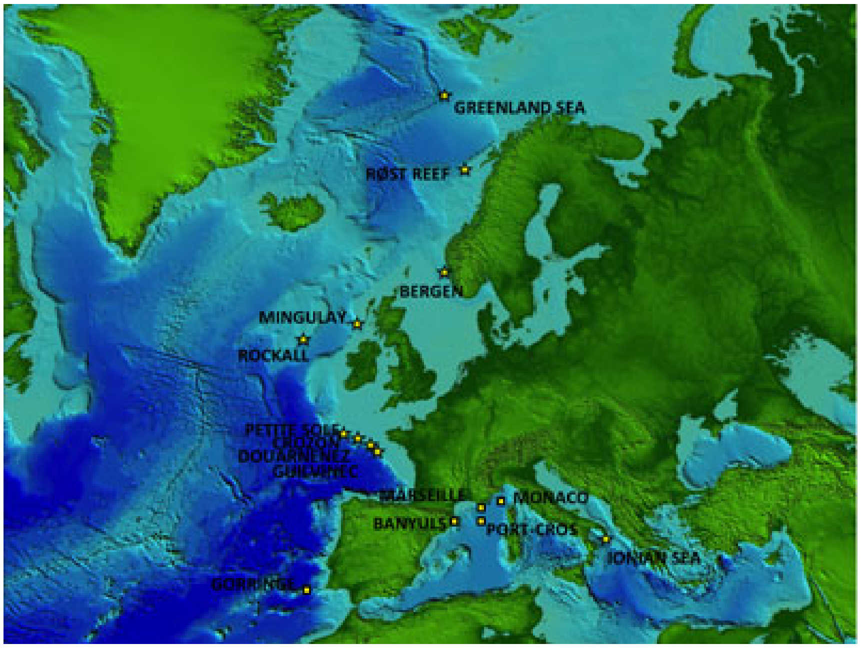
Different sponge species have highly specific, stable microbiomes

January 21 2014



This is a map displaying *Hexadella* sampling locations: deep-sea sites (star shape) and shallow-water sites (square shape). Credit: Map provided by the project Hotspot Ecosystems Research and Man's Impact on European Seas (HERMOINE).

The sea sponge is about as simple as an animal can get, but its associated bacterial community—its microbiome —is known to approach the complexity of the diverse microbiome in the human gut.

Now, scientists at the Marine Biological Laboratory (MBL) have shown that different species of *Hexadella* sponges each have a highly specific and stable microbiome, not only in terms of the most abundant members of the associated microbial community, but the rare members as well. They published their results recently in the *International Society for Microbial Ecology (ISME) Journal*.

"When we looked at what microbial community occurred in a species of sponge, we always found the same community, no matter where geographically and at which depth the sponge [lived]," says lead author Julie Reveillaud, a postdoctoral associate in the MBL's Bay Paul Center.

Reveillaud's team was interested in whether closely related sponge species display a higher degree of similarity in the composition of their microbiomes than do more distantly related sponge species. They found a weak correlation between the sponges' relatedness and their microbiomes, indicating *Hexadella* species did not inherit their entire microbiomes from their parents (vertical transmission), but also acquired microbes horizontally from the environment.

What's interesting, Reveillaud says, is while both horizontal and vertical transmission of microbes are occuring, the microbiomes were found to be highly specific to their sponge host species. That indicates that the microbes acquired horizontally are not just randomly selected from the environment and maintained. "There is a mechanism by which the sponge and the microbiome are specifically selecting each other," Reveillaud says.

Hexadella dedritifera (yellow) is sampled with the ROV Victor in the deep-sea reefs in Europe. Credit: Ifremer, France.

Using "ultra-deep" DNA sequencing technology to obtain very fine-grained pictures of the microbiomes' compositions, the team compared seven sponge species from the genus *Hexadella* whose habitats range from the Mediterranean Sea to the Greenland Sea, and who live at depths ranging from 15 to 1,000 meters. It was exciting to discover the high degree to which the microbiomes are specific to their hosts across such a wide geographic distribution, Reveillaud says.

Several other scientists in the Bay Paul Center collaborated on the study, including Loïs Maignien, A. Murat Eren, Julie Huber, and Mitchell Sogin.

More information: Reveillaud J, Maignien L, Eren AM, Huber JA, Apprill A, Sogin ML and Vanreusel A (2014) Host-specificity among abundant and rare taxa in the sponge microbiome. *ISME Journal*, advance online publication January 9; DOI: 10.1038/ismej.2013.227

Provided by Marine Biological Laboratory

Citation: Different sponge species have highly specific, stable microbiomes (2014, January 21) retrieved 23 April 2024 from
https://phys.org/news/2014-01-sponge-species-highly-specific-stable.html