

The Haeckelian short(er)fall: a reassessment of tadpole descriptions reveals deeper knowledge gaps on anuran larvae

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Abstract

Tetrapods are among the best-studied animals. However, substantial knowledge gaps persist in larval stages of amphibians, the most threatened vertebrates. Anurans, comprising ~ 88% of extant amphibians, exhibit a unique biphasic life cycle with specialized larvae (tadpoles). We reassess the global extent of the lack of knowledge in tadpoles by incorporating information on species identification and completeness of descriptions. Using a global dataset of 7,818 species, applying standardized criteria, we evaluate identification methods and description quality. Only 36.3% of all species have formally described larvae. Although most existing descriptions are detailed and illustrated (83.7%), identification methods vary widely, with fewer than 20% employing DNA barcoding. The knowledge gap, unevenly distributed across taxa and geography, is greater than expected. Only ~ 5% of all species have a reliably described tadpole. This poses a sharp contrast to the fact that globally ~ 40% of all anurans are threatened with extinction and hampers conservation efforts.

Introduction

There are more than 2 million extant species of known animals, land plants, fungi and protists scientifically documented, and many more are expected to exist, with estimates of up to 3 trillion [1, 2]. A comprehensive knowledge of these species is essential to understand ecological and evolutionary processes. Moreover, species are the cornerstone of nature conservation and policymaking [3, 4]. Among animals, it is a general consensus that tetrapods are amidst the better known and that huge knowledge gaps exist outside that clade [5, 6].

Amphibians are a species-rich tetrapod group with more than 9,000 currently recognized extant species in three orders [7] with new species being continuously discovered and described [8, 9]. As anamniotic tetrapods, they are characterized by a 'biphasic life cycle' (versus a 'single life cycle' in amniotes), with commonly a free-living aquatic larval stage that undergoes a metamorphosis to become a terrestrial stage [10]. The order of frogs (Anura) comprises approximately 88% of the extant amphibians (ca. 7,950 species [7]), and their larval stage – known as tadpole – is special. Unlike other amphibian orders, the bauplan of anuran larvae differs markedly from that of adults, as a result of extensive reorganization during metamorphosis [10–12]. This is unique not only among tetrapods, but also among all deuterostomians, and is perhaps only comparable to holometabolic insects.

Tadpoles can be highly diverse, e.g., they can be adapted to lentic or lotic environments, can be endotrophic or exotrophic, microphagous or macrophagous, and their dietary habits range from herbivorous, omnivorous, carnivorous and cannibalistic to highly specialized, such as oophagy [11–14]. Nearly 75% of the anuran species are considered to have free-swimming tadpoles [15]. In the remaining ca. 2000 species the ontogeny assumingly does not include a free-living larval stage, either because premetamorphic development occurs within a terrestrial egg (direct development) or attached to or retained within the parental body (different forms of viviparity [11]). However, these numbers remain vague, as knowledge of anuran larval stages has only recently been quantified at a global scale. The first

assessments of the Haeckelian shortfall (i.e., concerning the species ontogeny [16]) in anurans revealed that empirical observations are lacking for nearly 60% of the species [15, 17]. This lack of knowledge of anuran larvae varies across geographical, ecomorphological and taxonomic dimensions, thereby hampering our understanding of amphibian evolution and biology and hindering effective conservation efforts [15, 17]. This is particularly important of the latter. Amphibians are the most threatened vertebrate class globally, with 40.7% of all species (39% of all anuran species) threatened with extinction according to The IUCN Red List of Threatened Species [18, 19]. Amphibian conservation profits from integrative taxonomic knowledge, which specifically addresses a profound knowledge on larval stages [20, 21]. We see an enormous impediment in efforts to overcome the amphibian extinction crisis.

The estimated Haeckelian shortfall for anurans may even be substantially greater if two aspects, disregarded in the first, largely quantitative assessments, are taken into account and evaluated accurately: quality of tadpole identification and quality of tadpole description. The first is rooted in the fact that given the radical morphofunctional decoupling between larval and adult stages (e.g., [22–24]), the specific assignment of larvae (and attribution to corresponding adult specimens) remains challenging, and misidentifications can occur (among many others, e.g., *Allobates talamancae* vs. *Silverstoneia nubicola*, *Paratelmatobius lutzi* vs. Hylidae species [25, 26]). The proportion of erroneous assignments of tadpoles to nominal species remains unknown, and many tadpole descriptions may be unreliable, as explicit justification is often lacking (e.g., [27]). In other cases, species identification is confirmed by rearing tadpoles through metamorphosis, at which point species-specific diagnostic characters can be identified (e.g., [28]). The introduction of DNA barcoding marks a turning point, as it increases significantly the accuracy of lineage assignment of a given individual (e.g., [29–31]), which very often can be translated into species identification. For the first time, in the early 2000s, DNA barcoding was used for tadpole-species assignments (e.g., [32]), and has since become an important tool in taxonomic, ecological, and systematic studies (e.g., [33–35]).

The second aspect concerns what a tadpole description should include to be considered a scientifically appropriate description. In previous contributions [15, 17], tadpoles were considered known when they were referred to in a variety of sources, ranging from full, article-like descriptions to brief mentions or character scoring (including anatomical characters, for example in matrices used for phylogenetic analyses). A more refined categorization that first defines a threshold, namely a set of criteria that a tadpole ‘description’ should fulfill, could alter current estimates and result in a greater number of unknown tadpoles.

To better assess how the tadpole knowledge gap could exacerbate the worldwide amphibian extinction crisis, we reassessed the Haeckelian shortfall in anurans by quantifying tadpole descriptions and discriminating how tadpoles have been identified in the first place, and which aspects were included in their descriptions. There have been similar categorization approaches applied to regional anuran faunas (e.g., [36–38]), but our study is the first to apply this approach at the global scale. To facilitate comparison with data of previous contributions, we interpret these results in taxonomic and zoogeographic contexts.

Methods

Species list and data collection

We follow the taxonomy and nomenclature of Frost (as available until March 20, 2025 [39]). Thus, we considered 7,818 anuran species distributed in 52 families, plus the superfamily Brachycephaloidea comprising six families (viz. Brachycephalidae, Caligophrynidae, Ceuthomantidae, Craugastoridae, Eleutherodactylidae, Neblinaphrynidae) and two genera with no familial allocation (*Atopophrynus*, *Geobatrachus*). The complete list of species and accompanying data can be found in Supplementary Table S1. Phylogenetic relationships follow [40].

We updated the datasets of [17] and [15], and reviewed the existing scientific literature by searching Web of Science, Google Scholar, ResearchGate, and the literature list in [41] for tadpole descriptions published up to March 2025. Following former approaches and the fact that all anurans go through some sort of metamorphosis (cryptic larval development [12]), we consider descriptions of any comparable premetamorphic specimen as ‘tadpole description’, without distinction among free-living larvae, direct developing embryos, or all the ecomorphological variants in between. Developmental stages were considered, and only those descriptions dealing with specimens at representative ontogenetic phases showing distinct larval traits (i.e., Gosner Stages 30–41, Niewkoop & Faber 48–62, Townsend & Stewart ca. 7–13 [42–44]) were counted. The databases were updated and original sources, not only compilations and the most recent work on a certain taxon, were consulted and checked when possible. When multiple descriptions for a certain species were available, we prioritized the first description published. Notwithstanding, we chose subsequent descriptions when they met more of the defined criteria (see below), or when the species identification was considered more reliable. To analyze the data in a global spatial context, we scored species as belonging to zoogeographic realms, following [45]: Afrotropical, Australian, Madagascan, Neotropical, Nearctic, Oceanian, Oriental, Palearctic, Panamanian, Saharo-Arabian, and Sino-Japanese. Species distribution information was obtained from [7] and [19].

Tadpole identification

To assess the reliability of tadpoles’ specific allocations in the descriptions, we defined five criteria to evaluate identification accuracy: ID1, the description does not contain a rationale on how the larva was allocated to a particular species. We include here cases where tadpole identification relies only on species distribution, or cases where doubts about identity are explicitly mentioned. With a conservative criterion, we also categorize here some compilations or books we consulted (for availability or prioritizing the quality of descriptions) where no explicit mention to tadpole identification is provided but descriptions are based on tadpoles described in previous works, where that information might likely be provided; ID2, species allocation was based on comparison of larval morphology with existing species keys or images, by raising part of the tadpoles into metamorphs, and/or on the presence of presumed conspecific adult specimens when collecting the tadpoles; ID3, collected larvae were taken from identified adults in captivity or in the field or raised until adulthood. Alternatively, species were identified based on distinct reproductive behavior (such as back riding, nest-attending adults, or viviparity); ID4, the

specific allocation of collected tadpoles was based on DNA barcoding (e.g., using GenBank sequences as reference), without information on the presence of adults while collecting tadpoles; ID5, the specific allocation of collected tadpoles was via DNA barcoding using contemporaneously collected adults.

Tadpole description

We considered a tadpole to be formally described when the following information is provided: (1) a description of a set of external diagnostic characters; (2) some morphometric data; (3) description or illustration of mouthparts, including if applicable the labial tooth row formula (LTRF). Since we consider comparable premetamorphic specimens at stages representative of larval life, we did not include descriptions or illustrations of eggs, early embryos, advanced metamorphic specimens, or froglets. To assess the quality of tadpole descriptions we established 10 criteria based on and expanded from [37]. The criteria are: D1, abbreviated description with no illustration; D2, abbreviated description with illustration; D3, extended description with no illustration; D4, extended description with illustration; D5, only information on the LTRF; D6, only illustrations; D7, only measurements; D8, only textual description; D9, no measurements; D10, no LTRF information. The first four categories meet the definition of full description we set above and only discriminate some aspects that turn useful to score the literature; we consider abbreviated descriptions those that occupy only a few lines or characterizations included in keys, while extended descriptions range from a paragraph listing distinct features to complete descriptions published as full articles. In turn, reports scored as D5 to D10 fail to meet the three description criteria and were not included along with proper formal descriptions.

Results and discussion

The neglected tetrapod

Our results show that 2,840 of the 7,818 considered nominal anuran species (36.3%) have described larval stages according to our criteria. This represents a 5% decrease compared to previous calculations in [17] and [15], primarily driven by a more restrictive definition of ‘description’ rather than updates to the dataset (ca. 280 species were excluded; Supplementary Table S1). Species with tadpoles lacking confirmed descriptions belong to 33 families and, overall, the proportion of descriptions per clade does not differ substantially from previous estimates (Fig. 1). The most affected groups in terms of the number of species with described tadpole are Rhacophoridae (ca. 40 spp. excluded), Bufonidae and Hylidae (ca. 30 spp. each), and, in relative terms, some species-poor families, such as Sooglossidae (50%), Brevicipitidae and Conrauidae (ca. 10% each), as well as more species-rich families such as Dendrobatidae and Pyxicephalidae (ca. 10% each).

Anuran families with tadpoles described for 100% of the species contained remain largely the same ten families, with changes involving Alytidae (as tadpoles of *Discoglossus galganoi* are now considered as not formally described) and Pelodytidae (where the recent synonymization of *Pelodytes hespericus* with *P. punctatus* rendered in all the four species having described tadpoles [46]). About half of the 53 clades considered have at least 50% of species with tadpoles described. These include, for instance, Hylidae

and Dendrobatidae, for which many reports have been excluded (mainly because they consist only of anatomical studies or unpublished data), but the description percentages remain high.

One third of the excluded tadpole descriptions belongs to groups with endotrophic development (i.e., Brachycephaloidea, Brevicipitidae, Ceratobatrachidae, Sooglossidae, plus some hemiphractid, microhylid, and rhacophorid genera), for which only brief mentions or incomplete descriptions exist. This renders the overall deep knowledge gap involving these groups [17] even more pronounced. In Brevicipitidae and Sooglossidae, for instance, the refined description criteria result in the proportion of described larval descriptions in both families dropping to zero. Ericabatrachidae and three families within Brachycephaloidea (Caligophrynidae, Ceuthomantidae and Neblinaphrynidae) complete the six families with 0% of tadpoles described; all are also known or suspected to be direct developers [47, 48]. Vera Candioti et al. [17] interpret the knowledge gaps particularly affecting species with direct development as related to biological and methodological issues (e.g., non-standard ways of collection, raising, description). On the other hand, tadpoles of *Allophryne ruthveni* (Allophrynidae) were described recently [49], thus rendering all families with likely free-living larvae having at least one species with its tadpole known.

Overall, amounts of tadpole descriptions have differed over time. The first descriptions date back to before 1900 (e.g., [50]) and remained relatively low until ca. 1970, when numbers began to increase markedly (Fig. 2). Historically, most years had fewer than 50 descriptions, with an increase in descriptions after 2005, when most years had more than 50 descriptions. The high numbers of described tadpoles in the years 2012, 2013, 2015, and 2022 are in fact the result of having considered compilations of specific regional faunas (e.g., [28, 48, 51]). Over the past approximately 1.5 years, subsequent to the dataset provided by [17], tadpoles were described for about twenty additional species.

Taxonomy, time and space of tadpole descriptions

A summary of the categorization of tadpole identification and description is given in Fig. 3. Results show that for the majority (53.2%) of descriptions, specific allocation was justified by comparative morphology, by raising tadpoles until metamorphosis, or by the presence of adult specimens when larvae were collected (ID2). Approximately 12.9% of the described larvae were obtained from lab-breeding specimens or met comparable criteria (ID3). In less than 20% of the descriptions, DNA barcoding was employed, either on tadpoles only (ID4, 4.4%) or additionally including information of adult specimens (ID5, 13.8%). The proportion of descriptions classified as ID1 (the least trustworthy criterion; 15.8%) may be overestimated due to the respective literature consulted (i.e., compilations in which this information is not always repeated).

With respect to the description quality, our results demonstrate that the vast majority (83.7%) of the available descriptions are complete and provide illustrations (D4). In 3.6% of the cases, the description was extended, but no illustrations were provided (D3). Brief descriptions account for 12.7% of the cases, with (D2, 10.2%) and without illustration (D1, 2.5%). Combining both criteria shows that, of the total

number of complete, illustrated descriptions available, more than half are based on tadpoles identified by ID2 (56%), and about one third from breeding adults or DNA methods (34%).

The application of the various criteria for tadpole identification and description was analyzed over time (Fig. 3), among zoogeographic realms (Fig. 4) and taxonomic groups (Fig. 5). Good quality descriptions, being detailed and including illustrations, have predominated throughout time from the earliest descriptions (Fig. 3). The prevalent format has generally shifted from faunistic accounts in specific regions (e.g., [50, 52–54]) to current modalities such as articles exclusively dedicated to exhaustive description of tadpoles of a single species (e.g., [55–57]), or taxonomic revisions of species groups or entire families (e.g., [58–60]). This was equally observed in most zoogeographic realms (Fig. 4), and the predominance of abbreviated descriptions in the Sino-Japanese region reflects the distinctive style of the literature from there [61]. Likewise, there are no marked differences among taxonomic groups other than the expected variation within most diverse groups (Fig. 5; Supplementary Table S1). Complete and illustrated descriptions predominate in nearly all families and are the exclusive category in 12 of them, including some species-rich groups (e.g., Limnodynastidae, Cycloramphidae). Providing illustrations takes precedence over the length of the descriptive text in most families as well, and brief descriptions with no images are present in 15 families only. Finally, incomplete descriptions are sporadic and concern several families from both major neobatrachian clades (i.e., Indianura and Notogaeonura).

Identification criteria vary more markedly depending on the variables considered. With a few exceptions, identification by raising tadpoles to metamorphosis or comparative morphology (or similar aspects considered in ID2) has predominated over other criteria through time (ID2 is only surpassed by ID3 and ID5 in 2022; Fig. 3) and across the anuran tree of life (Fig. 5). In most zoogeographic realms, it constitutes the prevalent criterion for the species assignment of tadpoles (Fig. 4). Conversely, describing tadpoles from breeding adults (ID3) is uncommon, and the highest proportion of this category in Dendrobatoidea (and thus in the Neotropics) is explained by the collection of tadpoles from the parent's dorsum (tadpole transport is a synapomorphic trait of this group [62]). The percentages of species with ID1 in species-rich families, such as Hylidae, Megophryidae, and Ranidae, are mostly due to categorization performed on specific compilations in which this information is not always reported (e.g., [61, 63]).

DNA barcoding (ID4 and ID5) was introduced in the early 2000's and its use has steadily increased since then (Fig. 3). Application of these methods varies among zoogeographic realms. It was mostly used to identify tadpoles from Madagascan and Oriental species (Fig. 4), after years of systematic prospecting efforts (e.g., [51, 64–66]). Accordingly, families where genetic identification methods were predominantly applied are Mantellidae, Megophryidae, and Rhacophoridae (Fig. 5). Also, DNA barcoding methods were used to identify most species of Pelodytidae [67], Odontobatrachidae [60] and the only described tadpoles of Micrixalidae [68]. The scarcity of DNA studies on Nearctic tadpoles can be explained by that most research in that realm began in the early 19th century (see [17]), and that studies on tadpoles of this realm were probably fairly complete before the development of molecular techniques. Similarly, DNA methods were rarely used to identify Australian tadpoles, likely because pioneer studies had already

produced comprehensive and useful compilations relying on different identification methods (e.g., tadpoles mostly raised to metamorphosis [28]).

Present and future of tadpole descriptions

As stated in the foundational paper by Faria et al. [16], the impact of the Haeckelian shortfall is particularly significant in animal groups with complex life cycles, where knowledge (i.e., description) of a particular semaphoront also interrelates with other shortfall types that may vary along ontogeny (e.g., larvae and adults occupying different niches). In this regard, even before the formal definition of this shortfall type, contributions quantified gaps in the knowledge on ontogeny of some fish and insect groups (e.g., [69, 70]). Most of these studies also discussed the issue of accuracy of larval identification (e.g., [69, 71, 72]) or summarized the quality of larval descriptions (e.g., [73]). In a study on chironomids, the identification of larvae was addressed analytically, and pros and cons of specific assignments through morphology, molecular methods, and a combination of both are summarized through a SWOT (Strengths, Weaknesses, Opportunities and Threats) analysis [74]. Not surprisingly, an integrated approach overcomes problems inherent to morphological (e.g., cryptic species, phenotypic plasticity) or molecular methods alone (e.g., limited accessibility in some regions, incomplete or erroneous reference libraries) and is increasingly promoted in studies on biodiversity and environmental policy (e.g., [72, 75, 76]).

Our data highlights that more than 60% of anuran species still lack basic information on their premetamorphic stages. Among the ca. 36% of species with their tadpoles described, although the vast majority of these descriptions (ca. 84%) are fairly complete and of good quality, assessment of species identity must be considered not completely reliable in some cases. In a non-depreciable 10%, species assignment could be not explicitly justified. This is hopefully being reverted, once details of tadpole identification increasingly become a standard part of published descriptions. Half of the proper tadpole descriptions relied on morphological comparisons for species allocation. Challenges for identification of amphibian larval stages have been thoroughly discussed and are mainly attributed to conservative anatomy among closely related species, intraspecific variation related to development and distribution, and patterns of convergence and parallelism (e.g., [30, 77]). Finally, only a fifth of all tadpole descriptions employed molecular methods for supposedly reliable species allocation – although DNA sequences very often allow the match between adults and larvae, that not necessarily means the species allocation is correct. Following the implications by [78], who identified a concerning high portion of apparent errors in the GenBank genetic repository, we should be aware that molecular identification by comparison with vouchered adult sequences here considered to be reasonably reliable, may overestimate correct assignments, thus further reducing the proportion of reliably identified tadpoles. Moreover, even for well-trained taxonomists, and with several sources of evidence (e.g., breeding adults, metamorphic morphology, unequivocal species distributions, molecular identification), the existence of known species complexes (where identification of adults can be highly questionable) and a considerable amount of cryptic diversity remain obstacles to the proper allocations of adults and larvae. Multiple studies have identified the existence of ‘hidden’ species diversity in most groups of anurans, including

the identification of so-called candidate species, which are partly morphologically very similar to its nominal relatives, but clearly represent independent evolutionary lineages deserving species status (e.g., [79–83]). In these cases, existing tadpole descriptions may require subsequent specific reallocation. Also, this can go the other way around and taxonomic inflation also affects species assignment [84].

Given these concerns and projecting these to a global scale, we certainly face a knowledge shortfall deeper than previously estimated, ranging from (1) an optimistic scenario, including complete descriptions based on tadpoles identified using explicit criteria, where 27% of anuran species could be considered to have their tadpole described (as opposed to the initial 40% quantified in [15], to (2) the pessimistic scenario, that includes only contemporary tadpoles and adults identified by molecular methods, where only 4.7% of all anuran species would have a reliably described larva.

We stress that this work provides only an approximate estimate of the true magnitude of knowledge shortfalls in anuran tadpoles, since like previous contributions [15, 17], it only deals with the interface of the Haeckelian-Linnean shortfall types. Knowledge on many other crucial aspects of tadpole biology lags considerably behind and emphasizes the pertinence of addressing the rest of shortfall types (e.g., Hutchinsonian, fundamental niche; Prestonian, population dynamics; Eltonian, biotic interactions; Raunkiaeran, functional traits; [85] in anuran larval stages. For instance, several authors have emphasized the lack of data on internal morphology (e.g., [12, 86]). Moreover, data on fundamental aspects of tadpole biology are mostly missing, raising questions such as “what do tadpoles really eat?” ([87], which, like many comparable questions, remain largely unanswered ([14]. We advocate for new tadpole descriptions to ideally include some basic aspects of natural history, such as information on macro- and microhabitat, behavior and ecology. On the other hand, large datasets summarizing information at the global level are increasingly available and can be extremely useful for integration into comprehensive approaches (e.g., [88–90]).

Exacerbating the amphibian extinction crisis

Despite enormous efforts and strategies to combat the amphibian extinction crisis (e.g., [91, 92]), the amounts of species threatened with extinction under the IUCN Red List have dramatically increased in the last two decades from ~ 32% to ~ 41% [18]. On the other extreme, Vera Candioti et al. [17] drew attention to the fact that nearly half of the anuran species categorized as Least Concern lack descriptions of their larval stages. A rough estimate based on our compiled data shows that fewer than one fifth of the LC species with described tadpoles meet the strictest molecular identification criteria and provide extended descriptions (unpublished data), so that the gap is anew larger. This shortfall in tadpole knowledge has direct and consequential impacts and impede conservation efforts. Monitoring and conservation action plans are mainly based on adults, their biology, and their ecological needs, whereas larval forms are mostly neglected (e.g. [92, 93]). Given that anurans with their specialized larvae account for almost 90% of the extant Amphibia, this bias, together with the herein identified knowledge shortfalls, obscures the actual conservation status not only of anurans but amphibians in general. It prevents early detection of population declines and threats, as our understanding of ecological needs is

partially missing. Tadpole biology is unique and connecting the information on different semaphoronts is pivotal to ensure a complete and more reliable basis for protecting anuran diversity [21]. Given that amphibians are the most threatened vertebrate group on this planet [19], closing these knowledge gaps on tadpoles is essential to overcome the amphibian extinction crisis.

Declarations

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Data availability All data generated or analyzed during this study are included in this published article and its supplementary information files.

Competing interests The authors declare no competing interests.

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Figures

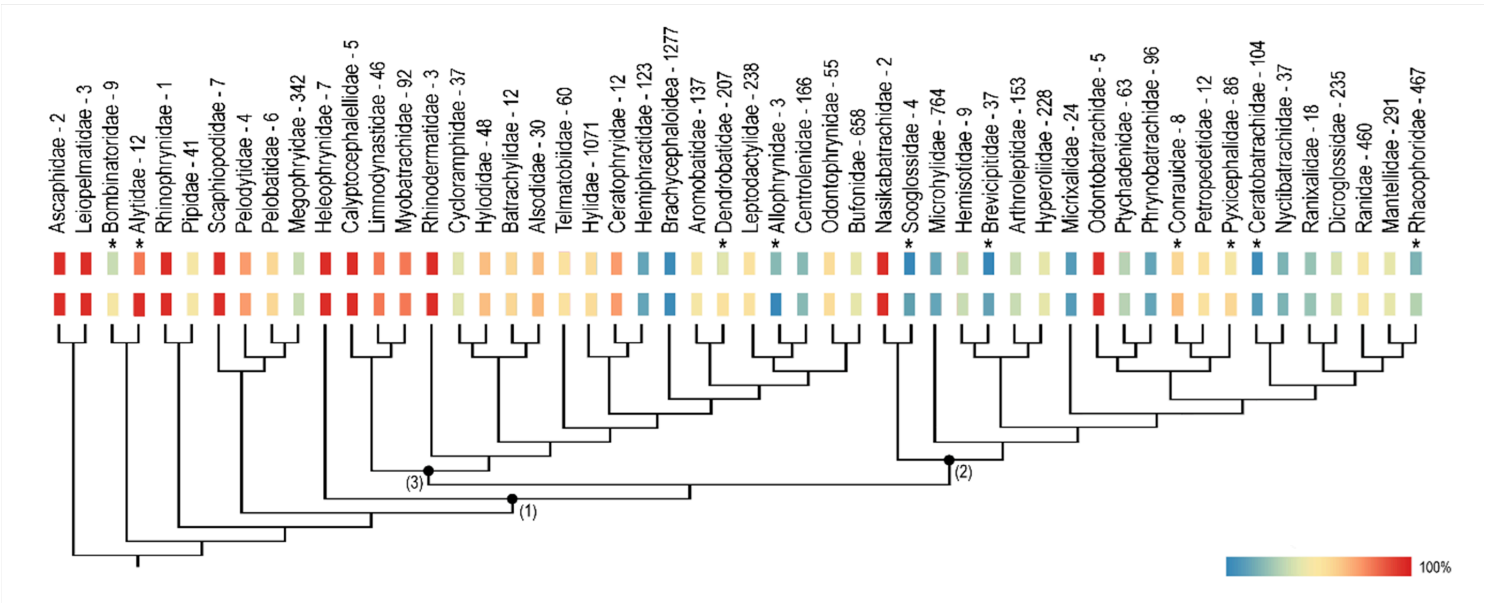


Figure 1

Percentage of anuran species with tadpoles described per family. Portik et al. [40] phylogenetic hypothesis is used as reference, and labeled clades are (1) Neobatrachia, (2) Indianura, and (3) Notogaeonura; numbers next to branch names indicate species content. Colored squares at branches indicate the percentage of tadpole description per clade, following the color scale: squares at the top line correspond to percentages of tadpoles formally described considering criteria defined here, and those at the bottom line are results from [17]. A new anuran family, Ericabatrachidae, was erected after the [40] survey and it is not included in the reference phylogenetic hypothesis; larval stages of the single species it contains (*Ericabatrachus baleensis*) are not known. Note the overall general pattern, with main differences in some punctual clades (asterisks; detailed comparison in Supplementary Table S1).

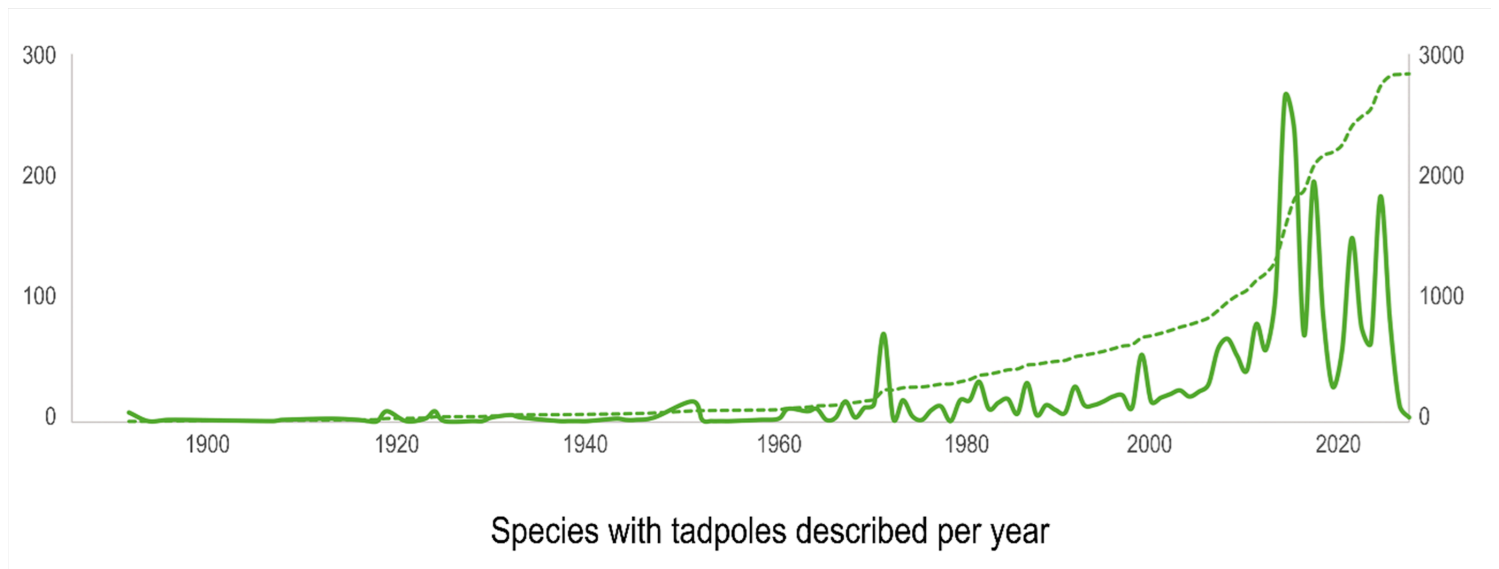


Figure 2

Number of species with tadpoles described per year (solid line; left Y-axis) and cumulative values (dashed line; right Y-axis). Note the marked increase after the 1970's.

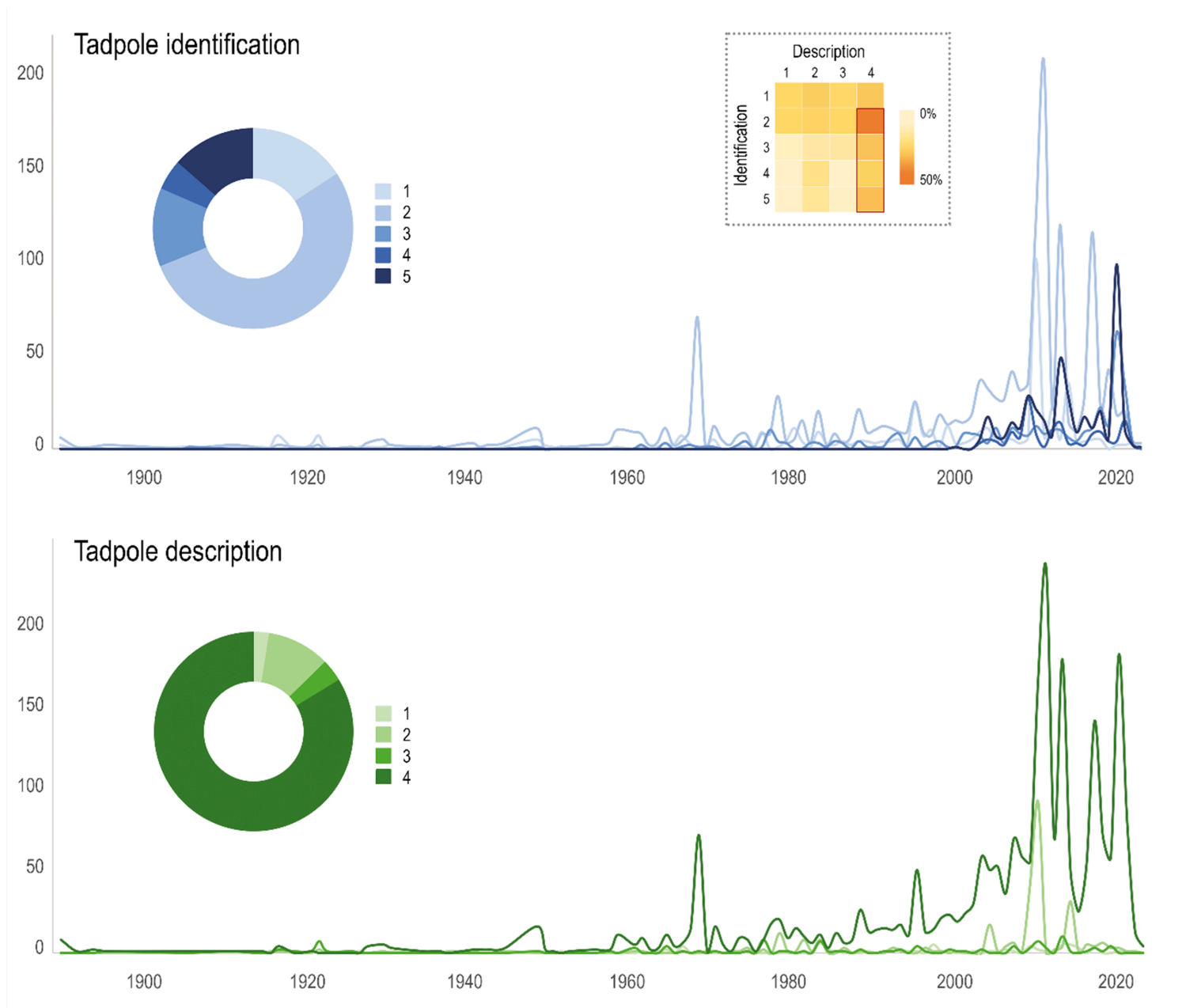


Figure 3

Proportions of the different criteria used to identify and describe tadpoles, in total (donuts) and per year (lines). Blue and green shades and numbers represent the reliability (ID1-5) and quality (D1-4) of descriptions, from no justification about species allocation and brief description without illustration, to tadpoles and adults identified by DNA barcoding and extended, illustrated descriptions. The heat map shows combination percentages of criteria. Note the overall good quality of descriptions, the increasing application of DNA identification methods, and the high percentage (ca. 75%, dark orange squares) of properly described tadpoles and with identification criteria explicit.

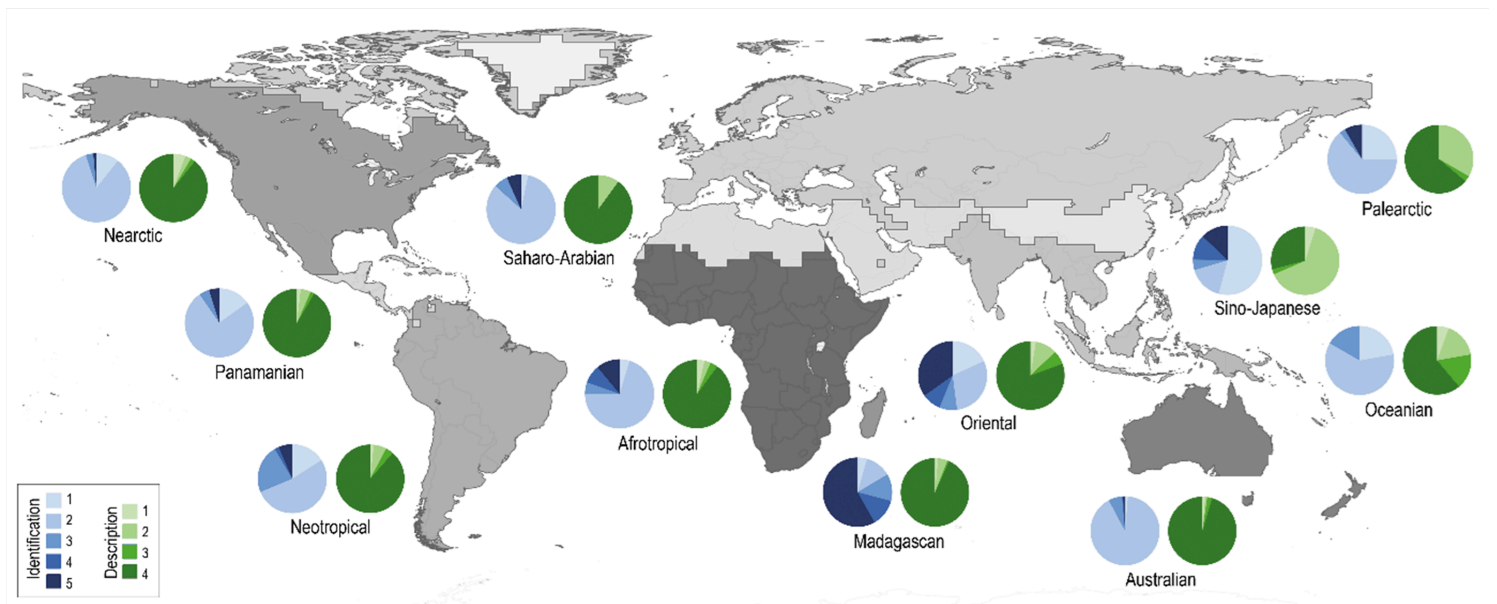


Figure 4

Percentage of criteria adopted for tadpole identification (shades of blue, ID1-5) and quality of the description (shades of green, D1-4) per zoogeographic realms. Note the prevalence of DNA identification methods in Madagascan and Oriental realms.



Figure 5

Taxonomic distribution of categories for tadpole identification and description. Portik et al. [40] phylogenetic hypothesis is used as reference, and numbers next to branch names indicate percentages of tadpole descriptions; labeled clades are (1) Neobatrachia, (2) Indianura, and (3) Notogaeana. Bubbles show the amount (raw numbers) of species per category. In the “Identification” plot, the darker the blue, the more accurate the tadpole identification mode. In the “Description” plot, green colors identify the 4 categories for tadpoles considered described, and red colors those that fail to consider some descriptive criteria (e.g., LTRF, measurements).

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [TableS1.pdf](#)