The Scientist
www.the-scientist.com

Taxonomy isn't black and white

DNA barcoding method put to the test reveals new cryptic bird and butterfly species | By Nick Atkinson

Two studies published this week by the University of Guelph's Paul Hebert and colleagues appear to confirm DNA barcoding as a powerful tool in taxonomic diagnostics. But claims and counterclaims about just what the method can and can't deliver continue unabated.

In the first study, published in PLoS Biology, Hebert and colleagues present an analysis of 260 known North American bird species. DNA barcodes—a 648-bp region of the mitochondrial gene cytochrome *c* oxidase I (COI)—are either identical or very similar within species, but differ between species. Of the 260 species examined, all were distinguished using barcodes, and four new cryptic species were discovered.

The second study, appearing this week in PNAS, uses the same technique to demonstrate that the neotropical skipper butterfly *Astraptes fulgerator* is actually a species complex consisting of at least 10 species. According to Felix Sperling, who was not involved in either study, Hebert's work is "an excellent demonstration of the power of DNA barcoding to make sense of a confusing welter of ecological and color pattern variation."

A comprehensive library of DNA barcodes should aid species identification in the field, Herbert said. "Single gene reads will deliver an unambiguous species identification in more than 95% of [animal] cases within a decade," he told *The Scientist*. Very young species might prove the stumbling block, though, for which additional sequences might be informative. "However, a move to multigenic systems for species diagnosis makes no more sense than invoking a scanning electron microscope to separate species that can be recognized by eye," he added.

But Sperling, a taxonomist at the University of Alberta, has reservations concerning some of the claims made by proponents of the technique. "Some of the barcoding apologists have done a disservice to systematics and especially taxonomy by overselling the strengths of the approach in such a single-minded fashion," he said.

"That has created an unrealistic set of expectations among people who are not aware of the weaknesses of the approach, but who have used it to justify replacing classical taxonomy rather than supplementing and strengthening it," Sperling continued.

Craig Moritz and Carla Cicero, authors of a commentary in PLoS Biology, echo these concerns. In what the University of Georgia's John Avise describes as an excellent review of the pros and cons of DNA barcoding, the authors attempt to damp down some of its hype. "The field, as it currently stands, tends to be structured around merely one gene, which for many well known reasons can be misleading about biological connections and discontinuities in nature," said Avise.

A practical difficulty with the approach is to capture molecular geographic variation within each species, said Avise, who was not involved with the studies. "This is especially important for low-dispersal or geographically structured taxa, which probably include the majority of the world's species," he said, adding that Hebert's bird analysis might have fallen foul of this difficulty. "Birds tend to be vagile creatures, and therefore less likely—all else being equal—to show substantial geographic variation than more sedentary species, such as snails or small mammals," Avise explained.

David Schindel, executive secretary of the Consortium for the Barcode of Life, sees the real impact of DNA barcoding as its ability to address applied problems. "Many fields need to draw on systematic expertise for the reliable identification of species, but these potential users have limited access to taxonomic experts. Genetic barcodes provide a kind of interface between taxonomy and the users of taxonomic data," he said.

However Charles Godfray, professor of evolutionary biology at the Natural Environment Research Council Centre for Population Biology, feels that DNA barcoding itself will evolve. "It will complement rather than replace a 250-year tradition of Linnean taxonomy. Whilst studies using the COI sequence are an excellent place to start, the rapidly advancing pace of molecular techniques makes it hard to predict what methods will be used in 20 or even 10 years' time."

Godfray believes that it's up to both camps to shift their positions. "Claims that molecular techniques are a panacea for all taxonomy's ills are overblown," he told *The Scientist*. "However, the subject must embrace and absorb new methods if it's to stay in touch with the real needs of the people who use taxonomic information."

Links for this article
Paul Hebert
http://www.uoguelph.ca/~phebert/

M.L. Blaxter, "The promise of a DNA taxonomy," *Philos Trans R Soc Lond B Biol Sci*, 359:669-79, April 2004.
[PubMed Abstract]

P.D.N. Hebert et al., "Identification of birds through DNA barcodes," *PLoS Biology*, 2:e312, DOI: 10.1371/journal.pbio.0020312, October 2004.
http://www.plosbiology.org

P.D.N. Hebert et al., "Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astraptes fulgerator*," *PNAS*, DOI:10.1073/pnas.0406166101, September 2004.

http://www.pnas.org

Felix A.H. Sperling
http://www.biology.ualberta.ca/faculty/felix_sperling/

C. Moritz, C. Cicero, "DNA barcoding: promise and pitfalls," *PLoS Biology*, 2:e354, DOI:10.1371/journal.pbio.0020354, October 2004.
http://www.plosbiology.org

John C. Avise
http://www.genetics.uga.edu/faculty/bio-Avise.html

Consortium for the Barcode Of Life
http://www.barcodinglife.com/

Natural Environment Research Council Centre for Population Biology
http://www.cpb.bio.ic.ac.uk/