ABSTRACT

Amphibians are a clade of over 8,400 species that provide unique research opportunities and challenges. With amphibians undergoing severe global declines, we posit that assessing our current understanding of amphibians is imperative. Focusing on the past five years (2016–2020), we examine trends in amphibian research, data, and systematics. New species of amphibians continue to be described at a pace of ~150 per year. Phylogenomic studies are increasing, fueling a growing consensus in the amphibian tree of life. Over 3,000 species of amphibians are now represented by expert-curated accounts or data in AmphibiaWeb, AmphibiaChina, BioWeb, or the Amphibian Disease Portal. Nevertheless, many species lack basic natural history data (e.g., diet records, morphological measurements, call recordings) and major gaps exist for entire amphibian clades. Genomic resources appear on the cusp of a rapid expansion, but large, repetitive amphibian genomes still pose significant challenges. Conservation continues to be a major focus for amphibian research and threats cataloged on AmphibiaWeb for 1,261 species highlight the need to address land use change and disease using adaptive management strategies. To further promote amphibian research and conservation, we underscore the importance of database integration and suggest that other understudied or imperiled clades would benefit from similar assessments of existing data.

INTRODUCTION

Amphibians are an ancient, diverse lineage of vertebrates that have been studied in research fields from evolution and ecology to engineering and medicine. Although amphibians are often considered to be sensitive to perturbation, they have survived the last four global mass extinction events and have a nearly worldwide distribution (Wake and Vredenburg, 2008; Kerby et al., 2010; Barnosky et al., 2011; Alroy, 2015). Most have biphasic lifestyles, serving as a vital link for energy and nutrient flows between terrestrial and aquatic systems (Finlay and Vredenburg, 2007). Many species have large populations and fast growth rates, occupying key roles in food webs as abundant food sources whilst simultaneously shaping the functional diversity of their own prey communities (Colón-Gaud et al., 2009; Zipkin et al., 2020). Despite the ecological importance of amphibians and their diverse evolutionary histories, we lack basic natural history and geographic distribution data for a large proportion of species, with 16.4% (1,185 species) classified as Data Deficient by the IUCN – the highest proportion of data deficiency for any vertebrate class (IUCN, 2021).

Amphibian research has grown rapidly over the last few decades, expanding from an early focus on several model species to an exploration and description of the evolution, ecology, and diversity of amphibians found globally. Researchers have developed amphibian model systems that are associated with sophisticated molecular and genomic tools based on decades of concentrated research into the molecular biology of three species – *Xenopus laevis*, *Xenopus tropicalis*, and *Ambystoma mexicanum* (Getwan and Lienkamp, 2017). Although these three model species scarcely capture the diversity of Amphibia (over 8,400 species; AmphibiaWeb 2021), they have served important roles during the last half century, providing insight into tetrapod evolution (Edholm et al., 2013; Rozenblit and Gollisch, 2020), developmental biology, molecular biology, neurobiology (Dascal, 1987; Yakushiji et al., 2009; Harland and Grainger, 2011), and tissue regeneration (Nye et al., 2003; Freitas et al., 2019). Research on many other amphibian genera has made notable historical contributions to biology: e.g., *Plethodon cinereus* in behavioral ecology and development (Dent 1942; Heatwole 1962; Kleeberger and Werner 1982; Wyman and Hawksley-Lescault 1987; Kerney 2011; Kerney et al. 2012); *Engystomops* in sexual selection (Ryan et al., 1990); *Rana* in cloning (Briggs and King, 1952); *Rana* and (Lefcort et al., 1998; Hopkins et al., 2000; Bridges, 2000; Pollet and Bendell-Young, 2000) *Acris* (Fleming et al., 1982; Clark et al., 1998; Reeder et al., 1998) in community ecology and toxicology. New tools have since promoted the emergence of more model systems from classically “non-model” species and systems, such as dendrobatid poison frogs for the neurobiology of parental care (Roland and O’Connell, 2015; O’Connell, 2020) and the molecular evolution of chemical defense (Saporito et al., 2012; Tarvin et al., 2017; Caty et al., 2019; Alvarez-Buylla et al., 2022), toxic salamanders and resistant garter snakes for co-evolution (Geffeney et al., 2005; Bucciarelli et al., 2022), *Spea* for phenotypic plasticity and life-history evolution (Levis et al., 2015, 2020), and *Nanorana parkeri* for adaptation to high elevation (Sun et al., 2015, 2018; Wang et al., 2018). As we will highlight here, the growing availability of amphibian genomes and other molecular resources poises amphibian researchers to further develop other amphibians as new “model” species.

New genetic tools and increasing availability of amphibian sequence data are also reshaping and expanding our knowledge of amphibian phylogeny and evolution (Blackburn et al., 2019). Until recently, many deeper phylogenetic relationships remained unresolved, resulting in frequent taxonomic changes. Moreover, new species continue to be described, two or three each week on average. Since 2000, there has been an average of 150 new species described every year, with no sign of slowing down (AmphibiaWeb, 2021).

Nevertheless, understanding current amphibian biodiversity is imperative, as amphibians are undergoing severe global population declines. The modern amphibian lineage is ancient (~300 million years old; Wake and Koo, 2018) and is now the most endangered vertebrate class in the ongoing Holocene Extinction (Stuart et al. 2004; Wake and Vredenburg 2008; Barnosky et al. 2011). Roughly 3% of anuran and caudatan diversity are believed to have declined to the point of extinction since the 1970s (Alroy, 2015), and an estimated 40% of extant species are threatened with extinction (IUCN, 2021). Continued research on amphibian biology, as well as efforts to share the fruits of this research through public databases, can guide efforts to mitigate the threats of habitat loss, climate change, and infectious diseases—particularly in light of opportunities presented by broad global initiatives to protect biodiversity, such as the proposal to protect 30% of the earth's surface by 2030 (Kubiak, 2020; HAC, 2021).

Given the ever-increasing accumulation of biological information, the expanding scale at which research is undertaken, and the urgent need for knowledge to combat amphibian declines, we aim to summarize the state of amphibian research to both improve awareness of existing resources and highlight gaps in knowledge. Focusing on the five years from 2016 to2020, we assess the following: 1) trends in publishing, 2) advances in amphibian conservation research, 3) trends and updates in systematics and amphibian diversity, and 4) a review of existing community resources.

MATERIALS AND METHODS

Trends in publishing.–

To assess changes in the focal topics of amphibian research from 2016 to 2020, we performed a standardized literature search in Web of Science (© Copyright Clarivate 2022). First, we quantified the total number of amphibian scholarly articles published from 2016 to 2020, as well as the total number within each individual year, that had the following search term in their abstract: "amphibian" OR "amphibians" OR “Caudata” OR “salamander” OR “salamanders” OR “newt” OR “newts” OR “Anura” OR "anuran" OR "frog" OR "frogs" OR “toad” OR “toads” OR “Gymnophiona” OR “caecilian” OR “caecilians”. Next, we quantified the total number of amphibian scholarly articles published in those years (and within each year) in specific subfields of biology by adding additional search terms to the one above. The full list of added subfield search terms was: “behavior”, “development”, “diet”, “cell” AND “molecular”, “climate”, “conservation”, “ecology”, “eDNA”, “fossil” OR “fossils”, "genetic" OR "genetics", "genomic" OR "genomics", “genetic” OR “genetics” OR “genomic” OR “genomics”, “phylogenetic” OR “phylogenetics”, “phylogenomic” OR “phylogenomics”, “microbiome”, “morphology”, “physiology” and “trait” OR “traits”. In addition to reporting the absolute numbers of amphibian publications from 2016 to 2020, we report the percent change in amphibian publications (overall and within each subfield) over that five-year period (number of articles published in 2020/number of articles published in 2016). We searched the total number of scholarly articles published (all publications, no search terms) in 2016 and in 2020 to determine the background percent change in publication rate to serve as a reference point for the percent change in amphibian publications from 2016 to 2020. We documented which journals published the amphibian papers recovered in our 2016–2020 literature search and how many languages were represented in these publications. We also review name changes of herpetology-focused journals. In an effort to examine how many publications focused on model amphibian species, we determined how many amphibian publications in each research field also mentioned *Xenopus laevis, Xenopus tropicalis,* OR *Ambystoma mexicanum* in their abstracts.

Advances in amphibian conservation research.–

To understand the major contributors to amphibian declines, for each species we obtained IUCN Red List status (or provisional IUCN Red List statuses from the AmphibiaWeb database) and associated drivers of decline from AmphibiaWeb species accounts (see supplemental data files; AmphibiaWeb and IUCN data were downloaded as of September 2021). The twenty-five AmphibiaWeb drivers of decline were collapsed into ten broad categories which, owing to the nature of these threats, do not form entirely discrete, non-overlapping units. For instance, the following categories all ultimately relate to habitat modification or loss, but were divided as follows to allow for more granular insight into important amphibian threats: a ‘habitat alteration and loss’ category includes general habitat alteration and loss, secondary succession, subtle changes to necessary specialized habitat, and habitat fragmentation; a ‘resource exploitation’ category includes habitat modification from deforestation or logging related activities, mining, and intensified agriculture or grazing; a ‘roads and urban development’ category includes urbanization, disturbance or death from vehicular traffic, barriers to movement, and accidental traps; and an ‘intentional changes to hydrology’ category includes drainage of habitat and dams changing river flow and/or covering habitat. The remaining threat categories were as follows: a ‘pollutants’ category includes local and long-distance pesticides, toxins, fertilizers, and pollutants; a ‘climatic factors’ category includes climate change, prolonged drought, floods, increased UVB, or increased sensitivity to it; a ‘disease and immune functioning’ category includes disease, parasitism, and weakened immune capacity; a ‘predators and competitors’ category includes changing dynamics with both introduced and native species; an ‘intentional mortality’ category includes over-harvesting, the pet trade, and collecting; and a ‘genetic degradation’ category includes loss of genetic diversity from small population phenomena and loss of distinctiveness through hybridization. We visualized these data by order and IUCN status for each decline category and discussed in the context of major new findings on habitat loss and disease as drivers of amphibian declines between 2016 and 2020.

Trends and updates in amphibian diversity and systematics.–

To visualize the accumulation of new species over time, we used the complete AmphibiaWeb database of new species between 2007 and 2020 (see supplemental data files) to provide a baseline comparison to identify any trend changes during 2016–2020. We joined the type localities of these new species to country and biogeographic realm using Quantum GIS (vers. 3.2, QGIS Development Team, 2021). We made a heatmap of the type localities of the new species (2016–2020) using the heatmap option in QGIS and calculated the number of new species per region using the QGIS point cluster option with radius distance set to 800 km for both the heatmap and clusters. We summarized the cumulative number of new species graphically in R (R Core Team, 2021) using ggplot2 v3.3.5 (Wickham, 2016), cowplot v1.1.1 (Wilke, 2020), lubridate v1.80 (Grolemund and Wickham, 2011), rentrez v1.2.3 (Winter, 2017), tidyverse v1.3.1 (Wickham et al., 2019), XML v3.99-0.8 (Lang, 2021), and included data in the phylogenetic matrix as described in the section below ("A review of community resources"). We also review higher level taxonomic changes in modern amphibians, largely based on recent phylogenomic studies.

A review of community resources.–

We compiled a list of published amphibian genomes by searching the NCBI Genome database with the "Organism" field set to "Amphibia" and reviewing Google Scholar results for "amphibian genome". We obtained a list of all available amphibian genetic sequences in the NCBI Sequence Read Archive (SRA; on 21 June 2021) by setting the "Organism" search field to "Amphibia" and downloading metadata files from Run Selector. To obtain metadata on the available sequences in the NCBI GenBank Nucleotide database, we used the Entrez retrieval tool (Clark et al., 2016; NCBI Resource Coordinators, 2016). GenBank data were downloaded on 27 June 2021 in 1-month batches from January 1982 to December 2020 using esearch (-db nuccore -query "amphibia [ORGN]" -mindate "$yr/$month" -maxdate "$yr/$month"), extracting the following elements from the document summary: Caption, Title, CreateDate, TaxId. We used the CreateDate information as the deposit date for each sequence. Using regular expressions and lists of keywords in R, we categorized each sequence as mitochondrial DNA (title containing one or more of the words "cytochrome oxidase", "COX", "tRNA", "ND", "ribosomal RNA", "rRNA", "NADH dehydro", "mitochondri", "cyt[.]b","cytochrome b", "ATP8", "ATP6", "control region", "d-loop", or "cytb"), as mRNA (title containing one or more of the words "mRNA", "transcript, or "TSA:"), or genomic DNA (all other sequences). To assign a taxonomic order to each sequence in the SRA and GenBank datasets, we merged sequence metadata with the NCBI taxonomy database (https://ftp.ncbi.nlm.nih.gov/pub/taxonomy/new_taxdump/) using tools from the R package 'dplyr' v1.0.6 (Wickham et al., 2021). See supplemental data files for raw data.

To count the cumulative number of species represented in the SRA database over time, we summed the number of unique species names in SRA metadata across years. We note, however, that these numbers are artificially inflated because of unspecified (e.g., " *Hyloxalus* sp. 1 WG-2019"), subspecies (e.g., "*Cryptobranchus alleganiensis bishopi*"), and hybrid (e.g., "*Hyla intermedia* x *Hyla* sp. n. DJ-2018") samples that are included in the data. To more accurately count the number of species added to NCBI databases each year, we used the *entrez_search* function from the R package 'rentrez' v1.2.3 (Winter, 2017) to query the ncbi taxonomy database by year and by Order, with additional search terms to filter out ambiguous or unspecified sequences (query = "<Order> and [SubTree] AND <year> AND species[Rank] NOT uncultured[prop] NOT unspecified[prop]").

To quantify the representation of amphibian species in other public databases, we collated metadata from several databases that contain information about amphibians. We identified all major bioacoustic repositories by surveying relevant literature and asked leading experts in bioacoustics. For each repository, we used website searches to obtain the number of available recordings and the number of species represented (see supplemental data files). If those data were not available, we contacted the person in charge of the website to obtain the database of the recordings. For microCT data, we identified all amphibian scans available on MorphoSource (https://www.morphosource.org, Boyer et al., 2016), DigiMorph (http://digimorph.org), and Phenome10K (https://www.phenome10k.org; see supplemental data files for MorphoSource and Phenome10K results). We downloaded Amphibian Disease Portal data on *Batrachochytrium dendrobatidis* (Bd) swabs taken and swabs testing positive for Bd, and summarized by amphibian family, by year, and by geography in R v4.1.0 (R Core Team, 2021) and plotted geographic representation of the database over time (see supplemental data files). Finally, in addition to these trait- or data type-specific databases, we also review existing large databases that provide information on amphibian morphological, ecological, and life-history traits.

We summarized the phenotypic, genetic, and disease data available for each anuran family in a phylogenetic matrix plot using a trimmed version of the phylogeny from Hime et al., 2021. We added four families to match the AmphibiaWeb taxonomy, Allophrynidae, Micrixalidae, Ranixalidae, and Chikilidae, that were not in the original tree by either using a species within a sister family to represent the missing family (in the cases of Allophrynidae and Chikilidae) or artificially adding branches to the tree using the bind.tree function (in the cases of Micrixalidae and Ranixalidae).

Data analysis and visualization.–

Plots and data formatting were performed in R v4.1.0 (R Core Team, 2021) with the following packages: cowplot v1.1.1 (Wilke, 2020), dplyr v1.0.7 (Wickham et al. 2021), ggplot2 v3.3.5 (Wickham, 2016), reshape2 v1.4.4 (Wickham, 2007), stringr v1.4.0 (Wickham, 2010), tidyr v1.1.3 (Wickham, 2017), and tidyverse v1.3.1.9 (Wickham et al., 2019). For phylogenetic data formatting, analysis, and plotting we used R v4.1.0 (R Core Team, 2021) with the following packages: ape v5.5 (Paradis and Schliep, 2019), geiger v2.0.7 (Pennell et al., 2014), phytools v0.7.8, (Revell, 2012), and tidyverse v1.3.1.9, (Wickham et al., 2019).

RESULTS

Trends in publishing

Research topics.–

We identified 13,208 articles published from 2016 through 2020 that included at least one of our amphibian-specific search terms in their abstracts. Overall, amphibian publications increased by 15% from 2016 to 2020, which equals the 15% increase in total publications (no search filters) during that time period (Fig. 1a; Table S1). The majority of amphibian publications were in five subfields: development (1,865), conservation (1,757), genetics OR genomics (1,506), behavior (1,023), and phylogenetics (999). Relatively few amphibian publications mentioned phylogenomics (32), microbiome (83), or eDNA (86; Fig. 1b; Table S1). Almost all subject areas increased in amphibian publications, with the exception of fossil publications (30 in 2016 and 29 in 2020), cell and molecular publications (41 in 2016 and 40 in 2020), and behavior publications (205 in 2016 and 203 in 2020). The fastest growing subject areas, microbiome, phylogenomics, eDNA, morphology, and diet all showed a 50% or greater increase in amphibian publications from 2016 through 2020 (Fig. 1a; Table S1).

Of the 13,208 total amphibian publications from 2016 through 2020, 629 (5%) mentioned *Xenopus laevis, Xenopus tropicalis,* OR *Ambystoma mexicanum* in their abstracts. These model amphibian publications were not evenly distributed among research areas, making up a substantial proportion of cell AND molecular (23%), development (13%), genomic(s) (10%), and physiology (9%) publications, but only 5% or less of all other research areas (Fig. S1).

Journals.–

The peer-reviewed journals with the largest number of amphibian publications from 2016 through 2020 were *PLOS One* (317), *Scientific Reports* (247), *Zootaxa* (186), *PeerJ* (174), and *Ecology and Evolution* (172; Table S2). Although our literature search recovered amphibian publications in 23 languages, the vast majority (98%) of amphibian publications recognized in our search were written in English (Table S3).

In the last five years, two herpetological journals acquired new names: *Revista Latinoamericana de Herpetología* in 2017 (formerly *Revista Mexicana de Herpetología*), and *Ichthyology and Herpetology* (formerly *Copeia*) in 2021. The latter is published by the American Society of Ichthyologists and Herpetologists, which acknowledged the racist views of eponymous herpetologist Edward Drinker Cope and whose Board of Governors approved the name change in July 2020. Thus, the title change reflects the wider movement towards making the discipline more inclusive (Cahan, 2020).

Advances in amphibian conservation research

Factors driving decline in the largest number of amphibian species.-

Based on our review of AmphibiaWeb data, the principal driver of amphibian declines is habitat alteration and loss (Fig. 2). The drivers subsumed in our habitat alteration and loss category threaten at least 46.6% of amphibian species with accounts on AmphibiaWeb. Furthermore, pooling the habitat alteration and loss category with resource exploitation, roads and urban development, and intentional changes to hydrology categories—which all encompass the repercussions of physical changes to amphibian habitat—the percentage of affected species increases to 51.2%.

Though habitat loss and degradation are undebatable drivers of amphibian declines, it is important that we interpret these data (Fig. 2) with the caveat that certain drivers are easier to measure than others, and that some drivers have only recently been studied. For example, habitat loss can be described based on observational data alone, while the low percentage of amphibian species for which genetic degradation is a documented driver of decline (50 species) can partly be attributed to the requirement of molecular work and knowledge of the species' evolutionary history for its ascertainment, which requires tools that have only recently been developed and democratized. Likewise, we know that climate change and disease threaten a large proportion of extant amphibian diversity (Warren et al., 2013; Olson et al., 2021), but these drivers have only been focal points in amphibian conservation over the past two to three decades. Meanwhile, pollutants are better documented as a driver of decline, but have been a focus for at least sixty years (225 amphibian species being documented as declining due to pollutants versus 170 species for climatic factors and 149 for disease and immune functioning; Fig. 2).

Factors largely associated with endangered or extinct amphibian species.-

When prioritizing which drivers of amphibian decline should receive limited conservation attention and resources, we should consider not only the raw count of amphibian species affected by a driver, but also which threats drive the most severe declines or tend to impact already vulnerable species. For example, while habitat alteration and loss may be the most common threat, the threat categories most closely associated with endangered or extinct species are disease and weakened immune functioning (59.11% of EN, CR, EX/EW species) and genetic degradation (56%). Thus, these two types of threats may tend to drive sudden and dramatic declines, particularly for endangered species that are also facing other stressors (Knapp et al., 2016; Fisher and Garner, 2020). The overrepresentation of highly endangered or extinct species in certain threat categories makes them clear strategic targets for conservation programs.

Trends and updates in amphibian diversity and systematics

Amphibian diversity.–

From 2016 to 2020, 780 new species of amphibians were described (Fig. 3), a higher number than in the previous five years (732 species between 2011 and 2015). Most (705) of the new species described in the last five years were from the largest amphibian order, Anura; salamanders gained 66 species and caecilians gained 9. Six new genera of frogs were described based entirely on newly discovered species: *Astrobatrachus* (Vijayakumar et al., 2019, also representing the new subfamily Astrobatrachinae); *Blythophryne* (Chandramouli et al., 2016); *Mini* (Scherz et al., 2019; Fig. 3f); *Siamophryne* (Suwannapoom et al., 2018); *Sigalegalephrynus* (Smart et al., 2017); and *Vietnamophryne* (Poyarkov et al., 2018).

At a regional level, most new species added from2016 to2020 are from Latin America (40.8%), Asia (37.2%) and Africa (12.0%; Fig. 4a). Less than 10% of the new species were from the other regions: Oceania-Australia, North America and Europe. All regions had more described species between 2016–2020 than during 2011–2015, except for Oceania-Australia (22 fewer species). The countries with the most new species added from2016 to2020 were China (100 species), Brazil (95 species), Ecuador (67 species), Madagascar (56 species), and Peru (56 species). Regions with a high density of new species described are southern Andes of Ecuador, northern Madagascar, and southern China (Fig. 4A). If the global trend continues as in the last decade (10–11% species increase every five years), we can expect to reach 9,000 amphibian species by the end of 2024.

Remarkably, the yearly rates of increase in the numbers of anurans, caudatans, and gymnophionans are quite consistent (Fig. 4bc). The steeper increase in anuran species indicates that we are still very much in the age of discovery for amphibian diversity. It remains unclear how much of this pattern is tied to the recognition of cryptic species based on molecular studies. We suggest that much of the substantial cryptic diversity remains unaccounted for taxonomically as many taxa are given informal identifiers such as “Hyla species 1” in published papers and on GenBank, but many GenBank accessions are not updated when the species is formally named. This phenomenon is captured by Fig. 4d, which illustrates the growing number of GenBank sequences representing unspecified amphibian species. New species were described in the majority of amphibian families, and Strabomantidae and Microhylidae had the absolute greatest number of new species (Fig. 5).

Amphibian systematics.–

In contrast with the first 15 years of the new millennium, during which dramatic changes occurred in both our understanding of the higher-level phylogeny of amphibians and in the corresponding taxonomy, the past five years have seen much less flux. This stability has been maintained despite the transition from Sanger-sequencing-based multilocus phylogenetic approaches and mitogenomic analyses to phylogenomic analyses based on new datasets of hundreds to thousands of sequenced loci (e.g., Lemmon and Lemmon, 2012; Portik et al., 2016; Hutter et al., 2021). There is complete agreement among recent phylogenomic studies regarding the family-level relationships of salamanders (Shen et al., 2013; Hime et al., 2021) and caecilians; among the recent major studies, only Hime et al. (2021) included caecilians, but their findings are in agreement with prior understanding of caecilian relationships based on Sanger data, such as Kamei et al. (2012). Even among the anurans, the various major studies have found nearly complete agreement except within Hyloidea, where some weakly supported arrangements are resolved differently across studies (e.g., Feng et al., 2017; Streicher et al., 2018; Hime et al., 2021). Even the major relationships among the 19 families that comprise Ranoidea have been largely stable in recent treatments. There is now remarkable agreement and taxonomic stability in terms of the higher level phylogenetic relationships among and within all three amphibian orders.

The most significant changes in our understanding of the deep relationships of amphibians comes from phylogenomic analyses of neobatrachians. Within ranoid frogs, phylogenomic analyses support a sister relationship between the Afrobatrachia (Arthroleptidae, Brevicipitidae, Hemisotidae, Hyperoliidae) and Natatanura (Feng et al., 2017; Hime et al., 2021) in contrast to previous analyses that found a sister relationship between Microhylidae and Afrobatrachia. Within the Natatanura, these same analyses resolve a clade of the six families endemic to continental Africa (Conrauidae, Odontobatrachidae, Petropedetidae, Phrynobatrachidae, Ptychadenidae, Pyxicephalidae). This is the sister-group of all other nataturans (Feng et al., 2017; Yuan et al., 2018; Hime et al., 2021). Yuan et al. (2018) provided strong support for Ranixalidae + Nyctibatrachidae; this clade is the sister-group of other natatanurans excluding the clade of six endemic African families. No phylogenomic analyses have simultaneously included the Micrixalidae, Nyctibatrachidae, and Ranixalidae—all endemic to India. However, other analyses that combine available loci with phylogenomic datasets found a close relationship between Micrixalidae and Ranixalidae (Feng et al., 2017), suggesting that these three families might together form a clade.

Phylogenomic analyses also are beginning to make sense of the diverse hyloid radiation. Rhinodermatidae is strongly supported as the sister to all other South American hyloids, followed by a clade of four families (Alsodidae, Batrachylidae, Cycloramphidae, Hylodidae) referred to as the Neoaustrana (Feng et al., 2017; Streicher et al., 2018; Hime et al., 2021). This is followed by the Telmatobiidae and then by a strongly supported clade of three families (Ceratophryidae, Hemiphractidae, Hylidae) referred to as the Amazorana (Feng et al., 2017; Streicher et al., 2018). All remaining hyloids form a well supported clade, though recent studies differ in the relationships among these taxa.

A review of community resources

Genomes.–

A total of 28 amphibian genomes with representatives from 14 different families have been sequenced as of July 2021 (Figs. 5 and 6). Of these, 13 are assembled to chromosome-level (scaffold N50 = 0.42 ± 0.29 Gb; mean ± standard deviation), eight are scaffolded (scaffold N50 = 0.24 ± 0.24 Mb), and six are contigs (contig N50 = 880 ± 610 bp) (Table S4). The first genome sequenced was that of *Xenopus tropicalis* in 2010 (Hellsten et al., 2010), and it remained the sole amphibian genome until *Nanorana parkeri* became available in 2015 (Sun et al., 2015). Since then, sequencing of amphibian (mostly anuran) genomes has slowly but steadily increased (Fig. 6). The largest amphibian genome sequenced to date is *Ambystoma maculatum*, with an estimated diploid genome size of ~34 Gb (Nowoshilow et al., 2018). Not surprisingly, all but one (*Nanorana parkeri*) of the chromosome-scale genomes used a combination of sequencing technologies, while those that remain as scaffolds or contigs were built using only the Illumina system short-read technologies (Table S4).

NCBI Sequence Read Archive.–

The amount of next-generation sequencing data deposited into the NCBI Sequence Read Archive (SRA) since its origin in 2008 (Leinonen et al., 2011) has been steadily increasing for both model and non-model amphibian species (Fig. 7a). In 2019, the amount of data available for non-model anurans surpassed that of model anurans (i.e., *Xenopus laevis, X. tropicalis*). The cumulative number of SRA studies (Fig. 7b) and cumulative number of species (Fig. 7c) increased in parallel over time. By the end of 2020, nearly 1000 species of amphibians (815 of which are anurans) had sequences deposited in the SRA (Fig. 5; Fig. 7c; note that these numbers are inflated because they include unspecified, subspecies, and hybrid samples; see Fig 4d).

NCBI GenBank Nucleotide database.–

Although the NCBI GenBank database was established in 1982 (Choudhuri, 2014), very few amphibian species were represented in the database until 2000 (Fig. 8). Early amphibian data were almost exclusively from *Xenopus* (Fig. 8, solid line, green circles). Since then, the number of represented species in NCBI databases has increased dramatically, to 6,203 (of a total of 8,268 known species) in 2020 (Fig. 8). However, despite this linear increase in representation, non-model species were not represented by large numbers of sequences until 2016; even today, most existing amphibian sequences in GenBank are from *Xenopus* (Fig. 8).

While the number of mtDNA sequences for anurans has risen gradually over time, the number for salamanders and caecilians has remained relatively flat (Fig. 8 mtDNA panel). In contrast, the number of nDNA and mRNA sequences added to GenBank has been stochastic and likely reflects specific large-scale sequencing projects (Fig. 8). For example, in 2012, >100,000 nDNA sequences of *Xenopus tropicalis* and *X. laevis* were deposited as part of new genome data that were beginning to be published at that time (Hellsten et al., 2010); many of these sequences were generated from Bacterial Artificial Chromosomes (BAC). Earlier BAC-generated sequences from *X. tropicalis* are responsible for the peak in 2003 of nDNA sequences (Wells et al., 2011). The notable increase in model-anuran mRNA from 2000 to 2007 is largely from the NCBI full-length cDNA project, which added *Xenopus* to its list of focal species in 2002 (Klein et al., 2002; Gerhard et al., 2004). Additional notable contributors to increases in nDNA include whole-genome shotgun sequences from *X. laevis* (Session et al., 2016) and

Nanorana parkeri (Sun et al., 2015), as well as other large-scale sequencing projects (e.g., Ultra Conserved Element sequences from *Kaloula,* Alexander et al., 2017; Fig. 8). In addition, several notable increases in non-model mRNA and nDNA sequence deposition likely are related to other new genomes (e.g., *Rana catesbeiana* in 2017 [Hammond et al., 2017]; *Microcaecilia unicolor* in 2019 and *Geotrypetes seraphini* in 2020, both from the Vertebrate Genomes Project, https://vertebrategenomesproject.org/; Koepfli et al. 2015) and transcriptomes (e.g., *Bombina variegata variegata* in 2016, *R. catesbeiana* in 2017; both in Transcriptome Shotgun Assembly [TSA] formats, which are primarily built from short-read technology [Suzuki et al., 2016; Nürnberger et al., 2016]).

Acoustic data.–

We identified eight major repositories that collectively contain 156,514 amphibian recordings (Table 1): Macaulay Library, Fonozoo, La Sonothèque, AmphibiaWeb, Fonoteca Neotropical Jacques Vielliard, Anfibios del Ecuador BIOWEB, Australian Museum FrogID Project, and Chinese National Specimen Resource Sharing Platform. Collectively, these call repositories contain calls for 1,985 unique species from 45 anuran families and four salamander families. The anuran families Pipidae (41 species), Mantellidae (232 species), Myobatrachidae (133 species), Scaphiopodidae (seven species), and Rhinophrynidae (one species) each have calls recorded for more than 50% of the family’s species (Fig. 5). Fonozoo contains the highest number of species represented, although FrogID contains the greatest number of recordings (Table 1). Of note among these databases are the Fonoteca Neotropical Jacques Vielliard (FNJV), which is the largest public and institutional online audiovisual repository in Latin America, and the Australian Museum FrogID Project, which is Australia's first national community-science frog identification initiative.

CT-scan data.–

Since 2016, CT-scan datasets for 1,947 amphibian specimens, including image stacks and 3D mesh files, have been shared via MorphoSource (www.morphosource.org). These include 1,530 anuran specimens representing 976 species (in 402 genera; 88%

of genera), 362 caudatan specimens representing 184 species (in 66 genera; 97%), and 55 gymnophionan specimens representing 40 species (in 32 genera; 97%; Fig. 5). Many of these data were generated as part of the NSF openVertebrate (oVert) Thematic Collections Network. In addition, there are a few CT-scans of extinct crown-group amphibians, such as 26 fossils of *Beelzebufo* deposited in 2015. MorphoSource also now houses most, if not all, of the CT-scan media from the Digital Morphology project (DigiMorph; www.digimorph.org). DigiMorph began in the early 2000s and still has CT-scan media available from 25 anuran species (in 21 genera), 28 caudate species (in 16 genera; plus one extinct salamander), and seven caecilian species (in seven genera).

Phenome10K also hosts 3D mesh files of amphibian skulls associated with several recent publications (Marshall et al., 2019; Fabre et al., 2020; Bardua et al., 2021). As of October 2021, the website (www.phenome10k.org) makes available 3D mesh files of skulls for 105 anuran species (in 94 genera), 104 caudate species (in 51 genera), and seven gymnophionan species (in seven genera). In many cases, the image stacks for these specimens also are available on MorphoSource.

Other trait databases.–

From 2016 through 2020, two large amphibian trait databases were published: AmphiBIO (Oliveira et al., 2017) and a Colombian anuran database (Mendoza-Henao et al., 2019). AmphiBIO (Oliveira et al., 2017), the largest species-level amphibian trait database that can be readily downloaded, contains 6,776 species and a broad range of ecological and life-history traits (e.g., microhabitat, diet, activity time, clutch size), but the matrix completeness is only 21%. Although the Colombian anuran database is much more complete, it contains morphological data from fewer species (239), which represent 38% of Colombian anuran diversity. Of note, the Colombian anuran database includes individual-level data for 4,623 museum specimens, with a range of 1 to 118 individuals (median = 8) measured per species. Three other existing databases were identified: one includes conservation, ecological, and life-history traits of 86 European species (Trochet et al., 2014); another, the Anuran Traits of the United States (ATraiU, Moore et al., 2021), contains ecological, morphological, and life history data of 106 anuran species, representing 91% of frog species in the USA (AmphibiaWeb, 2021). Finally, NSF-funded VertNet (http://vertnet.org/) aggregates individual-level amphibian trait data from records published by museum collections (e.g., body length, mass) that are tied to the location where individuals were collected and sometimes other traits (e.g., lifestage, sex). At the conclusion of 2020, VertNet had 1,261 individual records of amphibian body lengths (covering 897 species) and 455 individual records of amphibian body mass (covering 337 species).

Online portals for amphibians: AmphibiaWeb.–

In 2020, AmphibiaWeb celebrated its 20th anniversary, marking its commitment to its original vision—that "a healthy future for all life on Earth must include thriving amphibians, and the means to conserving amphibians is to enable and facilitate better research and education with an accessible, consolidated, and curated information system for all amphibian species" (AmphibiaWeb, 2021: https://amphibiaweb.org/about/index.html). Many of the core activities of AmphibiaWeb remain the same in the last two decades—a web page for every amphibian species with literature-based accounts and spatial data. Photos for species are provided through CalPhotos, a service also administered by UC Berkeley and used by other natural history projects (e.g., ReptileDatabase, etc). Much of AmphibiaWeb's data (e.g., species accounts, type localities, range maps and traits) have been used in research studies (reviewed in Uetz et al., 2021), including this article.

Usage of AmphibiaWeb (tracked by Google Analytics) continues to be strong, averaging 28,000 users per month (between June and November 2021) from 215 countries or sovereignties. Of the over 35% of users who shared demographic data, users trended female (54.5%) and young (33% 18–24 years old, 27% 25–34 years old). The site averaged 1.74 million page views per year in the last five years, with a high of 2.5 million page views during the pandemic of 2020 (page views are a measure of the number of times a page has been visited even in a single session of a single user).

Over the last five years, the AmphibiaWeb team has added 277 species accounts, a set of family-richness maps, and improved methods to access data and materials including a searchable public repository (https://github.com/AmphibiaWeb/aw-assets). It now hosts over 3,500 species accounts with over 42,200 photos embedded from CalPhotos, representing 4,766 species. Newly added educational materials range from a primer on why phylogeny, taxonomy, and nomenclature are useful in the study of amphibians to Spanish and English educational materials aimed for K–12 students. Recent outreach initiatives have been the art contest with original AmphibiaWeb designs ("#ArtYourAmphibian") and a quarterly newsletter.

Online portals for amphibians: Anfibios del Ecuador-BIOWEB.–

With 656 amphibian species (as of November 2021), Ecuador is the third most species rich country in the world. In 2018, the zoology museum of the Catholic University of Ecuador (QCAZ) launched the website Anfibios del Ecuador (https://bioweb.bio/faunaweb/amphibiaweb) to give access to comprehensive information about all amphibian species of Ecuador, which represent nearly 8% of the amphibian species worldwide. Anfibios del Ecuador was inspired by AmphibiaWeb and has a similar scope but at a country level. Anfibios del Ecuador replaced the previous portal "AmphibiaWebEcuador," which operated between 2010 and 2017. The website is currently part of a larger Ecuadorian biodiversity database called BIOWEB.

Anfibios del Ecuador provides detailed species accounts, which include an extensive photo gallery with 206,785 images. Species phenotypic variation is well documented with an average number of photographs per species of 323 (maximum 8746 for *Pristimantis achatinus*) and a median of 144. Species distribution is documented with a database of over 50,000 geographic records from the literature and the specimen database of the QCAZ museum. Those records are used to build species distribution models under current and future environmental conditions using the MAXENT algorithm (Phillips et al., 2017).

The website also presents overviews of the biogeography, species richness, and the conservation status of the Ecuadorian amphibians. Overviews of the Natural Regions, geography and climate of Ecuador are also provided. Anfibios del Ecuador gives access to: (1) the database of the amphibian QCAZ collection, the largest for Ecuadorian amphibians (76,500 specimens), and (2) the QCAZ sound collection with 1,297 recordings for 222 species (Table 1).

Crucially, Anfibios del Ecuador is in Spanish and helps to provide scientific data in languages other than English. For most species, Anfibios del Ecuador presents the only comprehensive species accounts available online in Spanish. Since 2018, Anfibios del Ecuador has been connected with AmphibiaWeb through a web API that allows visualizing the Spanish-language species accounts and photographs from Anfibios del Ecuador within AmphibiaWeb.

Anfibios del Ecuador has high visitor traffic (data from Google Analytics). Between June and November 2021, for example, it received approximately 16,000 monthly visitors from 106 countries or sovereignties. 51% of visitors shared demographic data, of which 72% were women and 28% men. Younger age groups are the most frequent visitors: 18–24 years old represented 37% of the visits, followed by 25–34 years (23%).

Online portals for amphibians: AmphibiaChina.–

In November of 2015, the Kunming Institute of Zoology, Chinese Academy of Sciences launched the website AmphibiaChina (www.amphibiachina.org) as an online database for Chinese amphibians (Che and Wang, 2016). China currently hosts 587 amphibian species (as of December 12, 2021) and many new species are being described each year. AmphibiaChina aims to provide a platform for sharing research progress and promoting accessibility to people and institutions (e.g., scientists, governmental agencies, and the public) who are interested in Chinese amphibians. Visitors to AmphibiaChina from 2016–2020 come from over 100 countries each year.

During the past five years, AmphibiaChina has undergone some structural changes, including a comprehensive update to version 2. AmphibiaChina has the following major sections: Classification, Species Identifications, Chinese Amphibian Tree of Life, News, and Photo Gallery. Users can navigate the Classification section using the hierarchical system of formal taxonomy or by geographic region (province). An up-to-date phylogeny of Chinese amphibians is provided. Comprehensive information on each species is available, and multiple species can be compared in a single page. The photograph gallery is extensive, with 9,042 images representing 433 species. AmphibiaChina also offers two online species identification tools: an amphibian image recognition module that uses deep learning and image processing techniques to automatically identify the species in user images, and a search engine which compares user-uploaded mtDNA sequences to a sequence database using BLAST. Since 2016, AmphibiaChina has linked reciprocally to accounts on AmphibiaWeb for species occurring in China.

Online portals for amphibians: Amphibian Species of the World.–

An online resource launched around the same time as AmphibiaWeb in 2000 that extended work first presented by Frost (1985), the Amphibian Species of the World database provides a critical bibliography of all amphibian taxonomy and species with reciprocal links to several of the other listed online resources here (Frost, 2021).

Online portals for amphibians: IUCN Red List.–

The International Union for Conservation of Nature (IUCN; https://www.iucnredlist.org) sets the most comprehensive global ranking and listing of conservation status for animal, plant, and fungi species including amphibians based on expert assessments. The Red List, as the compilation of conservation statuses is called, includes categories from Extinct and Critically Endangered to Least Concern. Species which lack enough information for a conservation status are listed as Data Deficient. Details on threats, trends in population, conservation actions, basically any information that helped determine the status are available on their website as are spatial range data. Many of these data are linked or incorporated in other portals listed here.

Online portals for amphibians: Amphibian Ark, Conservation Needs, and Conservation Evidence.–
The Amphibian Ark organization was borne from the need to implement the IUCN Amphibian Conservation Action Plan (Gascon, 2007), specifically charged to focus on *ex situ* conservation, hence Amphibian Ark maintains and provides valuable husbandry and *ex situ* conservation publications on many amphibian species (*https://www.amphibianark.org/husbandry-documents*). Amphibian Ark and their partners also develop, manage and share Conservation Needs Assessments (CNA; https://www.conservationneeds.org) which integrate both *in situ* and *ex situ* conservation actions for species at either the regional or national level. Links to species-specific CNAs are incorporated into AmphibiaWeb species pages as part of the Conservation Status table.

Finally, more than 500 papers on conservation efforts with amphibians are collated in a Conservation Evidence database (https://www.conservationevidence.com), which has summary functions that allow users to review evidence for the most effective approaches to amphibian conservation.

Online portals for amphibians: Amphibian Disease Portal.–
Following the discovery of the pathogen Bsal in Europe (Martel et al., 2013), biologists in the USA, Mexico, and Canada formed the North American Bsal Task Force to address the potential for Bsal-caused chytridiomycosis outbreak in North America. AmphibiaWeb became the co-lead for the Data Management effort with the USDA Forest Service and launched an effort to to establish a new open-access repository and archive for both Bd and Bsal data (Koo et al., 2021) called the Amphibian Disease Portal (https://amphibiandisease.org). The portal addresses two urgent needs: 1) to create a sustainable, modernized repository to aggregate and rapidly share global data on the fungal pathogens of amphibians Bd and Bsal; and 2) to upgrade and migrate the discontinued Bd-Maps database (Olson et al., 2013) to a new repository. The Amphibian Disease Portal reciprocally links with AmphibiaWeb species pages to display species-specific Bd and Bsal data. Since its introduction in 2017, it now encompasses a

broad global and temporal coverage of Bd (Fig. 9) and Bsal data (for details, see Olson et al., 2021; Koo et al., 2021). The amphibian disease portal contains Bd samples from all but five amphibian families (missing are two frog, two caecilian, and one salamander family) and positive Bd samples from all but sixteen amphibian families (Fig. 5). Currently, the Disease Portal dashboard displays dynamic counts of sample data by country, species and diseases tested and provides species-specific pie charts and links to original, downloadable datasets.

Discussion

Current picture and future projections for amphibian biodiversity.–
The pace of amphibian species descriptions continues unabated, with ~150 new species being described each year. However, our picture of amphibian diversity is changing in some predictable ways. The majority of new species are being described in Latin America (Vasconcelos et al., 2019) and Asia and specifically are concentrated in diverse families such as the Strabomantidae and Megophryidae. For example, the number of new species listed on AmphibiaChina increased from just four new species in 2015 (Murphy, 2016), to 41 new species reported in 2020 (Chen et al., 2021). Furthermore, our understanding of the relationships among amphibian families remains largely stable, however there remain several diverse lineages, including both subfamilies and genera, for which thorough and synoptic revisionary phylogenetic studies are needed.

On the other end of the spectrum from the description of previously unknown amphibian diversity, the study of amphibian declines has continued to be a central theme in amphibian biology. However, though the role of habitat loss and modification as principal drivers of amphibian declines is not a new finding (IUCN, 2021), relative to their importance these pivotal drivers have been deemphasized in amphibian conservation research (Green et al., 2020). Even still, over the last five years large-scale meta-analyses have confirmed several basic expectations of the repercussions of habitat degradation for amphibians : (i) land use change decreases amphibian species richness (Cordier et al., 2021), (ii) amphibian abundance declines towards the edge of fragmented habitat (Schneider-Maunoury et al., 2016), and (iii) habitat conversion tends to hurt specialist amphibians, driving the phylogenetic homogenization of communities (Thompson et al., 2016; Nowakowski et al., 2018a). Lamentably, the most amphibian-rich communities undergo the most species loss and turnover after habitat modification, and communities fail to recover completely over time (Thompson and Donnelly, 2018; Goldspiel et al., 2019; Cordier et al., 2021). Models of the impact of habitat loss and a 'middle of the road' climate and development scenario predict that 10% of known amphibians will be lost by 2070 (Powers and Jetz, 2019). We cannot prevent the loss of amphibian species to climate change altogether, but protecting areas from further land use change will be critical to mitigating further losses (Chen et al., 2017).

Among diseases driving amphibian declines, a primary concern over the past five years has continued to be chytridiomycosis, the disease caused by the fungal pathogens *Batrachochytrium dendrobatidis* (Bd) and *B. salamandrivorans* (Bsal). Some long-term monitoring projects of Bd-exposed amphibian species or communities are reaching their tenth or twentieth year, making large-scale meta-analyses possible. Bd has now been detected in 55% of amphibian species and 69% of countries sampled (Olson et al., 2021), contributing to declines across many families (Scheele et al., 2019)—though disentangling the extent of its impact is still challenging (Lambert et al., 2020). In some sites, populations declined or were extirpated synchronously with Bd epizootics, and have not recovered under the burden of Bd and additional stressors (Adams et al., 2017b; Bosch et al., 2021). Other populations may be recovering, despite the continued presence of Bd (Knapp et al., 2016; Seimon et al., 2017; Voyles et al., 2018). The broader impacts of amphibian declines on ecosystems are largely unknown, though steep amphibian declines in Panama appear to have induced a trophic cascade, driving declines in snake diversity and body condition (Zipkin et al., 2020).

Species recovering after Bd-associated declines appear to have altered their response to Bd (Palomar et al., 2016; Knapp et al., 2016; Kosch et al., 2019), with instances of positive directional selection documented in the major histocompatibility complex (MHC) and other immunogenes (Savage and Zamudio, 2016; Kosch et al., 2016; Voyles et al., 2018), while species continuing to decline in the wild remain susceptible to Bd despite prolonged exposure (Catenazzi et al., 2017). Such continued declines might be particularly common in systems with additional stressors like climate change, pollution, and habitat fragmentation, which synergistically impair amphibians' capacity to respond to any individual stressor (Nowakowski et al., 2016; Scheele et al., 2016; Rollins-Smith, 2017; Cohen et al., 2017, 2019; Adams et al., 2017a; Greenspan et al., 2017; McCoy and Peralta, 2018).

Unlike Bd, which is no longer causing mass amphibian die-offs in most regions, Bsal continues to drive steep local declines and extirpations (Schmeller et al., 2020; Thein et al., 2020; Vences and Lötters, 2020). It has spread across Northern Europe, even in areas with low host densities, causing collapses in susceptible species (Spitzen-van der Sluijs et al., 2016; Schmidt et al., 2017; Stegen et al., 2017). Alarmingly, we do not yet have evidence for acquired immunity to Bsal, and Bsal pathogenicity has not attenuated over time (Stegen et al., 2017). Herpetologists continue to monitor for Bsal elsewhere in the world, as it could drive devastating biodiversity decline in places like North America, which contains half of global salamander diversity (Richgels et al., 2016; Iwanowicz et al., 2017; Parrott et al., 2017; Yap et al., 2017; Waddle et al., 2020). Continued widespread surveillance for Bd and Bsal, and platforms promoting the accessibility of these data (see Community resources section), will help us improve our capacity to mitigate the impacts of these pathogens through monitoring, policy, and management.

Challenges and opportunities in amphibian research.–

Large amphibian genome sizes remain one of the greatest challenges in amphibian research. The size and repetitive content of amphibian genomes has hindered whole-genome sequencing efforts (Sun et al., 2020). For comparison, >500 fish genomes (Randhawa and Pawar, 2021; average size of 808 Mb) and >300 bird genomes have been sequenced (Feng et al., 2020; average size of 1.13 Gb, (Randhawa and Pawar, 2021), yet only 28 amphibian genomes are available. The average sizes of sequenced amphibian genomes (excluding contig-level assemblies (4.03 Gb for Anura [N = 18], 33.99 Gb for Caudata [N = 1], 4.75 Gb for Gymnophiona [N = 3]) are below the average amphibian genome sizes (4.28 Gb for Anura, 35.95 Gb for Caudata, 6.44 Gb for

Gymnophiona, based on values reported in Liedtke et al., 2018. Nevertheless, the number of species represented in NCBI sequence databases continues to increase, as does the use of high-throughput technologies for non-model species. A concerted effort to review and update the taxonomic identities of GenBank sequences will become more and more necessary as the database continues to grow.

We expect to see exponential growth in genomic data for amphibians in the coming years, especially as more reference genomes are made available. Moreover, we expect growth in the development of new tools for other emerging amphibian model species, such as medical applications arising from research on regeneration in *Notophthalamus viridescens* (Joven et al., 2019), freezing tolerance in *Rana sylvatica* (Joanisse and Storey, 1996; Gerber et al., 2016; Costanzo, 2019), and chytrid disease in *Atelopus zeteki* (McCaffery et al., 2015; Cohen et al., 2017; Byrne et al., 2021), along with even more innovative advances in existing model systems like the self-replicating biological robots created from *Xenopus* tissue (“xenobots”; Kriegman et al., 2021). These advances in genetic tools paired with more accessible and inexpensive sequencing technologies will accelerate research in areas currently underrepresented in amphibian publications, such as research focused on phylogenomics, microbiomes, and eDNA.

Although there is a wealth of accessible amphibian data online (Fig. 5), we still lack basic natural history and phenotypic data for a large portion of amphibian genera and families. For example, although most anuran families have calls recorded, certain families that contain species thought or known to call (Ceuthomantidae, Ranixalidae, Odontobatrachidae, Conrauidae, Petropedetidae, Brevicipitidae, and Heleophrynidae) have no call records in the databases examined here and many other families (Arthroleptidae, Craugastoridae, Megophryidae, Micrixalidae, Phrynobatrachidae, Pyxicephalidae, and Telmatobiidae) have calls recorded for fewer than 10% of species. Interviews conducted at two herpetology conferences found that nearly 80% of herpetologists did not catalog collected sound data because they did not have the time or expertise, or felt that the efforts were unnecessary (Dena et al., 2020). Additionally, although all amphibian families (except Chikilidae) have publicly available CT-scans for at least one species, most families (41 of 74 total) have CT-scans available for fewer than one quarter of their family's species. Ecological and natural history databases often lack information for many genera and families (e.g., ~80% missing data in AmphiBIO; Oliveira et al., 2017), and Paluh et al. (2021) recently found that 161 of 456 total frog genera lacked any dietary records from the wild. Furthermore, while data exist for Bd and Bsal for many amphibian families, much of those data are not yet in a centralized database like the Amphibian Disease Portal. These data deficits and the lack of integration among databases make comparative work and synthetic studies difficult, putting amphibian research at a disadvantage compared to other tetrapod clades with more complete databases (e.g., EltonTraits for birds and mammals; Wilman et al., 2014). Increasing natural history studies, and storing natural history data in publicly accessible, easy-to-download databases are necessary aids to amphibian research and conservation. In addition, it is crucially important to link data and specimens across repositories so that researchers and policy-makers can integrate and track different data types (e.g., DNA sequences, CT-scans, audio recordings, pathogen data) for the same individual or population.

Publication biases highlight obstacles to research progress.–
Inequality in the demography of amphibian research can sideline diverse and locally relevant viewpoints that would otherwise aid in tackling amphibian research challenges. Numerous studies published from2016 to 2020 have shown that, as in other STEM (science, technology, engineering, and mathematics) disciplines (Huang et al., 2020; Urbina-Blanco et al., 2020; Maas et al., 2021), female authors are still under-represented in peer-reviewed publications of amphibian biology (Rock et al., 2021). Nevertheless, the proportion of female authors in herpetological research has increased over time, from 8% in 1973–1982, 15% in 1983–1993 (Wilson, 1998) to 31% in 2010–2015 and 33% in 2016–2019 (Rock et al., 2021), at a remarkably constant rate (although we note that these two studies considered different datasets and journals).

Several factors likely underlie these patterns of underrepresentation of female authors. Within herpetology, papers with male first or last authors are less likely to have female co-authors than papers with female first or last authors (Salerno et al., 2019; Rock et al., 2021; Grosso et al., 2021). The trend of increasing numbers of women leaving academia as their career progresses (the "leaky pipeline") might partially explain the discrepancy in the relatively faster growing proportion of female first versus last authors found by Rock and colleagues (2021). A low proportion of senior female academics affects many aspects of publishing in herpetology through gender inequity of editorial boards, leadership positions, and committees of professional societies (Liévano-Latorre et al., 2020; Chuliver et al., 2021; Grosso et al., 2021). Although we lack a concrete understanding of the primary barriers to authorship inequality in amphibian research specifically, many are likely consistent with barriers and bias found in other STEM disciplines, such as male homophily (Helmer et al., 2017; Salerno et al., 2019; Rock et al., 2021; Grosso et al., 2021), attrition of women and underrepresented groups (Chuliver et al., 2021; Rock et al., 2021), bias in peer review (Silbiger and Stubler, 2019), and the culture of the geographic location of the authors (Fox et al., 2018; Huang et al., 2020; Maas et al., 2021). In addition, region-specific gaps in amphibian data (e.g., trait data) indicate geographic bias in amphibian research, further accentuating the importance of increased support for amphibian research and equitable collaborations worldwide.

Double-blind reviews are a potential solution to minimize bias during the reviewing process (Tomkins et al., 2017) and some herpetological journals are currently transitioning to double-blind reviews: e.g., *Revista Latinoamericana de Herpetología* and *Herpetological Conservation and Biology, The Herpetological Journal (UK), Ichthyology & Herpetology*. Amphibian research would benefit from further analyses of amphibian-specific publishing inequalities for identities beyond gender and assessments of whether changing publishing practices can affect change.

Using centralized portals for amphibian biology to translate research into policy and management.–

Amphibian conservation biology is a crisis discipline: the urgency of amphibian declines means that difficult decisions must be made even in cases with deep uncertainty. We no longer speculate on the prospect of a sixth mass extinction but rather document its progress (Wake and Vredenburg, 2008; Ceballos et al., 2015). One of the motivations for this review is to help consolidate major findings, trends, and public databases that can have immediate impact on policy and management. We urge for increased adoption of adaptive management practices by relevant agencies, non-governmental organizations (NGOs), and research units, where decisions are made under best current information, closely monitored, and then actions are updated accordingly (Meredith et al., 2016; Berger et al., 2016; Grant et al., 2016; Adams et al., 2018). Here, we highlight public databases for molecular (NCBI), acoustic (Table 1), phenotypic and natural history data (Trochet et al., 2014; Oliveira et al., 2017; Mendoza-Henao et al., 2019; Moore et al., 2021), as well as expert-curated reference databases (AmphibiaWeb, AmphibiaWebEcuador, AmphibiaChina, IUCN Red List, and Conservation Evidence), that can be vital tools in designing and updating adaptive management strategies by centralizing and collating information relevant to conservation-oriented policy and management from a diffuse literature.

An example of an exciting new opportunity to deploy these public databases in the interests of more effective, scientifically-informed conservation is provided by global 30x30 initiatives—commitments by governments to protect 30% of the Earth's land and oceans by 2030 (Kubiak, 2020; HAC, 2021). If new 30x30 protected areas are to serve amphibian conservation needs, sites with coverage of amphibian functional, phylogenetic, and taxonomic diversity should be selected, a process greatly facilitated by centralized databases. Additionally, sites that alleviate cataloged decline drivers (e.g., selecting sites that create climate corridors to protect species threatened by climate change) could be a focus (Gonçalves et al., 2016; Subba et al., 2018; Zellmer et al., 2020). In cases where Bd has been detected, *in situ* mitigation has had such limited success that the most robust strategy for improving amphibian outcomes may be to address other synchronous stressors (Knapp et al., 2016; Fisher and Garner, 2020). For example, restoring or creating water features, promoting the development of microhabitat to buffer amphibians against climate change, removing invasive species, managing pollution from activities like mining, and addressing barriers to amphibian movement are all methods that can promote amphibian population health (Reeves et al., 2016; Nowakowski et al., 2016, 2018b; Hamer, 2016; Laufer and Gobel, 2017; Arntzen et al., 2017; Magnus and Rannap, 2019; Goldspiel et al., 2019; Mayani-Parás et al., 2019; Simpkins et al., 2021).

Conclusion.–

The wealth of amphibian data offers both opportunities and challenges in the coming years. New species continue to accumulate at a steady rate and genomic data is exponentially increasing. Conservation continues to be a major focus in amphibian research and the most recent findings highlight both the role of adaptive management and the importance of managing multiple stressors. To facilitate research and conservation, we urge scientists to continue building and contributing to centralized public databases capable of informing conservation decision-making. We aim to provide a timely overview of research trends and major databases with the idea that the resources and gaps highlighted here will spark and facilitate basic and applied amphibian research. Finally, the overview of literature and data resources presented herein provides a framework that can be adapted for other organism clades and revisited over time to highlight major advances and identify opportunities for research growth.

DATA ACCESSIBILITY

Data summarized within this manuscript along with the R scripts to generate all figures (except Figs. 3 and 4) are available at a public repository: https://github.com/AmphibiaWeb/State-of-the-Amphibia.

A Spanish-language translation of the manuscript and Chinese and French translations of the abstract are available in our supplementary materials. The Spanish-language text was first machine-translated with DeepL and then human-verified by ES, SR, and AC; the Chinese translation was conducted by JC (车静) and Yunke Wu (吴耘珂); and the French-language text was first machine-translated with DeepL and then human-verified by AC. We hope that these translations make our work more accessible to a broad audience and that our open-access, human-verified translation can be used in training data sets to further improve machine translation technologies.

CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

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Figure Legends

Figure 1. Trends in amphibian research from 2016 through 2020 by (a) proportion change in publication number and (b) absolute number of publications in each biological subfield. The additional categories of “amphibian” and “background” in panel A refer to the proportional change of all amphibian publications and all publications (not amphibian-specific) from 2016 to 2020.

Figure 2. The number of species in each Order threatened by different drivers of amphibian decline, where each species can be represented by multiple drivers. IUCN conservation status categories are: extinct or extinct in the wild (EX/EW), critically endangered (CR), endangered (EN), vulnerable (VU), near threatened (NT), least concern (LC), and data deficient (DD). Of species with accounts on AmphibiaWeb, 53.3% (1261 of 2,364 species) have data on at least one factor driving their decline

Figure 3. Images of several new species described in the last five years. (a) *Ichthyophis benjii* from Mizoram, India (Lalremsanga et al., 2021), photo by Hmar Tlawmte Lalremsanga; (b) *Hydromantes samweli* (Bingham et al., 2018), holotype from Shasta County, CA, USA, photo by Robert Hansen; (c) *Nasutixalus medogensis (Jiang et al., 2016)*, holotype from Medog, Tibet, China, photo by Ke Jiang ; (d) *Rhinella lilyrodriguezae* (Cusi et al., 2017), holotype from Cordillera Azul National Park, Perú, photo by Anton Sorokin; (e) *Pristimantis verrucolatus* (Páez and Ron, 2019), holotype from Azuay Province, Ecuador, photo by Santiago Ron; (f) *Mini mum* (Scherz et al., 2019), holotype from Manombo Special Reserve, Madagascar, photo by Mark Scherz.

Figure 4. Additions of amphibian species over time. (a) Geographic heat map and point cluster of new species described between 2016 and 2020. The countries with the highest numbers of new species in this time period are China (100 species), Brazil (95 species), Ecuador (67 species), Madagascar (56 species), and Peru (56 species). Inset graphs indicate the cumulative number of new species described by region between 2007 and 2020; years 2016–2020 are highlighted with the blue rectangle; y-axis scale indicated for Latin America is the

same for all insets. Total cumulative number of (b) species and (c) genera in AmphibiaWeb taxonomy database, split by order. (d) Cumulative numbers of formal and unspecified (informal) species names in the GenBank Taxonomy database. Examples of unspecified names are "*Hyla* cf *arenicolor*" or "*Hyla* sp. B". See supplemental data files for data used to generate this figure.

Figure 5. Phylogenetic heat map showing the number and proportion of species within each family that were described in 2016–2020 and the proportion of species within each family that have accessible phenotypic, genetic, and disease data. Lighter to darker colored matrix cells represent lower to higher species-level representation for each family and white cells indicate that no species from the corresponding family have those data types available. From left to right in the matrix: 1) the proportion of new species added in 2016–2020, 2) the proportion of species with call data available in one of the seven databases listed in Table 1, 3) the proportion of species with microCT data available on morphosource.org or Phenome10K, 4) the proportion of species with sequenced genomes, 5) the proportion of species with sequences in NCBI GenBank 6) the proportion of species with sequences in the NCBI Sequence Read Archive 7) the proportion of species in the Amphibian Disease Portal that have been tested for Bd, 8) the proportion of species in that have positive tests for Bd documented in the Amphibian Disease Portal. Data used to generate this figure can be found in Table S5.

Figure 6. (a) Cumulative number and (b) size of sequenced amphibian genomes by year. The blue box highlights the years 2016–2020.

Figure 7. The (a) cumulative amount of data and (b) number of studies in the Sequence Read Archive, separated by model (*Ambystoma mexicanum, Xenopus laevis, Xenopus tropicalis*) and non-model (all other) species (c) total number of species represented in the Sequence Read Archive. Years missing data points indicate that no data were submitted that year for that order.

Figure 8. The cumulative number of mitochondrial DNA (mtDNA), nuclear DNA (nDNA), and messenger RNA (mRNA) sequences, as well as species, added to the GenBank Nucleotide database from 1982 to 2020, highlighting the last five years, 2016–2020, in blue. Some of the projects that contributed substantially to increase sequence numbers are highlighted on the figure; see text for references. Years missing data points indicate that no data were submitted that year for that order.

Figure 9. *Batrachochytrium dendrobatidis* samples in the Amphibian Disease Portal. (a) A log-scale histogram of Bd swab counts, binned by the five-year time span in which the amphibian swabbed was captured. (b) A stacked histogram showing the proportional representation of swabs taken from different continents, binned by the same five-year blocks. Bsal data archived in the portal only includes sample data in the US (Waddle et al., 2020) and from the Bsal Consortium Germany (Vences and Lötters, 2020).

Supplementary File information

Figure S1. Number and proportion of amphibian publications within each research area that mention model organisms (*Xenopus laevis, Xenopus tropicalis,* OR *Ambystoma mexicanum*) in their abstract.

Table S1. Literature search results
Table S2. Number of publications by journal
Table S3. Number of amphibian publications by language
Table S4. Amphibian-Genomes - *metadata for the 28 amphibian species with genomes published when this manuscript was prepared, including the 7 released as of July 2021*
Table S5. Family-level_PhylogeneticHeatMapData - *data used to generate figure 5*

Supplementary Data files uploaded “not for review”

Data files

1. ncbi_nuccore-data.csv - *metadata for all sequences deposited into the NCBI*

Nucleotide Core between 1982 and 2020, downloaded on 27 June 2021

2. ncbi_taxonomy-database.csv - *NCBI taxonomy database, downloaded on 21 June 2021*
3. sra_metadata-20210621.txt - *metadata for all sequences deposited into the NCBI SRA between 2008 and 2020, downloaded on 21 June 2021*
4. GenBank-Amphib.tsv - *raw and cumulative counts of specified and unspecified amphibian taxa represented by sequences in GenBank, downloaded on 28 October 2021*
5. AWeb-taxonomy-archive-master_2012-2020.zip - *monthly lists of amphibian species represented in AmphibiaWeb, spanning November 2012 until December 2020, downloaded on 14 May 2021*
6. AmphibiaWeb_newspecies.csv - *list of new species described by year of description, obtained from AmphibiaWeb*
7. orders_accounts.csv - *data on AmphibiaWeb species accounts available*
8. Aweb-threats_2021-09-21.csv - *data on factors driving amphibian declines as logged in AmphibiaWeb species accounts, downloaded on 21 September 2021*
9. Amphibian_disease_data_processed.csv - *data from the Amphibian Disease Portal*
10. DiseaseData_ForPhylogeneticHeatMap.csv - *count species sampled is the number of species sampled within each family, disease tested is always just "Bd", Bd tested is the number of Bd swabs taken for members of that family, Bd positive is the number of those tested Bd swabs that were Bd+ for that family*
11. SpeciesLevel_CallData.csv - *number of calls for each amphibian species contained in each of the call databases in Table 1*
12. Morphosource_TaxonomyCTscans_2021126.csv - *all Anura, Caudata, and Gymnophiona CT scans on morphosource.org*
13. Phenome10k_CTscans.csv - *all Anura, Caudata, and Gymnophiona CT scans on Phenome10k.org*

R scripts

1. Figs1andS1_LiteratureSearchSummary.R *R script to generate Figures 1 and S1*
2. Fig2_ConservationScripts.R *Scripts in R to create figures for conservation and disease segments of manuscript*
3. Fig5_PhylogeneticHeatMapData.R *R script to generate Figure 5*
4. Figs6-8_genetic-data.R *R script to generate Figures 6-8*

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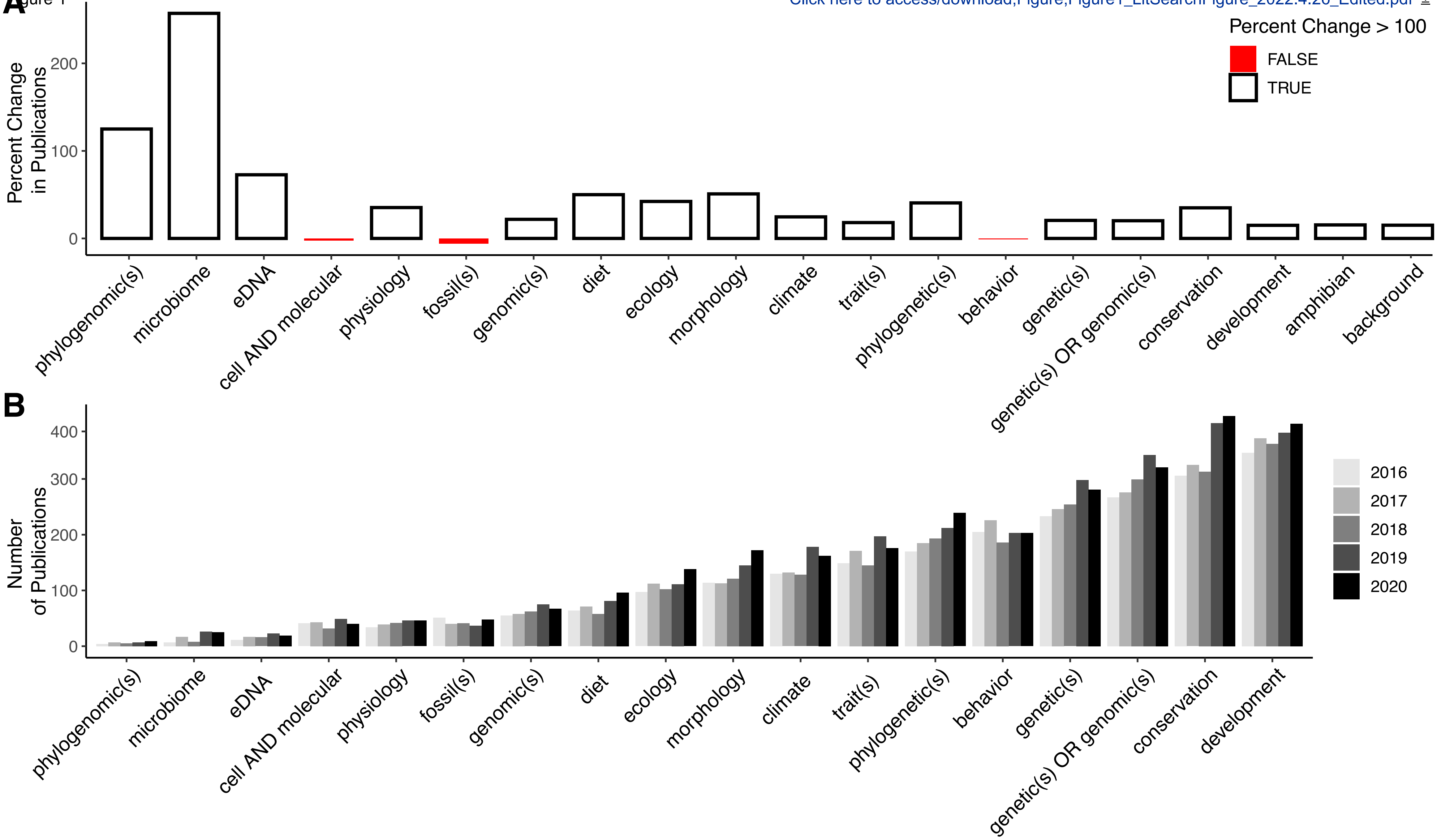
Table 1. The most comprehensive amphibian call databases available online. For geographic regions, Af = African, Au = Australians, Ne = Nearctic, Nt=neotropical, Or = Oriental, Pa= Paleartic. Unless otherwise noted, all recordings are available for download online.

Database	**Maintained by**	**No. species**	**No. calls**	**Regions represented (% of calls)**	**Accessibility for researchers**
Fonozoo	Museo Nacional de Ciencias Naturales de Madrid, Spain	886	9,794	Nt (49%), Af (29%), Pa (16%), Or (4%), Ne (1%); 63 countries	1098 can be played online. Other recordings require an online form and in some cases author permission.
Macaulay Library	Cornell Lab of Ornithology	788	11,460	Nt (38%), Or (6%), Ne (52%); 73 countries	Recordings are available for download online through a request form.
Fonoteca Neotropical Jacques Vielliard	Audiovisual Collection,Museu de Diversidade Biológica	568	5,959	Nt (>99%), Pa (<1%), Af (<1%); 19 countries	89% can be downloaded after curator authorization; 11% are available with author permission.
AmphibiaWeb	Museum of Vertebrate Zoology, UC Berkeley	557	813	Af (34%), Nt (31%), Au (14%), Ne (11%), Or (8%), Pa (3%); 59 countries	Recordings are available for download online.
Anfibios del Ecuador BIOWEB	QCAZ Museum of Pontificia Universidad Católica del Ecuador	222	1297	Nt (100%); nearly all from Ecuador	Recordings are available for direct download online.
FrogID	Australian Museum	182	126,169	Au (100%); all from Australia	Recordings are available for direct download online.
La Sonothèque	Muséum National d'Histoire Naturelle	61	953	Pa (75%), Nt (21%), Ne (2%), Af (1%); 14 countries	Recordings are available for direct download online.
Chinese National Specimen Resource Sharing Platform	Chinese National Specimen Information Infrastructure	35	69	Or (100%); all from China	Recordings are not available for download.


A
Percent Change in Publications
0
100
200
Percent Change > 100
FALSE
TRUE
phylogenomic(s)
microbiome
eDNA
cell AND molecular
physiology
fossil(s)
genomic(s)
diet
ecology
morphology
climate
trait(s)
phylogenetic(s)
behavior
genetic(s)
genetic(s) OR genomic(s)
conservation
development
amphibian
background
B
Number of Publications
0
100
200
300
400
2016
2017
2018
2019
2020

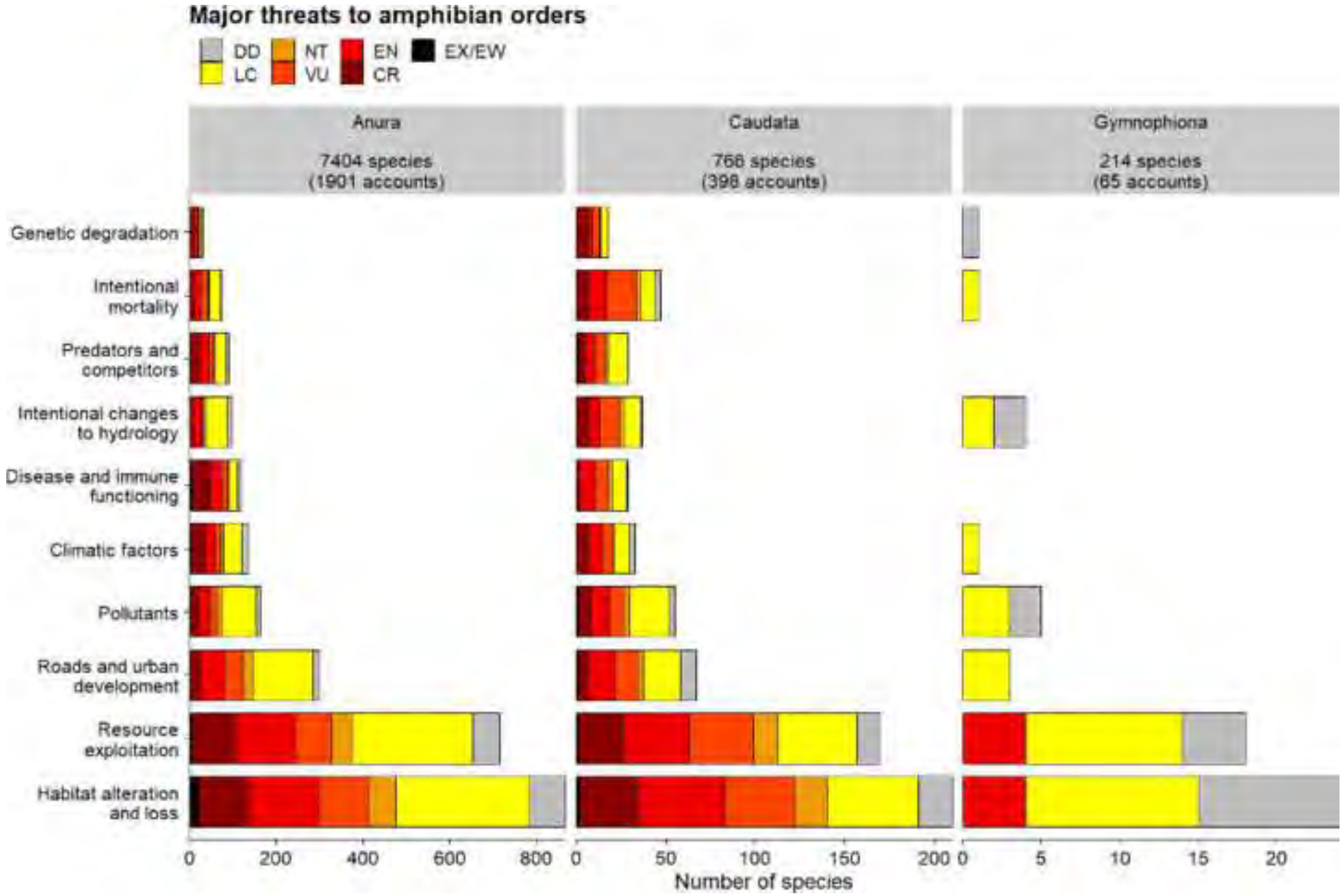

Major threats to amphibian orders
DD
LC
NT
VU
EN
CR
EX/EW
Anura
7404 species
(1901 accounts)
Caudata
768 species
(398 accounts)
Gymnophiona
214 species
(65 accounts)
Genetic degradation
Intentional mortality
Predators and competitors
Intentional changes to hydrology
Disease and immune functioning
Climatic factors
Pollutants
Roads and urban development
Resource exploitation
Habitat alteration and loss
0
200
400
600
800
0
50
100
150
200
0
5
10
15
20
Number of species

Figure 3

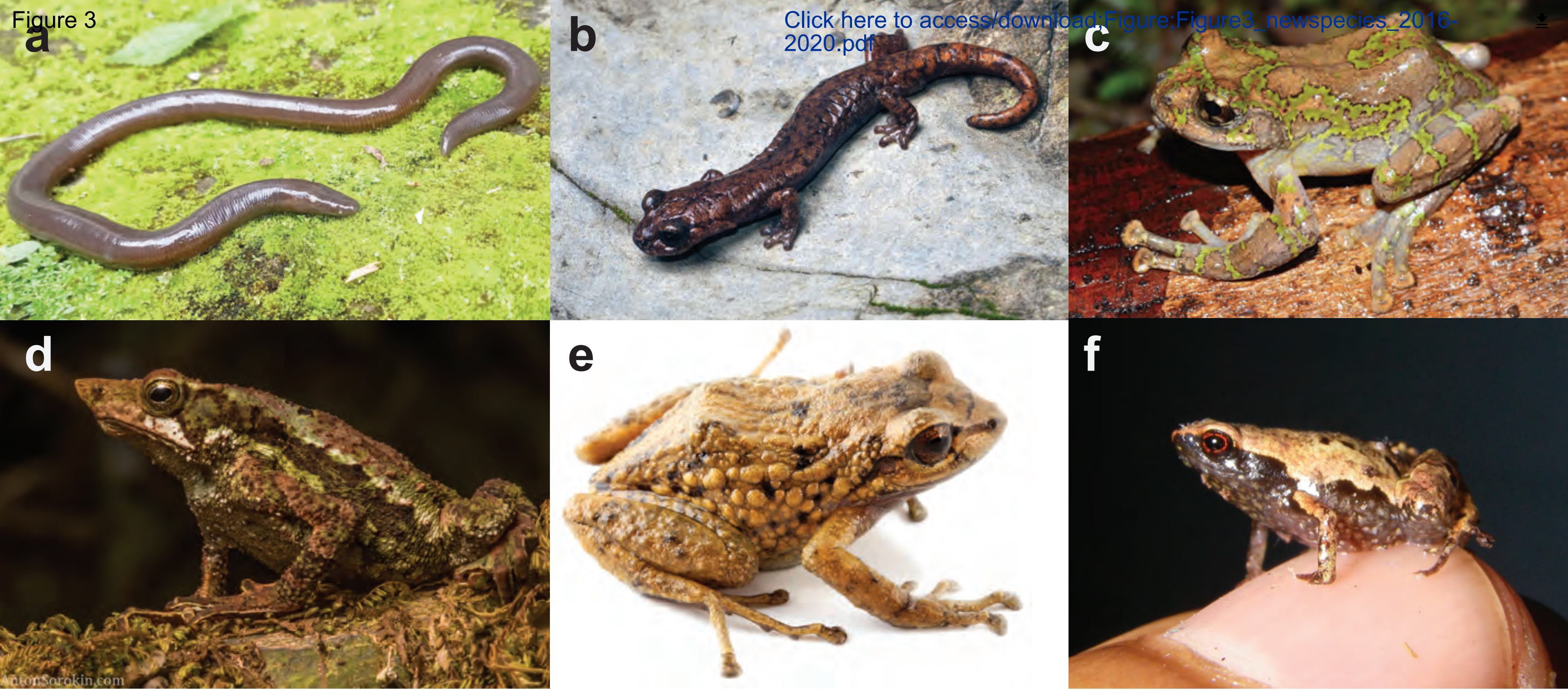


Figure 4

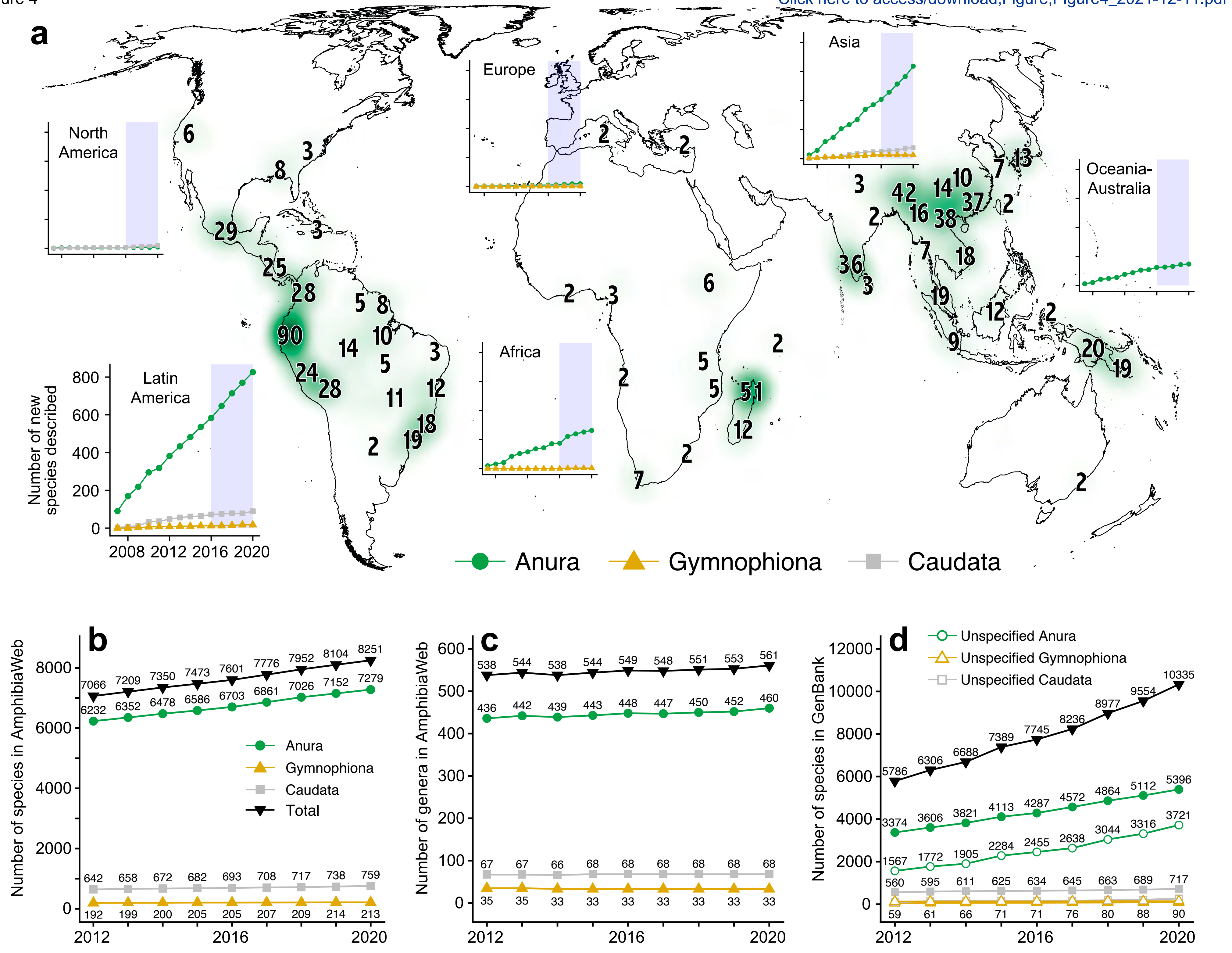

a
North America
Europe
Asia
Oceania-Australia
Africa
Latin America
Number of new species described
800
600
400
200
0
2008 2012 2016 2020
6
3
8
29
3
25
28
90
5
8
10
14
5
3
24
28
11
12
18
19
2
2
2
2
3
6
2
5
5
51
12
2
7
3
42
14
10
7
13
16
37
2
2
38
7
18
36
3
19
12
2
9
20
19
2
2
Anura
Gymnophiona
Caudata
b
Number of species in AmphibiaWeb
8000
6000
4000
2000
0
7066 7209 7350 7473 7601 7776 7952 8104 8251
6232 6352 6478 6586 6703 6861 7026 7152 7279
642 658 672 682 693 708 717 738 759
192 199 200 205 205 207 209 214 213
Anura
Gymnophiona
Caudata
Total
2012 2016 2020
c
Number of genera in AmphibiaWeb
600
500
400
300
200
100
0
538 544 538 544 549 548 551 553 561
436 442 439 443 448 447 450 452 460
67 67 66 68 68 68 68 68 68
35 35 33 33 33 33 33 33 33
2012 2016 2020
d
Number of species in GenBank
12000
10000
8000
6000
4000
2000
0
Unspecified Anura
Unspecified Gymnophiona
Unspecified Caudata
5786 6306 6688 7389 7745 8236 8977 9554 10335
3374 3606 3821 4113 4287 4572 4864 5112 5396
1567 1772 1905 2284 2455 2638 3044 3316 3721
560 595 611 625 634 645 663 689 717
59 61 66 71 71 76 80 88 90
2012 2016 2020

Figure 5

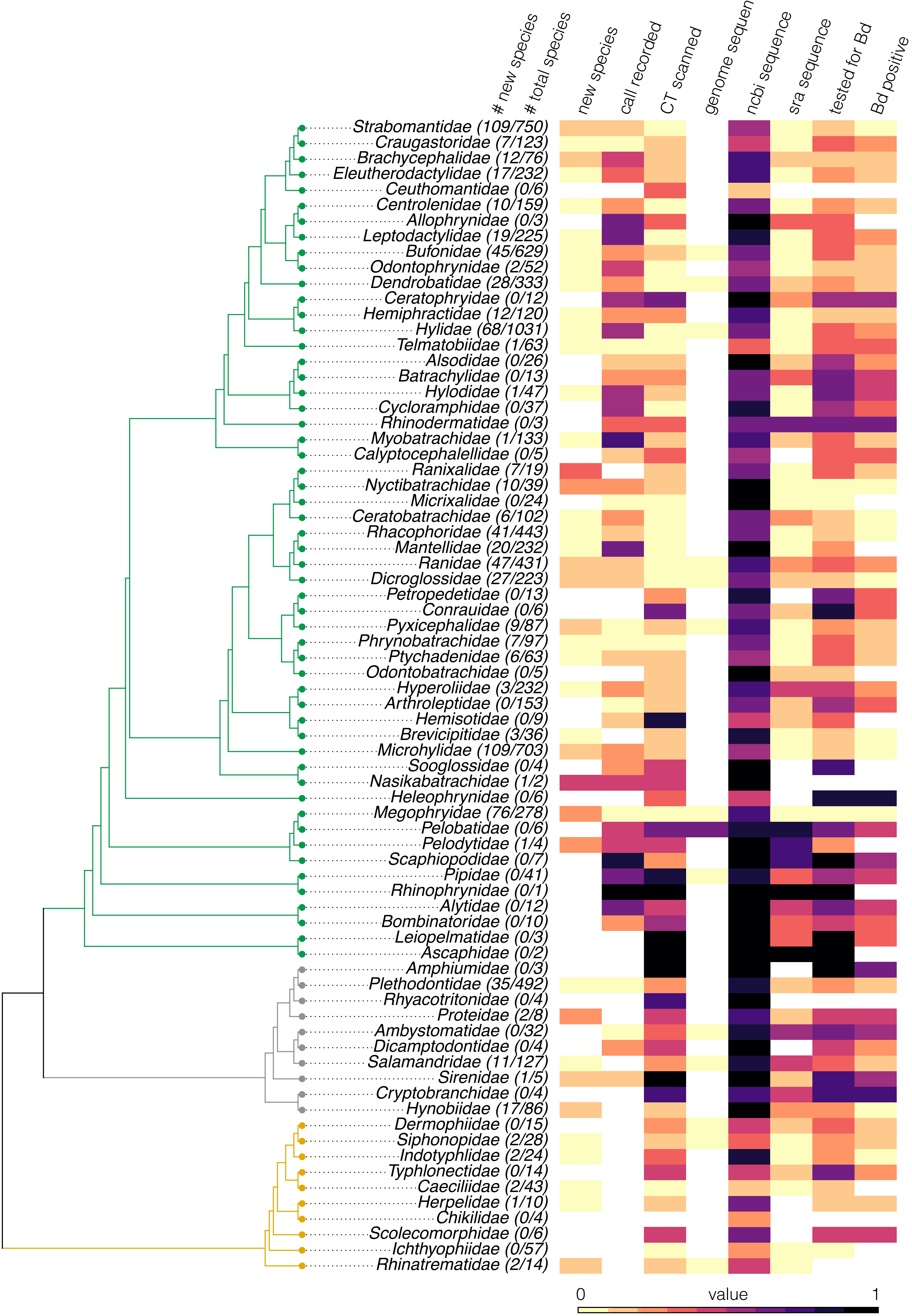

new species
total species
new species
call recorded
CT scanned
genome sequenced
ncbi sequence
sra sequence
tested for Bd
Bd positive
Strabomantidae (109/750)
Craugastoridae (7/123)
Brachycephalidae (12/76)
Eleutherodactylidae (17/232)
Ceuthomantidae (0/6)
Centrolenidae (10/159)
Allophrynidae (0/3)
Leptodactylidae (19/225)
Bufonidae (45/629)
Odontophrynidae (2/52)
Dendrobatidae (28/333)
Ceratophryidae (0/12)
Hemiphractidae (12/120)
Hylidae (68/1031)
Telmatobiidae (1/63)
Alsodidae (0/26)
Batrachylidae (0/13)
Hylodidae (1/47)
Cycloramphidae (0/37)
Rhinodermatidae (0/3)
Myobatrachidae (1/133)
Calyptocephalellidae (0/5)
Ranixalidae (7/19)
Nyctibatrachidae (10/39)
Micrixalidae (0/24)
Ceratobatrachidae (6/102)
Rhacophoridae (41/443)
Mantellidae (20/232)
Ranidae (47/431)
Dicroglossidae (27/223)
Petropedetidae (0/13)
Conrauidae (0/6)
Pyxicephalidae (9/87)
Phrynobatrachidae (7/97)
Ptychadenidae (6/63)
Odontobatrachidae (0/5)
Hyperoliidae (3/232)
Arthroleptidae (0/153)
Hemisotidae (0/9)
Brevicipitidae (3/36)
Microhylidae (109/703)
Sooglossidae (0/4)
Nasikabatrachidae (1/2)
Heleophrynidae (0/6)
Megophryidae (76/278)
Pelobatidae (0/6)
Pelodytidae (1/4)
Scaphiopodidae (0/7)
Pipidae (0/41)
Rhinophrynidae (0/1)
Alytidae (0/12)
Bombinatoridae (0/10)
Leiopelmatidae (0/3)
Ascaphidae (0/2)
Amphiumidae (0/3)
Plethodontidae (35/492)
Rhyacotritonidae (0/4)
Proteidae (2/8)
Ambystomatidae (0/32)
Dicamptodontidae (0/4)
Salamandridae (11/127)
Sirenidae (1/5)
Cryptobranchidae (0/4)
Hynobiidae (17/86)
Dermophiidae (0/15)
Siphonopidae (2/28)
Indotyphlidae (2/24)
Typhlonectidae (0/14)
Caeciliidae (2/43)
Herpelidae (1/10)
Chikilidae (0/4)
Scolecomorphidae (0/6)
Ichthyophiidae (0/57)
Rhinatrematidae (2/14)
0
value
1

Figure 6

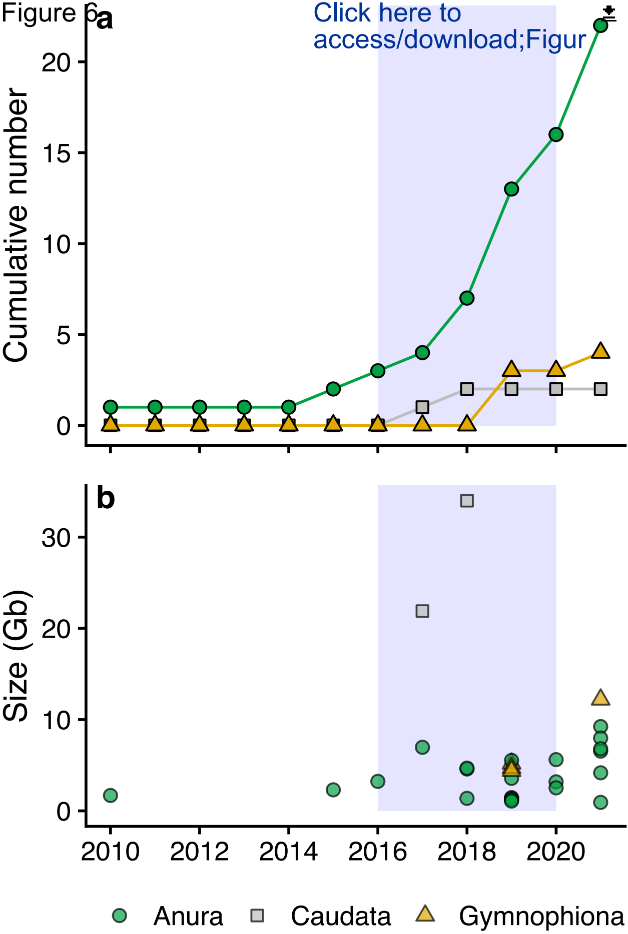

a
Cumulative number
0
5
10
15
20
b
Size (Gb)
0
10
20
30
2010
2012
2014
2016
2018
2020
Anura
Caudata
Gymnophiona

Figure 7

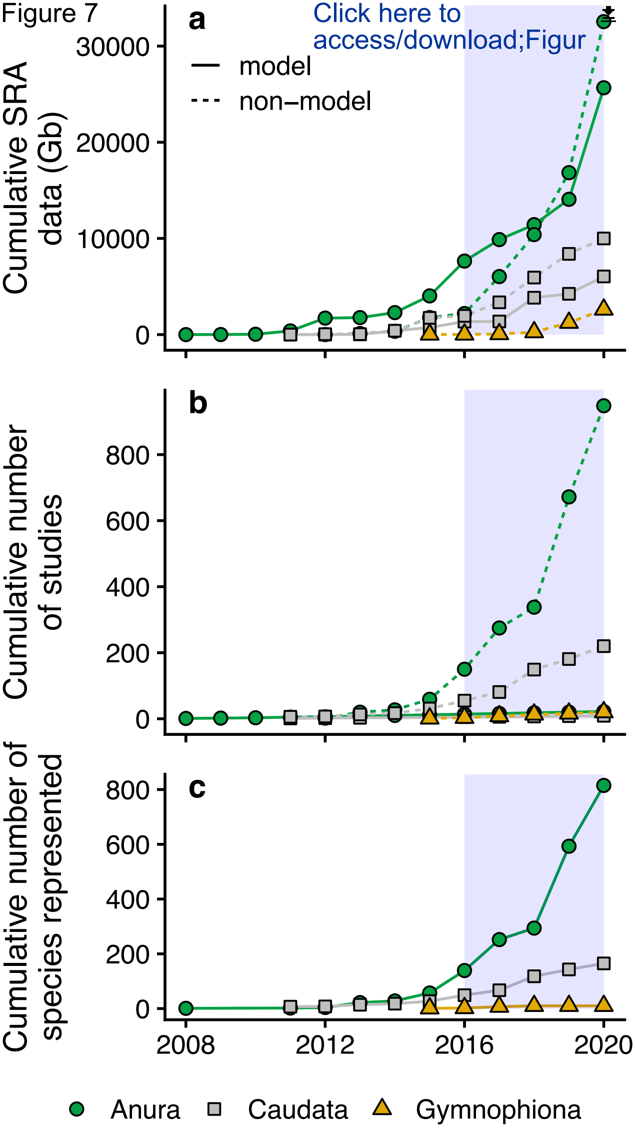
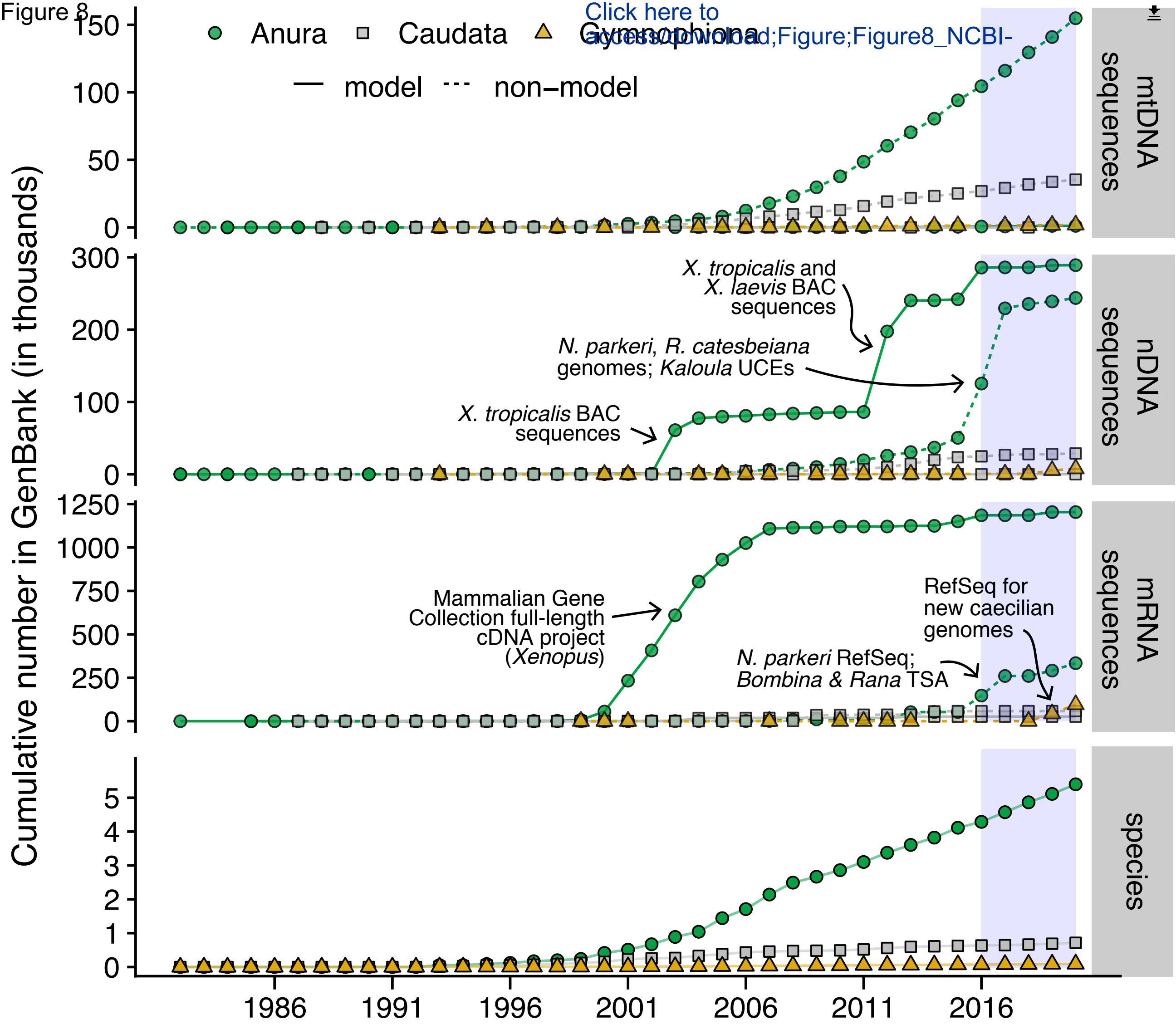
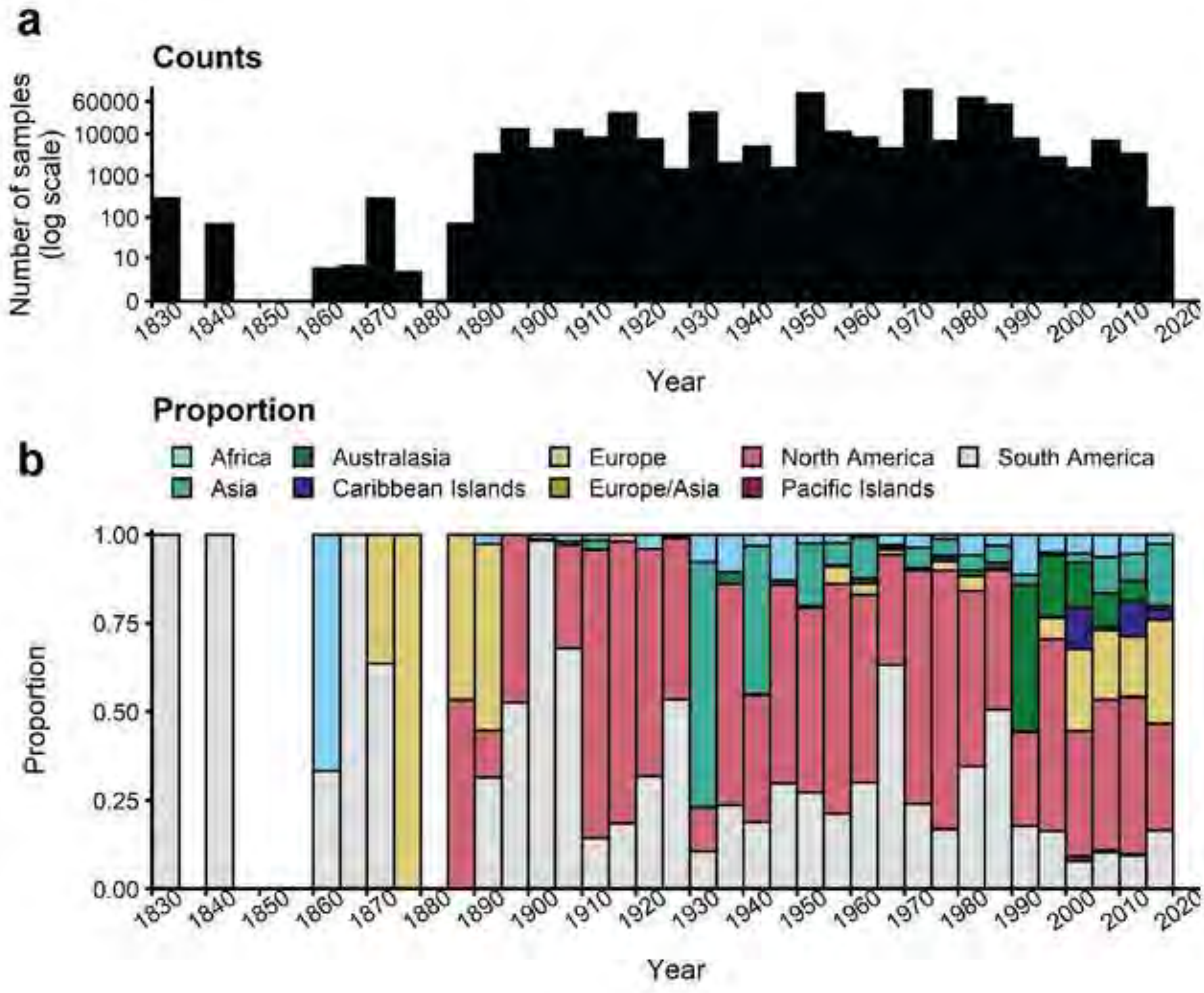

a
Cumulative SRA data (Gb)
30000
20000
10000
0
model
non−model
b
Cumulative number of studies
800
600
400
200
0
c
Cumulative number of species represented
800
600
400
200
0
2008
2012
2016
2020
Anura
Caudata
Gymnophiona

Figure 8


● Anura
■ Caudata
▲ Gymnophiona
— model
--- non–model
Cumulative number in GenBank (in thousands)
mtDNA sequences
nDNA sequences
mRNA sequences
species
150
100
50
0
300
200
100
0
1250
1000
750
500
250
0
5
4
3
2
1
0
1986
1991
1996
2001
2006
2011
2016
X. tropicalis and X. laevis BAC sequences
N. parkeri, R. catesbeiana genomes; Kaloula UCEs
X. tropicalis BAC sequences
Mammalian Gene Collection full-length cDNA project (Xenopus)
RefSeq for new caecilian genomes
N. parkeri RefSeq; Bombina & Rana TSA


a
Counts
Number of samples
(log scale)
60000
10000
1000
100
10
0
1830
1840
1850
1860
1870
1880
1890
1900
1910
1920
1930
1940
1950
1960
1970
1980
1990
2000
2010
2020
Year
b
Proportion
Africa
Asia
Australasia
Caribbean Islands
Europe
Europe/Asia
North America
Pacific Islands
South America
Proportion
1.00
0.75
0.50
0.25
0.00
1830
1840
1850
1860
1870
1880
1890
1900
1910
1920
1930
1940
1950
1960
1970
1980
1990
2000
2010
2020
Year

Supplemental Table 1

TableS1 - Literature Search Results

Search term	Category	2016	2017	2018	2019	2020	2016-2020_Total_ViaSearch_	Totals_Including "Xenopus laevis" OR "Xenopus tropicalis" OR "Ambystoma mexicanum"	percent_change	percent_model
"phylogenomic" OR "phylogenomics"	phylogenomic(s)	4	7	5	7	9	32	0	225	0
"fossil" or "fossils"	fossil(s)	51	40	41	37	48	217	1	94.11764706	0.460829493
"ecology"	ecology	97	112	102	111	138	560	3	142.2680412	0.535714286
"microbiome"	microbiome	7	17	8	26	25	83	1	357.1428571	1.204819277
"phylogenetic" OR "phylogenetics"	phylogenetic(s)	170	185	193	212	239	999	17	140.5882353	1.701701702
"climate"	climate	130	132	128	178	162	730	13	124.6153846	1.780821918
"conservation"	conservation	306	325	313	400	413	1757	34	134.9673203	1.935116676
"diet"	diet	64	71	58	81	96	370	8	150	2.162162162
"trait" or "traits"	trait(s)	149	171	145	197	176	838	19	118.1208054	2.267303103
"behavior" OR "behaviour"	behavior	205	226	186	203	203	1023	30	99.02439024	2.93255132
"eDNA"	eDNA	11	17	16	23	19	86	3	172.7272727	3.488372093
"genetic" OR "genetics"	genetic(s)	233	246	254	298	281	1312	62	120.6008584	4.725609756
Amphibian_Base	Amphibian_Base	2468	2598	2592	2701	2849	13208	629	115.4376013	4.762265294
"morphology"	morphology	114	113	121	145	172	665	36	150.877193	5.413533835
"genetic" OR "genetics" OR "genomic" OR "genomics"	genetic(s) OR genomic(s)	267	276	299	343	321	1506	84	120.2247191	5.577689243

"physiology"	physiology	34	39	42	46	46	207	18	135.2941176	8.695652174
"genomic" OR "genomics"	genomic(s)	55	58	62	75	67	317	32	121.8181818	10.09463722
"development"	development	347	373	363	383	399	1865	238	114.9855908	12.7613941
"cell" AND "molecular"	cell AND molecular	41	43	32	49	40	205	48	97.56097561	23.41463415
background pub rate	background pub rate	2712548	2825899	2895835	3130321	3122765	14687368	1713	115.1229398	0.011663084

TableS2 - Amphibian Publications By Journal

2016		2020		2016-2020	
Journal	Number	Journal	Number	Journal	Number
PLOS ONE	84	SCIENTIFIC REPORTS	55	PLOS ONE	317
SCIENTIFIC REPORTS	47	ZOOTAXA	46	SCIENTIFIC REPORTS	247
MITOCHONDRIAL DNA PART A	40	PLOS ONE	45	ZOOTAXA	186
COPEIA	39	ECOLOGY AND EVOLUTION	38	PEERJ	174
JOURNAL OF HERPETOLOGY	34	PEERJ	32	ECOLOGY AND EVOLUTION	172
ZOOTAXA	30	AMPHIBIAN REPTILE CONSERVATION	26	HERPETOLOGICAL CONSERVATION AND BIOLOGY	126
AMPHIBIA REPTILIA	23	HERPETOLOGICA	25	JOURNAL OF HERPETOLOGY	117
ASIAN HERPETOLOGICAL RESEARCH	21	ZOOKEYS	25	COPEIA	105
ECOLOGY AND EVOLUTION	21	ASIAN HERPETOLOGICAL RESEARCH	23	AMPHIBIA REPTILIA	104
PEERJ	21	JOURNAL OF EXPERIMENTAL BIOLOGY	23	JOURNAL OF EXPERIMENTAL BIOLOGY	98
HERPETOLOGICAL CONSERVATION AND BIOLOGY	18	JOURNAL OF HERPETOLOGY	23	MOLECULAR ECOLOGY	92
AQUATIC TOXICOLOGY	17	MOLECULAR ECOLOGY	23	BIOLOGICAL CONSERVATION	86
BIOLOGICAL CONSERVATION	17	AMPHIBIA REPTILIA	21	HERPETOLOGICA	81
JOURNAL OF EXPERIMENTAL BIOLOGY	17	BIOLOGICAL CONSERVATION	20	HERPETOLOGICAL JOURNAL	80
BEHAVIORAL ECOLOGY AND	15	HERPETOLOGICAL CONSERVATION AND	20	ASIAN HERPETOLOGICAL	78

SOCIOBIOLOGY		BIOLOGY		RESEARCH	
ECOSPHERE	15	COPEIA	19	ZOOKEYS	78
BIOLOGY LETTERS	14	GLOBAL ECOLOGY AND CONSERVATION	18	SALAMANDRA	73
HERPETOLOGICAL JOURNAL	14	SALAMANDRA	18	BIOLOGICAL JOURNAL OF THE LINNEAN SOCIETY	72
MOLECULAR ECOLOGY	14	GENERAL AND COMPARATIVE ENDOCRINOLOGY	16	PROCEEDINGS OF THE ROYAL SOCIETY B BIOLOGICAL SCIENCES	72
ACTA HERPETOLOGICA	13	BIOLOGICAL JOURNAL OF THE LINNEAN SOCIETY	15	GENERAL AND COMPARATIVE ENDOCRINOLOGY	71
ANIMAL BEHAVIOUR	13	EVOLUTION	15	MOLECULAR PHYLOGENETICS AND EVOLUTION	68
BIOLOGICAL JOURNAL OF THE LINNEAN SOCIETY	13	ANIMALS	14	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA	67
CONSERVATION BIOLOGY	13	DIVERSITY BASEL	14	DISEASES OF AQUATIC ORGANISMS	66
ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH	13	ENVIRONMENTAL POLLUTION	14	RUSSIAN JOURNAL OF HERPETOLOGY	65
GENERAL AND COMPARATIVE ENDOCRINOLOGY	13	HERPETOLOGICAL JOURNAL	14	JOURNAL OF BIOGEOGRAPHY	64
HERPETOLOGICA	13	JOURNAL OF ANIMAL ECOLOGY	14	ENVIRONMENTAL TOXICOLOGY AND CHEMISTRY	61
RUSSIAN JOURNAL OF HERPETOLOGY	13	MOLECULAR PHYLOGENETICS AND EVOLUTION	14	SCIENCE OF THE TOTAL ENVIRONMENT	58
SALAMANDRA	13	ENVIRONMENTAL SCIENCE AND	13	JOURNAL OF ZOOLOGY	57

		POLLUTION RESEARCH			
CHEMOSPHERE	12	JOURNAL OF NATURAL HISTORY	13	AMPHIBIAN REPTILE CONSERVATION	54
DISEASES OF AQUATIC ORGANISMS	12	RUSSIAN JOURNAL OF HERPETOLOGY	13	ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH	54
JOURNAL OF BIOGEOGRAPHY	12	CHEMOSPHERE	12	ECOSPHERE	53
JOURNAL OF MORPHOLOGY	12	DEVELOPMENTAL DYNAMICS	12	EVOLUTION	53
JOURNAL OF ZOOLOGY	12	ECOLOGICAL INDICATORS	12	JOURNAL OF MORPHOLOGY	53
PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA	12	INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES	12	MITOCHONDRIAL DNA PART A	53
PROCEEDINGS OF THE ROYAL SOCIETY B BIOLOGICAL SCIENCES	12	JOURNAL OF EXPERIMENTAL ZOOLOGY PART A ECOLOGICAL AND INTEGRATIVE PHYSIOLOGY	12	MITOCHONDRIAL DNA PART B RESOURCES	53
CURRENT HERPETOLOGY	11	JOURNAL OF HELMINTHOLOGY	12	BIOLOGICAL INVASIONS	52
METHODS IN MOLECULAR BIOLOGY	11	MITOCHONDRIAL DNA PART B RESOURCES	12	ECOTOXICOLOGY AND ENVIRONMENTAL SAFETY	50
MITOCHONDRIAL DNA PART B RESOURCES	11	ACTA ZOOLOGICA	11	FRONTIERS IN MICROBIOLOGY	50
ZOOKEYS	11	ANTIBIOTICS BASEL	11	AQUATIC TOXICOLOGY	49
SOUTH AMERICAN JOURNAL OF HERPETOLOGY	10	CANADIAN JOURNAL OF ZOOLOGY	11	BEHAVIORAL ECOLOGY AND SOCIOBIOLOGY	49

ANATOMICAL RECORD ADVANCES IN INTEGRATIVE ANATOMY AND EVOLUTIONARY BIOLOGY	9	CONSERVATION BIOLOGY	11	CHEMOSPHERE	48
BEHAVIORAL ECOLOGY	9	FRESHWATER BIOLOGY	11	JOURNAL OF NATURAL HISTORY	48
ECOHEALTH	9	GLOBAL ECOLOGY AND BIOGEOGRAPHY	11	SOUTH AMERICAN JOURNAL OF HERPETOLOGY	48
ENVIRONMENTAL TOXICOLOGY AND CHEMISTRY	9	JOURNAL OF BIOGEOGRAPHY	11	ACTA HERPETOLOGICA	47
EVOLUTION	9	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA	11	DEVELOPMENTAL BIOLOGY	46
MOLECULAR PHYLOGENETICS AND EVOLUTION	9	PROCEEDINGS OF THE ROYAL SOCIETY B BIOLOGICAL SCIENCES	11	OECOLOGIA	46
OECOLOGIA	9	SCIENCE OF THE TOTAL ENVIRONMENT	11	ENVIRONMENTAL POLLUTION	45
SCIENCE OF THE TOTAL ENVIRONMENT	9	BIOTROPICA	10	CANADIAN JOURNAL OF ZOOLOGY	44
AMERICAN NATURALIST	8	BMC GENOMICS	10	CONSERVATION BIOLOGY	44
CANADIAN JOURNAL OF ZOOLOGY	8	CONSERVATION SCIENCE AND PRACTICE	10	FRESHWATER BIOLOGY	44
ECOLOGY	8	FRONTIERS IN MICROBIOLOGY	10	CURRENT HERPETOLOGY	43
FOREST ECOLOGY AND MANAGEMENT	8	HERPETOZOA	10	METHODS IN MOLECULAR BIOLOGY	42
HYDROBIOLOGIA	8	JOURNAL OF MORPHOLOGY	10	GLOBAL ECOLOGY AND CONSERVATION	41

JOURNAL OF EVOLUTIONARY BIOCHEMISTRY AND PHYSIOLOGY	8	OECOLOGIA	10	HERPETOZOA	39
JOURNAL OF EXPERIMENTAL ZOOLOGY PART A ECOLOGICAL AND INTEGRATIVE PHYSIOLOGY	8	SOUTH AMERICAN JOURNAL OF HERPETOLOGY	10	HYDROBIOLOGIA	39
JOURNAL OF WILDLIFE DISEASES	8	ENVIRONMENTAL TOXICOLOGY AND CHEMISTRY	9	JOURNAL OF EXPERIMENTAL ZOOLOGY PART A ECOLOGICAL AND INTEGRATIVE PHYSIOLOGY	39
MOLECULAR ECOLOGY RESOURCES	8	INTEGRATIVE AND COMPARATIVE BIOLOGY	9	NATURE COMMUNICATIONS	39
WETLANDS	8	INTEGRATIVE ZOOLOGY	9	DEVELOPMENTAL AND COMPARATIVE IMMUNOLOGY	37
AGRICULTURE ECOSYSTEMS ENVIRONMENT	7	JOURNAL OF ZOOLOGY	9	JOURNAL OF THERMAL BIOLOGY	37
BIOLOGY OPEN	7	TOXINS	9	AUSTRAL ECOLOGY	36
BMC EVOLUTIONARY BIOLOGY	7	ACTA HERPETOLOGICA	8	BIOLOGY LETTERS	36
BMC GENOMICS	7	BEHAVIORAL ECOLOGY AND SOCIOBIOLOGY	8	COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY A MOLECULAR INTEGRATIVE PHYSIOLOGY	36
COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY A MOLECULAR INTEGRATIVE PHYSIOLOGY	7	BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS	8	GLOBAL ECOLOGY AND BIOGEOGRAPHY	36
COMPARATIVE BIOCHEMISTRY AND	7	BIODIVERSITY AND CONSERVATION	8	JOURNAL OF ANIMAL ECOLOGY	36

PHYSIOLOGY B BIOCHEMISTRY MOLECULAR BIOLOGY					
ECOTOXICOLOGY AND ENVIRONMENTAL SAFETY	7	BIOLOGICAL INVASIONS	8	BEHAVIORAL ECOLOGY	35
EVOLUTIONARY ECOLOGY	7	DISEASES OF AQUATIC ORGANISMS	8	BMC GENOMICS	35
INTERNATIONAL JOURNAL OF DEVELOPMENTAL BIOLOGY	7	DIVERSITY AND DISTRIBUTIONS	8	DIVERSITY AND DISTRIBUTIONS	35
JOVE JOURNAL OF VISUALIZED EXPERIMENTS	7	FACETS	8	AMERICAN NATURALIST	34
NORTH WESTERN JOURNAL OF ZOOLOGY	7	GLOBAL CHANGE BIOLOGY	8	ANIMAL BEHAVIOUR	34
PROCEEDINGS OF SPIE	7	JOURNAL FOR NATURE CONSERVATION	8	INTEGRATIVE AND COMPARATIVE BIOLOGY	34
REVISTA MEXICANA DE BIODIVERSIDAD	7	JOURNAL OF THERMAL BIOLOGY	8	PHYLLOMEDUSA	34
ROYAL SOCIETY OPEN SCIENCE	7	JOURNAL OF WILDLIFE DISEASES	8	BIODIVERSITY AND CONSERVATION	33
ZOOLOGICAL SCIENCE	7	PHYLLOMEDUSA	8	ACTA ZOOLOGICA	32
ACTA ZOOLOGICA	6	SEMINARS IN CELL DEVELOPMENTAL BIOLOGY	8	ECOLOGICAL INDICATORS	32
AMERICAN MIDLAND NATURALIST	6	TOXICON	8	NORTH WESTERN JOURNAL OF ZOOLOGY	32
AUSTRAL ECOLOGY	6	VERTEBRATE ZOOLOGY	8	SOUTHEASTERN NATURALIST	32
BIOCHEMICAL AND BIOPHYSICAL RESEARCH	6	BIOACOUSTICS THE INTERNATIONAL JOURNAL OF ANIMAL	7	ZOOLOGICAL SCIENCE	32

COMMUNICATIONS		SOUND AND ITS RECORDING			
BIODIVERSITY AND CONSERVATION	6	BIOTA NEOTROPICA	7	BIOTROPICA	31
ECOTOXICOLOGY	6	CURRENT HERPETOLOGY	7	BMC EVOLUTIONARY BIOLOGY	31
ENVIRONMENTAL POLLUTION	6	ECOTOXICOLOGY AND ENVIRONMENTAL SAFETY	7	ECOGRAPHY	31
ETHOLOGY	6	ELIFE	7	INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES	31
JOURNAL OF COMPARATIVE NEUROLOGY	6	FOREST ECOLOGY AND MANAGEMENT	7	JOURNAL OF EVOLUTIONARY BIOLOGY	31
JOURNAL OF NATURAL HISTORY	6	HEREDITY	7	MOLECULES	31
JOURNAL OF THERMAL BIOLOGY	6	INTERNATIONAL JOURNAL FOR PARASITOLOGY PARASITES AND WILDLIFE	7	ROYAL SOCIETY OPEN SCIENCE	31
JOURNAL OF WILDLIFE MANAGEMENT	6	MOLECULES	7	ZOOLOGISCHER ANZEIGER	31
JOURNAL OF ZOO AND WILDLIFE MEDICINE	6	NATURE COMMUNICATIONS	7	CONSERVATION GENETICS	30
LECTURE NOTES IN COMPUTER SCIENCE	6	PARASITOLOGY RESEARCH	7	ETHOLOGY	30
PALAEOBIODIVERSITY AND PALAEOENVIRONMENTS	6	SPECTROSCOPY AND SPECTRAL ANALYSIS	7	ANATOMICAL RECORD ADVANCES IN INTEGRATIVE ANATOMY AND EVOLUTIONARY BIOLOGY	29
SOUTHEASTERN NATURALIST	6	WETLANDS	7	DEVELOPMENTAL DYNAMICS	29

TOXICON	6	ZOOLOGICAL JOURNAL OF THE LINNEAN SOCIETY	7	ECOLOGY	29
ZOOLOGY	6	ACTA OECOLOGICA INTERNATIONAL JOURNAL OF ECOLOGY	6	FOREST ECOLOGY AND MANAGEMENT	29
ACTA ZOOLOGICA BULGARICA	5	AQUATIC CONSERVATION MARINE AND FRESHWATER ECOSYSTEMS	6	FRONTIERS IN ECOLOGY AND EVOLUTION	29
AIP CONFERENCE PROCEEDINGS	5	ARCHIVES OF ENVIRONMENTAL CONTAMINATION AND TOXICOLOGY	6	TOXICON	29
ANIMAL CONSERVATION	5	AUSTRAL ECOLOGY	6	CONSERVATION PHYSIOLOGY	28
AQUATIC CONSERVATION MARINE AND FRESHWATER ECOSYSTEMS	5	BEHAVIORAL ECOLOGY	6	DIVERSITY BASEL	28
BIOLOGICAL INVASIONS	5	BIOLOGY LETTERS	6	ECOHEALTH	28
BIOTA NEOTROPICA	5	BIOMOLECULES	6	JOURNAL OF WILDLIFE DISEASES	28
BIOTROPICA	5	CELLS	6	ANIMAL CONSERVATION	27
COMPARATIVE PARASITOLOGY	5	COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY A MOLECULAR INTEGRATIVE PHYSIOLOGY	6	ECOLOGICAL APPLICATIONS	27
CONSERVATION PHYSIOLOGY	5	CONSERVATION PHYSIOLOGY	6	MOLECULAR ECOLOGY RESOURCES	27

TableS3 - Amphibian Publications By Language

Language	Pubs in 2016	Language	Pubs in 2020	Language	Pubs 2016-2020
english	1,517	english	1,768	english	7,915
spanish	17	russian	8	spanish	63
russian	16	german	6	russian	57
chinese	5	portuguese	4	chinese	40
portuguese	3	spanish	4	german	22
french	2	chinese	2	portuguese	13
german	2	afrikaans	1	dutch/flemish	12
polish	2	armenian	1	czech	5
czech	1	dutch/flemish	1	turkish	5
hungarian	1	hebrew	1	ukrainian	5
slovenian	1	indonesian	1	hungarian	4
turkish	1	malay	1	persian	4
		persian	1	french	3
		thai	1	hebrew	2
				polish	2
				slovak	2
				slovenian	2
				thai	2
				afrikaans	1
				armenian	1

				indonesian	1
				italian	1
				malay	1
				multiple languages	1

TableS4-Amphibian-Genomes
Part 1

Order	Family	Species	Genome Status	Scaffold N50	Scaffold N50 unit	Average Genome Size (Gb)	Sequencing technologies
Anura	Bombinatoridae	Bombina variegata	Contig	2005	bp	9.236	Illumina
Anura	Bufonidae	Bufo bufo	Chromosomal	0.64	Gb	6.54	10x, Arima HiC, Bionano, PacBio
Anura	Bufonidae	Bufo gargarizans	Chromosomal	0.54	Gb	5.614	Illumina, PacBio, BioNano, 10x Genomics, HiC
Anura	Ranidae	Glandirana rugosa	Scaffolded	0.747	Mb	7.971	Illumina
Anura	Hylidae	Dendropsophus ebraccatus	Chromosomal	0.609	Gb	2.52	10x, Arima HiC, Bionano, Illumina, PacBio
Anura	Megophryidae	Leptobrachium ailaonicum	Chromosomal	0.412	Gb	5.53	Illumina, PacBio, HiC
Anura	Megophryidae	Leptobrachium leishanense	Chromosomal	0.39	Gb	3.56	HiC, Illumina, PacBio
Anura	Myobatrachidae	Limnodynastes dumerilii	Scaffolded	0.286	Mb	3.179	Illumina
Anura	Ranidae	Rana catesbeiana	Scaffolded	0.069	Mb	6.966	Illumina, 10X Chromium
Anura	Dicroglossidae	Nanorana parkeri	Chromosomal	0.00105	Gb	2.3	Illumina
Anura	Dendrobatidae	Oophaga pumilio	Scaffolded	0.116	Mb	4.586	Illumina, RNAseq
Anura	Myobatrachidae	Platyplectrum ornatum	Scaffolded	0.027	Mb	0.929	Illumina, Oxford Nanopore
Anura	Pyxicephalidae	Pyxicephalus adspersus	Chromosomal	0.158	Gb	1.369	Illumina, HiC, Chicago
Anura	Ranidae	Rana temporaria	Chromosomal	0.481	Gb	4.169	PacBio, 10X Genomics Chromium, BioNano, and Arima Hi-C
Anura	Dendrobatidae	Ranitomeya imitator	Scaffolded	0.397	Mb	6.8	10X Chromium, Oxford Nanopore, PacBio
Anura	Bufonidae	Rhinella marina	Scaffolded	0.168	Mb	4.681	PacBio, Illumina

Anura	Scaphiopodidae	Scaphiopus couchii	Contig	362	bp	1.45	Illumina
Anura	Scaphiopodidae	Scaphiopus holbrookii	Contig	514	bp	1.353	Illumina
Anura	Scaphiopodidae	Spea bombifrons	Contig	522	bp	1.208	Illumina
Anura	Scaphiopodidae	Spea multiplicata	Scaffolded	0.071	Mb	1.07	Illumina, PacBio, Oxford Nanopore
Anura	Pipidae	Xenopus laevis	Chromosomal	0.155	Gb	3.23	Illumina, PacBio (unclear if they were both used in latest assembly)
Anura	Pipidae	Xenopus tropicalis	Chromosomal	0.154	Gb	1.685	PacBio, Illumina
Caudata	Ambystomatidae	Ambystoma mexicanum	Chromosomal	1.2	Gb	33.99	improvement of two previous scaffolds (the first generated with PacBio, Illumina, BioNano, the second improved with meiotic mapping and FISH) using HiC
Caudata	Salamandridae	Pleurodeles waltl	Contig	1136	bp	21.89	Illumina
Gymnophiona	Dermophiidae	Geotrypetes seraphini	Chromosomal	0.27	Gb	5.187	10x, Dovetail HiC, Bionano, PacBio
Gymnophiona	Ichthyophiidae	Ichthyophis bannanicus	Contig	740	bp	12.2	Illumina
Gymnophiona	Siphonopidae	Microcaecilia unicolor	Chromosomal	0.376	Gb	4.69	10X, Arima HiC, BioNano, Dovetail Genomics, PacBio
Gymnophiona	Rhinatrematidae	Rhinatrema bivittatum	Chromosomal	0.487	Gb	4.374	10X, PacBio, Arima HiC, BioNano

Part 2 (same table, additional columns)

Year of latest version	Citation/link, latest version	Year of first version	Citation/link, first version(s)	Link to latest genome
--	--	2021	Cizkova, D. and Nurnberger, B. Institute of Vertebrate Biology, CAS, Kvetna 8, 603 65 Brno, Czech Republic	https://www.ncbi.nlm.nih.gov/assembly/GCA_905336975.1

--	--	2021	VGP (https://vgp.github.io/genomeark/Bufo_bufo/)	https://www.ncbi.nlm.nih.gov/assembly/GCF_905171765.1/
--	--	2020	Lu et al. 2020 (https://onlinelibrary.wiley.com/doi/epdf/10.1111/1755-0998.13319)	https://www.ncbi.nlm.nih.gov/genome/8043
--	--	2021	Katsura et al. 2021 (https://www.life-science-alliance.org/content/4/5/e202000905)	https://www.ncbi.nlm.nih.gov/assembly/GCA_018402905.1/
--	--	2020	VGP (https://vgp.github.io/genomeark/Dendropsophus_ebraccatus/)	https://vgp.github.io/genomeark/Dendropsophus_ebraccatus/
--	--	2019	Li et al. 2019 (https://academic.oup.com/gigascience/article/8/9/giz114/5572531)	http://gigadb.org/dataset/100624
--	--	2019	Li et al 2019 (https://www.nature.com/articles/s41467-019-13531-5)	https://www.ncbi.nlm.nih.gov/assembly/GCA_009667805.1/
--	--	2020	Li et al. 2020 (https://gigabytejournal.com/articles/2)	https://www.ncbi.nlm.nih.gov/assembly/GCA_011038615.1/
2017		2017	Hammond et al. 2017 (https://www.nature.com/articles/s41467-017-01316-7; https://www.ncbi.nlm.nih.gov/assembly/GCA_002284835.1/)	https://www.ncbi.nlm.nih.gov/assembly/GCA_002284835.2/
--	--	2015	Sun et al. 2015 (https://www.pnas.org/content/112/11/E1257)	https://www.ncbi.nlm.nih.gov/assembly/GCF_000935625.1/
2021	Rodríguez et al. 2021 (https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-020-6719-5)	2018	Rogers et al. 2018 (https://academic.oup.com/mbe/article/35/12/2913/5106668)	https://zenodo.org/record/3696842; https://www.ncbi.nlm.nih.gov/assembly/GCA_009801035.1/
--	--	2021	Lamichhaney et al. 2021 (https://www.pnas.org/content/118/11/e2011649118)	https://www.ncbi.nlm.nih.gov/assembly/GCA_016617825.1/
--	--	2018	Denton et al. bioRXiv (https://www.biorxiv.org/content/10.1101/329847v2)	https://www.ncbi.nlm.nih.gov/assembly/GCA_004786255.1/

--	--	2021	Darwin Tree of Life (https://portal.darwintreeoflife.org/data/root/details/Rana%20temporaria)	https://www.ncbi.nlm.nih.gov/assembly/GCA_905171775.1
--	--	2021	Stuckert et al. 2021 (https://onlinelibrary.wiley.com/doi/10.1111/mec.16024)	https://www.ncbi.nlm.nih.gov/assembly/GCA_905332335.1/
--	--	2018	Edwards et al. 2018 (https://academic.oup.com/gigascience/article/7/9/giy095/5067871)	https://www.ncbi.nlm.nih.gov/assembly/GCA_900303285.1/
--	--	2019	Seidl et al. 2019 (https://academic.oup.com/g3journal/article/9/12/3909/6028079)	https://www.ncbi.nlm.nih.gov/assembly/GCA_009364435.1/
--	--	2019	Seidl et al. 2019 (https://academic.oup.com/g3journal/article/9/12/3909/6028079)	https://www.ncbi.nlm.nih.gov/assembly/GCA_009364455.1
--	--	2019	Seidl et al. 2019 (https://academic.oup.com/g3journal/article/9/12/3909/6028079)	https://www.ncbi.nlm.nih.gov/assembly/GCA_009364475.1
--	--	2019	Seidl et al. 2019 (https://academic.oup.com/g3journal/article/9/12/3909/6028079)	https://www.ncbi.nlm.nih.gov/assembly/GCA_009364415.1/
2021	https://www.ncbi.nlm.nih.gov/assembly/GCF_017654675.1/	2016	Session et al. 2016 (https://www.nature.com/articles/nature19840; https://www.ncbi.nlm.nih.gov/assembly/GCF_001663975.1/)	https://www.ncbi.nlm.nih.gov/assembly/GCF_017654675.1/
2019	Mitros et al. 2019 (https://www.sciencedirect.com/science/article/pii/S0012160618303890?via%3Dihub)	2010	Hellsten et al. 2010 (https://science.sciencemag.org/content/328/5978/633)	https://www.ncbi.nlm.nih.gov/assembly/GCF_000004195.4
2021	Schloissnig et al. 2021 (https://www.pnas.org/content/118/15/e2017176118)	2018	Nowoshilow et al 2018 (doi:10.1038/nature25458), Smith et al. 2019 (https://genome.cshlp.org/content/29/2/317.long)	https://www.ncbi.nlm.nih.gov/assembly/GCA_002915635.3
--	--	2017	Elewa et al. 2017 (https://www.nature.com/articles/s41467-017-01964-9)	genome assembly available upon request
2021	VGP	2019	VGP	https://www.ncbi.nlm.nih.g

	(https://vgp.github.io/genomeark/Geotrypetes_seraphini/)		(https://www.ncbi.nlm.nih.gov/assembly/GCF_902459505.1)	ov/assembly/GCA_902459505.2
--	--	2021	Wang et al. 2021 (https://www.sciencedirect.com/science/article/pii/S1672022921000528?via%3Dihub)	assembly unavailable but reads are on NCBI
2021	VGP (https://vgp.github.io/genomeark/Microcaecilia_unicolor/)	2019	VGP (https://www.ncbi.nlm.nih.gov/assembly/GCF_901765095.1/)	https://www.ncbi.nlm.nih.gov/assembly/GCA_901765095.2
2021	VGP (https://vgp.github.io/genomeark/Rhinatrema_bivittatum/)	2019	VGP (https://www.ncbi.nlm.nih.gov/assembly/GCF_901001135.1/)	https://www.ncbi.nlm.nih.gov/assembly/GCA_901001135.2

TableS5 - Family-level Phylogenetic Heat Map Data

Family	Order	Genera	Species	new_species	PropSp_New	PropSp_Calls	PropSp_CTscan	PropSp_genomes	PropSp_ncbi	PropSp_sra	PropSp_DiseaseTested	PropSp_DiseasePositive
Hynobiidae	Caudata	9	86	17	0.19767442	0	0.10465116	0	0.91860465	0.20930233	0.23255814	0.03488372
Cryptobranchidae	Caudata	2	4	0	0	0	0.75	0	0.75	0.5	0.75	0.75
Salamandridae	Caudata	21	127	11	0.08661417	0	0.27559055	0.00787402	0.87401575	0.40944882	0.38582677	0.16535433
Dicamptodontidae	Caudata	1	4	0	0	0.25	0.5	0	1	0	0.5	0.25
Ambystomatidae	Caudata	1	32	0	0	0.03125	0.3125	0.03125	0.875	0.59375	0.6875	0.5625
Proteidae	Caudata	2	8	2	0.25	0	0.5	0	0.75	0.125	0.5	0.5
Rhyacotritonidae	Caudata	1	4	0	0	0	0.75	0	1	0	0	0
Plethodontidae	Caudata	28	492	35	0.07113821	0.00406504	0.21747967	0	0.83943089	0.1097561	0.29065041	0.13414634
Amphiumidae	Caudata	1	3	0	0	0	1	0	1	0	1	0.66666667
Sirenidae	Caudata	2	5	1	0.2	0.2	1	0	1	0.2	0.8	0.6
Ascaphidae	Anura	1	2	0	0	0	1	0	1	1	1	0
Leiopelmatidae	Anura	1	3	0	0	0	1	0	1	0.33333333	1	0.33333333

Bombinatoridae	Anura	2	10	0	0	0.3	0.6	0	1	0.4	0.5	0.4
Alytidae	Anura	3	12	0	0	0.66666667	0.41666667	0	1	0.41666667	0.66666667	0.5
Rhinophrynidae	Anura	1	1	0	0	1	1	0	1	1	1	0
Pipidae	Anura	4	41	0	0	0.6097561	0.87804878	0.04878049	0.85365854	0.36585366	0.58536585	0.48780488
Calyptocephalellidae	Anura	2	5	0	0	0.2	0.4	0	0.6	0	0.4	0.4
Myobatrachidae	Anura	21	133	1	0.0075188	0.77443609	0.16541353	0	0.79699248	0.16541353	0.33834586	0.18796992
Rhinodermatidae	Anura	2	3	0	0	0.33333333	0.33333333	0	0.66666667	0.66666667	0.66666667	0.66666667
Cycloramphidae	Anura	3	37	0	0	0.54054054	0.08108108	0	0.86486486	0.05405405	0.54054054	0.32432432
Hylodidae	Anura	4	47	1	0.0212766	0.59574468	0.10638298	0	0.63829787	0.08510638	0.61702128	0.4893617
Batrachylidae	Anura	4	13	0	0	0.23076923	0.23076923	0	0.61538462	0.38461538	0.61538462	0.46153846
Alsodidae	Anura	3	26	0	0	0.15384615	0.19230769	0	0.92307692	0.15384615	0.57692308	0.26923077
Dendrobatidae	Anura	20	333	28	0.084084	0.24924	0.0840840	0.003003	0.6276276	0.135135	0.21021021	0.12912913

					08	925	8		3	14		
Odontophrynidae	Anura	3	52	2	0.03846154	0.44230769	0.07692308	0	0.53846154	0.01923077	0.19230769	0.13461538
Bufonidae	Anura	52	629	45	0.07154213	0.22257552	0.19236884	0.00317965	0.64069952	0.08426073	0.31319555	0.15103339
Leptodactylidae	Anura	13	225	19	0.08444444	0.69777778	0.08	0	0.85333333	0.04444444	0.37333333	0.20444444
Allophrynidae	Anura	1	3	0	0	0.66666667	0.33333333	0	1	0.33333333	0.33333333	0
Centrolenidae	Anura	12	159	10	0.06289308	0.29559748	0.06918239	0	0.67924528	0.03773585	0.21383648	0.11320755
Ceuthomantidae	Anura	2	6	0	0	0	0.33333333	0	0.16666667	0	0	0
Eleutherodactylidae	Anura	4	232	17	0.07327586	0.31465517	0.13793103	0	0.7887931	0.03448276	0.28448276	0.14655172
Brachycephalidae	Anura	2	76	12	0.15789474	0.44736842	0.19736842	0	0.75	0.17105263	0.14473684	0.10526316
Craugastoridae	Anura	2	123	7	0.05691057	0.08130081	0.11382114	0	0.48780488	0.04065041	0.38211382	0.27642276
Strabomantidae	Anura	19	750	109	0.14533333	0.168	0.02666667	0	0.556	0.01466667	0.18133333	0.08266667
Hemiphractidae	Anura	6	120	12	0.1	0.24166	0.2916666	0	0.725	0.041666	0.2	0.16666667

						667	7			67		
Ceratophryidae	Anura	3	12	0	0	0.58333333	0.66666667	0	0.91666667	0.25	0.58333333	0.58333333
Hylidae	Anura	51	1031	68	0.06595538	0.50339476	0.09893307	0.00096993	0.64500485	0.09214355	0.3385063	0.22308438
Telmatobiidae	Anura	1	63	1	0.01587302	0.06349206	0.07936508	0	0.38095238	0.03174603	0.3968254	0.33333333
Nasikabatrachidae	Anura	1	2	1	0.5	0.5	0.5	0	1	0	0	0
Sooglossidae	Anura	2	4	0	0	0.25	0.5	0	1	0	0.75	0
Microhylidae	Anura	58	703	109	0.15504979	0.20625889	0.12660028	0	0.53485064	0.06970128	0.11948791	0.03556188
Dicroglossidae	Anura	15	223	27	0.12107623	0.11210762	0.09865471	0.0044843	0.69058296	0.10313901	0.19282511	0.07174888
Ranidae	Anura	24	431	47	0.10904872	0.18793503	0.07424594	0.00232019	0.76102088	0.22969838	0.37587007	0.21113689
Mantellidae	Anura	12	232	20	0.0862069	0.60775862	0.09482759	0	0.90086207	0.06034483	0.28017241	0
Rhacophoridae	Anura	21	443	41	0.09255079	0.11286682	0.04740406	0	0.69751693	0.06094808	0.11738149	0.04288939
Nyctibatrachidae	Anura	3	39	10	0.25641026	0.20512821	0.1025641	0	0.94871795	0.07692308	0.05128205	0.05128205

Ranixalidae	Anura	2	19	7	0.36842105	0	0.15789474	0	0.68421053	0.05263158	0.31578947	0.10526316
Micrixalidae	Anura	1	24	0	0	0.04166667	0.08333333	0	0.95833333	0.04166667	0.04166667	0
Ceratobatrachidae	Anura	4	102	6	0.05882353	0.26470588	0.09803922	0	0.64705882	0.24509804	0.1372549	0.01960784
Odontobatrachidae	Anura	1	5	0	0	0	0.2	0	1	0.2	0.2	0
Ptychadenidae	Anura	3	63	6	0.0952381	0.11111111	0.11111111	0	0.57142857	0.07936508	0.38095238	0.14285714
Phrynobatrachidae	Anura	1	97	7	0.07216495	0.05154639	0.05154639	0	0.68041237	0.01030928	0.39175258	0.18556701
Pyxicephalidae	Anura	12	87	9	0.10344828	0.03448276	0.17241379	0.01149425	0.7816092	0.06896552	0.29885057	0.18390805
Conrauidae	Anura	1	6	0	0	0	0.66666667	0	0.66666667	0.16666667	0.83333333	0.33333333
Petropedetidae	Anura	3	13	0	0	0	0.23076923	0	0.84615385	0	0.69230769	0.38461538
Brevicipitidae	Anura	5	36	3	0.08333333	0	0.19444444	0	0.88888889	0.05555556	0.16666667	0.02777778
Hemisotidae	Anura	1	9	0	0	0.11111111	0.88888889	0	0.44444444	0.11111111	0.33333333	0

Arthroleptidae	Anura	8	153	0	0	0.07189542	0.16339869	0	0.67973856	0.12418301	0.58169935	0.31372549
Hyperoliidae	Anura	18	232	3	0.01293103	0.20689655	0.14224138	0	0.70258621	0.48706897	0.43103448	0.25862069
Heleophrynidae	Anura	2	6	0	0	0	0.33333333	0	0.5	0	0.83333333	0.83333333
Scaphiopodidae	Anura	2	7	0	0	0.85714286	0.28571429	0	1	0.71428571	1.14285714	0.71428571
Pelodytidae	Anura	1	4	1	0.25	0.5	0.5	0	1	0.75	0.25	0
Pelobatidae	Anura	1	6	0	0	0.5	0.66666667	0.66666667	0.83333333	0.83333333	0.66666667	0.5
Megophryidae	Anura	12	278	76	0.27338129	0.07553957	0.06115108	0.00719424	0.75539568	0.06834532	0.10071942	0.01079137
Rhinatrematidae	Gymnophiona	3	14	2	0.14285714	0	0.14285714	0.07142857	0.5	0.07142857	0	0
Ichthyophiidae	Gymnophiona	2	57	0	0	0	0.0877193	0	0.28070175	0.01754386	0.07017544	0
Scolecomorphidae	Gymnophiona	2	6	0	0	0	0.5	0	0.66666667	0	0.5	0.5
Caeciliidae	Gymnophiona	2	43	2	0.04651163	0	0.04651163	0	0.1627907	0.02325581	0.11627907	0
Typhlone	Gymn	5	14	0	0	0	0.428	0	0.428	0.14	0.642857	0.285714

ctidae	ophiona						57143		57143	285714	14	29
Indotyphlidae	Gymnophiona	7	24	2	0.08333333	0	0.33333333	0	0.83333333	0.04166667	0.25	0.04166667
Siphonopidae	Gymnophiona	5	28	2	0.07142857	0	0.17857143	0.03571429	0.39285714	0.07142857	0.25	0.10714286
Dermophiidae	Gymnophiona	4	15	0	0	0	0.26666667	0.06666667	0.46666667	0.13333333	0.33333333	0.13333333
Chikilidae	Gymnophiona	1	4	0	0	0	0	0	0.25	0	0	0
Herpelidae	Gymnophiona	2	10	1	0.1	0	0.2	0	0.7	0	0.2	0.2

Supplemental Text - French Language Abstract

Les amphibiens constituent un clade de plus de 8400 espèces qui offrent des possibilités et des défis de recherche uniques. Les amphibiens subissant un grave déclin au niveau mondial, nous postulons qu'il est impératif d'évaluer notre compréhension actuelle des amphibiens. En nous concentrant sur les années de 2016 à 2020, nous examinons les nouveaux acquis et les nouvelles perspectives de la recherche et de la systématique des amphibiens. De nouvelles espèces d'amphibiens continuent d'être décrites à un rythme de ~150 par an. Les études phylogénomiques sont en augmentation, alimentant un consensus croissant dans la phylogénie des amphibiens. Plus de 3000 espèces d'amphibiens sont désormais représentées par des descriptions ou par des données gérées par des experts au sein d'AmphibiaWeb, AmphibiaChina, BioWeb ou le portail sur les maladies des amphibiens. Néanmoins, de nombreuses espèces ne disposent pas de données de base sur leur histoire naturelle (concernant, par exemple, leur régime alimentaire, les mesures morphologiques et les vocalisations) et des lacunes importantes existent pour des clades entiers d'amphibiens. Les ressources génomiques semblent être à l'aube d'une expansion rapide, mais les grands génomes répétitifs des amphibiens posent encore des défis importants. La conservation reste un axe majeur de la recherche sur les amphibiens. Les menaces cataloguées sur AmphibiaWeb pour 1261 espèces soulignent la nécessité de faire face aux changements d'utilisation des terres et aux maladies en utilisant des stratégies de gestion adaptative. Afin de promouvoir davantage la recherche et la conservation des amphibiens, nous soulignons l'importance de l'intégration des bases de données et nous pensons que d'autres clades peu étudiés ou en danger pourraient bénéficier d'évaluations similaires des données existantes.

Supplemental Figure 1