

that accompany this article, Will and Hebert respond to 10 questions selected by V.S. to reflect the balance of issues raised by the PEET audience (Hebert and Gregory, 2005; Will et al., 2005). Alternatively, you can follow the original debate as all 2 hours of the complete symposium are available to watch as a streaming video from <http://streamer.cen.uiuc.edu/seminars/peet/peet2-3-4.wmv> (Windows Media Player required).

ACKNOWLEDGEMENTS

I thank Kipling Will and Paul Hebert for taking part in the debate, Mike Irwin and Gail Kampmeier for organizing the fifth biennial PEET conference, and the National Science Foundation for financially supporting this meeting. Kevin Cummings, Martin Hauser, Andrew Miller, Mark Wetzle, and Kazunori Yoshizawa provided specimens and in some cases unpublished DNA sequences that were used during the species identification demonstration in this session. Martin Hauser, Mathys Meyer, Floyd Shockley, Daniela Takiya, and Jamie Zahniser assisted in the running of the debate. The symposium video was filmed and edited by Ritch Strom on behalf of the office of continuing education at the University of Illinois. Rasplus Jean-Yves, Kevin Johnson, Rod Page, Diana Percy, Vincent Savolainen, Jason Weckstein, and an anonymous reviewer provided comments on an earlier (and considerably different) version of this manuscript. This work was supported by a grant from the National Science Foundation (DEB-0107891).

REFERENCES

- Anonymous. 2003. What's in a name? *Economist* 366:62.
- Blaxter, M. 2003. Counting angels with DNA. *Nature* 421:122–124.
- Godfray, H. C. J., and S. Knapp. 2004. Introduction [to a theme issue 'Taxonomy for the twenty-first century']. *Phil. Trans. R. Soc. Lond. B* 359:559–569.
- Gotelli, N. J. 2004. A taxonomic wish-list for community ecology. *Phil. Trans. R. Soc. Lond. B* 359:585–597.
- Hebert, P. D. N., A. Cywinska, S. L. Ball, and J. R. deWaard. 2003. Biological identifications through DNA barcodes. *Proc. R. Soc. Lond. B* 270:313–322.
- Hebert, P. D. N., and T. R. Gregory. 2005. The promise of DNA barcoding for taxonomy. *Syst. Biol.* 54:852–859.
- Hebert, P. D. N., M. Y. Stoeckle, T. S. Zemlak, and C. M. Francis. 2004. Identification of birds through DNA barcodes. *PLoS Biol.* 2:1657–1663.
- Holmes, B. 2004. Barcode me. *New Scientist* 182:32–35.
- Kurosawa, O., and M. Washizu. 2004. Acquisition and amplification of targeted position of electrostatically stretched DNA. *J. Inst. Electrostat. Jpn.* 28:59–64.
- Lipscomb, D. L., N. Platnick, and Q. D. Wheeler. 2003. The intellectual content of taxonomy: a comment on DNA taxonomy. *TREE* 18:65–66.
- May, R. M. 2004. Tomorrow's taxonomy: Collecting new species in the field will remain the rate-limiting step. *Phil. Trans. R. Soc. Lond. B* 359:733–734.
- Moritz, C., and C. Cicero. 2004. DNA barcoding: Promise and pitfalls. *PLoS Biol.* 2:1529–1531.
- NCBI. 2005. National Center for Biological Information. GenBank statistics available at <http://www.ncbi.nlm.nih.gov/About/tools/restable.stat.html>.
- Nicholls, H. 2003. DNA: The barcode of life? Originally published on behalf of Elsevier by BioMedNet. Now available at <http://www.uoguelph.ca/~phebert/media/BioMedNet%20News%20article.pdf>.
- Pennisi, E. 2003. Modernizing the tree of life. *Science* 300:1692–1697.
- Rodman, J. E., and J. H. Cody. 2003. The taxonomic impediment overcome: NSF's Partnerships for Enhancing Expertise in Taxonomy (PEET) as a model. *Syst. Biol.* 52:428–435.
- Schindel, D. E., and S. E. Miller. 2005. DNA barcoding a useful tool for taxonomists. *Nature* 435:17.
- Tautz, D., P. Arctander, A. Minelli, R. H. Thomas, and A. P. Vogler. 2003. A plea for DNA taxonomy. *TREE* 18:70–74.
- Taylor, R. W. 1983. Descriptive taxonomy: Past, present, and future. Pages 93–134 in *Australian systematic entomology: A bicentenary perspective* (E. Highley, and R. W. Taylor, eds.). CSIRO, Canberra.
- Vincent, M., Y. Xu, and H. Kong. 2004. Helicase-dependent isothermal DNA amplification. *EMBO Rep.* 5:795–800.
- Will, K. W., B. D. Mishler, and Q. D. Wheeler. 2005. The perils of DNA barcoding and the need for integrative taxonomy. *Syst. Biol.* 54:844–851.

First submitted 23 March 2005; reviews returned 9 June 2005;
final acceptance 12 July 2005
Associate Editor: Vincent Savolainen

Syst. Biol. 54(5):844–851, 2005
Copyright © Society of Systematic Biologists
ISSN: 1063-5157 print / 1076-836X online
DOI: 10.1080/10635150500354878

The Perils of DNA Barcoding and the Need for Integrative Taxonomy

KIPLING W. WILL,¹ BRENT D. MISHLER,² AND QUENTIN D. WHEELER³

¹ESPM Department—Insect Biology and ²Department of Integrative Biology, University of California, Berkeley, California 94720, USA

³Natural History Museum, Cromwell Road, London, SW7 5BD, UK

"Your work, Sir, is both new and good, but what's new is not good and what's good is not new."

Samuel Johnson

We argue that DNA barcoding has both new and good elements, but unfortunately no elements that are both. We are strongly in favor of the good idea of using DNA for identification, but that is old hat—the use of DNA for identification goes back to the beginning of molecular

systematics. The DNA barcoders cannot take any credit for that. Their new idea that DNA barcoding can replace normal taxonomy for naming new species and studying their relationships is worse than bad, it is destructive. Statements by some barcoding proponents suggest an inevitable replacement of taxonomic research rather than augmentation of technology to taxonomic science, e.g., "a COI-based identification system will undoubtedly

provide taxonomic resolution that exceeds that which can be achieved through morphological studies. Moreover, the generation of *cox1* (= COI) profiles will provide a partial solution to the problem of the thinning ranks of morphological taxonomists by enabling a crystallization of their knowledge before they leave the field." (Hebert et al., 2003a:319) and "If taxonomists fail to embrace molecular technology, Hebert is clear about the consequences: "There is no more likely death of a discipline than the failure to innovate.'" (P. Hebert as quoted by Nicholls [2003]).

Rather than such a gloomy and narrow prospect for taxonomy we promote using all available resources to build real capacity to do the job right. An overemphasis on the barcoding approach could easily distract taxonomy from its scientific goals and siphon off resources for systematics just at the time it is poised to blossom, thanks to all the integrative programs underway at the U.S. National Science Foundation (NSF) and elsewhere. Contrary to their posturing as cutting-edge, by emphasizing a single gene as a "universal barcode" (Powers, 2004:371), DNA barcoders are returning to an ancient, typological, single-character-system approach. Note that we are not defending "traditional taxonomy" here, but instead we argue that the real cutting-edge future for systematics and biodiversity research is *integrative taxonomy*, which uses a large number of characters including DNA and many other types of data, to delimit, discover, and identify meaningful, natural species and taxa at all levels.

The following text is in direct response to 10 questions selected from issues raised during a DNA barcoding debate between K. Will and P. Hebert held at as part of the fifth PEET conference at the University of Illinois in Champaign-Urbana (20–23 September, 2004). Further details can be found in the adjoining articles in this issue (Smith, 2005; Hebert and Gregory, 2005). Our article is intended to be balanced by responses written by P. Hebert to the same questions. The tone and content of this submission reflects the ad hominem nature of the debate, limitations set by the questions themselves, and context at the time of the debate. Though some aspects of this article may seem to some as "dated" by the time they reach publication, we believe that most of the serious issues remain.

SUBMITTED QUESTIONS AND OUR ANSWERS

1. *Given two billion US dollars (the amount a comprehensive program of DNA barcoding is estimated to cost [Whitfield, 2003]), how would you spend this money to benefit taxonomic and biodiversity research, and what would be the legacy of these data?*

We would use it for education and capacity building, with a true vision for the future! Very simply, the well-worn analogy of the boy and the fish applies here—Give a boy a fish, he eats for a day. Teach a boy to fish and he eats for life. Clearly we have the potential to gain massively if we are willing to invest in the value option of taxonomy and the development of a complex understanding of the

natural world. The basic understanding of what species and higher-taxa are is fundamental to biology and still so controversial that it would be both arrogant and foolish to fail to invest in the human resources necessary to discover, enumerate, and, most importantly, understand biodiversity.

Because of the long history of taxonomy in many Holarctic countries, the major effort and richest taxonomic work, coupled with a broad array of life history data, has been done by taxonomists living within these countries and on their fauna. The most important regions of biodiversity and our worst ignorance of that diversity are in other parts of the world. The greatest long-term impact of this imagined money would come from establishing training opportunities and positions for researchers and students in the parts of the world with the greatest biodiversity to discover. Each of us knows mentors that have produced a cadre of students who collectively have had a tremendous impact on taxonomy, systematics, and biology. Establishment of programs based on models like PEET (www.nhm.ku.edu/peet/), LINNE (Page et al., 2005) (www.flmnh.ufl.edu/linne/default.htm), and ATOL (www.nsf.gov) throughout the world, and support of taxonomic research positions in universities and museums would have a propagating effect into the future of biological research.

The on-going NSF sponsored workshops for LINNE (Legacy Infrastructure Network for Natural Environments) offers a visionary cyber-infrastructure for collections-based "descriptive" taxonomy that would diminish or eliminate many of the obstacles to rapid growth of taxonomic knowledge. Such an approach is driven by taxonomy as a science and would rapidly generate the kind of sound knowledge needed to understand the diversity of life at and above the species level. That research lays the appropriately scientific foundation upon which DNA identification tools should be built. \$US 2 billion would easily fund LINNE and a veritable army of taxonomists who could discover and describe species, expand natural history museums and herbaria to reflect the living world, and elucidate the fascinating patterns of biology worthy of our detailed future study. None of these benefits accrue from a massive barcoding exercise. Capitalizing on theoretical advances in systematics in combination with cyber-infrastructure is a far superior approach and one that paves the way for truly useful DNA and morphological markers to identify species.

With two billion dollars neither DNA barcoding nor a robustly funded effort to address biodiversity using an integrative approach would achieve 100% success by any reasonable measure. The question then is what is gained for the investment. Undoubtedly more "items," in a typological sense, might be enumerated by focusing on a small piece of DNA, but this would necessarily leave details of what is meaningful aside. However, even if fewer items are enumerated per dollar by an integrative approach, these will be evolutionarily significant units, and the ultimate product is scientific with far reaching impacts.