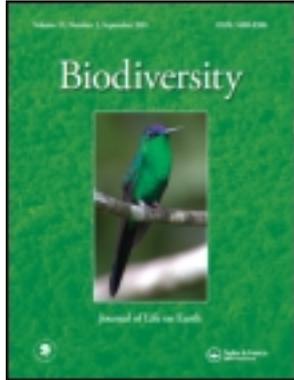


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DNA BARCODING: FAST-TRACKING SPECIES IDENTIFICATION

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**DNA BARCODING:
FAST-TRACKING SPECIES IDENTIFICATION**

“Our job is to reveal how many species there are on the planet and provide really simple tools to tell one species from another.” Paul Hebert

“I want something out of my back pocket that for one cent gives me one name in one second.” Dan Janzen

Less than a fifth of the earth’s 10 million species of plants and animals have been cataloged (1.7 million out of a possible 10 million according to some estimates, as high as 20 million according to others). Taxonomists are backlogged with requests to apply their specialist knowledge to identification problems. Since Linnaeus, biologists have used distinguishing features in taxonomic keys to apply binomial species names, such as *Homo sapiens*. Then, as a master key opens all the rooms in a building, the binomial species name accesses all knowledge about a species. From insects to birds, evidence now shows that short DNA sequences from a uniform locality on genomes can also be a distinguishing feature. As a Linnaean binomial is an abbreviated label for the morphology of a species, the short sequence is an abbreviated label for the genome of the species. The wait for a simple way of identifying species may be drawing to a close; if an idea known as DNA barcoding should prove as effective as its advocates say.

DNA barcoding, by analogy with the bar codes on supermarket products, depends on analyzing part of just one gene, the same gene in all cases, for every species. If and when a DNA bar code database of all terrestrial plant and animal species is established, a field biologist could take a tiny piece of tissue, like a scale or hair or leaf, from the unknown specimen, and feed it into a hand-held device for analysis. With a cellphone call to the database, the device would identify the species and present its photo and description. DNA barcoding is the idea of Dr. Paul D. N. Hebert, a population geneticist at the University of Guelph in Ontario. It has attracted support from the Alfred P. Sloan Foundation of New York, where it has been championed by a program officer, Jesse H. Ausubel of Rockefeller University. Out of this relationship grew the *Consortium for the Barcode of Life* (CBOL), an international collaboration of natural history museums, herbaria, biological repositories, and biodiversity inventory sites, together with academic and commercial experts in genomics, taxonomy, electronics, and computer science. The initial organizational support for CBOL is provided by a 2.5 year grant from the Sloan Foundation. The mission of CBOL is to rapidly accelerate compiling of DNA barcodes of known and newly discovered plant and animal species, establish a public library of

sequences linked to named specimens, and promote development of portable devices for DNA barcoding. Advocates believe that this will assist as many people as possible to quickly and cheaply recognize known species and retrieve information about them. The question is, ‘will this speed the discovery of the millions of species yet to be named ?’

Researchers have developed numerous ways to identify species by DNA, typically tailoring the approach to answer a specific question in a limited set of species. Like convergence on one or a few railroad gauges, barcoding aims to capture the benefits of standardization. Standardization typically lowers costs and lifts reliability, and thus speeds diffusion and use. For barcoding, standardization should help accelerate construction of a comprehensive, consistent reference library of DNA sequences and development of economical technologies for species identification.

The goal is that anyone, anywhere, anytime will be able to identify quickly and accurately the species of a specimen whatever its condition. Results so far suggest that a mitochondrial gene barcode will enable identification of most animal species. For plants, mitochondrial genes do not differ sufficiently to distinguish among closely related species. Promising approaches to standardize plant identification using one or possibly two barcode regions are under development.

Mitochondria, energy-producing organelles in plant and animal cells, have their own genome. Twenty years of research have established the utility of mitochondrial DNA sequences in differentiating among closely related animal species. Four properties make mitochondrial genomes especially suitable for identifying species.

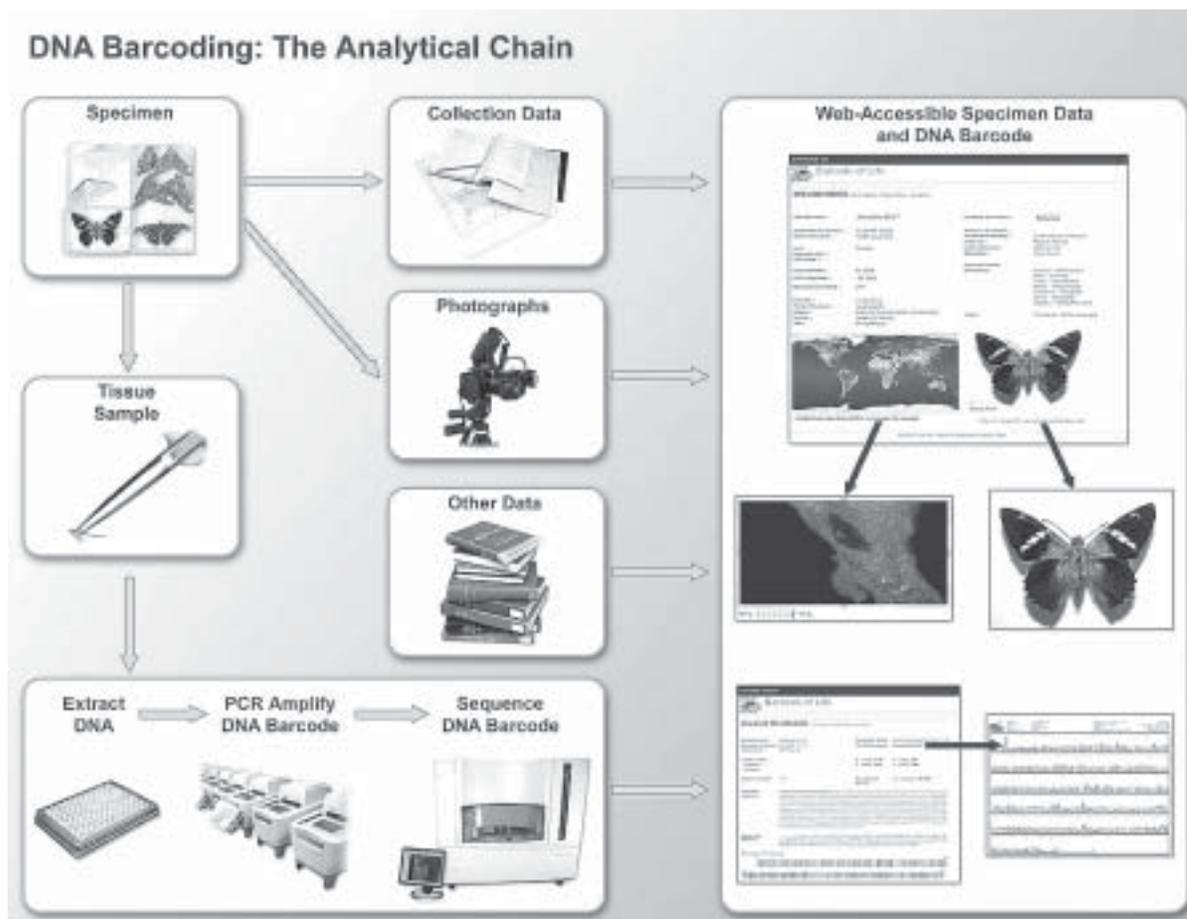
Copy number. While each cell typically contains only 2 copies of nuclear DNA sequences, the same cell encompasses 100-10,000 mitochondrial genomes. Recovering mitochondrial DNA sequences succeeds



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A Heron and its DNA barcode.

DNA barcoding can be an integral part of the analytical chain of specimen data collection ultimately providing an online accessible database.



much more often than nuclear sequences, especially from small or partially degraded samples. Greater success with smaller samples means lower processing costs.

Greater differences among species. Sequence differences among closely related animal species average 5- to 10-fold higher in mitochondrial than nuclear genes. Thus, shorter segments of mitochondrial DNA distinguish among species, and because they are shorter, less expensively.

Few differences within species. Intraspecific variation in mitochondrial DNA is low in most animal species. This may reflect rapid loss of ancestral polymorphisms due to maternal inheritance or selective sweeps following emergence of advantageous mutations. Regardless of cause, small intraspecific and large interspecific differences signal distinct genetic boundaries between most species, enabling precise identification with a mitochondrial barcode.

Absence of introns. In animals, mitochondrial genes rarely contain introns, which are non-coding sequences interspersed between the coding regions of a gene. Thus, amplification of mitochondrial DNA is usually straightforward. In contrast, amplification of coding regions of nuclear genes is often limited by introns, which may be long.

What are the main limits to barcoding encountered so far?

Groups with little sequence diversity. An example was found among a small number of corals and anemones from the marine phylum Cnidaria. The prevalence of such groups is not yet known, as researchers have analyzed only a few Cnidaria, and mitochondrial DNA sequences do distinguish some closely related species from this group. A comparison of mitochondrial sequences from 2238 species in 11 animal phyla showed 98% of closely related species pairs had more than 2% sequence difference, which is enough for successful identification of most species.

Resolution of recently diverged species. Collections of closely related organisms that have recently passed the threshold to win the status of species challenge separation by any method, including morphology. In some cases, a mitochondrial barcode may narrow identification to two (or more) closely related species and no further. The frequency of species with shared barcodes is low in groups studied so far.

Hybrids. Identification systems based on a single gene (nuclear or mitochondrial) will not allow the certain identification of hybrids, that is, individuals whose male and female parent are from different species. Such specimens may be misidentified morphologically as well.

Nuclear pseudogenes. Pseudogenes, which are inactive copies of genes usually containing multiple mutations and/or deletions, can complicate identification by either mitochondrial or nuclear genes. Pseudogenes have proven a minor limitation to using a mitochondrial barcode in groups studied so far.

Why select the barcode sequence from within one gene?

With a few exceptions, animal mitochondria contain an identical set of genes: 13 protein-coding, 2 ribosomal RNA, and 22 transfer RNA genes. While the order of the genes and their polarity (location on plus or minus strand) differ markedly among animal phyla, sequences from diverse organisms can be easily compared as long as the barcode locality is limited to one gene. Staying within the boundaries of a single gene also eases development of broad range techniques for recovery of barcode sequences from diverse organisms.

Why standardize on COI for animals?

The mitochondrial protein-coding genes generally contain more differences than the ribosomal genes and thus are more likely to distinguish effectively among closely related species. Sequence comparisons among protein coding genes are easier because they generally lack insertions or deletions frequently present in ribosomal genes. Among candidate protein-coding gene regions, the cytochrome *c* oxidase I (COI) locality contains sequence differences representative of those in other mitochondrial protein-coding genes. Possible gains in accuracy or cost from using a different protein-coding domain would likely be small in light of the general similarity of these regions. The COI region that is rapidly gaining currency represents approximately the first half of the gene and is 648 base pairs, a length easy to process in one “grab” with current technology and thus cheap.

Results to date indicate that this COI barcode is:

- 1) easy to recover from diverse taxa, using a limited set of primers.
- 2) readily aligned for sequence comparisons.
- 3) effective in distinguishing among closely related animal species from a variety of invertebrate and vertebrate taxa.

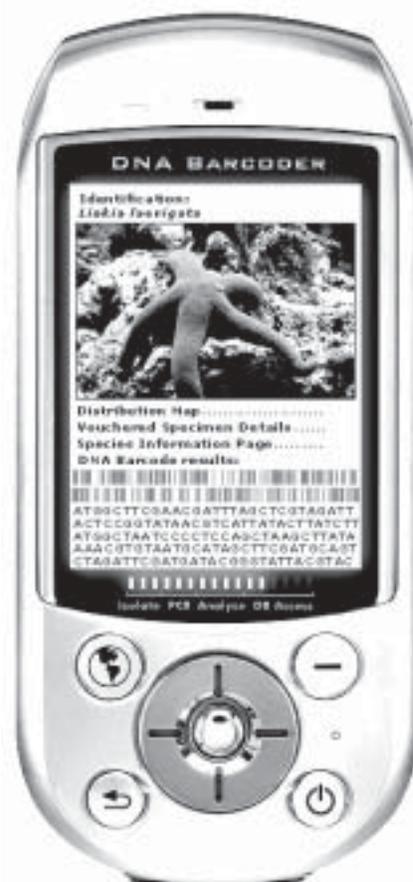
Dr. Hebert believes that variation within a species is reduced by the evolutionary mechanism called a selective sweep. Sweeps occur because most changes in the COI gene are so important that they rapidly spread through all members of a species. This erasure of natural variability within a species is the critical feature that creates a distinctive genetic signature for each species and makes barcoding possible. But critics say they are not yet convinced that the signatures will be distinctive in every group of animals.

What do barcode differences among and within animal species studied so far suggest?

COI barcode sequences differ much more among than within species. For example, among 260 species of North American birds, differences between closely related species averaged 18-times higher than differences within species. Thus, a COI barcode alone should identify most bird species. Exceptions occur among some species that diverged very recently or hybridize regularly. Alternatively, low barcode differences between specimens attributed to different species may indicate synonymy, i.e., single species incorrectly split into separate taxa, or misidentified specimens. Large barcode differences of specimens within a species may signal the presence of species mistakenly lumped together by current taxonomy.

Can barcodes aid understanding history of animal and plant species?

While barcoding's goal is identification of specimens at the level of species, various rules also assemble groups of barcodes in “trees” suggesting evolutionary distances and relationships among species. For centuries biologists have worked to construct a tree of life or phylogeny showing the history of species. These efforts benefit from analysis of multiple characters, especially across long eras and varied groups. In the few cases examined so far, genetic distances among



Mockup of a handheld DNA Barcoder. How does it work ?

COI barcodes are largely congruent with understanding developed through traditional taxonomy, suggesting a library of barcodes will help evolutionary study.

Barcoding – future functions

CBOL (<http://barcoding.si.edu/>) is devoted to developing DNA barcoding as a global standard in taxonomy. Based at the Smithsonian Institute, the Consortium has more than 130 Member Organizations from 40 countries. The mission is to create a DNA barcoding database that would be linked to identified specimens in their collections. Such a system, if it works as promised, will help field biologists identify known species and assist immensely in the urgent task of cataloging unknown species before their ranks are decimated by extinction. Public health authorities could identify whether mosquitoes were of a type likely to carry deadly diseases. Since barcoding works on tissues, inspectors could test animal feed for forbidden items likely to spread mad cow disease. And because DNA bar codes can be obtained from museum specimens up to 20 years old, curators throughout the world could bar code their collections, making their priceless storehouses of taxonomic knowledge available to everyone and easily accessible.

Despite its promise and quick start, DNA barcoding has not yet won the unanimous support of a core constituency, the taxonomists and biologists who would be its principal creators and users. The resistance stems from doubt that DNA barcodes can distinguish between closely related species. There may be other sources for the muted enthusiasm, like insiders' habitual reserve toward outsiders' help, and the traditional difference of perspective between those who study whole animals and those interested only in their DNA.

Two reports have demonstrated the striking power of DNA barcoding. In an article in *The Proceedings of the National Academy of Sciences*, a team led by Dr. Hebert and Dr. Daniel H. Janzen of the University of Pennsylvania showed that members of a Costa Rican butterfly species, *Astrartes fuligator*, possessed a total of 10 bar codes. The finding meant that the butterflies were not a single species, as long assumed, but a complex of 10 species occupying overlapping territories. Researchers had suspected something of the kind because the caterpillars looked quite different and preferred different food plants, as if each had long diverged away from a distant ancestral species. But all looked the same as adults, as if that particular appearance - livery that includes a splash of iridescent blue scales across the body and wings - carried such a survival advantage that none of the descendant species could stray from it. In another article, in *Public Library of Science Biology*, Dr. Mark Stoeckle of Rockefeller University and colleagues developed DNA bar codes for 260 species of North American birds. They found

that all had different DNA barcodes except four species in which two bar codes were present, suggesting in each case that a single species was really two. However critics have argued that the study was too narrow geographically and taxonomically to prove that bird species can be reliably distinguished through DNA.

The idea is not to supplant taxonomy, say the proponents, but to build on it and expand its power and utility. It is true that one gene is unlikely to distinguish all species perfectly but, come to think of it, traditional taxonomic methods are not so close to perfect either. The sensible criterion, say bar code backers, is practicality, not perfection: does DNA barcoding track traditional taxonomic classifications closely enough to be widely useful? The central idea of barcoding is standardization, but the COI gene alone may not have sufficient powers of discrimination for all animal groups. If so, a second mitochondrial gene could be chosen to help with these groups. Plant biologists have already decided that COI is not the right gene to distinguish among plant species and may prefer two genes on the chloroplast, the light-trapping subunit of plant cells.

CBOL has also announced another major project—one that uses a novel bar code for plants—which will test the method on 8000 plant species in Costa Rica. Partners in this project include scientists from Costa Rica, the Royal Botanic Gardens at Kew, U.K., the University of Pennsylvania in Philadelphia, and the Smithsonian Institution in Washington, D.C. (where botanist John Kress is developing a new plant bar code). Hebert, dubbed the “father of barcoding”, explained one reason for the current optimism among those in the field: The price for reading bar codes is dropping. Hebert said the cost of testing a specimen for COI variation is now about \$2, not counting labor, or about 10% of what it was 2 years ago. This means that barcoding all of life would be “relatively cheap in terms of other big science projects”: less than \$1 billion.

CBOL's executive secretary, David Schindel of the Smithsonian, said that the push has already begun. The big genome databases—GenBank in the United States and its partners in Europe and Japan— have “quietly” set up a bar codes section that includes the precise location the specimen came from, he says. About 1000 entries have been made so far, according to Scott Federhen of the National Center for Biological Information in Bethesda, Maryland. Guelph's Hebert and Bob Ward of Australia's Commonwealth Scientific and Industrial Research Organisation aim to supply tags for 15,000 marine and 8000 freshwater fish by 2010. During this time Stoeckle and a group of collaborators plan to bar-code 10,000 bird species. In an independent project, Ann Bucklin of the University of New Hampshire, Durham, and colleagues are gathering bar codes on ocean plankton.

Some big obstacles remain.

One is technical: Experts are not sure that simple bar codes will work for all species. Plants, for example, cannot be tracked with the COI gene. Kress proposes to use a combination that includes a bit of highly variable DNA between two genes on the chloroplast genome. It worked well in a test on Plummer's Island near Washington, D.C., he says, and is now being tried in Costa Rica. Amphibians also pose a challenge because for many, the COI gene varies so much from one individual to the next that it cannot be used reliably to mark species, said Miguel Vences of the Institute for Biodiversity and Ecosystem Dynamics in Amsterdam, the Netherlands. Herpetologist James Hanken, director of Harvard University's Museum of Comparative Zoology, suggested that for certain species such as the amphibians he studies, COI variation may need to be supplemented by extra tests. And very young species—including orangutans—may not be easily distinguished by COI barcoding.

Another challenge is to find money: Jesse Ausubel of the Alfred P. Sloan Foundation in New York City has steered support to this area and helped launch CBOL ever since hearing Hebert describe the idea in 2002. Others have joined in, but so far foundations have helped pay for start-up work. To scale up, research groups will need to tap into government budgets, and it remains to be seen how much policymakers want to spend. Ausubel said the field is gathering momentum and that funding will follow. He pointed out that several have invested in the field, including the bioprospecting firm Diversa Corp. of San Diego, California, gene chip maker Affymetrix of Santa Clara, California, and enzyme supplier New England Biolabs of Beverly, Massachusetts. Government agencies, including the U.S. Food and Drug Administration and the U.S. Department of Homeland Security, are also jumping in. "Environmental genomics is going to be huge," says Ausube.

Barcoding in action: recent studies reveal many "overlooked" species of birds and bats .

Twin papers on barcoding the DNA of birds and bats, were published online Feb. 19, 2007, by the UK journal *Molecular Ecology Notes* ([http:// www.barcodeoflife.org/barcode/batsbirds/](http://www.barcodeoflife.org/barcode/batsbirds/)).

At unprecedented levels of difficulty involving highly biodiverse and continent-sized landscapes, the scientists successfully tested their ability to identify and DNA "barcode" entire assemblages of species – the prelude to a genetic portrait of all animal life on Earth. They report having assembled a genetic portrait of birdlife in the U.S. and Canada, and announce the startling discovery of 15 new genetically-distinct species, nearly indistinguishable to human eyes and ears and consequently overlooked in centuries of bird studies.



Unique DNA barcodes were obtained from look-alike specimens of: A, Curve-billed Thrasher; B, Marsh Wren on phragmites; C, Ross's Goose with Snow Goose. (Photos courtesy of Doug Wechsler, Director VIREO, the Academy of Natural Sciences in Philadelphia. URL <http://acnatsci.org/vireo/>).

The barcoders also successfully logged the DNA attributes of 87 bat species of Guyana and reveal six new species (appendix 4), characterized by unique genetic make-up. One of the new species, a look-alike of *Trachops cirrhosus*, feasts on frogs. As well, the scientists report that 14 pairs of North American bird species with separate identities are in fact DNA twins, two trios of species are DNA triplets, and no less than eight gull species are virtually DNA identical (appendix 3). The complementary papers describing the bird and bat initiatives were authored by researchers from Guelph, Ottawa and Toronto, Canada, and from New

York City and Washington D.C., USA

The Birdcodes

The bird researchers; Mark Stoeckle, Program for the Human Environment, Rockefeller University, New York; Carla Dove and Lee Weigt, Smithsonian Institution, National Museum of Natural History, Washington, DC; Kevin Kerr, University of Guelph; and Charles Francis, Canadian Wildlife Service, Environment Canada, Ottawa, obtained DNA from “voucher” specimens in museums, augmented by samples sent in by scores of people. In all, more than 2,500 specimens were barcoded. The DNA portrait of 643 bird species, from the Arctic tundra to the temperate woodlands to the Florida Keys, represents 93% of 690 known breeding species in the U.S. and Canada. Work continues to collect DNA of the remaining 47 listed North American species, as well as several more considered extinct, specimens of which exist in museums (see <http://www.barcodingbirds.org/>).

“Now with the vast majority – 93-94% – of birds on the continent barcoded it’s hard to argue that barcoding might work for the easy stuff but miss the difficult cases of closely-related taxa,” says Dr. Paul Hebert of the Biodiversity Institute of Ontario, Guelph University, Canada, who co-authored both the bird and bat papers.

“People have watched birds for so long we might think every different tweet has been heard, every different color form observed,” says Dr. Hebert. However, “there are a number of cases of deep genetic divergences within what are currently called single species,” he says. The “cryptic species” are those with unique DNA barcodes but differences of song and plumage so subtle as to make them virtually indistinguishable from some other species. They are typically “small brown ground-dwelling shrubby birds that don’t attract a lot of human attention.”

Even though birds may appear very similar to human observers, a species with a distinct DNA barcode very rarely interbreeds; they literally find birds of a feather as mates. Also, the fauna (birds and bats) newly distinguished by virtue of unique DNA do not yet have unique names. That issue and process is the subject of scientific discussion and debate. “Did we find concordance between barcode results and conventional taxonomy? The answer is, resoundingly, yes. In 95% of cases, entities recognized as species are barcode distinct,” adds Dr. Hebert.

People who put tiny bands on birds to help track migrations contributed samples for the study. Banders are extremely good at identifying species “but even they can’t always identify a bird in the hand,” says Dr. Hebert. “In such cases, they appreciate having a barcode record to identify with certainty the bird they

banded.” Dr. Stoeckle of Rockefeller University says the world recognizes about 10,000 bird species today and predicts that, at a global scale, DNA barcoding will distinguish 500 to 1,000 more. The researchers hope to complete an all-bird DNA inventory by 2011. Given the continent’s legions of bird specialists, he says he was surprised by the extent of “hidden diversity” revealed in North America, and by the clear DNA distinctions between species. Dr. Stoeckle cautions that “some pairs of listed species now shown to be DNA twins may be relatively young species and prove different over time.” As well, he notes, there is no universal scientific agreement on what defines a species.

The Batcodes

Dr. Hebert and University of Guelph colleague Elizabeth Clare co-authored the bat study with Burton Lim, Mark Engstrom and Judith Eger of the Royal Ontario Museum, Toronto.

“Wouldn’t you think we’d have all of the world’s 5,500 mammals identified by now? The scientific community has been at it for 250 years,” says Dr. Hebert. Roughly 1,100 or 20% of the world’s 5,500 mammals are bats. Adding six new bat species to the 87 surveyed from Guyana is a surprisingly high percentage, he notes. In all, some 840 bat specimens were barcoded. “We wanted to give barcoding the toughest test possible. The bats of Guyana have been the subject of intensive taxonomic work and yet we found we could recognize 100% of the surveyed species and discovered a number of overlooked bats.”

Barcodes Important to Commerce, Security and Conservation

Barcoding can identify a species from bits and pieces. When fully established, the barcode database may help quickly identify undesirable animal or plant material in food and detect regulated species in the marketplace. Barcoding could potentially help reconstruct food cycles by identifying fragments in stomachs and assist plant science by identifying roots sampled from soil layers. A standardized library of barcodes will enable more people to identify species – whether abundant or rare, native or invasive – engendering appreciation of biodiversity locally and globally.

The importance of this work to conservation is particularly critical. The Solitary Sandpiper shorebird, its habitat increasingly under pressure from land development and climate change, was not known previously to have two forms, yet their DNA reveals two distinct groups split about 2.5 million years ago. “How can you develop strategies to preserve highly different genetic entities if you don’t know they’re there? Our work is providing the first molecular evidence of



Provisional new bat species. Unique DNA barcodes were obtained from look-alike specimens of: A, *Noctilio lbiventris* (photo by Ivan Kuzman); B, *Trachops cirrhosus*; C, *Platyrrhinus helleri*; D, *Phylloderma stenops*; E, *Myotis riparius*; F, *Carollia brevicauda*. (Photos credit to Alex Borisenko, Biodiversity Institute of Ontario / Royal Ontario Museum)

some of these splits," says Dr. Hebert.

The work with birds and bats also helps aviation and is supported in part by the U.S. Federal Aviation Authority and U.S. Air Force. According to Carla Dove of the Smithsonian Institution: "Knowing which birds are most often struck, and the timing, altitude and routes of their migrations, could avert some of the thousands of annual collisions between birds and aircraft, military and civilian." In a few years, field researchers, indeed many interested citizens, could employ handheld DNA devices for nearly instant species identification. Says Dr. Hebert: "For cases

where it is not convenient to identify species based on shape, sound and color, even non-experts could identify them based on DNA strings." Once minaturized, the many potential uses of quick DNA barcoding embrace food and agriculture, forestry and security, including certification of species for market, controlling pest animals and preventing invasions of species via international trade. A DNA barcoder could name the vegetables in your soup.

Perhaps the biggest surprise is that DNA barcoding works as well as it does, that a relatively short code of genes distinguishes species so clearly and there isn't more

blurring between species, says Dr. Stoeckle. Barcoding has prompted speculation and theories about mechanisms that strip variation out of species and keep them sharply distinct – periodic “selective sweeps” – and the reasons behind them. “This work is raising questions about how evolution works and what species are,” he says.

So far, the Barcode of Life Data Systems (www.barcodinglife.org) has catalogued more than 25,000 species of all types, and over 200,000 individual records; both numbers more than doubled in the past year. Whenever possible, museum specimens have been used to create

the DNA barcode reference library, enabling scientists to recheck and verify any puzzling results

The researchers are looking to raise US \$100 million to create 10 million records of 500,000 animal species by 2014. Says Dr. Hebert: “What it will mean effectively is that researchers will find a barcode linked to just about anything encountered anywhere on the planet. By 2014 I think you can count on having a functional barcode library linking barcodes to the binomial names that link to the accumulated knowledge about them. And I think you can count on having a handheld device.”

HERE ARE TEN REASONS TO SUPPORT BARCODING!

- 1. Works with fragments.** Barcoding can identify a species from bits and pieces. When established, barcoding can be used to quickly identify undesirable animal or plant material in processed foodstuffs and detect commercial products derived from regulated species. Barcoding can help reconstruct food cycles by identifying fragments in stomachs and assist plant science by identifying roots sampled from soil layers.
- 2. Works for all stages of life.** Barcoding can identify a species in its many forms, from eggs and seed, through larvae and seedlings, to adults and flowers.
- 3. Unmasks look-alikes.** Barcoding can distinguish among species that look alike, uncovering dangerous organisms masquerading as harmless ones and enabling a more accurate view of biodiversity. For example, Anopheles mosquitoes are vectors for human malaria but only a few of the 430 known species transmit infection.
- 4. Reduces ambiguity.** Written as a sequence of four discrete nucleotides - CATG – along a uniform locality on genomes, a barcode of life provides a digital identifying feature, supplementing the more analog gradations of words, shapes and colors. A library of digital barcodes will provide an unambiguous reference that will facilitate identifying species invading and retreating across the globe and through centuries.
- 5. Makes expertise go further.** The bewildering diversity of about 2 million species already known confines even an expert to morphological identification of only a small part of the plant and animal kingdoms. Foreseeing millions more species to go, scientists can equip themselves with barcoding to speedup the process of identifying known organisms and facilitate rapid recognition of new species.
- 6. Democratizes access and promotes appreciation.** A standardized library of barcodes will empower many more people to be confident in the identification of species around them, whether abundant or rare, native or invasive, engendering appreciation of biodiversity locally and globally.
- 7. Opens the way for an electronic handheld field guide - the Life Barcoder.** Barcoding links biological identification to advancing frontiers in DNA sequencing, miniaturization in electronics, and computerized information storage. Integrating those links will lead to portable desktop devices and ultimately to hand-held barcoders. Imagine the promise of a schoolchild with a barcoder in hand learning to read wild biodiversity, the power granted to a field ecologist surveying with a barcoder and global positioning system, or the security imparted by a port inspector with a barcoder linked to a central computer!
- 8. Sprouts new leaves on the tree of life.** Since Darwin, biologists seeking a natural system of classification have drawn genealogical trees to represent evolutionary history. Barcoding the similarities and differences among the nearly 2 million species already named will provide a wealth of genetic detail, helping to draw the tree of life on Earth. Barcoding newly discovered species will help show where they belong among known species, sprouting new leaves on the tree of life.
- 9. Demonstrates value of collections.** Compiling the library of barcodes begins with the multimillions of specimens in museums, herbaria, zoos and gardens, and other biological repositories. The spotlight that barcoding shines on these institutions and their collections will strengthen their ongoing efforts to preserve Earth's biodiversity. For example the National Museum of Natural History has over 600,000 bird specimens representing more than 80% of the world's known species.
- 10. Expedites the encyclopedia of life.** Compiling a library of barcodes linked to vouchered specimens and their binomial names will enhance public access to biological knowledge, helping to create an on-line encyclopedia of life on Earth, with a web page for every species of plant and animal

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ILL FARES THE LAND: REFLECTIONS ON SUSTAINABLE ORGANIC AGRICULTURE

Humans have, for millennia, raised food for themselves and others, selling the excess grain or vegetables for money. If money is scarce, they barter their food for things they don't have or cannot manufacture. This equilibrium that prevented to some degree famine or hunger is under attack all over the world, especially in societies that have returned to an industrialized version of feudalism. This is a dark agessystem of food production and land ownership whereby a very few farmers or corporations control an exceptionally large part of the country's agricultural and food economy. The United States and other "industrialized" countries deny their agricultural economy is feudal because, in theory, slavery is illegal. Yet, in practice, the economy of industrialized farming relies on purchased slavery, that of hundreds of thousands of migrant farm workers, most of them foreign, replicating the lives of slaves. So factory farmers dress up their feudal nature with pseudo-science, calling their practices "advanced," "modern" and other lipstick-like epithets.

The reason for this regression is political. The wars of the twentieth century returned most of the world to the dark ages. Agribusiness feudalism, mechanized and armed to the teeth with biological and chemical warfare weapons, has been a logical product of this toxic age. American agribusinesses practically own the land grant universities from which they extract technics, be they pesticides, bird flu vaccines, animal growth hormones, massive tractors and genetic engineering. Agribusinesses are also in charge of US agricultural policy, becoming the beneficiaries of government-funded research and lucrative subsidies with the result they have driven out most family farmers from rural America while, for all practical purposes, they enslave those who become "contract workers," to manage their animal farms.

In this political context, organic farming emerged in the shadow of feudal agribusiness, becoming merely a boutique niche for food "certified" clean of toxins, genetic engineering and sludge. Americans became tempted by this version of clean food so organic food, since 1990, began to grow by about 25% per year, earning its practitioners some \$13 billion in 2005. Agribusiness, however, since the 1980s has wanted to kill the organic experiment lest Americans conclude that the food they buy from the supermarkets is not clean and may be hazardous to their health. But the enormous public support for organic food in the late 1990s put agribusiness on notice. Agribusiness entered the market of organic farming and food on a large scale, subverting the rules of clean food, and making a killing in the process.

Introduction..

There's practically nothing that captures the human soul more than land, perhaps because life, including human life, would be inconceivable without it. Land was all that most humans had for millennia. It's only in the last 100 years or so that people in Europe and America abandoned their land and agrarian roots, most of them living in cities with food ending up on their table through a convoluted and dangerous highway of factories and markets.

"Industrializing" farming started in the 1860s without a thought about the quality of life or civilization that would follow such an upheaval. The men who launched the world into the kingdom of tractors, animal farms, synthetic fertilizers, and chemical-warfare farm sprays were the same men who benefited from the global slaughters of 1910s and 1940s. These men, or, more accurately, business conglomerates, have had no use for peasants, small family farmers or the natural world. Their primary goal remains the enslavement or killing of the first, the displacement of the second, and the taming or industrialization of the third.

They adopted the plantation of cash crops (now going under the pseudonyms of scientific agriculture, high tech