

# Chapter 16

## The Roles of Taxonomy and Systematics in Bat Conservation

Susan M. Tsang, Andrea L. Cirranello, Paul J.J. Bates  
and Nancy B. Simmons

**Abstract** Taxonomy—the description, naming, and classification of organisms—and systematics—the study of the evolutionary relationships of organisms—are both crucial components in conservation, providing a necessary framework for any conservation initiative. With more than 200 new bat species identified or raised from synonymy in the past decade and additional taxa described monthly, the Age of Discovery is ongoing for bats. New taxonomic and systematic discoveries clarify the status of populations, and the recognition of distinct species and lineages allows appropriate conservation strategies to be crafted, increasing the likelihood of recovery. In addition to identifying species and specimens, taxonomists care for vouchers, provide species lists for localities, and communicate taxonomic ideas to non-experts, especially through descriptions, keys, and field guides. Taxonomists can also provide conservation planning tools such as inventory data, estimates of extinction risk and extinction rate, and information for defining protected areas. Despite the importance of taxonomy, a lack of financial and institutional support impedes the training and employment of taxonomists and such factors need to be

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S.M. Tsang (✉)

Department of Biology, City College and the Graduate Center at the City  
University of New York, New York, NY 10031, USA

e-mail: stsang@amnh.org

S.M. Tsang · A.L. Cirranello · N.B. Simmons

Department of Mammalogy, Division of Vertebrate Zoology, American Museum  
of Natural History, New York, NY 10024, USA

e-mail: andreacirranello@gmail.com

N.B. Simmons

e-mail: simmons@amnh.org

P.J.J. Bates

Harrison Institute, Bowerwood House, St. Botolph's Road, Sevenoaks, Kent TN13 3AQ, UK

e-mail: pjjbates2@hotmail.com

overcome. Taxonomic and systematic discoveries, especially those involving cryptic species and unrecognized diversity, are rapidly increasing with the advent of modern genetics. Researchers must be cautious to argue from multiple lines of evidence when naming new species and be clear about the species concept they employ, as these have wide ranging impacts beyond taxonomy. Creating new ties between taxonomists and non-experts will be crucial in conservation of a diverse range of organisms in increasingly fragile landscapes.

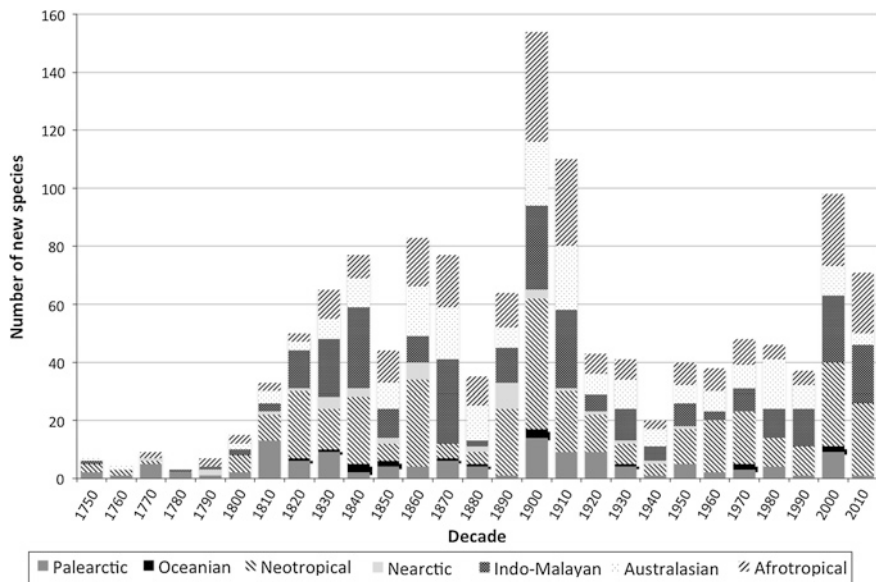
## 16.1 Introduction

Global biodiversity is being lost at an unprecedented rate as a result of environmental change and human activity. Like other organisms, bats are at risk and many populations and species are threatened. As of 2013, the International Union for Conservation of Nature and Natural Resources (IUCN) Red List recognized 81 bat species as Near Threatened, 95 as Vulnerable, 51 as Endangered, 26 as Critically Endangered, and 5 as Extinct (IUCN 2014). It is clear that decisions must be made now to combat ongoing loss of species and populations. However, appropriate management decisions cannot be made without a marriage among conservation biologists, taxonomists, and legislators. Before conservation strategies can be implemented, the species composition of a locality must be well understood; otherwise, the effectiveness of any conservation effort cannot be accurately quantified.

Clearly defining species boundaries—while often difficult—is crucial to basic research and conservation. Some level of agreement on the organisms and populations considered part of any species is necessary for studying and tracking the health of organisms and ecosystems. Taxonomy—the description, naming, and classification of organisms—provides this necessary framework. Taxonomy, along with classification, often is conflated with systematics (Schuh 2000), which is more properly defined as the study of the diversification and evolutionary relationships of organisms through time. Despite often being used interchangeably, they are distinctly different, though systematic research includes recognition of taxa (i.e., taxonomy) as a necessary ingredient to reconstructing the past. Phylogenies produced by systematists provide a crucial foundation for examining biological phenomena and hypotheses, such as adaptive radiation or biogeographic scenarios, some of which are important for informing conservation decisions. Phylogenies help predict where biodiversity hotspots may be located, inform how distinct populations may be from one another, and identify unique lineages that preserve critical genetic diversity. Without systematics, other aspects of natural history lose their historical framework; and without taxonomy, systematics loses its basic operational unit. This chapter will demonstrate the many ways in which taxonomy and systematics have contributed to past conservation efforts and how they will continue to enrich protection of bat species globally.

## 16.2 The Continuing Age of Discovery

Taxonomy is not a dead science; the Age of Discovery is ongoing, especially for bats (Fig. 16.1). The number of bats discovered in the last couple of decades is higher than expected when compared to other mammalian orders (Reeder et al. 2007). With each subsequent volume of *Mammal Species of the World* (Honacki et al. 1982; Wilson and Reeder 1993, 2005), the number of recognized bat species has increased dramatically, with new species described from every corner of the world. Between publication of the last edition in 2005 and the end of 2013, nearly 200 new bat species were described or resurrected from synonymy, including 120 species new to science (Table 16.1), putting the total number of bat species at just over 1300 at the time of writing of this chapter. The continuing high rate of discovery (or recognition) of new bats can be a potential impediment to conservation since it is difficult to assess the status of each newly discovered species within a short period of time, and because it is difficult to make management plans in the absence of abundance or natural history information (both of which are typically lacking for newly recognized taxa). However, new discoveries may clarify the status of isolated populations, and the recognition of these distinct species can allow appropriate conservation and management strategies to be crafted.



**Fig. 16.1** Number of new bat species described per decade since 1750. Species were categorized to zoogeographic region (as defined by Newton 2003) of discovery according to type localities. Species since 2010 only reflect discoveries prior to the writing of this chapter (early 2014). New species are constantly being described from the tropics, with rates of discovery in the Afrotropics and Indo-Malayan regions catching up with the Neotropics

**Table 16.1** New bat species by family since the previous edition of Mammal Species of the World (Wilson and Reeder 2005)

Family	Species	Year	Family	Species	Year
<i>Phyllostomidae</i>	<i>Anoura cadenai</i>	2006	<i>Vespertilionidae</i>	<i>Barbastella beijingensis</i>	2007
	<i>Anoura carashina</i>	2010		<i>Eptesicus lobatus</i>	2009
	<i>Anoura fistulata</i>	2005		<i>Eptesicus taddai</i>	2006
	<i>Carollia benkeithi</i>	2006		<i>Glischropus bucephalus</i>	2011
	<i>Carollia manu</i>	2004		<i>Harpioala isodon</i>	2006
	<i>Carollia monohernandezi</i>	2004		<i>Hypsugo lanzai</i>	2011
	<i>Chiroderma vizottoi</i>	2010		<i>Kerivoula kachinensis</i>	2004
	<i>Dryadonycteris capixaba</i>	2012		<i>Kerivoula titania</i>	2007
	<i>Lonchophylla cadenai</i>	2006		<i>Murina balaensis</i>	2013
	<i>Lonchophylla chocoana</i>	2004		<i>Murina beelzebub</i>	2011
	<i>Lonchophylla formicata</i>	2007		<i>Murina bicolor</i>	2009
	<i>Lonchophylla orcesi</i>	2005		<i>Murina chrysochaetes</i>	2011
	<i>Lonchophylla orienticollina</i>	2009		<i>Murina eleryi</i>	2009
	<i>Lonchophylla pattoni</i>	2006		<i>Murina fionae</i>	2012
	<i>Lonchophylla peracchii</i>	2013		<i>Murina gracilis</i>	2009
	<i>Lophostoma kalkoae</i>	2012		<i>Murina guilleni</i>	2013
	<i>Lophostoma yasuni</i>	2004		<i>Murina harpioloides</i>	2008
	<i>Micronycteris buriri</i>	2011		<i>Murina harrisoni</i>	2005
	<i>Micronycteris giovaniae</i>	2007		<i>Murina jainitiana</i>	2012
	<i>Micronycteris yatesi</i>	2013		<i>Murina loreleiae</i>	2011
	<i>Platyrrhinus alberticoi</i>	2005		<i>Murina pluvialis</i>	2012
	<i>Platyrrhinus angustirostris</i>	2010		<i>Murina recondita</i>	2009
	<i>Platyrrhinus fusciventris</i>	2010		<i>Murina shuipuenensis</i>	2011
	<i>Platyrrhinus guianensis</i>	2014		<i>Murina tiensa</i>	2007
	<i>Platyrrhinus ismaeli</i>	2005		<i>Murina walstoni</i>	2011

(continued)

Table 16.1 (continued)

Family	Species	Year	Family	Species	Year
	<i>Platyrhinus masu</i>	2005		<i>Myotis annatessae</i>	2013
	<i>Platyrhinus matapalensis</i>	2005		<i>Myotis badius</i>	2011
	<i>Platyrhinus nitelinea</i>	2009		<i>Myotis dieteri</i>	2005
	<i>Sturnira bakeri</i>	2014		<i>Myotis diminutus</i>	2011
	<i>Sturnira burtonlimi</i>	2014		<i>Myotis handleyi</i>	2013
	<i>Sturnira koopmanhilli</i>	2006		<i>Myotis indochinensis</i>	2013
	<i>Sturnira perla</i>	2011		<i>Myotis izecksohni</i>	2011
	<i>Sturnira sorianoi</i>	2005		<i>Myotis lavali</i>	2011
	<i>Uroderma bakeri</i>	2014		<i>Myotis midastactus</i>	2014
	<i>Xeronycteris vieirai</i>	2005		<i>Myotis phanluongi</i>	2008
<i>Emballonuridae</i>	<i>Coleura kibomalandy</i>	2012		<i>Neoromicia robertsi</i>	2012
	<i>Paraemballonura tiavato</i>	2006		<i>Neoromicia roseveari</i>	2013
	<i>Peropteryx pallidoptera</i>	2010		<i>Nyctophilus corbeni</i>	2009
<i>Thyropteridae</i>	<i>Thyroptera devivoi</i>	2006		<i>Nyctophilus shirleyae</i>	2009
	<i>Thyroptera wynneae</i>	2014		<i>Pipistrellus hanaki</i>	2004
<i>Molossidae</i>	<i>Chaerephon atsinanana</i>	2010		<i>Pipistrellus raceyi</i>	2006
	<i>Chaerephon jobimena</i>	2004		<i>Plecotus strelkovi</i>	2005
	<i>Eumops wilsoni</i>	2009		<i>Rhogeessa bickhami</i>	2012
	<i>Molossus alvarezi</i>	2011		<i>Rhogeessa menchuae</i>	2012
	<i>Mops bakarii</i>	2008		<i>Scotophilus andrewreborii</i>	2014
	<i>Mormopterus eleryi</i>	2008		<i>Scotophilus ejetai</i>	2014
	<i>Mormopterus francoismoutoui</i>	2008		<i>Scotophilus livingstonii</i>	2014
	<i>Mormopterus halli</i>	2014		<i>Scotophilus marovaza</i>	2006
	<i>Mormopterus kitcheneri</i>	2014		<i>Scotophilus tandrefana</i>	2005
	<i>Mormopterus lumsdenae</i>	2014		<i>Scotophilus trujilloi</i>	2014

(continued)

Table 16.1 (continued)

Family	Species	Year	Family	Species	Year
<i>Pteropodidae</i>	<i>Casinycteris campomaanensis</i>	2014		<i>Tylonycteris pygmaeus</i>	2008
	<i>Desmalopex microleucopterus</i>	2008	<i>Natalidae</i>	<i>Natalus lamatus</i>	2005
	<i>Dyacopterus rickartii</i>	2007	<i>Myzopodidae</i>	<i>Myzopoda schliemanni</i>	2006
	<i>Epomorphorus anselli</i>	2004	<i>Miniopteridae</i>	<i>Miniopterus aelleni</i>	2008
	<i>Pteralopex flammeryi</i>	2005		<i>Miniopterus brachytragos</i>	2009
	<i>Pteropus allenorum</i>	2009		<i>Miniopterus egeri</i>	2011
	<i>Pteropus coxi</i>	2009		<i>Miniopterus griffithsi</i>	2009
	<i>Syloctenium mindorensis</i>	2007		<i>Miniopterus mahafaliensis</i>	2009
	<i>Thoopterus suhaniahae</i>	2012		<i>Miniopterus maghrebenensis</i>	2014
	<i>Rhinolophus chiewkveeae</i>	2005		<i>Miniopterus mossambicus</i>	2013
	<i>Rhinolophus cohenae</i>	2012		<i>Miniopterus petersoni</i>	2008
	<i>Rhinolophus huamanus</i>	2008		<i>Miniopterus sororculus</i>	2007
	<i>Rhinolophus indorouxi</i>	2013		<i>Hipposideridae</i>	<i>Asellia arabica</i>
	<i>Rhinolophus kahuzi</i>	2013	<i>Hipposideros boeadi</i>		2007
<i>Rhinolophus mabuensis</i>	2012	<i>Hipposideros einnaythu</i>	2011		
<i>Rhinolophus mossambicus</i>	2012	<i>Hipposideros griffini</i>	2012		
<i>Rhinolophus schmitzleri</i>	2011	<i>Hipposideros khaokhouayensis</i>	2006		
<i>Rhinolophus smithersi</i>	2012	<i>Hipposideros khasiana</i>	2006		
<i>Rhinolophus willardi</i>	2013	<i>Paratriaenops pauliani</i>	2008		
<i>Rhinolophus xinanzhongguensis</i>	2009	<i>Triaenops menamena</i>	2009		
<i>Rhinopomatidae</i>	<i>Rhinopoma hadramauticum</i>	2009	<i>Triaenops parvus</i>	2009	

Most species discoveries in the past decade have been made in Neotropical families, though more genetic and phonic data on Rhinolophidae and Hipposideridae are now uncovering greater species diversity in the Palearctic

Species discoveries and recognition may bring attention to previously overlooked areas or act as a symbol of local pride. For example, in the Mekong Delta of Vietnam, a sixteenth-century Khmer pagoda in Soc Trang City called Wat Matahup, or Chua Doi—the Bat Pagoda—is home to a mixed colony of thousands of flying foxes (*Pteropus vampyrus* and *Pteropus lylei*), which are listed by the IUCN as Near Threatened and Vulnerable, respectively. The pagoda is a cultural and historic icon and the only pagoda in the region with a resident bat colony. The locals feel a sense of pride, as these rare bats roost only in the trees within the temple grounds. Monks actively protect the bats from increasing hunting pressure. This interest has resulted in the creation of bat and sustainability education campaigns by locals. These programs are aimed at educating young children on the importance of the bats to the ecosystem.

### 16.3 The Role of the Taxonomist in Conservation

The most basic contribution of the taxonomist to conservation is to identify and name the species being protected (Table 16.2). Being unable to differentiate among species makes it virtually impossible to manage wildlife, leads to poor decision-making, and causes unforeseen ecological consequences. Taxonomists are often the only people who can identify an animal—an underappreciated skill. For bats, this is of special importance as bats are an extremely diverse group, and many bat species are cryptic and therefore cannot be readily identified by amateurs and other biologists based on obvious external features. Taxonomists also form the backbone of any museum system. They are responsible for identification of voucher specimens that include whole organisms, skins, skeletons, skulls, and, increasingly, frozen tissues. Along with other museum personnel, they are responsible for ensuring that these specimens are preserved as a reference for future researchers. Natural history collections curate and maintain critical data associated with specimens including species identification, locality, sex, date of collection, collector, and other pertinent information. Much important taxonomic work takes place in these collections, with major taxonomic revisions of museum material often clarifying the status of particular species.

One of the most common requests to taxonomists from other researchers is for a species list for a particular locality. Without an easy way to identify species, non-taxonomists may not be able to accurately interpret collected data that are relevant to conservation, including information on habitat, geographic distribution, abundance, and basic features of ecology (e.g., roost sites for bats). Field researchers collect these ecological data; but many field researchers only observe animals and do not collect vouchers. Their observations—e.g., “bat species X and Y occur in caves all along the northwest coast”—form the basis of our understanding of fauna and species distributions alike. But, without vouchers, current and future research may not actually address the questions at hand. What happens when species Y is later recognized to be three species? What happens if species X has been

**Table 16.2** The process of describing a new species can be broken down into two parts: the research necessary prior to description and the publication

Part 1: Research prior to description	
<i>Collect data corroborating unique species identity</i>	
Several lines of evidence	
Morphological, genetic, behavioral, ecological, phonic	
<i>Literature review</i>	
Is it a variant?	
Was it previously reduced to synonymy?	
Is it a new record in that area for a known species?	
Did it use the wrong name?	
<i>Visit reference collections</i>	
Compare to reference, voucher, or type (if possible) specimens of similar species	
Collaborate with systematist if necessary	
Part 2: Publication	
<i>What kind of paper?</i>	
Species description	Redescription
Revision	Synopsis
Review	Catalog
Monograph	Phylogeny
Checklist	Subspecies description
Description of Higher Taxon	
<i>Create scientific binomial following rules set by ICZN</i>	
<i>Establish type specimen(s) and type locality</i>	
<i>Sections</i>	
Diagnosis (distinguishing characters only)	
Description (all traits)	
Taxonomic characters	Color
Life history characters	Quantitative characters
Life stages	Behavioral/ecological characters
Discussion—significance?	
Ecology	
Distribution	
Material examined	

The above-mentioned table is derived from taxonomic procedures described in Winston (1999), a reference which is recommended by the International Commission on Zoological Nomenclature (ICZN)

misidentified? In such circumstances, how are we to know which bats are really present in the area? Effective gathering, consolidation, and analysis of data for conservation efforts require accurate species identifications as well as collection of voucher material, if possible.

Taxonomists must also communicate their work to non-experts, including other biologists. The taxonomic literature is notoriously inaccessible to non-specialists as it is often filled with obscure terminology and outdated names. Many



historically important papers were published in journals that are not accessible to researchers in developing countries. Taxonomic revisions are not always readily available and widely circulated, allowing old names to persist in the literature and, more recently, Web-based faunal lists. This may complicate species delimitation and confuse consolidation of other ecologically important information necessary for effective conservation.

Best practices for species identification/documentation include the following: (1) use of a broad range of data to support species identifications, including morphological, genetic, and (if relevant) echolocation data; (2) a thorough review of the literature for names applied to the group(s) or specimens examined so that the oldest valid name is used; and (3) publication in an open-access journal for the broadest possible exposure. Examples of recent papers that use one or more of these best-practice approaches are as follows:

1. Larsen et al. (2010), who raised a previously recognized South American subspecies of *Artibeus*, *Artibeus jamaicensis aequatorialis*, to full species, *A. aequatorialis*, based on combined morphometric, mitochondrial, and AFLP (amplified fragment length polymorphism) data. The paper provided detailed context, including a review of the history of research on the species and a literature review of previous work on the genus. The study also provided a clear species account of *A. aequatorialis* and was published in the widely available journal *Zootaxa*.
2. Taylor et al. (2012), who recognized, on the basis of distinct echolocation calls, possible cryptic species within the *Rhinolophus hildebrandtii* complex of southern Africa. Subsequently, he described four new species supported by a combination of acoustic, morphometric, and molecular data.
3. Buden et al. (2013), who revised the Micronesian species *Pteropus insularis*, recognizing two subspecies, *P. pelagicus pelagicus* and *P. pelagicus insularis*. The authors examined a series of specimens and evaluated morphological features and conducted a thorough literature review of past names prior to revising the taxonomy of this species.
4. Velazco et al. (2014), who described the new species *Thyroptera wynneae* from South America. In this case, the morphological data unambiguously supported specific status for the collected voucher material, despite there being several other congeners found in sympatry.

The studies of *P. pelagicus* and *T. wynneae* were both published in the open-access journal, *ZooKeys* and *American Museum Novitates*, respectively, and are readily available to researchers from developing countries.

Products produced by taxonomists for use by experts and educated non-experts alike include keys and descriptions. Keys use mutually exclusive statements that help lead users to identifications of unknown organisms. Good keys use diagnostic features illustrated by line drawings or photographs to differentiate between species and include redundancy to ensure correct identifications at earlier steps. Incomplete keys often cause problems when they are the only means available to identify an animal. A good key enhances the work of land managers and other

decision makers as well as researchers studying ecology, zoonotic diseases, and agriculture by allowing them to identify easily confused species and to access updated information on taxonomic nomenclature.

Taxonomists must understand the skills and facilities that are available where the key will be used. Keys that rely on external characters from a living animal must take precedence over features that can only be seen in museum preparations or with the use of a microscope (although some craniodental data may be needed to supplement external characters, especially in bats). Microscopes may not be available under field conditions, or at all at the locality under study. Extracting and cleaning skulls, or measuring morphological features requires training. Good examples of accessible keys are Barquez et al. (1993), which is available bilingually, and Taylor (2000), which includes acoustic profiles. Both of these keys use easily distinguishable external characteristics along with illustrations to assist in identification.

Taxonomists sometimes also produce field guides, drawing on knowledge of collection records, phylogenetic relationships, species distributions, and natural history to enlighten experts and non-experts alike. Field guides engage the scientifically literate public and can act as an illuminating form of outreach for bats. Top-notch field guides, such as those by Francis (2008) for the mammals of Southeast Asia and Reid (2009) for the mammals of Central America, are produced by experts and include detailed notes on species identification, natural history, distribution maps, and color illustrations or high-quality photographs. While not quite a field guide, Bat Conservation International freely provides species profiles on their Web site for all 47 species of North American bats. It is likely that Web-based field guides, or mobile device apps, will come to play a larger role in field identifications in the future, and these resources will benefit from attention by taxonomists during their development.

## 16.4 Taxonomy and International Agreements

The importance of taxonomy is recognized by the Convention on Biological Diversity's (CBD) Global Taxonomy Initiative program. Inadequate taxonomic information is recognized as an obstacle to making informed management decisions in conservation, sustainable use of resources, and availability of genetic resources (Secretariat of the Convention on Biological Diversity 2008). The legally binding CBD was signed by 193 governments in 1992–1993 at the UN Conference for Environment and Development. Article 7 (identification and monitoring), Article 12 (research and training), and Article 17 (public awareness and education) of the CBD directly address the need for taxonomic research to be conducted and used for conservation. Furthermore, the strategy plan for 2011 to 2020 specifically referenced the need to “improve the status of biodiversity and by safeguarding ecosystems, species, and genetic diversity” (Secretariat of the Convention on Biological Diversity 2012). The CBD indicates a willingness of

governments to recognize the importance of taxonomy in resolving environmental challenges.

The importance of taxonomy in protecting species is most immediately visible under the Convention for International Trade of Endangered Species (CITES) agreement. With 179 Parties having now joined the Convention, to which they agree to voluntarily adhere, CITES provides a rank system with varying degrees of protection to more than 35,000 plant and animal species. Under CITES, all *Acerodon* and *Pteropus* species, or flying foxes, are listed as Appendix I or II. Appendix I species are deemed as threatened by extinction and all international trade is prohibited except for non-commercial purposes (e.g., scientific research). Appendix II affords protection to species that are not currently threatened, but may become threatened without controlled trade. Appendix II also protects similar-looking species in order to discourage illegal wildlife trafficking. All members of *Acerodon* and *Pteropus* are listed at both the genus and species level because many species have very restricted ranges and some are endangered, but species identification—especially by non-experts—is extremely difficult. The only non-pteropodid currently listed by CITES is the Uruguay population of the white-lined broad-nosed bat (*Platyrrhinus lineatus*), which is listed under Appendix III. Appendix III species are protected within a signatory country, but that signatory country has indicated it requires extended cooperation from other countries to prevent exploitation.

The importance of taxonomy in international agreements is also evident in the Convention on Migratory Species' (CMS) EUROBATS Agreement, which originally recognized 37 species, but now includes all 52 bat species (both migratory and non-migratory) in Europe, North Africa, and the Middle East. EUROBATS sets legal protection standards and develops and promotes management and conservation strategies across international borders, with 35 of 63 states within the targeted range as signatories. Revisions to the number of species listed, with an increase of 7 new species since 1995, are due to continuing taxonomic work in the region (CMS 2013).

## 16.5 Taxonomy as a Conservation Planning Tool

Taxonomy may be used as part of conservation either directly (e.g., generating species lists, defining hotspots in need of protection, inventories and monitoring, providing global perspective) or indirectly (e.g., estimating extinction risk, estimating rate of extinction). For example, the Southeast Asian Bat Conservation Research Unit (Kingston 2010) identified advancement in taxonomy and systematics research as a regional priority even though this consortium focuses on capacity building and conservation, not taxonomy. What follows is a summary of practices that conservation biologists currently employ, and also new perspectives and methods that taxonomy and systematics may bring to conservation management.

### ***16.5.1 A Basic Question: What is a Species?***

Effective species conservation requires defined taxonomic units that reflect biological reality and can be documented and tracked through space and time using survey and inventory methods appropriate to the organism and ecosystem. Defining and identifying such units is frequently much harder than it sounds. The most commonly used taxonomic unit in conservation biology is the species, though populations are occasionally considered unique enough to merit protection (Justice Department et al. 1996). Species are considered by both scientists and the public to be real, physical entities worthy of conservation. The fact that species have names makes it easier for non-experts to understand and protect them. However, species concepts in biology are far from simple (Cracraft 1989; de Queiroz 1998; Wheeler and Meier 2000; Baker and Bradley 2006; de Queiroz 2011) and applying a set of practical rules to standardize species units is helpful for making species lists in any given area. Taxonomic units for conservation recovery planning must acknowledge the ever-evolving nature of these units in natural systems. While methods of species definition and recognition are debated among researchers [e.g., reproductive isolation for the Biological Species Concept, monophyly for the Phylogenetic Species Concept (PSC), and genetic divergence for the Genetic Species Concept (GSC)], each recognizes that species are composed of populations and that by their nature they are dynamic, not static, units (de Queiroz 2005).

Compared to species of insects and birds, bats are relatively taxonomically stable, and issues related to new cryptic taxa are relatively minor in the sense that cryptic bat species are usually confined to within the boundaries of what was previously considered a single species (Jones et al. 2009). Cryptic species excepted, new information or the application of new species concepts has not tended to change species limits in most bat taxa, suggesting that species limits in bats (or at least those subject to revisionary studies within the last 25 years) are already defined to maximize stability (e.g., buffering against phylogenetic uncertainty) (Lee 2005). Despite hopes to the contrary, it seems unlikely that all taxonomists will ever agree on a single species concept, even for taxa within a relatively restricted group such as Chiroptera. A variety of factors influence the species concept employed in different studies: available data (e.g., morphology, molecules, echolocation calls, behavior), past history of work on the group, type(s) of training received by the researchers, sample sizes in the study, and available analytical tools may all play a role. In this context, it is important for taxonomists to be explicit about the species concept they employ in a study in order to make their data and conclusions transparent to other researchers.

### ***16.5.2 Listing Species for Protection***

The species lists that taxonomists assemble form the basic units used by international, national, and local authorities that provide protection to wildlife. Quantitative analysis has shown that the longer a species has been placed on a

list of threatened or endangered species, the more likely it is to recover (Taylor et al. 2005). Many agencies have taxonomic standards that must be met prior to inclusion in a listing. For example, the IUCN requires that names be validly published in accordance with Codes (e.g., The International Code for Zoological Nomenclature or ICZN), and checklists, such as *Mammal Species of the World* (Wilson and Reeder 2005), should be employed where possible. The IUCN accepts the following taxa for listing: species, subspecies, varieties (only for plants), and geographically separate subpopulations. It may also allow undescribed species to be listed under extraordinary circumstances. International legislation includes multilateral environmental agreements (e.g., CITES and CMS) that directly support bat conservation, but other free-trade agreements can also uphold the goals of conservation by combating illegal wildlife trade and promoting species persistence. For example, the North American Free Trade Agreement created the Commission for Environmental Cooperation to identify and address reasons for the decline of widespread species such as the monarch butterfly (Commission for Environmental Cooperation 2010).

Protection on the national level may vary from country to country, but in most cases the species is the unit of concern. In addition to protecting species, many nations recognize the importance of protecting habitats as well; examples include both the Endangered Species Act (ESA) in the USA (US Fish and Wildlife Service 2013), the Species at Risk Act (SARA) in Canada (Species at Risk Act 2013), and the Habitats Directive of the European Union (European Commission 2014). These pieces of legislations all rely on a species list to provide protections with the listing process critical to successful conservation. Within the USA, there have been numerous critiques of the ESA from both scientific perspectives (e.g., Rohlf 1991; Pennock and Dimmick 1997; but see Waples 1998) and policy perspectives (Doremus 1997). Often species listed as threatened by IUCN are not similarly recognized as such by ESA. Taxa listed by the ESA include subspecies that are not listed by the IUCN; three of the eleven bat species on the ESA's threatened and endangered list are listed at the subspecific level (Table 16.3). Within the EU, Annex II of the Habitats Directive calls for the establishment of a Special Area of Conservation to protect recognized species, and Annex IV calls for a strict protection regime across the entire natural range of the species in the EU (Council Directive 92/43/EEC, European Commission 2014).

Differences in listing among countries and NGOs, such as IUCN, may reflect different definitions of "threatened" or "endangered," or reflect the varying ways that priority is afforded to a taxon during assessment. Monotypic genera are sometimes afforded greater priority in evaluation and listing than species, down to the level of population. The phylogenetic uniqueness of a species is an important factor in conservation assessments (IUCN 1980; McNeely et al. 1990; Tisdell 1990). Consequently, the taxonomic mindset of specialists on the group ("splitters" versus "lumpers") may play a very critical role in their decisions concerning when and if a taxon is afforded protection.

There are a handful of instances in which recognition of a new species has resulted in direct conservation action. In Thailand, the discovery of Kitti's

**Table 16.3** Conservation status of bat species protected under the US's Endangered Species Act (ESA) compared to the global IUCN Red List

Species name according to ESA	US ESA	IUCN
<i>Leptonycteris nivalis</i>	E	E
<i>Tadarida brasiliensis</i>		LC
<i>Macrotus californicus</i>		LC
<i>Myotis grisescens</i>	E	NT
<i>Diphylla ecaudata</i>		LC
<i>Lasiurus cinereus semotus</i>	E	LC
<i>Choeronycteris mexicana</i>		NT
<i>Myotis sodalis</i>	E	E
<i>Leptonycteris curasoae</i>		V
<i>Leptonycteris (curasoae) yerbabuena</i>	E	V
<i>Pteropus tokudae</i>	E	EX
<i>Pteropus mariannus</i>	T	E
<i>Plecotus rafinesquii</i>		LC
<i>Corynorhinus (Plecotus) townsendii</i>		LC
<i>Corynorhinus (Plecotus) townsendii ingens</i>	E	
<i>Corynorhinus (Plecotus) townsendii virginia</i>	E	
<i>Eumops underwoodi</i>		LC
<i>Eumops floridanus</i>	E	CR
<i>Emballonura semicaudata rotensis</i>	C	E
<b>Non-American bats</b>		
<i>Craseonycteris thonglongyai</i>	E	V
<i>Aproteles bulmerae</i>	E	CR
<i>Pteropus rodricensis</i>	E	CR
<i>Hipposideros ridleyi</i>	E	V
<i>Emballonura semicaudata semicaudata</i>	C	E

Blanks represent lack of listing (ESA) or lack of recognition of species or subspecies (IUCN). The ESA also lists and extends protection to some foreign bat species to discourage people under American jurisdiction from further contributing to species decline. Listing of foreign species may increase in situ conservation action and provide limited financial assistance and training

ESA abbreviations: *E* Endangered, *T* Threatened, *C* Candidate

IUCN abbreviations: *EX* Extinct, *CR* Critically Endangered, *E* Endangered, *V* Vulnerable, *NT* Near Threatened, *LC* Least Concern

Source US Fish and Wildlife Service Environmental Conservation Online System, Species Report, Listed Species; IUCN Red List

hog-nosed bat (*Craseonycteris thonglongyai*; Hill 1974) and the recognition of the distinctiveness of the taxon with the definition of a new family, led to the creation of the 500 km<sup>2</sup> Sai Yok National Park in 1980 under the Wildlife Animal Reservation and Protection Act, B.E. 2535. However, a population subsequently discovered outside the park in Myanmar is not protected, and relatively little is known from its status. The Myanmar population is genetically distinct from the Thai population but morphologically indistinguishable from it (e.g., cryptic), raising questions about whether or not it should be considered a distinct taxon or simply an isolated

population (Bates et al. 2001; Pereira et al. 2007; Puechmaille et al. 2011). These discoveries have led to changes in the dynamic of conservation for *Craseonycteris*, since conservation priorities are often related to species range sizes. Similarly, ongoing discovery of cryptic species in Africa, such as Rosevear's serotine (*Neoromicia roseveari*), has led to calls for protection of the Upper Guinean forests, which are threatened by rampant human disturbance (Monadjem et al. 2013).

There are times when national recognition of a species as endangered comes too late, resulting in extinction. In some cases, this is in part due to taxonomic confusion—a circumstance that underlines the importance of taxonomy for conservation. The Christmas Island pipistrelle (*Pipistrellus murrayi*) is an unfortunate example from Australia. The only native insectivorous bat on Christmas Island, it was once widespread but underwent dramatic population declines by the mid-1990s (Beeton et al. 2010). The reasons for this decline remain unclear, but likely include introduction of non-native species (e.g., common wolf snake, feral cats, giant centipedes, and yellow crazy ants) that either disturbed roost sites or preyed on bats (Lumsden et al. 2007). It is also possible that control efforts focused on yellow crazy ants (*Anoplolepis gracilipes*) might have inadvertently poisoned the bats (Beeton et al. 2010). The muddled taxonomic history of the Christmas Island pipistrelle apparently contributed to poor management decisions. Koopman (1973, 1993) considered *P. murrayi* to be a synonym of *P. tenuis*, a common Southeast Asian species, apparently based on general morphological similarity. Hill and Harrison (1987) treated *P. murrayi* as a separate species based on the presence of a distinctive baculum, but this gained little attention at the time. Lack of a focused taxonomic treatment of the pipistrelle species complex resulted in lack of any real consensus about the status of the Christmas Island pipistrelle. The Australian government was slow to act upon findings from a long-term monitoring program, which recommended captive breeding programs for the Christmas Island pipistrelle in 2006 (Martin et al. 2012). It was only after genetic studies by Beeton et al. (2010) corroborated that *P. murrayi* was a distinct species that an emergency response was initiated in 2009 (Martin et al. 2012). However, these efforts came too late—the Christmas Island pipistrelle apparently became extinct in 2009 (Lumsden 2009).

Placing a species on international or national lists may be a prerequisite for local conservation actions such as habitat restoration or protection. The Indiana bat (*Myotis sodalis*) is listed as Endangered under the US's ESA. As such, the species is protected in the USA, meaning that commercial expansion must take into consideration the levels of disturbance to the population before development or operation may proceed in a given area. This has led to US Fish and Wildlife guidelines for businesses such as coal mining companies and wind farms (e.g., US Fish and Wildlife Service 2012) that describe development without harming local wildlife, such as Indiana bat populations. In a recent case against a wind energy company in West Virginia that failed to perform a due-diligence survey prior to development, the courts ordered an injunction against the company and required that it apply for incidental take permits before continuing operations. The wind turbines were allowed to be powered on only in the winter when the bats were hibernating (Woody 2009). In another case, a bat habitat restoration project has

been proposed in Ozark National Forest, Arkansas, after ice storm-damaged acres of forest. The idea in this case is to ensure there will be enough healthy stands of trees for the Indiana bat (USDA 2012).

### ***16.5.3 Downsides of Species Listing***

Although well intentioned, adoption of global endangered species lists may in some cases be detrimental to more localized protection and conservation efforts. Many countries, and some subnational units, have simply adopted the IUCN Red List of species into their legislation. This practice can be inappropriate, as is recognized by IUCN itself. The criteria used in the IUCN list are specifically designed to identify the species that are most endangered at a global level, not within a region, nation, or specific locality. Consequently, the IUCN has issued “Guidelines for Application of IUCN Red List Criteria at Regional and National Levels” (IUCN 2012) to aid in the application of IUCN principles to more regional surveys. National governments that adopt IUCN listings in their entirety typically do not conduct their own taxonomic and systematic assessment of the species and population status of species that reproduce in or regularly visit the region within their borders. The IUCN advises using the globally derived Red List to set regional conservation priorities under only two conditions: (1) when there are a high number of endemics or threatened near endemics in the region, and (2) when there are little to no data concerning the species within a region. In all other situations, the IUCN advises following IUCN guidelines to assess extinction risk at the geographic scale of interest (local, national, and regional) and publishing Red Lists at this scale. Full compliance with the guidelines allows the country or region to state that their regional Red List follows the IUCN system.

Application of global lists at the local level may miss some species that need local protection. Alternatively, negative conservation outcomes may result if local values are compromised as a result of uncritical national protection of IUCN-listed species. For example, if the presence of a protected species impedes economic development, landowners in a region may destroy the species’ habitat or deny the existence of that species to avoid local legal consequences stemming from its IUCN listing (Possingham et al. 2002). Planners and legislators need to appreciate that there are many dimensions to threat and protection and provide landowners and other stakeholders with incentives to protect endangered species.

### ***16.5.4 Inventory and Monitoring Programs***

Monitoring bat populations can be an important tool in efforts to understand the condition of an ecosystem, since bats have long been recognized as good indicator species (Fenton et al. 1992; Medellín et al. 2000; Jones et al. 2009). An indicator



species is one whose presence, absence, and condition is suggestive of environmental health (Noss 1990). Since bats provide many ecosystem functions, such as pollination and seed dispersal, they are intrinsically linked to plant populations where they live (Fujita and Tuttle 1991; McConkey and Drake 2006). The predation of bats on insects may also reflect arthropod abundance and species diversity (Kalka et al. 2008). Bats can also be indicative of global climatic shifts. For instance, *Pteropus alecto* and *Pteropus poliocephalus* experienced increasingly frequent massive die-offs during extreme heat spikes in Australia (Welbergen et al. 2008). In early 2014, a record-breaking heat wave in central and eastern Australia resulted in one of the most catastrophic die-offs ever recorded—more than 45,000 flying foxes of the three native species (*P. alecto*, *P. poliocephalus*, and *Pteropus scapulatus*) died and more than 1000 juveniles were orphaned (Welbergen et al. 2014). These mass mortality events appear to coincide with the increasing frequency and intensity of extreme climate events that are predicted for Australia due to climate change (IPCC 2012).

Collection of voucher specimens, while sometimes controversial, is widely regarded by systematists and taxonomists as critical to inventory projects (Voss and Emmons 1996; Simmons and Voss 1998, 2009). Vouchers are necessary for any future work such as reassessments of the initial study or further extension of the initial work when new information or methods become available. Vouchers, including tissue samples, are especially necessary when species are cryptic or nearly so—some bat species can only be identified by minute morphological differences, (e.g., cranial characters, or in small vespertilionids, the baculum (penis bone) (Hill and Harrison 1987) or by molecular means (e.g., Clare et al. 2013). Vouchers are also necessary to provide type specimens (minimally a holotype but preferably also paratypes) if a new species is discovered (ICZN 2012).

In some regions of the world, taxonomists may be the only biologists with active research programs and therefore may be the only scientists positioned to collect the population and ecological data required for conservation assessments. They may also be the only biologists on hand to provide information about threats to species at particular localities. These taxonomists often have studied species throughout their ranges and are able to offer a more accurate assessment of conservation status by thinking globally instead of locally. For example, for the current revision of the Old World Fruit Bat Action Plan, the team leaders have reached out to a number of bat researchers, many of whom are taxonomists, to determine the most appropriate IUCN Red List status for each species. Most of the current specialist groups of the IUCN Red List include at least one taxonomic expert. This allows for the establishment of international versus national priorities and the creation of appropriate management strategies at the correct taxonomic level. For instance, in Britain, all bats and their roosts are protected by multiple domestic and international laws, even though a majority of these species are listed as Least Concern by IUCN (Bat Conservation Trust 2013). The UN's Global Biodiversity Outlook 3 also repeatedly references trends in population size and diversity of different taxa (Secretariat of the Convention on Biological Diversity 2010). These trends are based on species-specific data—data that are worthless without proper taxonomic identifications of the species in question.

To counter the lack of taxonomic experts during surveys, a technique called parataxonomic sorting was introduced in the late 1980s for entomological surveys in the Neotropics (Janzen 1991) and subsequently for plant surveys (Baraloto et al. 2007; Abadie et al. 2008). Parataxonomy focused on the use of “morphospecies” to sort collected specimens into Recognizable Taxonomic Units (RTUs) (Cranston and Hillman 1992; Oliver and Beattie 1993) as a preliminary method of assessment in the absence of enough taxonomic expertise. RTUs are not truly recognized biological species, and the sorting method is recognized as non-scientific, but the efficiency of the method quickly turned a preliminary sorting method into a source of data for biological surveys. However, results of parataxonomy are inconsistent and these methods have been criticized for the low quality of data and incorrectly grouped individuals (Krell 2004; Baraloto et al. 2007). Parataxonomy is largely uninformative when it comes to inventories, biogeographic studies, area selection for conservation, autecology, and habitat comparisons although it may still be useful in limited capacities for global comparisons of gross species richness or single-site descriptions of species richness of some taxa (Krell 2004). However, bats are particularly ill-suited to parataxonomic efforts because taxa are difficult to distinguish and the process of collecting specimens is time-intensive and requires specialized training and permits that are difficult to obtain even when one is an expert. Parataxonomy seems to hold little promise for chiropteran studies.

### 16.5.5 Defining Protected Areas

One commonly used method for defining protected areas is identification of “biodiversity hotspots” with “exceptional concentrations of endemic species...experiencing exceptional loss of habitat” (Myers et al. 2000). Generally, methods of prioritizing areas for conservation based on measuring endemism, phylogenetic diversity, or taxon richness represent variations of the hotspot approach—they all measure some proxy for species representation and identify areas for conservation based on these variables. Such methods stand in contrast to area selection approaches that focus on threatened or degraded habitats. The hotspot approach to choosing protected areas has been criticized as susceptible to taxonomic instability (Isaac et al. 2004). Some authors have suggested that hotspots should use higher level taxonomy to identify areas that warrant protection and sidestep issues related to unstable taxonomy (Balmford et al. 2000; Amori and Gippoliti 2003). Genera and species were found to be highly correlated and may select for the same priority areas, whereas family and order are not very informative (Balmford et al. 2000; Amori and Gippoliti 2003). This approach may be inappropriate for bats, as young, rapid radiations may result in higher species diversity than would be predicted based on generic diversity. For example, in the Palearctic, site-wide diversity is primarily driven by only a few genera (e.g., *Hipposideros*, *Rhinolophus*, *Kerivoula*) (Kingston et al. 2003). This pattern is also seen in the Neotropics, although to a lesser extent (e.g., *Artibeus/Demanura*,

*Micronycteris*, *LophostomalTonatia*) (Voss and Emmons 1996; Simmons and Voss 1998). Selection of hotspots based on species richness would value a site where selection based on genera would not, potentially leading to missed conservation opportunities.

To combat issues related to taxonomic stability, conservation should implement approaches that emphasize the uniqueness of taxa or areas (Gippoliti and Groves 2012). Newer methods for conservation often emphasize evolutionary uniqueness in concert with extinction risk when choosing priority protection areas (Collen et al. 2011). However, regardless of taxonomic resolution, the hotspot approach may be unlikely to reduce extinction risk in areas such as the Andes, where high species richness is correlated with areas with low human disturbance (Fjeldså 2000). The hotspot approach in this case ignores species at greatest risk in areas with high levels of human contact and may result in directing more resources to areas that require little intervention. Complementarity takes into account human development, selecting sites that may not have high biodiversity, but would result in conservation of more species in the area.

The relative taxonomic stability of bats means that some conservation decisions may be easier to make. But it does not mean that hotspot approaches are always appropriate. Instead of focusing on overall species richness, some area selection approaches focus on an umbrella species, or a variation thereof: focal, keystone, flagship, or threatened species (Lambeck 1997; Roberge and Angelstam 2004), with the assumption that protection of their habitat will benefit other organisms in the area. This approach often focuses on “charismatic megafauna,” such as tigers, elephants, and primates, that are large-bodied as these species tend to have larger area requirements (Roberge and Angelstam 2004) and overlooks species with specialized habitat requirements or niche habitats, such as limestone karsts, that are irrelevant to large animals. Such niche habitats may be crucial to the survival of rare and endemic taxa with small ranges and narrow niches, such as threatened bat species such as Kitti’s hog-nosed bat (*C. thonglongyai*) and the Thailand leaf-nosed bat (*Hipposideros halophyllus*).

### ***16.5.6 Estimating Extinction Risk and Extinction Rate: The Role of Phylogenetics***

Much emphasis is placed on extinction risk by conservation biologists in relation to climate change, habitat fragmentation, and habitat loss, but we cannot determine current rates of extinction and compare them to past rates of extinction without accurate knowledge of global biodiversity and updated phylogenies. Phylogenies allow researchers to test hypotheses related to character trait evolution, including traits related to natural history and extinction risk (Jones et al. 2003). Shared ecological traits from any one clade are by definition non-independent since all the species in a clade are linked by common ancestry. Analysis of patterns requires the removal of the historical signal in the data through the

phylogenetic comparative method, otherwise known as “correcting” for phylogeny (Felsenstein 1985). Taxonomic bias for risk of extinction and for susceptibility to invasion is a known issue for conservation biologists (Fisher and Owens 2004). It may not be possible to conduct detailed research on every at-risk species within a short time span, but the comparative method allows for a quick assessment of conservation priorities based on shared risk of extinction in vulnerable clades. This may also provide perspective on causes of species decline. All of these data may allow for conservation actions to be taken sooner rather than later, with early action being more cost-effective and more successful (Fisher and Owens 2004).

Jones et al. (2003) conducted a multivariate analysis of correlation between extinction risk in bats (represented by IUCN threat level) and various natural history and morphological traits known to correlate with extinction risk in other taxa (Purvis et al. 2000; Isaac et al. 2005; Forero-Medina et al. 2009). Jones et al. (2003) found extinction risk to be highly correlated with evolutionary history, meaning clades shared similar levels of threat. Correlation of extinction risk with evolutionary history indicates the necessity of accounting for the phylogenetic history of clades when making such determinations, opening opportunities for determining the critical factors for clades. For example, geographic range size was the most important predictor of extinction risk across Chiroptera, though it was found to be an order of magnitude higher in pteropodids, which have smaller mean geographic ranges, than other bats. Among non-pteropodid bats, larger body size, larger group size, and low wing aspect ratios were significantly correlated with higher extinction risk. In pteropodids, smaller litter size was significantly correlated with extinction risk. These findings explained approximately half of the variance in extinction risk, and more work remains to be done. In a recent study of vespertilionid bats, those in threatened categories were more likely to be dietary specialists than those listed as Least Concern (Boyles and Storm 2007). As robust phylogenies are assembled and more ecological data are collected, the comparative method will be of great use for identifying important contributors to extinction risk in bats.

High genetic variation is generally thought to be associated with lower extinction risk, as species with greater amounts of variation are more able to adapt to changing environmental conditions (Lacy 1997; Hermisson and Pennings 2005). Endangered species generally have reduced genetic variability and, even after their numbers have recovered, may not be able to recover genetic variability and thus still face high extinction risk (Frankham 2005). While recovery rates may vary depending on how long populations were bottlenecked, a slow recovery would be predicted for bats, as they generally have low reproductive rates. Since populations recover too slowly, there would be a greater loss of genetic diversity as well. Rapid and irreversible loss of genetic diversity further increases extinction risk of a species and underscores the need for preemptive conservation action. However, reduced genetic variability must be shown to be truly a recent bottleneck through anthropogenic disturbance, as in the case of sea otters being impacted by the fur trade (Larson et al. 2002). In other mammalian species, such as cheetahs (Menotti-Raymond and O'Brien 1993) and wolverines (Schwartz et al. 2007), low genetic

variability is a result of previous historical demographic changes (e.g., bottlenecking from Pleistocene glacial cycles, founder effects at periphery of distribution). Phylogenetic research is necessary to approximate expected levels of genetic variation before statements about genetic health of an endangered species can be made. There are currently no examples in bats using these methods, but comparisons of extant populations to historical specimens in museum collections may help determine whether threatened populations are experiencing anthropogenic bottlenecks. This research is now made possible by new methods in high-throughput sequencing of ancient DNA from degraded material (Gilbert et al. 2007; Mason et al. 2011; Dabney et al. 2013) and modeling of heterochronous data (Ho et al. 2007; Navascués et al. 2010; Drummond et al. 2012).

Estimations of speciation and extinction rates may also be made from phylogenies (Ricklefs 2007; Fitzjohn et al. 2009; but see Rabosky 2010 about the need for inclusion of fossil data) using speciation–extinction models derived from birth–death models in population ecology. Greater availability of time-calibrated phylogenetic trees now makes this method viable for estimating the likelihood that a clade will go extinct during a particular time slice. However, these estimates of likelihood of speciation and extinction are tied to the completeness of the phylogeny, meaning more phylogenetic work must be completed if these estimates are to be used for making predictions about species diversity in that clade. These model-based methods allow researchers to investigate speciation or extinction rates as compared to random chance. Anthropogenic effects on extinction can thus be more accurately assessed. Such research may also be used as a second test of hypotheses of species loss in concert with current methods favored by conservation biologists, such as species–area relationship and endemics–area relationship (e.g., Lane et al. 2006).

From phylogenetic studies, researchers now know that some species may be the only remaining representative of an old lineage, while others are one of many in very diverse clades. These old lineages, known as relict species, have genes and traits that have survived from deep timescales and tell a tale of resilience (and luck) in the face of regime shifts and faunal turnover. These taxa may have survived previous major extinction events, and researchers can study them to understand how species may continue to survive in the face of the current extinction crisis (Habel and Assmann 2010). Relict species may also represent the only living relatives of fossil taxa, allowing systematists to place fossil taxa correctly in a tree. Representing both extant and extinct taxa is necessary for accurate estimates of extinction rates (Rabosky 2010). How accurate these estimates may be for bats is still unclear, as there are few dated phylogenies and the only study in non-volant mammalian extinction rates found that clade age was not correlated to higher extinction (Verde Arregoitia et al. 2013). *Mystacina tuberculata* is an example of a relict species. It is a New Zealand endemic and the sole extant representative of an entire family that was once more widespread. The fossil record of mystacinids includes the bat genus *Icarops* from the Oligocene and Miocene of Australia (Hand et al. 2001), but the family also includes *Mystacina robusta*, a species that went extinct in historic times (Daniel 1990). Even with molecular

tools, researchers have had difficulties resolving the sister taxon of *Mystacinidae*, likely a result of deep, rapid radiations that created short internal branches with conflicting phylogenetic signal (Kennedy et al. 1999).

## 16.6 Impediments to Taxonomic Research

A decline in both amateur and professional taxonomists has been documented (e.g., Stuessy and Thomas 1981; Hopkins and Freckleton 2002), with reductions or elimination of jobs in museums and universities for those trained in taxonomy. There are few skilled and trained bat taxonomists, slowing fieldwork as well as the publication of comprehensive taxonomic revisions, species lists, field guides, and popular works on bats. In part, this appears due to what has been described as a “classic market failure” for taxonomy (Aylward et al. 1993; Hoagland 1996). Taxonomy is an “externalized” cost:

Growing out of a tradition of reciprocity and collegiality, taxonomists frequently do not charge clients directly for their specialized services and products, such as identifications and biodiversity databases, even though the users of these services and products now extend far beyond their fellow taxonomists. These service activities are often ancillary to a taxonomist’s basic monographic work, for which he or she receives grant funds, or subsidizes on his own or through his employers. The cost of doing taxonomy is not factored into most biodiversity or ecology projects. Research grants (even in taxonomy) and ecological monitoring activities rarely include funds for the curation and care of voucher specimens, or the establishment and maintenance of museums. (Hoagland 1996)

The result? A reluctance by employers to hire those who do not bring in funds and cause a perceived drain on the institution, and a reluctance by students to pursue taxonomy as a career in favor of fields offering more money and jobs. While there are a growing number of young bat taxonomists in the developing world (Anwarali Khan et al. 2010; Douangboubpha et al. 2012; Soisook et al. 2013) where educational institutions are newly committed to developing and protecting local biodiversity, the lack of funds for taxonomy still presents a substantial impediment (Aylward et al. 1993). The few taxonomic experts in developed countries that still remain are discouraged from pursuing taxonomy in regions of the world where both the biota and their ecosystems are most understudied due to a combination of stricter local specimen export laws and lack of funding. Additionally, the low impact factor of taxonomic journals is a major impediment for academics at non-museum institutions whose performance reviews for promotion hinge largely upon the impact factor of journals in which they publish (Venu and Sanjappa 2011).

In most scientific fields, including other disciplines of systematics, specialists have grouped themselves in associations that publish journals and act as lobbies to promote their discipline and defend their members. However, there exists no international or national scientific society specifically devoted to the promotion of taxonomy, the publication of general papers on the discipline, its theoretical

background, its history, or its problems and its future. In part as a result, taxonomists are typically under-represented in official or unofficial bodies that play significant roles in shaping scientific policies, budgets, and definition of priorities. Yet, taxonomists are critically needed for research in understudied groups, such as bats, especially in developing countries. Without any formalized society, it becomes difficult to pass on the expertise and shared standards that are essential to all other fields in biology, including conservation.

The reduction in numbers of taxonomists in institutions in developed countries and the increase seen in developing countries is complicated by a great deal of historical baggage. Type specimens (the actual specimens to which scientific names are attached) and important taxonomic literature are still based in institutions in developed countries, and there is still an imperative need for repatriation of information as well as capacity building outside these centers. Capacity building can occur at three different levels: individual (build individual ability to contribute to taxonomy), institutional (modernize museum infrastructure and policies, increase the level of curatorial proficiency in staff), and societal (engage the public in understanding and learning about biodiversity and being held accountable for it). Lack of access to available information is then also a part of the taxonomic impediment to conservation, not just lack of research in the discipline.

Progress has been made recently to increase accessibility of resources housed in institutions in developed countries. Digitization of type specimens of bats by some of the larger museums (e.g., American Museum of Natural History), increased availability of literature through online sources, increased training in developing countries, and increased collaborations between Western taxonomists with young taxonomists from developing countries have begun to counter gaps in knowledge and training. Collections research fellowships are now available at some institutions to provide researchers with funds needed for visiting museums and inspecting specimens first-hand. Developing countries now see an increase in new bat taxa described in international, open-access journals by in-country scientists. New, well-maintained, and actively used natural history collections now exist in places like the University of Phnom Penh, Cambodia; Prince of Songkla University, Thailand; and the National University of Laos, thanks to local support and funding by NGOs such as the Darwin Initiative, the Systematics Association, and the MacArthur Foundation. Older collections in species-rich tropical countries, such as at the National Museum of the Philippines, the Museo de Zoología-Mamíferos, Pontificia Universidad Católica del Ecuador, and the Museu Nacional, Universidade Federal do Rio de Janeiro in Brazil, have refurbished outdated collections spaces and benefited from increased access to information and increased local capacity as talented local scientists have helped reignite interest in conservation and biodiversity initiatives.

Museum collections and historic taxonomic descriptions themselves may, counterintuitively, present impediments to taxonomic research. While today's taxonomists use morphological and genetic data (when available) to establish species limits, such modern methods have only come to the fore recently. Many older species names are attached to poorly preserved type specimens, sometimes dry

skins, museum taxidermy mounts, or specimens that survived long sea voyages pickled in rum or other spirits. These specimens may be so damaged that viewing important features, or any features, from the published descriptions is impossible, leading to confusion regarding the recognition of the species in question. In some cases, the type specimens have been lost or destroyed and new type specimens (known as neotypes) must be designated, again introducing the possibility of confusion. Older names are often based on brief and sometimes inadequate descriptions that fail to provide sufficient detail to facilitate distinction from similar species. Even when faunas have been well surveyed, these issues of taxonomy frequently cause confusion about the number and identity of species inhabiting a particular region. Taxonomic confusion may contribute to the inability to properly attribute a name to organisms or integrate new data, barring species from protection that they may have been granted had they been accurately recognized and complicating conservation efforts.

## 16.7 Conservation in the Era of Molecular Phylogenetics

Molecular tools have given systematists new ways to resolve phylogenies and population networks and thus new ways to delimit species and other units of conservation concern. Genetics has created new ways of thinking about what a species is, and this has led to healthy debates about species delimitation. In some countries such as Germany, conservation legislation takes into account the genetics of organisms as well as their species limits. The Nationale Strategie zur Biologischen Vielfalt (National Strategy for Biological Diversity of Germany, BMU 2007) recognizes that the entire gene pool of a species must be protected. While this may not always be possible, the reason for this approach is based on the desire to protect distinct lineages.

Populations are often locally adapted and may be on different evolutionary trajectories even within what is recognized as a single species. The term Evolutionary Significant Unit or ESUs was originally coined to reflect the importance of these units in conservation decisions (Ryder 1986; Moritz 1994). ESUs may be at the species level or below and ESU definitions generally include the idea that the ESU is currently geographically isolated from other ESUs, that there is genetic differentiation at neutral markers, or that there is local phenotypic variation. The term ESU has since changed to reflect both evolutionary processes along with ecological exchangeability. The crosshair analysis advocated by Crandall et al. (2000) uses tests of null hypotheses in four categories (genetic, ecological, recent, and history) to determine whether populations should be considered ESUs or not. Species are not static, but evolving; if given enough time, ESUs may evolve into entities that require a different taxonomic status, e.g., a population may become a new species. ESUs may represent unique gene pools and may be of special conservation concern; proper conservation action can be taken only if they are recognized.



Molecular genetics has also allowed researchers to identify cryptic species, species that are morphologically indistinguishable (or nearly so) but exhibit significant genetic divisions that form species boundaries (Pfenninger and Schwenk 2007). These discoveries have helped systematists further understand the mechanisms that drive the speciation process, such as sympatric reproductive isolation without morphological differentiation, but they also have conservation implications (Bickford et al. 2007). Cryptic species represent a previously unrecognized part of the biota of a region and thus may be important to conservation biologists who are interested in identifying and understanding biodiversity hotspots. In bats, many previously unrecognized cryptic species are now being found through molecular assays even in very well-studied areas (Mayer et al. 2007). Early results from bar coding work in Southeast Asia suggest that the number of bat species may be twice that currently recognized (Francis et al. 2010). The level of discovery of new taxa in the last decade has generally corroborated this estimate (Table 16.1).

A classic example of a cryptic species hiding in plain sight is the European pipistrelle (*Pipistrellus pipistrellus*). One of the most common bats throughout its range, the European pipistrelle was not recognized as a cryptic complex until echolocation data suggested the presence of more than one species of pipistrelle occurring in sympatry throughout much of Europe (Jones and van Parijs 1993; Barlow 1997; Barlow and Jones 1997). Since the early echolocation studies, mitochondrial data (Hulva et al. 2004), microsatellite data (Hulva et al. 2010), information on foraging (Davidson-Watts and Jones 2005), and habitat selection data (Davidson-Watts et al. 2006) have further corroborated the split of the European pipistrelle into two distinct species (*P. pipistrellus* and *Pipistrellus pygmaeus*). Similar echolocation studies in Southeast Asia of hipposiderid bats (Kingston et al. 2001; Thabah et al. 2006) and African *Rhinolophus* (Taylor et al. 2012) have shown that these groups likely contain many cryptic species that can be distinguished by distinct phonic profiles, but not so easily by morphology. In many cases, molecular work remains to be conducted to clarify the numbers and limits of species in these complexes.

Molecular tools can now be used to characterize biodiversity in a more efficient manner than could be done in the past, particularly in poorly studied regions of the world. However, these tools must be used with caution, as not every new mitochondrial clade warrants recognition as a distinct species—some genes are known to be hypervariable and poor indicators of species limits (Engstrom et al. 2004; Lohse 2009; Galtier et al. 2009). The phylogenetic signal for hybridizing species may look very similar to incomplete lineage sorting (e.g., both phenomena would result in non-monophyletic trees) and therefore requires more genetic data and stricter quantitative assessments of genetic data to test different evolutionary scenarios (Maddison 1997; Yu et al. 2012). Many molecular studies of bats published in recent years have failed to review important elements such as the morphology or echolocation call structure of putative species, or have failed to include a sufficient number of genes or individuals. Mitochondrial clades may point to the need for more research into a potential species complex, but such

clades cannot be readily assumed to represent a new species. The recent discovery of multiple allopatric mitochondrial lineages of *Pteronotus parnellii* (Clare et al. 2011) *Chrotopterus auritus*, *Glossophaga soricina*, and *Saccopteryx bilineata* (Clare 2011) indicates that deep divergences may exist within these species, but further study of genetic, morphological, or behavioral characters is needed as noted by these authors. Even in well-studied regions, such as Europe, cryptic species may have only been recently recognized as new phylogenetic methods and more nuclear data have become available, such as the Natterer's bat (*Myotis nattereri*) complex (Salicini et al. 2011). Mitochondrial divergence may also reflect sex-based differences in dispersal rather than new species. For example, Ozark big-eared bats (*Corynorhinus townsendii ingens*) have low levels of mitochondrial divergence between caves, but their microsatellite data indicate that there is likely male-mediated gene flow between populations (Weyandt et al. 2005).

Examples exist of cases where mitochondrial data have been misleading in bats. A cautionary tale is that of two subspecies of *Myotis lucifugus* (*M. lucifugus* and *M. carissima*), which exhibited enough mitochondrial divergence that they could have been recognized as separate species on the basis of molecular evidence alone (Dewey 2006). However, analyses of ten additional nuclear markers have shown that both these subspecies are experiencing high levels of gene flow, resulting in the absence of population structure even if these were historically separate populations. Additionally, no morphological characters diagnose the mitochondrial clades (Lausen et al. 2008). Consequently, there is no justification, despite the mitochondrial indicators, for recognizing these subspecies as separate species.

In contrast, Goodman et al. (2009) used a combined molecular and morphological dataset to resolve cryptic species in *Miniopterus manavi*. This study demonstrates a "best practices" approach to resolving widespread species complexes. Previous research using only mitochondrial data suggested that *M. manavi* in Madagascar and the Comoros represented unique lineages. However, sampling was limited and the relationships between clades were not fully resolved (Weyeneth et al. 2008). Using increased geographic sampling and morphological comparisons of type specimens, each of the clades was more clearly defined. *Miniopterus aelleni* was recognized as a new species, and its species diagnosis and description was accompanied by photographs of a live individual and skulls, and illustrations of dental characters (Goodman et al. 2009). Despite the relative rarity of *M. aelleni* to *M. manavi* on Madagascar, both species were found in several protected areas and the authors did not suggest further conservation action.

Extensive sampling throughout the geographic range of the relevant species is needed when attempting to resolve the relationships within a species complex. Simulation data suggests that more complete taxonomic sampling improves phylogenetic accuracy (Pollock et al. 2002). Too much missing data, either in the form of missing characters (e.g., missing genetic loci or using only mitochondrial data for some taxa) or missing taxa (e.g., incomplete geographic sampling) can lead to unresolved trees or incorrect inferences through phenomena such as long-branch attraction (Wiens 2003, 2006).

Currently, the field of molecular phylogenetics is undergoing a major shift away from locus-by-locus data collection to next-generation sequencing methods (also called high-throughput sequencing) that will allow for the collection of massive datasets in a relatively short period of time (Faircloth et al. 2012; Lemmon et al. 2012; Lemmon and Lemmon 2012). As prices fall and computational pipelines are developed to deal with the influx of data, taxonomically complex problems may be resolved by the increased availability of molecular character data. Genomic advances will also allow for detection of signs of natural selection in recent history (e.g., Pickrell et al. 2009 in humans; vonHoldt et al. 2010 in dogs), which could be used to determine how recent historical events such as climate change or human disturbance have affected natural populations. Having more data may not be the only solution to taxonomic problems, however—more powerful computational models means greater ability to analyze multilocus datasets that are already available. By taking cues from population genetics and phylogeography, historical models can now be incorporated into analyses to understand the effects of microevolutionary processes on species histories (Edwards and Beerli 2000). Establishing that a tip on a phylogenetic tree is truly representative of a species, and not just a genetic lineage, is fundamental to the goals of systematics and necessary prior to further analyses about speciation and diversification (Edwards 2009).

## 16.8 The Problem of “Taxonomic Inflation”

Taxonomic inflation caused by improper species delimitation can have profound effects on conservation, as biodiversity hotspots may be misidentified, or conservation priorities are selected based on poor evidence. With the advent of molecular phylogenies, imprudent application of the PSC or the GSC has been criticized for greatly inflating the number of recognized species in mammals, where many subspecies have been raised to full species rank. The examples cited by critics, such as Zachos et al. (2013) for Cetartiodactyla and Isaac et al. (2004) and Mace (2004) for Primates, however, are not due to application of the PSC or molecular phylogenetics; instead, they are generally due excessive splitting of inadequate datasets. For instance, critics cite splitting the mainland serow (*Capricornus sumatraensis*) into six species from one as evidence of taxonomic inflation. Yet the split of this species was based on pelage characteristics and was complicated by small sample sizes (Groves and Grubb 2011), and as such it has nothing to do with a new understanding of genetics. While the mainland serow may not have warranted such splitting, the critiques against taxonomic inflation ignore the fact that newly recognized species in these complexes may reflect biological reality (Gippoliti and Groves 2012; Gutiérrez and Helgen 2013). A more comprehensive set of data may be needed to confirm species boundaries, but new research should not be thrown out in favor of older taxonomy just because the latter is more convenient. Like other branches of science, our knowledge, and views of taxonomy change, other researchers also need to embrace this aspect of defining species.

Gippoliti and Groves (2012) responded to criticisms of taxonomic inflation by citing several examples of how integrative modern taxonomy (including multiple lines of evidence) has positively affected conservation. Critics of taxonomy are not wholly against the findings of modern taxonomy. For example, Zachos et al. (2013) recognized several legitimate cases of cryptic species in African elephants, giraffes, and European badgers. In each case, multiple lines of evidence corroborated species boundaries and warranted species-level recognition. Critics of taxonomic inflation seek the same comprehensive data collection that taxonomists do and generally make the same recommendations that we have outlined above. If uncertainty surrounding preliminary mitochondrial data exists, decision makers should determine if clades of interest correspond to any ESU or other management units (Miralles and Vences 2013), not throw out the new taxonomic information entirely.

It is important for taxonomists to state methods used to delimit species so that new candidate assessments can be easily made in the future. Explicit enumeration of methods, species concepts, and data makes taxonomic assessments more repeatable and testable by others. Clearly written species descriptions based on multiple lines of evidence help maintain the species identity over time, reducing confusion in the long run about the species and its associated name. A recent study in the Malagasy lizard genus *Madascincus* found that different species-delimitation protocols (e.g., Bayesian Assignment Test, HaploWeb, or Generalized Mixed Yule Coalescent Approach) result in wildly different recognized species, with the Bayesian Assignment test approach being in the most agreement with integrative taxonomy (Miralles and Vences 2013). Clearly stating methods can also reduce noise from new species concepts or new data, since it can be quickly determined if this new information will change how the species is viewed and understood. If species limits are known to be stable, that helps maintain the credibility of the lists that legislators and agencies so heavily rely upon for conservation.

## 16.9 Conclusion

The Age of Discovery is not over for chiropteran taxonomists, who play a critical role in efforts to ensure the documentation and protection of bat diversity by providing a necessary framework for conservation initiatives. Use of a broad range of data (morphological, molecular, behavioral, acoustic) has had a marked effect on the number of bat species identified in the past decade; molecular and acoustic data have indicated that there may be numerous cryptic bat species that cannot be successfully identified using morphology alone.

In addition to identifying species and caring for museum specimens, taxonomists create species lists for localities and communicate taxonomic ideas to non-experts, especially through species lists, descriptions, keys, and field guides. These activities lead to important opportunities for outreach via public exhibits at home institutions or in the field. Taxonomists also provide conservation planning tools

such as inventory data, estimates of extinction risk, and information to help define protected areas. These activities allow researchers and government agencies to lower extinction risks and improve the likelihood of species recovery.

More training should be provided to non-taxonomic experts through short workshops focusing on specimen collection and identification techniques. When conducting research, taxonomists may provide the first close-up look at bats to local populations. Capitalizing on this opportunity to inform people about their local biota through leaflets, talks, and training, can advance local and regional conservation goals.

Impediments to the training of new taxonomists remain substantial, including a lack of funding for the identification and storage of voucher specimens, the absence of a taxonomy “lobby” and journal devoted to taxonomic practice, and the low status often accorded to taxonomic publications. However, accessibility to museum materials in developed countries—both voucher material and literature—is increasing through ongoing digitization efforts. Worldwide interest in local biodiversity is also increasing and new bat taxonomists, with new or growing collections, are now practicing around the globe. It is our hope that all taxonomists advocate for appropriate management strategies for bats on a global scale by reaching out to local populations, non-expert scientists, and legislators; effectively communicating complex scientific ideas and listening to local concerns; and continuing to provide a robust scientific basis for conservation as we work to prevent bat extinctions in the Anthropocene.

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