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DNA Barcoding: An Instance of Technology-driven Science?

KIRK FITZHUGH

The recent surge of interest in DNA barcoding as a rapid method for species identification is reminiscent of some recent trends in phylogenetics in which computer-based methods such as maximum likelihood, Bayesianism, and super trees have swept through the systematics community, generating much excitement (Felsenstein 2004). Innovations in computer and nucleotide sequencing technologies have provided biologists of all sorts with a multitude of methodological options. The problem with such advances, however, is that one must beware of them becoming the force driving developments in a field at the expense of the philosophical foundations that form the basis for doing science and judging the merits of methods.

DNA barcoding is a case in point. The results of nucleotide sequencing among organisms of a population seem to demand application to some perceived problem—the problem in this case being species identification. Unfortunately, the focus of most papers on DNA barcoding has been the question of utility, that is, can species (new ones as well as established ones) be accurately identified through the use of some set of sequence data? For instance, a recent volume of the *Philosophical Transactions of the Royal Society of London B: Biological Sciences* is dedicated to just this topic, with a paper by Savolainen and colleagues (2005) providing a nice overview of the method. Yet although proponents and detractors of barcoding have presented many arguments, virtually nothing has been said by either side regarding its philosophical and scientific underpinnings. What I wish to address here is that the convenience of technology seems to have blinded us from identifying the fundamental issue that calls into question the scientific merits of DNA barcoding: the interpretation of the term "species."

Are species classes, that is, the mental constructs consisting of compilations of objects, based on properties of those objects? Or do species have the ontological status of objects or individuals? (Objects and individuals, in contrast to classes, exist independent of our perceiving them, although they must have discernible properties for us to recognize them.) Or is a species something else altogether, as I contend, neither class nor individual? Such vexing questions have resulted in a voluminous literature—there are over 20 species concepts from which to choose (e.g., Mayden 1997). Yet no answer is in sight that would indicate that biologists are approaching any sort of consensus. The lack of a generally accepted definition for the term is a problem that advocates of DNA barcoding are unwise to ignore.

For DNA barcoding to be successful, it must function like a sieve or net. Just as the appropriate mesh size for a net will determine whether or not target individuals are collected, we might hope that screening using appropriate nucleotide sequences—barcodes—will ensure that existing and new species are unambiguously identified. But for DNA barcoding to be used this way, species must be assumed to have the status of individuals that can be discerned through nucleotide sequences.

The view that species are individuals has been popular for the past 30 years or so. Species are said to have this status because they are born, are temporally and spatially restricted during their existence, and eventually die. But a more fundamental criterion for recognizing individuality must be met. Individuals, as opposed to classes or any other sort of mental construct, can be experienced by way of the properties of those individuals. As a consequence, we do not experience species, but rather individual organisms. We perceive the properties of those organisms, not of species or other taxa. A nucleotide sequence is a property of a given organism, not of a species. Such a sequence could not therefore be used to discern a species as individual.

I have argued elsewhere (Fitzhugh 2005, 2006) that species names refer to neither individuals nor classes, but rather to scientists' explanatory hypotheses. These hypotheses account for specifiable properties of organisms as the products of a set of past reproductive events distinct from other possible sets of such events. If individuals a, b, and c have nucleotide sequences of type α, the species name X signifies that the presence of α among a, b, and c is a collective effect of past reproductive events among past individuals with α, in contrast to individuals with sequences of type ß, γ, δ, etc. Such hypotheses about individual organisms in the past provide understanding of the perceived properties of organisms in the present. Although the past events involved individual organisms, the hypotheses are not themselves individuals, but rather explanatory constructs.

On the other hand, could barcoding be used to identify species as hypotheses? I have pointed out (Fitzhugh 2005, 2006) that species hypotheses, as well as supra-

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specific (i.e., phylogenetic) hypotheses, are the products of nondeductive reasoning. One of the central tenets of nondeductive reasoning is that inferences must fulfill what is known as the requirement of total evidence. This requirement simply states that for one to rationally believe a conclusion on the basis of some set of evidence, then all available relevant evidence must be taken into consideration (Carnap 1950). Evidence is relevant if it provides support for or against a conclusion; it is irrelevant if it provides neither positive nor negative support.

The requirement of total evidence makes it impossible for advocates of barcoding to claim that species can be rapidly identified just through the analysis of a segment of nucleotide sequence. If a species is a hypothesis, a systematist who observes the properties of an organism engages in an inferential process that brings the effects of past reproductive events into an explanatory nexus. This must be based on all relevant evidence, not just sequence data. The requirement of total evidence cannot be satisfied if species hypotheses are based only on nucleotides, to the exclusion of other relevant properties in need of explanation in terms of past reproductive events. To assert that sequences for a group of organisms form the basis for inferring a species hypothesis, a DNA barcoding advocate would have to assume that there is no other available relevant evidence to be considered. If this assumption cannot be met, then the basis for accepting the hypothesis is less than rational, and it should not be tolerated in science.

DNA barcoding has garnered favorable interest because it is a potentially productive technological advance that might serve noble motives. Yet successful species identification cannot be the principal criterion for evaluating the viability of the method. Advocates of barcoding have not addressed adequately the matter of what is meant by the term "species." That issue alone should preclude large-scale implementation of barcoding for species identification until there is a consensus of opinion. But if it is true that species represent explanatory hypotheses, not classes and not individuals or objects—thereby denying the whole notion of "identification"—then the requirement of total evidence presents an insurmountable obstacle to the method. Rather than arguing about methodological nuances of DNA barcoding, biologists should be facing up to more significant, philosophical problems that need to be overcome first.

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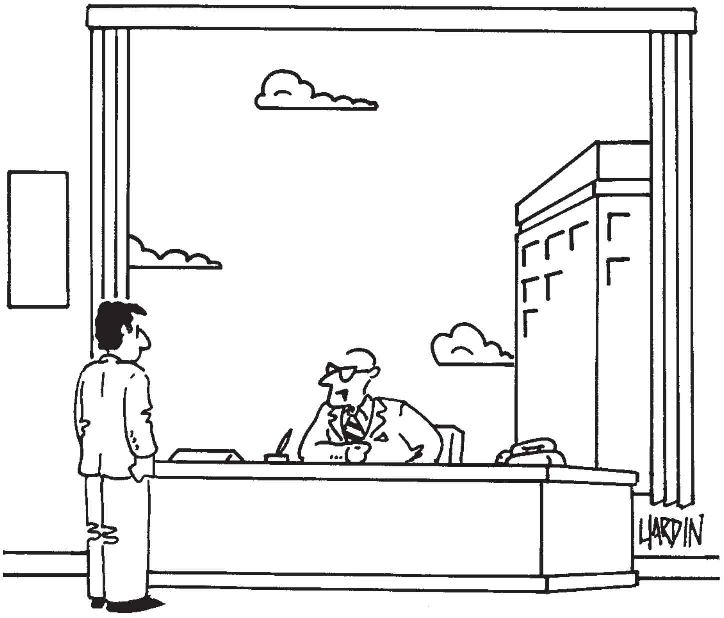

"Henderson! Find some DNA that matches mine and be quick about it!"