

Taxonomy

All bar none?

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There may be more species on Earth than previously imagined

IT IS bad enough that the Earth may be experiencing the largest mass extinction since the dinosaurs died out. Almost as bad—at least for science—is that as many as 90% of those species are dying without ever having been recorded. However, a new, rapid method for classifying species may ameliorate the latter problem, and help researchers to get at the question of just how much is being lost.

DNA barcoding, a technique proposed last year by Paul Hebert of the University of Guelph, in Ontario, Canada, has just had its first big trials, and has passed them with flying colours. It works by examining a particular part of a particular gene that is found in all animal species. The gene in question is called cytochrome c oxidase I (COI). It is easy to study because every cell contains lots of copies of it in simple, easily isolated structures called mitochondria. By contrast, most genes are hidden away in a cell's nucleus, where they are much harder to get at. Mitochondrial genes also tend to mutate rapidly, so meaningful differences between species build up quickly. And by concentrating on a mere part of COI—a section which is 648 genetic “letters” long—Dr Hebert has simplified the process still further. It is this sequence that he refers to as the “barcode”. All members of a species would be expected to have similar barcodes, but those codes should differ from species to species.

The first trial, just published in *PLoS Biology*, an online journal, sought to establish that the results of genetic barcoding agree with those of traditional taxonomy—the labour-intensive process of classifying species by their physical characteristics. (The formal biological definition of a species is a group of individuals that breed together, to the exclusion of others, in the wild. But the practical definition is usually based on reliable differences in anatomy between such groups.) In the study, DNA samples from birds classified by traditional taxonomy into 260 species were subjected to the technique. In almost all cases, the two classifications agreed. But Dr Hebert's technique went further. It suggested that four of the traditional species are each made up of two closely related species, and should be split.

That observation presaged the second study, which explicitly addresses the question of such “cryptic species”. This study, just published in the *Proceedings of the National Academy of Sciences*, examined a butterfly called *Astrartes fulgerator*. At least, that is what the traditionalists call it—and have done so since 1775, when it was first classified. But there have, for a long time, been doubts about whether *Astrartes fulgerator* really is a single species. That is because although the adults look similar, the caterpillars vary quite a lot, and also seem to prefer different food plants.

Barcoding showed that these suspicions are well-founded. Ten sorts of barcode turned up, suggesting that *Astrartes fulgerator* actually consists of at least ten species—and that is only the

number from the part of north-western Costa Rica where the specimens tested came from. Since *Astrartes fulgerator* ranges from northern Argentina to the southern United States, there is probably quite a bit more variety to be found in this one "species" alone.

Put into widespread use, therefore, DNA barcoding could begin to settle basic questions such as how much diversity there actually is in the living world. At the moment, estimates for the number of multicellular species in existence range from 10m to 100m—hence the uncertainty about how fast they are becoming extinct. Barcoding might also let scientists identify hot spots of genetic diversity, and work to protect those areas first.

There are still some sceptics around. In a commentary published in the same issue of *PLoS Biology*, Craig Moritz and Carla Cicero, of the University of California, Berkeley, say the method will probably run into practical problems. Species which diverged recently might not show enough difference in their barcodes to be recognised as separate. And some species might not be detectable using only the COI gene. But Dr Hebert thinks these problems can be resolved. The pilot studies suggest that 96% of animal species can be identified precisely with his method. Even problem species could be classified approximately, and then handed over to traditional taxonomists for a final once-over.

Already the Canadian government has provided C\$5m (\$3.9m) to begin cataloguing the 10,000 most economically important fish, birds, mammals and agricultural pests. Meanwhile, in April, the Consortium for the Barcode of Life, a collaboration of natural history museums and herbaria, launched an international effort to build a comprehensive library of species' barcodes. The supermarket of life, it seems, is now open for business.