



Handheld DNA Scanners to ID Species Instantly?

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Imagine a muggy summer night—steak sizzling on the barbeque, cold drink in hand, and hundreds of insects mobbing the porch light. Suddenly a mosquito dive-bombs your bare arm. You flatten it with a smack but not before it sucks a drop of your blood. Did you just contract the West Nile virus?

If Paul Hebert gets his way, in about ten years all you'll need to do is feed a fragment of the flattened bug into your handheld scanner for analysis. Moments later, the little machine will identify the species with a photo and description, allowing you to determine if you are at risk.

Hebert, a zoologist at the University of Guelph in Ontario, Canada, is the father of an idea known as DNA bar coding. The notion holds that just about every plant and animal species on the planet can be identified by quickly analyzing a short stretch of DNA—in much the same way that scanner reads bar codes in a store.

"The technology will be so simple to use that anyone can identify any organism they encounter," he said.

A tiny piece of tissue—a scale, a hair, a leaf—is all that is required for identification. Once it's fed into the machine, any organism can be known by such fragments.

Hebert imagines many possible applications for such a device:

- Aviation agencies could identify birds that impact aircraft;
- biologists could pinpoint a frog's last meal;
- health inspectors could look for undesirable plant and animal material in processed foods; and
- anyone could wander into the backyard and learn about its flora and fauna.

DNA "bar codes" also promise to expedite the discovery of new species, according to David Schindel, executive secretary of the Consortium for the Barcode of Life. The initiative is funded by the Alfred P. Sloan Foundation of New York to promote the use of DNA bar codes in species identification.

Launched in May 2004, the consortium is based at the Smithsonian Institution's National Museum of Natural History in Washington, D.C. To date, taxonomists have identified about two million of the estimated ten million species of plants and animals thought to live on Earth.

Schindel noted that, using DNA bar codes, scientists could highlight species that have no match in a database of bar codes, freeing up taxonomists "to focus their attention on things that are new and exciting."

Bar Code Meeting

Next month scientists will meet in London, England, for the consortium's first international conference. There, they'll discuss progress in DNA-bar-coding science and kick-start international collaborations to create a bar code database for Earth's estimated ten million species.

The database will be housed at GenBank, the United States National Institutes of Health's publicly accessible database of DNA sequences.

In addition, Hebert and his colleagues have already begun to compile a bar code database at the University of Guelph. Discussions are being held to make sure the two databases are complementary, Schindel said.

To make the bar code database an economical, effective, and useful tool, the consortium is focused on a portion of a single gene common to all life, known as *COI*, or cytochrome c oxidase 1. Variations in this segment of DNA distinguish species in much the same way that bar codes in a supermarket might distinguish brands of cereals.

"What we have said is that the *COI* ... gene seems to work very well for most animal groups," Schindel said. "So if you're going to use bar codes, start with that one."

The *COI* gene is found in mitochondria, the energy-producing subunits of cells that are inherited only from an organism's mother. (Most DNA is found in the nuclei of cells and is inherited from both the mother and father of an organism.)

Hebert, the Canadian zoologist, said mitochondrial DNA accumulates mutations up to ten times faster than nuclear DNA. As a result, the mitochondrial DNA of closely related species differs more than their nuclear DNA, making it easy to tell the species apart.

"It's not just rapid rates of evolution but rapid divergence," Hebert said. "Nuclear DNA retains old variation, while old mitochondrial variants are much more rapidly lost, making species separation very straightforward."

The *COI* gene is also simple to isolate in a variety of animals, and a broad range of animal life has been shown to have distinct *COI* sequences, Hebert said. However *COI* does not work well for vascular plants (plants with tube systems for conducting fluid, such as ferns and flowering plants).

Scientists will discuss possible plant genes that can be used to quickly identify species at the February conference.

Proof of Concept?

Two studies published in October 2004 illustrate the power of DNA bar codes.

In a *PLoS Biology* paper, researchers led by Hebert sequenced DNA bar codes for 260 species of North American birds. Each had a unique bar code. Variation between species was, on average, 18 times higher than between individuals of the same species.

During the course of the study, Hebert and his colleagues also found two divergent groups of *COI* bar codes within each of four species. This indicated that in each case, a single species was really two—the DNA bar codes revealed four new species of North American birds.

Meanwhile researchers led by Daniel Janzen, a biologist at the University of Pennsylvania in Philadelphia, used DNA bar codes to show that a common butterfly in Costa Rica, *Astrartes fulgerator*, is actually ten different species. The study was published in the *Proceedings of the National Academy of Sciences*.

The researchers were tipped off to the possibility when they realized that more than 2,500 wild-caught *A. fulgerator* caterpillars could be separated into several groups according to slight variations in color and food preferences. The adult butterflies, however, are indistinguishable.

"Given the vast range of the supposed *A. fulgerator* species, it doesn't take much imagination to realize that there are probably a great many more hidden species out there," Janzen said in a media statement. The butterflies are found from the southern United States to northern Argentina.

Vertebrate zoologists Craig Moritz and Carla Cicero of the University of California, Berkeley, commented on the Hebert-led study of North American birds in *PLoS Biology*. There, the pair echoed the major criticism against DNA bar codes, questioning whether the technique can reliably distinguish between closely related species.

Mortiz and Cicero wrote that DNA bar coding, used in combination with other taxonomic practices, can help to identify individuals and to increase rates of species discovery. But the pair remained skeptical on when and where the technique will be useful, noting that "the real challenge lies with tropical taxa. ... "

Schindel, of the Consortium for the Barcode of Life, said his organization is open to such criticism of bar coding. But he does not believe bar code limitations should prevent taxonomists from having the technique in their toolboxes.

"I think the most important question is, Does DNA bar coding contribute to the process of taxonomic revision and refinement? And I think the answer is very clearly yes," he said.