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State of the Amphibia 2020: A Review of Five Years of Amphibian Research and Existing Resources

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### Authors

Womack, Molly C  
Steigerwald, Emma  
Blackburn, David C  
[et al.](#)

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## 1 **ABSTRACT**

2

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

21

## 22 **INTRODUCTION**

23

24 Amphibians are an ancient, diverse lineage of vertebrates that have been studied in  
25 research fields from evolution and ecology to engineering and medicine. Although  
26 amphibians are often considered to be sensitive to perturbation, they have survived the  
27 last four global mass extinction events and have a nearly worldwide distribution (Wake  
28 and Vredenburg, 2008; Kerby et al., 2010; Barnosky et al., 2011; Alroy, 2015). Most  
29 have biphasic lifestyles, serving as a vital link for energy and nutrient flows between  
30 terrestrial and aquatic systems (Finlay and Vredenburg, 2007). Many species have  
31 large populations and fast growth rates, occupying key roles in food webs as abundant



32 food sources whilst simultaneously shaping the functional diversity of their own prey  
33 communities (Colón-Gaud et al., 2009; Zipkin et al., 2020). Despite the ecological  
34 importance of amphibians and their diverse evolutionary histories, we lack basic natural  
35 history and geographic distribution data for a large proportion of species, with 16.4%  
36 (1,185 species) classified as Data Deficient by the IUCN – the highest proportion of data  
37 deficiency for any vertebrate class (IUCN, 2021).

38  
39 Amphibian research has grown rapidly over the last few decades, expanding from an  
40 early focus on several model species to an exploration and description of the evolution,  
41 ecology, and diversity of amphibians found globally. Researchers have developed  
42 amphibian model systems that are associated with sophisticated molecular and  
43 genomic tools based on decades of concentrated research into the molecular biology of  
44 three species – *Xenopus laevis*, *Xenopus tropicalis*, and *Ambystoma mexicanum*  
45 (Getwan and Lienkamp, 2017). Although these three model species scarcely capture  
46 the diversity of Amphibia (over 8,400 species; AmphibiaWeb 2021), they have served  
47 important roles during the last half century, providing insight into tetrapod evolution  
48 (Edholm et al., 2013; Rozenblit and Gollisch, 2020), developmental biology, molecular  
49 biology, neurobiology (Dascal, 1987; Yakushiji et al., 2009; Harland and Grainger,  
50 2011), and tissue regeneration (Nye et al., 2003; Freitas et al., 2019). Research on  
51 many other amphibian genera has made notable historical contributions to biology:  
52 e.g., *Plethodon cinereus* in behavioral ecology and development ([Dent 1942](#); [Heatwole](#)  
53 [1962](#); [Kleeberger and Werner 1982](#); [Wyman and Hawksley-Lescault 1987](#); [Kerney](#)  
54 [2011](#); [Kerney et al. 2012](#)); *Engystomops* in sexual selection (Ryan et al., 1990); *Rana* in  
55 cloning (Briggs and King, 1952); *Rana* and (Lefcort et al., 1998; Hopkins et al., 2000;  
56 Bridges, 2000; Pollet and Bendell-Young, 2000) *Acris* (Fleming et al., 1982; Clark et al.,  
57 1998; Reeder et al., 1998) in community ecology and toxicology. New tools have since  
58 promoted the emergence of more model systems from classically “non-model” species  
59 and systems, such as dendrobatid poison frogs for the neurobiology of parental care  
60 (Roland and O’Connell, 2015; O’Connell, 2020) and the molecular evolution of chemical  
61 defense (Saporito et al., 2012; Tarvin et al., 2017; Caty et al., 2019; Alvarez-Buylla et  
62 al., 2022), toxic salamanders and resistant garter snakes for co-evolution (Geffeney et

63 al., 2005; Bucciarelli et al., 2022), *Spea* for phenotypic plasticity and life-history  
64 evolution (Levis et al., 2015, 2020), and *Nanorana parkeri* for adaptation to high  
65 elevation (Sun et al., 2015, 2018; Wang et al., 2018). As we will highlight here, the  
66 growing availability of amphibian genomes and other molecular resources poises  
67 amphibian researchers to further develop other amphibians as new “model” species.

68

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

76

77 Nevertheless, understanding current amphibian biodiversity is imperative, as  
78 amphibians are undergoing severe global population declines. The modern amphibian  
79 lineage is ancient (~300 million years old; Wake and Koo, 2018) and is now the most  
80 endangered vertebrate class in the ongoing Holocene Extinction ([Stuart et al. 2004;](#)  
81 [Wake and Vredenburg 2008; Barnosky et al. 2011](#)). Roughly 3% of anuran and  
82 caudatan diversity are believed to have declined to the point of extinction since the  
83 1970s (Alroy, 2015), and an estimated 40% of extant species are threatened with  
84 extinction (IUCN, 2021). Continued research on amphibian biology, as well as efforts to  
85 share the fruits of this research through public databases, can guide efforts to mitigate  
86 the threats of habitat loss, climate change, and infectious diseases—particularly in light  
87 of opportunities presented by broad global initiatives to protect biodiversity, such as the  
88 proposal to protect 30% of the earth's surface by 2030 (Kubiak, 2020; HAC, 2021).

89

90 Given the ever-increasing accumulation of biological information, the expanding scale at  
91 which research is undertaken, and the urgent need for knowledge to combat amphibian  
92 declines, we aim to summarize the state of amphibian research to both improve  
93 awareness of existing resources and highlight gaps in knowledge. Focusing on the five

94 years from 2016 to 2020, we assess the following: 1) trends in publishing, 2) advances  
95 in amphibian conservation research, 3) trends and updates in systematics and  
96 amphibian diversity, and 4) a review of existing community resources.

97

## 98 **MATERIALS AND METHODS**

99

### 100 ***Trends in publishing.***–

101 To assess changes in the focal topics of amphibian research from 2016 to 2020, we  
102 performed a standardized literature search in Web of Science (© Copyright Clarivate  
103 2022). First, we quantified the total number of amphibian scholarly articles published  
104 from 2016 to 2020, as well as the total number within each individual year, that had the  
105 following search term in their abstract: "amphibian" OR "amphibians" OR "Caudata" OR  
106 "salamander" OR "salamanders" OR "newt" OR "newts" OR "Anura" OR "anuran" OR  
107 "frog" OR "frogs" OR "toad" OR "toads" OR "Gymnophiona" OR "caecilian" OR  
108 "caecilians". Next, we quantified the total number of amphibian scholarly articles  
109 published in those years (and within each year) in specific subfields of biology by adding  
110 additional search terms to the one above. The full list of added subfield search terms  
111 was: "behavior", "development", "diet", "cell" AND "molecular", "climate", "conservation",  
112 "ecology", "eDNA", "fossil" OR "fossils", "genetic" OR "genetics", "genomic" OR  
113 "genomics", "genetic" OR "genetics" OR "genomic" OR "genomics", "phylogenetic" OR  
114 "phylogenetics", "phylogenomic" OR "phylogenomics", "microbiome", "morphology",  
115 "physiology" and "trait" OR "traits". In addition to reporting the absolute numbers of  
116 amphibian publications from 2016 to 2020, we report the percent change in amphibian  
117 publications (overall and within each subfield) over that five-year period (number of  
118 articles published in 2020/number of articles published in 2016). We searched the total  
119 number of scholarly articles published (all publications, no search terms) in 2016 and in  
120 2020 to determine the background percent change in publication rate to serve as a  
121 reference point for the percent change in amphibian publications from 2016 to 2020. We  
122 documented which journals published the amphibian papers recovered in our 2016–  
123 2020 literature search and how many languages were represented in these  
124 publications. We also review name changes of herpetology-focused journals. In an

125 effort to examine how many publications focused on model amphibian species, we  
126 determined how many amphibian publications in each research field also mentioned  
127 *Xenopus laevis*, *Xenopus tropicalis*, OR *Ambystoma mexicanum* in their abstracts.  
128

129 ***Advances in amphibian conservation research.–***

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

156 context of major new findings on habitat loss and disease as drivers of amphibian  
157 declines between 2016 and 2020.

158

159 ***Trends and updates in amphibian diversity and systematics.–***

160 To visualize the accumulation of new species over time, we used the complete  
161 AmphibiaWeb database of new species between 2007 and 2020 (see supplemental  
162 data files) to provide a baseline comparison to identify any trend changes during 2016–  
163 2020. We joined the type localities of these new species to country and biogeographic  
164 realm using Quantum GIS (vers. 3.2, QGIS Development Team, 2021). We made a  
165 heatmap of the type localities of the new species (2016–2020) using the heatmap option  
166 in QGIS and calculated the number of new species per region using the QGIS point  
167 cluster option with radius distance set to 800 km for both the heatmap and clusters. We  
168 summarized the cumulative number of new species graphically in R (R Core Team,  
169 2021) using ggplot2 v3.3.5 (Wickham, 2016), cowplot v1.1.1 (Wilke, 2020), lubridate  
170 v1.80 (Grolemund and Wickham, 2011), rentrez v1.2.3 (Winter, 2017), tidyverse v1.3.1  
171 (Wickham et al., 2019), XML v3.99-0.8 (Lang, 2021), and included data in the  
172 phylogenetic matrix as described in the section below (“A review of community  
173 resources”). We also review higher level taxonomic changes in modern amphibians,  
174 largely based on recent phylogenomic studies.

175

176 ***A review of community resources.–***

177 We compiled a list of published amphibian genomes by searching the NCBI Genome  
178 database with the “Organism” field set to “Amphibia” and reviewing Google Scholar  
179 results for “amphibian genome”. We obtained a list of all available amphibian genetic  
180 sequences in the NCBI Sequence Read Archive (SRA; on 21 June 2021) by setting the  
181 “Organism” search field to “Amphibia” and downloading metadata files from Run  
182 Selector. To obtain metadata on the available sequences in the NCBI GenBank  
183 Nucleotide database, we used the Entrez retrieval tool (Clark et al., 2016; NCBI  
184 Resource Coordinators, 2016). GenBank data were downloaded on 27 June 2021 in 1-  
185 month batches from January 1982 to December 2020 using esearch (-db nuccore -  
186 query "amphibia [ORGN]" -mindate "\$yr/\$month" -maxdate "\$yr/\$month"), extracting the

187 following elements from the document summary: Caption, Title, CreateDate, TaxId. We  
188 used the CreateDate information as the deposit date for each sequence. Using regular  
189 expressions and lists of keywords in R, we categorized each sequence as mitochondrial  
190 DNA (title containing one or more of the words "cytochrome oxidase", "COX", "tRNA",  
191 "ND", "ribosomal RNA", "rRNA", "NADH dehydro", "mitochondri", "cyt[. ]b", "cytochrome  
192 b", "ATP8", "ATP6", "control region", "d-loop", or "cytb"), as mRNA (title containing one  
193 or more of the words "mRNA", "transcript, or "TSA:"), or genomic DNA (all other  
194 sequences). To assign a taxonomic order to each sequence in the SRA and GenBank  
195 datasets, we merged sequence metadata with the NCBI taxonomy database  
196 ([https://ftp.ncbi.nlm.nih.gov/pub/taxonomy/new\\_taxdump/](https://ftp.ncbi.nlm.nih.gov/pub/taxonomy/new_taxdump/)) using tools from the R  
197 package 'dplyr' v1.0.6 (Wickham et al., 2021). See supplemental data files for raw data.

198  
199 To count the cumulative number of species represented in the SRA database over time,  
200 we summed the number of unique species names in SRA metadata across years. We  
201 note, however, that these numbers are artificially inflated because of unspecified (e.g., "  
202 *Hyloxalus* sp. 1 WG-2019"), subspecies (e.g., "*Cryptobranchus alleganiensis bishopi*"),  
203 and hybrid (e.g., "*Hyla intermedia* x *Hyla* sp. n. DJ-2018") samples that are included in  
204 the data. To more accurately count the number of species added to NCBI databases  
205 each year, we used the *entrez\_search* function from the R package 'rentrez' v1.2.3  
206 (Winter, 2017) to query the ncbi taxonomy database by year and by Order, with  
207 additional search terms to filter out ambiguous or unspecified sequences (query =  
208 "<Order> and [SubTree] AND <year> AND species[Rank] NOT uncultured[prop] NOT  
209 unspecified[prop]").

210  
211 To quantify the representation of amphibian species in other public databases, we  
212 collated metadata from several databases that contain information about amphibians.  
213 We identified all major bioacoustic repositories by surveying relevant literature and  
214 asked leading experts in bioacoustics. For each repository, we used website searches  
215 to obtain the number of available recordings and the number of species represented  
216 (see supplemental data files). If those data were not available, we contacted the person  
217 in charge of the website to obtain the database of the recordings. For microCT data, we

218 identified all amphibian scans available on MorphoSource  
219 (<https://www.morphosource.org>, Boyer et al., 2016), DigiMorph (<http://digimorph.org>),  
220 and Phenome10K (<https://www.phenome10k.org>; see supplemental data files for  
221 MorphoSource and Phenome10K results). We downloaded Amphibian Disease Portal  
222 data on *Batrachochytrium dendrobatidis* (Bd) swabs taken and swabs testing positive  
223 for Bd, and summarized by amphibian family, by year, and by geography in R v4.1.0 (R  
224 Core Team, 2021) and plotted geographic representation of the database over time  
225 (see supplemental data files). Finally, in addition to these trait- or data type-specific  
226 databases, we also review existing large databases that provide information on  
227 amphibian morphological, ecological, and life-history traits.

228

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

236

### 237 ***Data analysis and visualization.***–

238 Plots and data formatting were performed in R v4.1.0 (R Core Team, 2021) with the  
239 following packages: `cowplot` v1.1.1 (Wilke, 2020), `dplyr` v1.0.7 (Wickham et al. 2021),  
240 `ggplot2` v3.3.5 (Wickham, 2016), `reshape2` v1.4.4 (Wickham, 2007), `stringr` v1.4.0  
241 (Wickham, 2010), `tidyr` v1.1.3 (Wickham, 2017), and `tidyverse` v1.3.1.9 (Wickham et al.,  
242 2019). For phylogenetic data formatting, analysis, and plotting we used R v4.1.0 (R  
243 Core Team, 2021) with the following packages: `ape` v5.5 (Paradis and Schliep, 2019),  
244 `geiger` v2.0.7 (Pennell et al., 2014), `phytools` v0.7.8, (Revell, 2012), and `tidyverse`  
245 v1.3.1.9, (Wickham et al., 2019).

246

## 247 **RESULTS**

### 248 **Trends in publishing**

249

250 **Research topics.–**

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

264

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

271

272 **Journals.–**

273 The peer-reviewed journals with the largest number of amphibian publications from  
274 2016 through 2020 were *PLOS One* (317), *Scientific Reports* (247), *Zootaxa* (186),  
275 *PeerJ* (174), and *Ecology and Evolution* (172; Table S2). Although our literature search  
276 recovered amphibian publications in 23 languages, the vast majority (98%) of  
277 amphibian publications recognized in our search were written in English (Table S3).

278



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

286

## 287 **Advances in amphibian conservation research**

288

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

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

297

298 Though habitat loss and degradation are undebatable drivers of amphibian declines, it  
299 is important that we interpret these data (Fig. 2) with the caveat that certain drivers are  
300 easier to measure than others, and that some drivers have only recently been studied.  
301 For example, habitat loss can be described based on observational data alone, while  
302 the low percentage of amphibian species for which genetic degradation is a  
303 documented driver of decline (50 species) can partly be attributed to the requirement of  
304 molecular work and knowledge of the species' evolutionary history for its ascertainment,  
305 which requires tools that have only recently been developed and democratized.  
306 Likewise, we know that climate change and disease threaten a large proportion of  
307 extant amphibian diversity (Warren et al., 2013; Olson et al., 2021), but these drivers  
308 have only been focal points in amphibian conservation over the past two to three

309 decades. Meanwhile, pollutants are better documented as a driver of decline, but have  
310 been a focus for at least sixty years (225 amphibian species being documented as  
311 declining due to pollutants versus 170 species for climatic factors and 149 for disease  
312 and immune functioning; Fig. 2).

313

### 314 ***Factors largely associated with endangered or extinct amphibian species.-***

315

316 When prioritizing which drivers of amphibian decline should receive limited conservation  
317 attention and resources, we should consider not only the raw count of amphibian  
318 species affected by a driver, but also which threats drive the most severe declines or  
319 tend to impact already vulnerable species. For example, while habitat alteration and  
320 loss may be the most common threat, the threat categories most closely associated with  
321 endangered or extinct species are disease and weakened immune functioning (59.11%  
322 of EN, CR, EX/EW species) and genetic degradation (56%). Thus, these two types of  
323 threats may tend to drive sudden and dramatic declines, particularly for endangered  
324 species that are also facing other stressors (Knapp et al., 2016; Fisher and Garner,  
325 2020). The overrepresentation of highly endangered or extinct species in certain threat  
326 categories makes them clear strategic targets for conservation programs.

327

### 328 **Trends and updates in amphibian diversity and systematics**

329

#### 330 ***Amphibian diversity.-***

331 From 2016 to 2020, 780 new species of amphibians were described (Fig. 3), a higher  
332 number than in the previous five years (732 species between 2011 and 2015). Most  
333 (705) of the new species described in the last five years were from the largest  
334 amphibian order, Anura; salamanders gained 66 species and caecilians gained 9. Six  
335 new genera of frogs were described based entirely on newly discovered species:  
336 *Astrobatrachus* (Vijayakumar et al., 2019, also representing the new subfamily  
337 *Astrobatrachinae*); *Blythophryne* (Chandramouli et al., 2016); *Mini* (Scherz et al., 2019;  
338 Fig. 3f); *Siamophryne* (Suwannapoom et al., 2018); *Sigalegalephrynus* (Smart et al.,  
339 2017); and *Vietnamophryne* (Poyarkov et al., 2018).

340

341 At a regional level, most new species added from 2016 to 2020 are from Latin America  
342 (40.8%), Asia (37.2%) and Africa (12.0%; Fig. 4a). Less than 10% of the new species  
343 were from the other regions: Oceania-Australia, North America and Europe. All regions  
344 had more described species between 2016–2020 than during 2011–2015, except for  
345 Oceania-Australia (22 fewer species). The countries with the most new species added  
346 from 2016 to 2020 were China (100 species), Brazil (95 species), Ecuador (67 species),  
347 Madagascar (56 species), and Peru (56 species). Regions with a high density of new  
348 species described are southern Andes of Ecuador, northern Madagascar, and southern  
349 China (Fig. 4A). If the global trend continues as in the last decade (10–11% species  
350 increase every five years), we can expect to reach 9,000 amphibian species by the end  
351 of 2024.

352

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

365

### 366 ***Amphibian systematics.***–

367 In contrast with the first 15 years of the new millennium, during which dramatic changes  
368 occurred in both our understanding of the higher-level phylogeny of amphibians and in  
369 the corresponding taxonomy, the past five years have seen much less flux. This stability  
370 has been maintained despite the transition from Sanger-sequencing-based multilocus

371 phylogenetic approaches and mitogenomic analyses to phylogenomic analyses based  
372 on new datasets of hundreds to thousands of sequenced loci (e.g., Lemmon and  
373 Lemmon, 2012; Portik et al., 2016; Hutter et al., 2021). There is complete agreement  
374 among recent phylogenomic studies regarding the family-level relationships of  
375 salamanders (Shen et al., 2013; Hime et al., 2021) and caecilians; among the recent  
376 major studies, only Hime et al. (2021) included caecilians, but their findings are in  
377 agreement with prior understanding of caecilian relationships based on Sanger data,  
378 such as Kamei et al. (2012). Even among the anurans, the various major studies have  
379 found nearly complete agreement except within Hyloidea, where some weakly  
380 supported arrangements are resolved differently across studies (e.g., Feng et al., 2017;  
381 Streicher et al., 2018; Hime et al., 2021). Even the major relationships among the 19  
382 families that comprise Ranoidea have been largely stable in recent treatments. There is  
383 now remarkable agreement and taxonomic stability in terms of the higher level  
384 phylogenetic relationships among and within all three amphibian orders.

385

386 The most significant changes in our understanding of the deep relationships of  
387 amphibians comes from phylogenomic analyses of neobatrachians. Within ranoid frogs,  
388 phylogenomic analyses support a sister relationship between the Afrobatrachia  
389 (Arthroleptidae, Brevicipitidae, Hemisotidae, Hyperoliidae) and Natatanura (Feng et al.,  
390 2017; Hime et al., 2021) in contrast to previous analyses that found a sister relationship  
391 between Microhylidae and Afrobatrachia. Within the Natatanura, these same analyses  
392 resolve a clade of the six families endemic to continental Africa (Conrauidae,  
393 Odontobatrachidae, Petropedetidae, Phrynobatrachidae, Ptychadenidae,  
394 Pyxicephalidae). This is the sister-group of all other nataturans (Feng et al., 2017; Yuan  
395 et al., 2018; Hime et al., 2021). Yuan et al. (2018) provided strong support for  
396 Ranixalidae + Nyctibatrachidae; this clade is the sister-group of other natatanurans  
397 excluding the clade of six endemic African families. No phylogenomic analyses have  
398 simultaneously included the Micrixalidae, Nyctibatrachidae, and Ranixalidae—all  
399 endemic to India. However, other analyses that combine available loci with  
400 phylogenomic datasets found a close relationship between Micrixalidae and Ranixalidae  
401 (Feng et al., 2017), suggesting that these three families might together form a clade.

402  
403 Phylogenomic analyses also are beginning to make sense of the diverse hyloid  
404 radiation. Rhinodermatidae is strongly supported as the sister to all other South  
405 American hyloids, followed by a clade of four families (Alsodidae, Batrachylidae,  
406 Cycloramphidae, Hylodidae) referred to as the Neoaustrana (Feng et al., 2017;  
407 Streicher et al., 2018; Hime et al., 2021). This is followed by the Telmatobiidae and then  
408 by a strongly supported clade of three families (Ceratophryidae, Hemiphractidae,  
409 Hylidae) referred to as the Amazorana (Feng et al., 2017; Streicher et al., 2018). All  
410 remaining hyloids form a well supported clade, though recent studies differ in the  
411 relationships among these taxa.

412

### 413 **A review of community resources**

414

#### 415 **Genomes.–**

416 A total of 28 amphibian genomes with representatives from 14 different families have  
417 been sequenced as of July 2021 (Figs. 5 and 6). Of these, 13 are assembled to  
418 chromosome-level (scaffold N50 =  $0.42 \pm 0.29$  Gb; mean  $\pm$  standard deviation), eight  
419 are scaffolded (scaffold N50 =  $0.24 \pm 0.24$  Mb), and six are contigs (contig N50 =  $880 \pm$   
420  $610$  bp) (Table S4). The first genome sequenced was that of *Xenopus tropicalis* in 2010  
421 (Hellsten et al., 2010), and it remained the sole amphibian genome until *Nanorana*  
422 *parkeri* became available in 2015 (Sun et al., 2015). Since then, sequencing of  
423 amphibian (mostly anuran) genomes has slowly but steadily increased (Fig. 6). The  
424 largest amphibian genome sequenced to date is *Ambystoma maculatum*, with an  
425 estimated diploid genome size of  $\sim 34$  Gb (Nowoshilow et al., 2018). Not surprisingly, all  
426 but one (*Nanorana parkeri*) of the chromosome-scale genomes used a combination of  
427 sequencing technologies, while those that remain as scaffolds or contigs were built  
428 using only the Illumina system short-read technologies (Table S4).

429

#### 430 **NCBI Sequence Read Archive.–**

431 The amount of next-generation sequencing data deposited into the NCBI Sequence  
432 Read Archive (SRA) since its origin in 2008 (Leinonen et al., 2011) has been steadily

433 increasing for both model and non-model amphibian species (Fig. 7a). In 2019, the  
434 amount of data available for non-model anurans surpassed that of model anurans (i.e.,  
435 *Xenopus laevis*, *X. tropicalis*). The cumulative number of SRA studies (Fig. 7b) and  
436 cumulative number of species (Fig. 7c) increased in parallel over time. By the end of  
437 2020, nearly 1000 species of amphibians (815 of which are anurans) had sequences  
438 deposited in the SRA (Fig. 5; Fig. 7c; note that these numbers are inflated because they  
439 include unspecified, subspecies, and hybrid samples; see Fig 4d).

440

#### 441 **NCBI GenBank Nucleotide database.–**

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

450

451 While the number of mtDNA sequences for anurans has risen gradually over time, the  
452 number for salamanders and caecilians has remained relatively flat (Fig. 8 mtDNA  
453 panel). In contrast, the number of nDNA and mRNA sequences added to GenBank has  
454 been stochastic and likely reflects specific large-scale sequencing projects (Fig. 8). For  
455 example, in 2012, >100,000 nDNA sequences of *Xenopus tropicalis* and *X. laevis* were  
456 deposited as part of new genome data that were beginning to be published at that time  
457 (Hellsten et al., 2010); many of these sequences were generated from Bacterial Artificial  
458 Chromosomes (BAC). Earlier BAC-generated sequences from *X. tropicalis* are  
459 responsible for the peak in 2003 of nDNA sequences (Wells et al., 2011). The notable  
460 increase in model-anuran mRNA from 2000 to 2007 is largely from the NCBI full-length  
461 cDNA project, which added *Xenopus* to its list of focal species in 2002 (Klein et al.,  
462 2002; Gerhard et al., 2004). Additional notable contributors to increases in nDNA  
463 include whole-genome shotgun sequences from *X. laevis* (Session et al., 2016) and

464 *Nanorana parkeri* (Sun et al., 2015), as well as other large-scale sequencing projects  
465 (e.g., Ultra Conserved Element sequences from *Kaloula*, Alexander et al., 2017; Fig. 8).  
466 In addition, several notable increases in non-model mRNA and nDNA sequence  
467 deposition likely are related to other new genomes (e.g., *Rana catesbeiana* in 2017  
468 [Hammond et al., 2017]; *Microcaecilia unicolor* in 2019 and *Geotrypetes seraphini* in  
469 2020, both from the Vertebrate Genomes Project,  
470 <https://vertebrategenomesproject.org/>; Koepfli et al. 2015) and transcriptomes (e.g.,  
471 *Bombina variegata variegata* in 2016, *R. catesbeiana* in 2017; both in Transcriptome  
472 Shotgun Assembly [TSA] formats, which are primarily built from short-read technology  
473 [Suzuki et al., 2016; Nürnberger et al., 2016]).

474

#### 475 **Acoustic data.–**

476 We identified eight major repositories that collectively contain 156,514 amphibian  
477 recordings (Table 1): Macaulay Library, Fonozoo, La Sonothèque, AmphibiaWeb,  
478 Fonoteca Neotropical Jacques Vieliard, Anfibios del Ecuador BLOWEB, Australian  
479 Museum FrogID Project, and Chinese National Specimen Resource Sharing Platform.  
480 Collectively, these call repositories contain calls for 1,985 unique species from 45  
481 anuran families and four salamander families. The anuran families Pipidae (41 species),  
482 Mantellidae (232 species), Myobatrachidae (133 species), Scaphiopodidae (seven  
483 species), and Rhinophrynidae (one species) each have calls recorded for more than  
484 50% of the family's species (Fig. 5). Fonozoo contains the highest number of species  
485 represented, although FrogID contains the greatest number of recordings (Table 1). Of  
486 note among these databases are the Fonoteca Neotropical Jacques Vieliard (FNJV),  
487 which is the largest public and institutional online audiovisual repository in Latin  
488 America, and the Australian Museum FrogID Project, which is Australia's first national  
489 community-science frog identification initiative.

490

#### 491 **CT-scan data.–**

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

495 of genera), 362 caudatan specimens representing 184 species (in 66 genera; 97%), and  
496 55 gymnophionan specimens representing 40 species (in 32 genera; 97%; Fig. 5).  
497 Many of these data were generated as part of the NSF openVertebrate (oVert)  
498 Thematic Collections Network. In addition, there are a few CT-scans of extinct crown-  
499 group amphibians, such as 26 fossils of *Beelzebufo* deposited in 2015. MorphoSource  
500 also now houses most, if not all, of the CT-scan media from the Digital Morphology  
501 project (DigiMorph; [www.digimorph.org](http://www.digimorph.org)). DigiMorph began in the early 2000s and still  
502 has CT-scan media available from 25 anuran species (in 21 genera), 28 caudate  
503 species (in 16 genera; plus one extinct salamander), and seven caecilian species (in  
504 seven genera).

505  
506 Phenome10K also hosts 3D mesh files of amphibian skulls associated with several  
507 recent publications (Marshall et al., 2019; Fabre et al., 2020; Bardua et al., 2021). As of  
508 October 2021, the website ([www.phenome10k.org](http://www.phenome10k.org)) makes available 3D mesh files of  
509 skulls for 105 anuran species (in 94 genera), 104 caudate species (in 51 genera), and  
510 seven gymnophionan species (in seven genera). In many cases, the image stacks for  
511 these specimens also are available on MorphoSource.

512

### 513 ***Other trait databases.–***

514 From 2016 through 2020, two large amphibian trait databases were published:  
515 AmphiBIO (Oliveira et al., 2017) and a Colombian anuran database (Mendoza-Henao et  
516 al., 2019). AmphiBIO (Oliveira et al., 2017), the largest species-level amphibian trait  
517 database that can be readily downloaded, contains 6,776 species and a broad range of  
518 ecological and life-history traits (e.g., microhabitat, diet, activity time, clutch size), but  
519 the matrix completeness is only 21%. Although the Colombian anuran database is much  
520 more complete, it contains morphological data from fewer species (239), which  
521 represent 38% of Colombian anuran diversity. Of note, the Colombian anuran database  
522 includes individual-level data for 4,623 museum specimens, with a range of 1 to 118  
523 individuals (median = 8) measured per species. Three other existing databases were  
524 identified: one includes conservation, ecological, and life-history traits of 86 European  
525 species (Trochet et al., 2014); another, the Anuran Traits of the United States (ATraiU,



526 Moore et al., 2021), contains ecological, morphological, and life history data of 106  
527 anuran species, representing 91% of frog species in the USA (AmphibiaWeb, 2021).  
528 Finally, NSF-funded VertNet (<http://vertnet.org/>) aggregates individual-level amphibian  
529 trait data from records published by museum collections (e.g., body length, mass) that  
530 are tied to the location where individuals were collected and sometimes other traits  
531 (e.g., lifestage, sex). At the conclusion of 2020, VertNet had 1,261 individual records of  
532 amphibian body lengths (covering 897 species) and 455 individual records of amphibian  
533 body mass (covering 337 species).

534

### 535 ***Online portals for amphibians: AmphibiaWeb.***–

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

548

549 Usage of AmphibiaWeb (tracked by Google Analytics) continues to be strong, averaging  
550 28,000 users per month (between June and November 2021) from 215 countries or  
551 sovereignties. Of the over 35% of users who shared demographic data, users trended  
552 female (54.5%) and young (33% 18–24 years old, 27% 25–34 years old). The site  
553 averaged 1.74 million page views per year in the last five years, with a high of 2.5  
554 million page views during the pandemic of 2020 (page views are a measure of the  
555 number of times a page has been visited even in a single session of a single user).

556

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

566

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

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

577

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

586

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

593

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

600

601 Anfibios del Ecuador has high visitor traffic (data from Google Analytics). Between June  
602 and November 2021, for example, it received approximately 16,000 monthly visitors  
603 from 106 countries or sovereignties. 51% of visitors shared demographic data, of which  
604 72% were women and 28% men. Younger age groups are the most frequent visitors:  
605 18–24 years old represented 37% of the visits, followed by 25–34 years (23%).

606

#### 607 ***Online portals for amphibians: AmphibiaChina.–***

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

616

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

630

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

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

636

637 ***Online portals for amphibians: IUCN Red List.–***

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

647

648 **Online portals for amphibians: Amphibian Ark, Conservation Needs, and**  
649 **Conservation Evidence.–**

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

660

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

665

666 **Online portals for amphibians: Amphibian Disease Portal.–**

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

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

686

## 687 **Discussion**

688

### 689 ***Current picture and future projections for amphibian biodiversity.***–

690 The pace of amphibian species descriptions continues unabated, with ~150 new  
691 species being described each year. However, our picture of amphibian diversity is  
692 changing in some predictable ways. The majority of new species are being described in  
693 Latin America (Vasconcelos et al., 2019) and Asia and specifically are concentrated in  
694 diverse families such as the Strabomantidae and Megophryidae. For example, the  
695 number of new species listed on AmphibiaChina increased from just four new species in  
696 2015 (Murphy, 2016), to 41 new species reported in 2020 (Chen et al., 2021).  
697 Furthermore, our understanding of the relationships among amphibian families remains  
698 largely stable, however there remain several diverse lineages, including both  
699 subfamilies and genera, for which thorough and synoptic revisionary phylogenetic  
700 studies are needed.

701

702 On the other end of the spectrum from the description of previously unknown amphibian  
703 diversity, the study of amphibian declines has continued to be a central theme in  
704 amphibian biology. However, though the role of habitat loss and modification as  
705 principal drivers of amphibian declines is not a new finding (IUCN, 2021), relative to  
706 their importance these pivotal drivers have been deemphasized in amphibian  
707 conservation research (Green et al., 2020). Even still, over the last five years large-  
708 scale meta-analyses have confirmed several basic expectations of the repercussions of  
709 habitat degradation for amphibians : (i) land use change decreases amphibian species

710 richness (Cordier et al., 2021), (ii) amphibian abundance declines towards the edge of  
711 fragmented habitat (Schneider-Maunoury et al., 2016), and (iii) habitat conversion tends  
712 to hurt specialist amphibians, driving the phylogenetic homogenization of communities  
713 (Thompson et al., 2016; Nowakowski et al., 2018a). Lamentably, the most amphibian-  
714 rich communities undergo the most species loss and turnover after habitat modification,  
715 and communities fail to recover completely over time (Thompson and Donnelly, 2018;  
716 Goldspiel et al., 2019; Cordier et al., 2021). Models of the impact of habitat loss and a  
717 'middle of the road' climate and development scenario predict that 10% of known  
718 amphibians will be lost by 2070 (Powers and Jetz, 2019). We cannot prevent the loss of  
719 amphibian species to climate change altogether, but protecting areas from further land  
720 use change will be critical to mitigating further losses (Chen et al., 2017).

721 Among diseases driving amphibian declines, a primary concern over the past five years  
722 has continued to be chytridiomycosis, the disease caused by the fungal pathogens  
723 *Batrachochytrium dendrobatidis* (Bd) and *B. salamandrivorans* (Bsal). Some long-term  
724 monitoring projects of Bd-exposed amphibian species or communities are reaching their  
725 tenth or twentieth year, making large-scale meta-analyses possible. Bd has now been  
726 detected in 55% of amphibian species and 69% of countries sampled (Olson et al.,  
727 2021), contributing to declines across many families (Scheele et al., 2019)—though  
728 disentangling the extent of its impact is still challenging (Lambert et al., 2020). In some  
729 sites, populations declined or were extirpated synchronously with Bd epizootics, and  
730 have not recovered under the burden of Bd and additional stressors (Adams et al.,  
731 2017b; Bosch et al., 2021). Other populations may be recovering, despite the continued  
732 presence of Bd (Knapp et al., 2016; Seimon et al., 2017; Voyles et al., 2018). The  
733 broader impacts of amphibian declines on ecosystems are largely unknown, though  
734 steep amphibian declines in Panama appear to have induced a trophic cascade, driving  
735 declines in snake diversity and body condition (Zipkin et al., 2020).

736 Species recovering after Bd-associated declines appear to have altered their response  
737 to Bd (Palomar et al., 2016; Knapp et al., 2016; Kosch et al., 2019), with instances of  
738 positive directional selection documented in the major histocompatibility complex (MHC)  
739 and other immunogenes (Savage and Zamudio, 2016; Kosch et al., 2016; Voyles et al.,

740 2018), while species continuing to decline in the wild remain susceptible to Bd despite  
741 prolonged exposure (Catenazzi et al., 2017). Such continued declines might be  
742 particularly common in systems with additional stressors like climate change, pollution,  
743 and habitat fragmentation, which synergistically impair amphibians' capacity to respond  
744 to any individual stressor (Nowakowski et al., 2016; Scheele et al., 2016; Rollins-Smith,  
745 2017; Cohen et al., 2017, 2019; Adams et al., 2017a; Greenspan et al., 2017; McCoy  
746 and Peralta, 2018).

747 Unlike Bd, which is no longer causing mass amphibian die-offs in most regions, Bsal  
748 continues to drive steep local declines and extirpations (Schmeller et al., 2020; Thein et  
749 al., 2020; Vences and Lötters, 2020). It has spread across Northern Europe, even in  
750 areas with low host densities, causing collapses in susceptible species (Spitzen-van der  
751 Sluijs et al., 2016; Schmidt et al., 2017; Stegen et al., 2017). Alarming, we do not yet  
752 have evidence for acquired immunity to Bsal, and Bsal pathogenicity has not attenuated  
753 over time (Stegen et al., 2017). Herpetologists continue to monitor for Bsal elsewhere in  
754 the world, as it could drive devastating biodiversity decline in places like North America,  
755 which contains half of global salamander diversity (Richgels et al., 2016; Iwanowicz et  
756 al., 2017; Parrott et al., 2017; Yap et al., 2017; Waddle et al., 2020). Continued  
757 widespread surveillance for Bd and Bsal, and platforms promoting the accessibility of  
758 these data (see Community resources section), will help us improve our capacity to  
759 mitigate the impacts of these pathogens through monitoring, policy, and management.  
760

### 761 ***Challenges and opportunities in amphibian research.***–

762 Large amphibian genome sizes remain one of the greatest challenges in amphibian  
763 research. The size and repetitive content of amphibian genomes has hindered whole-  
764 genome sequencing efforts (Sun et al., 2020). For comparison, >500 fish genomes  
765 (Randhawa and Pawar, 2021; average size of 808 Mb) and >300 bird genomes have  
766 been sequenced (Feng et al., 2020; average size of 1.13 Gb, (Randhawa and Pawar,  
767 2021), yet only 28 amphibian genomes are available. The average sizes of sequenced  
768 amphibian genomes (excluding contig-level assemblies (4.03 Gb for Anura [N = 18],  
769 33.99 Gb for Caudata [N = 1], 4.75 Gb for Gymnophiona [N = 3]) are below the average  
770 amphibian genome sizes (4.28 Gb for Anura, 35.95 Gb for Caudata, 6.44 Gb for



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

776

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

789

790 Although there is a wealth of accessible amphibian data online (Fig. 5), we still lack  
791 basic natural history and phenotypic data for a large portion of amphibian genera and  
792 families. For example, although most anuran families have calls recorded, certain  
793 families that contain species thought or known to call (Ceuthomantidae, Ranixalidae,  
794 Odontobatrachidae, Conrauidae, Petropedetidae, Brevicipitidae, and Heleophrynidae)  
795 have no call records in the databases examined here and many other families  
796 (Arthroleptidae, Craugastoridae, Megophryidae, Micrixalidae, Phrynobatrachidae,  
797 Pyxicephalidae, and Telmatobiidae) have calls recorded for fewer than 10% of species.  
798 Interviews conducted at two herpetology conferences found that nearly 80% of  
799 herpetologists did not catalog collected sound data because they did not have the time  
800 or expertise, or felt that the efforts were unnecessary (Dena et al., 2020). Additionally,  
801 although all amphibian families (except Chikilidae) have publicly available CT-scans for

802 at least one species, most families (41 of 74 total) have CT-scans available for fewer  
803 than one quarter of their family's species. Ecological and natural history databases often  
804 lack information for many genera and families (e.g., ~80% missing data in AmphiBIO;  
805 Oliveira et al., 2017), and Paluh et al. (2021) recently found that 161 of 456 total frog  
806 genera lacked any dietary records from the wild. Furthermore, while data exist for Bd  
807 and Bsal for many amphibian families, much of those data are not yet in a centralized  
808 database like the Amphibian Disease Portal. These data deficits and the lack of  
809 integration among databases make comparative work and synthetic studies difficult,  
810 putting amphibian research at a disadvantage compared to other tetrapod clades with  
811 more complete databases (e.g., EltonTraits for birds and mammals; Wilman et al.,  
812 2014). Increasing natural history studies, and storing natural history data in publicly  
813 accessible, easy-to-download databases are necessary aids to amphibian research and  
814 conservation. In addition, it is crucially important to link data and specimens across  
815 repositories so that researchers and policy-makers can integrate and track different data  
816 types (e.g., DNA sequences, CT-scans, audio recordings, pathogen data) for the same  
817 individual or population.

818

819 ***Publication biases highlight obstacles to research progress.–***

820 Inequality in the demography of amphibian research can sideline diverse and locally  
821 relevant viewpoints that would otherwise aid in tackling amphibian research challenges.  
822 Numerous studies published from 2016 to 2020 have shown that, as in other STEM  
823 (science, technology, engineering, and mathematics) disciplines (Huang et al., 2020;  
824 Urbina-Blanco et al., 2020; Maas et al., 2021), female authors are still under-  
825 represented in peer-reviewed publications of amphibian biology (Rock et al., 2021).  
826 Nevertheless, the proportion of female authors in herpetological research has increased  
827 over time, from 8% in 1973–1982, 15% in 1983–1993 (Wilson, 1998) to 31% in 2010–  
828 2015 and 33% in 2016–2019 (Rock et al., 2021), at a remarkably constant rate  
829 (although we note that these two studies considered different datasets and journals).

830

831 Several factors likely underlie these patterns of underrepresentation of female authors.  
832 Within herpetology, papers with male first or last authors are less likely to have female

833 co-authors than papers with female first or last authors (Salerno et al., 2019; Rock et al.,  
834 2021; Grosso et al., 2021). The trend of increasing numbers of women leaving  
835 academia as their career progresses (the “leaky pipeline”) might partially explain the  
836 discrepancy in the relatively faster growing proportion of female first versus last authors  
837 found by Rock and colleagues (2021). A low proportion of senior female academics  
838 affects many aspects of publishing in herpetology through gender inequity of editorial  
839 boards, leadership positions, and committees of professional societies (Liévano-Latorre  
840 et al., 2020; Chuliver et al., 2021; Grosso et al., 2021). Although we lack a concrete  
841 understanding of the primary barriers to authorship inequality in amphibian research  
842 specifically, many are likely consistent with barriers and bias found in other STEM  
843 disciplines, such as male homophily (Helmer et al., 2017; Salerno et al., 2019; Rock et  
844 al., 2021; Grosso et al., 2021), attrition of women and underrepresented groups  
845 (Chuliver et al., 2021; Rock et al., 2021), bias in peer review (Silbiger and Stubler,  
846 2019), and the culture of the geographic location of the authors (Fox et al., 2018; Huang  
847 et al., 2020; Maas et al., 2021). In addition, region-specific gaps in amphibian data (e.g.,  
848 trait data) indicate geographic bias in amphibian research, further accentuating the  
849 importance of increased support for amphibian research and equitable collaborations  
850 worldwide.

851  
852 Double-blind reviews are a potential solution to minimize bias during the reviewing  
853 process (Tomkins et al., 2017) and some herpetological journals are currently  
854 transitioning to double-blind reviews: e.g., *Revista Latinoamericana de Herpetología*  
855 and *Herpetological Conservation and Biology*, *The Herpetological Journal (UK)*,  
856 *Ichthyology & Herpetology*. Amphibian research would benefit from further analyses of  
857 amphibian-specific publishing inequalities for identities beyond gender and  
858 assessments of whether changing publishing practices can affect change.

859 ***Using centralized portals for amphibian biology to translate research into policy***  
860 ***and management.***—

861 Amphibian conservation biology is a crisis discipline: the urgency of amphibian declines  
862 means that difficult decisions must be made even in cases with deep uncertainty. We no

863 longer speculate on the prospect of a sixth mass extinction but rather document its  
864 progress (Wake and Vredenburg, 2008; Ceballos et al., 2015). One of the motivations  
865 for this review is to help consolidate major findings, trends, and public databases that  
866 can have immediate impact on policy and management. We urge for increased adoption  
867 of adaptive management practices by relevant agencies, non-governmental  
868 organizations (NGOs), and research units, where decisions are made under best  
869 current information, closely monitored, and then actions are updated accordingly  
870 (Meredith et al., 2016; Berger et al., 2016; Grant et al., 2016; Adams et al., 2018). Here,  
871 we highlight public databases for molecular (NCBI), acoustic (Table 1), phenotypic and  
872 natural history data (Trochet et al., 2014; Oliveira et al., 2017; Mendoza-Henao et al.,  
873 2019; Moore et al., 2021), as well as expert-curated reference databases  
874 (AmphibiaWeb, AmphibiaWebEcuador, AmphibiaChina, IUCN Red List, and  
875 Conservation Evidence), that can be vital tools in designing and updating adaptive  
876 management strategies by centralizing and collating information relevant to  
877 conservation-oriented policy and management from a diffuse literature.

878 An example of an exciting new opportunity to deploy these public databases in the  
879 interests of more effective, scientifically-informed conservation is provided by global  
880 30x30 initiatives—commitments by governments to protect 30% of the Earth's land and  
881 oceans by 2030 (Kubiak, 2020; HAC, 2021). If new 30x30 protected areas are to serve  
882 amphibian conservation needs, sites with coverage of amphibian functional,  
883 phylogenetic, and taxonomic diversity should be selected, a process greatly facilitated  
884 by centralized databases. Additionally, sites that alleviate cataloged decline drivers  
885 (e.g., selecting sites that create climate corridors to protect species threatened by  
886 climate change) could be a focus (Gonçalves et al., 2016; Subba et al., 2018; Zellmer et  
887 al., 2020). In cases where Bd has been detected, *in situ* mitigation has had such limited  
888 success that the most robust strategy for improving amphibian outcomes may be to  
889 address other synchronous stressors (Knapp et al., 2016; Fisher and Garner, 2020). For  
890 example, restoring or creating water features, promoting the development of  
891 microhabitat to buffer amphibians against climate change, removing invasive species,  
892 managing pollution from activities like mining, and addressing barriers to amphibian  
893 movement are all methods that can promote amphibian population health (Reeves et

894 al., 2016; Nowakowski et al., 2016, 2018b; Hamer, 2016; Laufer and Gobel, 2017;  
895 Arntzen et al., 2017; Magnus and Rannap, 2019; Goldspiel et al., 2019; Mayani-Parás  
896 et al., 2019; Simpkins et al., 2021).

### 897 **Conclusion.–**

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

### 911 **DATA ACCESSIBILITY**

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

915 A Spanish-language translation of the manuscript and Chinese and French translations  
916 of the abstract are available in our supplementary materials. The Spanish-language text  
917 was first machine-translated with DeepL and then human-verified by ES, SR, and AC;  
918 the Chinese translation was conducted by JC (车静) and Yunke Wu (吴耘珂); and the  
919 French-language text was first machine-translated with DeepL and then human-verified

920 by AC. We hope that these translations make our work more accessible to a broad  
921 audience and that our open-access, human-verified translation can be used in training  
922 data sets to further improve machine translation technologies.

## 923 **CONFLICT OF INTEREST STATEMENT**

924

925 The authors declare no conflict of interest.

926

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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\_nucore-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*

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*

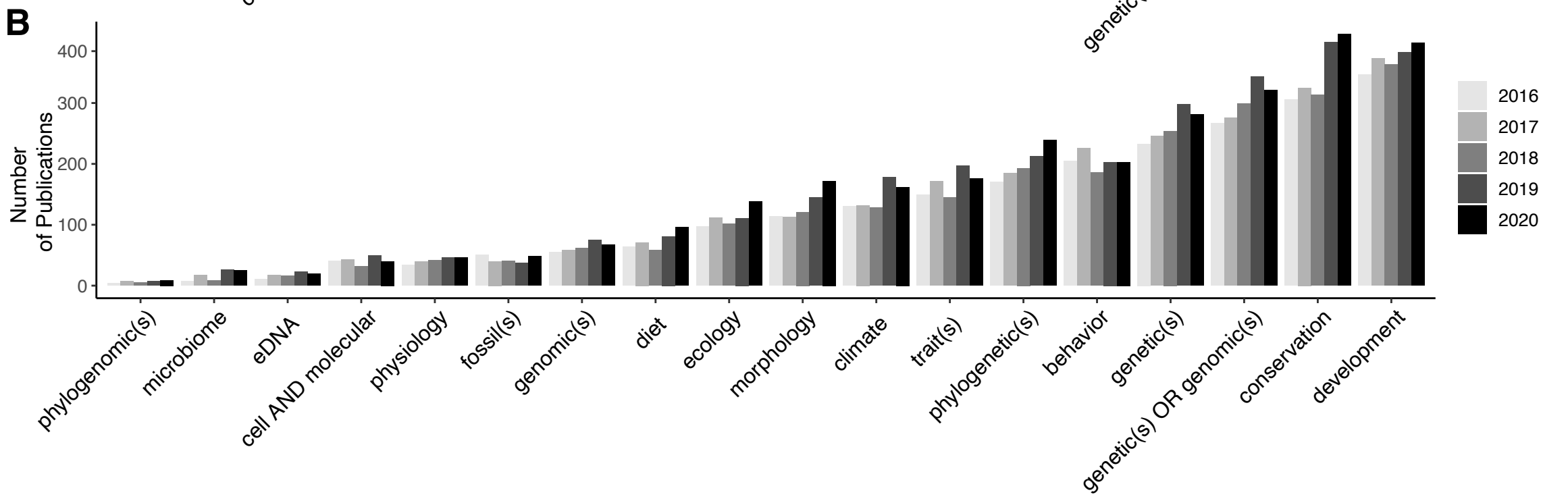
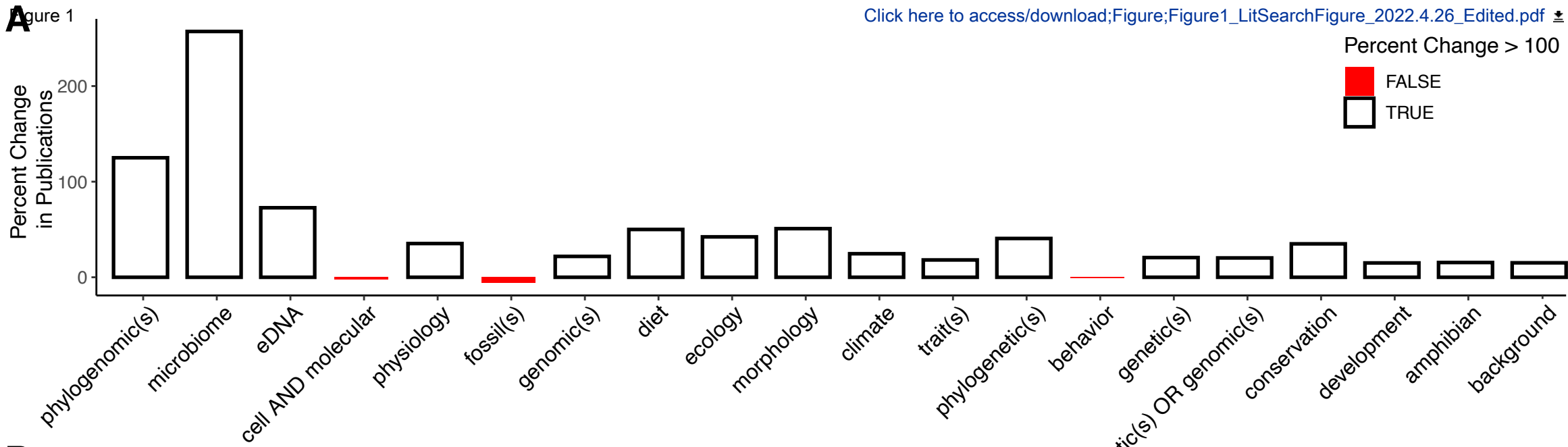
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Table 1. The most comprehensive amphibian call databases available online. For geographic regions, Af = African, Au = Australians, Ne = Nearctic, Nt=neotropical, Or = Oriental, Pa= Palearctic. Unless otherwise noted, all recordings are available for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







### Major threats to amphibian orders

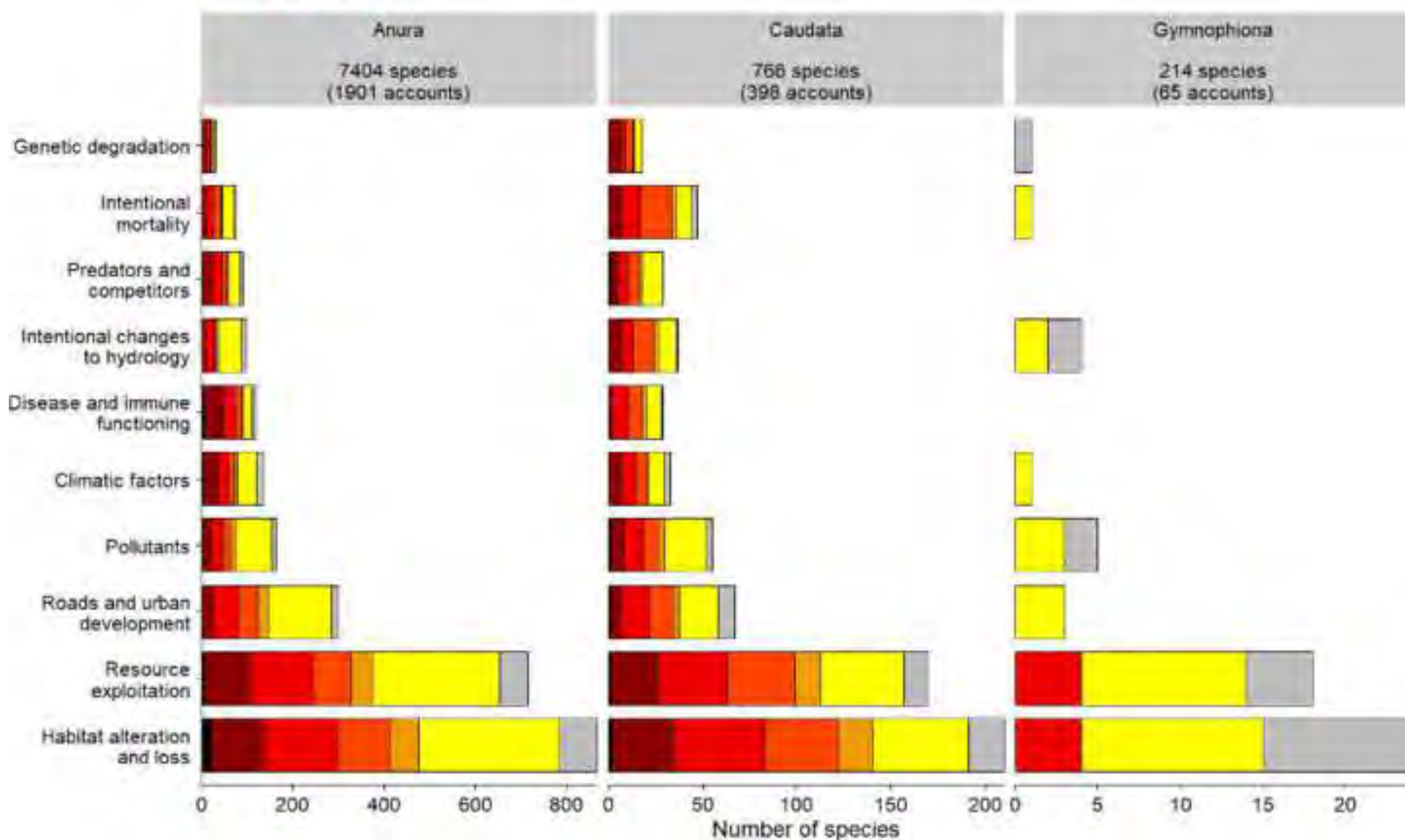


Figure 3

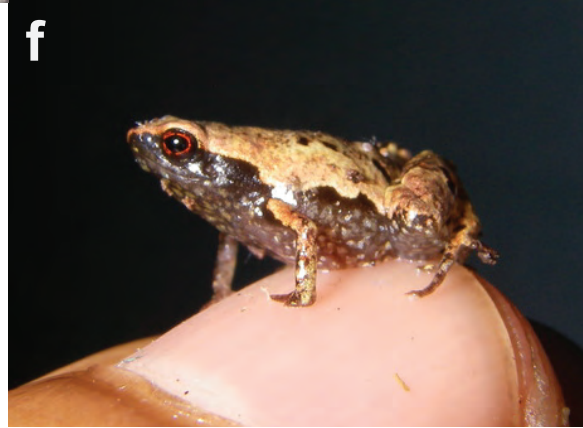
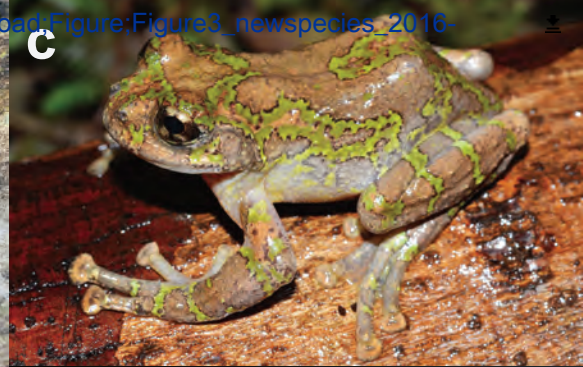
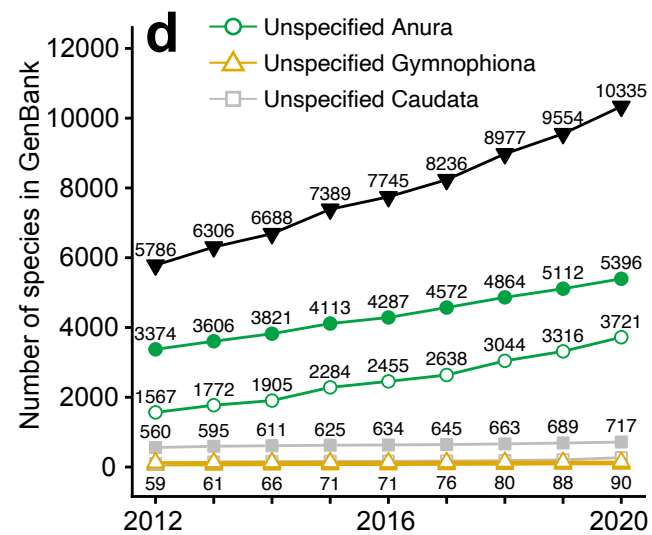
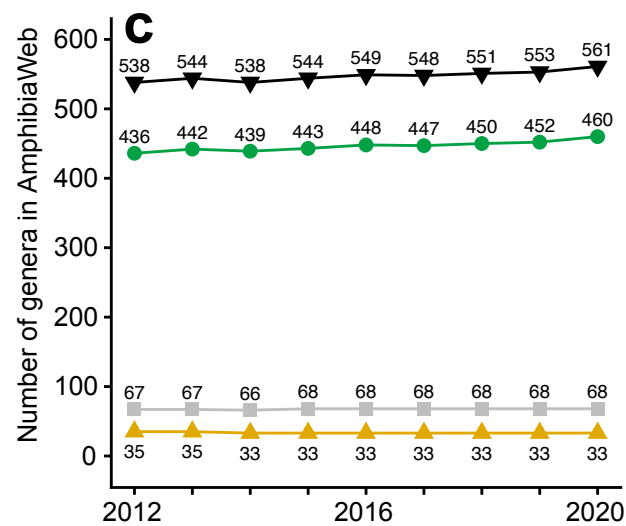
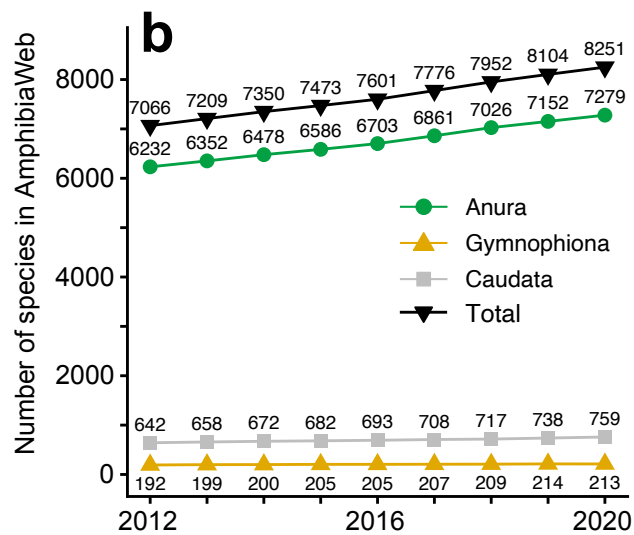
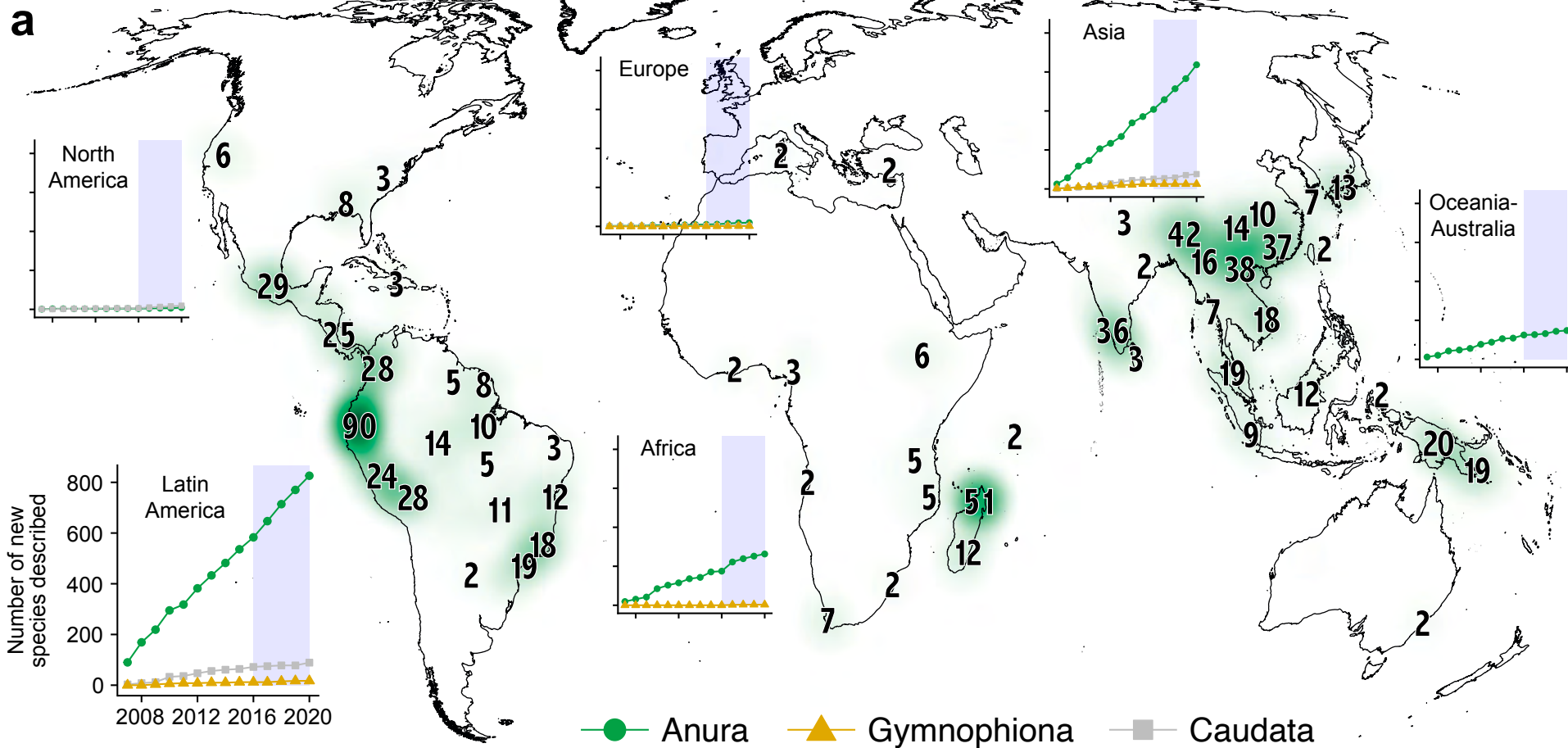


Figure 4

[Click here to access/download;Figure;Figure4\\_2021-12-11.pdf](#)





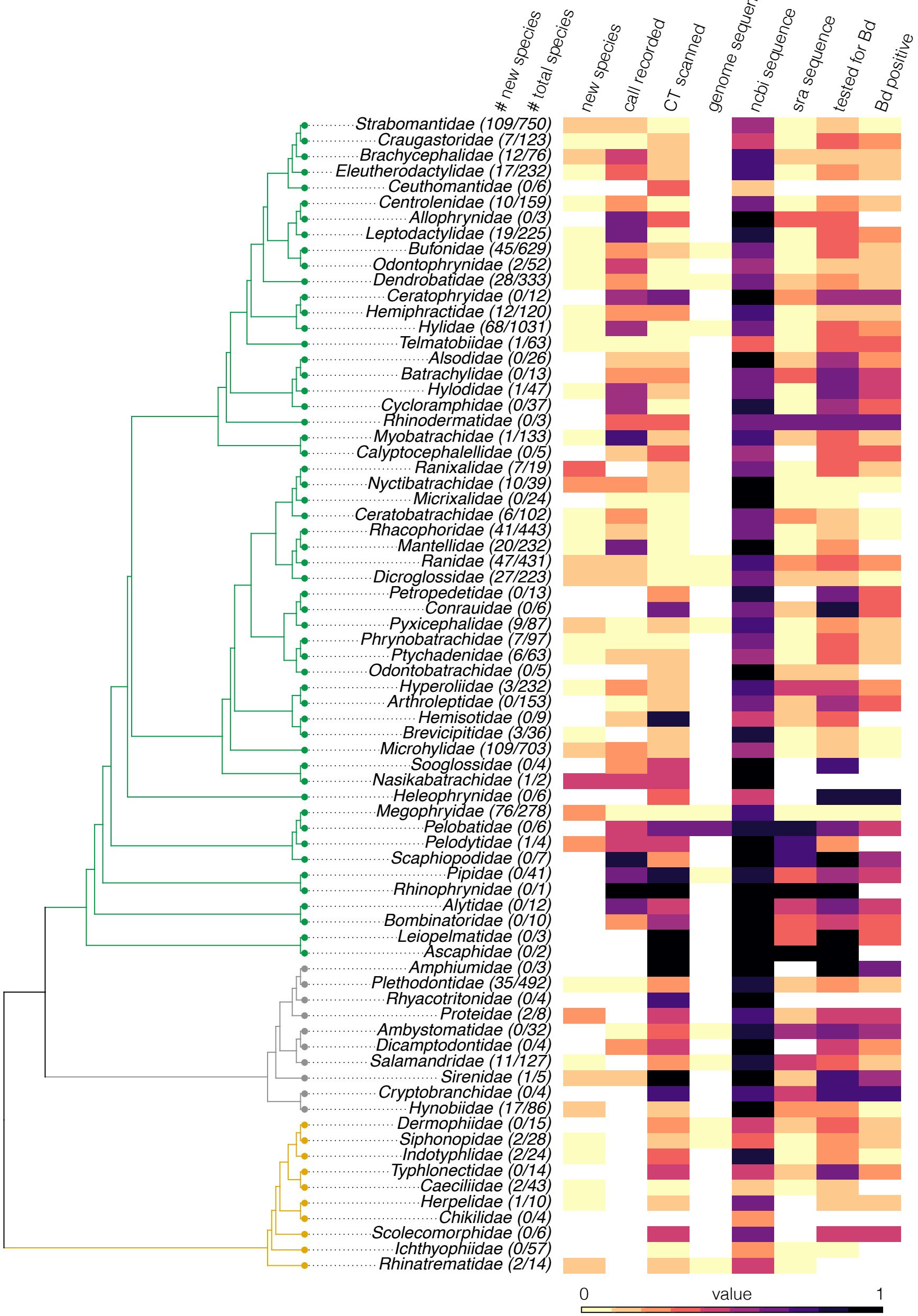
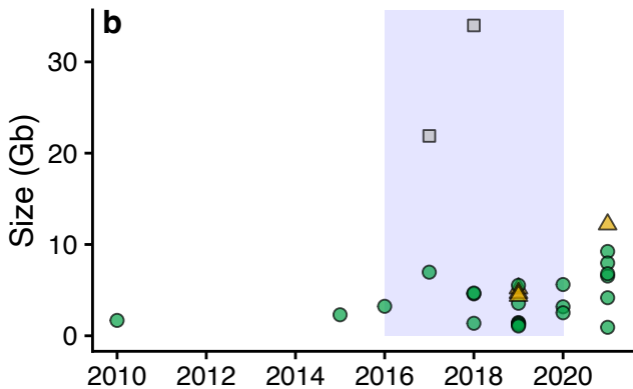
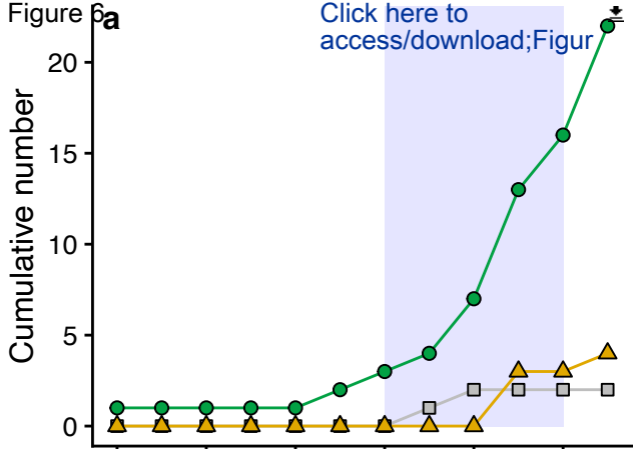
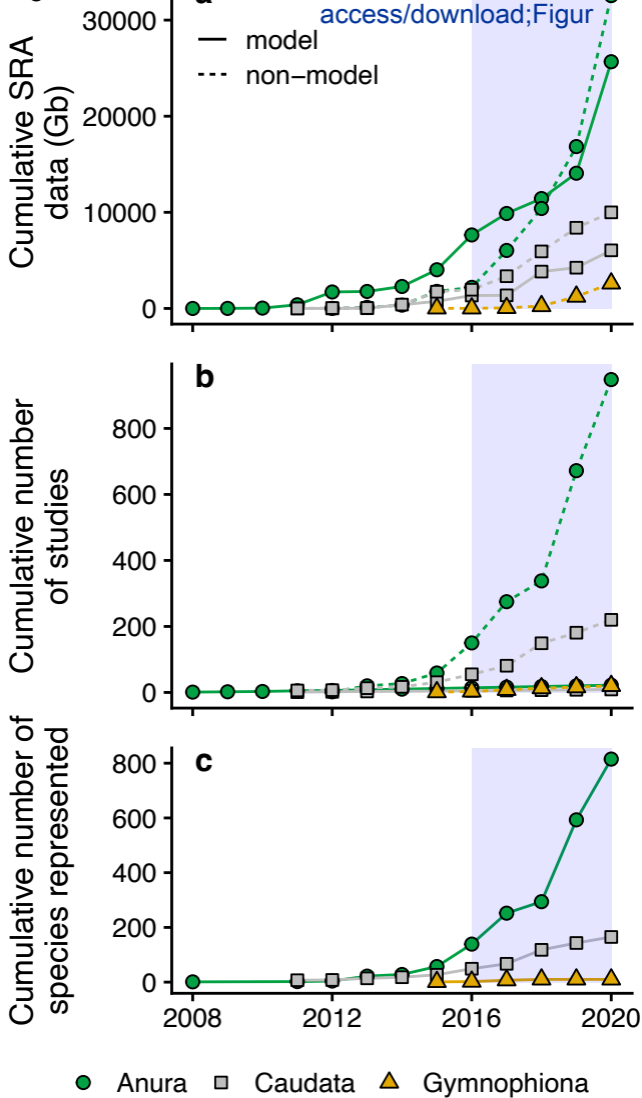


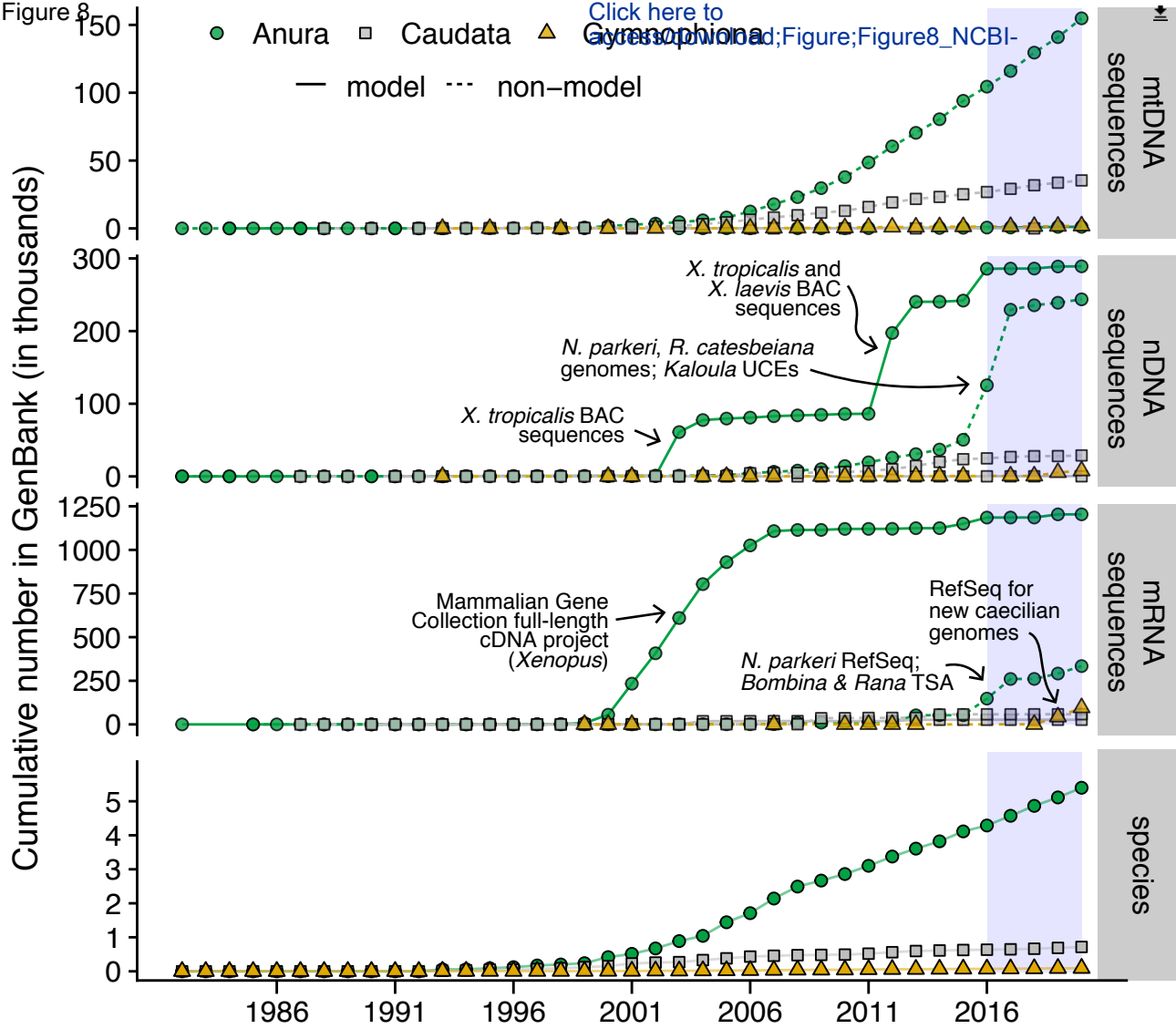
Figure 6



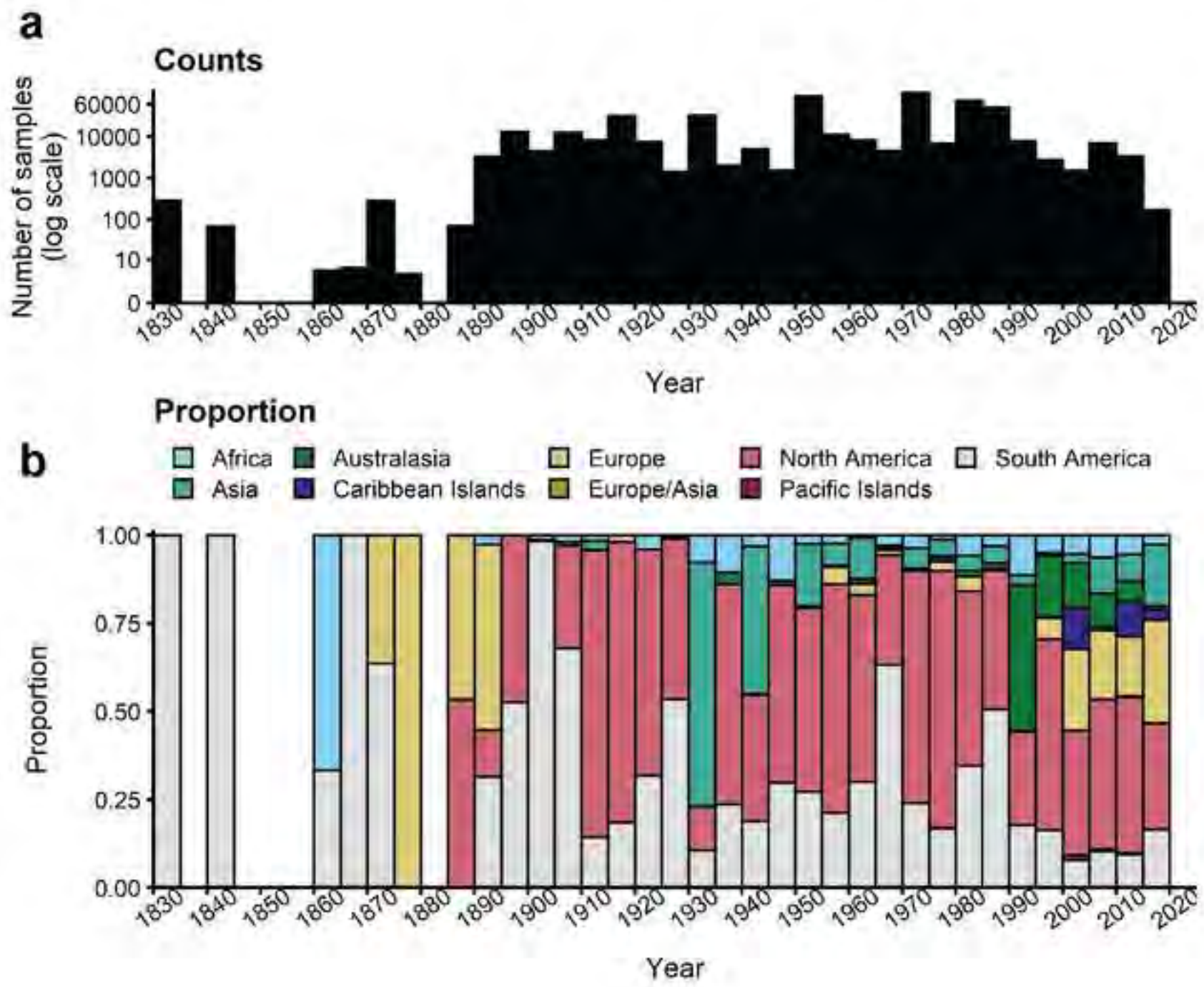
● Anura    □ Caudata    ▲ Gymnophiona

Figure 7









TableS1 - Literature Search Results

Search term	Category	2016	2017	2018	2019	2020	2016-2020_Totals	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	14	94.1176	0.46082
"ecology"	ecology	97	112	102	111	138	560	30	142.268	0.53571
"microbiome"	microbiome	7	17	8	26	25	83	18	357.142	1.20481
"phylogenetic" OR "phylogenetics"	phylogenetic(s)	170	185	193	212	239	999	17	140.588	1.70170
"climate"	climate	130	132	128	178	162	730	13	124.615	1.78082
"conservation"	conservation	306	325	313	400	413	1757	34	134.967	1.93511
"diet"	diet	64	71	58	81	96	370	8	150	2.16216
"trait" or "traits"	trait(s)	149	171	145	197	176	838	19	118.120	2.26730
"behavior" OR "behaviour"	behavior	205	226	186	203	203	1023	30	99.0243	2.93255
"eDNA"	eDNA	11	17	16	23	19	86	3	172.727	3.48837
"genetic" OR "genetics"	genetic(s)	233	246	254	298	281	1312	62	120.600	4.72560
Amphibian_Base	Amphibian_Base	2468	2598	2592	2701	2849	13208	629	115.437	4.76226
"morphology"	morphology	114	113	121	145	172	665	36	150.877	5.41353
"genetic" OR "genetics" OR "genomic" OR "genomics"	genetic(s) OR genomic(s)	267	276	299	343	321	1506	84	120.224	5.57768

"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	34	37	36	38	39	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	27	28	28	31	31	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
PALAEODIVERSITY 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	Bufo	Bufo bufo	Chromosomal	0.64	Gb	6.54	10x, Arima HiC, Bionano, PacBio
Anura	Bufo	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	Bufo	Rhinella marina	Scaffolded	0.168	Mb	4.681	PacBio, Illumina

Anura	Scaphiopodi dae	Scaphiopus couchii	Contig	362	bp	1.45	Illumina
Anura	Scaphiopodi dae	Scaphiopus holbrookii	Contig	514	bp	1.353	Illumina
Anura	Scaphiopodi dae	Spea bombifrons	Contig	522	bp	1.208	Illumina
Anura	Scaphiopodi dae	Spea multiplicata	Scaffolded	0.071	Mb	1.07	Illumina, PacBio, Oxford Nanopore
Anura	Pipidae	Xenopus laevis	Chromoso mal	0.155	Gb	3.23	Illumina, PacBio (unclear if they were both used in latest assembly)
Anura	Pipidae	Xenopus tropicalis	Chromoso mal	0.154	Gb	1.685	PacBio, Illumina
Caudata	Ambystoma tidae	Ambystoma mexicanum	Chromoso mal	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	Salamandri dae	Pleurodeles waltl	Contig	1136	bp	21.89	Illumina
Gymnoph iona	Dermophiid ae	Geotrypetes seraphini	Chromoso mal	0.27	Gb	5.187	10x, Dovetail HiC, Bionano, PacBio
Gymnoph iona	Ichthyophii dae	Ichthyophis bannanicus	Contig	740	bp	12.2	Illumina
Gymnoph iona	Siphonopid ae	Microcaecilia unicolor	Chromoso mal	0.376	Gb	4.69	10X, Arima HiC, BioNano, Dovetail Genomics, PacBio
Gymnoph iona	Rhinatrema tidae	Rhinatrema bivittatum	Chromoso mal	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	<a href="https://www.ncbi.nlm.nih.gov/assembly/GCA_905336975.1">https://www.ncbi.nlm.nih.gov/assembly/GCA_905336975.1</a>

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



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

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

TableS5 - Family-level Phylogenetic Heat Map Data

Family	Order	Gen era	Spe cies	new_ speci es	Prop Sp_N ew	Prop Sp_ Calls	PropS p_CTscan	PropSp _genomes	PropS p_ncb	Prop Sp_sra	PropSp_Di seaseTest ed	PropSp_D iseasePos itive
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	0.66667	0.41667	0	1	0.4167	0.66667	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	0.8534	0.3658566	0.58536585	0.48780488
Calyptoccephalellidae	Anura	2	5	0	0	0.2	0.4	0	0.6	0	0.4	0.4
Myobatrachidae	Anura	21	133	1	8	0.007518609	0.774436093	0.16541350	0.79699248	0.165413586	0.33834586	0.18796992
Rhinodermatidae	Anura	2	3	0	0	0.33333	0.33333	0	0.66667	0.66667	0.66667	0.66667
Cycloramphidae	Anura	3	37	0	0	0.540546	0.08108	0	0.8646	0.0505	0.54054054	0.32432432
Hylodidae	Anura	4	47	1	6	0.021276468	0.59574468	0.10638298	0.63829787	0.08510638	0.61702128	0.4893617
Batrachylidae	Anura	4	13	0	0	0.23076923	0.23076923	0	0.6152	0.3838	0.61538462	0.46153846
Alsodidae	Anura	3	26	0	0	0.15615	0.19230769	0	0.9232	0.1515	0.57692308	0.26923077
Dendrobatiidae	Anura	20	333	28	4084	0.08924	0.24084	0.003003	0.6276276	0.135135	0.21021021	0.12912913

					08	925	8		3	14		
Odontop hrynidae	Anura	3	52	2	0.03 8461 54	0.44 230 769	0.076 9230 8	0	0.538 4615 4	0.01 9230 77	0.192307 69	0.134615 38
Bufo nidae	Anura	52	629	45	0.07 1542 13	0.22 257 552	0.192 3688 4	0.0031 7965	0.640 6995 2	0.08 4260 73	0.313195 55	0.151033 39
Leptodac tylidae	Anura	13	225	19	0.08 4444 44	0.69 777 778	0.08 0	0	0.853 3333 3	0.04 4444 44	0.373333 33	0.204444 44
Allophry nidae	Anura	1	3	0	0 666 667	0.66 3333 3	0.333 3 0	0	1 33 33	0.33 3333 33	0.333333 33	0
Centrole nidae	Anura	12	159	10	0.06 2893 08	0.29 559 748	0.069 1823 9	0	0.679 2452 8	0.03 7735 85	0.213836 48	0.113207 55
Ceuthom antidae	Anura	2	6	0	0 0	0 0	0.333 3333 3	0	0.166 6666 7	0 0	0 0	0
Eleuther odactylid ae	Anura	4	232	17	0.07 3275 86	0.31 465 517	0.137 9310 3	0	0.788 7931	0.03 4482 76	0.284482 76	0.146551 72
Brachyce phalidae	Anura	2	76	12	0.15 7894 74	0.44 736 842	0.197 3684 2	0	0.75 1052	0.17 63	0.144736 84	0.105263 16
Craugast oridae	Anura	2	123	7	0.05 6910 57	0.08 130 081	0.113 8211 4	0	0.487 8048 8	0.04 0650 41	0.382113 82	0.276422 76
Strabom antidae	Anura	19	750	109	0.14 5333 33	0.16 6666 8	0.026 6666 7	0	0.556 4666	0.01 67	0.181333 33	0.082666 67
Hemiphr actidae	Anura	6	120	12	0.1 0.1	0.24 166	0.291 6666	0	0.725 1666	0.04 0.2		0.166666 67

						667	7			67		
Ceratophryidae	Anura	3	12	0	0	0.583333	0.666667	0		0.916667	0.25	0.583333
						333	6666	7	0	6666	33	0.583333
Hylidae	Anura	51	103	68	0.0638	0.50476	0.098330	0.0009	0.0048	0.092143	0.338506	0.223084
						5955	339	9330	6993	5	55	3
Telmatobiidae	Anura	1	63	1	0.0102	0.06349	0.0793650	0		0.3809523	0.031746	0.333333
						206	8	0	8	03	4	33
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	0.1579	0.20889	0.1266002	0		0.5348506	0.069701	0.035561
						79	889	8	0	4	28	91
Dicroglossidae	Anura	15	223	27	0.1223	0.11762	0.0986547	0.0044	0.0044	0.6905829	0.103139	0.071748
						23	762	1	843	6	01	11
Ranidae	Anura	24	431	47	0.1072	0.18503	0.0742459	0.0023	0.0023	0.7610208	0.229698	0.211136
						72	503	4	2019	8	38	07
Mantelliidae	Anura	12	232	20	0.0809	0.60862	0.0948275	0		0.9008620	0.060344	0.280172
						9	862	9	0	7	83	41
Rhacophoridae	Anura	21	443	41	0.0979	0.11682	0.0474040	0		0.6975169	0.060948	0.042889
						79	682	6	0	3	08	49
Nyctibatrachidae	Anura	3	39	10	0.2526	0.20512	0.1025641	0		0.9487179	0.076923	0.051282
						26	821	5641	0	5	08	05

Ranixalidae	Anura	2	19	7	0.36842105	0.15789474	0.68421053	0.05263158	0.31578947	0.10526316	
Micrixalidae	Anura	1	24	0	0.04166667	0.08333333	0.95833333	0.04166667	0.04166667	0	
Ceratobatrachidae	Anura	4	102	6	0.0582353	0.26470588	0.09803922	0.64705882	0.24509804	0.1372549	0.01960784
Odontobatrachidae	Anura	1	5	0	0	0.2	0	1	0.2	0.2	0
Ptychadenidae	Anura	3	63	6	0.0952381	0.11111111	0.11111111	0.57142857	0.07936508	0.38095238	0.14285714
Phrynobatrachidae	Anura	1	97	7	0.07216495	0.05154639	0.05154639	0.68041237	0.01030928	0.39175258	0.18556701
Pyxicephalidae	Anura	12	87	9	0.10344828	0.03448276	0.17241379	0.01149425	0.7816092	0.29885057	0.18390805
Conrauidae	Anura	1	6	0	0	0.66666667	0.66666667	0.66666667	0.16666667	0.83333333	0.33333333
Petropedetidae	Anura	3	13	0	0	0.23076923	0.84615385	0.69230769	0.38461538		
Brevicipitidae	Anura	5	36	3	0.08333333	0.19444444	0.88888889	0.05555556	0.16666667	0.02777778	
Hemisotidae	Anura	1	9	0	0	0.11111111	0.88888889	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	03	0.012931655	0.206896558	0	0.70258621	0.48706897	0.43103448	0.25862069
Heleophrynidae	Anura	2	6	0	0	0	0.3333333	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	0.66666666	0.5
Megophryidae	Anura	12	278	76	0.2729	0.07957	0.06115108	0.00719424	0.75539568	0.06834532	0.10071942	0.01079137
Rhinatreumatidae	Gymnophiona	3	14	2	0.1414	0	0.14285714	0.07142857	0.5	0.0757	0	0
Ichthyophiidae	Gymnophiona	2	57	0	0	0	0.0877193	0	0.28070175	0.01754344	0.07017544	0
Scolecophoridae	Gymnophiona	2	6	0	0	0	0.5	0	0.66666667	0	0.5	0.5
Caeciliidae	Gymnophiona	2	43	2	0.0463	0	0.04651163	0	0.1627907	0.028107	0.11627907	0
Typhlonectes	Gymnophiona	5	14	0	0	0	0.428	0	0.428	0.14	0.642857	0.285714



ctidae	ophio na						5714 3		5714 3	2857 14	14	29
Indotyph lidae	Gymn ophio na	7	24	2	0.08 3333 33	0	0.333 3333 3	0	0.833 3333 3	0.04 1666 67	0.25	0.041666 67
Siphono pidae	Gymn ophio na	5	28	2	0.07 1428 57	0	0.178 5714 3	0.0357 1429	0.392 8571 4	0.07 1428 57	0.25	0.107142 86
Dermop hiidae	Gymn ophio na	4	15	0	0	0	0.266 6666 7	0.0666 6667	0.466 6666 7	0.13 3333 33	0.333333 33	0.133333 33
Chikilida e	Gymn ophio na	1	4	0	0	0	0	0	0.25	0	0	0
Herpelid ae	Gymn ophio na	2	10	1	0.1	0	0.2	0	0.7	0	0.2	0.2

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.

**A** Supplemental Figure 1

