

LETTERS

Edited by Jennifer Sills

A genomics revolution in amphibian taxonomy

Amphibians feature the highest rates of both new species discoveries and species declines among vertebrates worldwide (1). To characterize this diversity faster than it disappears, zoologists have been using molecular data to rapidly describe new frog and salamander lineages, from species to family levels (2). About a third of the approximately 8500 known amphibian species (3) were first described in 2005 or later (4). However, mainstream species description practices relying on one or a few genes are critically flawed.

The majority of taxonomic descriptions rely on a few mitochondrial or nuclear-encoding genes (known as DNA barcodes). Because the variation of a small set of genes is often poorly indicative of the true evolutionary history of populations, overreliance on DNA barcodes distorts our perception of species diversity and distributions (5). In addition, a substantial proportion of newly identified amphibians merely consist of populations of the same species separated

by geography that differ at the few genes analyzed. The ongoing trend of splitting such genetic lineages into multiple species (“phylogenetic species”) artificially increases the total number of species identified on Earth (an issue known as “taxonomic inflation”), a shortcoming that complicates conservation, social, and economic decision-making (6).

Emerging genomic data are demonstrating the risks of these practices (7). The unreliability of frequently used DNA barcodes appears to be more common than previously assumed. Any new amphibian taxon supported mostly by mitochondrial divergence could be a “ghost lineage” (i.e., not a real extant species). Furthermore, it might be affiliated to the wrong clade, and its rank as a “species” might be inappropriate. Its name might also be mistaken because the type locality (i.e., the reference population where the taxon was first described) was misidentified (7).

Because of these ambiguities, the massive number of recent amphibian species descriptions will undoubtedly require time-consuming taxonomic revisions in the near future. To limit the confusion, we call for more cautious interpretations of genetic data in testing new species hypotheses. Given their higher resolution, genomic datasets will ultimately recover any structured population as unique

genetic lineages, rendering the idea of “phylogenetic species” obsolete (8). The rise of genomics in taxonomy will inevitably require a conceptual revolution.

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Comprehensive support for diversity in STEM

In their Policy Forum “Achieving STEM diversity: Fix the classrooms” (3 June, p. 1057), J. Handelsman *et al.* explain that past interventions have not resulted in equitable representation for students from historically excluded communities in science, technology, engineering, and mathematics (STEM). We agree that implementation of their suggested classroom changes would likely contribute to greater persistence and retention in STEM throughout college. However, fixing the classroom alone will not be sufficient. If we are to achieve a fully inclusive workforce (1, 2), we need a comprehensive approach that simultaneously and collaboratively addresses factors both within and outside the classroom (3).

Recruitment into a scientific discipline requires classroom experiences that stimulate curiosity and foster the sense that a career in the field is possible (4, 5). Once student interest is piqued, retention demands financial, mentoring, and advising support (6), all of which occur outside the classroom. Achieving positive change in workplace demographics requires increased attention to postgraduation factors. For instance, employers must reconsider where and how they advertise positions to reach diverse populations. They must also recognize that stating preferences for candidates with work or



The green toad (*Bufotes sitibundus*) has been misidentified as a result of overreliance on single-gene barcoding.

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