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Myth of the molecule: DNA barcodes for species cannot replace morphology for identification and classification

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Abstract

So-called DNA barcodes have recently been proposed to answer the problem of specimen identification and to quantify global biodiversity. We show that this proposition is wanting in terms of rationale, methodology and interpretation of results. In addition to falling short of all its stated goals, the method abandons the benefits of morphological studies in favor of a limited molecular identification system that would ultimately impede our understanding of biodiversity.
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''If the only tool you have is a hammer, you tend to see every problem as a nail.' Abraham Maslow

DNA barcodes for species-level identification may, at first glance, seem to represent an appropriate use of new technology to solve an old problem—identifying and classifying the world's biodiversity. Working toward this goal of understanding biodiversity is commendable, but we see serious flaws in the rationale, methodology, and interpretation of results involved in abandoning morphological studies in favor of a narrow and wholly molecular identification system, as suggested by Hebert et al. (2003a). Recently the concept of DNA taxonomy, of which the DNA barcode is one instance, has been hotly debated (Tautz et al., 2002, 2003; Lipscomb et al., 2003; Pennisi, 2003; Scotland et al., 2003a; Seberg et al., 2003) and the DNA barcode concept in general has been challenged (Scotland et al., 2003a; Sperling, 2003). Despite these significant challenges and existing literature suggesting that the method of DNA barcodes is unsound, claims that the technique has been validated are still being published (Hebert et al., 2003b; Stoeckle et al., 2003; Stoeckle, 2003; Whitfield, 2003; including many references at the website). Herein we demonstrate, using the examples published by Hebert et al., that the methodology fails not only theoretically, but also on a practical level. Additionally, we develop arguments and synthesize previously published views (e.g. Scotland et al., 2003a; Sperling, 2003), specifically applying them to claims made by Hebert et al. (2003a). The intent of this paper is to clarify the practical and theoretical shortcomings that would result from the adoption of a DNA barcoding system to identify biodiversity.

Discussion

Obviously there are many more species-level taxa to be recognized and specimens to be identified, even by conservative estimates (Novotny et al., 2002), than the present or predicted levels of manpower can handle given the limitations of current technology. As a result, users of biological classifications are interested in streamlining procedures to arrive at a confidently applied, uniform taxonomic concept for organisms under study. Hebert et al. (2003a) presented methods that attempted to shortcut these identifications and respond to the dearth of taxonomists.

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