

Barcoding helps biodiversity fly

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An essential part of good taxonomy is correctly identifying species. With correct identification, basic research objectives (e.g., correct ecological and evolutionary interpretation; ref. 1) and many practical applications (e.g., effective fisheries management, integrated pest control programs, and the conservation of biodiversity; refs. 2 and 3) are at least attainable. Without it, the odds of success in these realms are indeed slim. A recent addition to the taxonomical toolbox has been the application of DNA sequence information for both identifying and classifying an organism, much as a barcode identifies supermarket products (4, 5). In a recent issue of PNAS, Smith *et al.* (6) applied this increasingly common genetic methodology to cross-check species identifications of Tachinid flies in the genus *Belvosia* from the intensively studied Area de Conservacion Guanacaste in Costa Rica. In doing so, they have approximately doubled the local species count for these ecologically important parasitoids of herbivorous moth caterpillars and discovered that what had previously been thought to be three host-generalist species is in fact a suite of relatively host-specific cryptic species. These findings provide insight into a number of fascinating ecological and evolutionary questions and demonstrate the great potential for enlightened collaboration among ecologists, taxonomists, and geneticists who want to uncover and ultimately protect global biodiversity.

The simplest message coming from this work is that the number of recognized species on Earth is larger than we knew and likely much larger than we thought. Parasitoids are currently believed to constitute 8–25% of all insect species (7), and the discovery of cryptic, largely host-specific species will push both proportional and absolute numbers higher. As is the case with parasitoids in general, the Tachinid flies serve an extremely important ecosystem function: they help control outbreaks of the caterpillars that might otherwise defoliate large portions of the habitat (7–9). As such, correctly understanding the natural history of these parasitoids, the host caterpillars they feed on, and the host plants the caterpillars feed

on can have landscape-scale implications. Further, similar findings of cryptic or undiscovered species in other groups [bacteria (4, 10), algae (11), mycorrhizal fungi (12, 13), marine invertebrates (1, 14), and insects (15–18)] indicate that we are often woefully ignorant of what biotic diversity actually does exist and how it is distributed. In general, these kinds of studies consistently show more species with greater host specificity than previously thought. This cryptic diversity suggests that, even in the case of what appears to be extreme rarity of both hosts and conspecifics, individuals are usually able to find food and mates frequently enough so that the net effect is to keep their species viable.

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The observation of occasional cases in which a particular *Belvosia* species successfully parasitized a caterpillar species that is not normally its host is striking from a number of respects. Without the extensive collections and their detailed analyses, this signal would likely never be picked up (see refs. 15–18). Thus, within a general ecological pattern of very tight host specificity in these flies, there are apparently enough cases of host shifts or polyphagy (see refs. 15–18) to allow evolutionary opportunities for phylogenetic radiation across a suite of potential hosts (see ref. 15). Ultimately, the degree to which one observes or declares “host specificity” depends on how deeply one samples and whether the criterion is presence/absence versus relative abundance (see ref. 19). Likewise, the degree to which that host specificity is deemed important will hinge on whether the researcher is more interested in short-term ecological processes (e.g., for possible applied/biocontrol uses of the parasitoids) or longer-term evolutionary ones.

More broadly, Smith *et al.*'s study (6) represents the confluence of “Barcode of Life” genetic taxonomy (ref. 20 and www.barcodinglife.org), classical morphological taxonomy, and “use it or lose it” concepts of conservation of biodiversity (ref. 5 and <http://janzen.sas.upenn.edu>). In discussing their work, lead author Smith pointed out that these collaborations both suggest and make possible new research directions. The discovery of cryptic species is really just a starting point that enables more precise questions of coevolution, parasitoid ecology, and parasitoid physiology to be formulated and addressed. Coauthor Woodley concurred. Having sorted the specimens “blind” (without knowledge of host species), Smith *et al.* found that individuals within some of the groupings showed little morphological variation, whereas others showed considerably more. The additional data from genetics open a new set of possibilities for generating and testing hypotheses of how (or if) different types of morphological variation are connected to species boundaries.

All in all, these results, in conjunction with earlier work (15), support the notion that cryptic species are more prevalent in tropical regions than has been previously thought. Although not everyone is able to “Imagine a world where every child’s backpack, every farmer’s pocket, every doctor’s office, and every biologist’s belt has a gadget the size of a cell phone. A free gadget. Pop off a leg, pluck a tuft of hair, pinch a piece of leaf, swat a mosquito, and stick it on a tuft of toilet tissue. One minute later the screen says *Periplaneta americana*, *Canis familiaris*, *Quercus veriginiana*, or West Nile virus in *Culex pipiens*” (5), everyone should be able to appreciate the value of DNA barcoding in uncovering hidden diversity. This is especially true when coupled with traditional taxonomy and a keen appreciation of the fascinating details of basic natural history.

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