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Authors: EBACH, MALTE C., and HOLDREGE, CRAIG

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More Taxonomy, Not DNA Barcoding

MALTE C. EBACH AND CRAIG HOLDREGE

DNA barcoding is a term used to describe efforts to use the mitochondrial COI (cytochrome oxidase subunit I) gene as a molecular marker to allow easier and more efficient identification of specimens of known and unknown species. The Web sites of international barcoding projects (Barcode of Life, www.barcodinglife.org; Consortium for the Barcode of Life [CBOL], http://barcoding.si.edu/index_detail.htm) herald the technique's potential, informing readers that DNA barcoding will "revolutionize the task of identification" of species, allowing the identification of not only fragmentary specimens (a valuable application, without doubt) but also new species.

The barcoding organizations further note that taxonomists have identified only about 15 percent of all living species over the past 250 years, and imply that the rapid loss of biodiversity worldwide adds urgency to their task. Large-scale barcoding will drastically accelerate the rate of species identification, according to the technique's champions. They assure readers that this work can be carried out by a cadre of technicians who need none of the high-level expertise of present-day taxonomists. DNA barcoding is thus portrayed as a way of counting all the species in the world, in the hope of knowing something more about biodiversity.

This kind of hype often surrounds the development of new techniques. Over a decade ago, Francis Collins, the director of the National Human Genome Research Institute, described the mapping of the human genome as "the most important and the most significant project that humankind has ever mounted" (Kolata 1993). But after that project was finished in 2001, geneticists began admitting what they could have known earlier—that, as Sydney Brenner wrote in a 2003 editorial in *Science*, "we now know that the genome sequence is only the beginning and that a deduced

amino acid sequence is not a target for anything unless we know how it participates in the physiological processes in our bodies" (Brenner 2003). Sequence data do not tell you much about genes unless you can put them in a context. And that's the problem with the hype about DNA barcoding: it confuses gathering molecular information with meaningful knowledge.

We made this argument in a recent letter published in *Nature* (Ebach and Holdrege 2005). David Schindel, executive secretary of CBOL, and Scott Miller, its chairman, replied, "Ebach and Holdrege [2005] are correct in stating 'DNA barcoding generates information, not knowledge.' CBOL believes that this information can make systematists and the consumers of taxonomic information more knowledgeable. Therein lies its potential value" (Schindel and Miller 2005).

But systematists do not, merely by generating information, become more knowledgeable. In fact, the reverse is the case: DNA barcoding will provide meaningful information only if scientists can place it within the context of rich morphological, physiological, and behavioral knowledge. As a technique that generates information, barcoding will provide new illustrations of what we already know well: life is complex. But that information needs to be put into context to be useful. There is a real danger that a one-sided barcoding effort will lead to a glut of undigested facts, keeping many minds and machines busy while diverting attention from the real taxonomic issues that a new technique cannot address. Any call for barcoding demands an even more forceful call for intensified efforts to increase biologists' in-depth morphological and ecological understanding of Earth's organisms.

Imagine, for the sake of argument, that barcoders were able to tag each known taxonomic species with a DNA barcode, and that they discovered new and unique

sequences that might indicate a hitherto unknown species. Since barcoders maintain that there exist "DNA species" that are impossible to tell apart from known species except through sequence comparisons, many new species identified by barcoding would not be morphologically distinguishable. The resulting, much larger number of "species" would be a number that means very little. What that number might tell us about actually existing species would have to be intensively investigated, because barcodes cannot reveal the types of their corresponding real species, those species' relationships, or their behavior. In the end, we will be left with a very large and arbitrary number of supposed species. Since barcoding does not classify or create readily usable knowledge, it remains simply a technique, and should not be taken for more than that. What science really needs is more naturalists and taxonomists, not more barcoders.

The CBOL Web site claims that DNA barcoding is a "new and exciting addition to the taxonomists' toolbox." The observation prompts a question: What is already in a "taxonomist's toolbox"? It contains physical tools—such as a checklist, microscope, net, and plant press—and years of training and experience gained from studying the taxonomy of one or more groups. If barcoding could be viewed and managed as one subordinate physical instrument to be implemented in specific instances, it would be a useful addition. The question, in the present climate of high-tech hype, is whether researchers will realize that barcoding cannot replace any of the already existing tools, especially detailed knowledge of organisms. This is not a casual concern: wherever one looks in biology, molecular techniques are replacing the study of whole organisms and their relationships.

We can envision the potential usefulness of DNA barcoding to the conservation

ecologist and environmental consultant more easily than we can imagine its value to taxonomy. Barcoding could indeed be valuable in allowing quick species identification for rapid environmental assessment. It could, for example, help in allowing a rapid survey of the biodiversity in a polluted lake, or in a planned development site near an environmentally sensitive area. But even in these cases, a field guide, rubber boots, and a pair of binoculars are still perhaps the best and least invasive tools for identifying larger species. Barcoding would need specimens to be caught and possibly destroyed to provide cells whose DNA could be sequenced.

Museums, herbaria, and other institutions linked to taxonomy are pushing for a worldwide barcoding initiative, one that will fund a whole generation of technicians to sequence one barcode for each specimen in a type collection. The funding drive comes at a time when taxonomy is suffering from a shortage of funds and taxonomists. Barcoding supporters such as T. Ryan Gregory state that “the most unfortunate misunderstanding is that DNA barcoding competes with taxonomy for funding. Existing DNA barcoding networks have been funded by agencies that do not have a tradition of supporting taxonomic work. A global DNA barcoding initiative would be a ‘big science’ programme, and as such would compete for priority with projects of similar scale from physics, medicine and genomics—not taxonomy” (Gregory 2005).

Yet, if DNA barcoding receives major funding as a high-output, “big science” program, and as a result is viewed (wrongly)

as a modernized taxonomy, it will in fact begin supplanting taxonomic projects. It is naive to believe that the drive toward universal barcoding will not bring with it a radical shift in overall funding priorities. Museums fortunate enough to acquire funding for barcoding will place emphasis on building molecular biology laboratories, employing technicians, and expanding laboratory space dedicated to molecular techniques. Will there still be adequate funding to expand collections, to support research that identifies and describes new species, or to pursue systematic work in classification and the development of new keys? Most important, will there be funding for new taxonomic positions?

The role of museums, it should be remembered, is to further knowledge of life on Earth. They employ taxonomists who make discoveries in systematics, phylogenetics, physiology, ethnology, ecology, and biogeography. Museums will be unable to fulfill this role if they increasingly dedicate time, effort, and resources to molecular laboratories and barcode technicians.

In a funding climate focused on promoting sexy new high-output “solutions” to global problems, a scientific field that progresses by investing much time, energy, and funding into training taxonomists, doing careful fieldwork, and carrying out detailed morphological studies may seem outmoded. According to this view, taxonomists soon will become fossils in the strata of scientific evolution themselves. They must avoid this fate by promoting taxonomy for what it really is—“big science.” If they took this step, taxonomists could propose major fund-

ing initiatives for taxonomy, and so perhaps eliminate the need for barcoding consortiums (Wheeler 2004).

It is ironic that DNA barcoding is often portrayed as central to the effort to protect biodiversity. The implication seems to be that only enormous numbers of cataloged species, each with its own unique mitochondrial DNA sequence, will motivate human beings to gain, at last, respect for life. But this approach tells us next to nothing about the creatures we are supposed to care about. Would it not make much more sense to invest resources in getting to know better the whole organisms and their ecologies?

Malte C. Ebach (e-mail: ebach@ccr.jussieu.fr) is a researcher in the Laboratoire Informatique et Systématique at the University of Paris 6 (UPMC), UMR 5143, 12 rue Cuvier, 75005 Paris, France. Craig Holdrege is the director of The Nature Institute, 20 May Hill Road, Ghent, NY 12075.

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