ESSAY 11.10. FILLING THE BLACK HOLE: CHALLENGES IN TAXONOMY TO PROTECT AMPHIBIANS

Less than 10% of species on the planet have been discovered and fewer than 1% are known beyond brief anatomical descriptions (Wilson 2005). Without a doubt, our alarmingly inadequate knowledge of the Earth’s biodiversity is one of the most significant challenges to effectively protect threatened species, all the more urgent as biologically rich regions are destroyed at unprecedented rates.

An excellent example of the significance of this problem is provided by extinction risk assessments, such as those integral to the Global Amphibian Assessment. However, Red Lists of threatened species only evaluate formally described species. Although undescribed species may well have a high risk of extinction, they are ignored by conservation initiatives that rely on information contained within the IUCN Red List. Therefore, filling this taxonomic void should be a priority for the implementation of effective conservation programmes.

Among terrestrial vertebrates, sampling of amphibians appears to be particularly incomplete. This is indicated by the large number of species described during recent decades (for example, see Figure 1) at a rate of discovery that exceeds that of every other vertebrate group (Cannatella and Hillis 2004). During the period 1982–2003, the number of species of amphibians increased by 25% with most of the additions being new discoveries rather than subspecies elevated to the species rank (Kohler et al. 2006; and see Essay 1.1). Recent estimates indicate that the number of amphibians awaiting formal description in Southeast Asia and the Neotropics should be well above 1,000 (see below). These figures suggest that, at a global scale, the taxonomic deficit could be a serious obstacle for the success of any comprehensive programme to protect amphibians. Thus, intensive efforts in taxonomy and systematics are indispensable to secure adequate conservation measures.

Fortunately, the increasing use of genetic markers in systematics could increase the rate at which amphibian species are discovered. These tools quantify genetic variation within and among populations, which can expose genetic clusters that correspond to separate species. These data are usually complemented with geographic distribution, and morphological, or behavioral data to corroborate species identities. The use of genetic markers allows the identification of previously unsampled species and enables us to detect cryptic species that have previously been hiding under a single morphologically identified species. The available techniques include allozymes, ARPs, microsatellites, and, most prominently, DNA sequencing (including DNA bar-coding; see Essay 11.11).

Genetic markers have been used recently to estimate the number of species of amphibians that remain to be discovered. In a review of species-level molecular phylogenies of Neotropical amphibians, Ron et al. (2006) found that phylogenetic studies have lead to a 26% increase in the number of known species. The increase was higher (39%) for studies where taxon sampling has been more intensive (i.e., studies that included more than 50% of the described species). This indicates that a significant number of species have either been overlooked by morphology-based taxonomic reviews or have not been sampled at all.

Given that there are approximately 2,800 described species of amphibians in the Neotropics and assuming, conservatively, that the proportion of undescribed amphibians lies between 0.29 and 0.39, then the number of Neotropical species awaiting description should lie between 784 and 1,092. This estimate is considered conservative because the proportion of species discovered should increase with taxon sampling, which until now has been exhaustive only in a few Neotropical clades. Phylogenies with non-exhaustive sampling often include predominantly species of easy access, available in the pet trade (e.g., poison-arrow frogs of the genus Dendrobatidae) and/or distributed in habitats that, because of their relative accessibility and conspicuousness, are already described.

Applying the same logic and approach to another amphibian species-rich faunal region (Indo-China, and the island archipelagos of the Philippines, Malaysia, and Indonesia), we can provide estimates of the magnitude of the problem of underestimated biodiversity using the recent phylogenetic studies of Evans et al. (2003), Brown (2004), and Stuart et al. (2006). Our estimate of undetected species in this region lies between 271 and 384 undescribed forms. We can further examine the trends in one small oceanic island archipelago country (the Philippines) that has been the subject of recent intensive diversity assessment (see http://www.harpwatch.org) and “ground truth” these estimates with first-hand knowledge of new species awaiting description. The estimated numbers for the Philippines lie somewhere between 32 and 43 undescribed species (see Essay 3.3). We also have personal knowledge of approximately 55 undescribed species awaiting description in the genera Phyllomedusa and Litoria from the Philippines and Sulawesi (R. Brown, A. Diesmos, and A. Alcala, unpubl.), suggesting again that the estimation process is conservative.

Advertisement calls provide a cost-effective tool for species discovery and identification. Male Trachycephalus venulosus (Least Concern) call by inflating large lateral vocal sacs. They occur in dry forests in western Ecuador. © Santiago R. Ron.

A potential caveat with molecular techniques is that some genetic markers are inadequate to define species boundaries because they either have evolved too slowly or too fast. In addition, the use of genetic markers is still limited in developing countries, precisely in the regions where the taxonomic void is more extensive. Thus, species identification in many circumstances will continue to rely primarily on morphological or behavioural traits.

An alternative to discover morphologically cryptic species is through analysis of advertisement calls. In anurans, males produce advertisement calls which function to attract females, defend territories, or confront competing males. Because advertisement calls also have a function in species recognition and discrimination (Gerhardt and Huber 2002), they can be excellent indicators of species boundaries, in some cases as reliable as genetic markers. In one increasingly well-studied group, the Ceratobatrachidae frogs of Southeast Asia and the South-West Pacific (Alcala and Brown 1999), advertisement calls have provided a small group of modestly-funded researchers with a powerful means of species delimitation. Combined with analysis of mitochondrial gene sequences, advertisement calls have served as the primary set of characters for the recognition of more than 45 undescribed species over the past 10 years. Of approximately 60 species for which sequence data and call data are both available (Brown 2004, unpubl.), only two cases exist where sequence data and call data lead to differing conclusions with regards to the distinctiveness of a species. Both are cases in which populations of frogs possess very distinctive advertisement calls, but are genetically indistinguishable from sympatric congeners, and both are suspected cases of hybridization and introgression.

The overwhelming trend that results from this work is the general conclusion that genetic and call data are both very illustrative tools for identification of cryptic independent evolutionary lineages, particularly when used in complimentary fashion by field workers.

Figure 1. An example of the large number of amphibians that remain to be described is given by the accumulated number of formally described species of amphibians in Ecuador (period 1758–2006). The number of species has almost doubled since 1970 and additions continue at a fast rate, especially from montane habitats.

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References


