

# Sequencing billions of creatures between trillions of grains of sand

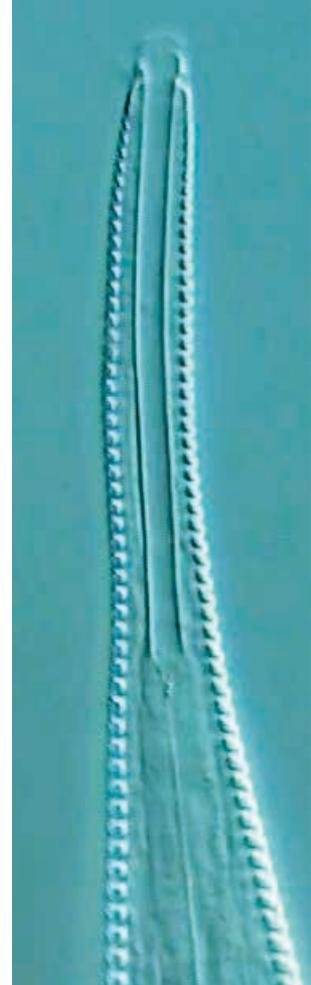
Scientists have tended to assume that microbes are so small and move so easily from place to place that they are randomly spread about the planet, rather than distributed according to the kind of ecological rules that govern bigger organisms. By using DNA sequencing, Simon Creer and colleagues have revealed that's not so – these tiny creatures aren't so different to the larger life-forms we see every day.

**W**e live in a period sometimes called the Anthropocene, and we are changing the environment faster and more profoundly than ever before. Scientists are increasingly focusing on the relationships between biodiversity and ecosystem function, since we rely on ecosystems for all of the benefits they provide. These 'ecosystem services' include food from the marine, terrestrial and freshwater environments.

Microbes play a fundamental role at the base of all food chains, supporting biogeochemical and nutrient recycling. If living things didn't decompose after they die, the ocean floor would be littered with detritus, your compost heap would no longer work and freshwater ecosystems would be clogged with organic matter. Luckily for us, an army of microbial species of incredible diversity and mind-boggling complexity perform such



jobs, helping energy flow through cycles of life and death. Bacteria and fungi are among the key groups that break down organic matter, with microscopic animals and microbes known as protists forming the next link up in the food chain. Yet microbes are so diverse, and the number of taxonomists who can actually identify them is so small, that even specifying the different organisms present in an environment is a major bottleneck. Before we can even start thinking about investigating how biodiversity affects the whole ecosystem's functioning, we need to know what lives there.



My interest in this was first ignited when I met a group of experts on nematode worms – at the International Seabed Authority in Kingston, Jamaica, 2005. We were there to discuss new ways of identifying microscopic communities in the world's oceans, and the meeting coincided with the publication of the first 'next-generation sequencing' genome paper in *Nature*.

We've long known that it is possible to use small variable stretches of genomic DNA that are shared by many species like 'barcodes' to identify particular species. But this was inefficient for large numbers of individuals, because there are so many of them and sequencing one creature at a time is costly and time consuming. In the bar afterwards Professor Kelley Thomas, a biologist from the University of New Hampshire, pointed out that we could harness the power of the new generation of DNA sequencers to sequence all the barcodes from a whole community simultaneously rather than looking at one individual at a time. The rest, as they say, is history.

Over the past decade, these techniques have transformed how we assess microbial biodiversity. They are now not just routinely

used on microbes, they have also been used on larger animals, plants, fungi and even whole food webs.

Part of my interest in the field lay in a desire to understand the distribution patterns of microscopic eukaryotes (organisms whose cells have complex internal structure) and how these patterns arose. Until we know this, it is hard to say how they will respond to climate and environmental change.

In particular, it has been predicted that species below a certain size weren't confined to particular geographical ranges. If this was true, studying microscopic communities in the context of climate change would become less relevant – organisms found all over the globe are less likely to be harmed by changes in temperature than ones that depend on particular local conditions.

### **Underestimating diversity**

It also became clear to me that previous researchers often lumped hugely diverse groups of living things together under subheadings like 'macroinvertebrates', or 'meiofaunal organisms' in ecological studies. Meiofauna are small animals up to about half a millimetre long. Most belong to three families – nematodes, flatworms and arthropods.

Sixty per cent of animal groups include meiofauna that live in the sand or mud of the seabed, and there are an awful lot of them. Nematodes alone can be present in abundances up to a hundred million individuals per square metre.

Nevertheless, because we were lumping different communities together or only focusing on specific animal groups within them, we couldn't understand how different groups of creatures respond to different ecological and environmental processes. By using DNA sequencing to discover all the groups and species that are present in a particular place instead of

trying to identify individuals under the microscope, we can now track the distribution of different groups and species in both space and time. This is something that's never been possible before, and is particularly cool!

Sequencing shows that marine microscopic animals are impressively diverse, with definable geographical distributions but also recognisable ecological preferences. This dispels the theory that these sorts of smaller creatures are distributed widely and lack biogeographical boundaries.

This in turn suggests that hidden microscopic communities are likely to be affected by environmental change, just as we see happening above the ground. Academics worry about how climate change may trigger local extinctions and biological invasions, with serious ecological consequences – how will this play out in microscopic communities?

Many assume that the microscopic world is so diverse, that it can withstand changes in composition. What we've learned through sequencing lets us study ecological change at relevant spatial scales. After all, it will be important to understand how resilient microscopic communities are to climate change, because these guys form the trophic links between true microbes and larger creatures in the ocean floor – about 70 per cent of the Earth's surface!

We have also found that certain groups, such as free-living predatory flatworms, are much more diverse than we'd thought. This suggests the way we've traditionally assessed marine benthic biodiversity largely ignores some of the key creatures higher up in food chains. In recent work with the UK Environment Agency in the Thames and Mersey estuaries (and in independent studies from Australia), we have also shown that different groups of microscopic life respond differently to environmental stresses, and that each estuary has its own distinctive microscopic community.

This is important for monitoring ecosystems' health. Not only are genetic approaches faster and cheaper than traditional methods, but they tell us more about the variety of life of microscopic communities and their ecological preferences. Microscopic animals are much more diverse than the bigger organisms that environmental agencies usually use to measure ecosystem health, so they should tell us much more about the status of whole ecosystems.

Further exciting developments in the field of molecular biodiversity assessment focus on the fact that many creatures leave traces of DNA in their environment. Many studies now show that directly sequencing all the DNA in filtered water taken from ponds, lakes, rivers, oceans (and even leeches!) can yield valuable insights into what lives in these habitats.

Combined with ever-developing sequencing technologies, we now hope to use environmentally derived DNA to link biodiversity to ecosystem processes and so understand the effects of change at the ecosystem scale. The next time you are by a river or lake, just think about how much eDNA may be flowing by – derived from the complex community of living things that live, eat, poo, moult and die in the water. It's quite amazing!

● Dr Simon Creer is a senior lecturer in the School of Biological Sciences at Bangor University.

Email: [s.creer@bangor.ac.uk](mailto:s.creer@bangor.ac.uk)

<http://mefgl.bangor.ac.uk/staff/si.php>