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Scientists seek DNA database of organisms

By Lisa M. Krieger
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It is quite likely that long-billed dowitchers and short-billed dowitchers can tell each other apart.


Long-billed dowitcher: This bird is a challenge for taxonomists because its coloring often resembles that of its short-billed cousin.

But when birds of these feathers flock together, they all look the same.

That's the challenge with traditional taxonomy, which relies on appearance to identify creatures. Despite the dowitchers' names, their bills aren't reliable markers; they are, on average, remarkably similar in length. Nor is their plumage any more distinct: Both species' feathers are brownish in the summer and gray in the winter. Both have narrow wings. Both have a white rump patch.

''The only safe way to tell them apart at this time of year is by their call,'' said Los Altos-based bird photographer Peter LaTourrette.


Short-billed dowitcher: Despite its name, this bird species sports a bill that's about as long as that of the long-billed dowitcher.

A controversial new approach to species identification, now debated within the biological community, could offer help.

This technique would create a sort of bar code from a small segment of DNA in the genome of each living thing, a tag that would definitively discriminate between species.

Proposed by Paul D.N. Hebert, an evolutionary biologist at the University of Guelph in Ontario, it borrows a coding concept from the retail industry, which uses 10 digits to create 100 billion bar-code combinations that identify products from diapers to caviar.

A coding system is used by nature, too. The genes within DNA that spell out operating instructions are written in a code involving four chemical bases -- adenine (A), cytosine ©, guanine (G) and thymine (T).

One key gene, cytochrome c oxidase I, or COI, plays a crucial role in metabolism and is present in all animals. But its sequence -- the exact order of its chemical bases -- varies substantially and is unique for each species. This makes it a prime candidate to serve as a bar code. The bar code of one animal might read AACACTGTAT, while another would be TACTCTTTA.

''In a very real sense, these sequences can be viewed as genetic 'bar codes' that are embedded in every cell,'' Hebert and his colleagues wrote in a paper published in the Proceedings of the Royal Society B, where the idea was first presented in September 2002.

Codes for all?

Although different genes might be used for broad categories of organisms -- animals, plants, fungi, bacteria and viruses -- scientists believe some type of bar coding could apply to every domain of life.

Last March, 40 leading scientists involved in taxonomy -- the classification of organisms -- met at New York's Cold Spring Harbor for the first conference to plan the creation of an international bar-coding system. Organizers included Harvard University, Rockefeller University and Philadelphia's Academy of Natural Sciences.

To test the technique, Herbert has examined 1,000 species of insects -- ants, bees, dragonflies, mayflies, moths and butterflies -- and found he could tell all but a few apart. In a box filled with legs of 50 Central American butterflies thought to be from a single species, he found at least 10 genetically distinct species.

He dreams of building a database that might someday serve as the basis for a giant identification system for all living things. DNA-based identification will start with animals but over time can expand to include all life, Hebert hopes.

A global inventory of animal life would take no longer than 20 years and cost about $1 billion, he said. This is far less than what was spent on other major initiatives such as the Human Genome Project or the International Space Station.

More than 250 years ago, Swedish scientist Carolus Linnaeus created a system based on physical traits to divide the natural world into categories such as phylum, class, order, genus and species. Organisms belong to the same species if they have the potential to successfully interbreed.

This traditional approach isn't working, Hebert asserts. There are an estimated 10 million to 100 million species on our planet, but only 1.7 million have been formally described, he said. It's rumored that some of the specimens from Charles Darwin's collection still sit, unnamed, on museum shelves in Britain.

''Whereas physicists deal with a cosmos assembled from 12 fundamental particles, biologists confront a planet populated by millions of species,'' Hebert wrote.

To make matters more difficult, some creatures are identifiable only at a particular life stage. Only males, or only females, may be recognizable. Quite a few plants are identifiable only by their flowers, which blossom once a year.

''We know that if the only sample you have is an egg -- and you want to know, 'Is that salamander B or salamander C?' -- a DNA technique would be very useful,'' said taxonomist Mark Stoeckle, an investigator in the Program for the Human Environment at Rockefeller University in New York City.

''In mosquitoes, eggs are not identifiable,'' Stoeckle said. ''And adults are difficult. You can only really distinguish mosquitoes from their larvae. This makes targeted control difficult.''

If scientists could easily identify which mosquito species carry the West Nile virus, for instance, they could spray only in areas where it's really needed, he said.

Some species remain a mystery. In 1900, naturalist C.H. Merriam classified mountain red foxes as a distinct species, separate from lowland red foxes. Then subsequent scientists lumped all North American red foxes into one species, Vulpes vulpes. But many experts still consider three isolated mountain fox populations in the West as a breed apart. Only DNA would tell for sure.

Despite a vast number of creatures, there are dwindling numbers of taxonomists. Very few humans can recognize and recall subtle variations in morphology -- that is, appearance -- between species. Since any given expert can identify only about 0.01 percent of the species on Earth by their physical characteristics alone, a community of 15,000 people is required, in perpetuity, to identify life using traditional tools, Hebert calculates.

The DNA bar-coding project has captured the imagination of some of biology's best blue-sky thinkers.

''Imagine a world where every child's backpack, every farmer's pocket, every doctor's office and every biologist's belt has a gadget the size of a cell phone -- for free,'' envisioned Dan Janzen, professor of biology at the University of Pennsylvania.

''Pop off a leg, pluck a tuft of hair, pinch a piece of leaf, swat a mosquito, and stick it in on a tuft of toilet tissue,'' he said. One minute later, the proper Latin name of the organism pops up on a screen, identifying it as an American cockroach, domestic dog, live oak or Northern house mosquito, a carrier of West Nile virus.

''A chip the size of your thumbnail could carry 30 million species-specific gene sequences,'' Janzen said. Push a button, and the screen offers basic natural history and images for that species at your point on the globe. ''Push it twice, and you are in dialogue with central for more complex queries,'' he said. ''Such a gadget would allow access to true bioliteracy for all humanity.''

Some experts hesitant

Any idea this big deserves to be debated, biologists agree.

However, many are leery of any proposal to replace the time-honored skill of visual observation.

‘‘I don’t like this idea of ‘We’re running out of taxonomists, so we need a whole new system,’ ’’ said Peter Fritsch, associate curator of botany at the California Academy of Sciences in San Francisco.

‘‘The answer is to train more taxonomists. Then, as an adjunct, use DNA techniques,’’ he said. ‘‘I don’t believe that you can replace the taxonomists by pushing a button.’’

He said that although the technique is not bad, it has limitations and may not provide enough information to distinguish recent splinter species , or species that have arisen through hybridization.

There is room for both approaches, Stoeckle said.

‘‘Traditional morphology will continue to be a mainstay. We’re not going to throw out 250 years of taxonomic knowledge,’’ he predicted. ‘‘It helps us understand how an organism lives. What do the hairs on the back of its legs have to do with how it moves its legs? How does oxygen move in and out? What is its food supply? Morphology can answer those questions.’’

But it can be misleading -- and far too slow, he said. Technology can help.

To identify and name every living thing, in a single human generation, will take a combined approach, Stoeckle said.

Used together, he said, human observation and DNA analysis could reward us with a more complex sense of the natural world around us.

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