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DNA barcodes tag species

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Genetic sequence could give an instant biological identification.

Wouldn't it be great if every animal had an easy-to-read label, telling you to which species it belonged? Scientists are now one step closer to making this idea a reality, thanks to two studies showing that the DNA sequence of just one gene can tell very closely related species of birds and butterflies apart, and even flag up previously unrecognized ones.

Birds of closely related species can be differentiated using the DNA sequence of just one gene.

The concept is called DNA barcoding. And if it works, it could find numerous uses. When a foreign ship docks, for example, inspection services could automatically scan ballast water for nasty species that they are keen to keep out. Or researchers in remote locations could use a handheld scanner to get an instant species identification.

At the moment, identifying species is a laborious process, based on characteristics such as the shape of a beak or the colour of a wing. But with DNA barcoding, scientists simply work out 650 letters in the genetic sequence of a single gene, called cytochrome *c* oxidase I.

This gene tends to vary a lot between species. Proponents of the method believe it is so variable that most different species will have a characteristic code, but many researchers are more sceptical.

Birds and butterflies

To show the system can work, Paul Hebert of the University of Guelph, Canada, and his colleagues read and compared the DNA barcodes from museum specimens of 260 species of North American birds.

They found that birds in different species had very different barcodes, whereas birds within the same species did not. They also support suspicions that some of the birds fall into four new species, they write in the *Proceedings of the National Academy of Sciences*[1].

Working with a different team, Hebert focused on skipper butterflies in the forest of Costa Rica. The group analysed the DNA barcodes of over 480 specimens that had previously been grouped as one species (*Astraptes fulgerator*).

The barcodes fell into clear groups that suggested the butterflies belonged to ten distinct species. The researchers report in *PloS Biology* that the result matches known differences in their choice of foods and caterpillars[2].

DNA database

Researchers have used the genetic sequences of animals to help work out their evolutionary relationships for over two decades. But they use a variety of different genes, whereas barcoding focuses on just one.

The idea gained credence last year, when Hebert showed that DNA barcodes could tell apart almost 2,000 species[3]. Now a series of projects around the world is showing that the system works in different animal groups. Supporters ultimately aim to catalogue the DNA barcode of each species, with its name, in a central database.

Daniel Janzen at the University of Pennsylvania, Philadelphia, who collected the butterflies used in the recent study, is enthusiastic about DNA barcodes. To identify a species of caterpillar, he currently has to rear it until it transforms into a butterfly and then send it to an expert taxonomist. A DNA barcode would allow him to classify caterpillars on the spot, he says, and work out the "gazillion species that give taxonomists nightmares".

The system has two other advantages over traditional taxonomy. It can be used to identify species from only a fragment of tissue or shell. And if barcode scanners become available, they could be used by amateurs.

But some researchers have reservations, seeing barcodes as a threat to traditional taxonomy. And even supporters acknowledge that the system will struggle to distinguish species whose genetic sequence is extremely similar, such as ones that have only recently diverged from one another. "We have to be a little bit cynical about where it works and where it doesn't," says ecologist Craig Moritz at the University of California, Berkeley.

Moritz says that, in some cases, it may be necessary to analyse more than one gene to properly identify a species. "There's strong debate about whether one gene fits all," he says.

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References

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