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Response from Holdrege and Ebach: What about Taxa?

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

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DNA Barcoding in Taxonomy and the Perception of Species in Nature

In the recent Viewpoint by Ebach and Holdrege, "More Taxonomy, Not DNA Barcoding" (*BioScience* 55: 822–823), the authors doubt that the application of DNA barcoding (the use of short nucleotide sequences as molecular markers for species identification) will really become a serious alternative to more conventional taxonomic techniques. They claim that science needs more taxonomists, not more barcoders. They take into consideration that "barcodes cannot reveal the types of their corresponding real species."

I am afraid that this criticism represents more a misconception of what a "real species" is than a concern about the quality of forthcoming taxonomic practices. Diagnosing a species should not be confused with the ontological "thing" that a species really is in nature. Evolution is an ongoing change, and so is speciation. A completed species does not exist. Knowledge of the "real species" is one goal; operational diagnosis is another. Merging both goals into a single concept brings to light an obvious immanent conflict between these two desires. Whenever the criteria for species classification and identification are optimized, the ontological status of real species will become fuzzy, and vice versa.

The emphasis on diagnosis forces taxonomists to treat species as classes, not as things or individuals that exist as real entities in nature. Classes, however, have a very different ontological status than realities. The generation of classes depends on our current technology, and our skills for identifying similarities and differences will change with time.

One thing is clear: Barcoding is a method for recognizing differences among individual organisms. In this respect, it is no different from any other technique used in taxonomy, for example, counting the number of bristles on the legs of certain beetles. The call for "more taxonomy, not DNA barcoding" is comparable with a call for "more taxonomy, not bristle counting." However, not all characters are suited for dividing organisms into biologically meaningful groups. Preexisting ancestral intraspecific polymorphisms have to be recognized. Does the barcode pattern covary with other taxonomically relevant characters? This question, among others, has to be scrutinized if barcoding is put on the test bench. If barcoding passes these hurdles, then taxonomy needs more barcoders, and barcoding should compete with conventional methods for funding, since its pragmatic advantage is evident.

WERNER KUNZ
Werner Kunz (e-mail: kunz@uni-duesseldorf.de) is a professor of biology at the Institute for Genetics, Heinrich Heine University, Universitätsstrasse 1, D-40225 Düsseldorf, Germany.

Response from Holdrege and Ebach: What about Taxa?

The problem of recognizing "real species" as opposed to identifying operational units is best addressed by viewing organisms and populations as taxa—namely, by considering the interrelationships of their homologous characteristics. Whether we look at gene sequences or bristles, what really matters is that we consider each new characteristic within the broader context of overall relationships.

Molecular methods may provide a wealth of new data. But this information alone is neither taxonomic nor systematic, since it provides no criteria for distinguishing taxa. Current molecular methods are statistical and measure similarities, which tell us nothing about homologous relationships. After all, any two things in the world can be compared with one another. Do we know if a molecular classification is based on a possibly irrelevant statistical similarity?

The danger of DNA barcoding is not the technique itself. It's that the flood of decontexualized information produced by an automated technology may seduce us into believing that this information will provide critical answers to taxonomic questions. We are concerned that the fascination with a new source of information generation will deflect attention from the critical conceptual challenges associated with discovering natural classifications (monophyletic groups). The fundamental context for taxonomy will always be a deep and broad empirical knowledge of whole organisms.

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

A Critique of Svancara and Colleagues

The article by Svancara and colleagues ("Policy-driven versus Evidence-based Conservation: A Review of Political Targets and Biological Needs," *BioScience* 55: 989–995) has numerous failings that make the authors' analysis highly questionable. Space allows me to discuss only four. First, no corrections were made for discrepancies in how minimum area was expressed. The policy targets and most of the conservation assessments state minimum area as percent of total area. However, at least seven of their assessments reported minimum area as percent of available land or of survey area. This error is most apparent in figure 5, where the data points (10, 34.25), (10, 36), (25, 49), and (50, 76) become (10, 20.5), (10, 12.9), (25, 25), and (50, 49.9) after the proper correction. Incidentally, the point at (20, 70) should not be included in the regression. The analytical target for this study (Noss et al. 2002; see Svancara et al. for citation) does not conform to the independent variable in figure 5. After fixing these mistakes, a line with a slope close to 1 fits the data reasonably well.

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BioScience
1444 I Street, NW, Suite 200
Washington, DC 20005
E-mail: bioscience@aibs.org
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Second, the data set suffers from at least two forms of pseudoreplication. Seven of the references were review articles that based their minimum areas on some of the other references in the data set. In addition, at least three references were published in two forms (e.g., journal article and government report), and in all three cases both publications were used in the analysis.

Third, the authors overlooked the distinction between preservation and conservation. The policy targets specify the amount of land dedicated for nature preserves. The policy targets do not include other lands where biodiversity conservation is just one of many important goals. In contrast, some conservation assessments, such as those done by The Nature Conservancy, specify the amount of land needed for both preserves and conservation zones where extractive uses are allowed. Likewise, many of the threshold results could be accommodated by a mix of preserves and conservation zones. Hence, comparisons between the policy-driven targets and many of the evidence-based targets are not valid.

Last, and most important, the authors overlooked the significance of what they called "predefined analytical targets." Figure 5 (whether corrected or not) suggests that these targets may be the most important factor determining minimum area requirements. A majority of the conservation assessments had predefined analytical targets, and many of these targets were based on the subjective judgment of scientists. Noss and colleagues (2002) typify how such targets are formulated. They stated that their targets were those they "felt comfortable with." In other words, the targets were actually based on the scientists' feelings about acceptable risk. Attitudes toward risk are based more on ethical value judgments than on scientific expertise. (In research studies, subjective predefined analytical targets represent hypothetical ethical value judgments.) Svancara and colleagues rightly exposed the lack of science in the policy-driven targets, but they failed to recognize the value judgments underlying many of the "evidence-based" conservation assessments.

GEORGE F. WILHERE
George F. Wilhere is with the Washington Department of Fish and Wildlife in Olympia, Washington.

Response from Svancara and Colleagues

We appreciate the opportunity to respond to George Wilhere's comments. We could not find support for Wilhere's first criticism. We addressed different expressions of minimum area in figure 4. In figure 5, we used only those 13 articles (list available from authors) that expressed both predefined, analytical targets and required conservation areas. All 13 required percentages were based on total area.

Regarding Wilhere's second criticism, each review article proposed a value, or range of values, frequently much different from the values given in the original papers. Exclusion of the reviews gives average values for conservation assessments of 30.2 percent (cf. our 30.6 percent) and 42.3 percent for threshold analyses (cf. our 41.6 percent). Our database contains closely related publications (i.e., same author), but all report different objectives and/or results. Our conclusions remain valid.

Wilhere's third criticism is unconvincing. We are not aware that any policy targets stipulate achievement only with strict reserves. Achievement with multiple IUCN protected area categories, varying widely in management intent, is more likely. Similarly, some conservation plans (e.g., in South Africa) achieve targets with a mix of management strategies. It is reasonable that (a) both policy and evidence-based targets assume areas should be managed primarily, but not solely, for biodiversity conservation; and (b) the particular spatial mix of management and allowable land uses can only be resolved during site-by-site implementation.

We believe Wilhere's fourth criticism misses the point. Clearly, judgment is involved. In many cases, predefined analytical targets were qualified as arbitrary, illustrative, or based on policy. In others, scientists made no pretense about objectivity. Pressey and colleagues (2003) clearly state that targets are interpretations of goals using available data and require periodic revision. Even with spatially explicit population viability analysis (e.g., Noss et al. 2002), there is no objective, universally accepted probability of persistence. Decisions about targets are always subjective, but there is a big difference between subjective decisions based on objective information, logical reasoning, and peer review and those based on political whim.

LEONA K. SVANCARA
REE BRANNON
J. MICHAEL SCOTT
CRAIG R. GROVES
REED F. NOSS
ROBERT L. PRESSEY
Leona K. Svancara (e-mail: leonab@uidaho.edu) is with the National Park Service and the University of Idaho in Moscow, Idaho. Ree Brannon is with the University of Idaho, and J. Michael Scott is with the US Geological Survey and the University of Idaho. Craig R. Groves works for the Wildlife Conservation Society in Bozeman, Montana. Reed F. Noss is with the University of Central Florida. Robert L. Pressey is with the University of Queensland, Australia.

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