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PRESS RELEASE

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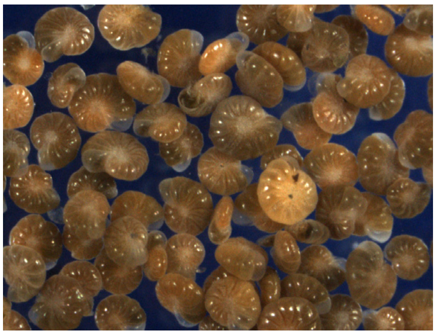
USING GENETICS TO MEASURE THE ENVIRONMENTAL IMPACT OF SALMON FARMING

Researchers at the University of Geneva (UNIGE), Switzerland, demonstrate that DNA bar-coding is a new and efficient tool for the large-scale identification of bioindicator species



0.3 mm foraminifera made up of a single cell surrounded by a limestone shell.

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Determining species diversity makes it possible to estimate the impact of human activity on marine ecosystems accurately. The environmental effects of salmon farming have been assessed, until now, by visually identifying the animals living in the marine sediment samples collected at specific distances from farming sites. A team led by Jan Pawlowski, professor at the Faculty of Science of the University of Geneva (UNIGE), Switzerland, analysed this type of sediment using a technique known as "DNA barcoding" that targets certain micro-organisms. Their research, which has been published in the *Molecular Ecology Resources* journal, reveals the potential of this new genomic tool for detecting environmental changes as accurately as with traditional methods – but more quickly and at lower cost.

Salmon farming is one of the most widespread activities in marine aquaculture. It has a considerable impact on the environment, which is largely due to three factors: the accumulation of food waste and faecal matter; the toxicity caused by the chemicals employed to clean the cages; and the drugs that are used.

The impact of such farms on the coastal environment is traditionally assessed by monitoring some of the small species that live in the sediments beneath the cages. The visual identification of these animals under a microscope is time consuming and extremely expensive. It also requires highly-trained taxonomy specialists, which renders the method unsuitable for large-scale use. But, as Jan Pawlowski, professor in the Department of Genetics and Evolution at UNIGE, explains: "It is now possible to address this problem using sophisticated tools that analyse the DNA and RNA extracted from sediment samples."

Genetic barcodes...

Working alongside researchers from the Scottish Association of Marine Sciences (UK) and the University of Aarhus (Denmark), Pawlowski collected sediment samples at specific distances from two salmon farms in the heart of the Scottish fjords. "We used genetic barcodes that recognise specific fragments of DNA and RNA extracted from the sediment samples," explains researcher Franck Lejzerowicz, a PhD student in the professor's team: "These 'genetic hooks' consist of DNA sequences that vary between species but remain stable within a given species."

The DNA barcodes used make it possible to identify the different foraminiferal species that are present in the sediments. These single-celled micro-organisms, which have a great diversity, are already recognised environmental bioindicators. As a result, the geneticists were able to process a large number of samples using high-throughput DNA sequencing. “Our study revealed large variations between foraminiferal species collected near farms and those from remote sites. In addition, species diversity diminishes on sites affected by the farms.”

... For monitoring the quality of the environment

This type of highly-accurate ecological analysis allowed to establish a correlation between species richness and distance from the cages, a correlation that is even more pronounced if the farm is only stirred by weak sea currents. The same type of correlation was also established based on the degree of oxygenation of the sediments. As Jan Pawlowski states: “The vast amount of organic compounds on the farming sites can even sometimes generate anoxic sediments, which makes it impossible for most species to survive.” The biologists were also surprised to discover a new species of foraminifera, which could serve as a bioindicator of organic enrichment.

This technology, known as “metabarcoding”, is spreading rapidly, and can be used to supply information on the overall diversity of the micro-organisms found in all samples. The method is suitable for large-scale tests because it is much quicker, more reliable and easier to standardise than the processes that are used at present. This study is one of the first attempts to use environmental genomics as a tool for assessing the impact of industries such as marine aquaculture or offshore drilling.

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