

# Evidence

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# A DNA based monitoring method for fish in lakes Project summary SC140018

This project develops a new DNA method that could revolutionise the way we monitor fish in lakes. It has been shown to detect 14 of 16 key fish species known to be present in Lake Windermere, compared to just four species found by conventional surveys. The work is part of a wider programme of research by UK agencies to develop DNA based methods for environmental monitoring and decision making.

Fish are sensitive indicators of water quality and their assessment is an important part of water management. In England, Wales and Scotland regular lake fish monitoring is not feasible with existing tools and resources. Netting can capture all the fish in an area, but it is costly and can injure or kill fish. We need a method that is cost effective and doesn't harm the fish.

This project tested a new approach to assess both the type and numbers of fish present in three large lakes in Cumbria (Windermere, Bassenthwaite and Derwentwater). The approach uses environmental DNA (eDNA) - the DNA that fish leave behind in the water from their skin, urine or faeces. This eDNA can be used to give us information on fish living in the lake. New technology allows all the DNA in a water sample to be sequenced and identified. This multi species identification method is rapid and sensitive and has real potential to change the way we carry out our ecological assessments.

The results show that the eDNA method is extremely sensitive for detecting different fish species. As in Lake Windermere, our eDNA analysis outperformed recent gill-net surveys in Bassenthwaite Lake and Derwentwater. There was also good agreement between estimates of rank abundance (how common or rare a fish species is) of fish species from eDNA sampling and recent net sampling and from expert judgement based on long-term knowledge of the lakes.

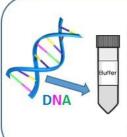
The analyses indicate that 10–20 samples may be adequate to show which species are present in a lake. More comprehensive sampling may be needed to estimate how many fish are living in the lake. We also found that sampling from the shore can be a good alternative to sampling from the whole lake.



Organisms shed cell debris into their surrounding environment creating a "soup" of floating eDNA.



Floating eDNA from all different organisms in the lake is collected and filtered. Many samples are taken from the shoreline and open water.



DNA from all the organisms in the sample is extracted and then the fish DNA is separated, amplified (make copies of it so there is enough to analyse) and sent for DNA sequencing on a next generation sequencer.



Thousands of DNA sequences are analysed and compared against a reference database to determine their identity. The relative abundance of the different types of fish is then calculated.

Figure 1 Simplified overview of eDNA metabarcoding. Steps to determining the types of fish and number of fish in a lake sample

This is good because sampling from the shore is easier and cheaper than using boats to sample from the whole lake. For example, 12 species were detected in just 6 samples collected along a short stretch of shoreline in Lake Windermere. However, deep water species, such as Arctic charr, were only detected during deep water sampling, indicating that shoreline sampling might be less effective for some species in deeper lakes.

Using eDNA is relatively new, and so far much of the research has focused on developing methods to assess the presence or absence of single species. This project has moved beyond that to provide the first demonstration of using eDNA to determine the identity of many different fish species at once and provide indications of their relative abundance in a lake in a non-destructive way.

The next step will be to demonstrate that the findings can be repeated at different times of the year and that the method has wider applicability to a greater range of water bodies, such as those with varied chemical and physical properties. This next step will be lead by The Scottish Environment Protection Agency (SEPA) and will include the assessment of Scottish lochs which are more nutrient poor and where fish (and eDNA) are likely to be found in much lower numbers as well as repeated assessment of Lake Windermere. This summary relates to information from project SC140018, reported in detail in the following output(s):

## Report: SC140018/R

**Title:** eDNA-based metabarcoding as a monitoring tool for fish in large lakes

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**Research Contractor:** University of Hull (Evolutionary Biology Group) and Centre for Ecology and Hydrology

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