Science Show

on ABC Radio National

Genetic Barcoding

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Genetic barcoding is a new technology using a short DNA sequence from a gene found in all animals which can identify a species.

Hide Transcript

Transcript

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David Schindel: DNA bar coding is a technique, it's about two years old, it was developed by Paul Hebert, a Professor at the University of Guelph in Ontario and it's quite simply a technique that has the potential to be able to distinguish species, animal, plant species one from the other using a very short stretch of DNA. So it's kind of the opposite of a genome project where you get the entire genome of one species. This is trying to get the minimum necessary bit of gene sequence from *all* species necessary to distinguish each other. In that sense we use the metaphor of the bar code, it's a unique identifier for each species.

Robyn Williams: How short can it be without confusion and overlap?

David Schindel: Well, so far the most successful gene region that's being used among animals, higher animals is called Cytochrome c oxidase 1, or some people call it c ox 1 and it's 650 base pairs long. But I want to emphasise *not all* of those base pairs are distinguishing characters within that 650 base pair stretch, there's probably a much smaller sub set which is sufficient to distinguish species one from the other.

Robyn Williams: And I presume from that that most of the higher organisms have got this. Do the lower organisms have it as well?

David Schindel: Not *all* lower organisms. Some microbes, aerobic microbes have mitochondria because they generate packets of energy the way higher organisms do, and they have the Cytochrome c oxidase 1 but many microbes don't and plants *do have* this gene in their mitochondria but it turns out to evolve much more slowly than it does in animals so it's not a useful DNA bar code region. So botanists have worked out several other regions, which they think are going to be effective as a bar code.

Robyn Williams: So when you come back from say, Costa Rico with a new creature and you've got a cell, how long does it take you to get from the bar code to an identification in the lab?

David Schindel: Well, the technique for obtaining the bar code is only a few hours now, in a high through put lab it takes four hours roughly to extract the DNA, purify it, amplify it - that is, make extra copies of it, and then run it through a sequencer. But then to *identify* you have to run that sequence against a reference library and we're in the process of building that reference library. So if you know, for example, that you're dealing with a particular genus of butterfly and all the species have been sequenced and those sequences are in the reference library, then it's really only a six hour process.

Robyn Williams: Well that's very nice, but in the old days clever people would say at a distance of, say 100 metres, they could recognise what it was and most of the time it would be right. In what circumstances would you want to have your molecular detective work come into play?

David Schindel: Well there's two reasons why your statement doesn't quite hold true. First, not anyone can identify a butterfly at a 100 metres, there are at most a handful of experts who really can tell the difference. So that creates a bottleneck. The taxonomy knowledge sources are quite few and they are not distributed all around the world. So, you know, where's a lepidopterist when you need them?

Second, we're discovering that there's a lot of hidden genetic variation, so what we thought was a species might turn out to be a species complex, so DNA bar coding is useful not just for assigning unknown specimens but it's a critical tool in the work of discovering, describing, analysing, deciding which species are which. So in that sense it really opens up that bottleneck, you no longer need to have the world's expert right with you in Costa Rico looking at that butterfly but a lab can extract the DNA, analyse it and run it against the data base and you don't need to be a taxonomic specialist in that group to be able to make an identification. So that's a real breakthrough.

Robyn Williams: And David, what's your role here in Washington DC on that quest?

David Schindel: Well, the Smithsonian has decided that it wants to host a consortium secretariat - this is really quite an extraordinary new kind of venture. The bar code initiative is an international movement, it's made up of people who want to explore the potential of this tool and put it to work, not just for taxonomy in the description of species but in the identification of specimens for real problem solving: border inspections for agricultural pests, public health where you want to know is this particular mosquito likely to be a disease vector or not. So these interested parties have gotten together to form a consortium and the Smithsonian is the host. This is really quite different in the tradition of biodiversity campaigns where they tend to be very large very long term all species, all place. We tend to be more focussed, starting with a particular group of interest or a particular problem of what it is that we need to know about a particular group of organisms because there's a user community that really wants to be able to identify species rapidly and cheaply.

Robyn Williams: What about reaching Australia, presumably we're in touch?

David Schindel: Ah yes, there's already a lot of activity, mostly through CSIRO. One of the big campaigns, the big mega projects in bar coding has already been launched, it's an effort called All Fishes, or Fishbowl, the bar code of life for fishes and Robert Ward, who's a researcher at CSIRO Marine Sciences is one of the principal leaders of that group.

He's done a project on Australian fishes already, it's one of the ground breaking efforts that shows that you *can* do this rapidly and cost effectively in fishes. There's going to be a workshop in Canada in June I believe where they do the major planning and they're hoping to be able to bar code all the fishes of the world by 2010.

Robyn Williams: And the advantage if you want to get a picture of what lives in a river say, you don't have to kill fish and invertebrates to sample their DNA. Just take some mud from the riverbed and check the bar codes in it.

Guests

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http://barcoding.si.edu/CBOLStaff.htm

Further Information

Consortium for the Barcode of Life
http://barcoding.si.edu/index_detail.htm

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Presented by
Robyn Williams

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