How DNA analysis of our rivers and lakes can reveal new secrets about their biodiversity

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Freshwater ecosystems are the lifeblood of the natural world, yet they are facing a silent crisis. A [2022 report](#) by the World Wildlife Fund revealed a staggering 83% decline in global freshwater vertebrate populations since 1970, a rate far exceeding that of any other habitat.

The level of degradation to nature is alarming, but ecosystems are complicated, as are the effects of human activity. So, the story is often more nuanced.

Our research shows how analyzing environmental DNA (eDNA)—the DNA left behind by organisms in life and death—could unlock the secrets hidden within freshwater streams, rivers and lakes. This offers hope for a more efficient monitoring of these vital ecosystems.

While fish and birds usually grab the spotlight, freshwater biodiversity is a hidden metropolis teeming with lesser-known residents. Macroinvertebrates such as mayflies and midges, visible to the naked eye, play a vital role in healthy ecosystems. They have been monitored for decades and can give us a more representative view of how freshwater habitats are responding to human pressures.

Different parts of the world also experience varying levels of threat from human activity. Across Europe, for example, the last century has seen great improvements in river water quality—largely due to better sanitation, de-industrialization and improved regulation, culminating in the recovery of macroinvertebrate biodiversity.

But this good news only goes so far. Since 2010, improvements in freshwater biodiversity have plateaued. Meanwhile, the environmental pressures of old are being replaced by new pressures ranging from climate change to emerging pollutants released from archaic sewage systems.

Arguably, understanding the health of freshwater ecosystems has never been more important. To do this effectively, widespread monitoring of which species are present is required. This is only possible by integrating new techniques—including the analysis of eDNA, which can come from a range of sources including poo, mucus and bits of tissue—alongside traditional monitoring programs.

Current methods of monitoring biodiversity

The bulk of current freshwater biodiversity monitoring focuses on a relatively narrow group of animals—fish and macroinvertebrates.

Fish are usually monitored by "electrofishing," where an electric current is passed through the water that temporarily stuns fish. Whichever fish float to the surface are identified and counted.

Macroinvertebrates are largely collected using "kick-net sampling," where a person stands in a river, kicks up the sediment, then catches whatever floats downstream in a net.

Both of these methods have limitations. With electrofishing, keeping the current consistent between sample runs can be difficult, due to differences in conductivity between rivers. Larger fish are also more susceptible to shock so there is a potential to miss smaller fish, which can introduce biases.

With kick-net sampling, certain river substrates can yield better results, while some species are better at avoiding or slipping through the net.

In both methods, some sites may not be amenable at all. Standardization between sites can be difficult, so results can be dependent on the experience of the sampler. These approaches are also time-consuming, labor-heavy and, above all, destructive.

Environmental DNA

On the other hand, eDNA can be filtered from a water sample, extracted from the filter, analyzed for the taxonomic group of interest, then sequenced in a process called "metabarcoding." This allows us to cross-reference results with a database, leading to the identification of the organism that the DNA came from.

There are many advantages to using eDNA. The work is easily standardized and automated. Sample collection is easy and does not require expertise, allowing for the involvement of citizen scientists. A far broader range of organisms can be identified, including a multitude of smaller organisms. And crucially, it leaves the environment undisturbed.

But eDNA analysis isn't without its limitations. Unlike traditional methods that might count individual fish, eDNA can't tell a juvenile salmon from a spawning adult. It also lacks the rich, multi-decade datasets that have been built up using traditional methods of analysis. This can make it difficult to use eDNA findings to inform current conservation policies.

There has also been concern that, in rivers, you are simply detecting the eDNA of organisms transported from many kilometers upstream—preventing you from understanding where, in an entire river catchment, a species signal has come from. This would render eDNA a poor tool for understanding biodiversity change.

However, our recent study shows this is not the case. We took 798 water samples at 14 sites and 19 time points over a year from the River Conwy in north Wales. We also took samples from rivers across England, Switzerland and the US. Our research shows that DNA shed by different creatures in the river doesn't travel far. Most becomes too faint to detect just one kilometer downstream.

This is great news—since each sample of eDNA taken in a river is representative of a relatively small stretch, this allows us to detect changes in the distribution of organisms across a river catchment. With this information, researchers can begin to unpick what is causing a decline in biodiversity even in local areas of a freshwater ecosystem, and then identify how to stop it.

As eDNA analysis gains traction, scientists like us are working to bridge the gap between research and real-world conservation. Initiatives such as the UKDNA Working Group foster collaboration, allowing us to share knowledge with government agencies and environmental stakeholders. By building comprehensive datasets that capture biodiversity changes across space and time, we can unlock secrets held within eDNA.

This newfound knowledge holds the key to crafting effective management solutions, and should ensure a brighter future for our precious freshwater ecosystems.

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