



Integrative taxonomists should use and produce DNA barcodes

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Put simply, DNA barcoding (DNAB) is an identification method that aims to relate short, specific DNA fragments from unidentified specimens to sequences of *previously identified* voucher specimens through comparison of sequence divergence (Hebert *et al.* 2003). DNAB has produced noticeable success in terms of scientific citation and media coverage because it is technically feasible, commercially attractive, and philosophically acceptable to many scientists (Smith 2005). Irrespective of the utility to the general public (Cameron *et al.* 2006), and contrary to other DNA-based methods with taxonomic purposes (Vogler & Monaghan 2006), identification through DNAB is becoming widely available (www.barcodinglife.org). While DNAB is rejected by some taxonomists who view it as a competitor for funds, or a danger to taxonomy (Will & Rubinoff 2004; Ebach & Holdrege 2005), we argue for the complete incorporation of DNAB into integrative taxonomy (*sensu* Will *et al.* 2005).

The goal of DNAB coincides with the first step of any taxonomic research: the sorting of collected specimens into previously described species and the detection of putative new ones. DNAB and classical (morphology-based) taxonomy suffer from similar impediments for completing biodiversity inventories. Some of these impediments are: (1) overlap in intra- and interspecific character variation (Vences *et al.* 2005), (2) incomplete geographic or taxonomic sampling (Wheeler 2004; Vences & Köhler 2006) and (3) the need to rely on pre-existing taxonomic hypotheses (Kerr *et al.* 2007). At this point, the joint effort of DNAB and classical taxonomy cannot be negative in any sense. However, DNAB does not overlap with the last step of any taxonomic research, that is, description and naming of new taxa. In other words, DNAB can be fully integrated into taxonomic practice without supplanting classical taxonomy.

It is well known that classical taxonomy has important problems that seriously impede taxonomic progress (Bello *et al.* 1995; May 2004). Most museum types wait decades to be revised by specialists. Many hypotheses, in the form of species names and synonyms, still need to be tested by other criteria. Unknown species remain hidden in jars on dusty stands of dark museum basements, awaiting the birth of a specialist or threatened by the imminent death of the last living one. Many described species are known only from a faded holotype, and often the types have been lost. Many species have not been found since the original descriptions. Most diversity is hidden in remote tropical areas where much collecting is still needed. In this scenario of limited funding and intimidating impediments, in a world where life recedes and there is no time to lose, DNAB should not be the enemy but the ally of taxonomy.

In fact, the Encyclopaedia of Life (Wilson 2003) was envisioned to be built on an integrative taxonomy, combining internet and other digital resources, natural history data and DNA sequences, before most species perish. Under this perspective, taxonomists and molecular biologists should collaborate in the establishment of appropriate guidelines for the use of DNA barcodes *for each taxon*. This would not only ensure that the transference of DNAB to the public would not be divorced from other taxonomic knowledge, but would also work against some of the taxonomic impediments. Current joint efforts of DNA barcoders and taxonomists are injecting new energy into museum research by promoting the digitization of databases and pictures, and the review and sequencing of specimens. The resulting information is being made available through the web (e. g. BOLD, All Bird Barcoding Initiative, All Leps Campaign, Fish BOL). For example, as posted by Gert Worheide on Evoldir (10th December 2006), the Sponge Barcoding Database ([available at www.spongebarcoding.org](http://www.spongebarcoding.org)) combines *sponge-specific* conventional taxonomic information with *DNA sequences* and integrates first-hand morphological descriptions by recognized taxonomists, voucher-associated DNA sequences, and distributional information. New sequence submissions must include a morphological description and species identification of the voucher that will be verified by an *expert in the group* before being made available to the public. This record is linked to the World Porifera Database, which provides updated information about species names.

However, DNAB of known species is not enough. If we are in a hurry because species are becoming extinct, molecular biologists should also encourage efforts to collect tissues, specimens, and natural history data in those areas

that are being destroyed. We doubt that even any classical taxonomist would oppose an international large-scale DNAB project where the collection of specimens and tissues and the integration of classical taxonomic knowledge were the first steps. Surely, integrative taxonomists would not reject such a proposal either.

In summary, we consider that DNA barcoders pursue similar goals to those proposed by taxonomists to overcome the taxonomic impediments. Integrative taxonomy must be their rendezvous, and this must be seen as one of the important challenges taxonomy has ahead to fulfil its necessary revitalization (Wheeler & Valdecasas 2005).

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