JHONNY JOSÉ MAGALHÃES GUEDES

IDENTIFYING FACTORS TO BOOST SPECIES DISCOVERIES AMONG REPTILE MUSEUM SPECIMENS

Dissertação apresentada à Universidade Federal de Viçosa, como parte das exigências do Programa de Pós-Graduação em Biologia Animal, para obtenção do título de *Magister Scientiae*.

Orientador: Renato Neves Feio

Coorientador: Mario Ribeiro Moura

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APROVADA: 19 de julho de 2019.

Jhonny José Magalhães Guedes
Autor

Renato Neves Feio
Orientador

"Nothing will ever replace the taxonomic knowledge and training that museums provide;
funding in this area should become a national priority. Otherwise, knowledge of this planet's
biodiversity, and of all the potential benefits therein, will be lost"
Suarez & Tsutsui 2004

Dedico este trabalho a todos os pesquisadores que dedicaram parte de suas vidas ao Museu Nacional, mas em especial aqueles que perderam seus projetos nas chamas daquele fatídico incêndio em setembro de 2018. Com o incêndio no museu mais antigo do Brasil, uma considerável e inestimável parte da história científico-cultural brasileira foi perdida. Este e outros tristes eventos ressaltam o grande descaso de um país onde educação, ciência e cultura são ainda desvalorizados pela maioria dos nossos governantes. Espero que num futuro não muito distante, instituições tão importantes como nossos museus recebam a devida atenção e investimentos, para que episódios como este não se repitam jamais.

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RESUMO

GUEDES, Jhonny José Magalhães, M.Sc., Universidade Federal de Viçosa, julho de 2019. **Identificando fatores para impulsionar a descrição de novas espécies de répteis depositados em museus.** Orientador: Renato Neves Feio. Coorientador: Mario Ribeiro Moura.

A maioria das espécies na Terra ainda são desconhecidas pela ciência, e podem ser extintas antes de detectarmos sua existência. Espécimes de muitas dessas espécies não descritas podem já ter sido coletados e armazenados em coleções científicas, embora tais espécimes possam permanecer “engavetados” por anos antes de serem formalmente descobertos pela ciência. Nós investigamos o gap temporal entre as datas de coleta e descrição de espécies de répteis, assim como seus possíveis determinantes. Revisamos a literatura das descrições de répteis globais entre 1992 e 2017, obtendo dados sobre variáveis biológicas e sociológicas para 2.661 espécies. Usamos análises de sobrevivência dentro de uma abordagem de modelo médio para investigar quais fatores contribuem para explicar variações do gap temporal. O gap temporal de répteis globais variou entre 0 a 155 anos (mediana = 5 anos). Mais de 25% das descrições envolveram espécimes armazenados em coleções por 12 anos ou mais. O gap temporal foi menor quando o coletor do holótipo foi também autor da descrição da espécie, e revisões taxonômicas revelaram espécies com maiores gaps temporais. Espécies desconhecidas eventualmente coletadas por não-taxonomistas podem, portanto, permanecer “engavetadas” por longos períodos de tempo em coleções científicas. Nesse ponto, revisões taxonômicas são fundamentais para reverter esta tendência e melhorar os benefícios fornecidos por pesquisadores não taxonomistas e cidadãos em geral, que porventura redirecionem espécimes a coleções científicas. Nossos resultados revelam características de répteis preservados em coleções que podem possivelmente representar espécies ainda não descritas pela ciência, mas já coletadas e armazenadas em coleções científicas.

Palavras-chave: Descoberta de espécies. Conservação da biodiversidade. Déficit Lineano. Impedimento taxonômico. *Tempo de gaveta*. Espécimes preservados. *Gap* temporal.

ABSTRACT

GUEDES, Jhonny José Magalhães, M.Sc., Universidade Federal de Viçosa, July, 2019. **Identifying factors to boost species discoveries among reptile museum specimens.** Advisor: Renato Neves Feio. Co-advisor: Mario Ribeiro Moura.

Most species on Earth remain unknown to science and might go extinct before we ever recognize their existence. Specimens belonging to many of those missing species may have been already collected and housed in scientific collections, although they can remain “shelved” for years without a formal name. We investigate the time lag between collection and description dates of recently described species, and its determinants. We reviewed the literature on species descriptions of global reptile species from 1992 to 2017, gathering data on biological and sociological variables for 2,661 species. We used time-to-event analysis in concert with a model averaging approach to investigate what factors contribute to explain variation in time lag. The time lag of global reptiles varied from zero to 155 years (median = 5 years). More than one-quarter of the descriptions involved specimens shelved for 12 years or more. Time lags were shorter when the collector of the holotype was an author of description, and taxonomic revisions uncovered species with longer time lags. Unknown species eventually collected by citizen scientists may therefore remain shelved for much longer in scientific collections. Taxonomic revisionary studies are crucial to reverse this trend and improve the benefits from citizen science. Our findings reveal which kind of preserved reptile specimens can likely represent yet unknown species in scientific collections.

Keywords: Species discoveries. Biodiversity conservation. Linnaean shortfall. Taxonomic impediment. Shelf life. Preserved specimens. Time lag.

SUMÁRIO

INTRODUÇÃO GERAL

Caso algum dia um alienígena amigável visite nosso planeta, qual seria uma de suas primeiras perguntas ao povo terráqueo? Certamente, uma delas seria sobre quantas espécies existem no nosso planeta. Embaraçosamente, não teríamos uma resposta precisa para essa questão (MAY, 2010). Seres humanos possuem, por natureza, o instinto de classificar e nomear coisas, desde objetos inanimados à seres vivos (HOPWOOD, 1957). Essa prática, conhecida como taxonomia, é datada desde a origem da linguagem humana, a centenas de anos antes de cristo (MANKTELOW, 2010). Atualmente, a taxonomia moderna se baseia no sistema de classificação binomial, proposto pelo botânico e zoólogo Carl Linnaeus em 1753. Nesse sistema as espécies constituem o nível de classificação taxonômico mais básico, sendo identificadas por duas palavras (gênero + epíteto específico) escritas em itálico; por exemplo, nós seres humanos pertencemos a espécie *Homo sapiens*.

Desde a criação do sistema binomial, nosso conhecimento sobre a biodiversidade tem crescido significativamente e, em pouco mais de 260 anos, já descrevemos e catalogamos mais de 1,2 milhão de espécies de animais, plantas, fungos e protozoários – bactérias constituem um 'mundo' a parte (SCHLOSS; HANDELSMAN, 2004). No entanto, estudos recentes apontam que essa diversidade representa apenas cerca de 15% das espécies que habitam a terra (MORA et al., 2011). Essa discrepância entre o número de espécies viventes e aquelas formalmente descritas é conhecida pelos pesquisadores como déficit Lineano (WHITTAKER et al., 2005), e mostra que o atual conhecimento sobre nossa biodiversidade ainda é incipiente e tem muito a ser melhorado. Para piorar este cenário, vários estudos tem reportado eventos de extinções de espécies e/ou populações em diversas partes do globo (CEBALLOS et al., 2015; CEBALLOS; EHRLICH, 2002; HUGHES; DAILY; EHRLICH, 1997; THOMAS et al., 2004; WORM et al., 2006), de modo que alguns pesquisadores argumentam que estamos vivenciando uma possível 6ª grande extinção em massa causada principalmente por ações humanas (BARNOSKY et al., 2011).

Espécies são importantes componentes dos ecossistemas, onde cada uma possui seu papel na manutenção de um ambiente saudável e equilibrado. Quando extintas, mesmo que localmente, o bom funcionamento dos ecossistemas é afetado, que por sua vez, impacta produtos e serviços que a sociedade usufrui dos ecossistemas, tais como alimentos, água potável, regulação do clima, controle biológico, dentre outros (CARDINALE et al., 2012). Visto que espécies são as 'unidades de trabalho' em diversos programas de conservação, aquelas ainda não descritas (a maioria) enfrentam perigo ainda maiores, podendo serem extintas mesmo antes de conhecidas pela ciência (COSTELLO; MAY; STORK, 2013; TEDESCO et al., 2014). Portanto, identificar fatores que acelerem descrições de novas espécies é crucial para minimizar os déficits de conhecimento sobre a biodiversidade, além de aprimorar medidas de conservação já existentes e contribuir para o desenvolvimento e implementação de novas medidas (HORTAL et al., 2015).

Diante do que foi visto, alguém pode se perguntar: como saberemos onde encontrar as espécies 'desaparecidas' de modo a impulsionar novas descrições? Bom, vários estudos fornecem dicas quanto a onde se encontram as peças faltantes do quebra-cabeça chamado biodiversidade. De um modo geral, a maioria destas espécies serão encontradas em regiões tropicais, especialmente em áreas pouco ou nada amostradas (COSTELLO et al., 2015), assim como em áreas conhecidas como *hotspots* pra conservarão da diversidade biológica – locais com elevada riqueza de espécies onde muitas só ocorrem nestas regiões – espécies endêmicas (MYERS et al., 2000). Novamente, alguém poderia se perguntar: se existem tantas espécies a serem descritas, e sabemos onde encontra-las, por que ainda não foram coletadas e descritas? É ai que entra um detalhe curioso e 'animador' – muitas destas espécies já foram coletadas, encontrando-se armazenadas em museus de história natural e herbários em todo o globo, só 'aguardando' que algum pesquisador as descreva. Por exemplo, estima-se que cerca de 70.000 espécies de angiospermas – plantas que produzem flores e frutos – ainda serão descritas até que o inventário desse grupo seja completo (JOPPA; ROBERTS; PIMM, 2011a). No entanto, um estudo publicado em 2010 estimou que mais da metade destas espécies já foram coletadas e estão depositadas em herbários, aguardando sua descrição formal (BEBBER et al., 2010).

Antes de uma espécie ser descrita, primeiramente ela tem de ser coletada. Após a coleta vem uma nova etapa do processo de descoberta, onde a chamada espécie 'candidata' precisa ser estudada e comparada com espécies parecidas ("parentes" próximos) para então ser separada e descrita como nova espécie para a ciência. Entretanto, estas duas etapas (coleta e descrição) aparentemente representam duas partes bem distintas e dissociadas entre si (BEBBER et al., 2010). Com isso, muitas das peças faltantes de nossa biodiversidade acabam permanecendo décadas engavetadas em coleções científicas até que finalmente sejam descritas (FONTAINE; PERRARD; BOUCHET, 2012). A dissociação entre coleta e descrição de uma nova espécie pode se dar por diferentes motivos: pode ser resultado de uma superlotação de coleções científicas associada a falta de experts locais (taxonomistas) atuando junto a referida instituição; problemas correlatos à mal curadoria; falta de equipamentos e infraestrutura necessários para investigação e estudo de espécimes, dentre outros. Portanto, o objetivo do presente trabalho foi entender quais são os fatores por trás da 'fila de espera' que muitas espécies enfrentam antes de seu ‘nascimento’ formal, o que é crucial para otimizarmos investimentos em instituições depositárias por todo o globo, uma vez que o acervo de tais instituições é muitas vezes sub-conhecido taxonomicamente. Nossos resultados podem ajudar a acelerar a descrição de novas espécies por atrair maior atenção de pesquisadores as coleções científicas, ‘casas’ onde inúmeras espécies a serem descritas encontram-se na lista de espera para sua descrição formal.

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Identifying factors to boost species discoveries among museum reptile specimens

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Abstract

Most species on Earth remain unknown to science and might even go extinct before we ever recognize their existence. Specimens belonging to many of those missing species may have already been collected and housed in scientific collections, although they can remain 'shelved' for years bearing a wrong name, or even without a formal name. We investigate the time lag between collection and description dates of 2,612 reptile species described worldwide between 1992 and 2017, and its determinants. We modeled the time lag to description using biological and sociological variables in a time-to-event analysis framework. The time lag of global reptiles varied from zero to 155 years (median = 5). More than one-quarter of the species descriptions involved specimens ‘shelved’ under an old name, or as undetermined taxa, for 12 years or more. Time lags were shorter when the collector of the holotype – the specimen serving as the name-bearer of the species – was an author of the description, while taxonomic revisions uncovered species with longer time lags. Unknown species eventually collected by non-taxonomists remain incorrectly identified for much longer in scientific collections. Taxonomic revisions are crucial to reverse this trend and improve the benefits of collecting. Our findings reveal the kinds of reptile specimens that most likely represent yet unknown species in scientific collections.

Keywords: species discoveries; biodiversity conservation; Linnaean shortfall; taxonomic impediment, shelf life, preserved specimens, time lag

Significance Statement

Billions of animal specimens are housed in natural history museums worldwide, and many of them might represent yet unknown species that await formal description. Understanding what drives the amount of time species remain undescribed or wrongly identified helps to elucidate ways to boost species discoveries and improve the biodiversity knowledge. We found that unknown species collected by non-taxonomists – e.g., ecologists and non-scientists such as farmers, forest rangers and firefighters – may remain unperceived for decades in scientific collections. Also, older museum specimens are more prone to be correctly identified, or even described as new taxa, during taxonomic revisions.

Introduction

We live in a fast changing world where biodiversity loss has reached unprecedented rates, especially due to anthropogenic activities (BARNOSKY et al., 2011). There is a huge discrepancy between the number of extant species inhabiting Earth and those formally described, a problem named ‘the Linnaean shortfall’ (WHITTAKER et al., 2005). Since described species are the ‘working units’ in many conservation approaches (e.g., the IUCN red lists), undescribed taxa are usually left out of conservation planning, management and decision-making (COSTELLO; MAY; STORK, 2013; TEDESCO et al., 2014). This issue has been recognized through international agreements such as the Convention on Biological Diversity (CBD) and its dedicated taxonomy initiative established to tackle the shortage of taxonomic knowledge (SECRETARIAT, 2010). Such shortage is often present in scientific collections in the form of insufficient taxonomists and curators (6–7; cf. 8). Consequently, many collected specimens might have never been properly studied, and some may represent unknown species that remain ‘shelved’ for years in scientific collections (BEBBER et al., 2010; FONTAINE; PERRARD; BOUCHET, 2012). Documenting which factors drive the amount of time species remain undescribed or misidentified helps identifying mechanisms to reduce both the taxonomic bottleneck and the Linnaean shortfall (KIM; BYRNE, 2006; SECRETARIAT, 2010).

The chances of being discovered and described early are not equal among species (COLLEN; PURVIS; GITTLEMAN, 2004; COSTELLO et al., 2015; GASTON; BLACKBURN; LODER, 1995; GASTON; SCOBLE; CROOK, 1995). Species with larger body size and, especially, wider geographic ranges, were usually described earlier (COLLEN; PURVIS; GITTLEMAN, 2004; DINIZ-FILHO et al., 2005; MEIRI, 2016). Although we have advanced on our understanding of correlates of species description dates (BLACKBURN; GASTON, 1995; COSTELLO et al., 2015; MEIRI, 2016), the processes leading to the recognition and description of new taxa after their collection in nature are poorly understood (BEBBER et al., 2010; FONTAINE; PERRARD; BOUCHET, 2012). After collection, specimens are usually housed in scientific collections, and some of them become type specimens – a unique set of specimens to which the scientific name of a new taxa is formally attached. Most importantly, a single specimen is described as the *holotype,* and it then serves as the name-bearer of the species – to which all putative conspecifics should be compared. Clearly, time is required to examine collected specimens and identify yet unknown species, but such times can be surprisingly long. The average time lag between collection and description dates of a random set of species described in 2007 was 21 years (FONTAINE; PERRARD; BOUCHET, 2012).

Among terrestrial vertebrates, reptiles are the most diverse group (UETZ; FREED; HOSEK, 2018), and are often used in conservation planning exercises (PAWAR et al., 2007; ROLL et al., 2017). It has been shown that lizard species only known from their type series were described, on average, 10 years after first collection (22). But the times to proper identification can be considerably longer. The Andean stout-tailed snake *Calamophis katesandersae*, for example, was described 137 years after the holotype was collected in 1875 (MURPHY, 2012). Some reptile species remain shelved for so long under an incorrect name, or even unidentified, that their wild populations have been driven to extinction by the time species descriptions are finally published (e.g., 21). More than 3.7 millions preserved reptile specimens are recorded on GBIF (*Global Biodiversity Information Facility*; https://www.gbif.org/). Of these, more than 400,000 (12%) remain unidentified at the species level, and many of those identified, however, are probably mislabeled (GOODWIN et al., 2015). Considering that several scientific collections have not been digitalized and incorporated into GBIF (24), actual numbers of unidentified reptile specimens are thus likely much higher. Given the high rate of reptile discoveries in the last decades (MEIRI, 2016; UETZ, 2010), it is almost certain that many of those preserved specimens actually represent undescribed species.

We investigate the time lag – also known as 'shelf life' (FONTAINE; PERRARD; BOUCHET, 2012) – between the collection and description dates of reptile species. Using species-level attributes of reptiles, and sociological attributes related to museums and taxonomists, we test nine interrelated hypotheses regarding the determinants of shelf life length. (i) The description of new species often require the analysis of several specimens to account for variation in examined characters (DAYRAT, 2005). We expect that descriptions based on few specimens show shorter time lags because taxonomists would wait less time either to collect or examine few type specimens. (ii) Species with many congeners may take longer to distinguish taxonomically from closely related taxa (GASTON; BLACKBURN; LODER, 1995), which would lead to longer shelf life. (iii) Larger animals generally attract more attention (ROLL et al., 2016), are easier to detect and collect, being thus described first (COLLEN; PURVIS; GITTLEMAN, 2004; COSTELLO et al., 2015; GASTON; BLACKBURN; LODER, 1995; MEIRI, 2008). Similarly, taxonomists may take more time to distinguish small bodied species, which can require better equipment and techniques (GASTON, 1991). Hence, we expect longer time lags for small-bodied species relative to larger ones. (iv) Advances in molecular biological techniques have facilitated the descriptions of unknown species (HEBERT; GREGORY, 2005). Such tools are nowadays routinely used to study museum specimens (PARHAM et al., 2004; SHOKRALLA et al., 2011). Until 20–30 years ago the commonly used fixatives and preservatives, such as formalin, often degrade the specimen's DNA. These were recently generally replaced with more DNA-friendly materials – and tissues are now commonly frozen for future genetic analyses. We therefore expect shorter time lags for species described with an accompanying molecular analysis, basically because it is nearly impossible to extract DNA from very old reptile specimens.

Most reptile species occur in the tropics (ROLL et al., 2017) and most undescribed taxa will likely be discovered in this region (BEBBER et al., 2010; GIAM et al., 2012;

MEIRI, 2016). (v) Given the vast collections of unstudied material from tropical regions coupled with shortage of experts to describe them (PEARSON; HAMILTON; ERWIN, 2011), we expect longer time lags for species collected at lower latitudes. (vi) We acknowledge that some species may be collected in the tropics but housed and later described in museums from temperate regions. The herpetological collections from temperate regions are often the largest ones. For example, the *Museum of Comparative Zoology* (Harvard University) and the *Smithsonian Institution* house about 195,000 and 190,000 reptile specimens, respectively. The *Natural History Museum* in London has 80,000–100,000, and collections in Europe and N. America are generally the largest in the world. These museums receive hundreds of knowledgeable taxonomists yearly that will sort their museum specimens, provide correct species identification, and uncover undescribed species faster. Therefore we expect shorter time lags for species housed in museums from higher latitudes. Alternatively, the sheer size of such collections may mean it is more difficult to find unique specimens there, lengthening the shelf lives between their collection and formal description. (vii) In the last decades, the number of authors per described species has grown (JOPPA; ROBERTS; PIMM, 2011b), which is also true for the reptile species described from 1992 to 2017 (Fig. S1). We hypothesize that such increasing collaboration among authors hastens descriptions of new taxa. (viii) Collectors of specimens in nature are not always taxonomists, with non-taxonomists playing an important role in biodiversity knowledge accumulation (MOURA et al., 2018). When non-taxonomists collect a specimen of a yet unknown species, they may deposit such specimen in a scientific collection without an expert on that particular taxon, where it may be ascribed, wrongly, to a widely distributed, highly variable taxon, or simply left unidentified. Such specimens may escape awareness of taxonomists and remain hidden on shelves for a long time. On the other hand, if a taxonomist collected the holotype, he/she may immediately recognize it as unique, and may have deliberately collected it in view of describing a new species. Therefore, the species description process might be initiated earlier and lead to shorter species' shelf life. (ix) During revisionary studies, taxonomists often visit several collections and analyze hundreds of specimens, which increases the odds of uncovering older specimens (BEBBER et al., 2010). We expect longer time lags for species described based on taxonomic revisions as it may reveal such old specimens from the pool of undescribed species.

In understanding which kind of species are most likely to remain shelved, taxonomists and curators can adjust efforts towards yet unknown taxa housed in scientific collections. We test which factors (if any) affect the time lag between collection and description dates of global reptiles based in a time-to-event model framework. Because the value of some covariates might be subject to temporal constraints, we applied a sensitivity analysis to account for the potential disproportionate influence of very old collection dates among reptile species.

Results

The time lag between collection and description dates of global reptile species ranged from zero to 155 years, with a median of five years. The species with the highest time lag was the gecko *Cnemaspis amith* (MANAMENDRA-ARACHCHI; BATUWITA; PETHIYAGODA, 2007), described 155 years after the holotype was collected. The snake species 'waiting' the longest to be described was Grismer's bronzeback *Dendrelaphis grismeri* (VOGEL; VAN ROOIJEN, 2008) that remained shelved for 146 years. More than one-quarter of reptile species involved specimens shelved for at least 12 years before their formal description. Shelf life varied across reptile groups (Fig. 1). Lizards median shelf life was 4 years (range = 0–155 years), and significantly shorter than that of snakes (median = 7.5 years, range = 0–146; Mood's median test: $\chi^2 = 74.639$, df = 1, $p < 0.001$) (Table S1).

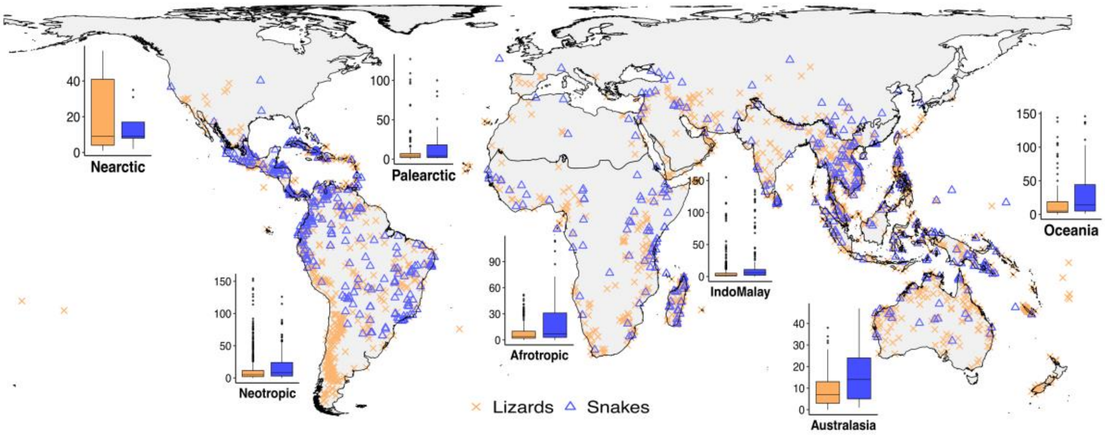

Fig. 1. Global distribution of holotype specimens of reptile taxa described from 1992 to 2017. Boxplots show the time lag (years) between collection and description dates of reptile species across each biogeographic realm.

The average weighted Accelerated Failure Time (AFT) model explained 30.5% of the variation in time lag of reptile species globally (27.6% in lizards and 34.7% in snakes; Tables S2). The most important predictor (e.g., strongest effect size) of time lag variation was the participation of the collector of the holotype as an author of the species description, decreasing time lag by 75% on average – from 12 to three years (Fig. 2). Descriptions based on revisionary studies showed higher median time lag (9 years) than other descriptions (4 years). Time lags were shorter for species whose descriptions were based on few type specimens and for species belonging to speciose genera. The effect of the most important covariates was robust to the successive discarding of specimens collected at older dates from the complete species dataset (Fig. 2, and see below).

Time lag to descriptions increased with decreasing latitude of the type locality – e.g., tropical reptiles had higher time lags. Time lags, however, increased with the latitude of the museum in which holotypes are housed: types were processed more slowly if the museums in which they were housed are in Europe or the USA, but such effects were inconsistent according to the sensitivity analyses (e.g., after discarding the oldest museum specimens; Fig. 2). The use of molecular in species description yielded shorter time lags, but this result was not consistent either. Effects of the number of specimens in the type series, and the number of species within the genus, were important for lizards but not for snakes. In addition, snakes showed higher time lags when holotypes were small-bodied, rather than large sized, and collected from lower latitudes, but only without discarding older specimens (Fig. 2). The loss of significance of taxonomic review for snakes can result from either a reduction in sample size after the successive discard of old specimens, or be due to the unbalanced sample size (Fig. S2). The number of authors describing each species was unimportant for any taxon (Table S2).

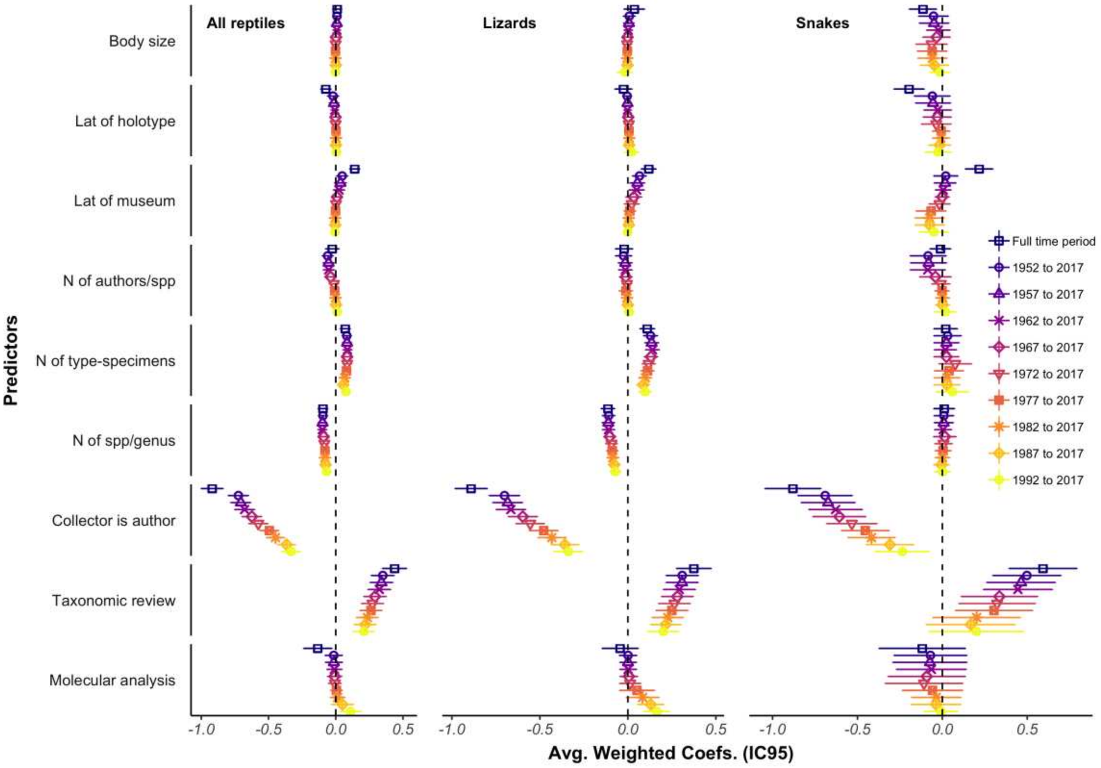

Fig. 2. Sensitivity analysis and its respective standardized coefficients from the average weighted Accelerated Failure Time (AFT) model for each iteration with different temporal

ranges for collection dates. The horizontal bars denote the 95% confidence intervals around each coefficient.

Discussion

Hundreds of millions of preserved specimens are housed in scientific collections worldwide (GBIF.ORG, 2019), and many of those probably represent yet unknown species waiting to be formally named. The time lag to description of those species can be explained by several factors, including biological, socioeconomic and geopolitical variables (BEBBER et al., 2010; FONTAINE; PERRARD; BOUCHET, 2012). We have shown that the time lag between collection and description dates of reptile species is shorter when collectors are authors of descriptions, increases as the number of specimens in the type series increase, and is shorter for species belonging to speciose genera. Moreover, species described based on revisionary taxonomic studies have longer time lags than otherwise, indicating that taxonomic reviews are more prone to uncover old specimens in scientific collections.

Among the most consistent findings in our study is the participation of the collectors of the holotype in the species description process. Collecting and describing new species are crucial stages of the discovery process, but they can be completely disconnected (BEBBER et al., 2010). If the collector of the holotype is an author of the formal description, she/he is most likely a taxonomist capable of recognizing such unknown taxon, and can henceforth start the species' formal description. In fact, such a person may have collected a type specimen *in order* to describe it. In contrast, if a non-taxonomist collects a specimen and deposits it in a scientific collection, the specimen may not be identified as a new species until an expert revises the group. This would contribute to increase the species 'shelf life'. 'Citizen scientists' – e.g., farmers, forest rangers, and firefighters – and professional biologists not trained in taxonomy – e.g., ecologists, physiologists – often collect reptiles that are found dead. If redirected to scientific collections, such specimens may eventually become type specimens of new species, as pointed out for Atlantic Forest reptiles in South America (MOURA et al., 2018). Although citizen-science is well established in some fields (e.g., ornithology), it is only starting to become a factor in herpetology (O'DONNELL; DURSO, 2014; PRICE; DORCAS, 2011). It is crucially important to make taxonomists available for museum collections, but also collections available for taxonomists, which can be accomplished by allowing visitation to scientific collections, lending specimens, digitizing not just databases, but also museum specimens using 3D scans or providing color plates, especially for type specimens (e.g., 43, 44). By doing so, unknown species collected by non-taxonomists can be properly handled and remain shelved for much shorter times.

Taxonomic reviews are important in detecting specimens collected a long time ago. Only a small portion of collected specimens are recognized as belonging to new species upon collection in the field (BEBBER et al., 2010; FONTAINE; PERRARD; BOUCHET, 2012). Most specimens are stored in museums often forming huge collections of unstudied material that could serve as a pool for new species descriptions (BEBBER et al., 2010). During taxonomic revisions, detailed comparisons among closely related species are carried out – frequently on hundreds of specimens housed in several museums. It is evident that such procedure allows the discovery of undescribed taxa represented by old specimens stored since long ago. For example, the skink lizard *Capitellum mariagalantae* was first collected sometime between 1830 and 1861, and described in 2012, during a revisionary work in which the authors examined ~750 preserved specimens from 24 scientific collections (HEDGES; CONN, 2012). Taxonomic revisions can also act synergistically with efforts provided by non-taxonomists. The anguid lizard *Abronia smithi*, for example, was described during a taxonomic revision in 1993. Its holotype was obtained by local collectors 15 years before (CAMPBELL; FROST, 1993).

We found shorter shelf life for lizard species described based on a fewer type specimens. This trend can be due to at least two factors. First, considering that most species are rare in nature (PRESTON, 1948), most new species when first collected are represented by few specimens – often only one (e.g., 45). Therefore, taxonomists describing new species based on several type specimens had to wait more time until they were able to describe a new species (FONTAINE; PERRARD; BOUCHET, 2012). In despite of this intuitive reasoning, we did not find a clear relationship between the range or variation in collection dates of type specimens and the size of type series (Fig. S3). It indicates that the processes behind such finding is possibly much more complex and may involve other factors. Second, it may be faster to analyze and obtain diagnostic features of candidate species based on a few type specimens than on many, although it might be difficult to investigate this latter possibility.

We expected longer time lag for species belonging to speciose genera, whose descriptions included taxonomic comparisons with many closely-related species (COLLEN; PURVIS; GITTLEMAN, 2004; GASTON; BLACKBURN; LODER, 1995). However, we observed the inverse relationship for lizards: species belonging to species-rich genera were described with shorter time lags. Speciose lizard genera such as *Anolis*, *Cyrtodactylus,* and *Liolaemus,* have gone through several taxonomic updates, which ultimately improved the knowledge of the distinguishing traits of each known species. It is possible that the availability of such information facilitates taxonomic comparisons across species, allowing a positive feedback that ultimately boosts the discovery process within speciose genera.

We have shown how species-level traits and sociological attributes of museums and taxonomists can contribute to 'shelve' yet unknown species for decades in scientific collections. However, other institutional-level factors, such as collection size, or the number of active taxonomists working at, or curating in them, likely affect the time lag in species discoveries. For instance, overloaded and understaffed scientific collections demand a comprehensive amount of time and effort of their staff to properly examine all housed specimens. Deficient workplace facilities and inadequate equipment can incapacitate researchers from properly analyzing collected but undescribed species. Such additional institutional-level variables are potential drivers of the species shelf life, deserving further investigation. Moreover, the average species shelf life can also be affected by temporal variations in the rates of either species descriptions – which are accelerating for reptiles (MEIRI, 2018; UETZ; FREED; HOSEK, 2018) – or specimen collections. If collection efforts were constant over time, an increasing rate of species discoveries would rapidly remove older specimens from the bulk of unknown species, ultimately decreasing the average time lag of global reptile species. Rates of specimen collections, holotype collections, and species descriptions, however, are not constant (Fig. S4).

In conclusion, we reveal to taxonomists what kind of reptile species have been shelved longer before their formal description. Our findings highlight how taxonomists can bridge the gap between natural history collections and non-taxonomists. The active participation of the collector of holotype in the discovery process is the major factor boosting the formal species descriptions. Although non-taxonomists greatly contribute to the growth of biodiversity knowledge (THEOBALD et al., 2015), their collecting tend to remain unappreciated or 'hidden in scientific collections' as specimens are either left undescribed or assigned to wide-ranging, well known taxa. At this point, revisionary taxonomic studies are crucial in uncovering older specimens from the bulk of undescribed species housed in scientific collection. Such taxonomic reviews should prioritize preserved specimens belonging to less speciouse genera, and collected by non-taxonomists. To boost species descriptions and reduce the Linnaean shortfall on Earth's biota, which represents one of the main goals established during the CBD, more funds must be targeted to research in natural history collections, and for taxonomist training programs. Despite the relevance of fieldwork to better understanding biodiversity, it is also important to better look at scientific collections, the houses where many undescribed species are ‘waiting’ for their formal description.

Materials and methods

Data collection. We reviewed the literature on descriptions of 2,612 valid reptile species published from 1992 to 2017 by reading their description papers (Dataset S1). This period reflects broadly similar scientific and socioeconomic influences on reptile descriptions, which differs considerably from 19th century and early 20th century practices. Unlike the extremely brief descriptions of old, often based on single individuals and a very limited set of characters, modern descriptions often involve many characters, detailed morphological examinations, and molecular analyses, as well as high resolution photographs and, increasingly, CT scans. We removed 254 of these species because of missing data – e.g., their holotype collection date is unknown. We measured the time lag of each species discovery as the interval (in years) between the species description date and collection date of the holotype. We selected the holotype because one is always available, and it will always be used to describe the species (e.g., even if a paratype is found to belong to a different species). Using other dates, such as the date of the oldest type specimen, would bias the time lag due to the sampling effect associated with increasing type series size – with more specimens, higher the chances to find a very old specimen. We analyzed all reptiles as well as lizards and snakes separately. Fewer than 50 turtles and amphisbaenians were described from 1992 to 2017. We therefore merged amphisbaenians with lizards in the taxon-specific analyses, and excluded turtles. We compiled data on nine potential predictors of species shelf life. Six were continuous covariates: (i) maximum body mass – obtained from (FELDMAN et al., 2015), and original descriptions; (ii) latitude from the locality harboring the holotype. When latitude was unavailable in the original description, it was estimated based on the mentioned type locality;

(iii) latitude of the museum in which the holotype is housed (Uetz et al.; unpublished data); (iv) The number of authors in the species description; and (v) number of specimens in the type series – were derived from the description papers; (vi) The number of congeners at the year of description was based on current taxonomy (UETZ; FREED; HOSEK, 2018). We acknowledge that the latter is not always a precise measure due to the recent splitting of some genera (e.g., *Lacerta, Mabuya, Sphenomorphus*). Three other predictors were binary covariates, which we gleaned from the description papers, and informed if (vii) collectors of the holotype participated in the species description; (viii) whether a molecular analysis was used as evidence in the species description; and (ix) if the description was based on a taxonomic revision. We defined a publication as a taxonomic revision if the work explicitly mentioned it – e.g., using words such as *revision/review/revise* – on its title, abstract, key words, or throughout the main text.

Statistical Analysis. The time lag in species discoveries was investigated through time-to-event analysis, also known as survival analysis (BRADBURN et al., 2003; CLARK et al., 2003). Time-to-event analysis are commonly applied to investigate factors affecting the probability of an event (e.g., failure time, death), but has also been used in ecological studies (e.g., 54). Our event of interest here is the time of a species' formal description. Specifically, we used Accelerated Failure Time (AFT) model, a parametric survival model that allows for the evaluation of covariate effects on acceleration/deceleration of survival time (BAGDONAVICIUS; NIKULIN, 2002).We $\log_{10}$ transformed the continuous predictors (number of type specimens, number of species on genus, and number of authors in descriptions) to reduce their skewness and improve linearity of the relationship with our response variable. We checked for multicollinearity among continuous variables using Variation Inflation Factors (VIFs; 56), which varies from 1 to +inf. Strong multicollinearity is normally attributed to VIF values > 10, indicating that variables should be removed from analysis (KUTNER et al., 2005). None of our continuous variables reached VIF > 2 and we thus kept them all (Table S3). We used an AICc-based model selection to identify the best error distribution (among exponential, weibull, lognormal, log-logistic, gamma, and gompertz) for the AFT model (BURNHAM; ANDERSON, 2002), and found the lognormal distribution as the most suitable one. We averaged all 511 models ($2^9 - 1$, no interaction terms) (CADE, 2015; SYMONDS; MOUSSALLI, 2011) based on their respective AICc weights.

Sensitivity Analysis. Some predictors are prone to temporal constraints. For example, the collector of the holotype is unlikely to be an author in the description of a post 1991 species if the holotype was collected before 1930. Likewise, the holotype of species descriptions using molecular analysis could probably not have been collected when formalin was widely used as fixative (e.g., probably until the late 20th century in most collections). Ultimately, these temporal constraints would overestimate the effect size of some covariates. To account for the potential differential influence of old specimens in our models, we performed a sensitivity analysis by successively discarding specimens collected very early. We defined 10 time periods covering the interval from *y* to 2017, where *y* is a 5-year interval from 1952 to 2017 (e.g. 1952–2017, 1957–2017, …, 1992–2017). We then filtered the species dataset to include only holotypes collected within each time period and repeated our analyses. In restricting the oldest collection dates from 1952–2017 towards 1992–2017, we constrained the temporal range of collection dates to be the same as that of the description dates, although such procedure inevitably reduces the number of samplings units (species) available for the analysis. Computations were performed in R 3.3.3 (R, 2017) using the *survival* (THERNEAU; T. LUMLEY, 2018), *survminer* (KASSAMBARA; KOSINSKI, 2018), *flexsurv* (JACKSON, 2016), *MuMIn* (BARTON, 2018), and *usdm* (NAIMI et al., 2014) packages. R scripts and raw datasets are available in the supplements: see Data Availability section.

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Author contributions

MRM conceived the ideas and designed methodology; JJMG and SM compiled the data; MRM and JJMG analyzed the data; JJMG led the writing. All authors contributed in the form of discussions and suggestions, and approved the final manuscript.

Conflict of Interest

The authors declare no conflict of interest.

Data Availability

Raw data and R script necessary for replicating the analysis and plotting figures must be requested from the corresponding author.

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Supplementary Material

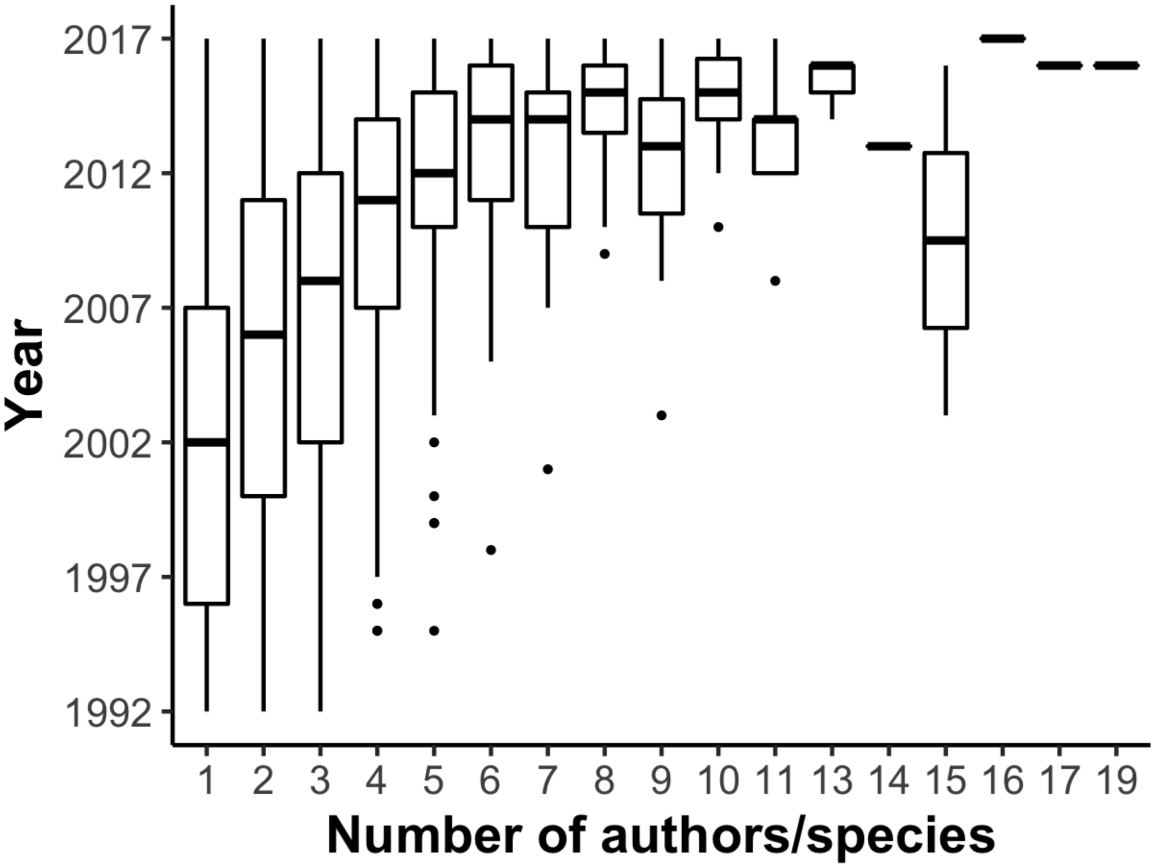

Fig. S1. Increase over the years in the number of authors per species descriptions – taxonomic effort – of reptiles described from 1992 to 2017.

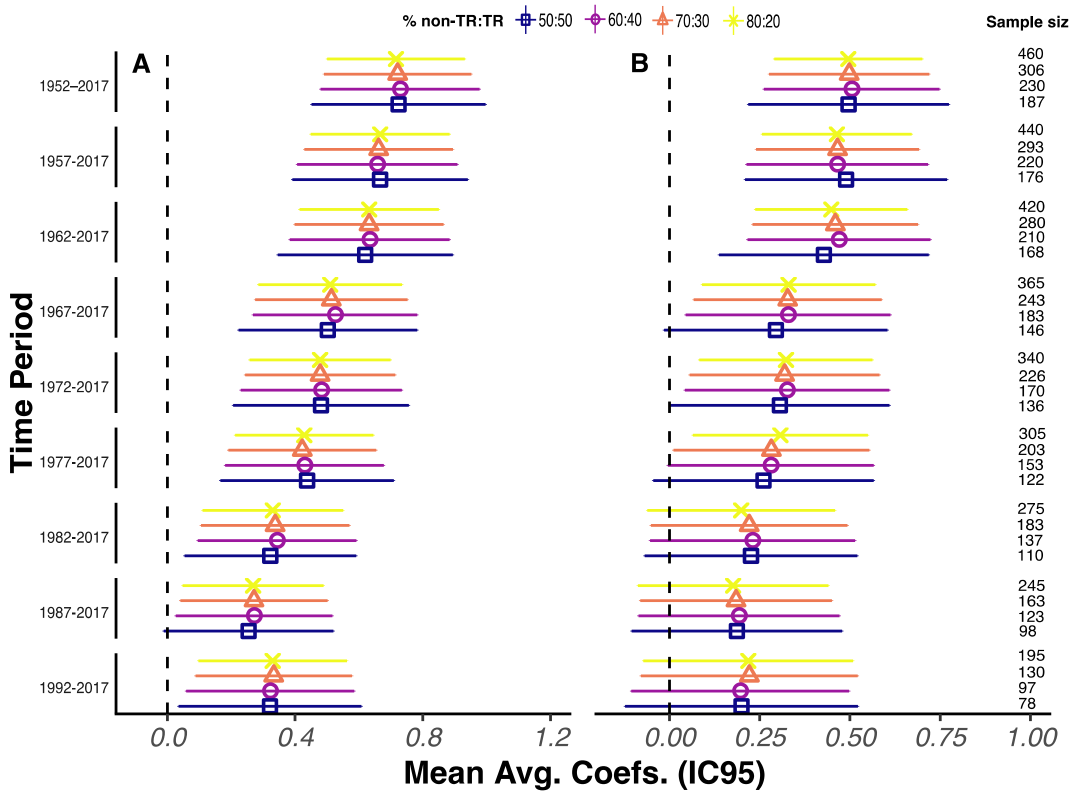

Fig. S2. Sensitivity analysis on the influence of sample size and unbalanced samples on the coefficients of the variable taxonomic review for snakes. The loss of significance of taxonomic review can result from either a reduction in sample size after the successive discard of older specimens, or be due to the unbalanced sample. The standardized coefficients are shown for models with taxonomic review as single predictor (A) and its respective coefficient based on the average weighted model with all nine predictors (B).

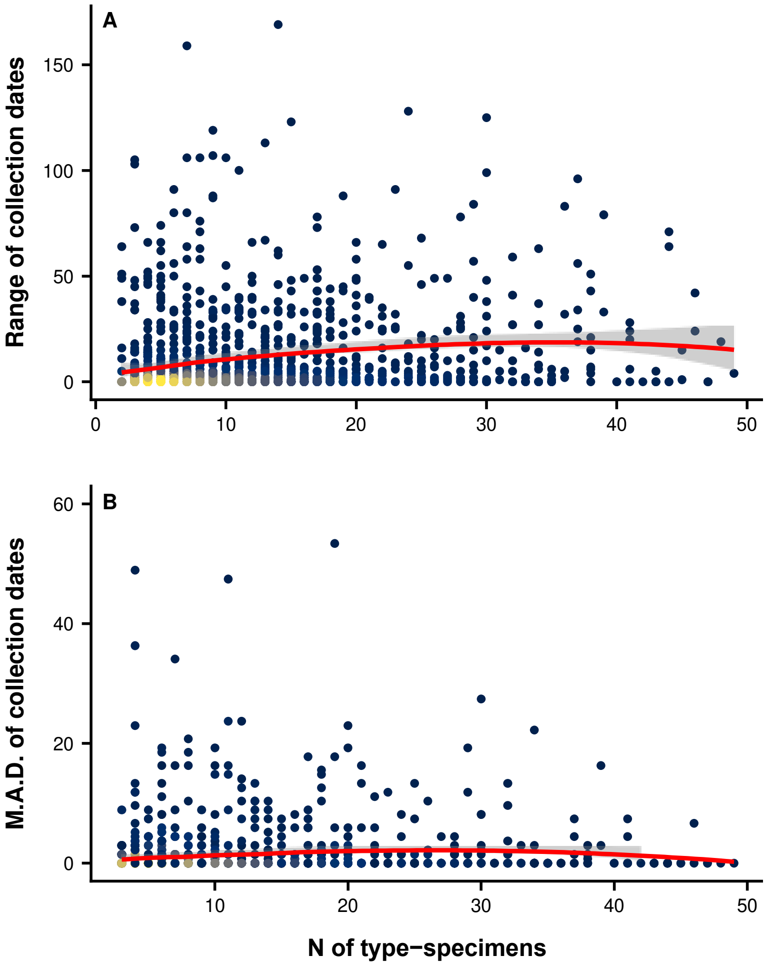

Fig. S3. Density plot for the relationship between the size of type series and the (A) range and (B) variation – median absolute deviation (MAD) – in collection dates of type specimens. The collection of three or more type specimens does not necessarily take longer.

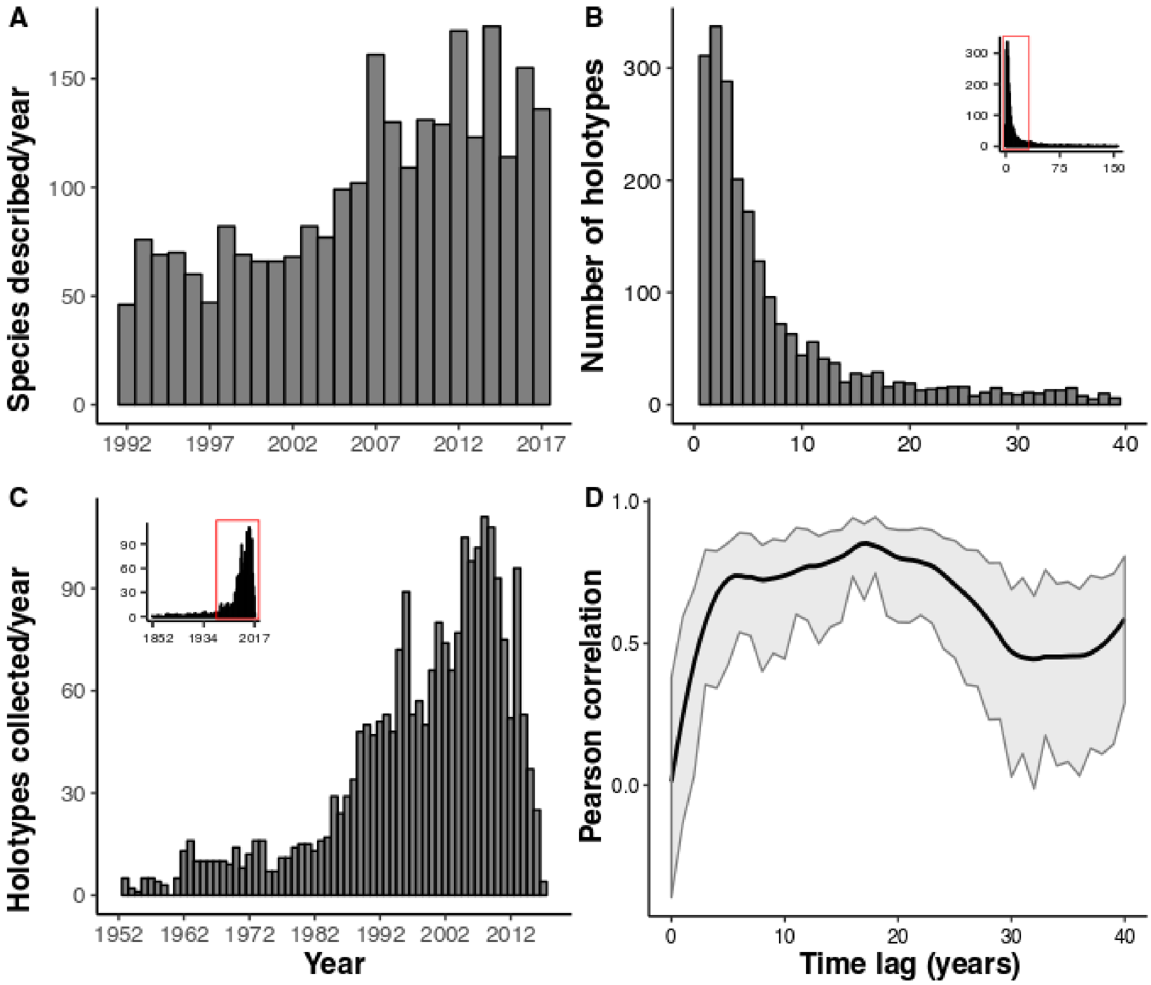

Fig. S4. Temporal variations in the rates of either species descriptions or specimen collections might affect the average species shelf life. A: Gradual increase of the number of reptile species described from 1992 to 2017. B: Most reptiles described during this time period have shorter time lags (median = 5 years). C: Rapid increase in the collection of holotypes after 1982, which could affect species descriptions in later years, and hence, the average time lag. D: Pearson correlation between the number of holotypes collected and the number of species described by a given time lag value (gray area denotes the 95% CI). It shows that the rate of reptile descriptions is also affected by the amount of holotypes collected in the past, particularly from 5 to 25 years before species description date.

Table S1. Raw time lag filtered by biogeographic realm, herpetofaunal group, and categorical predictor. N = number of species (samples) in each level.

Filters/levels		**Time lag (years)**						
		N	**min**	**max**	**median**	**mean**	**sd**	**se**
Biogeographic realm	Afrotropic	414	0	114	5	11.71	16.79	0.83
	Australasia	196	0	47	8	9.98	8.83	0.63
	IndoMalay	668	0	155	3	9.72	22.04	0.85
	Nearctic	32	1	57	9	18.63	17.67	3.12
	Neotropic	937	0	154	6	13.90	21.09	0.69
	Oceania	217	0	146	6	20.28	31.02	2.11
	Palearctic	148	0	127	4	13.13	24.43	2.01
Group	Lizards	1939	0	155	4	10.53	18.77	0.43
	Snakes	673	0	146	7.5	19.40	26.87	1.04
Collector is author	No	986	0	155	12	24.80	30.24	0.96
	Yes	1495	0	64	3	5.24	6.17	0.16
Molecular analysis	No	1845	0	155	5	14.50	23.77	0.55
	Yes	757	0	135	4	8.62	13.77	0.50
Taxonomic review	No	2040	0	144	4	10.25	17.78	0.39
	Yes	572	0	155	9	21.77	29.58	1.24

Table S2. Standardized coefficients of predictors in the average weighted accelerated failure time (AFT) models, both globally and by reptile group. * = 95% confidence interval of the coefficient that did not encompass '0'.

Predictor	***Global***		*Lizards*		*Snakes*	
	ß (s.e.)	exp(ß)	ß (s.e.)	exp(ß)	ß (s.e.)	exp(ß)
Nº of authors	**-0.026 (0.026)** *	0.974	-0.021 (0.025)	0.979	-0.011 (0.031)	0.989
Nº of type-specimens	0.071 (0.019)	1.074	**0.11 (0.022)** *	1.116	0.02 (0.036)	1.020
Nº of spp/genus	**-0.095 (0.018)** *	0.909	**-0.113 (0.02)** *	0.893	0.011 (0.032)	1.011
Body size	**0.011 (0.017)** *	1.011	0.037 (0.03)	1.038	**-0.114 (0.041)** *	0.892
Latitude of holotype	-0.074 (0.02)	0.929	-0.025 (0.025)	0.975	**-0.196 (0.045)** *	0.822
Latitude of museum	**0.141 (0.019)** *	1.151	**0.119 (0.022)** *	1.126	**0.217 (0.041)** *	1.242
Collector is author	**-0.919 (0.041)** *	0.399	**-0.891 (0.047)** *	0.410	**-0.88 (0.084)** *	0.415
Taxonomic review	**0.438 (0.046)** *	1.550	**0.375 (0.051)** *	1.455	**0.593 (0.102)** *	1.809
Molecular analysis	**-0.134 (0.054)** *	0.875	-0.044 (0.052)	0.957	-0.118 (0.13)	0.889
Pseudo-R^2	0.305		0.276		0.347	

Table S3. Variance inflation factor (VIF) values obtained among the six continuous predictors used in the Accelerated Failure Time (AFT) model.

Variables	VIF
Log10_mass	1.009032
Lat	1.115036
Lat_mz	1.096637
LogN_specimens_TS	1.04404
LogN_spp_genus	1.027872
LogN_authors	1.010069