Traces of diversity

Every litre of seawater is full of genetic material from all kinds of different organisms. Biologist Silke Laakmann and her team are pioneering techniques that use these DNA traces to determine the biodiversity of marine communities. This involves combining conventional methods of species identification with new genetic procedures.

Typical zooplankton found in the North Sea include copepods (top right), bristle worms (polychaetes, bottom right) and hydromedusae (left), a class of cnidaria. Many of the tiny organisms floating in the water are barely a millimetre long.

The procedure at the heart of the work of Laakmann and her five-member team is also very much on trend. “One key question is whether oyster larvae from the Borkum Reef Ground protected area move with the currents into other marine areas where they had not previously been restored,” explains Laakmann. As part of the project, which is funded by the Federal Ministry of Education and Research in the framework of the German Marine Research Alliance, the biologist and her team currently compile an eDNA archive for the North Sea, aimed at documenting the current status of biodiversity and the effects of future environmental changes.

Environmetal scientist Dr Kingsly Chuo Beng, a postdoctoral researcher in the focus group and an expert in eDNA research, manages the corresponding work package. The researchers in Laakmann’s team have been laying the groundwork for this over the past four years: “Recently, a shift has taken place in biodiversity research, from what you might call the classical morphological methods of species identification to molecular ones,” the researcher explains. From microscope to genes, in other words. Her own training started in the conventional methods. “During my doctoral studies at the University of Bremen and my time as a postdoc at
the samples for further analysis. Still on board, Kingsly Chuo Beng prepares for the sorting and identification of the zooplankton in the North Sea and the Baltic, but also analyses the zooplankton in Patagonia, the Arctic and South Africa. They have collected more than 3,000 samples which will be preserved for further studies at the HIFMB.

To obtain an overview of biodiversity levels, the scientists generally use three different methods. They still collect plankton in the traditional way using long, thin nets. This often brings on board a brownish, flaky mass of sea animals. A colleague at AWI, Astrid Corning, a comparison with conventional identification under the microscope. “I think it is important to make a connection with the organisms I study.”

“When the vast assemblage of genetic material in an environmental sample is analysed in parallel – a process that gives rise to thousands of different DNA sequences – this is known as “metabarcoding”. In our samples we have millions of these gene snippets from all sorts of organisms. After sequencing we compare the gene sequences with the database entries, so that in the end we have a list of species or groups,” Laakmann explains. Over the past four years the researchers have developed a special toolkit for dealing with the eDNA. “We were interested in questions such as: How much water do we need in order to capture as many species as possible in one area? How often do we need to take samples? What should the filter look like? What databases should we use?” the biologist notes.

The molecular biology methods used need in order to capture as many species as possible in one area? How often do we need to take samples? What should the filter look like? What databases should we use?” the biologist notes. The team also studied threshold values for the CREATE project they have already successfully identified the genetic material of the oyster larvae in water samples.

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Every now and then the researchers come across what are known as cryptic species – species that are genetically new but externally resemble other, already known species. Moreover, the genetic method increases the likelihood of finding rare or endangered species, including marine mammals. “We find more species than we could previously identify,” Laakmann stresses. All of these factors show the huge potential of eDNA in opening up previously hidden areas of biodiversity.

When it comes to the larvae found in the zooplankton samples of benthic organisms and fish, a whole new world is revealed. With conventional methods these minuscule organisms can only often be roughly assigned to the different animal groups. Metabarcoding, however, allows researchers to pinpoint what species many of these larvae belong to – provided they have already inventoried in a database. “Now, for the first time, we can identify which larvae are living in the water at what time of the year. This allows us to draw conclusions about their distribution and reproductive cycles,” Laakmann comments. Particularly in late spring and summer, when many organisms reproduce, eDNA analysis can detect up to four times as many species in zooplankton samples than with conventional methods.

The larvae of the European oyster are also almost impossible to identify under the microscope. At the free-swimming stage, when they are less than a millimetre in size, they resemble small blobs that move using lobe-like extensions, much like all other bivalve larvae. Laakmann and her team are nevertheless confident that they will be able to uncover the drift of the mollusc offspring in the vast expanses of the North Sea. In preparatory studies for the CREATE project they have already

Laakmann and her team use environmental DNA to research marine biodiversity.

Conventional identification methods are important to allow for a comparison with genetic methods.

At sea (here with the research vessel Heincke in the North Sea), the team collects water samples containing environmental DNA.

Still on board, Kingsly Chuo Beng prepares the samples for further analysis.