

# Museum collections: Mining the past to manage the future

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We are in the midst of the sixth mass extinction (1), and we are watching species disappear faster than we can describe them (2). Three of the major drivers of extinction, emerging infectious diseases (3), invasive species (4), and threats from climate change (5), are especially difficult to address because of their rapid spread, broad geographic effects, and widespread impacts on entire classes (6) or ecosystems (7). We urgently need a better catalog of the abundance and distribution of species on the planet and a broader understanding of biotic (e.g., parasites, diseases, seed dispersal, pollination, predation, and competition) and abiotic (e.g., ecophysiology and climate change) factors that influence species biology. Achieving this requires more field biologists, more collections, and more synthesis of existing data—a considerable challenge that is exacerbated by the strained budgets and rapid timelines at hand. We need to get creative. A study published in PNAS (8) exemplifies how we can make better use of existing research infrastructure and obtain information from old materials.

Cheng et al. (8) modify an established technique to develop a diagnostic for the presence of the lethal *Batrachochytrium dendrobatidis* (*Bd*) fungus in preserved amphibian specimens. Cheng et al. (8) use specimens of salamanders collected almost 40 y ago from Mexico, Guatemala, and Costa Rica to test the spreading pathogen hypothesis (SPH). They found that *Bd* first appeared immediately before population declines in each instance, supporting the SPH (9, 10) for northern Central America and extending the extent of proposed epidemic waves from Mexico in 1970 to Panama in 2010. This finding is important because of the debate surrounding the potential causes of declines of *Incilius [Bufo] periglenes*, the golden toad at Monteverde (10, 11), as well as reports that climate change might have been involved in declines of salamanders in Mexico and Guatemala (12).

This technique may help researchers determine the timing and location of arrival—or emergence—of *Bd* around the world. For example, examination of amphibian specimens in museum collections might provide better resolution of the timing of *Bd* arrival into populations of *Atelopus* in Andean South America and may inform the debate as to the role of climatic conditions in the



Fig. 1. An undescribed species of *Diasporus* from El Cope, Panama.

spread of *Bd* in these areas (13, 14). Closer to home, this technique will be especially useful in reconstructing the history of *Bd* in the United States. *Bd* is currently found throughout the country ([www.spatalepidemiology.net](http://www.spatalepidemiology.net)), but the timing of its arrival or emergence is not known, particularly in the Midwest and eastern United States. Despite widespread reports of population declines in woodland salamanders (15) reminiscent of those reported by ref. 12 in Mexico and Guatemala, *Bd* has yet to be definitively linked to historic population declines in these regions. Fortunately, thorough surveys, extensive collections, and baseline population data are available and offer rich avenues for exploring these questions. Finally, this (8) technique might help resolve the search for the first origins of *Bd*. Intriguing results from ref. 16 showed high genetic diversity of *Bd* in Japanese amphibians, which suggests a long co-evolutionary history. Examination of Japanese specimens using this technique might identify natural controls on *Bd* and shed light on the vectors and routes that led to its global distribution.

An especially interesting application of this (8) finding is that this technique may also aid in the discovery of microbial symbionts that may affect disease dynamics, such as *Janthinobacterium lividum* (*Jliv*). *Jliv* is a naturally occurring bacteria that lives on amphibians and can reduce or eliminate *Bd* infections (17). *Jliv* has been applied as an experimental treatment for *Bd* in wild populations (18). What is not known is the geographic or taxonomic distribution of *Jliv* either currently or historically, its association with amphibian populations, or its effect—if any—on the spread of *Bd* through those populations. By using this (8) approach, we can use museum collections to describe the history

of *Bd* and determine whether its spread has negatively affected the distribution of amphibian species (19) and if it has caused a corresponding increase in the distribution of *Jliv*. More generally, knowing where *Bd* and *Jliv* occur today, how they interact, and where they occurred in the past will help us understand the spread of both across the landscape and may help us keep *Bd* out of as yet uninfected areas such as Madagascar and Papua New Guinea.

However, despite the promising applications of this (8) tool, we are still limited in quantifying the true effect of *Bd* on amphibian biodiversity, and this hampers effective conservation efforts (Fig. 1). We lack information on population demography for most amphibian species and from many habitats around the world. We cannot understand population decline and recovery without accurate estimates of population size, life history traits, and changes in abundances after the arrival of *Bd*. If we had better estimates of abundance and survivorship among species and sites at different stages of disease, we could determine why some populations decline and do not recover, whereas others are able to persist. Knowing which life stages are most sensitive to losses and which are important for population recovery will be key in managing recovery. This requires time- and labor-intensive fieldwork, population modeling, and analysis.

Training more taxonomists and field ecologists—as well as parataxonomists and paraecologists—is part of this effort as is expanding international collaborations and building in-country capacity, but also part of this is the use of technology to provide access to museum materials to our colleagues around the world. Encouragingly, we have a rapidly growing toolbox to assist in cataloguing, describing, and studying biodiversity thanks to advances in technology and knowledge in the fields of bioinformatics, computational biology, molecular biology, remote sensing, and physiological modeling. This allows us to analyze minuscule amounts of material from valuable specimens or visualize internal anatomy with imaging technology and software.

Author contributions: K.R.L. wrote the paper.

The author declares no conflict of interest.

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Another strategic option is to be more creative in harnessing the power of the internet and an engaged community of citizen scientists to amass distributional data of widespread species around the globe. Using smart phones and other handheld devices, we can collect valuable location data through websites such as Amphibiaweb and INaturalist. We must continue to develop innovative communication and visualization technologies to allow electronic exchange of images, ideas, and written materials. By using photographs, expert identifications, and global positioning system locality data, scientists and citizens could collaborate to gather

data across entire regions to determine where species and populations are present. Additional data collection and experimentation can be incorporated into this research to determine whether climate, disease, or invasive species are associated with those declines.

In the face of global epidemics, our knowledge of historical amphibian richness, genetic variation, and a host of other ecological data (e.g., natural parasite loads, symbiotic bacterial communities, and commensals) is crucial for predicting and preventing extinctions. We need to expand our research, and in the meantime, we need to be more resourceful in increasing scientific knowledge, whether it is

in exploring remote regions of the world where collections are limited or improving distribution maps in our own backyard. Cheng et al. (8) exemplify just one opportunity to better use the products of existing research infrastructure. We must continue to improve our ability to obtain unique information from existing materials, combine old data in new ways, and synthesize existing information to derive new insights or direct the collection of new material.

**ACKNOWLEDGMENTS.** Work on amphibian disease ecology in my laboratory is supported by National Science Foundation Grants DEB 0815315 and DEB 0717741.

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