

DNA barcode- DNA Taxonomy

Differentiating DNA taxonomy and DNA barcode identification. Exclusive and mandatory use of DNA data to define species vs. use of a single piece of sequence data to identify species.

What proponents say it is or could be:

"A short DNA sequence that provides an aid to species recognition and identification in a particular domain of life." (Taxonomy, DNA, and the Barcode of Life website)

"We are convinced that the sole prospect for a sustainable identification capability lies in the construction of systems that employ DNA sequences as taxon 'barcodes'." (Herbert et al. 2002)

"...enabling the rapid and inexpensive identification of the estimated 10 million species on Earth" (Savolainen et al., 2005).

How it is proposed to work:

A short sequence (clearly COI is the target), ~600bp, potentially contains enough information to resolve 10-100million species.

A good DNA barcode sequence is conserved enough to be amplified with a broad range of primers while divergent enough to resolve closely related species. COI is thought to have these properties.

The "method"

1. Gather this short sequence from all species with mtDNA.
2. Build "profile" trees.
3. Add unknowns and their identity can be read from the resultant topology.

Purported good properties and possible applications:

Applicable to conservation biology and biodiversity surveys for rapid and accurate identifications. Enumeration of organisms with divergent sequences (MOTU, Gene species).

~1.7 million species described and at least 10 million others are yet to be named. DNA-based identification will allow for flagging specimen that probably represent undescribed taxa.

Will make full use of the knowledge built over the last 250 years of "classical" taxonomy as a scaffold.

When it becomes cheap, it will be available to local non_experts.

Problems acknowledged by Barcode proponents:

The right length of sequence data needed in any given group to recover correct results is not known and probably will vary across taxa. Must be able to distinguish between interspecific and intraspecific variation. Resolving recently diverged species and hybrids may be impossible for COI and there is no way to know when the answer is wrong except in well known and well sampled groups.

No single gene is conserved across all life. So it will take a few at least.

Reference sequences must be from "taxonomically confirmed" specimens.

Problems expanded:

Currently proposed method fails to work, works poorly and/or has only been applied to expensive, unrealistic test cases.

Proposed pilot projects on the Taxonomy, DNA, and the Barcode of Life website-

(all well known and relatively small groups) Primates of the world; Birds of the world; Turtles of the world; Sphingids of the world; Mosquitos of the world; Skipper butterflies of the world; Species of Costa Rica/INBIO Species of Great Smoky Mountains National Park; (circumscribed areas have little use beyond the boundaries and could result in spurious estimates based on the limited sample. Invasive/adventive spp could be misleading.)

What is being said:

"Barcodes are just new tools that like a good screwdriver, can either help immensely or injure mortally, depending upon how vigorously you apply it to sensitive issues." (J. Rawlins)

"Barcoding could also help to identify pest species, or to monitor commercial fishing, says Miller. But it won't replace the traditional methods of identifying and classifying species by their appearance, he says: "It's one more tool in the box, but we will always need backup." [Nature May 2003]

"But there are many,many skeptics, including UC Berkeley's Brent Mishler, who think it's highly unlikely that the cytochrome oxidase I gene can discriminate among all species. Mishler calls the approach "basically terrible and arbitrary," and he worries that spurious counts of biodiversity will result. Hebert predicts that a global bar_code project would require \$1 billion over the next 20 years. So far, NSF officials are lukewarm at best. "It's not research," says NSF's Rodman, who notes that bar codes are still unproven." [Science mag. June 2003]

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." [Biomednet Jan 2003].

"We may see comprehensive barcoding projects within five years," says Hebert, "and it's feasible to imagine a database of all animal life on the planet in 20 years." Such a scheme would cost about US\$2 billion, he says.[Nature May 2003] (~1400 sequences/day to do one each of 10 million species)

Identification does not equal Science: Identification is placing individuals into circumscribed groups or recognizing that they fit none that exist. The science (taxonomy and systematics) to determine those groups would have to be nearly finished for this to even be partially useful beyond identifying (possibly).

How is divergence in COI related to species and interesting biological questions? Fundamentally, barcoding ignores difficult issues of species concepts and boundaries, dynamics of biological classifications and taxonomic hypotheses.

It does not answer the Biodiversity crisis: species diversity; ecological cohesion, evolutionary relationships. Its applicability to conservation biology and biodiversity surveys for rapid and accurate identifications is wholly dependent on current knowledge and expert help.

Claims of using the knowledge built over the last 250 years of "classical" taxonomy seems to imply that there is no future contribution to be made by that type of research. A shift in focus and money would be devastating to biology as a whole, as it does not reduce the need for taxonomists only delays the hard work and reduces the potency of the "encyclopedia of life".