UNDERSTANDING CHANGES IN NEOTROPICAL AMPHIBIAN COMMUNITIES IN THE FACE OF ANTHROPOGENIC PRESSURES:

A SPATIAL, PHYLOGENETIC AND FUNCTIONAL APPROACH

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ABSTRACT

Amphibians are globally declining at an unprecedented rate with almost half of species now considered at risk of extinction. Several factors, including climate change, habitat loss and infectious diseases, have been identified as main drivers of amphibians declines; however, their impacts on the different facets of amphibian diversity across space and time are still poorly understood. There is, therefore, an urgent need to better understand the threats to amphibian diversity at both regional and local scales. In this thesis, I combine modeling and empirical data to evaluate changes in Neotropical amphibian communities in the Anthropocene. In Chapter 1, I use species distribution models for 2,269 species to explore how climate change may drive shifts in amphibian species richness, ecological specialism and phylogenetic diversity. I show that by 2070, the majority of anuran highland assemblages will exhibit increasing biotic homogenization, a consequence of gains in generalist species (and to a lesser extent of losses in specialists), leading to elevated taxonomic richness, but a reduction in phylogenetic diversity. In contrast, the majority of anuran lowland assemblages will become increasingly heterogeneous, a consequence of the local extinction of generalists, leading to reduced taxonomic diversity, and an increase in phylogenetic diversity. In Chapter 2, I evaluate the functional relevance of highly threatened anuran species, and the impact of their loss on taxonomic, functional and phylogenetic diversity at a regional scale. I show that within Ecuadorian anuran communities, highly threatened species are more functionally distinct than non-threatened species. I also show that the extinction of currently threatened anurans would result in increasing taxonomic, phylogenetic, and especially, functional homogenization of anuran assemblages across the Ecuadorian Andes, with potential consequence for the stability of local ecosystem functioning. In Chapter 3, I combine empirical data from historic and recent surveys to evaluate diversity changes in seven amphibian communities in the Ecuadorian Andes over the past 50 years. I use Bayesian models to test the role of climate change and habitat loss as drivers of local species losses. I reveal that most communities have experienced substantial species losses, on average almost 52% of species were lost, and these local extirpations are associated with climate warming. I also show that community changes in species composition have resulted in significant erosion of functional and phylogenetic diversity, and increased functional homogenization of communities across space. In Chapter 4, I use phylogenetic, morphological and bioacoustics analyses to explore cryptic anuran diversity in the Neotropics. I reveal that populations of the *Rhinella marina* species complex from the western side of the Ecuadorian Andes are a new species, and describe it here for the first time as *Rhinella bellus* sp. nov. The body of work I present in this thesis highlights large and consistent impacts of anthropogenic environmental change on anuran diversity that may have substantial ecosystem consequences. My research also shows that much of Neotropical diversity may still be undescribed, presenting a challenge to efforts aimed at reducing rates of biodiversity decline.

RÉSUMÉ

Les amphibiens déclinent dans le monde à un rythme sans précédent et près de la moitié des espèces d’amphibiens sont désormais considérées comme menacées d'extinction. Plusieurs facteurs, dont le changement climatique, la perte d'habitat et les maladies infectieuses, ont été identifiés comme les principaux moteurs du déclin des amphibiens; cependant, leurs impacts sur les différentes facettes de la diversité des amphibiens dans l'espace et le temps demeurent mal compris. Il est donc urgent de mieux comprendre les menaces qui pèsent sur la diversité des amphibiens aux échelles régionale et locale. Dans cette thèse, je combine la modélisation et les données empiriques pour évaluer les changements dans les communautés d'amphibiens néotropicaux dans l'Anthropocène. Dans le chapitre 1, j'utilise des modèles de distribution des espèces pour 2 269 espèces afin d’explorer comment le changement climatique peut entraîner des changements dans la richesse des espèces d'amphibiens, la spécialisation écologique et la diversité phylogénétique. Je démontre que d'ici 2070, la majorité des assemblages d’anoures dans les hautes terres présenteront une augmentation d’homogénéisation biotique, conséquence de gains d'espèces généralistes (et dans une moindre mesure de pertes en spécialistes), menant à une richesse taxonomique augmenté et à une diversité phylogénétique réduite. En revanche, la majorité des assemblages d’anoures dans les basses terres deviendront de plus en plus hétérogènes, conséquence de l'extinction locale des généralistes, menant à une diversité taxonomique réduite et à une diversité phylogénétique augmenté. Dans le chapitre 2, j'évalue la pertinence fonctionnelle des espèces d'anoures fortemenet menacées et l'impact de leur disparition sur la diversité taxonomique, fonctionnelle et phylogénétique à l'échelle régionale. Je démontre qu'au sein des communautés d’anoures équatoriennes, les espèces fortement menacées sont fonctionnellement plus distinctes que les espèces non menacées. Je démontre également que l'extinction des anoures actuellement menacés entraînerait une augmentation d'homogénéisation taxonomique, phylogénétique et surtout fonctionnelle des assemblages d'anoures à travers les Andes équatoriennes, avec des conséquences potentielles sur la stabilité du fonctionnement des écosystèmes locaux. Dans le chapitre 3, je combine des données empiriques provenant d'études récentes et historiques pour évaluer les changements de diversité au cours des 50 dernières années dans sept communautés d'amphibiens des Andes équatoriennes. J'utilise des modèles Bayésiens pour tester le rôle du changement climatique et de la perte d'habitat en tant que facteurs de pertes d'espèces locales. Je révèle que la plupart des communautés ont subi des pertes substantielles d'espèces (en moyenne près de 52% des espèces ont été perdues) et que ces disparitions locales sont associées au réchauffement climatique. Je révèle également que les changements communautaires dans la composition des espèces ont entraîné une érosion significative de la diversité fonctionnelle et phylogénétique et une homogénéisation fonctionnelle accrue des communautés à travers l'espace. Dans le chapitre 4, j'utilise des analyses phylogénétiques, morphologiques et bioacoustiques pour explorer la diversité des anoures cryptiques dans les régions néotropicales. Je révèle que les populations du complexe d'espèces *Rhinella marina* du côté ouest des Andes équatoriennes sont une nouvelle espèce, et je la décris ici pour la première fois sous le nom de *Rhinella bellus* sp. nov. L'ensemble des travaux que je présente dans cette thèse met en évidence les impacts importants et cohérents des changements environnementaux anthropiques sur la diversité des anoures, qui peuvent avoir des conséquences substantielles sur l'écosystème. Mes recherches démontrent également qu'une grande partie de la diversité néotropicale n'est peut-être pas encore décrite, ce qui pose un défi pour les efforts visant à réduire les taux de déclin de la biodiversité.

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This thesis is dedicated to my son Samu (mi pipo), who is my inspiration to keep moving forward, and with whom I discovered that love has no limits.

PREFACE

All manuscript chapters of this thesis constitute original contributions to scientific knowledge.

In chapter 1, I present the first assessment of the projected effects of future climate change on species assembly structure (beta diversity) in one of the most diverse and threatened groups – Neotropical amphibians, at a continental scale. I show that in tropical highlands, range expansion of generalists and the extinction of specialists will likely result in the homogenization of amphibian assemblages. In contrast, in tropical lowlands, assemblages are predicted to become more heterogeneous, mainly driven by local extirpations. These results have important implications for understanding the effect of climate change beyond species richness reductions, and for biodiversity conservation in the Anthropocene.

In chapter 2, I examine the functional importance of highly threatened amphibians and the potential impacts of their extinction on the functional diversity of Ecuadorian amphibian assemblages at a regional scale. I show that the potential extinction of highly threatened and functionally distinct species would drive the functional homogenization of anuran assemblages across the Andes of Ecuador, which may have significant consequences for ecosystem functioning. These results highlight the importance of examine more closely the declines in functional diversity that accompany species extinctions in biodiversity assessments and conservation strategies.

In chapter 3, I show empirically the dramatic erosion in anuran diversity over the past 50 years within the montane communities of Ecuadorian Andes. Nearly half of anuran species went locally extinct in the communities surveyed during the study period, and declines were associated with recent climate warming. I also show local extirpations are accompanied with disproportionate losses in phylogenetic and functional alpha and beta diversity. Together, these findings indicate that impacts of climate change on Neotropical amphibian diversity in the Anthropocene may be much greater than currently assumed .

In chapter 4, I examine cryptic amphibian diversity in the Neotropics using an integrative approach that incorporates phylogenetic, bioacoustic, morphometric and ecological data. I describe a new species within the *Rhinella marina* (Cane Toad) species group. The discovery of a new species within such a conspicuous group of anurans highlights the likely large unrecognized diversity within Neotropical regions, and emphasizes the need to better document cryptic diversity if we are to fully understand biodiversity change in the Anthropocene.

THESIS FORMAT

The present thesis is written in a manuscript-based format and includes: a general introduction, four manuscript chapters (Chapter 1-4), short linking statements to connect chapters, a general discussion & conclusion, and an appendix, which comprises supplementary material for all manuscript chapters. For all manuscript chapters, I am the lead author. Chapters 1 and 2 have been published previously in peer-reviewed journals. Chapter 3 and Chapter 4 will be submitted for publication. Each manuscript chapter is formatted according journal guidelines.

Chapter 1: Menéndez-Guerrero, P.A., Green, D.M. and Davies, T.J. (2020). Climate change and the future restructuring of Neotropical anuran biodiversity. *Ecography*, *43*(2), 222–235.

Chapter 2: Menéndez-Guerrero, P.A., Davies, T.J. and Green, D.M. (2020). Extinctions of Threatened Frogs may Impact Ecosystems in a Global Hotspot of Anuran Diversity. *Herpetologica*, *76*(2), 121–131.

Chapter 3: Menéndez-Guerrero, P.A., Carvajal-Endara, S., Ron, S.R., Vaca-Guerrero, G., Yánez-Muñoz, M.H., Bustamante, M.R., Green, D.M., and Davies, T.J. Diversity erosion of Neotropical mountain amphibian communities in the Anthropocene. *Prepared for submission to Journal of Animal Ecology*.

Chapter 4: Menéndez-Guerrero, P.A., dos Santos, S.P., Salazar-Nicholls, M.J., Green, D.M., and Ron, S.R. Cryptic Diversity in Toads of the *Rhinella marina* species group (Anura, Bufonidae) and a new species from Western Ecuador. *Prepared for submission to Zoological Journal of the Linnean Society.*

CONTRIBUTION OF AUTHORS

Chapter 1: Pablo A. Menéndez-Guerrero and T. Jonathan Davies designed the study; Pablo A. Menéndez-Guerrero collected the data, performed data analyses, and wrote the manuscript with input from Jonathan T. Davies and David M. Green.

Chapter 2: Pablo A. Menéndez-Guerrero designed the study with input from David M. Green; Pablo A. Menéndez-Guerrero collected the data, performed data analyses, and wrote the manuscript with input from Jonathan T. Davies and David M. Green.

Chapter 3: Pablo A. Menéndez-Guerrero designed the study; Pablo A. Menéndez-Guerrero collected the data in collaboration with Santiago R. Ron, George Vaca-Guerrero, Mario H. Yánez-Muñoz and Martín R. Bustamante. Pablo A. Menéndez-Guerrero and Jonathan T. Davies performed the data analysis; Pablo A. Menéndez-Guerrero wrote the manuscript with input from Jonathan T. Davies, Sofía Carvajal-Endara and David M. Green.

Chapter 4: Pablo A. Menéndez-Guerrero and Santiago R. Ron designed the research. Pablo A. Menéndez-Guerrero, María-José Salazar-Nicholls and Sueny P. dos Santos collected the data; Pablo A. Menéndez-Guerrero analyzed the data and wrote the manuscript with input from Santiago R. Ron, David M. Green and Sueny P. dos Santos.

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General Introduction

Although geographic ranges of species are always shifting, and biological communities are continually being rearranged, an unprecedented combination of global change drivers is rapidly and dramatically altering the diversity and structure of ecological communities (Lovejoy and Hannah, 2006; Cardinale et al., 2012. These changes, in turn, may have serious adverse impacts on the functioning of ecosystems and on the services and goods they provide (Oliver et al., 2015). Much attention has been focused on documenting species range shifts, but we have only recently started to explore how these human-caused range shifts might drive changes in the structure and composition of communities across space and time (e.g., Peterson et al., 2002; Thuiller et al., 2005; Buisson and Grenouillet, 2009; Reu et al., 2014, Molinos et al., 2016; Zwiener et al., 2018). To better understand the complexity of anthropogenic-related reshaping of biodiversity and the likelihood of decline in the resilience of ecosystems, we need integrative approaches that explicitly incorporate the different facets of biodiversity across scales from local to global (Morlon et al., 2011; Pavoine and Bonsall, 2011; Lefcheck et al., 2015; Isbell et al., 2017; Chase et al., 2019).

Global change drivers of shifts in species communities

Mounting evidence shows that climate change and habitat loss are the main anthropogenic drivers of biodiversity loss and community restructuring (Bennett and Saunders, 2010; Laurance, 2010; Lojevoy, 2010; Pecl et al., 2017). For instance, it is predicted that climate change-driven extinction of ecological specialist species and their replacement by widespread resilient generalist species, will result in ecological communities becoming less diverse and more homogeneous, i.e., have increased community similarity (McKinney and Lockwood, 1999; Clavel et al., 2011). These expectations have been confirmed by several observational studies (e.g., Menéndez et al., 2006; Jurasinski and Kreyling 2007; Davey et al., 2012; Savage and Vellend, 2015) and predictive models across multiple taxa (e.g., Buisson and Grenouillet, 2009; Molinos et al., 2016; Zwiener et al., 2018). Additional studies have documented compositional changes, for example shifts towards a higher dominance of heat-tolerant or arid-associated species with rising temperatures and decreasing precipitation, respectively (Gottfried et al., 2012; Feeley et al., 2013; Fadrique et al., 2018; Esquivel-Muelbert et al., 2019).

Climate change may drive homogenization through extinctions of specialist species (e.g., Rahel, 2002; Olden and Poff, 2003) and via promoting range expansions of disturbance-tolerant species (e.g. Zwiener et al., 2018). Thus shifts towards greater biotic homogenization are not necessarily accompanied by decreases in species richness (Dornelas et al., 2014; Magurran et al., 2015). Habitat loss and fragmentation can also drive biotic homogenization by selecting for those species best able to survive within the modified ecosystem. For instance, plant, insect and bird communities are shifting in composition towards a greater proportion of disturbance-adapted species and a lesser proportion of disturbance-sensitive or forest-specialized species (Olden and Poff, 2004; Ribeiro-Neto et al., 2016; Smart et al., 2006; Gómez-Martínez et al., 2020). Species introductions and invasive spread will also enhance homogenization. Some amphibian and fish communities are already experiencing such changes via species introductions from multiple sources, such as agriculture, aquaculture and aquarium escapees (Richter et al., 1997; Rahel, 2002; Nowakowski et al., 2018). The synergistic effects of climate change and habitat loss have been less well studied, but may also have profound influences on rates of biotic homogenization and the restructuring of biodiversity (Brook et al., 2009; Kampichler et al., 2012).

Species range shifts, in response to anthropogenic pressures, may also drive biotic heterogenization – the increasing differentiation of species communities (e.g., Moritz et al., 2008; Tingley and Beissinger, 2013; Molinos et al., 2015) – which is also recognized as a potential outcome of anthropogenic change (Socolar et al. 2016). The impacts of increasing heterogeneity are less clear, but it is possible it too could have detrimental effects upon ecosystems (Folke, et al., 2004, Ochoa-Ochoa, et al., 2012).

Biotic homogenization will likely become intensified due to increasing climate and land-use changes in coming years, and is now recognized as a major conservation concern (Cardinale et al., 2012; Molinos et al., 2016). The potential ecological consequences of biotic homogenization include a reduction of overall ecosystem functioning and stability and, over longer time periods, likely a decline in speciation rates and the adaptive capacity of communities in the face of future environmental changes (Olden et al., 2004). Importantly, the magnitude of biotic homogenization (or heterogenization) depends not only on intensity of anthropogenic drivers, but also the spatial and temporal scale at which communities are characterized (Keil et al., 2011; McGill et al., 2015), the rate at which species are gained and/or lost across the landscape, the composition and structure of the species pool from which invaders disperse, and the specific components of community diversity under consideration (Olden and Poff, 2003; Olden and Poff, 2004; Olden, 2006; Smart et al., 2006; de Castro Solar et al., 2015).

The importance of spatial scale

Spatial scale might influence the signature of anthropogenic impacts. Biodiversity changes and the increasing alteration of ecosystems occur at multiple spatial scales (Sax and

Gaines 2003; Reichstein et al., 2014; Isbell et al., 2017; Chase et al., 2019). Changes at a global scale are not necessarily manifested at smaller scales, and vice-versa (Smith et al., 1993; Chase et al., 2019). Commonly, changes in species richness can even contrast across scales, with overall declines in species richness at global scales and increases of species richness at smaller scales, suggesting that changes in biodiversity are spatially structured (Sax and Gaines, 2003; Millennium Ecosystem Assessment 2005; Sax and Gaines, 2008; Blowes et al., 2019). However, our consideration of spatial scale in studies of biodiversity change within the context of anthropogenic threats is still insufficient (Chase et al., 2019).

At a global scale, habitat degradation is an important factor triggering extinctions of native species and overall reduction of alpha diversity (i.e., the number of species), while at smaller scales these extinctions may be offset by the spread of non-native species. As a result, we might detect no change, or even an overall increase, in alpha diversity, but a reduction in spatial beta diversity (i.e., differences in species composition among communities), supporting a trend towards biotic homogenization (Trentanovi et al., 2013; Rahel, 2000; Sax et al., 2002; Finderup Nielsen et al., 2019; but see: Li et al., 2020). Similarly, climate warming may lead to either increases or decreases in alpha diversity at community scales (Williams and Jackson, 2007; Damschen, et al., 2010; Davey et al., 2013), but both of which could be accompanied by decreases in local-scale beta diversity, for example, by the facilitation of thermophilization (i.e. increasing dominance of warm-affinity species) of some biological communities or the upward migration of animal species (Raxworthy et al., 2008; Chen et al., 2011; Forero-Medina et al., 2011; Savage and Vellend, 2015; Burrows et al., 2019). How these climate-driven community composition changes at small scales translate into larger scales has been less explored (Zwiener et al., 2018), and evidence is mixed (Feeley et al., 2020).

The complexity of biodiversity change across spatial scales is further exacerbated by the scale dependence of different types of diversity measurements (Pereira et al., 2013; Jarzyna and Jetz, 2018). To achieve a robust understanding of contemporary biodiversity change we must, therefore, not only consider how processes operating at one scale manifest at another scale, but also consider the multiple facets of biodiversity (e.g., Morlon et al. 2011; Smith et al. 2013; Li et al., 2020).

Multiple facets of biodiversity

Efforts to assess contemporary changes in biodiversity have been largely focused on taxonomic diversity (Chase et al., 2018; e.g., Kappelle et al., 1999; Mendenhall et al., 2014). However, a thorough analysis on how global change drives the loss of species and the re-assortment of ecological communities, should consider the multiple dimension of biodiversity (Graham and Fine, 2008; Devictor et al., 2010; Iknayan et al. 2014). To accomplish this task, we must consider other biodiversity descriptors such as functional diversity (Tilman, 2001) and phylogenetic diversity (Faith, 1992).

Functional diversity reflects the diversity of ecological traits among species (Chapin et al., 2000; Petchey and Gaston, 2006). Major changes in functional diversity are expected to have far-reaching consequences for ecosystems (Mokany et al., 2008; Peterson et al., 2005; Naeem et al., 2012). The extinction or invasion of functionally rare species (i.e., species with unique and irreplaceable functional roles), for example, could have disproportionate impacts on ecosystems relative to the gain or loss of species less functionally distinct within a given community (Mouillot et al., 2012, 2013; Jain et al., 2014; Leitão et al., 2016; Van Cleemput et al., 2020).

Phylogenetic diversity is a biodiversity measure that quantifies the shared evolutionary history of species (Faith, 1992), and has been frequently used as a surrogate for functional diversity (Web et al., 2002; Winter et al., 2012, but see Mazel et al., 2018). Phylogenetic diversity allows us to assess the current biodiversity crisis in terms of the amount of evolutionary history gained (e.g. with invasions) or loss (with extinctions), rather than simply focusing on species counts (Purvis et al., 2000). Additionally, phylogenetic information may also help us to better understand extinction cascades in ecological networks that could have large destabilizing effects on ecosystem functions (Srivastava et al., 2012)

In general, ecological communities with higher functional and phylogenetic alpha and beta diversity tend to be more stable, more productive, and likely more resilient to perturbations (Ives and Carpenter, 2007; Lavergne et al., 2010). For example, more phylogenetically diverse communities are thought to have greater evolutionary potential to adapt to shifting environmental conditions (Forest et al., 2007; Mouilllot et al., 2013; but see Tucker et al., 2019). Phylogenetic, functional and species diversity are frequently highly correlated. However, different facets of biodiversity may respond to environmental stressors in different ways (Devictor et al., 2010; Purschke et al., 2013; Hurtado et al., 2020; Li et al., 2020). For instance, bird, fish and plant assemblages across the globe have shown a decoupling in trends in taxonomic and phylogenetic diversity with anthropogenic pressures (Li et al., 2020). These assemblages have shown increasing taxonomic alpha diversity but decreasing phylogenetic diversity, whereas shifts in homogenization (beta diversity) were largely consistent, revealing a trend towards increasing homogenization. Similar findings have been reported elsewhere, with a decoupling of trends in the change in taxonomic, functional, and phylogenetic beta diversity (Villéger et al., 2014; Nowakowski et al., 2018; White et al., 2018), In some instances, functional homogenization exceeds rates of taxonomic and phylogenetic homogenization, as a result of the invasions of functionally redundant species (Olden et al., 2004, 2018).

These findings showing different, and sometimes conflicting, trends in biodiversity change across the different facets of biodiversity, highlight the importance of integrating across scales and biodiversity dimensions. In this thesis, I explore shifts in the functional and phylogenetic diversity of amphibians in the Neotropics, one the most speciose regions of the globe (Stuart et al., 2004; Wake and Vredenburg, 2008).

Amphibians as a study model

More than 8,000 amphibian species have been formally described, with 1,680 of these discovered only during the past ten years (AmphibiaWeb, 2020). The rate of discovery of new amphibian species has never been higher than it is at the present time (e.g., Fouquet et al, 2007, Funk et al., 2012), and is expected to increase in coming years due to widespread use of new molecular techniques in systematics (Catenazzi, 2015). Among amphibians, toads and frogs (i.e., Anurans) are by far the most numerous and widely distributed group, representing ~ 90% of all amphibian species (AmphibiaWeb, 2020).

Amphibians are often the most abundant vertebrates in many terrestrial and freshwater habitats (Stebbins and Cohen 1997), and are, therefore, critical components of these ecosystems. Their ecological importance includes mediating energy flow through trophic chains, cycling of essential nutrients for ecosystem functioning, such as carbon, nitrogen and phosphorus, bioturbation, seed dispersal and biological control of pests (Valencia-Aguilar et al., 2013; Hocking and Babbitt 2014; Cortes-Gomez et al., 2015). Additionally, amphibians provide services for human society, for example by serving as models in medical research, as a food source, and as cultural symbols, appearing in the folklore, myths and legends of many cultures throughout human history (Hofrichte, 2000; Hocking and Babbit, 2014). Yet amphibians are globally in decline, as recognized by the scientific community approximately 30 years ago (Grant et al., 2020; Green et al., 2020).

Amphibian diversity is experiencing global-scale declines at an unprecedented rate (Wake, 1991; Stuart et al., 2004; Sodhi et al., 2008; Collins, 2010), with nearly half of all known species threatened with extinction (González-del-Pliego et al., 2019). Although most amphibian declines have occurred in the Australian, Mesoamerican and South American tropics (Scheele et al., 2019), the amphibians of the Neotropics deserve special attention due to their exceptional diversity and endemism (Young et al., 2004). Six out of the 10 countries with the greatest amphibian diversity by unit area are in this region (Ron et al., 2020). Moreover, a significant amount of cryptic diversity has been reported among Neotropical amphibians (Fouquet et al., 2007, Funk et al., 2012). Unveiling cryptic species and understanding how species are distributed are critical steps for quantifying biodiversity, identifying threats to it, and designing efficient conservation efforts.

There is large geographic and taxonomic variation in amphibian declines, and in the underlying factors driving those declines (Grant et al., 2016; Miller et al., 2018; Grant et al., 2020; Lannoo and Stiles, 2020). Historically, the most important factor leading to amphibian population declines has been habitat destruction, degradation and fragmentation (Dodd and Smith, 2003). However, in many instances, declines have also been recorded in well protected and relatively pristine areas (Lips, 2000). An emerging disease called chytridiomycosis (caused by the fungal chytrid pathogen *Batrachochytrium dendrobatidis*) and global climate change have been proposed as major contributors to current and future species declines (Carey and Alexander 2003; Wake, 2007; Scheele et al., 2019; Smalling et al., 2019; but see Lambert et al., 2020). However, potential synergies among drivers, stochastic threats, and variation in the geographical scale of studies make robust predictions challenging (e.g., Scherer et al., 2005; Brooks et al., 2008; Menéndez-Guerrero and Graham, 2013; Vredenburg et al., 2010). Recent efforts based on large-scale studies of long time series have suggested that amphibian declines are real, but not ubiquitous, and that climate change is an important driver of population declines in North America and Europe (Grant et al., 2020). Equivalent efforts are still lacking for highly diverse regions, such the Neotropics.

Thesis organization

This thesis assesses past, present and future changes of Neotropical amphibian communities in the Anthropocene, using a multi-spatial scale framework encompassing different facets of biodiversity.

In Chapter 1, I predict future (2070) climate change driven shifts in biotic homogenization of Neotropical anuran assemblages at a continental scale. I employ species distribution modelling for 2,269 species and traditional metrics of beta diversity. I then use generalized additive models to assess whether climate induced changes in species richness, ecological specialism and phylogenetic diversity might drive contrasting changes in beta diversity within anuran assemblages in highlands versus lowlands.

In Chapter 2, I explore how extinctions of currently endangered anurans may impact ecosystem functioning at a regional scale. I first assess the functional importance of highly threatened vs non-threatened species within assemblages. I then evaluate how different scenarios of species extinctions may lead to changes in taxonomic, phylogenetic and especially functional similarity of anuran assemblages in Ecuador, a hotspot of anuran biodiversity. Finally, I illustrate the conservation relevance of functional diversity. In this chapter, I use taxonomic, phylogenetic and functional diversity metrics along with species distribution modelling.

In Chapter 3, I test the relative importance of climate change versus habitat loss as drivers of biodiversity changes within anuran communities. I first assess temporal changes in amphibian diversity over the past 50 years in seven communities of the Ecuadorian Andes, and explore how shifts taxonomic diversity are translated into changes in functional and phylogenetic diversity. I use Bayesian statistical modelling and long-term monitoring data.

In Chapter 4, I explore cryptic amphibian diversity in the Neotropics. I evaluate the phylogenetic relationships within the *Rhinella marina* (Cane Toad) species complex, with a focus on Ecuadorian populations. I examine species boundaries using DNA, morphological, bioacoustic and ecological characters,. As a result of this work, I describe a new species in the genus *Rhinella* found on the western side of the Ecuadorian Andes.

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CHAPTER 1:

Climate change and the future restructuring of Neotropical anuran biodiversity

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Abstract

Climate change is likely to impact multiple dimensions of biodiversity. Species range shifts are expected and may drive changes in the composition of species assemblages. In some regions, changes in climate may precipitate the loss of geographically restricted, niche specialists and facilitate their replacement by more widespread, niche generalists, leading to decreases in β-diversity and biotic homogenization. However, in other regions climate change may drive local extinctions and range contraction, leading to increases in β-diversity and biotic heterogenization. Regional topography should be a strong determinant of such changes as mountainous areas often are home to many geographically restricted species, whereas lowlands and plains are more often inhabited by widespread generalists. Climate warming, therefore, may simultaneously bring about opposite trends in β-diversity in mountainous highlands versus relatively flat lowlands. To test this hypothesis, we used species distribution modelling to map the present-day distributions of 2669 Neotropical anuran species, and then generated projections of their future distributions assuming future climate change scenarios. Using traditional metrics of β-diversity, we mapped shifts in biotic homogenization across the entire Neotropical region. We used generalized additive models to then evaluate how changes in β-diversity were associated with shifts in species richness, phylogenetic diversity, and one measure of ecological generalism. Consistent with our hypothesis, we find increasing biotic homogenization in most highlands, associated with increased numbers of generalists and, to a lesser extent, losses of specialists, leading to an overall increase in alpha diversity, but lower mean phylogenetic diversity. In the lowlands, biotic heterogenization was more common, and primarily driven by local extinctions of generalists, leading to lower α-diversity, but higher mean phylogenetic diversity. Our results suggest that impacts of climate change on β-diversity are likely to vary regionally, but will generally lead to lower diversity, with increases in β-diversity offset by decreases in α-diversity.

Keywords: beta diversity, biotic heterogeneity, biotic homogenization, climate change, community structure, extinction, species distribution modelling, species range shifts

INTRODUCTION

Global climate change has the potential to affect profoundly the future distribution of biodiversity and the composition of ecological communities (Bellard et al. 2012). Potential effects of climate change include alterations in species range sizes, extinction probabilities

(Lovejoy and Hannah 2006, Ladle and Whittaker 2011), and local richness of species assemblages (Peterson et al. 2002, Thuiller et al. 2005, Lawler et al. 2009, Reu et al. 2014). Shifts in species' ranges will also alter the spatial composition of species assemblages across landscapes (i.e., their β-diversity; Tuomisto 2010a,b, Anderson et al. 2011). There is increasing interest in exploring changes in β-diversity with climate change (e.g. Buisson and Grenouillet 2009, Ochoa-Ochoa et al. 2012, Tisseuil et al. 2012, Molinos et al. 2016, Socolar et al. 2016, Zwiener et al. 2018) because shifts may influence both ecosystem functioning and provisioning of ecosystem services (Lovejoy and Hannah 2006, Cardinale et al. 2012).

In general, species assemblages should become less diverse, and thus more homogeneous, where climate change precipitates the loss of geographically restricted, niche specialists and their replacement by more widespread, niche generalists (McKinney and Lockwood 1999, Clavel et al. 2011). For example, climate-driven latitudinal and altitudinal shifts of species ranges have been associated with biotic homogenization in several taxonomic groups (Menéndez et al. 2006, Davey et al. 2012, Savage and Vellend 2015), generally without driving concomitant changes in species richness (Dornelas et al. 2014, Magurran et al. 2015). The ecological consequences of biotic homogenization may be significant, and can lead to reductions in overall community and ecosystem function, stability, and adaptability (Olden et al. 2004).

Examples of climate-induced increases in β-diversity have also been observed (Moritz et al. 2008, Rahel 2010, Tingley and Beissinger 2013). However, the drivers and impacts of increased biotic heterogeneity are still unclear, but any shift in the natural structure of species assemblages may have extensive ecosystem consequences (Folke et al. 2004).

We suggest that regional topography should be a strong determinant of changes in β-diversity. Mountainous areas generally are home to many geographically restricted species, especially in the tropics, where high elevation gradients and rugged terrain favours the presence of local endemic species. Lowlands and plains, however, are frequently inhabited by more widespread generalists as there are relatively few geographic barriers to dispersal and they can represent large extents of similar habitat types. We predict that highland regions, currently dominated by habitat specialists, will likely see increases in generalists and reductions in habitat specialists, as climates associated with present day lowland habitats shift to higher altitudes (Parmesan 2006, Moritz et al. 2008, Chen et al. 2011). These shifts will lead to decreasing β-diversity and increasing biotic homogeneity (e.g. Menéndez et al. 2006, Davey et al. 2012). In contrast, climate warming in lowland regions is likely to induce range contractions, with previously widespread lowland species becoming restricted to "islands" of remnant habitat. Local extirpations in lowlands may thus lead to reductions in α-diversity but increases in β-diversity, resulting in a regional biota that is increasingly heterogenous. To date, only few empirical studies (e.g. Burgmer et al. 2007, Davey et al. 2013, Savage and Vellend 2015) have evaluated directly the effects of climate change on patterns of regional β-diversity.

Climate model projections can be used to test predictions of regional trends in β-diversity. Here, we used information on anuran amphibians' (frogs and toads) present-day distributions and 21st century climate change scenarios to assess temporal changes in β-diversity across the Neotropical Region. The Neotropics, encompassing the Middle American Cordillera Central and the South American Andes Mountains which run nearly the entire north-south extent of the Neotropics over ca. 75° of latitude, the greatest latitudinal extent of any mountainous region in the world, provide an ideal case study. The Neotropics are also home to the greatest diversity of amphibians in the world, with approximately 3,000 known species (Frost 2017). Amphibians, specially anurans, are important components of both terrestrial and aquatic assemblages. As omnivores when larvae, and small insectivores and carnivores when adults, they serve as critical links between the lowest and highest trophic levels (Duellman and Trueb 1994). Tropical species assemblages, which are characterized by both high species richness and high endemism, tend to flourish best in warm, humid climate, but may be especially sensitive to climate change (Stuart et al. 2004, Buckley and Jetz 2008). Widespread declines have occurred among Neotropical amphibians in recent decades (Wake 1991, Pounds et al. 2006) and climate change has been implicated in these declines (Pounds et al. 1999, Kiesecker et al. 2001, Menéndez-Guerrero and Graham 2013).

Here, we used β-diversity metrics to quantify the degree of anuran assemblage dissimilarity among sites (e.g. Baselga 2010, 2012, Olden and Rooney 2006, Buckley and Jetz 2008, Dobrovolski et al. 2012). We then tested whether climate induced changes in species richness, ecological generalism, and phylogenetic diversity (PD) have potential to drive opposing changes in β-diversity within anuran assemblages in highlands versus lowlands.

METHODS

We used species distribution modelling (SDM) to explore changes in spatial patterns of anuran β-diversity across the Neotropics. We focused our analysis on anurans, frogs and toads, which represent the vast majority of Neotropical amphibians (~90%), and which demonstrate remarkable endemism (Duellman 1999). Correlative models used in SDM generally ignore the effect of distribution-limiting factors, such as dispersal limitations and biotic interactions, and thus tend to overestimate the actual extent of species distributions and summed species richness (Guisan and Rahbek 2011, Mateo et al. 2017). However, our focus here is on broad-scale biogeographic patterns and determinants of regional shifts in β-diversity due to climate change, not localized presence-absences. Our species distribution models (SDMs) delineate the environmental limits that define anuran distributions at relatively coarse scales. These models are not, therefore, intended to provide fine-scaled predictions of species distributions, where micro-climate, biotic interactions and local habitat variation will be increasingly important, reflecting the narrow environmental tolerances of anurans.

Biological and climate data

We extracted data on the current distribution of Neotropical anurans from IUCN digital range maps (available on line, IUCN [2015]) for 2669 species of the ~3000 known amphibian species in the Neotropics (see Supplementary material, Appendix A1, Table A1.1). We followed the taxonomy of Frost (2017), and Löwenberg-Neto (2014) and Morrone (2014) in the delimitation of the Neotropical realm, including the Andean region. Species with taxonomic discrepancies between the IUCN species names and the taxonomy of Frost (2017, *n* = 6), and species classified as introduced were excluded from the analyses.

Environmental data for baseline conditions were estimated using interpolated climatic variables from the WorlClim database (www.worldclim.org, Hijmans et al. 2005), with a temporal span of approximately 50 years, for the period 1950–2000, and a spatial resolution of 2.5 arc-minutes (i.e. ~ 4.5 km). We note this time period already encompasses recent climate change, but pre-climate change baseline data are lacking. Future climate scenarios, covering the period between 2041 and 2080 (hereafter referred to as 2070 scenarios), included three global climate models (GCMs) under the RCP 4.5 representative concentration pathways (Stocker et al. 2013), that assumes that global annual greenhouse emissions peak around 2040, with a slight improvement and stabilization of current emissions by 2100 (Van Vuuren et al. 2011a). We used the RCP 4.5 as a conservative greenhouse emission scenario, the lower-emission scenario–RCP 2.6–is unrealistic (requires negative emission, Van Vuuren et al. 2011b). We evaluated outputs from the following three GCMs, which illustrate contrasting temperature and precipitation predicted changes: the HadGEM2-ES model that predicts high temperature increase and a reduction in precipitation (Jones et al. 2011, hereafter referred to as the hotter/drier scenario), the GISS-E2-R model that predicts moderate temperature increase and comparatively constant precipitation rates (Schmidt et al. 2014, moderate scenario), and the IPSL-CM5a-LR model that predicts warm temperatures and reduction in precipitation (Dufresne et al. 2013, warmer/drier scenario). These GCMs are frequently used in SDM studies, including in Neotropical areas (e.g. Tomillo et al. 2015, Ihlow et al. 2016).

Species distribution modelling

Species range maps were rasterized at the resolution matching the climate data, and a climate model was then fit to the observed current distribution of each species including 19 baseline (current) climate variables using Random Forest (Breiman 2001). Range maps have been previously used in amphibian biogeographical studies at large spatial scales (e.g., McKnight et al. 2007, Buckley and Jetz 2008, Lawler et al. 2009), and recent findings showed a strong agreement between SDMs trained with IUCN range maps and SDMs trained with true occurrences (Fourcade 2016). Random forests are machine learning algorithms based on classification of regression trees returning the class that is the mode of the classes output by individual trees (Breiman 2001); they have been widely used in SDMs, and proven to be effective for predictive modelling (Prasad et al. 2006, Mi et al. 2017). Random forest classifiers are robust to over-fitting but tend to better fit the observed data than other algorithms, and hence producing more accurate predictions of species' ranges (Lawler et al. 2006). Areas inside the extent of the species ranges were treated as presences, and 10,000 background points outside of the ranges were randomly selected as pseudo-absences. We modelled only species with at least three locations (following van Proosdij [2016], see Appendix A2). For each species, the calibration region (i.e. the mobility and accessible M area *sensu* Soberón and Peterson [2005]) was restricted to occupied ecoregion(s) following the regionalisation of Morrone (2014), see Barve et al. (2011) and Cooper and Soberón (2018, Appendix A3, Table A3.2).

All models were fit in R (R Development Core Team 2015) using the package BIOMOD2 (Thuiller et al. 2014), with default settings (as suggested by Thuiller et al. 2009) and using 80% of the presences and pseudo-absences for calibration. The remaining 20% of the data were used to test model performance. Models were evaluated based on the true skill statistic (TSS, Allouche et al. 2006), that varies from -1 to +1, where 0 or less represent no discrimination and +1 represents perfect discrimination (Araújo and New 2007). Models with TSS scores of < 0.70 were discarded from our analyses. A threshold set to the value at which TSS is maximized (TSSmax) was used to transform the model predictions (both current and future) into maps of presence/absence (Liu et al. 2011).

The fitted models were then projected under the three different GCMs (i.e. hotter/drier, moderate, and warmer/drier scenarios) to generate estimates of species distributional responses to climate change. For our purposes here, we assumed a full-dispersal scenario (i.e. perfect climate tracking), but see following section where we describe a relaxation of this assumption.

Uncertainties in forecasts of SDM

The projection of SDMs to predict shifts in the distribution of species under future climate change scenarios, where predictions cannot be cross validated, is challenging (see e.g. Thuiller 2004, Elith et al. 2010, Peterson et al. 2018). We therefore evaluated some of the key factors that may affect the accuracy and transferability of the models to assess the robustness of our downstream analyses (see Appendix A4):

- ***Number and grain size of predictor variables***: To evaluate the effect of these two common sources of uncertainty (Pearson and Dawson 2003, Braunisch et al. 2013, Manzoor et al. 2018), we reestimated baseline and future conditions using climatic variables with a spatial resolution of 10 arc-minutes (i.e. ~ 20km). We then refit the SDMs on the eight least correlated variables (|rho| <0.75) that have previously been identified as biological relevant (Menendez-Guerrero and Graham 2013, see Appendix A4).
- ***Extent of calibration area*** *(equivalent to M area)*: Several studies have highlighted significant effects of calibration area on SDM (e.g. Lobo et al. 2008, Barve et al. 2011). Restricting the calibration area to a hypothetically accessible area (M) relevant to the focal species is suggested to increase model performance (Saupe et al. 2012, Cooper and Soberón 2018). Our base models assume calibration areas based on the ecoregions of Morrone (2014), to evaluate model sensitivity, we also generated random pseudoabsences (or background data) at a maximal distance of two degrees from the species' range boundaries, following Barbet-Massin et al. (2012), see Appendix A4.
- ***Thresholding method***: This is a procedure by which continuous SDM outputs are transformed into presence/absence maps, and represents another common source of uncertainty in SDM studies (Thuiller 2004, Liu et al. 2013). Our base models threshold on the TSS, to further evaluate model sensitivity, we also selected the 10th percentile threshold (P10, Peterson et al. 2007). P10 is a conservative threshold that seems to be less sensitive to extreme environmental values (Radosavljevic and Anderson 2014). It

includes 90% of the presence records with the highest probability of occurrence from the predicted presence range, and thus may be better suited for our input data (i.e. species' ranges, see Appendix A4).

- ***Dispersal scenarios***: The importance of accounting for dispersal limitations when projecting SDMs is well recognised (Araújo and Guisan 2006, Midgley et al. 2007, Thuiller et al. 2008), especially for a group such as amphibians, whose dispersal capacity is lower than that observed in other vertebrates (Foden et al. 2013). Unfortunately, there is little data on dispersal for most Neotropical species (Stuart 2008). Our full dispersal scenario can be considered as representing potential range shifts, to evaluate how this scenario might depart from realised range shifts, we also implemented a dispersal scenario of 16.9 km per decade, following the meta-analysis across multiple taxa -mainly plants and insects- by Chen et al. (2011, see Appendix A4).
- ***Partitioning occurrence data for model evaluation*****:** Evaluating the accuracy of distribution models ideally requires testing them on independent data that accounts for spatial autocorrelation between testing and training localities, especially for studies involving transfer across time or space (Hijmans 2012, Wenger and Olden 2012). To assess the effect of temporal transferability, we used two spatial-partitioning schemes (see Appendix A4) for conducting spatially independent evaluations of our models (e.g. Muscarella et al. 2014).

Calculating β-diversity

To derive species composition of assemblages under current and future climatic conditions, we stacked (i.e. summed) the presences from the individual species models. We use a grid cell resolution of ~50-km (see Rahbek 2005) as range map data can be unreliable at finer spatial scales (Hurlbert and Jetz 2007, Hawkins et al. 2008), and because our focus was on the variation in the structure of biogeographical assemblages at broad spatial scales. We use the term species assemblage to refer to the set of species within a defined geographic area, following accepted usage in the fields of biogeography, macroecology, and paleoecology (Elton 1927, Vellend 2016), and it does not necessarily imply coexistence at local scales, such as within the context of community ecology. A grid cell was considered occupied if it overlapped any part of a species projected distribution (McKnight et al. 2007).

We quantified spatial patterns of β-diversity using the Sørensen pairwise dissimilarity index (βsor, Sørensen 1948). This index can be partitioned into two additive components: turnover (β_{sim}), accounting for species replacement, and nestedness (β_{nes}), reflecting the loss (or gain) of species (see Baselga 2010, 2012 for a detailed explanation). Here, we focused our analyses on the turnover component, β_{sim}, as it has been found to contribute more than nestedness to overall β-diversity among sites (Baselga et al. 2012, Xu et al. 2015), and nestedness is captured in our separate analysis of species richness differences (Carvalho et al. 2012, see below). We quantify turnover as:

$$\boldsymbol{\beta_{sim} = \min(b,c)/[a + \min(b,c)]}$$

where a is the number of species in both cells, b is the number of species exclusive to the focal cell and c is the number of species exclusive to the adjacent cell.

We calculated β_{sim} for each cell as the average of the β-diversity values between a focal cell and each of the eight neighboring cells (see Melo et al. 2009). Increasing the focal cell neighborhood (e.g. 24 or 48 cells) has shown to not substantially alter β_{sim} values (Melo et al. 2009). To evaluate changes in β_{sim} with climate change (reflecting how differences in species spatial composition changes over time), we projected species distributions using the future climate scenarios and recalculated β_{sim}, and then subtracted future projected β_{sim} from current β_{sim}. Negative values indicate a trend towards biotic homogenization, while positive values indicate a trend towards increasing biotic heterogeneity. All β-diversity metrics were calculated using functions in the betapart package implemented in R (Baselga and Orme 2012, R Development Core Team 2015).

Assessing spatial patterns of diversity change under future climates

We assessed whether changes in β_{sim} were associated with changes in species richness (species loss vs. species gains), phylogenetic diversity (PD), and ecological generalism.

Changes in species richness (ΔSR): We estimated projected ΔSR by subtracting future projected richness from current richness. Negative values represented projected species losses, while positive values represent projected species gains.

Changes in PD (ΔPD): We used the phylogenetic tree from (Pyron 2014), the most complete amphibian phylogeny at the time of analysis, to calculate Faith's PD (the sum of the phylogenetic branch lengths connecting all taxa in a set, Faith [1992]). Species missing from this tree (1315) were added as polytomies at the root node for the genus using the congeneric.merge function from the pez R library (Pearse et al. 2015). We used the standardized effect size of Faith's PD (SES.pd) to quantify PD corrected for species richness under both current and future climate scenarios. SES.PD was calculated by comparing observed PD values to null expectations (999 runs) generated through the independent-swap null model (Gotelli and Entsminger 2003). Negative SES values indicate species in assemblages are more related than expected by chance (clustered in the phylogenetic tree), while positive SES values indicate species in the assemblages are less related than expected by chance (overdispersed in the phylogenetic tree). PD analyses were conducted using functions in the R package picante (Kembel et al. 2010). Negative ΔPD indicate that assemblages are projected to become increasingly clustered, whereas positive ΔPD values indicated that assemblages are projected to become increasingly overdispersed.

Changes in ecological generalism (ΔEG): Species with wide environmental tolerances tend to have larger geographic ranges than specialists, with the latter being characterized by highly constrained niches and smaller geographic ranges (MacArthur 1972, Slatyer et al. 2013). Geographic range area may therefore provide a reasonable surrogate for the ecological generalism-specialism of species. We derived the mean of the current geographic range areas for the species present in each grid cell under both current and future climate scenarios, and calculated their difference. Here, positive values represent assemblages that are predicted to shift composition towards a greater proportion of generalists, whereas negative values represent assemblages that are predicted to shift composition towards a greater proportion of specialists. Range size provides just one proxy metric of ecological generalism, we therefore also estimated niche breadth assuming an alternative surrogate of ecological generalism (Brown 1984), using the inverse concentration metrics of Levin (1968). These metrics were calculated on the suitability score maps (which are functions of all climatic variables) generated by Random Forest, as described above, using the ENMTools R package (Warren 2016, see Appendix A5).

All geographic analyses were performed in R (R Development Core Team 2015), and ArcGIS 10.2 (ESRI 2013).

Statistical analyses

To describe changes in species assembly structure, we fitted generalized additive models (GAMs) with change in β_{sim} as the response variable, and four predictor variables: ΔSR, ΔEG, ΔPD, and elevation (derived from the Shuttle Radar Topography Mission [SRTM], Farr et al. 2007). GAMs were fit in the R library mgcv (Wood 2017) using default settings. All predictor variables were log transformed and standardised to a mean of 0 and a standard deviation to 1 prior to analysis. There was no significant multicollinearity among predictors (all VIFs < 2, Quinn and Keough 2002). We generated the set of all possible additive models using the MuMIn R package (Barton 2018), with the intention to average the best models according to the Akaike information criteria (AIC, Burnham and Anderson 2003). Models with an AIC difference below 2 (ΔAIC <2) were considered to have significant support (Burnham and Anderson 2003). To evaluate statistical significance of individual predictors, we used likelihood ratio tests to contrast the best model with reduced models, removing one term at a time. Because there is some controversy regarding the fitting of GAMs (Hastie 2017) and interpratting model coefficients can be complicated, we also performed ordinary least squares (OLS) regression, with ΔSR, ΔPD, ΔEG, elevation, and the spatial term (i.e. latitude*longitude) included as predictors.

RESULTS

Species distribution modelling

The average fit of the SDMs on present day climate was high ($\overline{X}$ TSS = 0.78). Although choice of climate change scenario impacted the magnitude of projected gains or losses of species, overall trends were similar across scenarios. For brevity, we present results for the warmer/drier scenario IPSL-CM5a-LR in the main text because we believe amphibians are likely more sensitive to these climate trends, results for the alternative scenarios are presented in Appendix A6 (Fig. A6.7, A6.8).

Our models predict large changes in anuran diversity across the Neotropics. Under 2070 projections, species retain, on average, just 58% of their current suitable area (42% range loss, see Appendix A7, Fig. A7.9), but with large variation among species (1st quartile = 83% range loss, 3rd quartile = 24% range loss). Our results match closely to previous estimates of shifts in Neotropical amphibian alpha diversity under climate change projections (e.g. Lawler et al. 2009, Hof et al. 2011), including a slight tendency for SDMs to overestimate species richness, especially in the Northern Andes (e.g. Lawler et al. 2009). The implications of these biodiversity changes have been discussed elsewhere, and we do not expand on them here.

Predicted changes of spatial patterns of β-diversity

We show that areas with high Neotropical amphibian β_{sim} are currently concentrated in the highlands, primarily in the South American Andes (Fig. 1.1a). In contrast, β_{sim} is relatively low over most of the lowland Neotropics, especially in the Amazonian, Guiana Shield and Cerrado region (Fig. 1.1a). These patterns are largely concordant with those of McKnight et al. (2007), who used the same metric to calculate anuran β-diversity for a smaller subset of species across the entire Western Hemisphere (see also Baselga et al. 2012).

On average, β_{sim} is projected to increase by ~36% per cell by 2070, but there is large variation across space. In the Neotropical lowlands, where β_{sim} is currently low, β_{sim} is predicted to generally increase (i.e. there is a trend towards biotic differentiation, $\overline{X}$ β-diversity change = 39% ± 40.29 SD, Fig. 1.1a, 1.2a,b). This pattern of β-diversity change is projected to be greatest in the Amazon Basin, and some areas of the Cerrado and Chaco regions (Fig. 1.2b). Exceptions include several highland assemblages in Mesoamerica, such as Mexico's Sierra Madre

Occidental mountain ranges, some parts of Sierra Madre Oriental and del Sur, and some highlands of Guatemala (Fig. 1.2b). In contrast, β_{sim} is predicted to decrease in approximately 75% of the Neotropical highlands, where current β_{sim} is high (i.e. there is a trend towards biotic homogenization, $\overline{X}$ β-diversity change = -8.5% ±6.66 SD, Fig. 1.1a, 1.2a,b), including most of the South American Andes and Guiana Shield highlands, some northern and central areas of Sierra Madre Occidental, and areas of Sierra Madre Oriental of the Mexican mountain system (Fig. 1.2b). Lowlands predicted to decrease in β_{sim} include the Pacific lowlands of South America, especially the northern South America, some Caribbean areas of Colombia, and the lowlands from southern Argentina and Chile (Fig. 1.2b).

Predictors of change in β-diversity

The full GAM including ΔSR, ΔEG, ΔPD, and elevation was the only model favoured by AIC (Table 1.1, $\Delta AIC < 2$). This model explained 65% of the total variance in β_{sim} change (Table 1.1). The results of the likelihood ratio tests showed that the inclusion of the each of individual predictors had a significant impact on the full model's predictive power (all $p < 0.001$, Table 1.1, Appendix A8, Table A8.3). Both ΔEG and ΔSR were negatively correlated with β_{sim} change, while ΔPD was positively correlated with β_{sim} change. The model including ΔEG as estimated by niche breath instead of range size (see Methods), showed qualitatively similar associations (Appendix A5, Fig. A5.6).

The increasing heterogeneity of lowland anuran assemblages (Fig. 1.2) is primarily driven by range contraction and local extinction of generalist species (Fig. 1.3a,b, see also red areas in Fig. 1.1b,c). Range contraction and local extinction also tend to drive decreases in species richness, but result in higher phylogenetic dispersion – thus future anuran assemblages in these regions will tend to be species-poor and comprised of taxa that are more distantly related than current assemblages (Fig. 1.3c, see also blue areas in Fig. 1.1d). The increasing heterogeneity of some Mesoamerican highland assemblages is largely explained by local species extinctions, which tend to impact more generalist species (see Appendix A9, Fig. A9.10).

The biotic homogenization predicted in the majority of highlands (Fig. 1.2), is driven by increases in generalist species (i.e. range expansion) and, to a lesser extent, loss of specialists (Fig. 1.3a,b). This pattern is especially clear in the central and southern Andes (Fig. 1.4c,d). Range expansion will tend to increase local species richness, but coincides with the loss of specialist species. In this region, future anuran communities are predicted to become more phylogenetically clustered (formed of taxa that are closer together on the phylogenetic tree) than current assemblages (Fig. 1.3c). Anuran assemblages in the northern Andes, will also tend to become more homogeneous with projected climate change. However, here the shift in community structure appears to be driven more by local extinctions of specialists, resulting in assemblages with lower species richness and dominated by generalists (Fig. 1.4a,b). The predicted homogenization of northern assemblages is estimated to be stronger than that in the southern Andes ($\overline{X}$ β-diversity change = -18.84% ± 7.31 SD vs. $\overline{X}$ β-diversity change = -6.81% ± 4.41 SD, respectively). The local extinction of specialists is similarly predicted to drive greater homogenization of anuran assemblages in the northern Pacific lowlands of South America, whereas local species gains (especially of generalists) will tend to homogenize the southern Pacific lowlands and some areas of the southern Andes (see Appendix A10, Fig. A10.11).

OLS models produced results analogous to those obtained in the GAMs, in which ΔSR and ΔEG were negatively associated with β-diversity change, and ΔPD was associated positively with β-diversity change (see Appendix A12, Table A12.4).

Model sensitivity and robustness

We explored robustness of our findings to various sources of uncertainty. To encompass variability in future emission scenarios, we used three different and contrasting GCMs, and show largely congruent patterns of β_{sim} changes (Appendix A6, Fig. A6.7, A6.8). Our predicted changes of β_{sim} are clearly dependent on the assumption of unlimited dispersal ability of species under climate change. However, assuming a more realistic dispersal-scenario (see Methods) did not importantly affect the general spatial patterns of β-diversity shifts described in this study (see Appendix A4). Given sufficient time, it is also possible that some species might be able to adapt to novel climatic conditions in their current locations (Bellard et al. 2012), in such cases our estimates of range contraction may be overestimates.

Although the IUCN digital range maps used here have been used widely in macroecological studies, the geographic distributions of some species are much better known than others. For example, the distribution models for anuran species in the "data deficient" (DD) category under the IUCN Red List (http://www.redlist.org/) are likely less reliable than those for species in other IUCN categories. Nori and Loyola (2015) recently emphasized the need to consider DD amphibian species in broad-geographic scale studies, especially for the effectiveness of future conservation assessments. To evaluate sensitivity of our results, we recalculated our β-diversity metrics excluding DD species, and found again that results were qualitatively similar (see Appendix A13, Fig. A13.13).

DISCUSSION

Climate change is expected to affect patterns of species diversity and the structure of species assemblages, particularly in tropical regions (Buckley and Jetz 2008). Here, we show that, within Neotropical anuran amphibians, a trend towards biotic homogenization may be observed in mountainous areas, whereas a trend towards biotic heterogenization may be more likely in lowland and plains landscapes characterized by only modest variation in altitude. Our models indicate that biotic homogenization is mainly driven by an increase in generalist species and, to a lesser extent, loss of specialists, resulting in overall greater local species richness, but lower phylogenetic diversity (PD). In contrast, increasingly biotic heterogeneity is explained by range contraction and local extinctions of generalists, resulting in reduced species richness, but higher phylogenetic dispersion of remaining species (see Appendix A14, Fig. A14.14 for changes in individual correlates of β-diversity). Such regional variation in shifts in β-diversity, which may have important consequences for ecosystem functioning (Lovejoy and Hannah 2006), indicate the importance of considering landscape-level variation in biodiversity responses to global change drivers.

Homogenization of Neotropical highlands

Our model predictions suggest biotic homogenization, especially along the Andean highlands, associated with a shift in assemblage composition towards higher species richness and a greater dominance by generalists, which also tend to be closely related. Our results showing increasing homogeneity are concordant with some empirical and model-based studies of other taxa (e.g. plants: Jurasinski and Kreyling 2007, Savage and Vellend 2015, Zwiener et al. 2018, birds: Davey et al. 2013, and fishes: Buisson and Grenouillet 2009, Tisseuil et al. 2012, Molinos et al. 2016). This has led some to suggest that we may be entering a new era—the

"Homogocene". However, the relative responses of specialist versus generalist species have rarely been considered (but see Zwiener et al. 2018).

Biotic homogenization may result not only as a consequence of the increasing spread of generalists, but also from the extirpation of more specialist, range-restricted, species (McKinney and Lockwood 1999, Rahel 2002, Olden and Poff 2003, Clavel et al. 2011). The Andes, especially the northern and central part, is one of the regions with the highest richness of range-restricted anurans in South America (Villalobos et al. 2013). Small range size obviously drives patterns of β-diversity, and range size has been shown to be a key predictor of anuran species vulnerability to extinction (Botts et al. 2013). In the north and southern Andes (and some of South American western lowlands), we observed an average increase in the mean geographic range size of anuran species within assemblages under climate projections, consistent with both an increase in large-ranged generalist species, and a local extinction of small ranged specialists. In the north, where there is a very high concentration of range-restricted species, extinctions are the primary driver of homogenization, as indicated by the decrease in local species richness projected under future climate change scenarios; whereas in the south the main driver is the range expansion of species, mainly generalists, as indicated by an increase in projected species richness. The more pronounced homogenization predicted in the northern versus southern Andes, suggests that climate-driven extinctions of specialists could have greater impact on patterns of β-diversity than the range expansions of generalists.

Heterogenization of Neotropical lowlands

Increasing biotic heterogeneity can also result from species extinctions (Rahel 2002, Olden and Poff 2003; e.g. Moritz et al. 2008, Molinos et al. 2016) and range shifts (e.g. Ochoa-

Ochoa et al. 2012). We predict an increase in beta diversity of assemblages in Neotropical lowlands, notably within the Amazon Basin, and some parts of the Cerrado and Chaco. This increase in heterogeneity is predominantly driven by local extinctions, often among closely related species, but also by range reductions of generalists, which results in species-poor assemblages dominated by a greater proportion of specialists. Other studies projecting future climate-induced shifts in amphibian species ranges have also identified the Amazon and the Cerrado regions as areas prone to high species losses, and with only few species gains (Lawler et al. 2009, Hof et al. 2011). However, our study is the first to translate such shifts into changes in β-diversity at a continental scale.

Predicting an uncertain future

In amphibians, it has been suggested that tropical communities may be particularly sensitive to climate change based on the tight linking between environmental conditions and β-diversity (Buckley and Jetz 2008, da Silva et al. 2014). Here we have shown how such changes may reassemble amphibian communities across the entire Neotropical region.

Concerns about using SDM to infer impacts of climate change have been discussed widely elsewhere (e.g. Thuiller 2004, Hijmans and Graham 2006, Wiens et al. 2009, Elith et al. 2010, Heikkinen et al. 2012, Peterson et al. 2018). For instance, the uncertainty around global climate models (GCMs) could be larger than other sources of uncertainty in SDM (Diniz-Filho et al. 2009, Buisson et al. 2010), and it is difficult to identify a GCM that performs better than another (Martinez-Meyer 2005). We evaluated the sensitivity of our estimated shifts in β-diversity to several types of uncertainty: GCM's, grain size, number of predictors, extent of calibration area, thresholding, dispersion, partitioning of occurrence data for model evaluation, and inclusion of IUCN data deficient species (see Methods). Predictions from these alternative models were generally highly congruent (see Appendix A4, A6, A13), increasing our confidence in the main findings we present here. Nonetheless, we acknowledge that our results showing potential changes in the spatial configuration of anuran assemblages represent just a few of many possible future scenarios (Buisson and Grenouillet 2009, see Appendix A4). However, perhaps the greatest uncertainty associated with our analyses surrounds the societal choices that will determine future emission scenarios.

Conservation implications

The distribution of β-diversity is a fundamental component of biodiversity relevant to conservation (Socolar et al. 2016). Here we show that, in the Neotropical highlands, future anuran communities will become increasingly homogeneous. While many species might track climate changes by moving upwards in elevation, potentially increasing local species richness in some regions, greater biotic homogenization might reduce ecological functioning and stability of anuran assemblages (Olden et al. 2004). The projected increase in β-diversity of lowland assemblages might appear to be a positive outcome; however, it is largely driven by range contraction and localized extinction of more generalist species. The local extinction of such species might have lesser impacts on ecosystem functioning due to the high functional redundancy in species-rich amphibian assemblages (Naeem 1998, Strauß et al. 2010), but as their losses compound we might experience non-linear and potential catastrophic loss of function in the future. The changing β-diversity landscape, alongside the sharp decline of the amphibian richness around the world, represents another challenge for conservation biologists.

DATA AVAILABILITY STATEMENT

IUCN digital range maps of Neotropical anurans are available on line at http://www.iucnredlist.org. Environmental data for baseline and future conditions are available at: www.worldclim.org. R code for SDM is available in Supplementary material, Appendix A15.

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Table 1.1 Results of the best (i.e., full) generalized additive model relating change in anuran β-diversity to change in species richness (ΔSR), elevation, change in the average level of ecological generalism (ΔEG), and change in phylogenetic diversity (ΔPD). Degrees of freedom (df), Akaike Information Criterion (AIC), and Log Likelihood (logLik) are presented. As measures of overall fit, the adjusted R^2 and the deviance explained are also presented. F-values (*F*) and their associated probabilities (*p*) for each variable are shown as well. Variables were standardised to a mean of 0 and standard deviation of 1 prior to analysis. See other models' AICs and logLiks in Appendix A8, Table A8.3.

Model (predictors)	**df**	**AIC**	**logLik**	**R^2(adj)**	**Deviance (%)**
ΔSR+Elevation+ΔEG+ΔPD	31	19699.8	9881.256	0.65	65%
	F	***p***			
ΔSR	208.24	<0.001			
Elevation	130.27	<0.001			
ΔEG	462.76	<0.001			
ΔPD	25.32	<0.001			

Figure 1.1. Bivariate maps depicting relative changes in biodiversity measures for Neotropical anurans between the present and ca. 70 years into the future. Colours indicate the relative amount of change. Reductions are depicted towards the red end of the spectrum whereas increases are depicted toward the blue end of the spectrum. Each transition in colour shading translates to a 10% quantile shift in the value of the variables. a) β-diversity, b) species richness (SR), c) average level of ecological generalism (EG), d) phylogenetic diversity (PD). Much of the area currently characterized as high β-diversity will remain proportionally high in β-diversity (i.e., yellow areas mainly in Central and South American Andes, except for northern Andes that are predicted to show a relative reduction in β-diversity [red areas]). In contrast, β-diversity is predicted to increase in some lowland areas (i.e., parts of the Amazon Basin, Cerrado, and Chaco regions) where β-diversity is currently low (blue areas); whereas β-diversity will remain largely unchanged in other lowlands (e.g., Guiana Shield and parts of Amazonia; light green areas). We used a function generated by José Hidasi-Neto to generate the map (http://rfunctions.blogspot.ca/2015/03/bivariate-maps-bivariatemap-function.html).

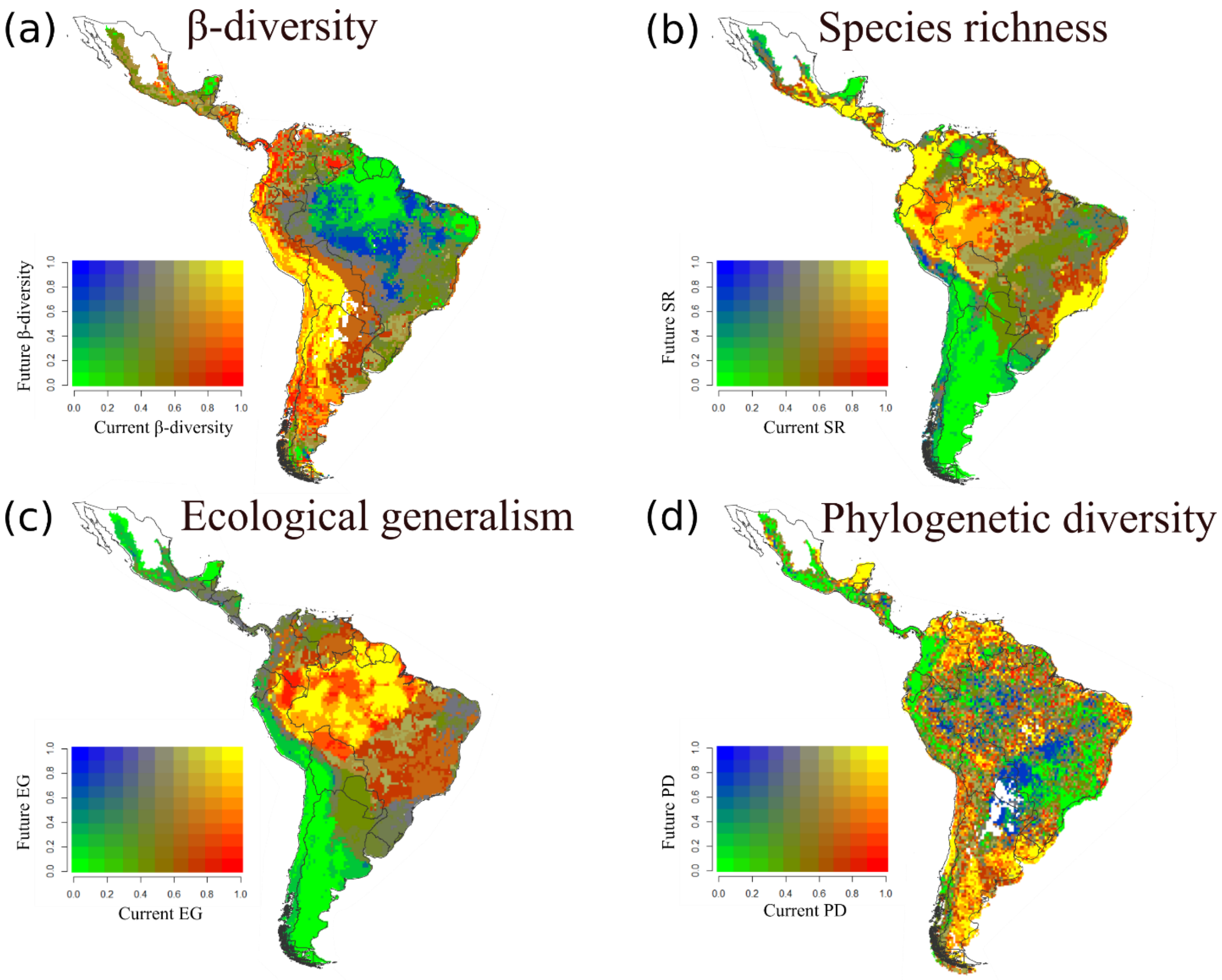


Figure 1.2. Projected changes in β-diversity of Neotropical anuran amphibians according to the "warmer/dryer" scenario of the IPSL-CM5a-LR global climate model. a) Violin plots showing variation (median, range, kernel density, 25th-75th percentiles) in changes in anuran β-diversity in Neotropical highlands (altitude > 1300 m.a.s.l.), in red, versus lowlands (altitude < 1300 m.a.s.l.), in green. b) Map of Neotropical America showing predicted distribution of areas of biotic homogenization with respect to anuran species diversity (i.e. decrease in β-diversity), in red, vs. biotic heterogenization (i.e. increase in β-diversity), in green. The majority of highland assemblages are predicted to become more homogeneous, whereas the majority of lowland assemblages are predicted to become more heterogenous (see violin plot). Analyses were performed under the assumption that a species can reach any area with suitable environmental conditions (universal dispersion).

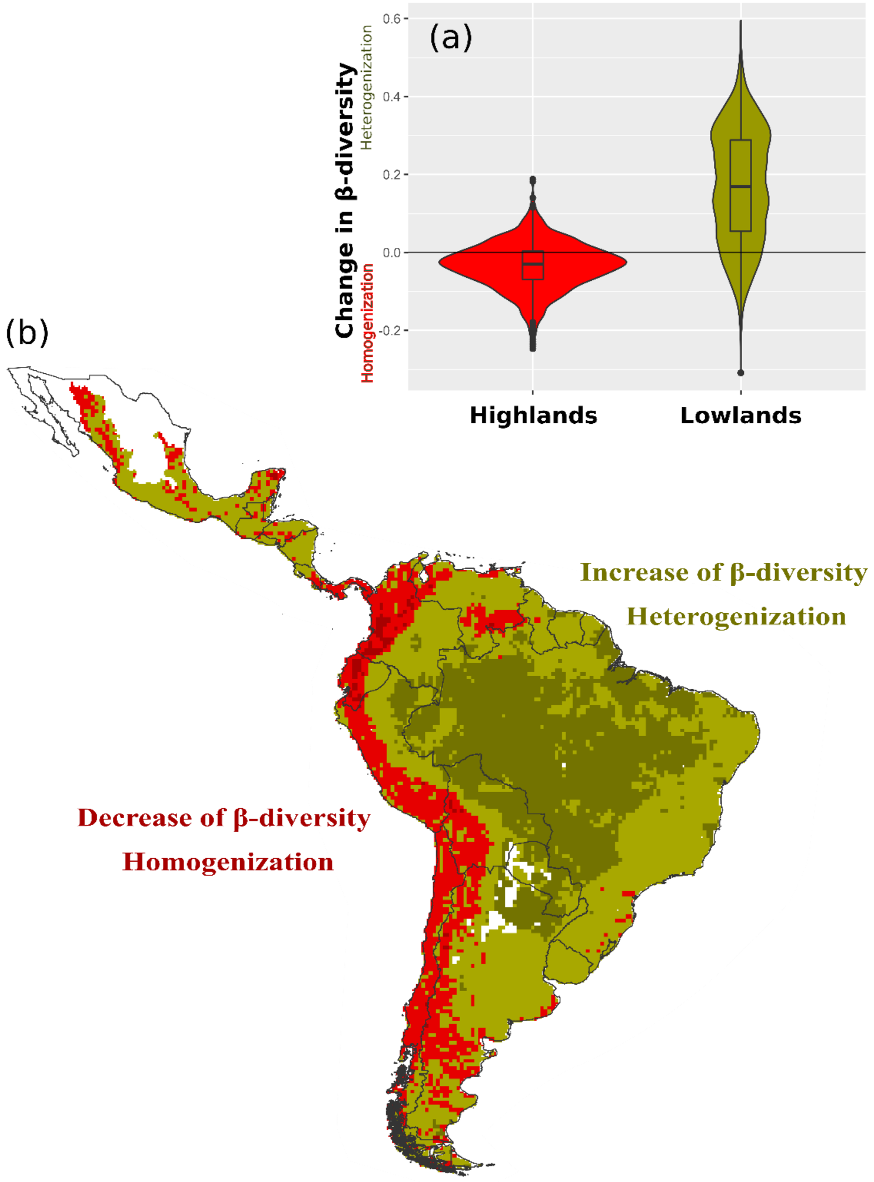


Figure 1.3. Biplots showing the predicted relationships between change in β-diversity and predictors retained in the best generalized additive model (GAM): a) Change in species richness (ΔSR); b) Change in the average level of ecological generalism (ΔEG) and c) Change in phylogenetic diversity (ΔPD). Fitted lines show the univariate generalized additive models (GAMs) with 95% confidence interval (dark gray), and residuals (light gray points). Rugs on the x axes (i.e., vertical lines above the x axes) show the predictors values, and how they are distributed. Labels on the y-axes indicate the smoothed function (s) for the term of interest (ΔSR, ΔEG and ΔPD), and the estimated degrees of freedom (following the term).

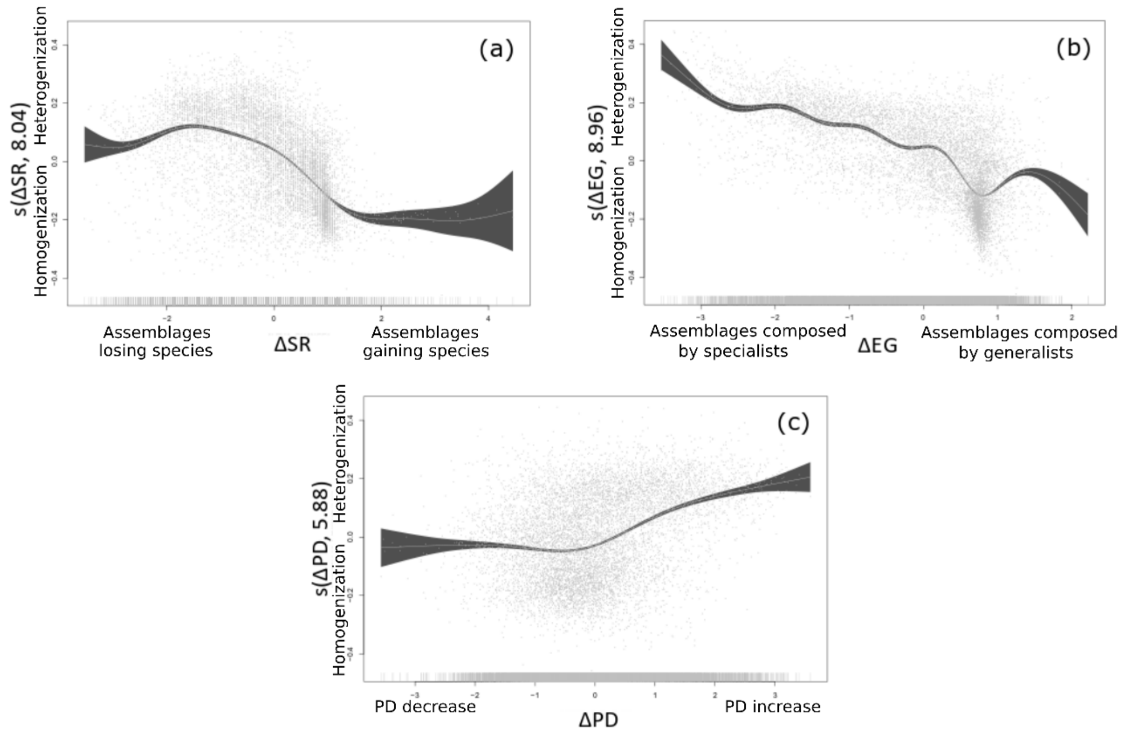
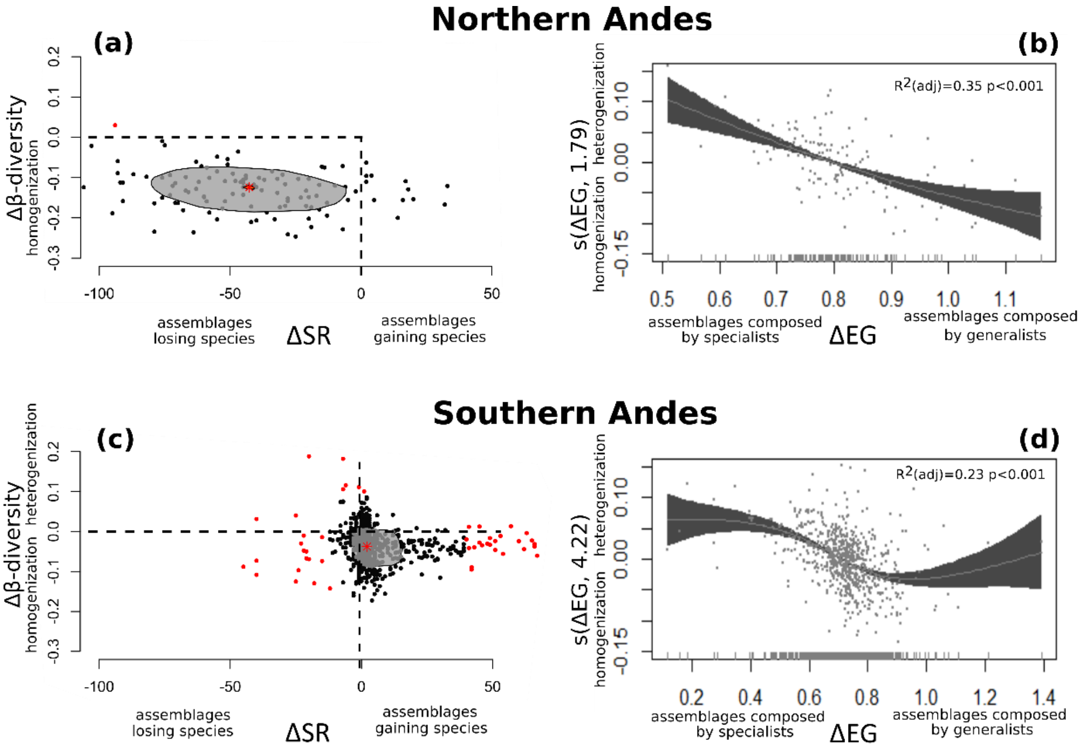


Figure 1.4. Plots of the relationships between change in β-diversity (homogenization vs. heterogenization) against change in species richness (ΔSR; species gains vs. species loss) and change in the average level of ecological generalism of the species (ΔEG) for the Andes.
(a) Bagplot of the relationship between change in β-diversity and ΔSR in the northern Andes.
(b) Biplot showing the predicted relationship between change in β-diversity and ΔEG in the northern Andes. (c) Bagplot of the relationship between change in β-diversity and ΔSR in the southern Andes. Median is shown as red asterisk, and outliers are shown in red. The light gray polygon (i.e., the bag) contains 50% of the data points. (d) Biplot showing the predicted relationship between change in β-diversity and ΔEG in the southern Andes.
Univariate generalized additive models (GAMs) were used to predict these relationships (light gray line), showing 95% confidence interval of the prediction shaded in dark gray and residuals (light gray points). Rugs on the x axes (i.e., vertical lines above the x axes) show the predictors values, and how they are distributed. Labels on the y-axes indicate the smoothed function (s) for the term of interest (ΔEG), and the estimated degrees of freedom (following the term). As measures of overall fit we present adjusted R^2 and the significance of predictors (p).



Linking Statement 1

In Chapter 1, I examined the effects of future climate change on the species composition of Neotropical amphibians assemblages (i.e., beta diversity) at a continental scale. I predict a future trend toward greater biotic homogenization in mountainous areas, and a trend towards greater biotic differentiation in lowlands. Climate-driven biotic homogenization was associated with an overall increase in species richness – mainly through range expansions of generalists –, but lower mean phylogenetic diversity. Increasing biotic differentiation, in contrast, was linked with a decrease in species richness – mainly driven by local extirpations of generalist species –, but higher mean phylogenetic diversity. These findings suggest that climate change will have differential and opposite effects on anuran community structure in different Neotropical regions; however, it will generally result in lower taxonomic diversity.

In Chapters 2 and 3 I assess how the climate-driven community composition changes predicted at large scales may translate into smaller scales in the Anthropocene. In Chapter 2, I investigate the consequences of local extinctions of endangered species on the functional structure of amphibian assemblages at a regional scale.

CHAPTER 2:

Extinctions of Threatened Frogs may Impact Ecosystems in a Global Hotspot of Anuran Diversity

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ABSTRACT: Human activity is accelerating rates of extinction around the world, and there is therefore an urgent need to understand the potential consequences of species loss on functional diversity and ecosystem functioning. It is frequently assumed that the extinction of threatened species, which are usually rare species, may have limited effects on ecosystem functioning, especially within highly diverse regions, given the low abundance of individuals of each species and the potentially high functional redundancy among them. However, these rare species may contribute unique and irreplaceable functional roles, and therefore their extinction could have disproportionate impacts on ecosystems. We assess the functional importance of highly threatened anurans (frogs and toads) and then explore how the loss of these threatened species would impact spatial patterns of β-diversity in Ecuador, a hotspot of anuran biodiversity and endemism. We found that highly threatened species are, on average, more functionally distinct at an assemblage level than are less threatened anurans. We then show that the potential extinction of these highly endangered species would drive the taxonomic, phylogenetic and, especially, functional homogenization of anuran assemblages across the Ecuadorian Andes. We suggest this could lead to profound alterations in the stability of local ecosystem functioning. Finally, we highlight the limited scope of the existing network of protected areas in Ecuador to effectively cover anuran assemblages predicted to become increasingly functionally homogenous. Our study underscores the potential losses of functional diversity that accompany species extinctions and the importance of considering the many facets of biodiversity in conservation decision making.

Key words: Anuran assemblages; Biotic homogenization; Ecuador; Endangered species; Functional distinctiveness; Functional homogenization; Functional redundancy; Phylogenetic homogenization

THE ON-GOING global extinction crisis (Ceballos et al. 2015; McCallum 2015) presents a major ecological challenge, and there is a pressing need to understand the causes and consequences of population declines and local extinction events on ecosystem functioning. Amphibians are one of the most vulnerable groups among vertebrates (Stuart et al. 2004; Wake and Vredenburg 2008). About 3% of amphibians are thought to have already succumbed to extinction, and approximately 50% of species are threatened with extinction, according to González-del-Pliego et al. (2019) and assessments by the International Union for Conservation of Nature (IUCN), the most comprehensive inventory of the conservation status of species in the world. Over the past three decades, several causes for the widespread decline in amphibians have been identified, including infectious diseases, climate change, habitat loss, introduced species, and environmental pollution (Sodhi et al. 2008; Hof et al. 2011; Scheele et al. 2019). However, the complex nature of this global phenomenon has precluded the application of effective conservation strategies to mitigate the general trend of amphibian biodiversity loss and the increasing risk of ecological collapse that may result (Mendelson et al. 2006; Grant et al. 2016). It is crucial, therefore, to evaluate the ecosystem role of at-risk species so as to anticipate potential ecological consequences of their disappearance in the near future (Collins 2010).

Species with the highest risk of extinction are usually rare, with small populations, restricted geographical ranges and/or narrow habitat tolerances (MacArthur and Wilson 1967; Rabinowitz 1981; Gaston 1994). Because they are typically rare, the role of highly endangered species in ecosystems is often unclear. On the one hand, their loss might have only a limited effect on local ecosystems, especially in highly diverse regions where functional redundancy among multiple species can provide insurance for ecosystem functioning (Grime 1998; Smith and Knapp 2003). On the other hand, highly endangered species could have distinctive functional traits, play unique roles in ecosystems, and disproportionally contribute to ecosystem functioning (Mouillot et al. 2013; Jain et al. 2014; Leitão et al. 2016). If functional distinctiveness is an important component of ecosystem contribution, then it is also possible that the contribution of rare species to ecosystem functioning will be conditional on the species composition of local assemblages, and may thus vary over space.

In aquatic and terrestrial ecosystems amphibians contribute to a number of key ecological processes, including nutrient cycling, bioturbation, seed dispersal, and energy flow through trophic chains (Valencia-Aguilar et al. 2013; Hocking and Babbitt 2014; Cortes-Gomez et al. 2015). Therefore, extinctions of amphibian species could have important effects on communities and ecosystem functioning at local scales (Whiles et al. 2006; Mohneke and Rödel 2009; Whiles et al. 2013). The extinction of amphibian species or populations could also have cascading impacts at larger scales and result in increasing homogenization of biotic assemblages across space (i.e., the loss of β-diversity; Smith et al. 2009; Nowakowski et al. 2018). This temporal trend of increasing similarity of assemblages over space, especially at a functional level, could reduce the functional diversity of ecosystems and their resilience in the face of environmental change (Clavel et al. 2011).

We address how the loss of threatened amphibian species could affect spatial patterns of β-diversity and ecosystem functioning in Ecuador, a highly biodiverse country. Using information on species' geographic distribution, phylogenetic relatedness, and functional traits for 539 species of Ecuadorian anurans, we first test the relationship between functional distinctiveness and IUCN threat categories over space. Second, we evaluate whether the potential extinction of the most threatened species would lead to decreases in β-diversity, which is detectable as biotic homogenization of anuran assemblages taxonomically, phylogenetically and functionally. We reason that if threatened species are functionally distinct, then we would expect their loss to drive functional homogenization. Finally, we determined whether areas in Ecuador predicted to become increasingly functionally homogenous, and thus potentially more vulnerable to threats, are under protection in Ecuador.

MATERIALS AND METHODS

Distributional Data

We used presence-only data for 539 anuran species out of the 592 species recorded in Ecuador to date (Ron et al. 2019; Table S1 in Supplemental Materials available online). Species occurrence data were obtained from the collection of Museo de Zoología, Pontificia Universidad Católica del Ecuador (QCAZ), available at the portal BIOWEB (http://bioweb.bio), which represents the most up-to-date and comprehensive database of Ecuadorian vertebrates (Ron et al. 2019), and from published literature compiled by the QCAZ staff. All occurrences (*n* = 21,227 unique occurrence records) were checked for accuracy using information on species' altitudinal limits and distribution maps from BIOWEB. Species taxonomy follows AmphibiaWeb (2019), and species endangerment status follows an updated version of IUCN categories for all Ecuadorian amphibian species (available at https://bioweb.bio/faunaweb/amphibiaweb/ListaRojaAWE/). According to this version, 9% of species are critically endangered (CR), 15% are endangered (EN), 8% are vulnerable (VU), 12% are near threatened (NT), 24% are least concern (LC), and 32% are data deficient (DD).

Phylogenetic and Species Trait Data

We acquired data on phylogenetic relationships from Jetz and Pyron (2018). We pruned their phylogenetic tree to only include species within Ecuador, resulting in a phylogeny for 490 of the 539 species. Species absent in the original phylogeny were inserted as polytomies within genera using the congeneric.merge function from the pez R library (Pearse et al. 2015).

We used information compiled from BIOWEB, complemented with information from Oliveira et al. (2017), to quantify four functional traits related to morphology, ecology and reproductive features of frogs (Supplemental Table S2, available online). Snout–vent lengths, for both males and females, were recorded as continuous data. Diel active period (diurnal, nocturnal or crepuscular) and habitat (aquatic, arboreal, fossorial or terrestrial) were recorded as binary data, and breeding strategy (direct or larval development) was treated as a binary variable. These selected traits have been used in previous studies of amphibian functional diversity (Díaz-García et al. 2017; Tsianou and Kallimanis 2019), and represent some of the most complete trait-data available for Ecuadorian anurans.

Environmental Data

We used four bioclimatic variables from the WorldClim2 database (Fick and Hijmans 2017) at a resolution of 30 arc seconds as environmental predictors: mean temperature of warmest quarter, mean temperature of the coldest quarter, precipitation of the wettest quarter, and precipitation of the driest quarter. These variables represent limiting climatic factors that often constrain tropical species distributions (Khaliq et al. 2014), are relatively uncorrelated, and have been shown to be useful predictor variables in previous analyses (Root 1988; Wiens et al. 2006; Bonetti and Wiens 2014). We clipped environmental variables to the extent of Colombia, Ecuador, Peru and Brazil.

Species Distribution Modeling

We fit MaxEnt (Phillips et al. 2006) correlative species distribution models for each amphibian species with Wallace v1.0.6.1 (Kass et al. 2018), written for R (R Development Core Team 2017) using the package shiny (Chang et al. 2017). MaxEnt is a widely used machine learning, presence-only species distribution algorithm that has high predictive power in identifying habitat suitability outside of known occurrences (Elith et al. 2006), even with small sample sizes (Wisz et al. 2008). We modeled only species with at least five unique records (Pearson et al. 2007; van Proosdij et al. 2016; Supplemental Table S3, available online). For each species, we restricted the background extent, i.e., the calibration area or accessible M area sensu Soberón and Peterson (2005), to the minimum convex polygon with a 0.7-degree buffer distance around the occurrence records, and 10,000 background points to increase model performance (Anderson and Raza 2010; Saupe et al. 2012; Cooper and Soberón 2018).

Models were fit using *k*-fold cross-validation, with $k = 2$ for species with between 21 and 99 unique occurrence records, and $k = 3$ for species with more than 99 occurrences (Hirzel et al. 2006). For species with less than 20 occurrences, we used the jackknife leave-one-out procedure (Shcheglovitova and Anderson 2013). For more details about these partitioning methods, see Muscarella et al. (2014).

Numerous recent studies have shown that tuning MaxEnt settings carefully may result in simpler and significantly better models than those built using default settings (Warren and Seifert 2011; Muscarella et al. 2014; Radosavljevic and Anderson 2014). Here, for each species, we constructed models using feature classes that span a varied range of complexities: L (Linear), LQH (Linear Quadratic Hinge), and LQHP (Linear Quadratic Hinge Product) with 1–4 regularization multipliers (β) and the multiplier step value set to 1. This procedure resulted in

5268 candidate models, equivalent to 12 models per each of 439 species. Species with less than five unique records (100 species) were excluded.

Model accuracy was evaluated using three of the most commonly used evaluation metrics. First, we used the area under the curve (AUC) of the receiver of a Receiver Operating Characteristic plot for test occurrences, i.e., the mean of the *k* test AUCs (avg.test.AUC; Peterson et al. 2011). Second, omission rates were calculated at the 10th percentile training presence threshold (Peterson et al. 2011). Lastly, we used the Akaike Information Criterion corrected for finite sample sizes (AICc) to evaluate model complexity (Warren and Seifert 2011). AICc was calculated on the full model only and thus does not consider *k* partitions (Kass et al. 2018). We selected the best models according to the following criteria (Swets 1988): (1) models with the highest AUC and (2) if more than one best model was available, models with the lowest omission rate or AICc. Twenty-three models with avg.test.AUC scores of < 0.70 were discarded.

The final models were generated using the best parameterizations and the full set of occurrences with logistic outputs. These models were then transformed into presence–absence maps using the 10th percentile threshold (Peterson et al. 2011). This is a conservative threshold that seems to be less sensitive to environmental outliers (Radosavljevic and Anderson 2014). It includes 90% of the presence records with the highest probability of occurrence from the predicted presence range.

Species Assemblages Composition

We estimated species assemblage composition for each 5 × 5 km^2 grid cell by stacking presences from the individual species distribution models ($n = 416$). This resolution is commonly used to study amphibian distributions (Pyron and Wiens 2013; Dufresnes et al. 2016; Betts et al. 2017) and for delineating taxon assemblages (Graham et al. 2017). Species whose models performed poorly (i.e., avg.test.AUC scores < 0.70; $n = 23$), and species with less than five unique records ($n = 100$) were assigned to the grid cells that overlapped with their occurrence records. Finally, we built a species presence–absence matrix ($n = 539$ species) to represent the occurrence of each species across all 6178 grid cells (i.e., assemblages).

Functional Distinctiveness of Anuran Species

To test the hypothesis that critically endangered (CR) species are more functionally distinct at the assemblage level, we first estimated Gower's pairwise functional distances (Gower 1971) between species across assemblages using the vegdist function in the R-package vegan (Oksanen et al. 2016). Gower distances allows us to quantify functionally differences using both continuous and categorical traits. We then computed a Principal Coordinates Analysis (PCoA) on the basis of the Gower distance functional matrix, with Lingoes correction (Lingoes 1971) for negative eigenvalues, and used this to describe multidimensional trait space and visualize differences between species classified under different IUCN categories using the R-package ape (Paradis et al. 2004).

We then calculated functional distinctiveness, *D*, for each species, *i*, within an assemblage (Grenié et al. 2018) as follows:

Eq.

$$D_i = \frac{\sum_{J=0,i\neq j}^{N} d_{ij}}{N-1}, \tag{1}$$

where D_i is the functional distinctiveness of species *i*, *N* the total number of species in the assemblage and d_{ij} the functional distance between species *i* and species *j* (Grenié et al. 2017). The distances d_{ij} were scaled between 0 (the focal species is identical to all the other species) and 1 (the focal species is most dissimilar to the other species). We computed functional distinctiveness using the R-package funrar (Grenié et al. 2017). We next used ANOVA to explore differences in species functional distinctiveness among IUCN extinction risk categories.

We ran models separately for Ecuadorian highlands (i.e., areas > 1000 m in the Andes mountains), and lowlands (i.e., areas < 1000 m; Veblen et al. 2015).

Calculating Beta Diversity (β-diversity)

To explore shifts in diversity with the loss of CR species by considering different facets of diversity (i.e., taxonomic, phylogenetic, functional), we used assemblage dissimilarity metrics (i.e., β-diversity metrics) based on species presence–absence matrices with and without CR species. First, for each grid cell, we calculated taxonomic, phylogenetic and functional β-diversity as the average of the β-diversity values between a focal grid cell and each of the eight neighboring grid cells (Melo et al. 2009). Second, we recalculated these measures of β-diversity excluding species listed as CR, and we subtracted β-diversity without CR species from current β-diversity. Positive values imply a trend towards increasing heterogeneity, while negative values indicate a trend towards homogenization. We also considered a scenario in which both CR and EN species become regionally extinct.

Taxonomic β-diversity.—To quantify spatial patterns of species dissimilarity among all assemblages, we used the Sørensen (1948) pairwise dissimilarity metric, βsor, which can be partitioned into turnover (β_{sim}), accounting for species replacement, and nestedness (βnes), reflecting the loss or gain of species (Baselga 2010, 2012). We focussed on the turnover component of taxonomic β-diversity as previous analyses have shown little spatial variation in the nestedness component across Ecuador (Menéndez-Guerrero et al. 2020). We therefore use taxonomic β-diversity to refer explicitly to species turnover, estimated as:

Eq. $$\beta sim = \min(b,c)/(\mathrm{a} + \min[b,c]) \quad (2)$$

where a is the number of species in both grid cells, b is the number of species exclusive to the focal grid cell, and c is the number of species exclusive to the adjacent grid cell.

Phylogenetic and functional β-diversity.—For phylogenetic β-diversity, which is a measure of how phylogenetic relatedness changes across space, we used the PhyloSor metric (Bryant et al. 2008), a phylogenetic analog of the Sørensen index (Swenson 2011). This pairwise metric uses information on the total length of the branches shared and not shared between grid cells. As with taxonomic β-diversity, we used only the turnover component of phylogenetic β-diversity (Baselga 2010). By linking ecological and evolutionary processes across space in time, phylogenetic β-diversity can bring insights into the mechanisms underlying current and future patterns of biodiversity (Graham and Fine 2008).

Prior to estimating functional β-diversity, which is a measure of how functional-trait composition of assemblages vary across space, we applied UPGMA to the Gower's pairwise distance matrix to construct a dendrogram that estimates species differences in functional space (Petchey and Gaston 2002). Then, branch lengths of the functional dendrogram were used to calculate the functional equivalent of PhyloSor. All β-diversity metrics were calculated using functions in the package betapart implemented in R (Baselga and Orme 2012).

Statistical Analyses

To explore the relationship between changes in assembly structure (i.e., β-diversity) along the three facets of diversity (taxonomic, phylogenetic, and functional), we fitted two linear models with change in phylogenetic and functional β-diversity as the response variable, respectively, and change in taxonomic β-diversity as the predictor variable. To control for spatial autocorrelation, we included a spatial term (latitude*longitude) as a co-predictor in the models. Changes in β-diversities represent the difference in β-diversities when dropping CR species. All predictor variables were log transformed and standardized to a mean of 0 and a standard deviation of 1 prior to analysis.

To compare extinction scenarios on the homogenization of anuran assemblages among different facets of diversity, we used Cohen's (1988) *d* (or standardized differences), defined as the difference between the means divided by the root mean square of two standard deviations, calculated using the R-package effectsize (Gamer et al. 2012). Larger Cohen's *d* values mean higher effect sizes. To evaluate how the potential loss of EN species may further affect homogenization patterns, we also ran linear mixed effect models on each of the three facets of homogenization, with the intensity of homogenization (i.e., percentage of negative change in βfdiversity) as response variable, extinction intensity (IUCN status) as a fixed effect, and altitude as a random effect. Models were fit using the R-package lme4 (Bates et al. 2015) on assemblages with at least a 5% predicted increase in homogeneity, i.e., a 5% decrease in β-diversity (Graham et al. 2017).

To assess whether the existing protected network effectively covered assemblages predicted to become increasingly homogeneous, we calculated the geographic overlap between residuals of the linear regression between functional homogenization and taxonomic homogenization, assuming loss of both CR and EN species, and the current National System of Protected Areas (MAE 2019). All statistical analyses were performed in R (v3.5.1; R Development Core Team 2017).

RESULTS

Species Distribution Modeling

The average performance of the best distribution models with an AUC above 0.7 was high ($\overline{X}$ AUC = 0.87; *n* = 416 species). Only 21 (~5%) models showed an AUC below 0.7 (see all evaluation metrics in Table S3).

Functional Distinctiveness (D_i) of Highly Endangered Anurans

The first two axes from the PCoA on the functional trait matrix explained 64% of the total variation in trait space (Fig. 2.1). CR species were primarily separated along the second PCoA axis, explaining 19.27% of the variation. This axis was mainly described by breeding strategy and body size, with the majority of CR species reproducing via larval development and with bigger body sizes than non-CR species (Fig. 2.1, and Supplemental Figs. S1 and S2, available online).

The average (± SD) of the mean functional distinctiveness (D_i) of all species across assemblages was 0.40 (± 0.09), with important variation among species (minimum = 0.19; maximum = 0.70). CR species were, on average, the most functionally distinct species in the highlands ($\overline{X}\ D_i = 0.47 \pm 0.12$; Fig. 2.2A), followed by EN species ($\overline{X}\ D_i = 0.40 \pm 0.11$), LC species ($\overline{X}\ D_i = 0.39 \pm 0.07$), VU species ($\overline{X}\ D_i = 0.38 \pm 0.09$) and NT species ($\overline{X}\ D_i = 0.38 \pm 0.09$). Linear models indicated that CR species differ from species in all other IUCN categories in the highland Ecuadorian Andes (Supplemental Table S4, available online) whereas, in the lowlands, there were no differences in functional distinctiveness between CR and other IUCN categories (Table S4; Fig. 2.2A). The majority of anuran assemblages in Ecuador lack CR species (Supplemental Fig. S3, available online), which are mainly distributed in the highlands. However, in the majority of Ecuadorian highland anuran assemblages (~70%), a CR species was the most, or the second most, functionally distinct species (Fig. 2.2B). CR species were the most functionally distinct in only a few assemblages in the lowlands, mainly in the Western Dry Lowlands of the Ecuadorian Pacific Coast (Fig. 2.2B).

Spatial Shifts in β-diversities due to the Extinction of Highly Endangered Anurans

In general, we found that the extinction of CR species will have only a small impact on the majority of Ecuadorian anuran species assemblages (Figs. 3A, B, C) as change in taxonomic β-diversity was < 5% for ca. 65% of all assemblages. However, there was an important spatial variation in the composition of species (Fig. 2.3B). Highland assemblages represent about 40% of all Ecuadorian anuran species assemblages. Among these, assemblages with reductions in taxonomic β-diversity, indicating increasing taxonomic homogeneity ($\overline{X}$ β-diversity change = –9.99% ± 5.15 SD), were concentrated in the Western and Eastern Montane Forest on the slopes of the Ecuadorian Andes (Fig. 2.3B). These assemblages showing increasing taxonomic homogeneity are mainly found at mid-elevations, between 1105 m (1st quartile) and 2771 m (3rd quartile), and represent approximately 65% of all anuran assemblages in the Andean highlands. In contrast, most of the Ecuadorian Inter-Andean Valley, mainly situated at high elevations between 2796 and 3800 m (Fig. 2.3B) were found to become increasingly taxonomically heterogeneous ($\overline{X}$ β-diversity change = 13.42% ± 5.76). Only a few lowland assemblages, such as those in some areas of the Chocoan Tropical Rain Forest and Deciduous Forest, showed a decrease in taxonomic β-diversity ($\overline{X}$ β-diversity change = –11.54% ± 7.90), and some were expected to show increases, mainly in areas of the Chocoan Tropical Rain Forest and Western Foothill Forest ($\overline{X}$ β-diversity change = 5.25% ± 0.09).

Changes in taxonomic β-diversity were significantly correlated with shifts in phylogenetic β-diversity ($R^2_{\text{adj}} = 0.85$; $P < 0.01$; Table 2.1) and, to a lesser extent, functional β-diversity ($R^2_{\text{adj}} = 0.2$; $P < 0.01$; Table 2.1). Anuran assemblages with the highest spatial congruence between taxonomic and phylogenetic homogenization (Table 2.2) were mainly in the western and eastern slopes of the Ecuadorian Andes (Fig. 2.3A, D), whereas assemblages predicted to become more taxonomically and functionally homogeneous were mainly restricted to the eastern slopes of the Andes (Fig. 2.3C, E). Anuran assemblages were predicted to become more taxonomically, phylogenetically and functionally heterogeneous across the Ecuadorian Inter-Andean Valley (Fig. 2.3D, E).

Influence of Species Extinctions on Homogenization

Functional homogenization (i.e., number of assemblages that became functionally more similar) was less frequent than phylogenetic or taxonomic homogenization under the CR species extinction scenario. However, the additional extinction of currently EN species (plus CR species) increased the trend towards functional homogenization nearly five-fold (Supplemental Table S5, and Supplemental Fig. S4, available online). Increasing trends were also observed for taxonomic and phylogenetic homogenization, but to a lesser extent (Fig. S4). Furthermore, the effect size of the extinction of CR species on the intensity of functional homogenization (i.e., negative change in β-diversity) was higher than for phylogenetic and taxonomic homogenization (Table 2.2; Fig. 2.4). With the extinction of EN species added, the increase in the intensity of functional homogeneity was about three times that for taxonomic homogeneity, and more than two times that for phylogenetic homogeneity (Cohen's $d = 0.78$ [medium effect size], Cohen's $d = 0.41$[small effect size], and Cohen's $d = 0.32$ [small effect size], respectively; Fig. 2.4; Table 2.2). All trends towards increasing homogenization were significant (Supplemental Table S6, available online).

Approximately 18% of anuran assemblages predicted to show disproportionate losses in functional heterogeneity relative to predicted changes in taxonomic heterogeneity fell within the Ecuadorian current National System of Protected Areas. Conservation shortfalls were found mainly to be located in the Southern Andes, especially in the Cordillera del Condor and

Cordillera de Cutucú and, to a lesser extent, in the Chocoan Tropical Rainforest of western Ecuador (Supplemental Fig. S5, available online).

DISCUSSION

We have shown that CR classified frogs and toads are, on average, more functionally distinct within anuran assemblages than those in lower IUCN threat categories. This functional distinctiveness mainly captures variation in reproductive strategy and body size, with CR species being larger and more often reproducing via larval development than non-CR species. The potential extinction of currently endangered species is likely to trigger increasing taxonomic, phylogenetic, and, especially, functional homogenization of anuran assemblages in the Ecuadorian Andes. The increase in similarity of trait composition (i.e., functional homogenization) among anuran assemblages could have even more extensive consequences on ecosystem functioning and stability than simple taxonomic homogenization (Villéger et al. 2014; Mori et al. 2015). Currently, the vast majority (~80%) of locations at high risk of becoming functionally homogeneous relative to predicted shifts in taxonomic homogeneity are unprotected as only ~20% overlap with the National System of Protected Areas. Our results indicate a need for further studies to examine impacts of loss of functional variation across biotic assemblages. They also emphasise the need for conservation efforts to consider the multiple facets of biodiversity.

Species are not functionally equivalent and variation in species' traits can help to explain the functional differences among species. Some traits may also influence species’ susceptibility to extinction, and hence current threat status (McKinney 1997; Bielby et al. 2006; Lee and Jetz 2010). Our results showing functional differences between CR and Non-CR species are concordant with previous studies on amphibians that have found that large species with dependency on aquatic habitats and reproduction are more prone to decline or be listed at higher IUCN threat categories (Lips et al. 2003; Sodhi et al. 2008; González-del-Pliego et al. 2019). These traits might mediate ecological functions that species perform in ecosystems. For example, body size is related to trophic ecology whereas reproductive strategy may reflect availability of food and energy (Wells 2007; Oliveira et al. 2019). To our knowledge, no previous studies have explicitly examined the relationship between functional distinctiveness and IUCN Red List Status in amphibians. Vasconcelos et al. (2019) identified the Andes, including the Ecuadorian Andes, as a region harboring many functionally distinct species. In other taxonomic groups, species with high extinction risk, which usually are rare (MacArthur and Wilson 1967; Pimm et al. 1995), also tend to be more functionally unique (Jain et al. 2014; Mouillot et al. 2013; Leitão et al. 2016; but see Chapman et al. 2018). Here, we have shown how this relationship is manifested in anuran species assemblages across the Ecuadorian Andes.

We predicted, and our data supported, a general tendency towards biotic homogenization due to extinctions of threatened and functionally distinct species in the majority of anuran assemblages occurring in the Andes. This trend is especially marked in areas where the greatest diversity of amphibians is found. For instance, we predicted high levels of increasing taxonomic, phylogenetic, and functional similarity across anuran assemblages on the slopes of Ecuadorian Andes, particularly in the Eastern Montane Forest. This ecoregion has the highest level of amphibian richness (~40%), and one of the highest percentages of amphibian endemism (~60%), in Ecuador (Ron et al. 2019). These findings may contradict the predictions of the biodiversity insurance hypothesis (Walker 1992; Yachi and Loreau 1999), which proposes that highly diverse ecosystems are buffered against extinction by high functional redundancy among species. In a continental-scale study on anurans, Menéndez-Guerrero et al. (2020) also identified the Ecuadorian Andes as an area vulnerable to increasing taxonomic homogenization due to species losses as a consequence of future climate change. However, they did not evaluate how such taxonomic shifts translated into changes in phylogenetic and functional homogeneity. Indeed, only a handful of studies (Smith et al. 2009; Nowakowski et al. 2018) have explored spatial shifts in phylogenetic homogeneity in amphibians. Similarly, spatial shifts in functional diversity towards functional homogenization in anurans has received considerably less attention than equivalent changes in taxonomic homogeneity across space (but see Smith et al. 2009). The ecosystem effects of the increased functional heterogeneity projected to occur in some regions of Ecuadorian Inter-Andean Valley are much less clear. However, ecosystem functioning may be impacted by any change in the natural functional structure of assemblages (Folke et al. 2004).

Recent studies have suggested that trends towards taxonomic, phylogenetic, and functional homogenization could be uncoupled (Villéger et al. 2014; Nowakowski et al. 2018; White et al. 2018). For example, invasions by functionally redundant species (i.e., species in the same ecosystem filling similar roles) or non-random extinctions of functionally distinct species could result in greater increase in functional homogeneity relative to taxonomic homogeneity (Olden et al. 2004, 2018). Similarly, a steeper decline in functional heterogeneity than in phylogenetic heterogeneity could result if particular traits correlate closely with extinction risk (Fritz and Purvis 2010; Oliveira et al. 2019). Some of the functional traits we examined in the present study, specifically large body size and aquatic-breeding, have been linked to population declines (Lips et al. 2003). Our results show a moderate association between taxonomic and phylogenetic homogenization with functional homogenization across anuran assemblages following the loss of currently threatened species. However, increases in functional homogenization exceed increases in taxonomic and phylogenetic homogenization nearly three-fold when both CR and EN species are assumed lost to extinction. Our findings perhaps reflect a general pattern across taxa, whereby shifts in taxonomic diversity cannot be used to predict changes in functional diversity (for reviews, see Olden et al. 2016, 2018), and challenge the paradigm of surrogacy among different facets of diversity. We suggest, therefore, that there is a need to recognise the unique contribution of functional diversity to ecosystems, and examine more closely the possible losses of functional diversity that occur with species extinctions. This need is particularly pressing for groups such as amphibians, which includes a high number of threatened species (González-del-Pliego et al. 2019).

Conservation Implications

An increasing number of studies are looking to better understanding the central link between species functional traits and ecosystem function via different mechanistic underpinnings (Cadotte et al. 2011; Gagic et al. 2015; Cadotte 2017). Decreases in functional β-diversity (increases in functional homogenization) across species assemblages represent an under-recognised facet of biodiversity loss. Very few studies have focussed on trends towards functional homogenization in such a diverse and threatened group as the Neotropical amphibians (Olden et al. 2016; Smith et al. 2009). Our results highlight the limitations of the current reserve network in Ecuador for maintaining functionally diverse amphibian assemblages. Gaining a better understanding of the ecological consequence of increased functional homogenization remains a critical ecological and conservation challenge.

SUPPLEMENTAL MATERIAL

Supplemental material associated with this article can be found online at https://doi.org/10.1655/Herpetologica-D-20- 00011.S1.

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TABLE 2.1.—Results of two linear models fitted with change (△) in phylogenetic β-diversity or functional β-diversity in response to change in taxonomic β-diversity. A spatial term (latitude*longitude) is included to control for spatial autocorrelation. Adjusted R^2 (R^2_{adj}) is used as a measure of goodness of fit. Estimates, standard error of estimates (Std. Error), *t*-values (*t*) and their associated probabilities (*P*-value) for each predictor are shown as well.

Response variable	Model predictors	R^2_{adj}	*P*-value		
△phylogenetic β-diversity	△taxonomic β-diversity + longitude*latitude	0.85	< 0.01		
		Estimate	Std. Error	*t*	*P*-value
	△taxonomic β-diversity	94.46	0.51	184.22	< 0.01
	longitude*latitude	0.01	0.006	2.08	< 0.05
△functional β-diversity	△taxonomic β-diversity + longitude*latitude	0.2	< 0.01		
		Estimate	Std. Error	*t*	*P*-value
	△taxonomic β-diversity	40.54	1.23	32.98	< 0.01
	longitude*latitude	0.1	0.02	6.21	< 0.01

TABLE 2.2.—Intensity of predicted biotic homogenization (i.e., percentage of negative change in β-diversity) of Ecuadorian anuran assemblages under two scenarios of species extinctions: extinction of critically endangered species (CR extinction) and extinction of both critically endangered and endangered species (CR–EN extinction). Mean and standard deviation (SD) of intensity of homogenization are shown.

Diversity facet	Scenario	Intensity of homogenization (mean ± SD)
Taxonomic homogenization	CR extinction	–9.98 ± 5.15
	CR–EN extinction	–13.75 ± 8.27
Phylogenetic homogenization	CR extinction	–11.69 ± 6.28
	CR–EN extinction	–16.37 ± 10.92
Functional homogenization	CR extinction	–19.85 ± 17.00
	CR–EN extinction	–38.80 ± 21.43

FIG. 2.1.—Principal coordinate analysis (PCoA) of Gower distance based on a functional trait matrix for anuran species. First and second principle components (PCs) and their explained variation are shown. Critically endangered species (red squares) mainly differ from species in other International Union for Conservation of Nature (IUCN) categories (brown circles) along PC2, which is primarily defined by breeding strategy and body size.

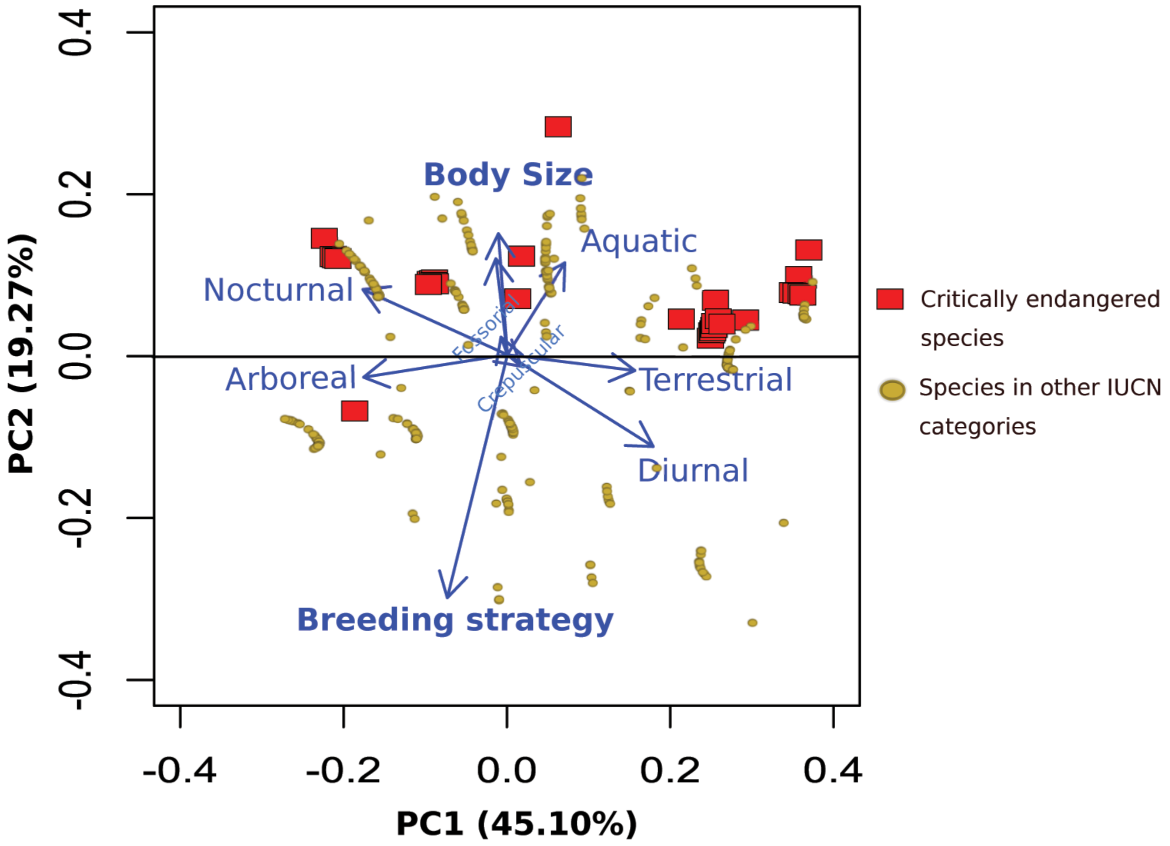


FIG. 2.2—Functional distinctiveness (*Di*) of anuran species. **(A)** Variation in *Di* of species classified under the International Union for Conservation of Nature Red List Categories: critically endangered (CR), endangered (EN), vulnerable (VU), near threatened (NT), and least concern (LC). The variation in *Di* is shown for highland species vs. lowland species. Median values of *Di* are shown (black horizontal line) with their respective 95% confidence interval (notches of box). The core boxes of boxplots indicate the interquartile range of data whereas the whisker lines extend to at most 1.5× the interquartile range from both ends of the box. Outliers are shown as black circles. **(B)** Spatial distribution of anuran assemblages, indicating CR species as the most (dark green), or the second most (light green), functionally distinct within the assemblages. The black line delineates the highlands (> 1000 m in elevation).

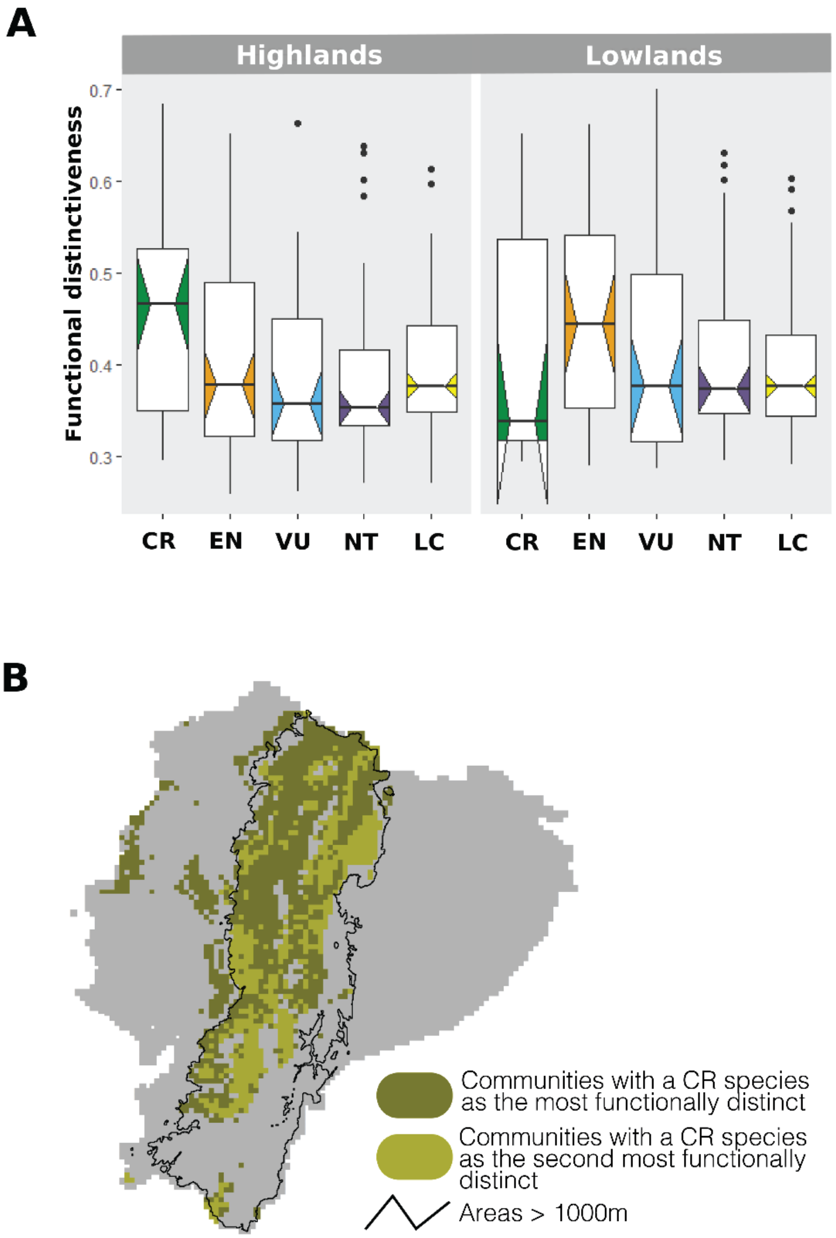


FIG. 2.3.—Shifts in spatial patterns of anuran β-diversities across Ecuador due to the extinction of CR species. Magnitude of shifts are shown as percentages. **(A)** Map showing shifts in phylogenetic β-diversity (△PBD): assemblages shifting composition towards increasing phylogenetic heterogeneity are in blue; those shifting towards increasing phylogenetic homogenization are in red. **(B)** Map showing shifts in taxonomic β-diversity (△TBD): assemblages shifting composition towards taxonomic heterogeneity are in blue; those shifting towards taxonomic homogenization are in red. **(C)** Map showing shifts in functional β-diversity (△FBD): assemblages shifting composition towards functional heterogeneity are in blue; those shifting towards functional homogenization are in red. **(D)** Bivariate map depicting the spatial congruence between shifts in taxonomic β-diversity (△TBD) and phylogenetic β-diversity (△PBD). **(E)** Bivariate map depicting the spatial congruence between shifts in taxonomic β-diversity (△TBD) and functional β-diversity (△FBD).

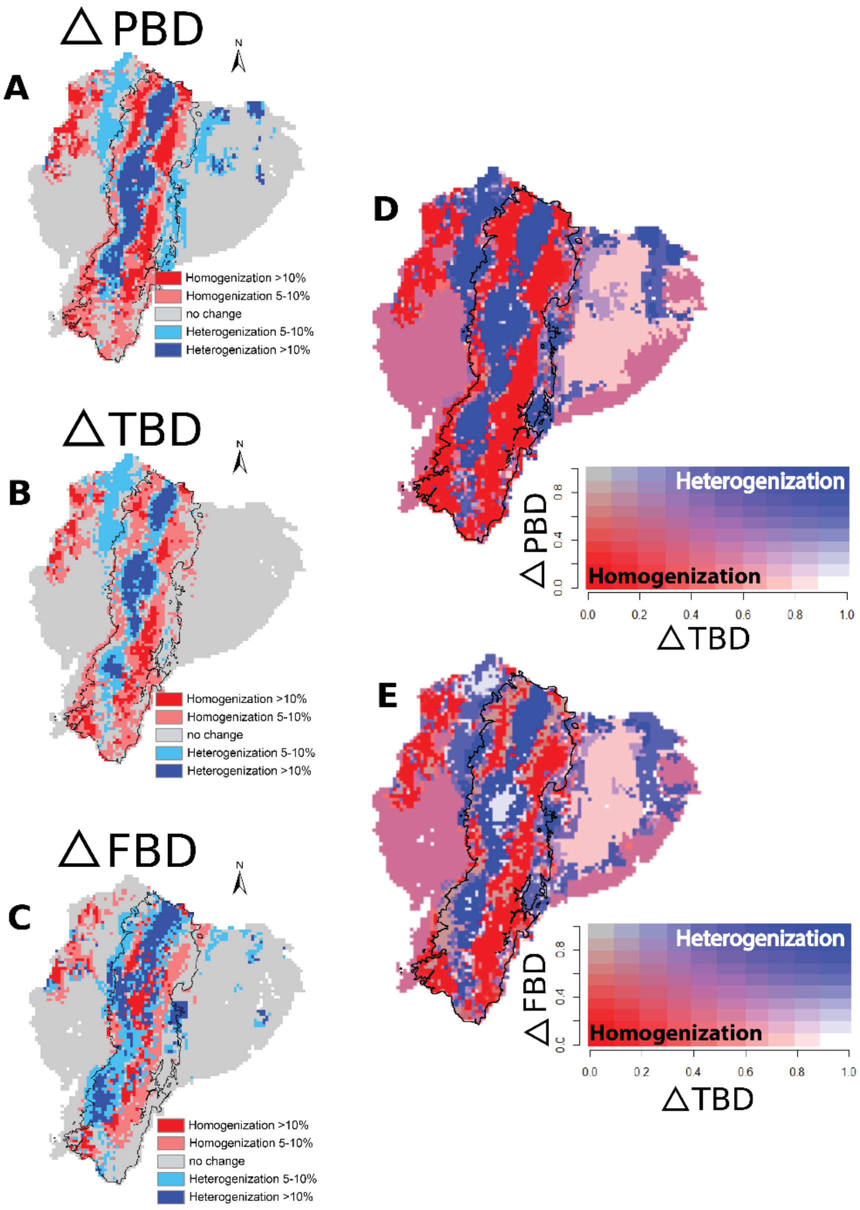
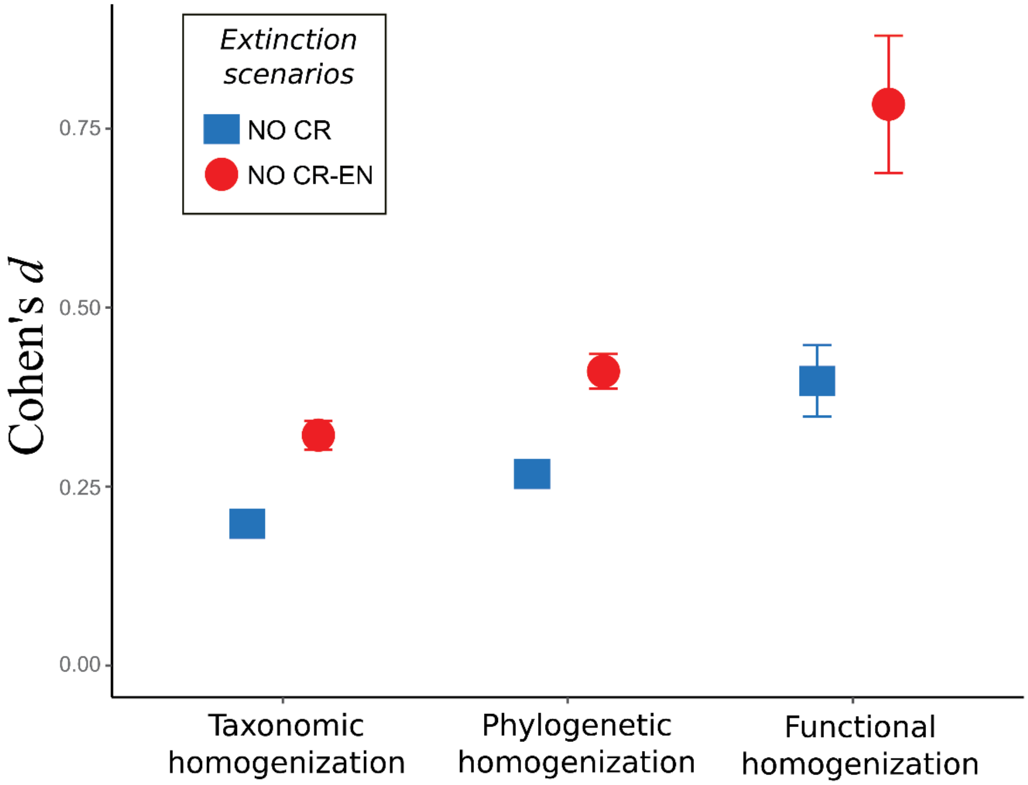


FIG. 2.4.—Effect size of the intensity of homogenization (i.e., negative change in β-diversity) under two scenarios of species extinctions: a No CR scenario in which CR species become extinct (in blue) and a No CR–EN scenario in which both CR and EN become extinct (in red). The intensity of homogenization is shown for the three different diversity facets on the x-axis. Effect size was calculated using Cohen's *d* (or standardized differences), defined as the difference between the means divided by the root mean square of two standard deviations. Cohen's *d* estimates and 95% confidence intervals are plotted.



Linking Statement 2

In Chapter 2, I assess the functional importance of the currently highly endangered amphibian species (following the IUCN Red List categories) within ecological communities, and model the functional consequences of their extinction within the Ecuadorian landscape. My analyses indicate that the extinction of endangered species will increase the functional homogeneity of communities across the Ecuadorian Andes. I suggest that increasing functional homogenization may lead to important alterations in the stability and functioning of local ecosystems, and I emphasize the need to consider the different facets of biodiversity in conservation assessments.

In Chapter 3, I use empirical data on amphibian communities to assess compositional changes in amphibian diversity in the tropical montane landscapes of Ecuador over the last five decades. I use Bayesian modelling and data from long-term historic and recent monitoring efforts, to explore the drivers of community change across the different facets of biodiversity.

CHAPTER 3:

Diversity erosion of Neotropical mountain amphibian communities in the Anthropocene

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ABSTRACT

Human activities have caused alarming trends of biodiversity loss at a global scale. However, at regional and local scales, patterns of species responses to anthropogenic pressures are less clear. A better understanding of the contemporary re-shaping of communities and how these shifts might affect stability of ecosystems functioning is critical specially for some groups that are declining stronger such as amphibian and reptiles. Here we empirically address the response of seven anuran communities from Neotropical highlands, a highly vulnerable region, to human-caused environmental changes over the last 50 years. In general, we show that most anuran communities experienced a substantial diversity erosion. First, we found that most communities show a decrease in species richness, in average almost 52% of species were locally lost. Then, we show that these local species losses are strongly associated with species climatic niches and extreme warm temperature events. In addition, we show that the reduction of local taxonomic diversity have resulted in larger phylogenetic and functional diversity reduction, which could hamper ecosystem functioning. Finally, we found that communities re-shaping has yielded an increment in functional homogenization across space. Our results suggest climate warming might have played an important role on amphibian montane declines and highlight the need to evaluate biodiversity shifts beyond species richness.

1 INTRODUCTION

Human activities have profoundly transformed the global environment (Vitousek et al., 1997; Lewis and Maslin 2015) causing a severe loss of biodiversity around the world (Barnosky et al., 2011; Ripple et al., 2017). Species extinction rates in the Anthropocene are estimated to be 100 to 1000 times higher than background rates (Pimm et al., 1995), and are threatening the stability of natural ecosystem functioning (Hautier et al., 2015) and human well-being. However, while this trend in biodiversity loss is clear at a global scale, mixed patterns of biodiversity changes are reported at regional and local scales (McGill et al., 2015; Primack et al., 2018). A number of communities facing anthropogenic impacts show stable, or even increased biodiversity trends (Vellend et al., 2017; Barnagaud et al., 2017; Gotelli et al., 2017), as is the case when local extinctions are balanced or offset by colonization of non-native species (Dornelas et al., 2014; Hillebrand et al., 2018).

The mismatch between local and global biodiversity trends highlights the importance of considering the variation in species' responses when predicting impacts of anthropogenic environmental changes (McGill et al., 2015). In the face of any given anthropogenic change, we might expect some species to decline or disappear, while others, which may be preadapted to the new conditions, persist or even increase in abundance (McKinney & Lockwood 1999; Hobbs et al., 2018). Addressing species-specific responses to local changes thus allows us to better understand contemporary reshaping of communities and help predict novel ecosystems.   the need to look beyond changes in species richness (Hillebrand et al., 2018). Local species richness estimates alone can fail to capture other facets of biodiversity (e.g. phylogenetic, functional, phenotypic diversity), species interactions, and processes working at larger spatial scales such as biotic homogenization (Primack et al., 2018; Hillebrand et al., 2018).

Among vertebrates, amphibians have the highest proportion of species (~40%) at risk of extinction (González-del-Pliego et al., 2019). Declines have increased significantly since the 1970s and 1980s, and show continued downwards trends over time (Stuart el al., 2004; Wake and Vredenburg 2008; Alroy 2015). At least 3.1% of frog species have disappeared, and within the next century 6.9% are expected to go extinct (Alroy 2015). While amphibian declines are geographically widespread, there appears to be no single causal driver (Grant et al., 2020). Analyses based on long-term demographic studies of single populations, focal species, and communities suggest that climate change and habitat transformation are among the most pervasive threats at large spatial scales (Grant et al., 2016). However, pressures from these and other drivers, such as infectious diseases and pollution, varies considerably across regions, species and sites (Grant et al., 2016; Miller et al., 2018).

The Neotropical highlands top the worldwide list of hotspots for endemism and number of amphibian species per unit area (Myers et al., 2000). However, it is also a region that has experienced some of the most dramatic amphibian population declines (Stuart el al., 2004; Lips et al., 2008; Stuart et al., 2008; Catenazzi, 2015). A number of studies have documented the role of chytridiomycosis (a zoonotic disease caused by the chytrid fungus *Batrachochytrium dendrobatids*) in catastrophic local amphibian declines (Lips et al., 2005, 2006; Voyles et al., 2009; Crawford et al., 2010; Scheele et al., 2019), but the importance of other extinction pressures, such as climate warming and habitat loss, is less clear.

As ectotherms, amphibians are especially sensitive to changes in environmental temperature and precipitation, which likely have large effects on both their physiology and biotic interactions (Beebee 1995; Carey and Alexander 2003; Pounds et al., 2006). As climate becomes warmer, amphibians must either disperse to more suitable environments, acclimate via preexisting phenotypic plasticity or evolutionary adaptation, or risk extinction (IPCC, 2014; McDonnell and Chapman, 2015). Land use change might have both direct impacts on amphibian populations, for example, through reducing the area of suitable habitat available to them, and indirect impacts, for example, via amplifying susceptibility to global warming (Pintanel et al., 2019; González-del-Pliego et al., 2020). To date, empirical evidence on species and community-wide responses to these threats, especially among tropical montane species, is scarce (e.g. Pounds et al., 1999; 2006; Bustamante et al., 2005; Raxworthy et al., 2008; Palmeirim et al., 2017). However, montane species are thought to be at elevated risk since they tend to have more restricted geographical ranges and narrower environmental niches. Future projections based on species bioclimatic models and spatial distribution of threats suggest that amphibians in the Andean region may experience some of the highest extinction rates in the world (Hof et al., 2011), and that community assemblages will become significantly more similar across space (Menéndez-Guerrero et al., 2020).

Here, we explore changes in the status of seven Ecuadorian high-altitude anuran assemblages over the last 50 years. Combining data from historical and contemporary sources, we ask (1) whether changes in anuran communities are dominated by species losses, (2) if local species extinctions are associated with anthropogenic environmental changes, such as climate warming or habitat loss, (3) if taxonomic diversity changes translate into proportional changes in phylogenetic and functional diversity, and (4) if anuran communities have become more similar across space. We show that most communities have lost species (ca. 52% of species lost in average). Local species losses are associated with species climatic niches, and are likely to have been driven by climate warming. Finally, we show that changes in community composition have a greater impact on functional and phylogenetic diversity than taxonomic diversity, and result in the increasing functional homogenization of communities across space.

2 MATERIALS AND METHODS

2.1 Study area

We selected seven localities in the Ecuadorian Andes between 1400–4200 m elevation (Fig. 3.1), showing high environmental heterogeneity and strong temperature and precipitation gradients. These localities were Bosque Protector Cashca Totoras (P1), Pilaló (P2), Paramo of Antisana (P3), Paramo of Guamaní (P4), Quebrada Zapadores (P5), Río Azuela (P6) and Río Faisanes (P7).

2.2 Data

2.2.1 Anuran community data over time

We compiled data on anuran composition and structure in the seven localities over three discrete time periods: 1967-1987 (TI), 2000-2003 (T2), and 2016-2018 (T3). For time periods T1 and T2 we extracted data from Bustamante et al. (2005). T1 data were obtained through visual encounter surveys, and were among the very first systematic assessments of amphibian species composition in the Ecuadorian Andes (Duellman, in lit.; Black, 1982; Bustamante et al., 2005). Exhaustive sampling performed in comparable habitats resulted in similar estimations of species richness (Lynch and Duellman, 1997; Bustamante et al., 2005) to those obtained in our T1 survey data, suggesting sampling effort was sufficient to reliably capture the diversity and structure of amphibian communities at each site. T2 data represented 5–14 diurnal and nocturnal sampling sessions at each locality (except at BPCT where surveys were much longer; Bustamante et al., 2005), exceeding the sampling effort of T1 (Table S1, Supporting information). Specimens from observed species were collected and housed at QCAZ museum from Pontificia Universidad Católica del Ecuador. For time period T3, between 2016 and 2018 we conducted 4–9 diurnal and nocturnal sampling sessions of between seven to nine hours using direct observation and active searching across habitat types (Table S1, Supporting information). Our sampling effort was always greater than in T1, and comparable to that in T2 (except at BPCT), however, the intensity of our samplings (i.e., number of persons sampling during each session) was higher than T2. When possible, surveys were undertaken during the same months or seasons as in T1 and T2. All collected specimens were housed at QCAZ or at the Museo Ecuatoriano de Ciencias Naturales (MECN), Instituto Nacional de Biodiversidad of Ecuador (INABIO).

2.2.2 Taxonomic remarks

We restricted our analysis to species with formal descriptions. Species that were not found during T2 but reported in T1 and T3 were added as present in T2 for all analyses. *Hyloscirtus ptychodactylus* was included as present in T1 and T2 since it was reported in T3 at Pilaló, and the species was described in the year 1990, with Pilaló as the type locality (Duellman and Hillis, 1990). *Pristimantis totoroi* from Bosque Protector Cashca Totoras was previously incorrectly reported as *P. phoxocephalus* in T1 and T2 (Páez and Ron, 2019). *Pristimantis w-nigrum* is a complex of cryptic species (Reyes et al., 2015), therefore, it was not used in the analyses.

2.2.3 Phylogeny and Ecological traits

We used data on phylogenetic relationships from Jetz and Pyron (2018), pruned to the set of species reported in the combined T1, T2 and T3 surveys.

We used a functional trait database compiled by Menéndez-Guerrero et al. (2020) containing information on four traits related to morphology, ecology, and reproductive characteristics for Ecuadorian anurans: (1) snout–vent length, for both males and females, as continuous data, (2) diel active period (diurnal or nocturnal), (3) habitat (aquatic, arboreal, or terrestrial) as binary data, and (4) breeding strategy (direct or larval development) as a binary variable. These data were extracted from the portal BIOWEB (http://bioweb.bio), and supplemented with information from Oliveira et al. (2017).

2.3 Changes in community composition

To characterize changes in species composition (i.e., dissimilarity) between sampling time periods, we used a temporal beta-diversity index ($D_{\%diff}$; Odum, 1950; Legendre and Gauthier, 2014; Shimadzu et al., 2015), calculated as:

$$D_{\%diff} = (B + C)/(2A + B + C)$$

where A = number of species that are common to the two surveys (i.e., unscaled similarity between two surveys), B = unscaled sum of species losses between two surveys, and C = unscaled sum of species gains between two surveys; (B+C) represents the unscaled dissimilarity (Legendre, 2014). The scaled versions of B and C allow us to calculate the relative contribution of species losses and species gains to the total dissimilarity for site, respectively (for details see Legendre, 2019). $D_{\%diff}$ in each locality (i.e., P1- P7) was measured between T1 and T2 , T2 and T3, and T1 and T3. We also estimated the mean of $D_{\%diff}$ across sites between times, and tested for significance using a permutational paired t-test with 9999 random permutations (Legendre, 2019). Analyses were performed using functions TBI() and plot.TBI() in the 'adespatial' package (Dray et al., 2019) in R Core Team (2017).

2.4 Potential determinants of species losses (i.e., local extinctions)

We assessed the effects of various climatic, ecological and anthropogenic drivers on local species extinctions between time periods.

Climatic niche breadth: We estimated niche breadth for each species by quantifying the high-dimensional ecological hypervolumes via a kernel density estimation method developed by Blonder et al. (2014). For all unique species occurrence records obtained from the collection of QCAZ, and available at BIOWEB (http://bioweb.bio), we extracted 19 climatic variables (WorldClim2 database at a resolution of 30 arc-seconds; Fick and Hijmans, 2017). Climatic values were also extracted for points generated from within a 6km buffer around each of the seven sampling localities (P1-P7), cropped to the altitudinal limits of each site (See Fig. 3.1). We then conducted a principle component analysis (PCA) on the climate correlation matrix, and used the top three principal components to characterize the niche hypervolume using the R packages 'hypervolume' (Blonder and Harris, 2017), and 'Raster' (Hijmans et al., 2020). We calculated hypervolumes only for species with at least four unique records (van Proosdij et al., 2016).

Niche unfit, which represented the climatic suitability of each of the sampling localities (P1-P7) for the surveyed anuran species, was estimated as the Euclidean distance between each species' hypervolume centroid (i.e., climatic niche centroid) and the centroid for the hypervolume (i.e., climatic space available) represented by each of the sampling localities where the species occur.

Extreme warm temperature events were quantified at each sampling locality as the highest yearly maximum temperature recorded between 1967 and 1999 (i.e., before T2), or between 2004 and 2015 (i.e., after T2 but before T3; Fig. S1, Supporting information).

Mean temperatures were calculated by taking the average of the yearly mean temperatures within each time window, described above.

Extreme drought events were calculated similarly, using the minimum yearly precipitation values between time periods (see above).

Mean precipitation were calculated as for changes in mean temperature.

Maximum temperatures, mean temperatures and precipitation values were obtained from the historical monthly weather data at 2.5 minutes (~21 km^2) spatial resolution of WorldClim (Harris et al., 2014; Fick and Hijmans, 2017), available at https://www.worldclim.org/data/monthlywth.html. Yearly means *were calculated* by averaging monthly values.

Habitat loss was calculated using land cover/land use data from digital maps that most closely matched the surveys years. The earliest available map dates back to 1990 and was used as an approximate estimate of land cover for T1; T2 land cover was estimated based on data for 2000, and T3 with data for 2016 (LC_T3). Land cover change was reported as the reduction in the percentage of natural vegetation cover across time points at each locality. Land cover maps were obtained from http://mapainteractivo.ambiente.gob.ec/portal of Ministerio de Medio Ambiente de Ecuador.

2.5 Statistical analyses

We fitted a hierarchical Bayesian binomial-logit model to estimate local species extinctions with niche breadth, niche dissimilarity, extreme temperature and habitat cover as predictors. We also included hierarchical effects of time period, and locality (as a grouping factor) to account for different conditions not included directly, plus a species-level phylogenetic correlation structure. We did not include mean temperature, mean precipitation, and drought in this model (but see Supporting information) as they were highly correlated with temperature extremes (Pearson $r >= 0.83$, $p < 0.01$; see Fig. S2, Supporting information). All predictor variables were standardised to a mean of 0 and a standard deviation of 1 prior to analysis. Models were fitted in Stan (Stan Development Team, 2017a; Carpenter et al., 2017) using the rstan R package (Stan Development Team, 2017b). We ran four independent chains of 4000 generations and a 3000 generation warmup. The posterior was thinned to retain every 10th generation , resulting in a total of 4000 posterior draws. Model convergence was verified by observation of Rhat values equal to 1 (Table 3.1), and explored using the R package shinystan (Stan Development Team, 2017c). Posterior predictive checks were performed to confirm model validity and fit to the data. To summarize the posterior distribution for our parameters, we used the 95% Highest Density Posterior Interval (HDPI; Hyndman, 1996). The HDPI describes the smallest range of parameter values that incorporates 95% of the posterior density, and hence there is 95% chance that the parameter is in the HDPI.

2.6 Assessing changes in taxonomic, phylogenetic and functional diversity

To examine how observed changes in taxonomic diversity translate into changes in functional and phylogenetic diversity, we calculated community-level phylogenetic and functional diversity indices across time points.

2.6.1 Phylogenetic and functional diversity

We used the mean pairwise phylogenetic distance (MPD) as a metric of phylogenetic diversity per locality per time period. MPD captures the average phylogenetic distance (i.e., branch lengths) among all pairs of species within a community, and is considered a basal metric of phylogenetic diversity (Webb et al., 2002). To remove the effect of species richness, we calculated the standard effect size of MPD (SESmpd) by comparing the observed community phylogenetic diversity to a null distribution generated by drawing species from the phylogeny pool (Kembel et al., 2010). Negative SES values indicate lower phylogenetic diversity than expected under the null model (i.e., phylogenetic clustering), whereas positive SES values indicate higher phylogenetic diversity than expected from the null (i.e., phylogenetic overdispersion). We also calculated Faith's phylogenetic diversity (PD) as the sum of the phylogenetic branch lengths connecting all taxa in a set (Faith 1992), and the equivalent standard effect size (SESpd). SESpd is a more terminal metric of phylogenetic structure, capturing structure towards the tips of the phylogeny (Mazel et al., 2016).

We employed an equivalent tree-based approach to compute functional diversity. We first constructed a matrix of Gower's pairwise functional distances (Gower, 1971) between species within each community, using the vegdist function in the R package vegan (Oksanen et al., 2016). We then constructed a functional dendrogram by applying the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) algorithm to the Gower's matrix for estimating species differences in functional space (Petchey and Gaston, 2002), and calculated matching SESmpd and SESpd from the functional dendrogram (see above).

SES metrics were calculated using the R package picante (Kembel et al., 2010).

2.6.2 Spatial phylogenetic and functional diversity

To explore temporal trends towards biotic homogenization across space, we first computed taxonomic beta diversity using Sorensen's pairwise similarity index (Sørensen, 1948) using the vegan R package (Oksanen et al., 2016). We then calculated phylogenetic and functional pairwise beta diversity (βMPD) among communities using the *comdist* function in the R package picante (Kembel et al., 2010). This function measures the among-community equivalent of MPD separating taxa across communities (Swenson, 2011).

To compare changes in the different facets of anuran diversity (i.e., taxonomic, phylogenetic and functional) across time points, we quantified differences using Cohen's (1988) *d* statistic (standardized effect size) using the R package effectsize (Gamer et al., 2012). Larger Cohen's *d*-values (positive or negative) indicate higher effect sizes.

3 RESULTS

Ecuadorian Andean anuran communities have lost species and diversity over the past 50 years. Species losses (i.e., local extinctions) were correlated with species niche properties, and appear to have been exacerbated by contemporary climate warming. Declines in taxonomic diversity translated into greater losses of phylogenetic and functional diversity, and resulted in increased phylogenetic and functional homogenization across space.

3.1 Changes in species richness.

A total of 83 anuran species were reported in the three surveys, 64 species in T1 (updated from Bustamante et al., 2005), 49 species in T2 (updated from Bustamante et al., 2005) and 44 species in T3 (Table S2, Supporting information). Overall, therefore, we recorded a 31.25% loss in taxonomic richness through time. Thirty-two species recorded in T1 were not found in T3 (i.e., 50% of species lost), 28 species recorded in T1 were not observed in T2, and 11 species recorded in T2 were not observed in T3. However, we also documented some additions. In T2, 17 species were new records and in T3, we recorded 7 additions relative to T2, of which two are probably new species to science: one occurring at Pilaló (P2) and the other one at Río Azuela (P6; Table S2, Supporting information). Losses exceeded additions at six out of seven of our sampling localities in the last 50 years (Fig. 3.2A; Table S3, Supporting information).

3.2 Changes in community composition

The temporal changes (i.e., dissimilarity) in community composition from T1 to T3 were dominated by species losses (permutational $t = -4.00$; $p < 0.05$), which accounted for 72.2% of the mean dissimilarity ($\overline{X}\ D_{\%\mathrm{diff}} = 0.42$), with species additions contributing the remaining

27.8%. Localities that contributed the most to mean dissimilarity (i.e., the mean of changes in species composition over all sites between sampling time periods) included the Paramo of Guamaní (P4), Río Azuela (P6), Quebrada Zapadores (P5) and Pilaló (P2; Fig. 3.2A; Table S3, Supporting information). Changes in community composition between T1 and T2 were of a similar magnitude ($\overline{X}\,D_{\%\mathrm{diff}} = 0.40$), and were again dominated by species losses (permutational $t = -4.55$; $p < 0.05$), which explained 64.67% of the mean dissimilarity, and with six out of seven sampling localities dominated by species losses (Fig. 3.2B; Table S3, Supporting information). There was small overall change in species composition between T2 and T3 ($\overline{X}\,D_{\%\mathrm{diff}} = 0.18$), so that while the percent contribution of losses was higher, accounting for 70.36% of the mean dissimilarity, the dominance of losses over gains was not significant (permutational $t = -1.80$; $p > 0.05$). Four out of seven sampling localities lost species between T2 and T3 (Fig 3.2C; Table S3, Supporting information).

3.3 Determinants of species losses

We found that local extinctions (i.e., losses of a species from a locality between sequential time periods) were strongly associated with species niche properties. Species with a narrow climatic niche breadth and those with a climatic niche that fit less well to the climatic conditions of the sampling locality at one time period, had a higher probability of being absent in subsequent samples at that locality (Table 3.1; Fig. 3.3, 3.4A,B).

Extinctions were also positively correlated with extreme warm temperature events (90% credible intervals do not overlap zero; Fig. 3.3; 3.5A), and negatively correlated with time period (50% credible intervals do not overlap zero; Fig. 3.3; 3.5B). There was a large variability (i.e., large credible intervals) in estimates of the strength of all these relationships, but the mean effect sizes of niche properties and extreme temperatures were much greater in magnitude than that for time period (Table 3.1; Fig. 3.3). The association between extinctions and time period supports the observation that the magnitude of species loss between T1 and T2 was greater than that between T2 and T3, even after adjusting for climate. We did not find support for a relationship between extinctions and habitat loss (Table 3.1; Fig. 3.3). Contrary to expectations, local extinctions were positively associated with increases in precipitation in the models including either mean precipitation or drought (Figure S3B,C, Supporting information), at least for the surveyed localities in this study. The model with mean temperature had a very similar fit to the model with extreme temperatures (Figure S3A, Supporting information).

3.4 Changes in phylogenetic and functional diversity relative to changes in taxonomic diversity

Taxonomic (i.e., species richness), phylogenetic and functional diversity (measured as the standard effect sizes of the mean pairwise distances between taxa; SESmpd) decreased markedly over the 50 years of the study (Table 3.2; Fig. S4, Supporting information). However, losses of phylogenetic and functional diversity were approximately four times that observed for taxonomic diversity (Cohen's *d* = -1.54, -1.53, and -0.38, for phylogenetic, functional and taxonomic diversity, respectively; Fig. 3.6A). Results for SESpd were qualitatively similar.

In contrast to the significant decreases in taxonomic diversity within sites, we found little change in the compositional similarity between sites over the last 50 year –as measured using Sorensen's index of beta diversity– (Cohen's *d* = 0.15 [negligible effect size]; Fig. 3.6B). Nonetheless, anuran communities have become more phylogenetically and functionally homogeneous (Table 3.3; Fig. 3.6B), with the trend toward increasing functional homogenization nearly four-fold that observed for phylogenetic homogenization (Cohen's *d* = -0.71 and *d* = -2.46, for phylogenetic and functional homogenization, respectively; Fig 3.6B).

4 DISCUSSION

Our study reveals that anuran biodiversity has dramatically decreased over the past five decades in the montane tropical communities of Ecuador. Changes in community composition are being driven primarily by species extirpations, with approximately half of all anuran species becoming locally extinct in the study period. Our analyses indicate that climate warming is the most plausible explanation for the observed population extirpations, and suggest that species climatic niche properties are good predictors of species' susceptibility to contemporary climate change. The erosion of anuran taxonomic diversity was accompanied by disproportionately larger losses in phylogenetic and functional diversity (nearly four-fold greater). These compositional changes have led to greater phylogenetic and functional homogenization (i.e., increase in similarity of trait composition among communities), which might have consequences for ecosystem processes (Villéger et al., 2014; Mori et al., 2015). Our results confirm the ongoing erosion of anuran diversity and highlight the central contribution of climate change to amphibian population extinctions and community shifts in the Neotropics.

We found that amphibian communities in the montane tropics of Ecuador have experienced elevated extinction rates over the past 50 years when compared with global averages. We estimated that ca. 1.03% of species are being extirpated locally each year, contrasting with declines of 0.14% in temperate biomes (Miller et al., 2018). A recent study compiling data on shifts of amphibian communities from five continents showed fewer local extinctions than our observations, with communities losing approximately 22% of species on average (Nowakowski et al., 2018) compared to our estimate of 52%, although the span of years of this dataset was not reported. Our estimates are more similar to climate-related extirpation rates reported recently by Román-Palacios and Wiens (2019) (an average extirpation rate of 44% of more than 500 plant and animal species over time periods ranging from 10 to 160 years). However, the idiosyncratic responses across species to global threats (Grant et al., 2016; Miller et al., 2018), the use of different metrics and statistical practices to estimate local extinctions (Williams et al., 2002; MacKenzie et al., 2003; Dornelas et al., 2019), the notable variation in intensity and frequency of anthropogenic drivers (Grant et al., 2016), and the lack of long-term community studies (Grant et al., 2020), especially in tropical regions, all make it difficult to draw comparisons among different studies. Thus, comparing species extirpations in different regions and/or at different times remains a challenge. The weight of evidence nonetheless supports the ubiquity of local species extinctions, alongside the already alarming global rate of amphibian extinctions (Stuart el al., 2004; Vredenburg et al., 2010; Alroy, 2015; Wiens, 2016).

Although there is much focus on species extinctions, anthropogenic change may also result in increases in diversity, especially at community scales (Sax and Gaines, 2003; Sax and Gaines, 2008; Blowes et al., 2019; Finderup Nielsen et al., 2019, Leung et al., 2020). For instance, Nowakowski et al. (2018) found that 17% of amphibian communities around the world showed increases in species richness, likely related to the migration of species adapted to disturbed habitats. We did not detect evidence for gains in species richness among the anuran communities we studied. However, we found an average of 1.6 new records per locality in the last sampling time period (T3) relative to T1 (Table S2, , Supporting information). The majority of these records, except for *Dendropsophus sarayacuensis* and *Nymphargus grandisonae*, belong to species in the direct developing genus *Pristimantis*, and all are characterized by having some degree of tolerance to habitat degradation (Ron et al., 2019). Likewise, six species extended their upper range limits between T1 and T2 (Bustamante et al., 2005) and one species between T2 and T3, consistent with expected species range responses to climate change (Raxworthy et al., 2008; Chen et al., 2011).

Cumulative evidence shows that climate change is among the main drivers of amphibian diversity loss and community reorganization (McCaffery and Maxell, 2010; Pecl et al., 2017; Grant et al., 2020). Here, we have provided clear evidence for an association between climate warming and local extinctions and, although we were not able to unambiguously disentangle the relative contributions of maximum temperature versus mean temperature, both support a link between elevated extinction risk and increasing temperature. Román-Palacios and Wiens (2019) reported widespread population extinctions across different taxa in communities facing smaller shifts in mean temperatures but larger shifts in maximum temperatures. However, the direction and degree of amphibian sensitivity to climate changes vary geographically, and among populations and species (Miller, 2018; Grant et al., 2020). For instance, species' sensitivity depends, in part, on geographical and ecological properties. Species with narrow physiological tolerances and populations at the peripheral extremes of the species' range may be more vulnerable to the stresses imposed by climatic fluctuations and temperature change than species with wider tolerances and populations towards the centre of species distributions (e.g. Brown et al., 1996; Broennimann et al., 2006; Paaijmans et al., 2013; Amburgey et al., 2018; but see Lomolino and Channell, 1995; Hoffman and Parsons, 1997; Gibson et al., 2009). Our analyses support these links, showing that species with narrow climatic niche breadths and populations more towards the extremes of a species' climate envelope were also more likely to go extinct.

Although habitat loss and fragmentation have also been recognized as major drivers of Neotropical amphibian extinctions (Cushman, 2006; Stuart et al., 2008; Catenazzi, 2015), we did not find evidence that habitat loss was an important cause of local extinctions in our study. Documented amphibian declines in relatively undisturbed areas suggest that habitat destruction may not necessarily be the most important factor driving the catastrophic amphibian declines that have been documented over the last several decades (Pounds et al., 2006; Menéndez-Guerrero and Graham, 2013). However, it is possible that the habitat degradation observed in some surveying localities may have amplified species susceptibility to climate warming (Pintanel et al., 2019).

The chytrid fungus (*Batrachochytrium dendrobatidis*) is thought to be another important extinction driver within neotropical montane amphibians (Lips et al., 2008; Scheele et al., 2019). The lack of information on chytridiomycosis infections during the first two surveying time periods prevented us from testing this link directly. However, there is an increasing evidence that climate change, especially extreme temperature events, interacts with fungal disease by depressing immunity of hosts – the “thermal mismatch hypothesis” (Cohen et al, 2017; 2019; 2020). The higher number of local extinctions we documented in the earlier time period, during the 1980s and1990s, relative to the later time period (post 2003) matches both the chytridiomycosis-associated amphibian mass extinctions reported in Neotropical montane regions elsewhere (e.g. Ron et al., 2003; Pounds et al., 2006; Whitfield et al., 2007; Lips et al., 2008) and the more extreme climatic events (in frequency and intensity) recorded in our sampling localities. Furthermore, the fewer lower extinction in the later time period might be explained by innate or acquired immune defenses against the fungal pathogen (Richmond et al., 2009), possibly in concert with milder climatic extremes (Ribas et al., 2009). More data on chytrid prevalence is needed to evaluate these potential links.

We have shown that decreasing anuran species richness is accompanied by an erosion of phylogenetic and functional distinctiveness. A focus only on taxonomic diversity might underestimate impacts of global change on biodiversity (Hillenbrand et al., 2018). For instance, it is only when we combine information on evolutionary history and functional traits that we are able to reveal temporal trends towards increasing biotic homogeneity. Functional homogenization could exacerbate the effects of amphibian extirpations on ecosystem functioning and stability (e.g. Tilman et al., 1997; Smith et al., 2009). Only a handful of studies have explored patterns of functional homogenization within amphibians (e.g. Smith et al., 2009; Menéndez-Guerrero et al., 2020; Oliveira et al., 2020). To the best of our knowledge, this is the first study to also explore the underlying drivers of change across axes of taxonomic, phylogenetic and functional diversity.

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Table 3.1. Summary of the Bayesian regression model of species loss, including posterior means, posterior standard deviations (SD), 2.5%, 25%, 50%, 75% and 97.5% quantiles, the effective sample size (n_eff), and the potential scale reduction statistic (Rhat).

Parameter	**mean**	**SD**	**2.5%**	**25%**	**50%**	**75%**	**97.5%**	**n_eff**	**Rhat**
Intercept	-0.7	0.5	-1.8	-1	-0.7	-0.4	0.4	1621	1
Climatic niche breadth	-1.6	0.4	-2.4	-1.9	-1.6	-1.3	-0.9	2765	1
Niche unfit	1.8	0.5	0.9	1.4	1.8	2.1	2.8	2150	1
Extreme warm temperature events	0.9	0.5	-0.1	0.6	0.9	1.2	2	1208	1
Habitat loss	-0.1	0.4	-1	-0.4	-0.2	0.1	0.8	1988	1
Time period	-0.4	0.5	-1.4	-0.7	-0.4	0	0.7	2955	1

Table 3.2. Community data on taxonomic diversity (TD), measured as species richness, phylogenetic diversity (PD) and functional diversity (FD), measured as SESmpd per locality per time period. Localities are as follow: Bosque Protector Cashca Totoras (P1), Pilaló (P2), paramo of Antisana (P3), paramo of Guamaní (P4), Quebrada Zapadores (P5), Río Azuela (P6) and Río Faisanes (P7). T1 refers to surveys conducting between 1967-1987, and T3 to surveys conducting between 2016-2018.

Locality	Time period	TD (species richness)	PD (SESmpd)	FD (SESmpd)
P1	T1	9	0.11	-0.51
P1	T3	5	-1.01	-1.11
P2	T1	10	0.85	1.31
P2	T3	8	-2.64	-0.64
P3	T1	3	0.99	1.12
P3	T3	2	0.42	-0.19
P4	T1	3	0.93	1.13
P4	T3	3	-2.04	-1.18
P5	T1	12	0.25	-0.96
P5	T3	7	-0.86	-0.36
P6	T1	21	1.59	0.91
P6	T3	13	0.23	-0.64
P7	T1	14	1.38	0.05
P7	T3	7	1.02	-0.32

Table 3.3. Mean and standard deviation (SD) of taxonomic beta diversity (TD) measured using Sorensen's pairwise similarity index, and phylogenetic beta diversity (PD) and functional beta diversity (FD) measured as the among-community equivalent of MPD. T1 refers to surveys conducting between 1967-1987, T3 to surveys conducting between 2016-2018.

Statistic	Time period	TBD (Sorensen)	PBD (MPD)	FBD (MPD)
Mean	T1	0.91	196.35	0.37
SD	T1	0.22	12.82	0.03
Mean	T3	0.95	183.78	0.29
SD	T3	0.11	19.60	0.03

Figure 3.1. Map of the study area, showing the seven sampling localities in the Ecuadorian Andes, with areas above 1000 m indicated in yellow. Bosque Protector Cashca Totoras (P1; 2800–3100 m), Pilaló (P2; 2300–2500 m), Paramo of Antisana (P3; 4200 m), Paramo of Guamaní (P4; 4020 m), Quebrada Zapadores (P5; 1900–2300 m), Río Azuela (P6; 1700–1800 m) and Río Faisanes (P7; 1300–1400 m).

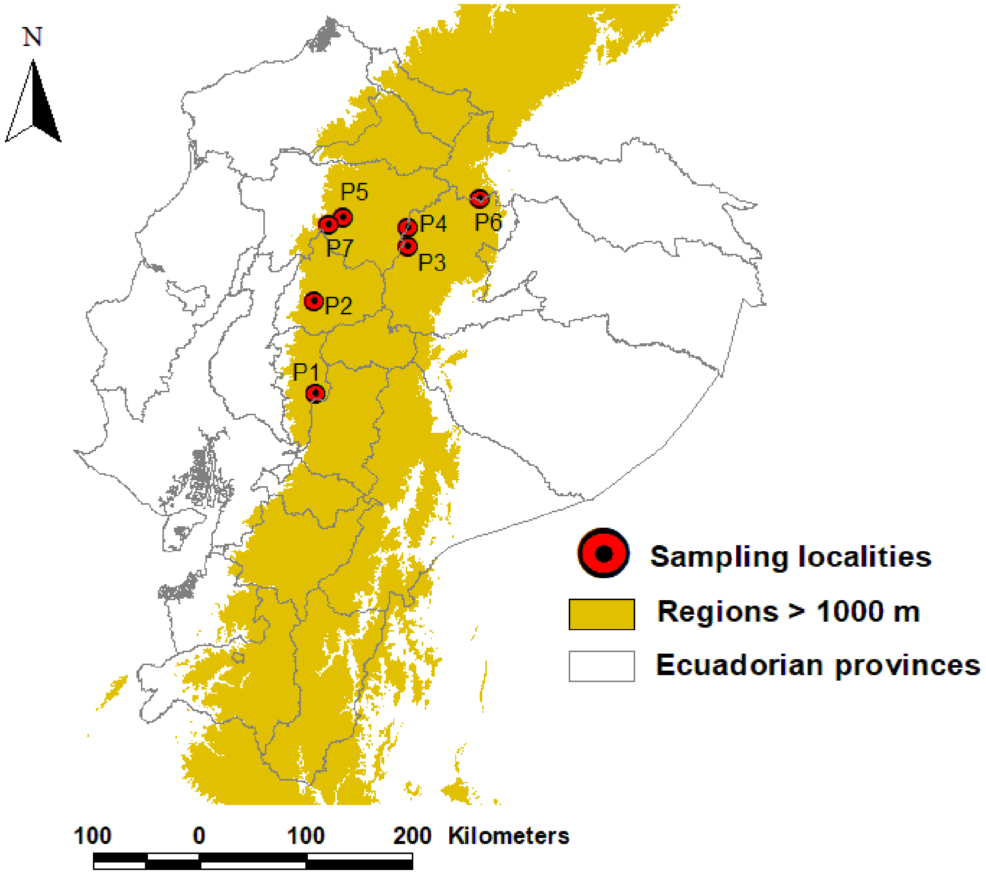


Figure 3.2. Comparisons of relative species gains and losses between time periods T1 and T3 (**A**), T1 and T2 (**B**), and T2 and T3 (**C**), for the seven localities (P1-P7). Losses were calculated as: B/ (2A+B+C), and gains as: C/ (2A+B+C), where A = number of species that are common to the two surveys, B = unscaled sum of species losses between two surveys and C = unscaled sum of species gains between two surveys (see Materials and Methods). The sampling localities are represented by symbols with diameters proportional to the site temporal beta-diversity index ($D_{\%diff}$; see Materials and Methods). Green line with slope of 1: line where gains equal losses. The red line is parallel to the green line and passes through the centroid of the points. Its position below the green line indicates that, on average, most sites fall below the line indicating that species losses dominate species gains. Localities are as follow: Bosque Protector Cashca Totoras (P1), Pilaló (P2), paramo of Antisana (P3), paramo of Guamaní (P4), Quebrada Zapadores (P5), Río Azuela (P6) and Río Faisanes (P7).

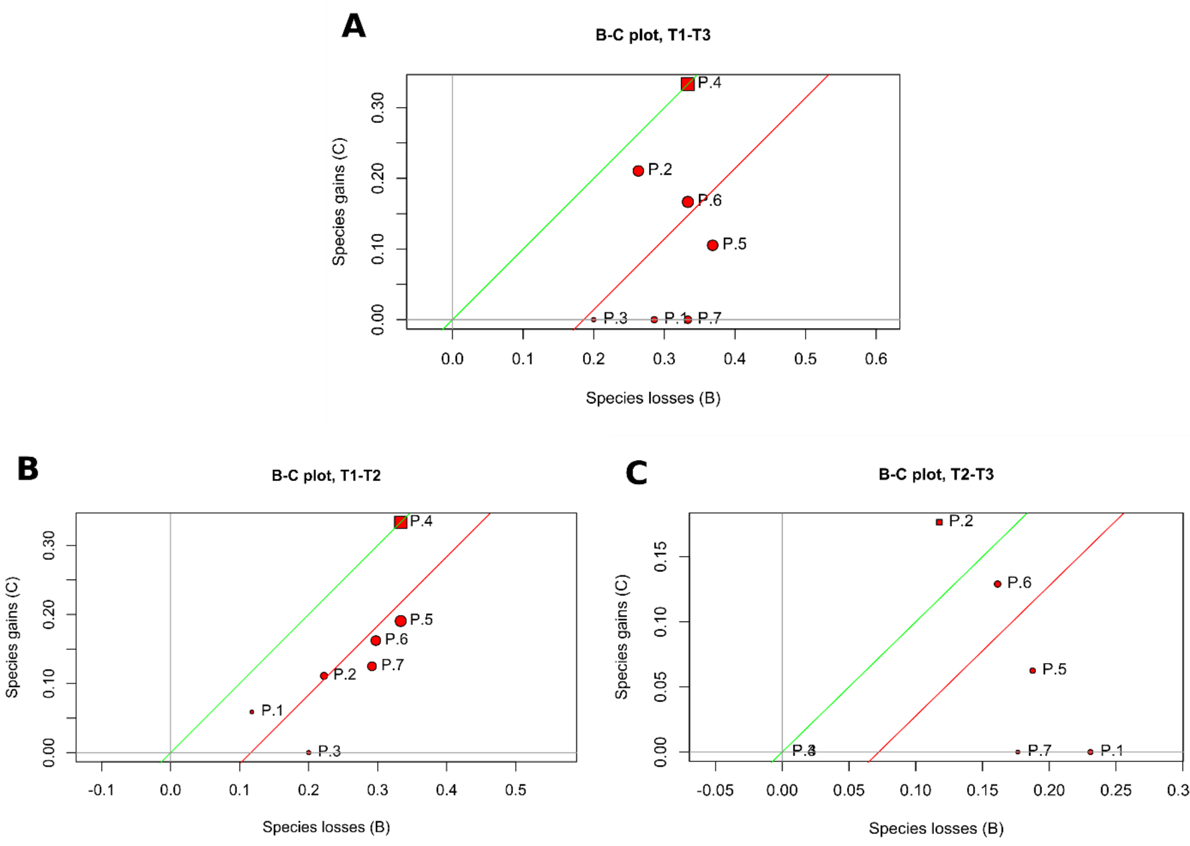


Figure 3.3. Estimated coefficients for predictors of extinctions from the Bayesian regression (Table 3.1). Red circles represent posterior means; blue horizontal bars represent 50% credible intervals; dark gray horizontal lines represent 95% credible intervals.

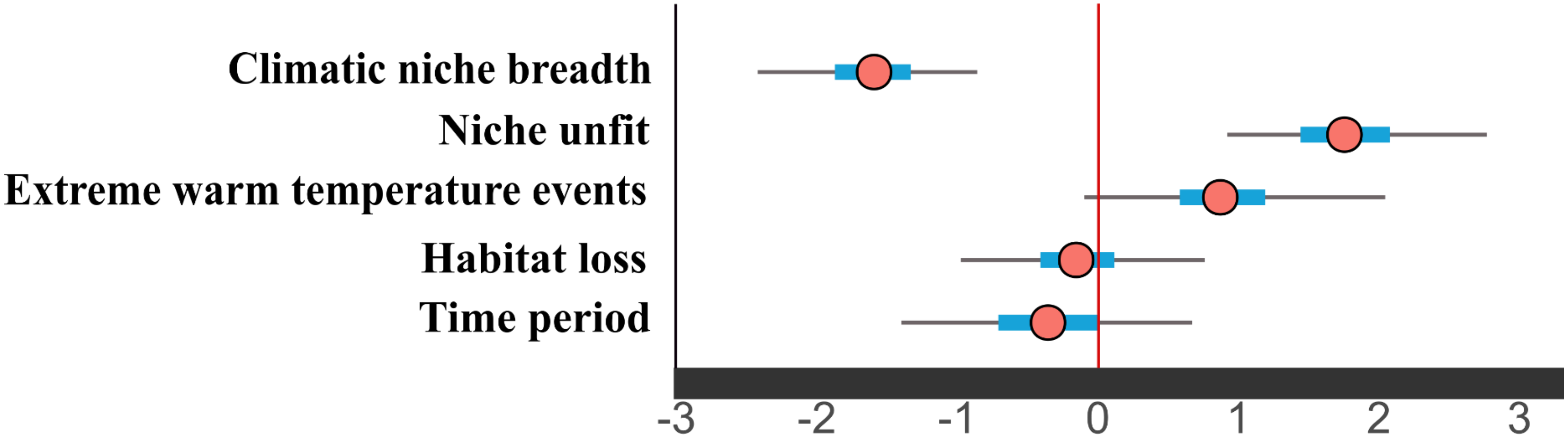


Figure 3.4. Bayesian posterior predictions of the probability of species extinctions as a function of Niche breadth (A) and Niche fit (B). Solid yellow lines represent the mean; red lines represent the upper and lower bounds of the 50% credible interval.

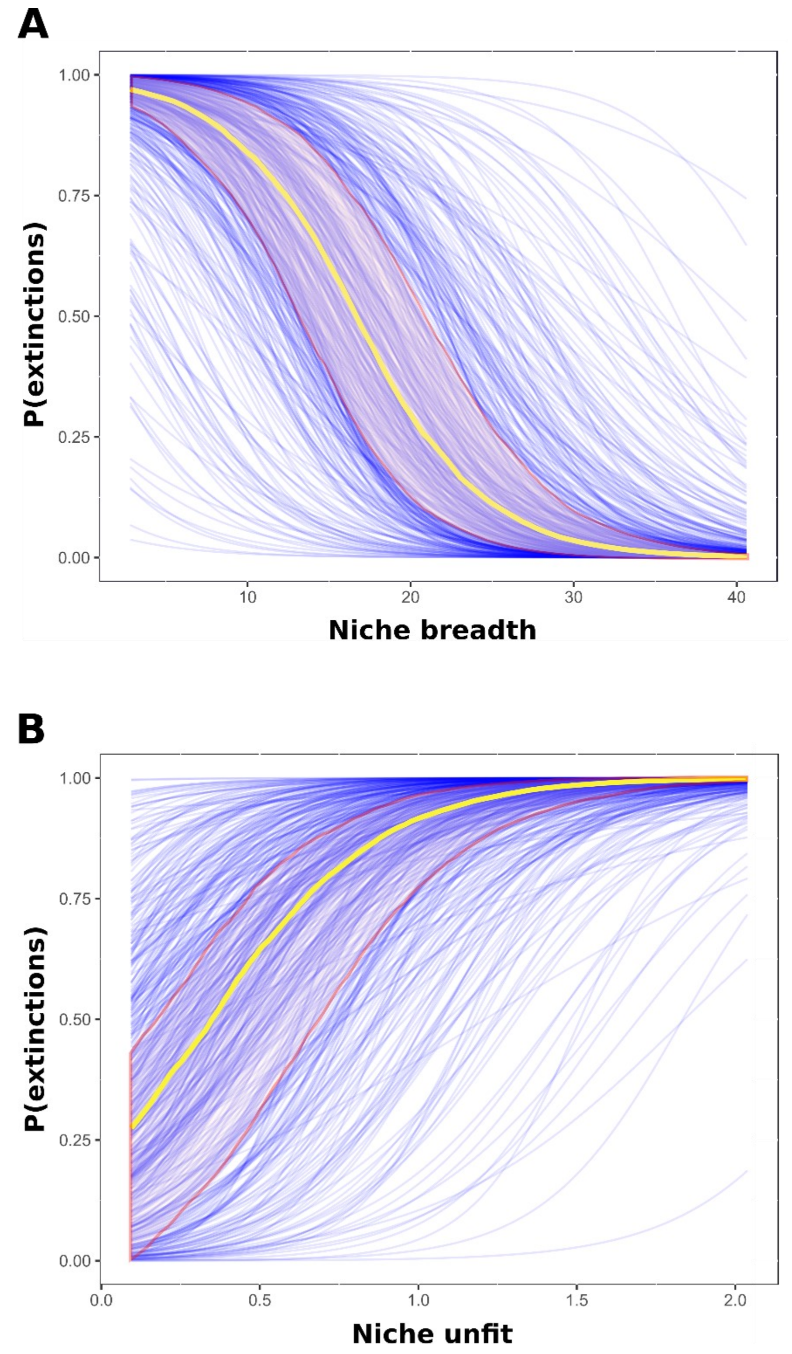


Figure 3.5. Extinctions associated with extreme warm temperature events (A) and time period (B). Blue dashed lines represent posterior means. Here, the blue lines (90% credible intervals in (A), and 50% in (B); analogous to a confidence interval in frequentist methods) do not overlap the zero-slope line (red), indicating that extreme warm temperature events are positively correlated with extinctions with relatively high certainty, and time period is negatively with extinctions, but with greater uncertainty.

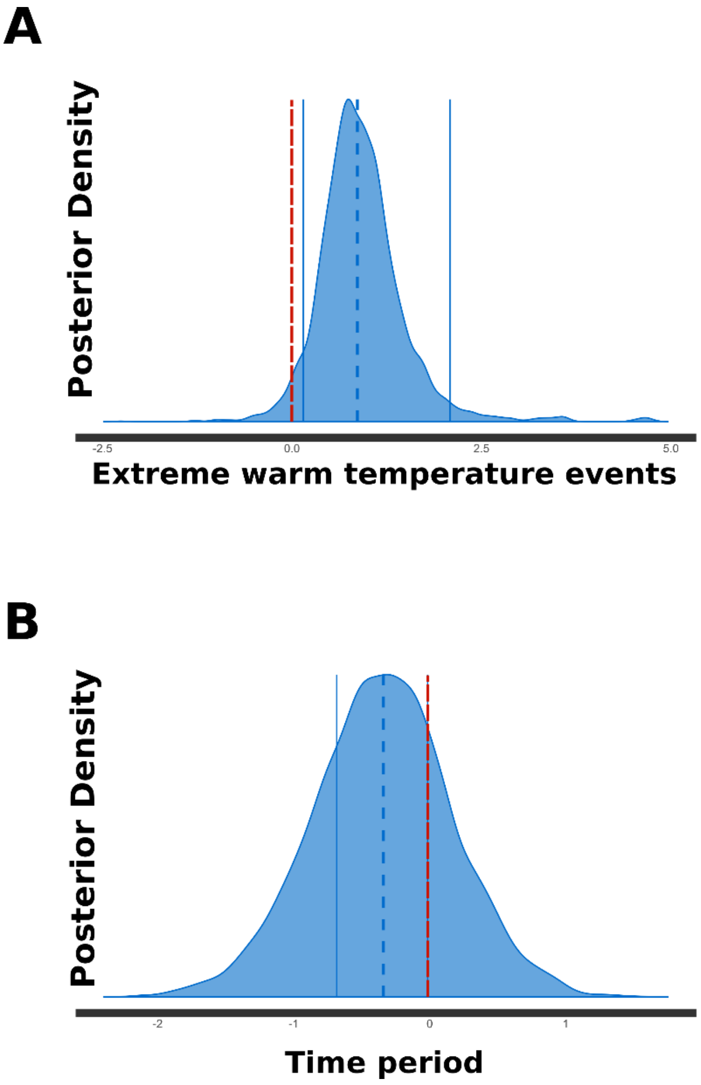
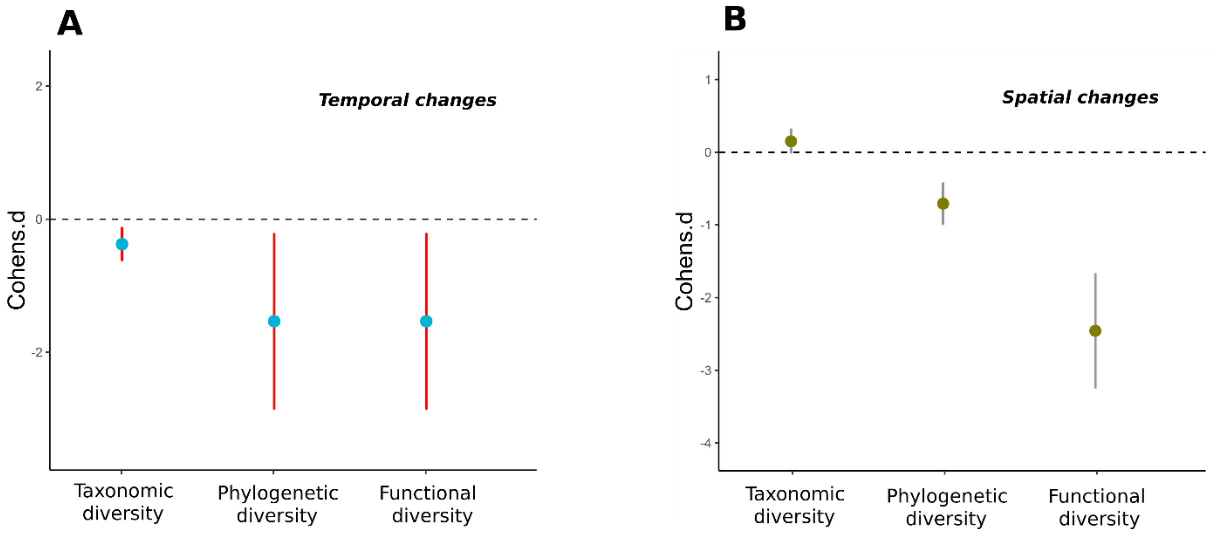


Figure 3.6. Changes in taxonomic, phylogenetic and functional diversity between period T1 and T3. **(A)** Temporal changes in alpha diversity – negative values reflect decreases in diversity (see Material and Methods). Taxonomic diversity represents species richness, phylogenetic and functional alpha diversity were measured as the standard effect size of MPD (SESmpd; see Materials and Methods). **(B)** Changes in beta diversity – negative values indicate a trend towards spatial biotic homogenization. Taxonomic beta diversity was calculated using the Sorensen index, phylogenetic and functional beta diversity were measured as MPD (see Methods and materials). Cohen's d (standardized effect size) estimates and 95% confidence intervals are shown.



Linking Statement 3

In Chapter 3, I explore changes in species composition within seven anuran communities in Ecuador over the past 50 years. I also assess how changes in taxonomic diversity translate into shifts in phylogenetic and functional diversity, and the relative importance of climate change versus habitat loss as drivers of biodiversity changes within communities. I show that anuran diversity has experienced a significant erosion over the past 50 years, with about 50% of species becoming locally extirpated. This diversity loss is associated with recent climate warming, and disproportionate losses in phylogenetic and functional diversity relative to species richness losses. My results suggest that current estimates of amphibian declines in the Neotropics are likely underestimated, and emphasize the need to better recognize the erosion of evolutionary and ecological dimensions of diversity.

Another reasons that we might underestimate the magnitude of the current biodiversity crisis is that much of biodiversity remains cryptic with no formal description, and this is especially true of Neotropical anuran diversity. In Chapter IV, I explore cryptic diversity within the Neotropical cane toads, and describe a new species within the *Rhinella marina* species complex – mainly restricted to the western side of the Ecuadorian Andes –, using DNA, morphological, bioacoustic and ecological characters.

CHAPTER 4:

Cryptic Diversity in Toads of the *Rhinella marina* species group (Anura, Bufonidae) and a new species from Western Ecuador

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ABSTRACT

Amphibians have the highest proportion of species at risk of extinction among vertebrates and therefore uncovering the extent of cryptic diversity among them is of considerable concern in areas where their diversity may be significantly underestimated. Within the *Rhinella marina* species complex of Giant or Cane Toads, *R. horribilis* (Wiegmann 1833) occurs from southern Texas through Central America and south along the Pacific Coast of South America to Ecuador west of the Andes Mountains. Within this extensive range, populations of *R. horribilis*, as currently recognized, have been suspected to conceal cryptic diversity. Based on extensive new collections of specimens from western Ecuador and the combined evidence of phylogenetic analyses based on mtDNA sequence variation, morphological data analyzed using both linear and geometric morphometric approaches, bioacoustics and environmental information, we tested whether populations of these toads from the western side of the Ecuadorian Andes represented an independent evolutionary lineage. Our results revealed that these western Ecuadorian populations constitute a well-supported, monophyletic clade that is distinctly different genetically, morphologically, acoustically and ecologically both from a sister clade composed of populations of *R. horribilis* from Central America and from populations in Amazon River drainage basin of eastern Ecuador ascribable to *R. marina* sensu stricto. The weight of evidence validates recognition of a new species, which we describe it here as *R. bellus* sp. nov. Our unmasking of this cryptic diversity with the *R. marina* species complex represents a significant contribution towards understanding biogeographic relationships and history in this widespread clade of neotropical toads.

INTRODUCCTION

Rhinella marina, the Cane Toad, has a long and complex taxonomic history. Once considered to be a single, widely distributed, neotropical species in the large and cosmopolitan genus, *Bufo*, *R. marina* is currently considered to be one of the 11 species in the *R. marina* species group (Martin, 1972). This group occur natively in the Americas from as far north as southern Texas in the United States to as far south as Uruguay in South America (Blair, 1972; Cei, 1972; Pauly *et al*., 2004; Maciel *et al*., 2010). Ten species, *R. achavali, R. arenarum, R. cerradensis*, *R. icterica, R. jimi, R. marina, R. poeppigii, R. rubescens, R. schneideri,* and *R. veredas,* are confined to South America, where the group most probably originated (Pauly *et al.*, 2004; Pramuk, 2006; Maciel *et al.*, 2010; Vallinoto *et al.*, 2010). The monophyly of this species group is supported by morphological, molecular, and skin-secretion evidence (Pramuk, 2006; Maciel *et al.*, 2010). A putative morphological synapomorphy is the presence of a jagged or "scalloped" suture present at the articulation of the medial ramus of the pterygoid with the parasphenoid alae (Pramuk, 2006).

Rhinella marina was described by Linnaeus (1758); its type locality is "America" and probably collected in Suriname (Müller & Hellmich, 1936). It is widely distributed in the Guianan region and the Amazon Basin, with introduced populations on the United States, Australia, Japan, Philippines, Taiwan, Papua New Guinea, Solomon Islands and many Caribbean and Pacific islands (Easteal, 1981, 1985; Lever, 2001; Shine, 2010; Acevedo *et al*., 2016; Frost, 2020). The taxonomy of *R. marina* has problems in need of resolution. One of them is the paraphyly reported by Vallinoto *et al.* (2010) and Slade & Moritz (1998). A study by Acevedo *et al.* (2016) proposed that populations west of the Andes in South America, Central America/Mexico, and southern Texas are a different species based on mitochondrial DNA and morphometric data for which the name *Rhinella horribilis* (Wiegmann 1833) is applicable. This change, suggested mainly by comparisons of Venezuelan populations for *R. horribilis* and *R. marina*, has been recently supported by Bessa-Silva *et al.* (2020) based on both mitochondrial DNA and nuclear data. However, it is likely that *R. horribilis*, as currently defined, includes more than one species. This scenario was suggested by Vallinoto *et al.* (2010), who found two allopatric mitochondrial DNA clades within "*R. horribilis*", one in Central America and the other in western Ecuador. Additional evidence of the existence of more than one species is given by an estimate of 10.9 My for the divergence between Central America populations and one sample from Western Ecuador (Mulcahy *et al*., 2006). This genetic evidence needs to be confronted with phenotypic characters to determine the taxonomic status of populations of the *R. marina* complex from western Ecuador.

In this study, we evaluate the phylogenetic relationships of populations of the *R. marina* complex with emphasis in Ecuadorian populations based on mitochondrial DNA and morphological and bioacoustic characters. Our sampling includes extensive new collections of specimens from Central America and Mexico (hereafter referred to as only Central America) and both the Pacific and Amazonian basins of Ecuador. If the populations from west of the Ecuadorian Andes are taxonomically discrete to the extent that they are an independent evolutionary lineage, they should comprise a monophyletic clade to the exclusion of other such populations and possess acoustic and/or morphological distinctions, and/or climatic differentiation. Finally, we include the description of the new species.

MATERIALS AND METHODS

Molecular phylogenetics

To resolve phylogenetic relationships among *Rhinella marina* species group toads, we combined published and new sequences of the mitochondrial genes 12S rRNA, tRNA-Val, and 16S rRNA. We obtained sequences from 55 specimens from GenBank, representing nine species of the *R. marina* species group: *R. achavali, R. arenarum, R. horribilis, R. icterica, R. jimi, R. marina, R. poeppigii, R. rubescens,* and *R. schneideri.* We also included seven species as outgroups: *R. crucifer, R. granulosa*, *Anaxyrus exsul*, *A. fowleri, A. microscaphus*, *Incilius alvarius and Incilius valliceps*. Published sequences for *R. marina sensu lato* included samples from the eastern Andes and Amazonia, as well from western Ecuador. Sequences of *R. horribilis* from Central America were available only for the 16S gene. We extended this data set by generating 68 new sequences for the 12S, tRNA-Val and 16S genes from specimens of *R. marina* species group collected on both the eastern and western sides of the Ecuadorian Andes (Fig. 4.1, Supporting information, Table S1). We assembled and aligned DNA sequences with Geneious Pro 5.5 (Drummond et al. 2011) using the GENEIOUS alignment algorithm, and used PartitionFinder v1.1.1 (Lanfear et al. 2012) to select the best-fit nucleotide substitution models, and the best partitioning scheme for our data matrix of 2476 bp.

We used both Bayesian and Maximum likelihood methods to estimate phylogenetic relationships. We performed four independent Bayesian analyses using MrBayes 3.2 (Ronquist *et al*., 2012). For each one, we ran 10^6 generations and four Markov chains with default heating values, sampling trees every 1000 generations. We used Tracer 1.6 (Rambaut *et al.*, 2013) to examine stationarity, posterior estimates, and effective sample size (ESS) for model parameters. After confirming convergence of the results from the four independent searches, we discarded the initial 10% of the generations as burn-in and the remaining generations were used to estimate a 50% majority rule consensus tree and the posterior probabilities for each node. We performed

Maximum likelihood analysis using PhyML (Guindon & Gascuel, 2003) with a subtree pruning and regrafting (SPR) topology search. We estimated node support based on 500 bootstrap replicates. In addition, we used MEGA 5 (Tamura et al. 2011) to estimate pairwise uncorrected (*p*) genetic distances among mitochondrial clades using partial sequences of the 16S gene (ca. 520 pb). To visualize the observed genetic distances, we performed a multidimensional scaling (MDS) plot of the pairwise distance matrix using the *cmdscale* function in program R (R Development Core Team 2017).

Acoustic analysis of calls

Recordings of advertisement calls were obtained from different sources: ten recordings from the audio archive of QCAZ, four from Museo Gustavo Orcés at Escuela Politécnica Nacional (MEPN), one from the audio CD "Frogs of Tambopata" (Cocroft *et al*., 2001). Three recordings were downloaded from FonoZoo (http://www.fonozoo.com), one recording from Universidad del Valle, Colombia, and four recordings from Macaulay Library at the Cornell Lab of Ornithology (https://www.macaulaylibrary.org). A total of 166 calls from 36 individuals were analyzed:17 individuals from western Ecuador, one from western Colombia, 13 from eastern side of the Andes and Amazonia (i.e. 12 from eastern Ecuador and one from eastern Peru), and five from Central America (i.e. of *R. horribilis*).

Calls were digitized using Raven 1.5 software (Cornell Lab of Ornithology, NY, USA; (www.birds.cornell.edu/raven) at a sampling rate of 44.1 kHz with 16-bit accuracy. The spectrogram analyses used settings of window type Hann, window size 890 samples and filter bandwidth 71.3 Hz, and a frequency resolution of 44.1 Hz. When available, several calls or notes were analyzed per individual to calculate an individual average. Temporal variables were measured on the oscillogram, spectral variables on the power spectrum. Measured call variables were as follows: (1) call length (time between onset of first pulse and offset of last pulse in a call); (2) call rise time (time required for a call to reach its maximum amplitude); (3) notes per call (number of notes); (4) pulses per note (number of pulses); (5) pulse rate (number of pulses repeated in a defined period of time within a note); (6) call repetition rate (number of calls/min); and (7) dominant frequency (frequency with the most energy, measured along all the call). These variables were used to run a PCA to assess the degree of acoustic variation among populations of *R. horribilis* from Central America (two males from Costa Rica, three males from Mexico), populations from western Ecuador (six males from Mindo, one male from Puyango, one male from Río Baba, two males from Yunguilla, four males from Río Palenque, three males from Zapotillo, and one male from Cali, Colombia), and populations from eastern Ecuador and Peru (three males from Cordillera del Cóndor [Campamento Las Peñas, next to the Machinaza river], one male from Montalvo, six males from Puerto Morona, two males from Via Maxus, and one male from Tambopata-Peru). Then we used the informative principal components (PCs) for a MANOVA, followed by post hoc multiple comparison analyses using the Bonferroni corrected approach (Rice, 1989).

Ambient temperature data was not provided for approximately half of the analyzed vocalizations, which precluded to accurately estimate an effect of temperature on the structure of calls (Gerhardt & Huber, 2002; Köehler *et al*., 2017). While we acknowledge this limitation, our available data shows low variation in recording temperature among populations (i.e. < 6.5 C degrees), suggesting that temperature may not explain the interpopulation call differences observed in our study (Caminer & Ron, 2014). Moreover, given the weak temperature dependence of dominant frequency in calls of anurans (Köehler *et al*., 2017), we performed

Mann–Whitney univariate tests to assess differences only in this call trait among toad populations.

Morphometric analysis

To assess the degree of morphometric variation and differentiation among Central American, Amazonian and western Ecuadorian *R. marina* populations, we used both linear and geometric morphometric techniques. To reduce the noise due to developmental variability, we only analyzed adult individuals. We determined sexual maturity of males by the presence of vocal slits, and/or nuptial excrescences, and by inspection of gonadal development. Sexual maturity of females was assessed by the presence of pigmented eggs and convoluted oviducts.

Linear morphological measurements were taken with digital calipers to the nearest 0.01 mm from a total of 106 individuals: 20 from Central America (i.e. *R. horribilis*), 26 from the eastern side of the Ecuadorian Andes, and 60 from the western side of the Ecuadorian Andes (Supporting information, Table S2). We used only well-preserved specimens fixed in 10% formalin and preserved in 70% ethanol (Simmons, 2002) and, following Duellman & Schulte (1992), took the following measurements: snout-vent length (SVL), tibia length (TL), foot length (FL), femur length (FEL), head length (HL), head width (HW), interorbital distance (IOD), internarial distance (IND), eye-nostril distance (END), eye diameter (ED), tympanum diameter (TD), thumb length (THL), third finger length (TF). We verified normal distribution of residuals from a linear regression of all measurements against SVL using Shapiro–Wilk tests (Sokal & Rohlf, 1995), and then transformed the variables to natural logarithms to improve properties of normality. Homogeneity of the residuals was tested using a visual check of the plots of the model residuals against their fitted values (Quinn & Keough, 2002).

We used geometric morphometric analysis (Zelditch *et al*., 2012) to assess variation attributable exclusively to shape, and focused only on the morphology of the skull, which can be related to a variety of functions (e.g. acquiring food, protecting the brain) and/or to sexual dimorphism (Birch, 1999). For this analysis we used a total of 84 specimens: 12 from Central America, 20 from the eastern side of the Ecuadorian Andes, and 52 from the western side of the Ecuadorian Andes. We took digital X-ray radiographs in the dorsal perspective of the head of each toad with a KUBTEC XPERT 80- L Cabinet X-ray System (Milford, CT, USA). To capture the shape of the skulls, following Birch (1999), we digitized a suite of 13 fixed landmarks on the right side of each specimen from each image (Supporting information, Fig. S1) using tpsDig software (Rohlf, 2006), after setting a 1 cm scale factor; available from http://life.bio.sunysb.edu/morph). We then used tpsRelW (Rohlf, 2007; available from http://life.bio.sunysb.edu/morph) to perform a Generalized Procrustes Analysis (GPA) to superimpose and align landmarks (Rohlf & Slice, 1990) and quantify geometric shape variables (Kendall, 1984, 1985; Bookstein, 1991). Partial warps (i.e. geometric shape variables) themselves cannot be treated as biologically/functionally independent variables and should not be interpreted in isolation (but see for example Zelditch & Fink, 1995 or Burke *et al*., 1996), instead, they must be interpreted all together as a joint multivariate distribution to describe the deformation of skull shape relative to the reference form, for example along canonical variate axes (Rohlf, 1998; Adrain *et al*., 2001). Furthermore, partial warp scores can be used in statistical tests without adjusting the degrees of freedom (Zelditch *et al.*, 2012). We examined the degree of morphometric variation and divergence among populations through use of principal component analysis (PCA) and canonical variate analysis (CVA), performing separate analyses for linear and geometric morphometric variables. We conducted a varimax rotation of the loading matrix after PCA in order to have more interpretable factors with a simpler structure than can be obtained using orthogonal rotation. We used rotated principal components scores to evaluate pairwise differences between population samples by performing Bonferroni corrected post-hoc multiple comparison tests (Rice, 1989). Multivariate analyses of shape variables were performed on partial warps and uniform component scores, that were extracted from the Generalized Procrustes Analyses to obtain relative warps in the case of PCA, or canonical variables in the case of CVA (Rohlf, 1993).

We acknowledge some of the criticisms of using CVA and discriminant function analysis in systematics, regarding their requirement for *a priori* definition of groups (e.g. Albrecht, 1992). However, the group memberships in our CVA is geographically based, therefore there is not any uncertainty on the identity of the groups. Our data showed heterogeneity across the within-group variance-covariance matrix (*Box's M* = 376.40, $P < 0.01$), therefore CVA was implemented using quadratic functions for discriminating among populations instead of linear ones (Quinn & Keough, 2002). Statistical analyses were implemented in R (R Development Core Team 2017), SPSS v. 20.0 (IBM Corp, 2011) and MorphoJ v. 1.06a (Klingenberg, 2011).

Climatic analysis

Species climatic envelopes (inferred through climatic characteristics at sites of species occurrence) have been used to improve inferences about species boundaries in cryptic species (e.g. Rissler & Apodaca, 2007; Florio *et al.*, 2012; Páez & Ron, 2019). To evaluate climatic differences among Central American, western Ecuadorian and populations from eastern Ecuador we only selected collection localities of the specimens used for the phylogenetic analysis ($n = 98$; see Molecular phylogenetics section and Supporting information, Table S1). We extracted values for 19 bioclimatic variables obtained from WorldClim database (Fick & Hijmans, 2017, <www.worldclim.org/data/worldclim21.html>) at 30 arc-second resolution. This climatic database is generated through interpolation of average monthly temperature and precipitation values and represent biologically meaningful variables for describing species ranges (Nix 1986). We conducted a principal component analysis (PCA) to examine the degree of climatic variation among populations. We then performed a MANOVA using informative rotated principal components (PCs), followed by post hoc multiple comparison analyses using the Bonferroni corrected approach (Rice, 1989) to evaluate pairwise differences between population samples.

RESULTS

Molecular phylogenetic analysis

Phylogenetic relationships were estimated for the non-partitioned 12S + tRNA-Val + 16S data set, using a GTR+ I + G model of evolution. Nearly identical phylogenies were obtained using Bayesian vs. Maximum Likelihood methods (Fig. 4.2). Both phylogenies placed samples of *Rhinella crucifer* within the *R. marina* species group making the group paraphyletic (Fig. 4.2). Samples from Central America (= *R. horribilis*) constituted a well-supported, monophyletic clade (Clade A in Figure 4.2); its sister clade also has strong support and is composed by samples from western Ecuador (Clade B = *R.* sp. nov.). Samples from Amazon Basin, including east of the Andes, did not assort into distinct, monophyletic clades consistent with current species-level taxonomy. One clade (Clade C) consisted of samples referable to *R. arenarum, R. achavali, R. icterica* and *R. rubescens* from Uruguay, Argentina and eastern Brazil, and another clade (Clade D) was composed of *R. poeppigii* and *R. marina* samples from east of the Ecuadorian and Peruvian Andes (but see Discussion section). Clade E contained samples of *R. poeppigii*, *R.*

schneideri, *R. jimi* and *R. marina* from Argentina, Paraguay, Brazil, Surinam and eastern Ecuador (but see Discussion section). The only monophyletic species found east of the Andes was *R. arenarum*, which formed a well-supported clade closely related to samples of *R. achavali, R. icterica,* and *R. rubescens* in Clade C (Fig. 4.2). *Rhinella marina sensu lato* was widely paraphyletic.

Uncorrected p-genetic distance between samples from western Ecuador (clade B of *R*. sp. nov.) and its sister clade, *R. horribilis* from Central America (clade A) is 5.0% (Table 4.1; Fig. 4.3). This distance is higher than the distances between Clade B (*R*. sp. nov.) and all other species in the *R. marina* species group (i.e. Clades C, D and E; Table 4.1; Fig. 4.2, 4.3) which ranged between 4.3% to 4.8%. This distance is also much higher than the distance of 0.4 to 0.9% found among all other currently recognized species of *R. marina* group (*R. achavali*, *R. arenarum*, *R. icterica*, *R. rubescens*; Table 4.1), and even higher than the 3.4 to 4.3% found between *R. crucifer* and all taxa/clades of the group (Table 4.1).

Bioacoustic analyses

Bioacoustic comparisons indicate significant differences (see PCA results below) in call structure between western Ecuador (*R*. sp. nov.) and both *R. horribilis* and the eastern Ecuador clade. Calls from western Ecuador are shorter, with fewer notes, and shorter rise time than calls from eastern Ecuador and *R. horribilis* (Table 4.2, 4.3; Fig. 4.4, 4.5). Results from Mann–Whitney tests indicated that western Ecuadorian populations differ significantly in dominant frequency from both *R. horribilis* ($P < 0.001$) and eastern Ecuadorian populations ($P < 0.05$). Western Ecuadorian toads tend to have higher dominant frequency that Central American and eastern Ecuadorian populations (Table 4.3; Fig. 4.6).

Our PCA of advertisement calls from 30 males resulted in two PCs with eigenvalues > 1.0. These two PCs accounted for 80.06% of the total variation. PC I (59.87% of the variance) had high loadings on call length, notes per call, call rise time and dominant frequency; PC II (20.19% of the variance) had high loadings on pulse rate and pulses per note (Table 4.2). The acoustic space (as represented by PC I and PC II; Fig. 4.4) showed significant differences between western Ecuador (*R*. sp. nov.) and both *R*. *horribilis*, and eastern Ecuador clades as determined by Pillai's trace test statistic ($F = 6.69$, $P < 0.001$). Univariate variance tests suggested that this dissimilarity occurs only in PC I ($F = 19.42$, $P < 0.001$; PC II: $F = 1.66$, $P > 0.05$). Multiple comparison analyses showed that western Ecuadorian populations differed from *R*. *horribilis* (P < 0.01), and from eastern Ecuadorian populations (P < 0.01) for PC I.

Morphometric analysis

Multivariate analysis of morphometric characteristics (using both linear and geometric morphometric approaches) showed differences among western Ecuadorian population (*R*. sp. nov.), *R*. *horribilis* (Central American population) and eastern Ecuador populations (*R. marina*). Sexes were analyzed together because males and females broadly overlapped in the PCA space applied to linear variables (Supporting information, Fig. S2), showing no differences between sexes ($P > 0.05$ in all populations on PC I). Likewise, there were no differences between sexes ($P > 0.05$ in all populations on PC I) in the PCA applied to shape variables.

Results from the PCA on linear variables showed most of the variables having high loadings (mainly SVL, Tympanum diameter, Tibia Length, Head Width, and Head Length) on the first component (52.20% of the variation explained). The second component (31.88% of the variation explained) was mainly based on Third Finger Length (Table 4.4). Although there is an important overlap in 2D morpho-space between western Ecuadorian populations and eastern Ecuadorian, and Central American populations (Fig. 4.7), results from MANOVA indicated that there were differences among populations for the first two PC's as determined by Pillai's trace test statistic ($F = 15.75$, $P < 0.001$). Univariate variance tests suggest that this dissimilarity occurs in both PCs individually (PC I: $F = 21.29$, $P < 0.001$; PC II: $F = 11.00$, $P < 0.001$). Multiple comparison analyses showed that toads from the western Ecuadorian populations differed from toads from *R*. *horribilis* only for PC I ($P < 0.001$), and from toads from eastern Ecuadorian populations for PC II ($P < 0.05$). Overall, individuals from western Ecuador were smaller, but with proportionally larger tympanum diameter, larger tibia, and wider and larger heads (*R*. sp. nov.; $\bar{x}$ SVL= 94.08; $\bar{x}$ TD/HL= 14.26%; $\bar{x}$ TL/SVL= 41.51%; $\bar{x}$ HW/SVL= 39.94%; $\bar{x}$ HL/SVL= 32.83%, respectively; Fig. 4.8) than individuals of *R*. *horribilis* ($\bar{x}$ SVL= 117.34; $\bar{x}$ TD/HL = 13.75%; $\bar{x}$ TL/SVL = 38.26%; $\bar{x}$ HW/SVL = 37.66%; $\bar{x}$ HL/SVL = 30.96%, respectively; Fig. 4.8). Western Ecuadorian populations tend to have proportionally shorter third fingers ($\bar{x}$ TF/FL= 33.23%) than individuals from eastern Ecuador (*R*. *marina*; $\bar{x}$ TF/FL = 34.75%; see Supporting information, Table S2). Additionally, similar results were obtained when we repeated the MANOVA and *post hoc* comparisons on PC I and PC II only with males (i.e. western Ecuadorian populations differed from Central American populations in PC I, and from eastern Ecuadorian populations for PC II [$P < 0.05$; Supporting information, Table S3]); and only with females (i.e. western Ecuadorian populations differed from Central American populations in PC I, and from western and eastern Ecuadorian populations for PC II [($P < 0.05$; Supporting information, Table S3)].

Canonical variate analysis on linear variables showed significant morphological differentiation among Central American, eastern, and western Ecuadorian populations (*Wilk's* λ

= 0.17, χ^2 =172.94, $P < 0.001$). The first canonical factor had an eigenvalue of 2.89, accounted for 84.60% of the total variability, and mainly separated toads from western Ecuadorian populations (*R*. sp. nov.) from *R. horribilis* (Fig. 4.9). Snout-vent length, Third Finger Length, Head Width and Head Length were the strongest discriminators along this factor (Supporting information, Table S4). Overall, individuals from Central America (*R. horribilis*) were larger, with proportionally shorter third fingers, and proportionally shorter heads than individuals from western Ecuador and than individuals from Amazonia and eastern Andes of Ecuador (see Supporting information, Table S2). The second canonical factor (15.40% of the total variability) had an eigenvalue of 0.53, and mainly separated toads of western Ecuadorian populations (*R*. sp. nov.) from Amazonian Ecuadorian populations (*R. marina*; Fig. 4.9). Head width and Tibia Length stand out as the most important variables for the discrimination of populations along this factor (Supporting information, Table S4; see Supporting information, Table S2).

The PCA applied to shape variables also showed partial overlap among clades in the space of the first two components of shape (Supporting information, Fig. S3). These two Relative Warps explained 74.60% of the total variation (RW 1 = 66.95%; RW 2 = 7.65%; Supporting information, Table S5). Results from MANOVA indicated that there are differences among populations for the first two RW axes as determined by Pillai's trace test statistic (F = 5.61, $P < 0.001$). Univariate variance tests suggested that this dissimilarity occurs only in RW 2 ($F = 9.10$, $P < 0.001$; RW 1: $F = 2.57$, $P > 0.05$). Multiple comparison analyses indicated that western Ecuadorian populations differed only from *R. horribilis* for RW 2 ($P < 0.001$).

Canonical variate analysis (CVA) on shape variables (i.e. partial warp scores) show separation among the three clades along the first (53.85% of the total variability) and second (46.15%) canonical factors (Table 4.5). Both canonical components were statistically significant

($P < 0.01$), with eigenvalues of 2.42 and 2.07, respectively, suggesting that some aspect of skull shape strongly separates the three studied populations (Fig. 4.10). Thin-plate splines deformation grids along CV I showed skull shape differences between western Ecuadorian and eastern Ecuadorian populations, especially around the premaxilla and the nasal bone (landmarks 1,2,3 and 4,7; Fig. 4.10). The western Ecuadorian specimens tended to display a relatively narrower premaxilla, but more elongated nasal bones than eastern populations. Deformations grids along CV II showed differences between western Ecuador (*R*. sp. nov.) and *R. horribilis* (Fig. 4.10), mainly around the quadratojugal and squamosal bones (landmarks 10, 12, 13), and the distal region of the frontoparietals (landmark 5). A depression of the quadratojugal-squamosal region, and elongation of the distal part of frontoparietal bones distinguished western Ecuador (*R*. sp. nov.) from *R*. *horribilis*.

Climatic analysis

The PCA on climatic variables resulted in four PCs with eigenvalues > 1.0. These four PCs accounted for 92.86% of the total variation (Table 4.6). The MANOVA showed that there are overall differences among populations as determined by Pillai's trace test statistic ($F = 60.23$, $P < 0.001$), however, univariate variance tests suggest that this dissimilarity does not occur in PC I (PC I: $F = 2. 65$, $P > 0.05$; PC II: $F = 66.08$, $P < 0.001$; PC III: $F = 85.77$, $P < 0.001$; PC IV: $F = 9.19$, $P < 0.001$). Along PC II (33.04% of the variation explained), that was mainly based on precipitation-related variables (Table 4.6), western Ecuadorian populations differed from *R. horribilis* and eastern Ecuadorian populations (both $P < 0.001$; Fig. 4.11). Along PC III (16.49% of the variation explained), based mainly on temperature seasonality (Table 4.6), western Ecuadorian populations clearly separated only from *R. horribilis* (Fig. 4.11). Overall, western populations tend to occur in drier and less seasonal in temperature areas than other populations (Fig. 4.11). Along PC IV (8.71% of the total variance), that was mainly explained by mean diurnal range (Table 4.6), western Ecuadorian populations differed from both *R. horribilis* and eastern Ecuadorian populations (both $P < 0.001$), however, this distinction was much less clear than the previous ones.

Our analyses of mtDNA, linear morphometrics, geometric morphometrics of cranial shape, calls and climatic envelopes within *R. marina* species group reveal a new species from the western side of Ecuadorian Andes, corresponding to Clade B in our phylogeny, that we considerer new to science and that we describe below as *R. bellus* sp. nov.

RHINELLA BELLUS SP. NOV.

(FIGS 4.12, 4.13; 4.14, TABLE S2)

Holotype: (Figs. 4.12, 4.13): QCAZ 23305, adult male, SVL = 87.11 mm, collected in Ecuador, Guayas Province, between Palmas and Balsas (ca. 2.003° S, 80.562° W) at 72 m.a.s.l., on 18 March 2003 by Santiago Ron. **Juveniles** (Fig. 4.14): QCAZ 13893, collected in Cañar Canton, Manta Real Community (ca. 2.554° S, 79.364° W) at 1100 m.a.s.l., on 21 December 1998 by Ricardo Oliva. QCAZ 28528, collected in Santo Domingo Canton, near to secondary road, near Tinalandia, jumping between puddles, (ca. 0.303° S, 79.041° W) at 694 m.a.s.l., on 05 January 2005 by Giovanna Romero. QCAZ 35433, collected in Pichincha Province, Pedro Vicente Maldonado, 6 Km to the Northwest at airport, (ca. 0.104° S, 79.103° W) at 544 m.a.s.l., on 17 April 2003 by Santiago Ron. QCAZ 40424, collected in Esmeraldas Province, Rosa Zarate Parish, Laguna del Cube, (ca. 0.415° S, 79.650° W) at 207 m.a.s.l., on 22 August 2007 by Santiago Ron. QCAZ 45989 and 46001, collected in Imbabura Province, Cotacachi-Cayapas

Reserve buffer zone, near the Aguas Verdes River, (ca. 0.331° S, 78.931° W) at 670 m.a.s.l., on 01 November 2009 by Diego Almeida. QCAZ 49447, collected in Manabí Province, Jama Canton, Reserva Lalo Loor Locality, (ca. 0.079° S, 80.148° W) at 150 m.a.s.l., on 02 September 2010 by Diego Salazar. QCAZ 50701 and 50702, collected in Manabí Province, 5 km north of Rocafuerte, San Andrés de Rocafuerte Locality, (ca. 0.868° S, 80.464° W) at 334 m.a.s.l., on 26 by Santiago Ron. **Males Adults** (Figs. 4.12, 4.13): QCAZ 12039, collected in Santo Domingo Province, 5 km north of Rocafuerte, Hotel Saracay Locality, (ca. 0.676° S, 76.399° W) at 334 m.a.s.l., on 05 April 1998 by Luis Eduardo López. QCAZ 17965, collected in Pichincha Province, Guayllabamba, under the bridge over the Guayllabamba river, (ca. 0.069° S, 78.372° W) at 1972 m.a.s.l., on 23 November 2001 by Verónica Sandoya. QCAZ 23324, collected in Santa Elena Province, Via Palmas-Balsas Locality, (ca. 2.031° S, 80.460° W) at 78 m.a.s.l., on 23 November 2001 by Santiago Ron. QCAZ 23486, collected in Guayas Province, Sendero de Cerro Más Vale Locality, in stone, in Cerro Blanco stream approximately 200 m, (ca. 2.399° S, 79.634° W) on 22 March 2003 by Santiago Ron. QCAZ 24579, collected in Manabí Province, Puerto Rico, Alándaluz Locality, in lagoon facing the north side beach, (ca. 1.640° S, 80.830° W) 18 February 2002 by David Cannatella. QCAZ 39353, collected in Pichincha Province, Tababela, New Quito International Airport, N-2 reservoir, at the edge of a water reservoir, (ca. 0.181° S, 78.334° W), on 09 September 2008 by Fernando Ayala. QCAZ 41327, collected in Guayas Province, Bosque Protector Cerro Blanco Locality, (ca. 2.182° S, 80.018 W), at 237 m.a.s.l., on 17 March 2008 by Gustavo Pazmiño. QCAZ 47444 and 47445, collected in Loja Province, San Bernabé Locality, (ca. 4.113° S, 79.304 W), at 1665 m.a.s.l., on 03 March 2010 by Elicio Tapia. **Female Adult**: QCAZ 50698, collected in Manabi Province, Puerto Cayo Locality, (ca. 1.344° S, 80.732 W), at 29 m.a.s.l., on 25 February 2011 by Santiago Ron.

Common names:

Cane toad (EN) or beautiful cane toad (EN); sapo grande de la Costa (SPA)

Diagnosis:

(Figs 4.12, 4.13): *Rhinella bellus* sp. nov. is a member of the *R. marina* species group characterized by: (1) average SVL in adult females 102.163 mm (*SD* = 13.746, *n* = 29), adult males 86.514 mm (*SD* = 13.945, *n* = 31; see Supporting information, Table S2 with sexes considered together); (2) short snout, subacuminated in dorsal view, truncated to rounded profile; (3) bony knob at angle of jaws absent; (4) presence of low and thick cephalic crests with borders with keratinized spicules, continuous with supraorbital, supratympanic, canthal rostral and preorbital crests; reduced infraorbital crests, and preorbital crests absent; (5) heel not reaching posterior margin of eye when hindlimbs depressed; (6) vertebral apophyses absent; (7) dorsal skin with medium and round tubercles usually with a keratinized spicule at the tip, with or without large scattered warts, most are pointed; (8) a thin middorsal line from snout to groin is present; (9) absence of dorsolateral fringe; (10) tympanic membrane and tympanic annulus distinct; (11) parotoid glands relatively big, elongate posteriorly, relatively prominent in dorsal view, with visible small pores, and with a keratinized spicule at the tip, width of parotoid glands varies from 9.17 to 14.27% of SVL; height of parotoid glands can vary from 15.91 to 22.44% of SVL; (12) upper eyelid with keratinized warts; (13) palms without rudimentary basal webbing between fingers, lateral fringes absent; small rounded knobs at tips of digits; finger lengths 3 > 4 > 2 > 1; (14) inner and outer metatarsal tubercles conical, protruding distally, outer usually similar size of inner tubercles; subarticular tubercles present; supernumerary with keratinized spicule at the tip distributed linearly on toes on plantar surface; (15) forelimbs and forearms robust with low and rounded warts keratinized; supernumerary tubercles rounded with different size, distributed irregularly on palm; palmar tubercle larger than thenar tubercle, both are oval; (16) foot with basal webbing between toes, lateral fringes present; small rounded knobs at tips of digits; toe lengths 4 > 5 > 3 > 2 > 1; (16) nuptial pads present.

Comparisons with other species:

Rhinella bellus sp. nov. is morphologically similar to *R. horribilis* and *R. marina*. However, the new species *R. bellus* differs morphometrically from populations of *R. horribilis* and Eastern Ecuador ("*R. marina*"; but mainly from the former) in having a smaller body size, along with proportionally larger tympanum diameter, larger tibia and a wider and larger head (Fig. 4.8; Supporting information, Table S2). Differences among species were also evident in the skull shape (see results of morphometric analyses). Acevedo *et al.* (2016) reported cranial morphology differences between populations of east (*R. marina*) and west (*R. horribilis*) side of the Venezuelan Andes, mainly around the pre- maxillar, nasal bones, and occipital region. We also found skull differences between populations of east (*R. marina*) and west (*R. bellus* sp. nov.) side of the Ecuadorian Andes mainly around pre-maxillar and nasal bones, however, the non-monophyletic status of the eastern and Amazon Basin populations (Vallinoto *et al.*, 2010; this paper) precluded us to make further comparisons with the findings of Acevedo *et al.* (2016). The new species is distinguishable from *R. horribilis* by a depressed area on the quadratojugal-squamosal contact region, and the elongation of frontoparietal bones at their most distant region (Fig. 4.10; Table 4.5).

Rhinella bellus sp. nov. differ in environmental envelope from *R. horribilis* and *R. marina* (Fig. 4.11; Table 4.6; for details see Climatic analysis section from Methods and Results) and is separated by high genetic distances from both species as well (Fig. 4.3; Table 4.1; see Molecular phylogenetic analysis from Methods and Results).

Advertisement calls of *R. bellus* sp. nov. are significantly shorter, with fewer notes and shorter rise time than those of *R. horribilis* and *R. marina* (Fig. 4.4; Table 4.2). The number of notes per call of *R. bellu*s sp. nov. (midrange = 23; range 6-40) is also lower than those reported in several other species within the *R. marina* species group (e.g. *R. arenarum* [midrange = 84, range 61–107; Straneck *et al*., 1993]; *R. marina* [midrange = 176.5, range 18 –335; present work]; *R. poeppigii* [midrange = 27.5, range 10 – 45; De la Riva *et al*., 1996]; and *R. schneideri* [midrange = 36.5, range 33 – 40; Köhler et al. 1997]). Furthermore, *R. bellus* sp. nov. toads produce calls with higher dominant frequency than toads of *R. horribilis* and *R. marina* (Fig. 4.6; Table 4.2,4.3).

Description of holotype:

Adult male; robust body; head wider (HW = 36.15 mm) than long (HL = 30.49 mm). Head shape in dorsal view subtriangular with short squared snout and straight lateral view, tip of the snout not surpassing anterior margin of maxilla in dorsal and ventral views. Intensive rounded tubercles with several keratinized spicules in dorsal view skin. Spaced granulation on top of the head. Presence of low cephalic crests with keratinized borders, continuous with supraorbital, supratympanic, canthal rostral and preorbital crests; reduced infraorbital crests, and preorbital crests absent. Tympanic membrane and tympanic annulus distinct; bony knob at angle of jaws absent; corner of mouth angular; vertebral apophyses absent; parotoid glands relatively big, elongate posteriorly, relatively prominent in dorsal view, with small pores visible, and tubercles keratinized; upper eyelid with keratinized warts. Forelimbs and forearms robust with low and rounded warts keratinized. Longitudinal mid-dorsal cream thin stripe from snout to groin present. Hand without rudimentary basal webbing between fingers, lateral fringes absent; small rounded knobs at tips of digits; finger lengths 3 > 4 > 2 > 1; subarticular tubercles low and rounded; supernumerary tubercles rounded with different size, distributed irregularly on palm; palmar tubercle larger than thenar tubercle, both are oval; nuptial pads on the dorsolateral surface of fingers I and II. Foot longer than tibia (TL/FL = 0.948); foot with basal webbing between toes, lateral fringes present; small rounded knobs at tips of digits; toe lengths 4 > 5 > 3 > 2 > 1; inner and outer metatarsal tubercles conical, protruding distally, outer similar size of inner tubercles (~ 4.18 mm); subarticular tubercles present; supernumerary keratinized tubercles rounded distributed linearly on toes on plantar surface.

Color of holotype in preservative:

(Fig. 4.12): Dorsum light gray, intense rounded tubercles between light cream and dark brown with dark brown spicules, also in dorsal surfaces of tights, shanks, and forelimbs which are lighter than dorsum; presence of few dark gray marks arranged irregularly. Nuptial pads dark brown. Ventral surfaces gray and in the center yellowish-cream with irregular dark brown marks arranged in irregular patterns; cream color across with black edges slightly posterior to gular region. Fingertips and subarticular tubercles yellowish-cream. Dark brown knobs at tips of digits; Tympanum region dark gray (Fig. 4.12).

Etymology: *"Bellus"* is Latin meaning for "beautiful", given in opposition to the Latin adjective *"horribilis"* of its sister taxa since ugliness can be viewed as just a variety of beauty.

Variation of coloration in preserved specimens

(Fig. 4.13): Background dorsal coloration varies from light gray (e.g. QCAZ 23305, 50698, 50701) to dark brown (e.g. QCAZ 41327,24579, 39353), with irregular black and yellowish marks (e.g. QCAZ 40806, 50702, 50698). A thin middorsal line from snout to groin is present, except QCAZ 47445. Ventral surfaces have a yellowish-cream to dark brown background; and several with irregular grey marks arranged in diverse patterns (e.g. QCAZ 12039, 17965 28528), absence in QCAZ 41327, 47445, 47444.

Vocalization: Based on an individual recorded (7818 FonoZoo) at Estación Biológica Río Palenque (Provincia Los Ríos) by W. E. Duellman on 12 April 1972 at 21:50 h, air temperature 24 °C, distance about 5.5 feet. The advertisement call consists of a short trill with a mean duration of 1.99 s, mean call rise time of 1.09 s, 20–40 notes per call, 3–5 pulses per note, a mean pulse rate of 89.92 pulses per second, mean dominant frequency of 750.00 Hz, and a repetition rate of 8 calls per minute.

Distribution and ecology:

In Ecuador, this species is restricted to the western side of the Andes, from the sea level to 2900 m.a.s.l., and frequently associated with open areas in disturbed urban and semi-natural habitats, but also sometimes found in undisturbed forests. The complete distribution of *R. bellus* sp. nov. remains unknown, mainly due to lack of distributional information in the Colombian Chocó Bioregion. However, the clustering of the call from southwestern Colombia into the *R. bellus* sp. nov. acoustic space along the first PC axis (see results and Fig. 4.4), suggests that populations from western Colombia might belong to the new species. Moreover, the limited seasonal temperature variation of the Colombian Chocó Bioregion matches the climatic envelope of the *R. bellus* sp. nov., suggesting its geographic range probably extends north to this region (see results of climatic envelopes and Fig. 4.11; Table 4.6). We also believe these toads are likely to be found in the extreme northwestern of Peru due to the close proximity of the collection sites from the extreme southwestern of Ecuador. We propose that the name *R. horribilis* is mainly restricted for populations in Central America and western Venezuela.

DISCUSSION

Our analyses reveal that populations from western Ecuador represent an independent lineage from all other known species of the *Rhinella marina* group. We base this conclusion in the congruence observed between genetic, bioacoustic, morphological and climate envelope information. Western Ecuadorian populations are genetically highly different from other species of the group. Its mtDNA divergence is much higher that observed between uncontroversial species pairs of the same group like *R. arenarum* and *R. icterica* or *R. schneideri* and *R. poeppigii*. Differences in advertisement calls are additional clear indication that those populations represent a candidate species within the *R. marina* group. We provide conclusive evidence, based on an integrative approach combining different sources of information, that there are two, independent lineages of *R. marina* group toads west of the Andes in northern South America and Central America. One, *R. horribilis*, further ranges north through Central America as far as southern Texas whereas the other, *R. bellus* sp. nov., occurs in Ecuador and probably as far north as southwestern Colombia and as far south as extreme northern Peru.

Past studies have shown two genetically distinct species within *R. marina* from east and west side of the Venezuelan Andes (Slade & Moritz, 1998), including the recent work of Acevedo *et al.* (2016), who suggested that the *R. horribilis* name should be revalidated for the western Andes and Central American populations. Additionally, Mulcahy *et al*. (2006), Pramuk (2006) and Vallinoto *et al.* (2010) had previously found important levels of genetic divergence between Central American and Ecuadorian samples, however, the incomplete sampling (only very few were included from western Ecuador) and the lack of bioacoustics, morphological (but see Pramuk, 2006) and ecological information, limited their conclusions. We provide novel evidence showing a new independent evolutionary lineage (i.e. a separate species) within the *R.*

marina species group, with the western Ecuadorian populations (*R. bellus* sp. nov.) being a new distinct species from the populations of Central America (*R. horribilis*), and from the populations from the Amazon Basin (*R. marina*).

In contrast to the cryptic morphological diversity notable throughout the genus *Rhinella* (Graybeal, 1997; Pramuk, 2006; Acevedo *et al.*, 2016), including the *R. marina* species group, our morphometric analyses (including the geometric morphometric-based) suggest that *R. bellus* sp. nov. (western Ecuadorian populations) is distinguishable from *R. horribilis* (Central American populations) and from *R. marina* (Amazon basin populations) as currently understood. Isolated from all other *R. marina* group toads except for *R. horribilis* by the Andes, *R. bellus* sp. nov. appears to be among the most geographically isolated and among the most morphologically distinctive of this group of species.

For the first time, we report significant acoustic differences between *R. horribilis, R. marina* and *R. bellus* sp. nov. (see Fig. 4.4, 4.5, 4.6) despite the generally conservative structure of advertisement calls among species of the *R. marina* group (Maciel *et al.*, 2007). The distinctly lower number of notes per call in *R. bellus* sp. nov. relative to other species within the *R. marina* group is significant. Similarly, the higher dominant frequency of *R. bellus* sp. nov. calls in comparison with calls of *R. horribilis* and *R. marina* is remarkable as this call trait is among the few not strongly dependent on operational temperature (Fig. 4.6), and has been proved to be useful to assess species limits (Köhler et al., 2017). This acoustic distinctiveness of *R. bellus* sp. nov. among *R. marina* group species, and especially from *R. horribilis*, suggests that calls may have diverged at faster rates compared to morphology in this group, as it has also been shown in other anuran species groups (e.g. Padial *et al.*, 2008; Angulo & Icochea, 2010; Funk *et al.*, 2012). These patterns could be due to sexual selection promoting rapid divergence in both male traits and female preferences, or strong selection on species recognition (Panhuis *et al.*, 2001). This may be particularly relevant to the calls of *R. bellus* sp. nov. vs. *R. horribilis* in that vocal character displacement where these two species meet (probably in southern Colombia) could promote mating isolation. Alternatively, mate-recognition traits as calls, may diverge faster than morphology due to a strong stabilizing selection on morphological traits (Funk *et al.*, 2012), which may be imposed by several ecological factors (Bickford *et al.*, 2007). Previous studies have not fully evaluated call differences within the *R. marina* species group, although acoustic information seems to be particularly useful for the delimitation of cryptic species (Funk *et al.*, 2012).

The comparison of climatic envelopes among studied populations provided important complementary evidence for species separation (see Fig. 4.11). Frog populations occurring in western Ecuador (*R. bellus* sp. nov.) have a climatic envelope with lesser temperature seasonality than populations of *R. horribilis* occurring further north in South America and Central America. Previous studies have shown temperature seasonality to be a major climatic factor limiting dispersal of amphibians (e.g. Wiens *et al.*, 2006), and others have proved climatic specialization of Neotropical species along temperature seasonality axes (e.g. Graham *et al.*, 2004). We would not expect notable and substantial morphological divergence between *R. bellus* sp. nov. and *R. horribilis* if speciation occurred mainly via geographic isolation related to climatic components, unless climate impose selection on morphology. However, the relative importance of climatic factors in the population divergence and speciation of these lineages deserve further investigation.

We also found that *R. marina* from the Amazon Basin remains non-monophyletic as previously found by Vallinoto *et al.* (2010). Samples of *R. marina* are nested within only one well supported clade (i.e. clade E in Figure 4.2), since the sample MJH 3678 of "*R. marina*" from clade D is probably misidentified and most likely correspond to *R. poeppigii*. The clade E is formed by "*R. poeppigii"* from Bolivia, *R. schneideri, R. jimi, R. marina* from the eastern side of Ecuadorian Andes, and *R. marina* from the Amazonian Basin. The sample MNCN/ADN6044 of *R. poeppig*ii, however, is likely misidentified and correspond to either *R. marina* or *R. schneideri*. Furthermore, Vallinoto et al. (2010), Ron et al. (2015), and the present study placed *R. crucifer* as sister to the *R. marina* group according to mtDNA sequence information. Although *R. crucifer* is not formally considered to be in the *R. marina* species group (Pramuk, 2006), morphological similarities and a close cytogenetic and phylogenetic relationship between it and members of the *R. marina* group have been noted previously (Blair, 1972; Cei, 1972; Duellman & Schulte, 1992; Baldissera *et al*., 1999; Pauly *et al.*, 2004; Pramuk, 2006).

The discrepancy between phylogenetic relationships and the taxonomic classification of species within *R. marina* species group could be influenced by several factors. First, the lack of an integrative taxonomy (i.e. species delimitation based on multiple sources of evidence; Padial *et al.,* 2010) that provides a more effective solution to refine the systematic of *R. marina* species group. Second, DNA sequences of some lineages (e.g. some populations previously known as *R. horribilis"*) available for only a small number of samples and/or with limited representation of the geographic distribution (Maciel *et al.*, 2010; Vallinoto *et al.*, 2010). Third, the evident lack of prominent diagnostic morphological characters for some lineages in this group can result in the misidentification of specimens. For instance, Venegas & Ron (2014) reported on 10 specimens of *R. poeppigii* deposited at Museo de Zoología, Pontificia Universidad Católica del Ecuador (QCAZ) that had previously been misidentified as *R. marina*. Finally, mitochondrial introgression, that could result from interspecific hybridization events between closely related species that occur in sympatry (e.g. Masta *et al.*, 2002; Green & Parent, 2003), may affect phylogenetic reconstruction by obscuring topology and divergence estimates. This could have been the case for some populations of *R. marina* and *R. schneideri* at the Amazon Basin (Sequeira *et al.*, 2011).

Cane Toads are economically important and invasive outside of their native range, having been introduced on many Caribbean and Pacific islands (Easteal, 1981, 1985; Lever, 2001; Shine, 2010, 2018) where they are often now considered pests. The impact of such a large, voracious, prolific and toxic amphibian on the ecology of northern Australia, for example, has been profound (Shine, 2018). Most of the evidence and historical record indicates that the Cane Toads currently in the Pacific originated from native populations in Venezuela, via Puerto Rico, Cuba and Florida. Considering the extent of cryptic taxonomic diversity of *R. marina* species toads, however, and the probability that new species such as *R. bellus* sp. nov. remain to be discovered within the complex, it is possible that the Cane Toads infesting Australia and many Pacific Islands may not actually be *R. marina.* If this is the case, some aspects of our current knowledge on global biological invasions of these species (e.g. Tingley *et al.*, 2014) would deserve reconsideration.

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Table 4.1. Genetic uncorrected distances (*p*) among taxa of *Rhinella marina* group. Values represent the means and the minimum–maximum range of the genetic differentiation among taxa and the main clades shown in the phylogeny of *R. marina* species group. Species names with asterisk belong to Clade C. Clade A corresponds to *R. horribilis*, Clade B to *R. bellus* sp. nov., Clade D most probably to *R. poeppigii* (see Discussion section) and E to *R. marina*. *Rhinella crucifer* refers to the outgroup.

	Taxa/Clade	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**
1	**Clade A**	-							
2	**Clade B**	0.05 0.042–0.061	-						
3	**Clade D**	0.046 0.042–0.057	0.044 0.037–0.055	-					
4	**Clade E**	0.049 0.044–0.064	0.043 0.035–0.057	0.02 0.015–0.029	-				
5	***R. achavali****	0.052 0.05–0.059	0.048 0.042–0.055	0.029 0.026–0.031	0.029 0.022–0.033	-			
6	***R. arenarum****	0.055 0.053–0.061	0.046 0.04–0.053	0.031 0.029–0.033	0.03 0.024–0.035	0.007 0.007–0.007	-		
7	***R. crucifer***	0.043 0.04–0.051	0.04 0.035–0.044	0.041 0.037–0.046	0.043 0.037–0.048	0.034 0.033–0.035	0.036 0.035–0.037	-	
8	***R. icterica****	0.055 0.053–0.061	0.048 0.04–0.057	0.031 0.029–0.033	0.029 0.024–0.035	0.007 0.007–0.007	0.009 0.009–0.009	0.036 0.035–0.037	-
9	***R. rubescens****	0.052 0.05–0.059	0.048 0.042–0.055	0.029 0.026–0.031	0.029 0.022–0.033	0.004 0.004–0.004	0.007 0.007–0.007	0.034 0.033–0.035	0.005 0.002–0.007

Table 4.2. Loadings, eigenvalues, and percentage of explained variance for first two principal components (PC's) of a Principal component analysis (PCA). This analysis was based on seven acoustic variables from the advertisement calls of 36 toads from western Ecuador (*Rhinella bellus* sp. nov.), eastern Ecuador (*R. marina*) and Central America (*R. horribilis*). Additionally, one individual from western Colombia, and one from eastern Peru were included in the analysis.

Variables	**PC I**	**PC II**
Call length	0.900	0.345
Call rise time	0.880	0.299
Notes per call	0.921	0.301
Pulses per note	-0.659	0.609
Pulse rate	-0.523	0.699
Call repetition rate	-0.642	-0.338
Dominant frequency	-0.800	0.376
Eigenvalue	**4.191**	**1.413**
% of variance explained	**59.87**	**20.19**
Cumulative %	**59.87**	**80.06**

Table 4.3. Descriptive statistics for call parameters of toad populations form Central America, western Ecuador and eastern Ecuador. Sample size (*n*), and Mean ± SD are given. Individuals from western Ecuador correspond to *Rhinella bellus* sp. nov., individuals from eastern Ecuador correspond to *R. marina*, and individuals from Central America correspond to *R. horribilis*.

Variables	**Central America** (***n*=5**)	**Western Ecuador** (***n*=17**)	**Eastern Ecuador** (***n*=12**)
Call length	6.33 ± 1.01	1.51 ± 0.43	5.28 ± 4.04
Call rise time	3.75 ± 1.86	0.94 ± 0.26	3.09 ± 2.19
Notes per call	83.98 ± 11.10	18.33 ± 5.70	81.66 ± 61.97
Pulses per note	3.55 ± 0.78	3.80 ± 0.59	3.16 ± 0.69
Pulse rate	90.57 ± 13.87	91.31 ± 11.70	88.92 ± 13.66
Call repetition rate	4.41 ± 1.61	8.57 ± 2.40	2.96 ± 0.86
Dominant frequency	633.02 ± 35.28	803.05 ± 75.7	705.52 ± 117.24

Table 4.4. Loadings, eigenvalues, and percentage of explained variance for two first principal components from a principal component analysis (PCA). The analysis is based on 13 continuously varying lineal morphological characters of 3 toad populations and 106 specimens (see methods in the main text). Abbreviations are: SVL = Snout-vent length; TL = Tibia length; FL = Foot length; FEL = Femur length; HL = Head length; HW = Head width; IOD = Interorbiltal distance; IND = Internarial distance; END = Eye-nostril distance; ED = Eye diameter; TD = Tympanum diameter; THL = Thumb length; TF = Third finger length.

Variables	**Code**	**PC I**	**PC II**
Snout-vent length	Log SVL	.854	.448
Tibia length	Log TL	.810	.537
Foot length	Log FL	.736	.609
Femur length	Log FEL	.736	.597
Head length	Log HL	.798	.525
Head width	Log HW	.805	.548
Interorbiltal distance	Log IOD	.690	.512
Internarial distance	Log IND	.730	.444
Eye-nostril distance	Log END	.733	.425
Eye diameter	Log ED	.694	.528
Tympanum diameter	Log TD	.823	.175
Thumb length	Log THL	.501	.758
Third finger length	Log TF	.278	.911
Eigenvalues		**6.79**	**4.15**
% of variance explained		**52.20**	**31.88**
Cumulative %		**52.20**	**84.08**

Table 4.5. Canonical coefficients and percentage of explained variance for canonical variables (CV) of the Canonical Variate Analysis (CVA) of 3 toad populations and 84 specimens. This analysis was based on shape variables (see main text).

Shape variables	**CV I**	**CV II**
x1	-29.5047	105.6930
y1	-137.1518	101.0467
x2	95.0278	-95.6869
y2	95.6099	-63.0279
x3	-12.6571	26.8945
y3	42.8372	-5.6094
x4	-103.9906	-19.3548
y4	-25.4385	9.6817
x5	19.2644	-18.6325
y5	-19.4825	-22.6826
x6	72.4379	17.1427
y6	-22.4482	14.6958
x7	93.5268	0.6927
y7	78.0845	9.5599
x8	-37.4333	-17.7027
y8	17.0133	-48.1208
x9	-35.4839	-36.8079
y9	2.8802	-18.1410
x10	26.1319	55.7962
y10	-19.5041	-12.9742
x11	-63.8547	15.6947
y11	11.8286	8.6709
x12	-47.9645	-10.7240
y12	8.2034	18.2051
x13	24.5003	-23.0049
y13	-32.4319	8.6958
% of variance explained	**53.85**	**46.15**
Cumulative %	**53.85**	**100**

Table 4.6. Loadings, eigenvalues, and percentage of explained variance for four first principal components from a principal component analysis (PCA). The analysis is based on 19 climatic variables (BIO1 – BIO19) from 98 collection localities of 3 toad populations' specimens used for the phylogenetic analysis (see Methods section).

Variables	**PC I**	**PC II**	**PC III**	**PC IV**
BIO1 - Annual Mean Temperature)	0.989	0.103	0.086	-0.045
BIO2 - Mean Diurnal Range(Mean(period max-min))	-0.056	-0.229	-0.233	0.865
BIO3 - Isothermality	0.13	0.306	0.879	-0.077
BIO4 - Temperature Seasonality (Coefficient of Variation)	-0.049	-0.228	-0.908	0.182
BIO5 - Max Temperature of Warmest Period	0.97	0.004	-0.149	0.181
BIO6 - Min Temperature of Coldest Period	0.881	0.196	0.342	-0.259
BIO7 - Temperature Annual Range	-0.121	-0.294	-0.709	0.623
BIO8 - Mean Temperature of Wettest Quarter	0.988	-0.003	-0.068	-0.071
BIO9 - Mean Temperature of Driest Quarter	0.949	0.215	0.192	-0.033
BIO10 - Mean Temperature of Warmest Quarter	0.993	0.046	-0.085	-0.019
BIO11 - Mean Temperature of Coldest Quarter	0.944	0.13	0.281	-0.092
BIO12 - Annual Precipitation	0.129	0.954	0.237	-0.104
BIO13 - Precipitation of Wettest Period	0.072	0.866	-0.117	-0.316
BIO14 - Precipitation of Driest Period	0.09	0.889	0.347	0.039
BIO15 - Precipitation Seasonality (Coefficient of Variation)	0.032	-0.795	-0.471	-0.088
BIO16 - Precipitation of Wettest Quarter	0.139	0.892	-0.028	-0.308
BIO17 - Precipitation of Driest Quarter	0.076	0.894	0.355	0.026
BIO18 - Precipitation of Warmest Quarter	0.077	0.714	0.018	-0.383
BIO19 -Precipitation of Coldest Quarter	0.174	0.832	0.405	0.018
Eigenvalues	9.118	5.394	1.942	1.19
% of variance explained	34.62	33.04	16.49	8.71
Cumulative %	34.62	67.66	84.15	92.86

Figure 4.1. Distribution of *Rhinella horribilis* from Central America (black circles; according to Acevedo et al. 2016), *R. bellus* sp. nov. (white circles; according to our results; previously *R. horribilis* according to Acevedo et al. 2016), and *R. marina* (black triangles). Symbols correspond to locations of specimens sequenced in this study (all records from western Ecuador, except AY680259 and DQ158474, and all from eastern Ecuador) and published sequences as well (records from Central America, Brazil and Peru; see main text and Supporting information, Table S1).

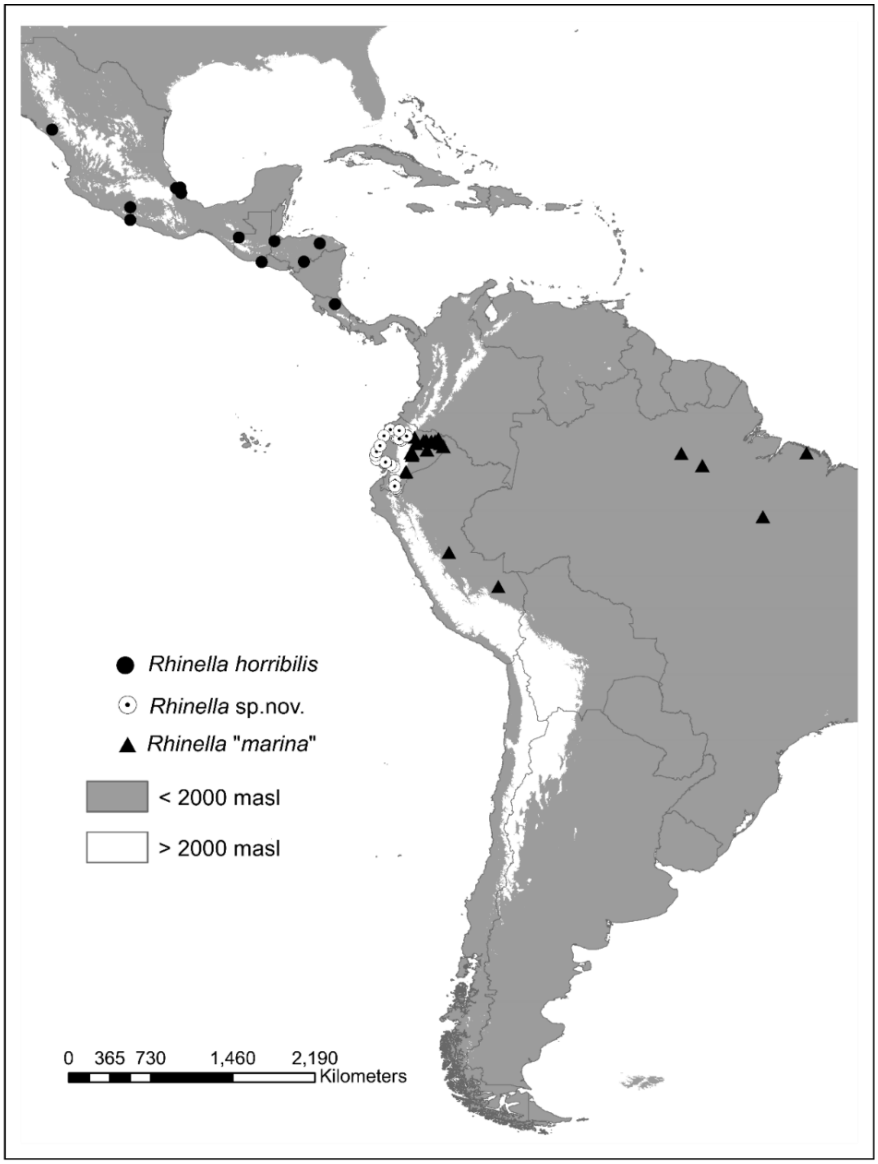

Figure 4.2. Phylogenetic relationships among species of the *Rhinella marina* group based on the Bayesian analysis of the 12S–16S fragment. Numbers above the branches are Bayesian posterior probability values and maximum likelihood bootstrap values. Posterior probabilities higher than 0.9, and maximum parsimony bootstrap values higher than 90% are marked with an asterisk (*). Clade A corresponds to *R. horribilis*, Clade B to *R. bellus* sp. nov., Clades D most probably to *R. poeppigii* (see Discussion section) and clade E to *R. marina*.

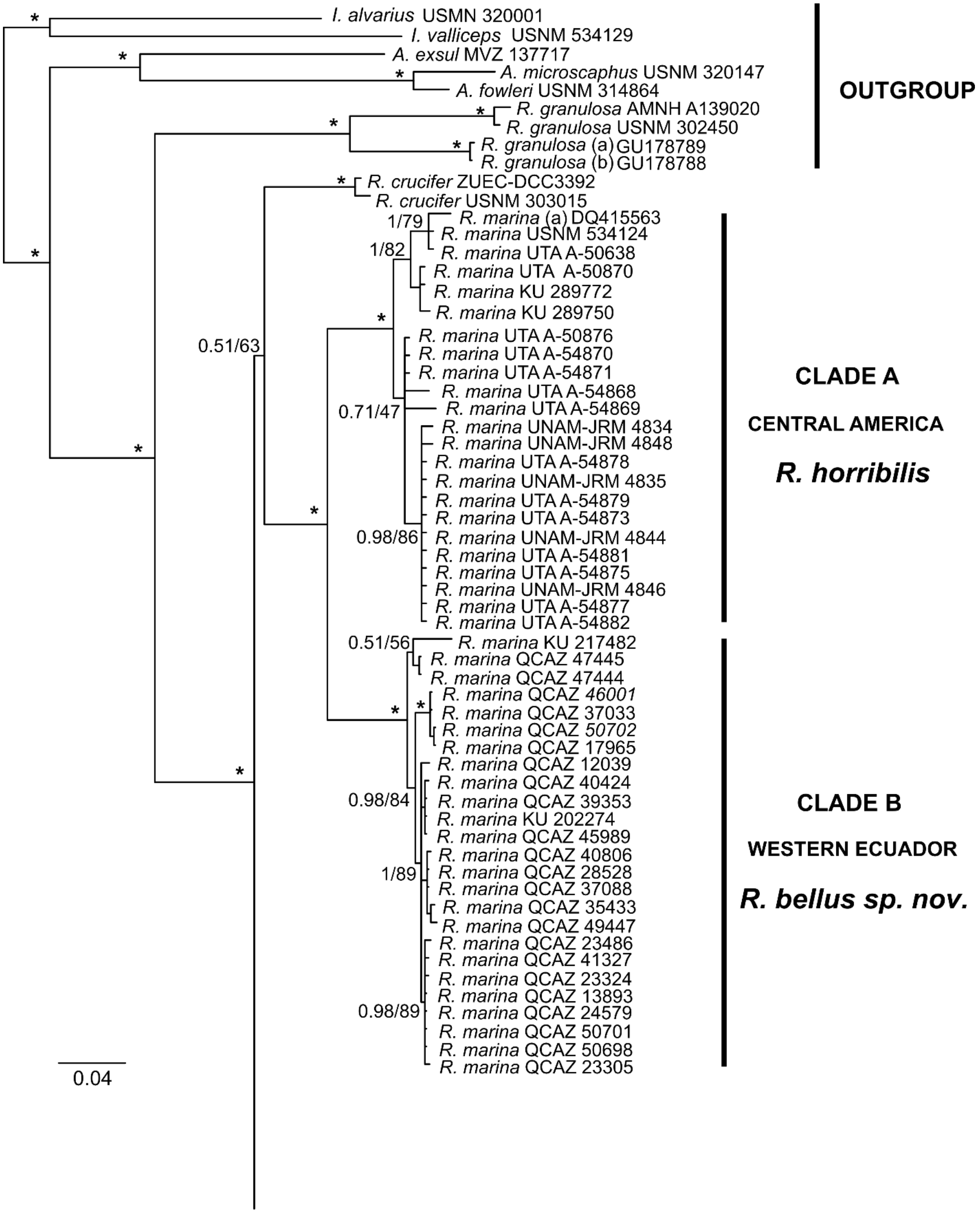

Figure 4.2. ***Continuation***

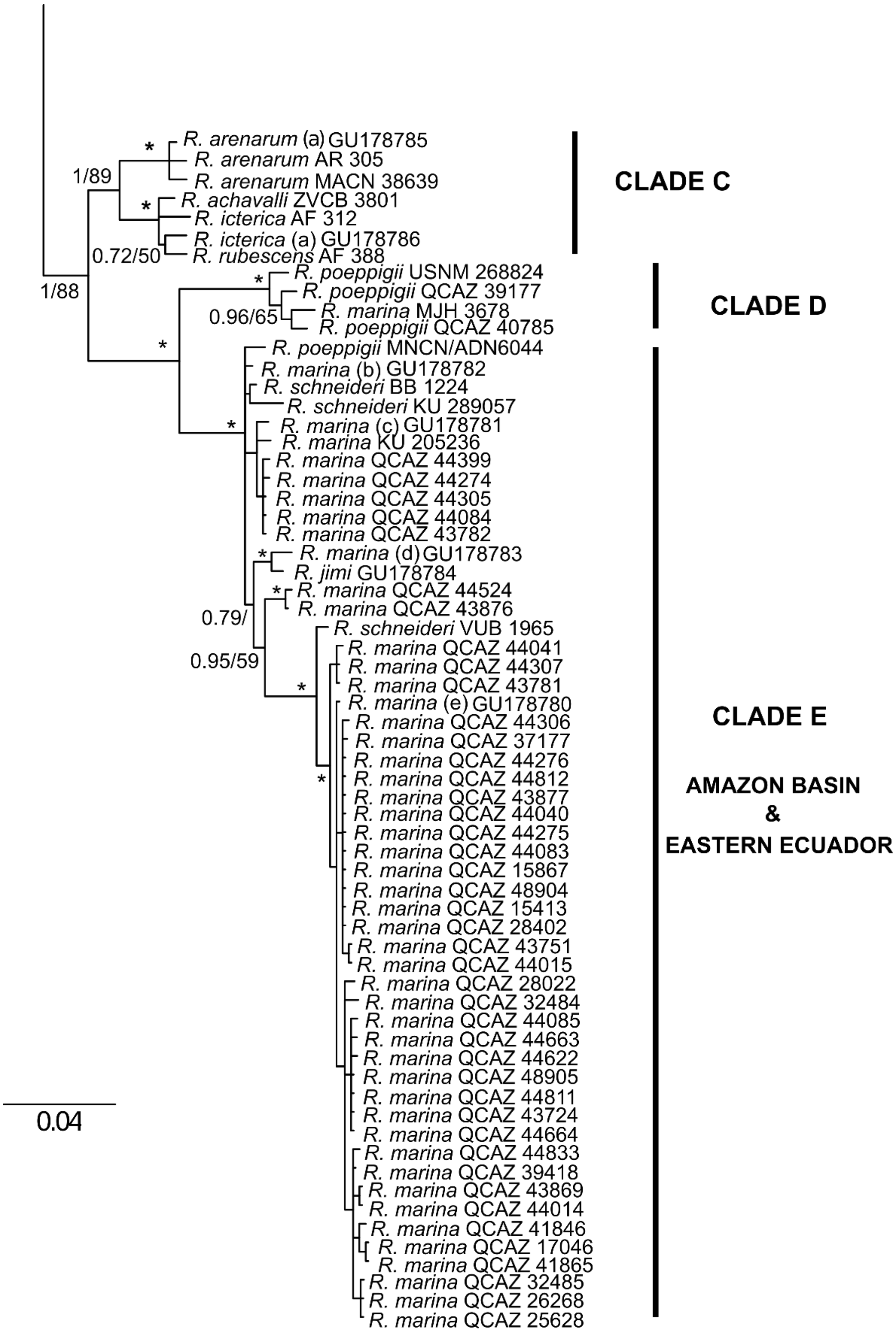

Figure 4.3. Multidimensional scaling plot of the pairwise genetic distances calculated between species of *Rhinella marina* group (see Table 4.1). Clade B corresponds to the new species *R. bellus*. Clade D most probably correspond to *R. poeppigii* (see Discussion section).

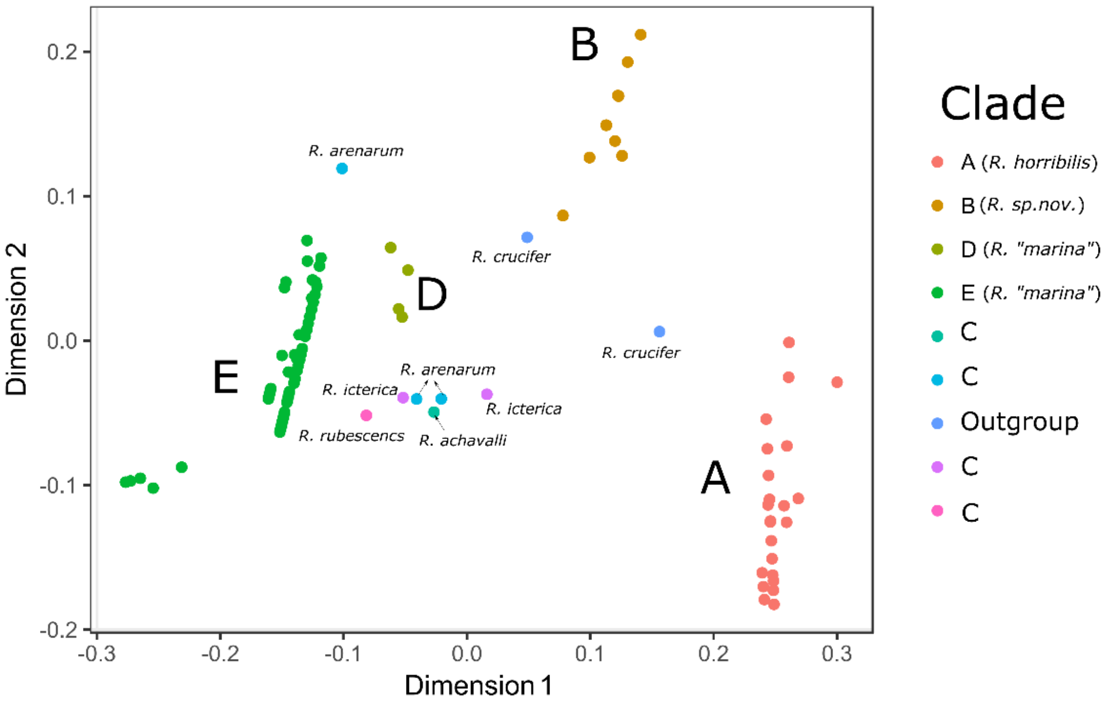

Figure 4.4. Plot of the first two axes (PC's) from principal components analysis (PCA) based on seven acoustic variables of the advertisement calls of 36 toads from western Ecuador (*Rhinella bellus* sp. nov.), eastern Ecuador (*R. marina*) and Central America (*R. horribilis*). Additionally, one individual from western Colombia, and one from eastern Peru were included in the analysis. Vertical dashed line separates populations from western side of the Andes from the rest of the studied populations along PC I.

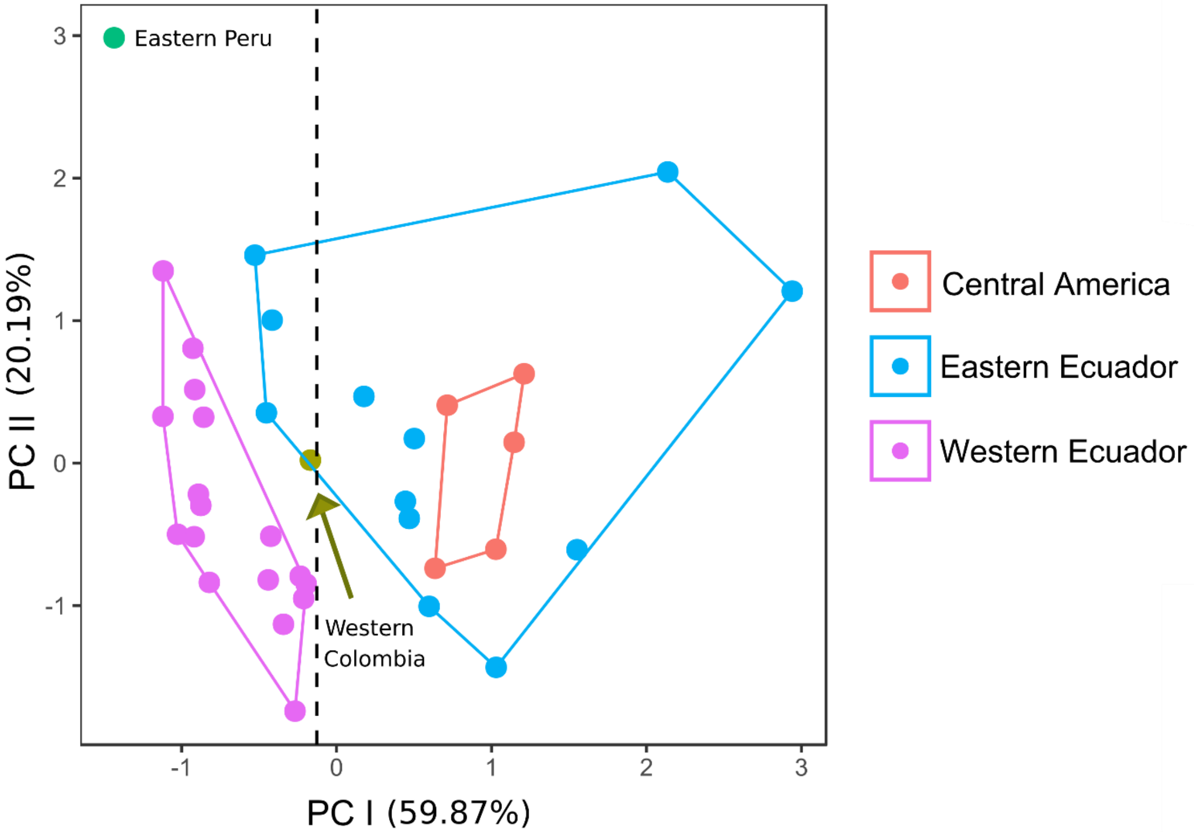

Figure 4.5. Calls of: **A–B** *Rhinella marina* from Vía Maxus km 58, Provincia Orellana, eastern Ecuador. **C–D** *R. bellus* sp. nov. from Yunguilla, Provincia Azuay, western Ecuador. **E-F** *R. horribilis* from 1.6 km WNW of Villa Neily, Puntaneras, Costa Rica, Central America. Oscilograms (A, C and E) and spectrograms (B, D and F).

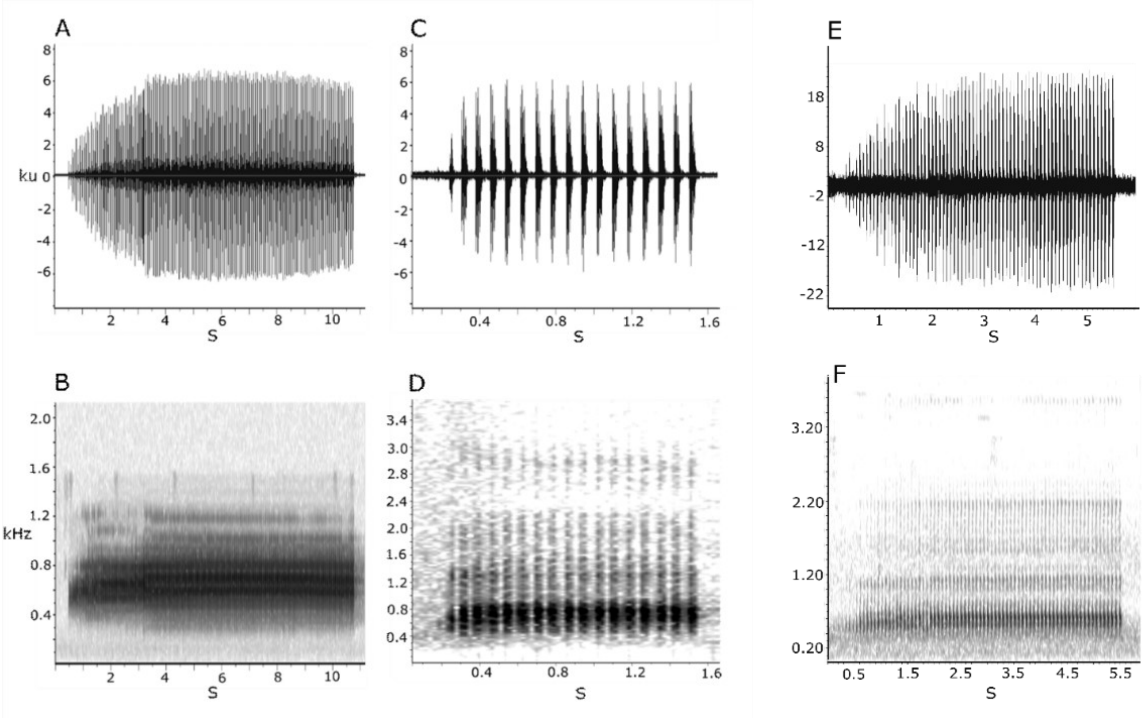

Figure 4.6. Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) in dominant frequency (Hz) of calls in toad populations from Central America (*n* = 5), eastern Ecuador (*n* = 12) and western Ecuador (*n* = 17). Individuals from western Ecuador correspond to *R*. *bellus* sp. nov., individuals from eastern Ecuador correspond to *R*. *marina*, and individuals from Central America correspond to *R*. *horribilis*.

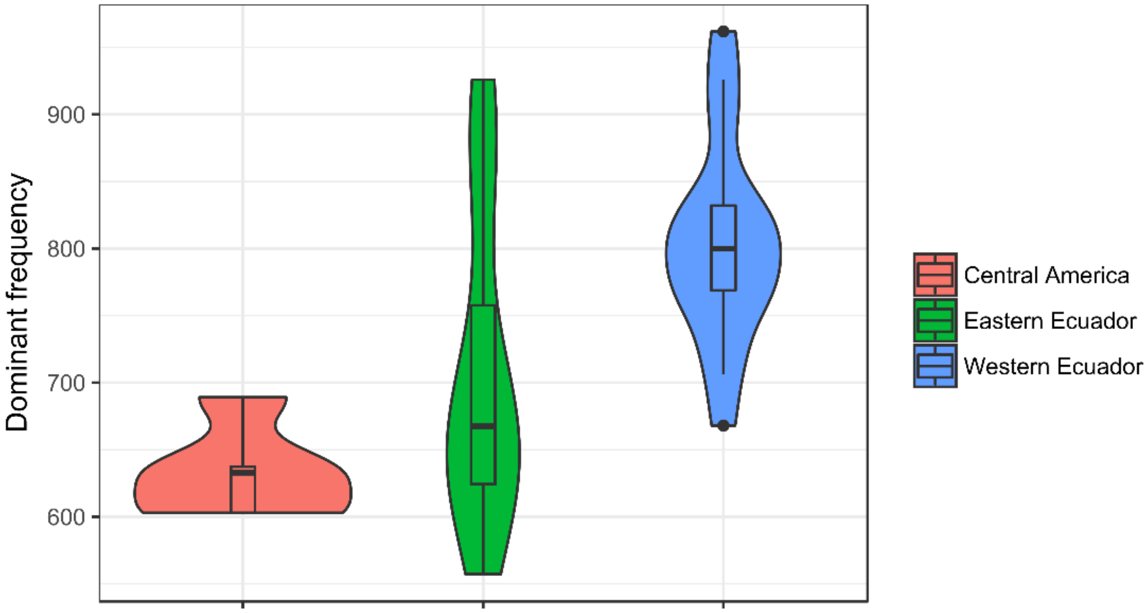

Figure 4.7. Principal components (PC's) from a PCA based on 13 continuously varying lineal morphological characters from 106 toads (*Rhinella marina* species group; see methods in the main text). Individuals are classified by geographic region, with 50% ellipse per group. For eigenvectors and eigenvalues see Table 4. Individuals from western Ecuador correspond to *R. bellus* sp. nov., individuals from eastern Ecuador correspond to *R. marina*, and individuals from Central America correspond to *R. horribilis*.

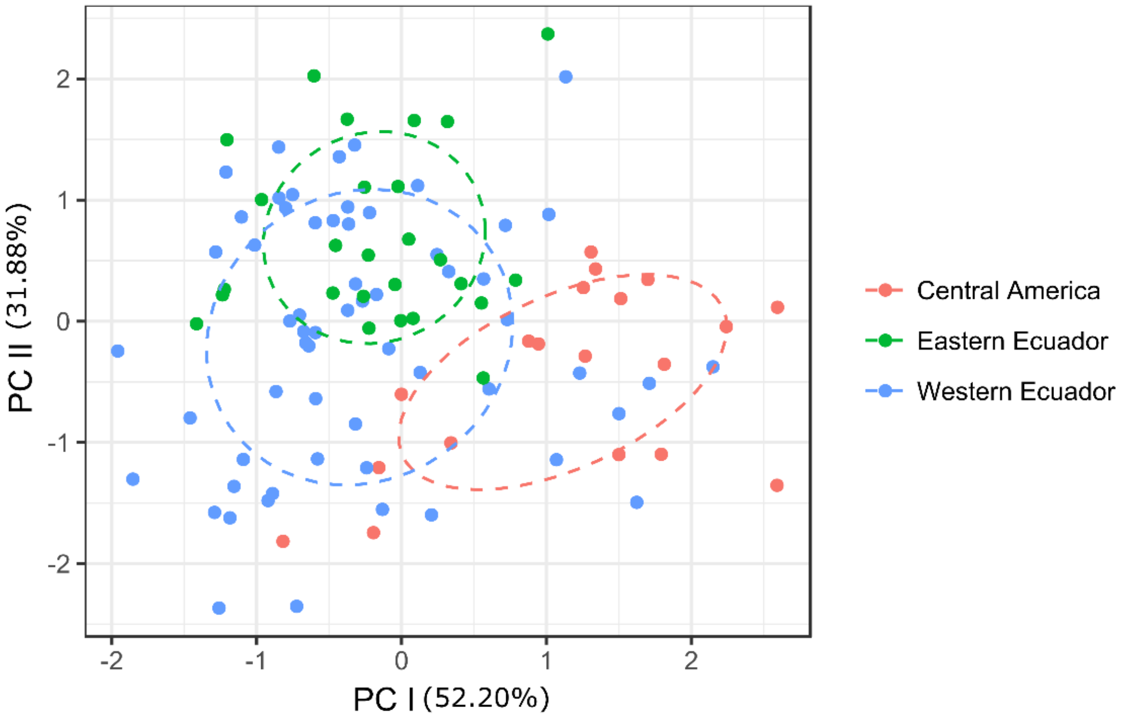

Figure 4.8. Violin plots showing the variation (median -unfilled diamond-, range, kernel density, 25th-75th percentiles) of the following measurements (in mm): **A.** Snout-vent length (SVL) of toad populations from Central America ($n = 20$) and western Ecuador ($n = 60$). Individuals from Central America correspond to *Rhinella horribilis* and individuals from western Ecuador correspond to *R. bellus* sp. nov. **B.** Tympanum diameter as a proportion (in percentage) of head length (TD/HL). **C.** Tibia length as a proportion (in percentage) of snout-vent length (TL/SVL). **D.** Head length as a proportion (in percentage) of snout-vent length (HL/SVL). **E.** Head width as a proportion (in percentage) of snout-vent length (HW/SVL).

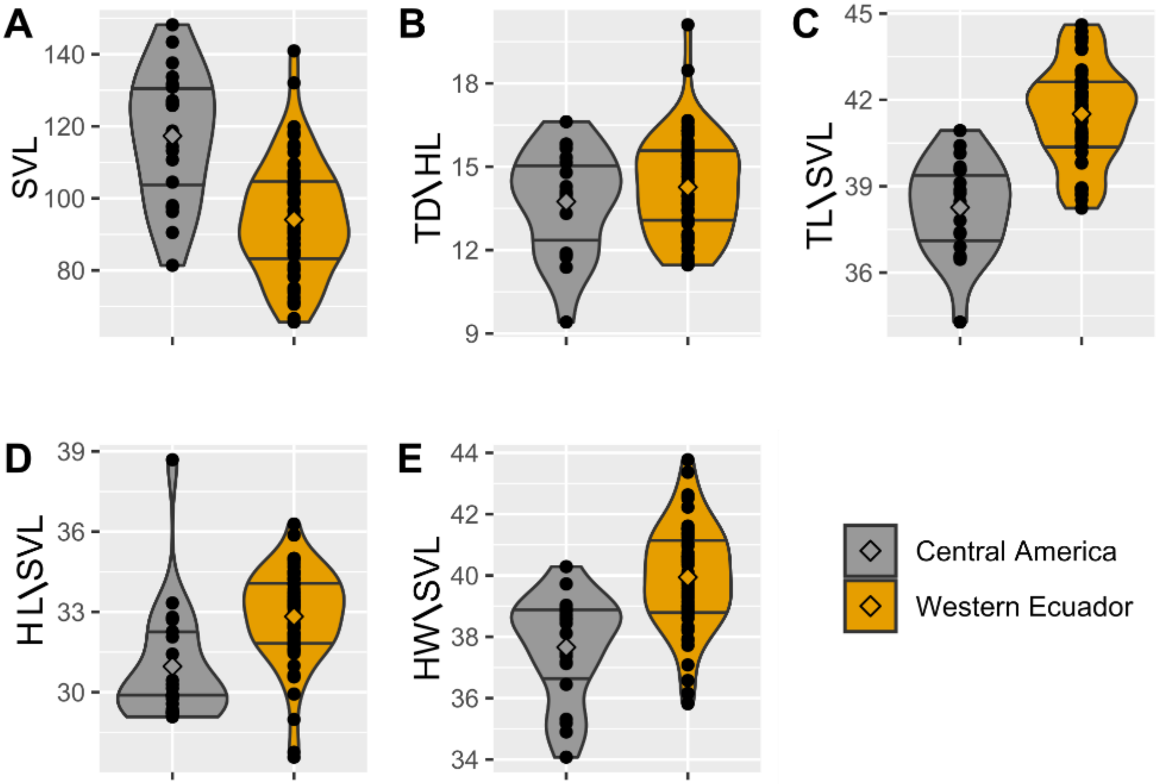

Figure 4.9. Plot of the first two canonical axes (I, II) from Canonical Variates Analysis (CVA) based on 13 continuously varying lineal morphological characters from 106 toads of three species from *Rhinella marina* species group (see methods). Individuals from western Ecuador correspond to *R. bellus* sp. nov., individuals from eastern Ecuador correspond to *R. marina*, and individuals from Central America correspond to *R. horribilis*.

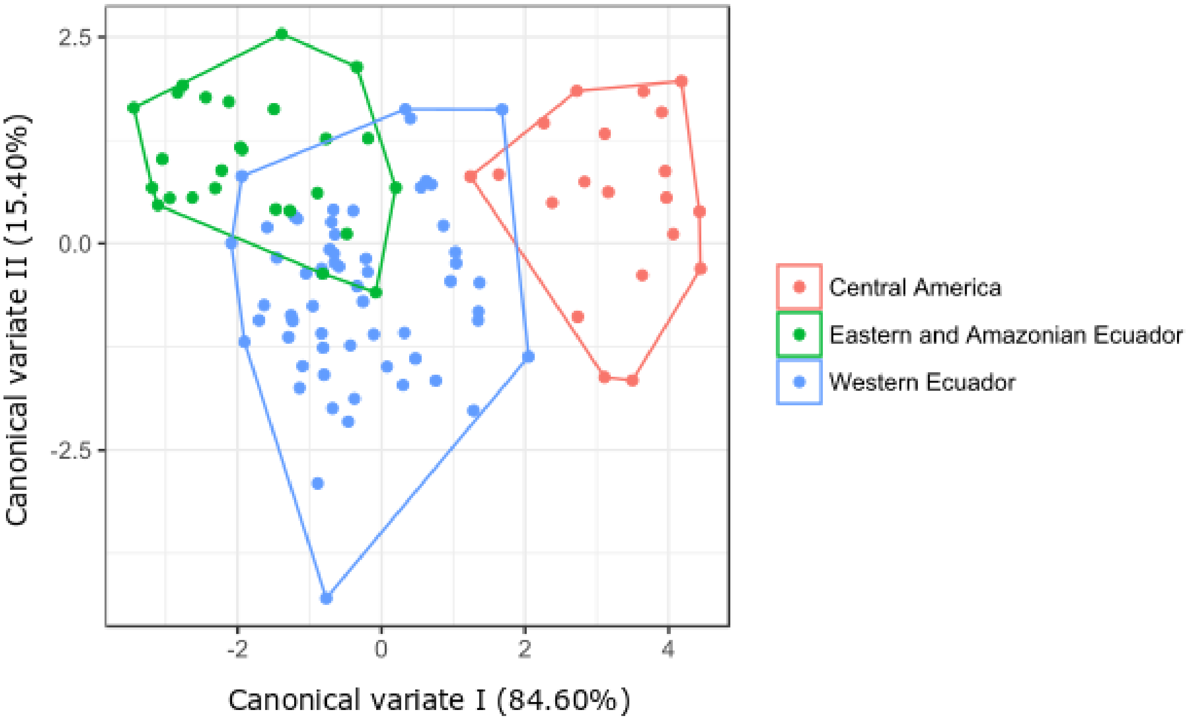

Figure 4.10. Morphological differences in skull shape among western Ecuadorian (*Rhinella bellus* sp. nov.), eastern Ecuadorian (R. *marina*), and Central American (*R. horribilis*) populations of *R. marina* species group. The plot of the first two canonical axes of Canonical Variates Analysis (CVA) based on shape variables from 84 toads (see methods in the main text), and changes with respect to the average on the deformation grids for the extreme points along each canonical variate axis are shown. Grid differences among populations have been exaggerated five-fold to make them more visible.

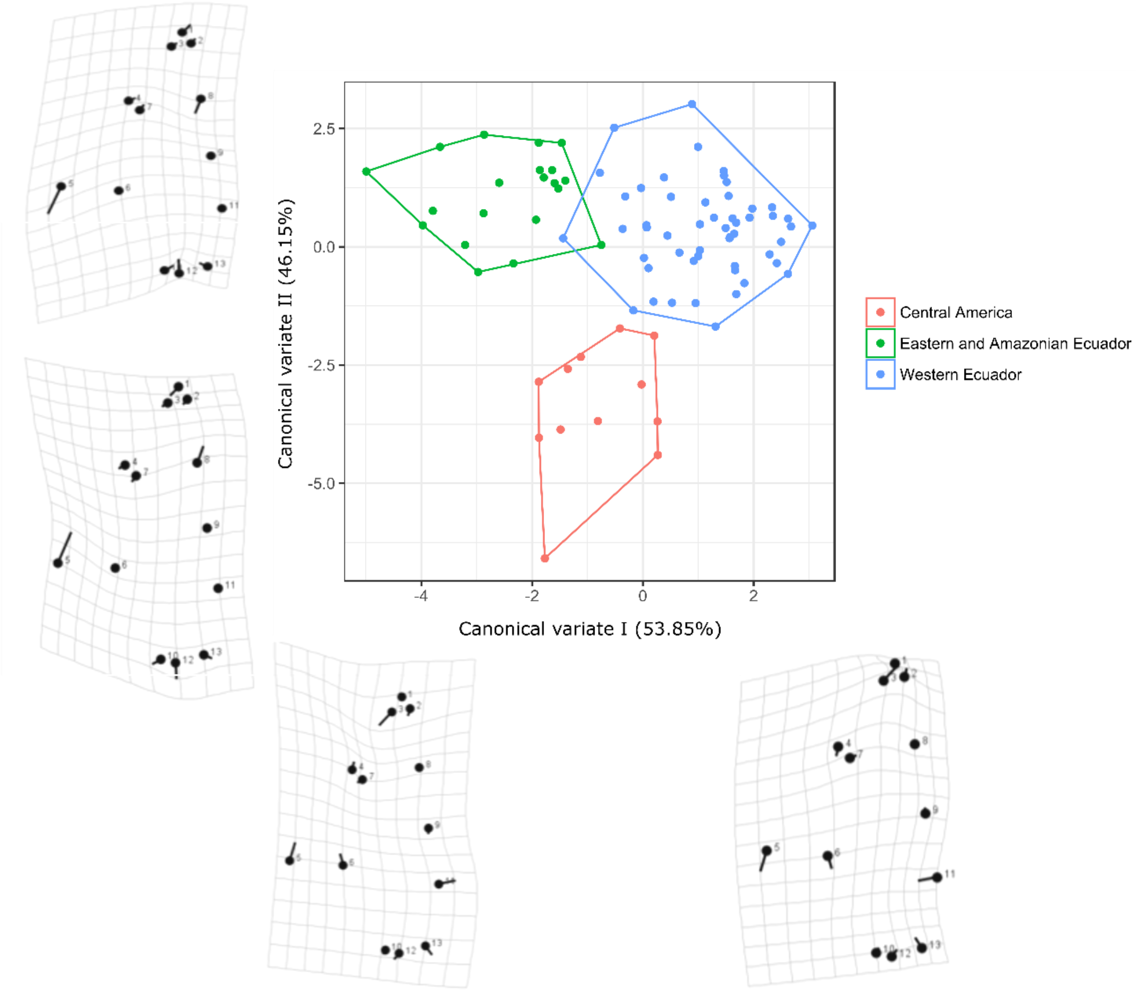

Figure 4.11. Principal components (PC's) from a PCA based on 19 climatic variables from 98 collection localities of specimens used for the phylogenetic analysis. Individuals are classified by geographic region, with 90% ellipse per group. For eigenvectors and eigenvalues see Table 6, Individuals from western Ecuador correspond to *Rhinella bellus* sp. nov., individuals from eastern Ecuador correspond to *R. marina*, and individuals from Central America correspond to *R. horribilis*.

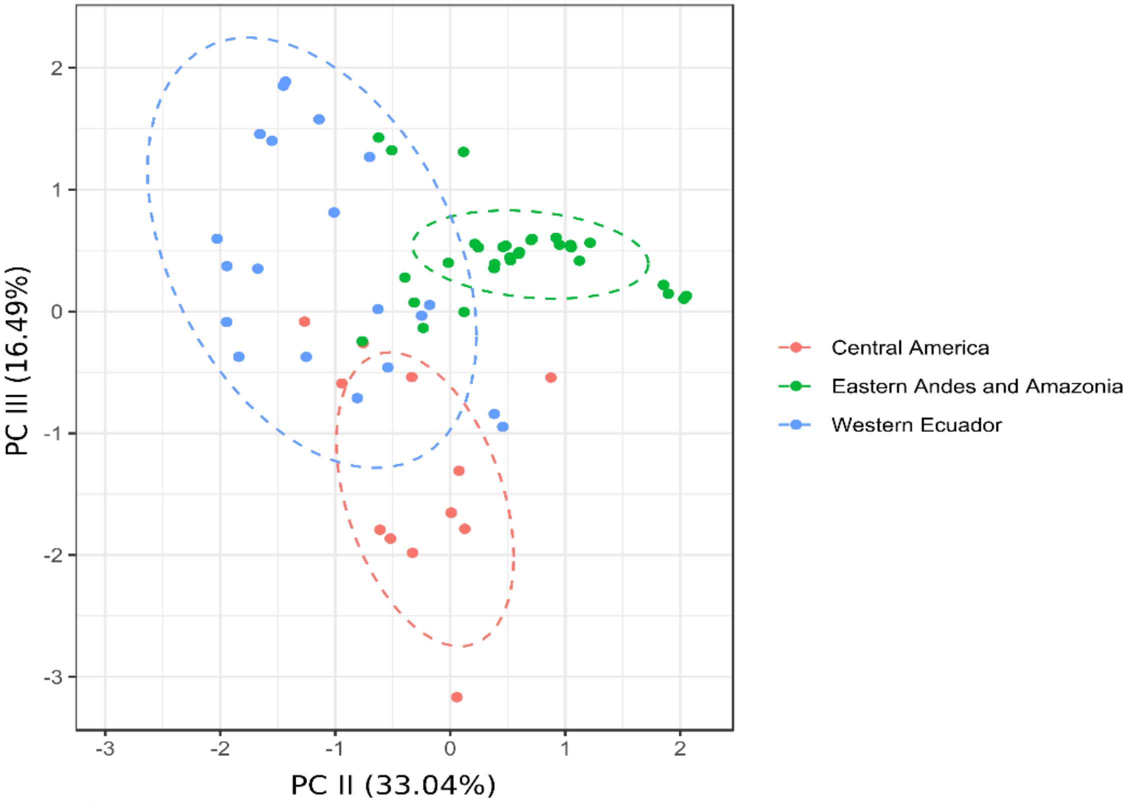

Figure 4.12. Dorsal, ventral and lateral views of the holotype of *Rhinella bellus* sp. nov. (QCAZ 23305, adult male).

Figure 4.13. Adult preserved specimens of *Rhinella bellus* sp. nov. showing variation in dorsal and ventral coloration. From left to right, first row: QCAZ 12039, 17965, 23324 (males); second row: QCAZ 23486, 24579, 39353 (males); third row: QCAZ 41327, 47444, 47445 (males), 50698 (female). See Table S1 for locality data. All specimens are shown at the same scale.

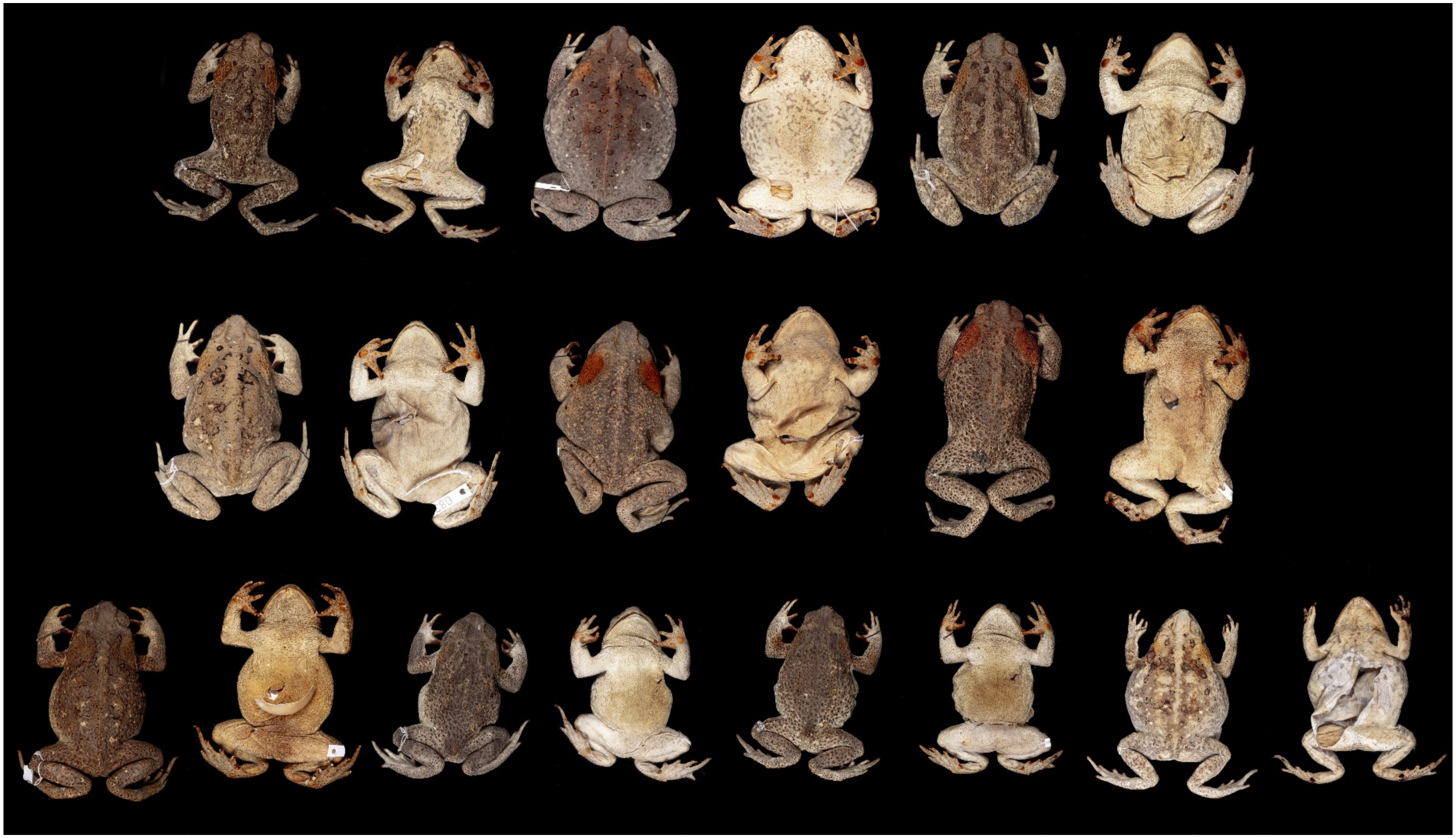

Figure 4.14. Juveniles preserved specimens of *Rhinella bellus* sp. nov. showing variation in dorsal and ventral coloration. From left to right, first row: QCAZ 13893, 28528, 35433; second row: QCAZ 40424, 45989, 49447, third row: QCAZ 50701, 50702. See Table S1 for locality data. All specimens are shown at the same scale.

General Discussion & Conclusions

The ongoing amphibian declines, especially in the Neotropics, represent perhaps the biggest biodiversity catastrophe. There are two reasons for this: the high proportion of known amphibian species at risk of extinction (nearly half), and the high estimated number of species still unknown (Mora et al., 2011) despite the current elevated rates of discovery of new species. More than 20% of the ca. 8,000 amphibian species known today have been described during the last ten years. Therefore, the real magnitude of the erosion of amphibian diversity most likely remains significantly underestimated, highlighting the critical need for integrative strategies to better understand this conservation crisis. In my thesis, I have used an integrative approach to assess past, present and future changes in the composition and structure of Neotropical amphibian communities in the Anthropocene. My research combines modelling and empirical data to quantify the increasing erosion of amphibian diversity at multiple spatial scales in response to human activities. I explicitly consider functional and phylogenetic attributes of species to evaluate the relative intensity and direction of anthropogenic-related changes across different facets of biodiversity. Finally, I discuss the potential ecosystem consequences of these changes, and contribute to the unveiling of cryptic amphibian diversity of the Neotropics.

In chapter one, I provide the first projection of the effect of future climate change on the spatial composition of anuran assemblages (i.e., beta diversity) across the entire Neotropical region. I used species distribution modelling and climate change scenarios by end of the 21st century to show that the majority of anuran highland assemblages will experience biotic homogenization with projected climate change. Several high-profile studies have previously suggested climate change as a major driver of future extinctions (e.g. Thomas et al., 2004;

Urban, 2015), but much less attention had been given to community restructuring. In this chapter, I suggest that shifts in beta diversity at continental scale may be as ecologically significant as predicted declines in alpha diversity. However, biodiversity changes are occurring at multiple spatial scales in response to climate warming, habitat loss and other wildlife pressures (Whittaker, 1960; MacArthur, 1965; Wagner et al. 2000), and it is unclear how the projected future disassembly and reassembly of amphibian communities at continental scales may reflect the reorganization and decline of species at smaller scales.

In chapter two, I model at the community-level, potential functional consequences of the very likely extinction scenario of current critically endangered species (following the conservation categories of the International Union for Conservation of Nature – IUCN). I show that highly threatened amphibian species (that are typically rare species) are significantly more functionally distinct than non-threatened species within communities. Furthermore, their extinction would drive increasing functional homogenization of anuran assemblages in the Ecuadorian Andes. This increase in functional homogenization could have more far-reaching consequences for ecosystem functioning than simple taxonomic homogenization. My results support the increasing evidence of the importance of rare species to ecosystem function across habitats and taxonomic groups (Mouillet, et al., 2013). Many studies have also highlighted the importance of considering different components of biodiversity when evaluating the responses of biological communities to global change drivers, with observations suggesting a decoupling of trends in changes in taxonomic, phylogenetic and functional diversity (e.g. Li et al., 2020). To date, the vast majority of research on amphibians has focused on taxonomic diversity as unit of biodiversity change and loss, and may therefore have underestimated impacts of global change on amphibian communities. While there has been concern that we may be entering a new era defined by an increasingly homogeneous biotic environment—the Homogocene—empirical data from long-term studies in amphibians remain sparse.

To help fill the gaps in amphibian decline research, in chapter three I empirically assess shifts in community composition on the different facets of amphibian diversity over the past 50 years in the Ecuadorian Andes. Using Bayesian modelling and long-term sampling data, I also explore the relative contribution of climate change and habitat loss as drivers of observed changes within seven amphibian communities. My findings, showing that amphibian extirpations are ongoing, and catastrophic in some locations, are consistent with recent evidence from long-term monitoring efforts on amphibian diversity in temperate ecosystems (see Grant et al., 2020 for a synthesis). In my study of amphibian communities in the Andes, half of species were lost during the time span of the study. I also show that, within Neotropical montane communities, the observed species extirpations may be close to the worst-case scenario, with several of the most phylogenetically and functionally distinct species become locally extinct over the duration of the study. These disproportionate losses in phylogenetic and functional diversity appear to have been exacerbated by contemporary climate warming, and could have consequential impacts on ecosystems. Together, these findings suggest that human-caused declines in amphibian diversity are likely greater than previously thought, and highlight the need to consider the multiple facets of biodiversity, which are typically overlooked in empirical and long-term amphibian studies (but see Smith et al., 2009; Nowakowski et al., 2018; Oliveira et al., 2020).

An additional challenge to estimating the true magnitude of biodiversity change and loss in the Anthropocene is the poor understanding of species diversity (Mora et al., 2011). For instance, there is likely high unrecognized cryptic species (i.e., morphologically similar species) diversity, especially in the Neotropics. A significant number of cryptic Neotropical anurans have been documented and described in recent years (Funk et al., 2012; Ortega-Andrade et al., 2015; Páez and Ron, 2019; Jaramillo et al., 2020), suggesting that diversity in this region remains strongly underestimated. Funk et al. (2012) reported exceptionally high levels of undescribed cryptic diversity within two Amazonian clades of anurans, with increases in species richness by more than 300%. However, efforts to discover and describe new species in biodiversity-rich regions are still few. In the final chapter of my thesis, I use an integrative analysis to help uncover cryptic diversity within the Neotropical cane toads of the *Rhinella marina* species group, and I describe a new species from west of the Ecuadorian Andes. The discovery of this new species, which belongs to a group of large, conspicuous and supposedly well-known toads, reveals just how much diversity there is still to discover in Neotropical regions. Importantly, since effective conservation of threatened species relies ultimately on accurate species classification, the observed decline of taxonomists and systematic biologists in recent decades (Mertl, 2002) could be devastating for conservation efforts. Our presently incomplete knowledge of biological diversity, and the rapid rates of biodiversity decline, indicates an urgent need for universities and research institutions to adopt new policies and strategies to recruit young scientists into the field of systematics and taxonomy.

To accurately predict how communities and ecosystems may cope with global change and understand the underlying human-related drivers of change, the integration of empirical and modeling approaches is necessary. This is especially critical given rapid rates of global change and the complexities of combined global change drivers. In my thesis, through the combination of modelling and empirical approaches across different spatial scales and time periods, I reveal the fingerprint of anthropogenic global change on Neotropical amphibian biodiversity. My main conclusions are the following:

1) The predicted climate change-related shifts in assemblage structure at a continental scale driven by local extinctions of specialist species in the northern Andes (Chapter I), are well reflected at a local scale in the observed temporal changes in the composition of Ecuadorian amphibian communities, which are dominated by local species extinctions linked to contemporary climate warming, (Chapter III).
2) The modelled increasing functional homogenization of assemblages at a regional scale, though extinction of endangered frogs in the Ecuadorian Andes (Chapter II), is concordant with the observed functional homogenization of communities linked with declines in taxonomic diversity at local scale (Chapter III).
3) Climate change emerges as an important driver of species extirpations and biotic homogenization of communities in Neotropical amphibians (Chapters I and III).
4) Amphibian diversity is more than just number of species, it is also the range of species' ecological roles in a community and the amount of unique evolutionary history they represent on the tree of life. These different facets of biodiversity need to be considered to ensure the effectiveness of conservation actions (Chapter II, III).
5) There is likely an appreciable underestimation of true amphibian diversity in the Neotropics that down-biases our current estimates of biodiversity loss (Chapter IV).

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APPENDIX

Supplementary Material Chapter 1

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Appendix A6 Maps of projected changes in β-diversity throughout the Neotropical Region by 2070 under alternative global climate models

Appendix A7 Percentage of species' range change by 2070 year due to climate change

Appendix A8 Results of generalized additive models (GAMs) explaining changes in β-diversity due to climate change

Appendix A9 Plots of the relationships between change in β-diversity and two predictors in the Mesoamerican highlands: change in species richness and change in the average level of ecological generalism

Appendix A10 Plots of the relationships between change in β-diversity and two predictors in the Pacific lowlands of South America: change in species richness and change in the average level of ecological generalism

Appendix A11 Maps of the predictor coefficients from univariate geographically weighted regressions

Appendix A12 Results of the multiple linear regression evaluating drivers of change in β-diversity under climate change

Appendix A13 Map of the projected changes in β-diversity throughout the Neotropical Region without species in the "data deficient" (DD) category of the IUCN Red List

Appendix A14 Maps of Projected changes in species richness, average level of ecological generalism and phylogenetic diversity by 2070 throughout the Neotropical Region

Appendix A15 R code to model species distributions

Appendix A1

Table A1.1. List of the 2669 species whose digital range maps were obtained to explore changes in spatial patterns of anuran β-diversity across the Neotropical region due to projected climate change. The IUCN extinction risk categories are as follows: Critically Endangered (CR), Endangered (EN), Vulnerable (VU), Near Threatened (NT), Least Concern (LC), and Data Deficient (DD).

SPECIES	IUCN	SPECIES	IUCN	SPECIES	IUCN
Adelastes hylonomos	DD	*Eleutherodactylus rivularis*	CR	*Plectrohyla celata*	CR
Adelophryne adiastola	LC	*Eleutherodactylus ronaldi*	VU	*Plectrohyla cembra*	CR
Adelophryne baturitensis	VU	*Eleutherodactylus rubrimaculatus*	VU	*Plectrohyla charadricola*	EN
Adelophryne gutturosa	LC	*Eleutherodactylus rufifemoralis*	CR	*Plectrohyla chryses*	CR
Adelophryne maranguapensis	EN	*Eleutherodactylus ruthae*	EN	*Plectrohyla chrysopleura*	CR
Adelophryne pachydactyla	DD	*Eleutherodactylus saxatilis*	EN	*Plectrohyla crassa*	CR
Adelophryne patamona	DD	*Eleutherodactylus schmidti*	CR	*Plectrohyla cyanomma*	CR
Adelphobates castaneoticus	LC	*Eleutherodactylus sciagraphus*	CR	*Plectrohyla cyclada*	EN
Adelphobates galactonotus	LC	*Eleutherodactylus semipalmatus*	CR	*Plectrohyla dasypus*	CR
Adelphobates quinquevittatus	LC	*Eleutherodactylus sisyphodemus*	CR	*Plectrohyla ephemera*	CR
Adenomera ajurauna	DD	*Eleutherodactylus sommeri*	EN	*Plectrohyla exquisita*	CR
Adenomera andreae	LC	*Eleutherodactylus symingtoni*	CR	*Plectrohyla glandulosa*	EN
Adenomera araucaria	LC	*Eleutherodactylus syristes*	EN	*Plectrohyla guatemalensis*	CR
Adenomera bokermanni	LC	*Eleutherodactylus teretistes*	DD	*Plectrohyla hartwegi*	CR
Adenomera coca	DD	*Eleutherodactylus tetajulia*	CR	*Plectrohyla hazelae*	CR
Adenomera diptyx	LC	*Eleutherodactylus thomasi*	EN	*Plectrohyla ixil*	CR
Adenomera heyeri	LC	*Eleutherodactylus thorectes*	CR	*Plectrohyla labedactyla*	DD
Adenomera hylaedactyla	LC	*Eleutherodactylus toa*	EN	*Plectrohyla lacertosa*	EN
Adenomera lutzi	DD	*Eleutherodactylus tonyi*	CR	*Plectrohyla matudai*	VU
Adenomera marmorata	LC	*Eleutherodactylus turquinensis*	CR	*Plectrohyla miahuatlanensis*	DD
Adenomera martinezi	LC	*Eleutherodactylus varians*	VU	*Plectrohyla mykter*	EN
Adenomera nana	LC	*Eleutherodactylus varleyi*	LC	*Plectrohyla pachyderma*	CR
Adenomera thomei	LC	*Eleutherodactylus ventrilineatus*	CR	*Plectrohyla pentheter*	EN
Agalychnis annae	EN	*Eleutherodactylus verrucipes*	VU	*Plectrohyla pokomchi*	CR
Agalychnis aspera	LC	*Eleutherodactylus verruculatus*	DD	*Plectrohyla psiloderma*	EN
Agalychnis buckleyi	LC	*Eleutherodactylus weinlandi*	LC	*Plectrohyla pycnochila*	CR
Agalychnis callidryas	LC	*Eleutherodactylus wetmorei*	VU	*Plectrohyla quecchi*	CR
Agalychnis dacnicolor	LC	*Eleutherodactylus wightmanae*	EN	*Plectrohyla robertsorum*	EN
Agalychnis danieli	DD	*Eleutherodactylus zeus*	EN	*Plectrohyla sabrina*	CR
Agalychnis granulosa	LC	*Eleutherodactylus zugi*	EN	*Plectrohyla sagorum*	EN
Agalychnis hulli	LC	*Engystomops coloradorum*	DD	*Plectrohyla tecunumani*	CR
Agalychnis lemur	CR	*Engystomops freibergi*	LC	*Plectrohyla teuchestes*	CR
Agalychnis medinae	DD	*Engystomops guayaco*	DD	*Plectrohyla thorectes*	CR
Agalychnis moreletii	CR	*Engystomops montubio*	LC	*Pleurodema bibroni*	NT
Agalychnis psilopygion	DD	*Engystomops petersi*	LC	*Pleurodema borellii*	LC
Agalychnis saltator	LC	*Engystomops pustulatus*	LC	*Pleurodema brachyops*	LC
Agalychnis spurrelli	LC	*Engystomops pustulosus*	LC	*Pleurodema bufoninum*	LC
Allobates alessandroi	DD	*Engystomops randi*	LC	*Pleurodema cinereum*	LC
Allobates algorei	LC	*Epipedobates anthonyi*	NT	*Pleurodema diplolister*	LC
Allobates bromelicola	DD	*Epipedobates boulengeri*	LC	*Pleurodema guayapae*	LC
Allobates brunneus	LC	*Epipedobates machalilla*	NT	*Pleurodema kriegi*	NT

Allobates caeruleodactylus	DD
Allobates cepedai	DD
Allobates conspicuus	DD
Allobates crombiei	DD
Allobates femoralis	LC
Allobates fratisenescus	DD
Allobates fuscellus	DD
Allobates gasconi	DD
Allobates goianus	DD
Allobates granti	LC
Allobates humilis	VU
Allobates insperatus	LC
Allobates juanii	CR
Allobates kingsburyi	EN
Allobates mandelorum	EN
Allobates marchesianus	LC
Allobates masniger	DD
Allobates mcdiarmidi	NT
Allobates melanolaemus	DD
Allobates myersi	LC
Allobates nidicola	DD
Allobates niputidea	LC
Allobates olfersioides	VU
Allobates ornatus	DD
Allobates paleovarzensis	NT
Allobates picachos	DD
Allobates pittieri	LC
Allobates ranoides	EN
Allobates sanmartini	DD
Allobates subfolionidificans	VU
Allobates sumtuosus	DD
Allobates talamancae	LC
Allobates trilineatus	LC
Allobates undulatus	DD
Allobates vanzolinius	DD
Allobates wayuu	VU
Allobates zaparo	LC
Allophryne ruthveni	LC
Alsodes australis	DD
Alsodes barrioi	VU
Alsodes gargola	LC
Alsodes hugoi	DD
Alsodes igneus	DD
Alsodes kaweshkari	DD
Alsodes montanus	CR
Alsodes nodosus	NT
Alsodes pehuenche	CR
Alsodes tumultuosus	CR
Alsodes valdiviensis	DD
Epipedobates narinensis	DD
Epipedobates tricolor	EN
Espadarana andina	LC
Espadarana callistomma	DD
Espadarana durrellorum	VU
Euparkerella brasiliensis	LC
Euparkerella cochranae	LC
Euparkerella robusta	VU
Eupsophus calcaratus	LC
Eupsophus contulmoensis	EN
Eupsophus emiliopugini	LC
Eupsophus migueli	EN
Eupsophus nahuelbutensis	EN
Eupsophus roseus	NT
Eupsophus septentrionalis	DD
Eupsophus vertebralis	NT
Excidobates captivus	LC
Excidobates mysteriosus	EN
Exerodonta abdivita	DD
Exerodonta bivocata	DD
Exerodonta catracha	EN
Exerodonta chimalapa	EN
Exerodonta juanitae	VU
Exerodonta melanomma	VU
Exerodonta perkinsi	CR
Exerodonta pinorum	VU
Exerodonta smaragdina	LC
Exerodonta sumichrasti	LC
Exerodonta xera	VU
Flectonotus fissilis	LC
Flectonotus fitzgeraldi	EN
Flectonotus pygmaeus	LC
Fritziana goeldii	LC
Fritziana ohausi	LC
Frostius erythrophthalmus	DD
Frostius pernambucensis	LC
Gastrophryne carolinensis	LC
Gastrophryne elegans	LC
Gastrophryne olivacea	LC
Gastrotheca abdita	DD
Gastrotheca aguaruna	NT
Gastrotheca albolineata	LC
Gastrotheca andaquiensis	NT
Gastrotheca angustifrons	VU
Gastrotheca antomia	VU
Gastrotheca antoniiochoai	DD
Gastrotheca aratia	LC
Gastrotheca argenteovirens	LC
Gastrotheca atympana	VU
Pleurodema marmoratum	LC
Pleurodema nebulosum	LC
Pleurodema somuncurense	CR
Pleurodema thaul	LC
Pleurodema tucumanum	LC
Pristimantis aaptus	LC
Pristimantis acatallelus	LC
Pristimantis acerus	EN
Pristimantis achatinus	LC
Pristimantis actinolaimus	EN
Pristimantis actites	VU
Pristimantis acuminatus	LC
Pristimantis acutirostris	EN
Pristimantis adiastolus	DD
Pristimantis aemulatus	DD
Pristimantis affinis	VU
Pristimantis alalocophus	NT
Pristimantis albericoi	CR
Pristimantis albertus	DD
Pristimantis altae	NT
Pristimantis altamazonicus	LC
Pristimantis altamnis	LC
Pristimantis amydrotus	DD
Pristimantis anemerus	DD
Pristimantis angustilineatus	EN
Pristimantis aniptopalmatus	DD
Pristimantis anolirex	NT
Pristimantis anotis	DD
Pristimantis apiculatus	DD
Pristimantis appendiculatus	LC
Pristimantis aquilonaris	LC
Pristimantis ardalonychus	DD
Pristimantis atrabracus	DD
Pristimantis atratus	EN
Pristimantis aurantiguttatus	DD
Pristimantis aureolineatus	LC
Pristimantis aureoventris	EN
Pristimantis avicuporum	DD
Pristimantis avius	DD
Pristimantis bacchus	EN
Pristimantis baiotis	DD
Pristimantis balionotus	EN
Pristimantis bambu	DD
Pristimantis baryecuus	EN
Pristimantis batrachites	DD
Pristimantis bearsei	DD
Pristimantis bellator	LC
Pristimantis bellona	EN
Pristimantis bernali	CR

Alsodes verrucosus	DD
Alsodes vittatus	DD
Amazophrynella bokermanni	LC
Amazophrynella minuta	LC
Ameerega andina	DD
Ameerega bassleri	NT
Ameerega berohoka	LC
Ameerega bilinguis	LC
Ameerega boehmei	LC
Ameerega boliviana	LC
Ameerega braccata	LC
Ameerega cainarachi	VU
Ameerega erythromos	DD
Ameerega flavopicta	LC
Ameerega hahneli	LC
Ameerega ingeri	CR
Ameerega macero	LC
Ameerega parvula	LC
Ameerega petersi	LC
Ameerega picta	LC
Ameerega planipaleae	CR
Ameerega pongoensis	VU
Ameerega pulchripecta	DD
Ameerega rubriventris	DD
Ameerega silverstonei	EN
Ameerega simulans	LC
Ameerega smaragdina	DD
Ameerega trivittata	LC
Ameerega yungicola	LC
Anaxyrus cognatus	LC
Anaxyrus compactilis	LC
Anaxyrus debilis	LC
Anaxyrus kelloggi	LC
Anaxyrus mexicanus	NT
Anaxyrus punctatus	LC
Anaxyrus speciosus	LC
Anaxyrus woodhousii	LC
Andinobates altobueyensis	VU
Andinobates bombetes	EN
Andinobates claudiae	DD
Andinobates daleswansoni	VU
Andinobates dorisswansonae	VU
Andinobates fulguritus	LC
Andinobates minutus	LC
Andinobates opisthomelas	VU
Andinobates tolimensis	VU
Andinobates viridis	VU
Andinobates virolinensis	EN
Andinophryne atelopoides	DD
Gastrotheca aureomaculata	NT
Gastrotheca bufona	EN
Gastrotheca carinaceps	DD
Gastrotheca christiani	EN
Gastrotheca chrysosticta	VU
Gastrotheca cornuta	EN
Gastrotheca dendronastes	VU
Gastrotheca dunni	LC
Gastrotheca ernestoi	DD
Gastrotheca espeletia	EN
Gastrotheca excubitor	VU
Gastrotheca fissipes	LC
Gastrotheca flamma	DD
Gastrotheca fulvorufa	DD
Gastrotheca galeata	DD
Gastrotheca gracilis	VU
Gastrotheca griswoldi	LC
Gastrotheca guentheri	VU
Gastrotheca helenae	DD
Gastrotheca lateonota	DD
Gastrotheca lauzuricae	CR
Gastrotheca litonedis	EN
Gastrotheca longipes	LC
Gastrotheca marsupiata	LC
Gastrotheca microdiscus	LC
Gastrotheca monticola	LC
Gastrotheca nicefori	LC
Gastrotheca ochoai	DD
Gastrotheca orophylax	EN
Gastrotheca ossilaginis	DD
Gastrotheca ovifera	EN
Gastrotheca pacchamama	DD
Gastrotheca peruana	LC
Gastrotheca piperata	LC
Gastrotheca plumbea	VU
Gastrotheca pseustes	EN
Gastrotheca psychrophila	EN
Gastrotheca rebeccae	DD
Gastrotheca riobambae	EN
Gastrotheca ruizi	EN
Gastrotheca splendens	EN
Gastrotheca stictopleura	EN
Gastrotheca testudinea	LC
Gastrotheca trachyceps	EN
Gastrotheca walkeri	DD
Gastrotheca weinlandii	DD
Gastrotheca williamsoni	DD
Gastrotheca zeugocystis	CR
Geobatrachus walkeri	EN
Pristimantis bicolor	VU
Pristimantis bicumulus	VU
Pristimantis boconoensis	VU
Pristimantis bogotensis	LC
Pristimantis boulengeri	LC
Pristimantis brevifrons	LC
Pristimantis briceni	VU
Pristimantis bromeliaceus	VU
Pristimantis buccinator	LC
Pristimantis buckleyi	LC
Pristimantis cabrerai	EN
Pristimantis cacao	EN
Pristimantis caeruleonotus	DD
Pristimantis cajamarcensis	LC
Pristimantis calcaratus	EN
Pristimantis calcarulatus	VU
Pristimantis cantitans	DD
Pristimantis capitonis	EN
Pristimantis caprifer	LC
Pristimantis carlossanchezi	DD
Pristimantis carmelitae	DD
Pristimantis carranguerorum	DD
Pristimantis carvalhoi	LC
Pristimantis caryophyllaceus	NT
Pristimantis celator	NT
Pristimantis cerasinus	LC
Pristimantis ceuthospilus	VU
Pristimantis chalceus	LC
Pristimantis chiastonotus	LC
Pristimantis chimu	DD
Pristimantis chloronotus	LC
Pristimantis chrysops	EN
Pristimantis citriogaster	DD
Pristimantis colodactylus	VU
Pristimantis colomai	EN
Pristimantis colonensis	DD
Pristimantis colostichos	VU
Pristimantis condor	VU
Pristimantis conspicillatus	LC
Pristimantis cordovae	VU
Pristimantis corniger	DD
Pristimantis coronatus	DD
Pristimantis corrugatus	LC
Pristimantis cosnipatae	EN
Pristimantis cremnobates	EN
Pristimantis crenunguis	EN
Pristimantis cristinae	DD
Pristimantis croceoinguinis	LC
Pristimantis crucifer	VU

Andinophryne colomai	CR
Andinophryne olallai	DD
Anomaloglossus atopoglossus	DD
Anomaloglossus ayarzaguenai	DD
Anomaloglossus baeobatrachus	DD
Anomaloglossus beebei	VU
Anomaloglossus breweri	VU
Anomaloglossus degranvillei	LC
Anomaloglossus guanayensis	DD
Anomaloglossus kaiei	LC
Anomaloglossus lacrimosus	DD
Anomaloglossus murisipanensis	VU
Anomaloglossus parkerae	DD
Anomaloglossus praderioi	DD
Anomaloglossus roraima	DD
Anomaloglossus rufulus	DD
Anomaloglossus shrevei	DD
Anomaloglossus stepheni	LC
Anomaloglossus tamacuarensis	DD
Anomaloglossus tepuyensis	DD
Anomaloglossus triunfo	DD
Anomaloglossus wothuja	DD
Anotheca spinosa	LC
Aparasphenodon bokermanni	DD
Aparasphenodon brunoi	LC
Aparasphenodon venezolanus	LC
Aplastodiscus albofrenatus	LC
Aplastodiscus albosignatus	LC
Aplastodiscus arildae	LC
Aplastodiscus callipygius	LC
Aplastodiscus cavicola	NT
Aplastodiscus cochranae	LC
Aplastodiscus ehrhardti	LC
Aplastodiscus eugenioi	NT
Aplastodiscus flumineus	DD
Aplastodiscus ibirapitanga	LC
Aplastodiscus leucopygius	LC
Aplastodiscus musicus	DD
Aplastodiscus perviridis	LC
Aplastodiscus sibilatus	DD
Aplastodiscus weygoldti	NT
Arcovomer passarellii	LC
Argenteohyla siemersi	EN
Aromobates alboguttatus	EN
Aromobates capurinensis	DD
Aromobates duranti	EN
Aromobates haydeeae	EN
Aromobates leopardalis	CR
Haddadus aramunha	DD
Haddadus binotatus	LC
Hamptophryne alios	DD
Hamptophryne boliviana	LC
Hemiphractus bubalus	NT
Hemiphractus fasciatus	NT
Hemiphractus helioi	LC
Hemiphractus johnsoni	EN
Hemiphractus proboscideus	LC
Hemiphractus scutatus	LC
Holoaden bradei	CR
Holoaden luederwaldti	DD
Holoaden pholeter	DD
Hyalinobatrachium aureoguttatum	NT
Hyalinobatrachium chirripoi	LC
Hyalinobatrachium colymbiphyllum	LC
Hyalinobatrachium duranti	DD
Hyalinobatrachium esmeralda	EN
Hyalinobatrachium fleischmanni	LC
Hyalinobatrachium fragile	VU
Hyalinobatrachium guairarepanense	EN
Hyalinobatrachium iaspidiense	DD
Hyalinobatrachium ibama	VU
Hyalinobatrachium orientale	VU
Hyalinobatrachium pallidum	EN
Hyalinobatrachium pellucidum	NT
Hyalinobatrachium ruedai	LC
Hyalinobatrachium talamancae	LC
Hyalinobatrachium tatayoi	LC
Hyalinobatrachium taylori	LC
Hyalinobatrachium valerioi	LC
Hyalinobatrachium vireovittatum	DD
Hydrolaetare caparu	DD
Hydrolaetare dantasi	LC
Hydrolaetare schmidti	LC
Hyla arboricola	DD
Hyla arenicolor	LC
Hyla bocourti	CR
Hyla cinerea	LC
Hyla euphorbiacea	NT
Hyla eximia	LC
Hyla nicefori	CR
Hyla plicata	LC
Hyla squirella	LC
Hyla walkeri	VU
Hyla wrightorum	LC
Hylodes amnicola	DD
Hylodes asper	LC
Pristimantis cruciocularis	VU
Pristimantis cruentus	LC
Pristimantis cryophilius	EN
Pristimantis cryptomelas	EN
Pristimantis cuentasi	DD
Pristimantis culatensis	DD
Pristimantis cuneirostris	DD
Pristimantis curtipes	LC
Pristimantis danae	LC
Pristimantis degener	EN
Pristimantis deinops	EN
Pristimantis delicatus	DD
Pristimantis delius	DD
Pristimantis dendrobatoides	LC
Pristimantis devillei	EN
Pristimantis diadematus	LC
Pristimantis diaphonus	VU
Pristimantis diogenes	VU
Pristimantis dissimulatus	EN
Pristimantis divnae	LC
Pristimantis dorsopictus	EN
Pristimantis douglasi	VU
Pristimantis duellmani	VU
Pristimantis duende	DD
Pristimantis dundeei	DD
Pristimantis elegans	VU
Pristimantis epacrus	DD
Pristimantis eremitus	VU
Pristimantis eriphus	VU
Pristimantis erythropleura	LC
Pristimantis esmeraldas	DD
Pristimantis eugeniae	EN
Pristimantis euphronides	EN
Pristimantis eurydactylus	LC
Pristimantis exoristus	DD
Pristimantis factiosus	LC
Pristimantis fallax	VU
Pristimantis fasciatus	EN
Pristimantis fenestratus	LC
Pristimantis fetosus	EN
Pristimantis flabellidiscus	DD
Pristimantis flavobracatus	DD
Pristimantis floridus	VU
Pristimantis frater	VU
Pristimantis gaigei	LC
Pristimantis galdi	NT
Pristimantis ganonotus	DD
Pristimantis gentryi	EN

Aromobates mayorgai	EN
Aromobates meridensis	CR
Aromobates molinarii	EN
Aromobates nocturnus	CR
Aromobates orostoma	EN
Aromobates saltuensis	EN
Aromobates serranus	EN
Atelognathus ceii	DD
Atelognathus nitoi	VU
Atelognathus patagonicus	EN
Atelognathus praebasalticus	EN
Atelognathus reverberii	EN
Atelognathus salai	VU
Atelognathus solitarius	VU
Atelopus andinus	CR
Atelopus angelito	CR
Atelopus ardila	CR
Atelopus arsyecue	CR
Atelopus arthuri	CR
Atelopus balios	CR
Atelopus bomolochos	CR
Atelopus boulengeri	CR
Atelopus carauta	CR
Atelopus carbonerensis	CR
Atelopus carrikeri	CR
Atelopus certus	EN
Atelopus chiriquiensis	CR
Atelopus chocoensis	CR
Atelopus chrysocorallus	CR
Atelopus coynei	CR
Atelopus cruciger	CR
Atelopus dimorphus	EN
Atelopus ebenoides	CR
Atelopus elegans	CR
Atelopus epikeisthos	CR
Atelopus erythropus	CR
Atelopus eusebianus	CR
Atelopus eusebiodiazi	CR
Atelopus exiguus	CR
Atelopus famelicus	CR
Atelopus farci	CR
Atelopus flavescens	VU
Atelopus franciscus	VU
Atelopus galactogaster	CR
Atelopus glyphus	CR
Atelopus guanujo	CR
Atelopus guitarraensis	CR
Atelopus halihelos	CR
Atelopus ignescens	EX

Hylodes babax	DD
Hylodes cardosoi	LC
Hylodes charadranaetes	DD
Hylodes dactylocinus	DD
Hylodes glaber	DD
Hylodes heyeri	DD
Hylodes lateristrigatus	LC
Hylodes magalhaesi	DD
Hylodes meridionalis	LC
Hylodes mertensi	DD
Hylodes nasus	LC
Hylodes ornatus	LC
Hylodes otavioi	DD
Hylodes perplicatus	LC
Hylodes phyllodes	LC
Hylodes pipilans	DD
Hylodes regius	DD
Hylodes sazimai	DD
Hylodes uai	DD
Hylodes vanzolinii	DD
Hylorina sylvatica	LC
Hyloscirtus albopunctulatus	LC
Hyloscirtus alytolylax	NT
Hyloscirtus armatus	LC
Hyloscirtus bogotensis	NT
Hyloscirtus callipeza	NT
Hyloscirtus caucanus	DD
Hyloscirtus charazani	EN
Hyloscirtus chlorosteus	CR
Hyloscirtus colymba	NT
Hyloscirtus denticulentus	EN
Hyloscirtus jahni	NT
Hyloscirtus larinopygion	NT
Hyloscirtus lascinius	LC
Hyloscirtus lindae	VU
Hyloscirtus lynchi	EN
Hyloscirtus pacha	DD
Hyloscirtus palmeri	LC
Hyloscirtus pantostictus	EN
Hyloscirtus phyllognathus	LC
Hyloscirtus piceigularis	EN
Hyloscirtus platydactylus	VU
Hyloscirtus psarolaimus	EN
Hyloscirtus ptychodactylus	CR
Hyloscirtus sarampiona	DD
Hyloscirtus simmonsi	EN
Hyloscirtus staufferorum	EN
Hyloscirtus torrenticola	VU
Hyloxalus abditaurantius	LC

Pristimantis ginesi	EN
Pristimantis gladiator	EN
Pristimantis glandulosus	EN
Pristimantis gracilis	VU
Pristimantis grandiceps	DD
Pristimantis gutturalis	LC
Pristimantis hectus	DD
Pristimantis helvolus	EN
Pristimantis hernandezi	EN
Pristimantis huicundo	DD
Pristimantis hybotragus	VU
Pristimantis ignicolor	EN
Pristimantis illotus	NT
Pristimantis imitatrix	LC
Pristimantis incanus	EN
Pristimantis incertus	DD
Pristimantis incomptus	VU
Pristimantis infraguttatus	DD
Pristimantis inguinalis	LC
Pristimantis insignitus	EN
Pristimantis inusitatus	VU
Pristimantis ixalus	DD
Pristimantis jaimei	DD
Pristimantis jester	LC
Pristimantis johannesdei	EN
Pristimantis jorgevelosai	EN
Pristimantis juanchoi	NT
Pristimantis jubatus	NT
Pristimantis kareliae	NT
Pristimantis katoptroides	EN
Pristimantis kelephus	VU
Pristimantis kichwarum	LC
Pristimantis labiosus	LC
Pristimantis lacrimosus	LC
Pristimantis lancinii	EN
Pristimantis lanthanites	LC
Pristimantis lasalleorum	DD
Pristimantis lassoalcalai	NT
Pristimantis laticlavius	DD
Pristimantis latidiscus	LC
Pristimantis lemur	EN
Pristimantis lentiginosus	DD
Pristimantis leoni	LC
Pristimantis leptolophus	LC
Pristimantis leucopus	DD
Pristimantis librarius	DD
Pristimantis lichenoides	CR
Pristimantis lindae	DD
Pristimantis lirellus	DD

Atelopus laetissimus	EN
Atelopus limosus	EN
Atelopus longibrachius	EN
Atelopus longirostris	EX
Atelopus lozanoi	CR
Atelopus lynchi	CR
Atelopus mandingues	CR
Atelopus mindoensis	CR
Atelopus minutulus	CR
Atelopus monohernandezii	CR
Atelopus mucubajiensis	CR
Atelopus muisca	CR
Atelopus nahumae	EN
Atelopus nanay	CR
Atelopus nepiozomus	CR
Atelopus nicefori	CR
Atelopus oxapampae	EN
Atelopus oxyrhynchus	CR
Atelopus pachydermus	CR
Atelopus palmatus	DD
Atelopus pastuso	CR
Atelopus patazensis	CR
Atelopus pedimarmoratus	CR
Atelopus peruensis	CR
Atelopus petersi	CR
Atelopus petriruizi	CR
Atelopus pictiventris	CR
Atelopus pinangoi	CR
Atelopus planispina	CR
Atelopus podocarpus	CR
Atelopus pulcher	CR
Atelopus pyrodactylus	CR
Atelopus quimbaya	CR
Atelopus reticulatus	CR
Atelopus sanjosei	DD
Atelopus seminiferus	CR
Atelopus senex	CR
Atelopus sernai	CR
Atelopus simulatus	CR
Atelopus siranus	DD
Atelopus sonsonensis	CR
Atelopus sorianoi	CR
Atelopus spumarius	VU
Atelopus spurrelli	VU
Atelopus subornatus	CR
Atelopus tamaense	CR
Atelopus tricolor	VU
Atelopus varius	CR
Atelopus walkeri	CR
Hyloxalus aeruginosus	DD
Hyloxalus anthracinus	CR
Hyloxalus awa	VU
Hyloxalus azureiventris	EN
Hyloxalus betancuri	DD
Hyloxalus bocagei	LC
Hyloxalus borjai	DD
Hyloxalus breviquartus	DD
Hyloxalus cevallosi	EN
Hyloxalus chlorocraspedus	DD
Hyloxalus chocoensis	DD
Hyloxalus craspedoceps	DD
Hyloxalus delatorreae	CR
Hyloxalus edwardsi	CR
Hyloxalus elachyhistus	EN
Hyloxalus eleutherodactylus	DD
Hyloxalus exasperatus	DD
Hyloxalus excisus	DD
Hyloxalus faciopunctulatus	DD
Hyloxalus fallax	DD
Hyloxalus fascianigrus	NT
Hyloxalus fuliginosus	DD
Hyloxalus idiomelus	DD
Hyloxalus infraguttatus	NT
Hyloxalus insulatus	DD
Hyloxalus lehmanni	NT
Hyloxalus leucophaeus	DD
Hyloxalus littoralis	LC
Hyloxalus maculosus	DD
Hyloxalus maquipucuna	DD
Hyloxalus marmoreoventris	DD
Hyloxalus mittermeieri	DD
Hyloxalus mystax	DD
Hyloxalus nexipus	LC
Hyloxalus parcus	DD
Hyloxalus peruvianus	LC
Hyloxalus pinguis	DD
Hyloxalus pulchellus	VU
Hyloxalus pulcherrimus	DD
Hyloxalus ramosi	DD
Hyloxalus ruizi	CR
Hyloxalus saltuarius	DD
Hyloxalus sauli	LC
Hyloxalus shuar	NT
Hyloxalus sordidatus	DD
Hyloxalus spilotogaster	DD
Hyloxalus subpunctatus	LC
Hyloxalus sylvaticus	DD
Hyloxalus toachi	EN
Pristimantis lividus	EN
Pristimantis llojsintuta	LC
Pristimantis loustes	EN
Pristimantis lucasi	DD
Pristimantis luscombei	DD
Pristimantis luteolateralis	NT
Pristimantis lutitus	DD
Pristimantis lymani	LC
Pristimantis lynchi	DD
Pristimantis lythrodes	LC
Pristimantis maculosus	EN
Pristimantis malkini	LC
Pristimantis marahuaka	VU
Pristimantis marmoratus	LC
Pristimantis mars	EN
Pristimantis martiae	LC
Pristimantis medemi	LC
Pristimantis megalops	NT
Pristimantis melanogaster	EN
Pristimantis melanoproctus	DD
Pristimantis memorans	DD
Pristimantis mendax	LC
Pristimantis meridionalis	DD
Pristimantis merostictus	EN
Pristimantis metabates	DD
Pristimantis minutulus	DD
Pristimantis miyatai	NT
Pristimantis mnionaetes	EN
Pristimantis modipeplus	EN
Pristimantis molybrignus	NT
Pristimantis mondolfii	DD
Pristimantis moro	LC
Pristimantis muricatus	VU
Pristimantis muscosus	DD
Pristimantis museosus	EN
Pristimantis myersi	LC
Pristimantis myops	DD
Pristimantis nebulosus	DD
Pristimantis nephophilus	VU
Pristimantis nervicus	LC
Pristimantis nicefori	LC
Pristimantis nigrogriseus	VU
Pristimantis nyctophylax	VU
Pristimantis obmutescens	LC
Pristimantis ocellatus	DD
Pristimantis ockendeni	LC
Pristimantis ocreatus	EN
Pristimantis olivaceus	DD
Pristimantis orcesi	LC

Atelopus zeteki	CR
Atopophrynus syntomopus	CR
Barycholos pulcher	LC
Barycholos ternetzi	LC
Batrachyla antartandica	LC
Batrachyla leptopus	LC
Batrachyla nibaldoi	DD
Batrachyla taeniata	LC
Bokermannohyla ahenea	DD
Bokermannohyla alvarengai	LC
Bokermannohyla astartea	LC
Bokermannohyla caramaschii	LC
Bokermannohyla carvalhoi	LC
Bokermannohyla circumdata	LC
Bokermannohyla claresignata	DD
Bokermannohyla clepsydra	DD
Bokermannohyla diamantina	DD
Bokermannohyla gouveai	DD
Bokermannohyla hylax	LC
Bokermannohyla ibitipoca	DD
Bokermannohyla itapoty	LC
Bokermannohyla izecksohni	CR
Bokermannohyla langei	DD
Bokermannohyla luctuosa	LC
Bokermannohyla martinsi	LC
Bokermannohyla nanuzae	LC
Bokermannohyla oxente	LC
Bokermannohyla pseudopseudis	LC
Bokermannohyla ravida	DD
Bokermannohyla sagarana	NT
Bokermannohyla saxicola	LC
Bokermannohyla sazimai	DD
Bokermannohyla vulcaniae	VU
Brachycephalus alipioi	DD
Brachycephalus brunneus	DD
Brachycephalus didactylus	LC
Brachycephalus ephippium	LC
Brachycephalus ferruginus	DD
Brachycephalus hermogenesi	LC
Brachycephalus izecksohni	DD
Brachycephalus nodoterga	DD
Brachycephalus pernix	DD
Brachycephalus pombali	DD
Brachycephalus vertebralis	DD
Bromeliohyla bromeliacia	LC
Bromeliohyla dendroscarta	CR
Bryophryne bustamantei	EN
Bryophryne cophites	EN
Bryophryne gymnotis	DD
Hyloxalus utcubambensis	DD
Hyloxalus vergeli	VU
Hyloxalus vertebralis	CR
Hyloxalus whymperi	DD
Hypodactylus adercus	DD
Hypodactylus araiodactylus	DD
Hypodactylus babax	LC
Hypodactylus brunneus	EN
Hypodactylus dolops	VU
Hypodactylus elassodiscus	EN
Hypodactylus fallaciosus	DD
Hypodactylus latens	EN
Hypodactylus lucida	CR
Hypodactylus mantipus	LC
Hypodactylus nigrovittatus	LC
Hypodactylus peraccai	DD
Hypopachus barberi	VU
Hypopachus pictiventris	LC
Hypopachus ustus	LC
Hypopachus variolosus	LC
Hypsiboas albomarginatus	LC
Hypsiboas alboniger	NT
Hypsiboas albopunctatus	LC
Hypsiboas alemani	DD
Hypsiboas atlanticus	LC
Hypsiboas balzani	LC
Hypsiboas beckeri	DD
Hypsiboas bischoffi	LC
Hypsiboas boans	LC
Hypsiboas buriti	DD
Hypsiboas caingua	LC
Hypsiboas calcaratus	LC
Hypsiboas callipleura	LC
Hypsiboas cinerascens	LC
Hypsiboas cipoensis	NT
Hypsiboas cordobae	DD
Hypsiboas crepitans	LC
Hypsiboas curupi	LC
Hypsiboas cymbalum	CR
Hypsiboas dentei	LC
Hypsiboas ericae	DD
Hypsiboas exastis	DD
Hypsiboas faber	LC
Hypsiboas fasciatus	LC
Hypsiboas fuentei	DD
Hypsiboas geographicus	LC
Hypsiboas goianus	LC
Hypsiboas guentheri	LC
Hypsiboas heilprini	VU
Pristimantis orcus	LC
Pristimantis orestes	EN
Pristimantis ornatissimus	VU
Pristimantis ornatus	EN
Pristimantis orpacobates	VU
Pristimantis orphnolaimus	DD
Pristimantis ortizi	DD
Pristimantis padrecarlosi	DD
Pristimantis paisa	LC
Pristimantis palmeri	LC
Pristimantis paramerus	EN
Pristimantis pardalinus	CR
Pristimantis pardalis	NT
Pristimantis parectatus	EN
Pristimantis parvillus	LC
Pristimantis pastazensis	EN
Pristimantis pataikos	VU
Pristimantis paulodutrai	LC
Pristimantis paululus	LC
Pristimantis pecki	DD
Pristimantis pedimontanus	DD
Pristimantis penelopus	VU
Pristimantis peraticus	LC
Pristimantis percnopterus	NT
Pristimantis percultus	EN
Pristimantis permixtus	LC
Pristimantis peruvianus	LC
Pristimantis petersi	VU
Pristimantis petrobardus	DD
Pristimantis phalaroinguinis	DD
Pristimantis phalarus	VU
Pristimantis philipi	DD
Pristimantis phoxocephalus	LC
Pristimantis phragmipleuron	CR
Pristimantis piceus	LC
Pristimantis pinguis	DD
Pristimantis pirrensis	DD
Pristimantis platychilus	VU
Pristimantis platydactylus	LC
Pristimantis pleurostriatus	DD
Pristimantis polychrus	EN
Pristimantis prolatus	EN
Pristimantis prolixodiscus	LC
Pristimantis proserpens	EN
Pristimantis pruinatus	DD
Pristimantis pseudoacuminatus	LC
Pristimantis pteridophilus	EN
Pristimantis ptochus	DD
Pristimantis pugnax	VU

Bryophryne hanssaueri	LC
Bryophryne nubilosus	LC
Bryophryne zonalis	DD
Calyptocephalella gayi	VU
Celsiella revocata	VU
Celsiella vozmedianoi	DD
Centrolene acanthidiocephalum	DD
Centrolene altitudinale	DD
Centrolene antioquiense	NT
Centrolene azulae	EN
Centrolene bacatum	DD
Centrolene ballux	CR
Centrolene buckleyi	VU
Centrolene condor	DD
Centrolene daidaleum	VU
Centrolene geckoideum	VU
Centrolene gemmatum	CR
Centrolene guanacarum	DD
Centrolene heloderma	CR
Centrolene hesperium	VU
Centrolene huilense	DD
Centrolene hybrida	LC
Centrolene lemniscatum	DD
Centrolene lynchi	EN
Centrolene medemi	DD
Centrolene notostictum	LC
Centrolene peristictum	VU
Centrolene petrophilum	EN
Centrolene pipilatum	EN
Centrolene quindianum	VU
Centrolene robledoi	LC
Centrolene sanchezi	DD
Centrolene savagei	VU
Centrolene scirtetes	DD
Centrolene solitaria	DD
Centrolene venezuelense	LC
Ceratophrys aurita	LC
Ceratophrys calcarata	LC
Ceratophrys cornuta	LC
Ceratophrys cranwelli	LC
Ceratophrys joazeirensis	DD
Ceratophrys ornata	NT
Ceratophrys stolzmanni	VU
Ceratophrys testudo	DD
Ceuthomantis aracamuni	VU
Ceuthomantis cavernibardus	DD
Ceuthomantis duellmani	LC
Chacophrys pierottii	LC
Chaltenobatrachus grandisonae	DD
Hypsiboas hobbsi	LC
Hypsiboas hutchinsi	LC
Hypsiboas jimenezi	LC
Hypsiboas joaquini	LC
Hypsiboas lanciformis	LC
Hypsiboas latistriatus	DD
Hypsiboas lemai	LC
Hypsiboas leptolineatus	LC
Hypsiboas leucocheilus	DD
Hypsiboas liliae	LC
Hypsiboas lundii	LC
Hypsiboas marginatus	LC
Hypsiboas marianitae	LC
Hypsiboas melanopleura	DD
Hypsiboas microderma	LC
Hypsiboas multifasciatus	LC
Hypsiboas nympha	LC
Hypsiboas ornatissimus	LC
Hypsiboas palaestes	DD
Hypsiboas pardalis	LC
Hypsiboas pellucens	LC
Hypsiboas phaeopleura	DD
Hypsiboas picturatus	LC
Hypsiboas polytaenius	LC
Hypsiboas pombali	LC
Hypsiboas prasinus	LC
Hypsiboas pugnax	LC
Hypsiboas pulchellus	LC
Hypsiboas pulidoi	DD
Hypsiboas punctatus	LC
Hypsiboas raniceps	LC
Hypsiboas rhythmicus	DD
Hypsiboas riojanus	DD
Hypsiboas roraima	DD
Hypsiboas rosenbergi	LC
Hypsiboas rubracylus	LC
Hypsiboas rufitelus	LC
Hypsiboas secedens	DD
Hypsiboas semiguttatus	LC
Hypsiboas semilineatus	LC
Hypsiboas sibleszi	LC
Hypsiboas stellae	LC
Hypsiboas stenocephalus	DD
Hypsiboas tepuianus	LC
Hypsiboas varelae	DD
Hypsiboas wavrini	LC
Ikakogi tayrona	VU
Incilius alvarius	LC
Incilius aucoinae	LC
Pristimantis pulvinatus	LC
Pristimantis pycnodermis	EN
Pristimantis pyrrhomerus	EN
Pristimantis quantus	VU
Pristimantis quaquaversus	LC
Pristimantis quinquagesimus	VU
Pristimantis racemus	LC
Pristimantis ramagii	LC
Pristimantis reclusas	DD
Pristimantis renjiforum	EN
Pristimantis repens	VU
Pristimantis restrepoi	LC
Pristimantis reticulatus	DD
Pristimantis rhabdocnemus	DD
Pristimantis rhabdolaemus	LC
Pristimantis rhigophilus	DD
Pristimantis rhodoplichus	EN
Pristimantis rhodostichus	VU
Pristimantis ridens	LC
Pristimantis rivasi	EN
Pristimantis riveroi	DD
Pristimantis riveti	NT
Pristimantis rosadoi	VU
Pristimantis roseus	NT
Pristimantis rozei	DD
Pristimantis rubicundus	EN
Pristimantis ruedai	VU
Pristimantis rufioculis	DD
Pristimantis ruthveni	EN
Pristimantis salaputium	DD
Pristimantis saltissimus	LC
Pristimantis samaipatae	LC
Pristimantis sanctaemartae	NT
Pristimantis sanguineus	NT
Pristimantis satagius	DD
Pristimantis savagei	NT
Pristimantis schultei	VU
Pristimantis scitulus	DD
Pristimantis scoloblepharus	EN
Pristimantis scolodiscus	EN
Pristimantis scopaeus	DD
Pristimantis seorsus	DD
Pristimantis serendipitus	VU
Pristimantis shrevei	EN
Pristimantis signifer	VU
Pristimantis silverstonei	NT
Pristimantis simonbolivari	EN
Pristimantis simonsii	CR
Pristimantis simoteriscus	EN

Charadrahyla altipotens	CR
Charadrahyla chaneque	EN
Charadrahyla nephila	VU
Charadrahyla taeniopus	VU
Charadrahyla trux	CR
Chiasmocleis alagoana	DD
Chiasmocleis albopunctata	LC
Chiasmocleis anatipes	LC
Chiasmocleis antenori	LC
Chiasmocleis atlantica	LC
Chiasmocleis avilapiresae	LC
Chiasmocleis bassleri	LC
Chiasmocleis capixaba	LC
Chiasmocleis centralis	DD
Chiasmocleis devriesi	DD
Chiasmocleis hudsoni	LC
Chiasmocleis leucosticta	LC
Chiasmocleis magnova	DD
Chiasmocleis mantiqueira	DD
Chiasmocleis mehelyi	DD
Chiasmocleis sapiranga	DD
Chiasmocleis schubarti	LC
Chiasmocleis shudikarensis	LC
Chiasmocleis tridactyla	LC
Chiasmocleis ventrimaculata	LC
Chimerella mariaelenae	VU
Cochranella balionota	VU
Cochranella duidaeana	DD
Cochranella erminea	DD
Cochranella euhystrix	DD
Cochranella euknemos	LC
Cochranella geijskesi	DD
Cochranella granulosa	LC
Cochranella litoralis	DD
Cochranella mache	EN
Cochranella megista	NT
Cochranella nola	NT
Cochranella phryxa	DD
Cochranella ramirezi	DD
Cochranella resplendens	LC
Cochranella riveroi	VU
Cochranella xanthocheridia	VU
Colostethus agilis	NT
Colostethus alacris	DD
Colostethus argyrogaster	LC
Colostethus brachistriatus	DD
Colostethus dysprosium	DD
Colostethus fraterdanieli	NT
Colostethus fugax	DD
Incilius bocourti	LC
Incilius campbelli	NT
Incilius canaliferus	LC
Incilius cavifrons	EN
Incilius chompipe	VU
Incilius coccifer	LC
Incilius coniferus	LC
Incilius cristatus	CR
Incilius cycladen	VU
Incilius epioticus	LC
Incilius fastidiosus	CR
Incilius gemmifer	EN
Incilius guanacaste	DD
Incilius holdridgei	CR
Incilius ibarrai	EN
Incilius leucomyos	EN
Incilius luetkenii	LC
Incilius macrocristatus	VU
Incilius marmoreus	LC
Incilius mazatlanensis	LC
Incilius melanochlorus	LC
Incilius nebulifer	LC
Incilius occidentalis	LC
Incilius periglenes	EX
Incilius peripatetes	CR
Incilius perplexus	EN
Incilius pisinnus	DD
Incilius porteri	DD
Incilius signifer	LC
Incilius spiculatus	EN
Incilius tacanensis	EN
Incilius tutelarius	EN
Incilius valliceps	LC
Insuetophrynus acarpicus	CR
Ischnocnema bolbodactyla	LC
Ischnocnema erythromera	DD
Ischnocnema gehrti	DD
Ischnocnema gualteri	LC
Ischnocnema guentheri	LC
Ischnocnema henselii	LC
Ischnocnema hoehnei	LC
Ischnocnema holti	DD
Ischnocnema izecksohni	DD
Ischnocnema juipoca	LC
Ischnocnema lactea	LC
Ischnocnema manezinho	NT
Ischnocnema nasuta	LC
Ischnocnema nigriventris	DD
Ischnocnema octavioi	LC
Pristimantis simoterus	NT
Pristimantis siopelus	EN
Pristimantis skydmainos	LC
Pristimantis sobetes	EN
Pristimantis spilogaster	EN
Pristimantis spinosus	NT
Pristimantis stenodiscus	DD
Pristimantis sternothylax	DD
Pristimantis stictoboubonus	DD
Pristimantis subsigillatus	LC
Pristimantis suetus	EN
Pristimantis sulculus	EN
Pristimantis supernatis	VU
Pristimantis surdus	EN
Pristimantis susaguae	DD
Pristimantis taciturnus	DD
Pristimantis taeniatus	LC
Pristimantis tamsitti	NT
Pristimantis tantanti	DD
Pristimantis tanyrhynchus	DD
Pristimantis tayrona	NT
Pristimantis telefericus	DD
Pristimantis tenebrionis	EN
Pristimantis terraebolivaris	LC
Pristimantis thectopternus	LC
Pristimantis thyellus	DD
Pristimantis thymalopsoides	EN
Pristimantis thymelensis	LC
Pristimantis toftae	LC
Pristimantis trachyblepharis	DD
Pristimantis truebae	EN
Pristimantis tubernasus	DD
Pristimantis turik	DD
Pristimantis turumiquirensis	EN
Pristimantis uisae	DD
Pristimantis unistrigatus	LC
Pristimantis uranobates	LC
Pristimantis urichi	EN
Pristimantis vanadise	NT
Pristimantis variabilis	LC
Pristimantis veletis	CR
Pristimantis ventrimarmoratus	LC
Pristimantis verecundus	VU
Pristimantis versicolor	VU
Pristimantis vertebralis	VU
Pristimantis vicarius	NT
Pristimantis vidua	EN
Pristimantis viejas	LC
Pristimantis vilarsi	LC

Colostethus furviventris	DD
Colostethus imbricolus	DD
Colostethus inguinalis	LC
Colostethus jacobuspetersi	CR
Colostethus latinasus	DD
Colostethus lynchi	DD
Colostethus mertensi	EN
Colostethus panamansis	LC
Colostethus poecilonotus	DD
Colostethus pratti	LC
Colostethus ramirezi	DD
Colostethus ruthveni	EN
Colostethus thorntoni	DD
Colostethus ucumari	LC
Colostethus yaguara	DD
Corythomantis greeningi	LC
Craugastor adamastus	DD
Craugastor alfredi	VU
Craugastor amniscola	DD
Craugastor anciano	CR
Craugastor andi	CR
Craugastor angelicus	CR
Craugastor aphanus	VU
Craugastor augusti	LC
Craugastor aurilegulus	EN
Craugastor azueroensis	EN
Craugastor batrachylus	DD
Craugastor berkenbuschii	NT
Craugastor bocourti	VU
Craugastor bransfordii	LC
Craugastor brocchi	VU
Craugastor campbelli	DD
Craugastor catalinae	CR
Craugastor chac	NT
Craugastor charadra	EN
Craugastor chingopetaca	DD
Craugastor chrysozetetes	EX
Craugastor coffeus	CR
Craugastor crassidigitus	LC
Craugastor cruzi	CR
Craugastor cuaquero	DD
Craugastor cyanochthebius	NT
Craugastor daryi	EN
Craugastor decoratus	VU
Craugastor emcelae	CR
Craugastor emleni	CR
Craugastor epochthidius	CR
Craugastor escoces	EX
Craugastor fecundus	CR
Ischnocnema paranaensis	DD
Ischnocnema parva	LC
Ischnocnema penaxavantinho	DD
Ischnocnema pusilla	DD
Ischnocnema randorum	DD
Ischnocnema sambaqui	DD
Ischnocnema spanios	DD
Ischnocnema venancioi	LC
Ischnocnema verrucosa	DD
Isthmohyla angustilineata	CR
Isthmohyla calypsa	CR
Isthmohyla debilis	CR
Isthmohyla graceae	CR
Isthmohyla infucata	DD
Isthmohyla insolita	CR
Isthmohyla lancasteri	LC
Isthmohyla melacaena	NT
Isthmohyla picadoi	NT
Isthmohyla pictipes	EN
Isthmohyla pseudopuma	LC
Isthmohyla rivularis	CR
Isthmohyla tica	CR
Isthmohyla xanthosticta	DD
Isthmohyla zeteki	NT
Itapotihyla langsdorffii	LC
Lepidobatrachus asper	NT
Lepidobatrachus laevis	LC
Lepidobatrachus llanensis	LC
Leptodactylus albilabris	LC
Leptodactylus bolivianus	LC
Leptodactylus bufonius	LC
Leptodactylus caatingae	LC
Leptodactylus camaquara	DD
Leptodactylus chaquensis	LC
Leptodactylus colombiensis	LC
Leptodactylus cunicularius	LC
Leptodactylus cupreus	DD
Leptodactylus didymus	LC
Leptodactylus diedrus	LC
Leptodactylus discodactylus	LC
Leptodactylus elenae	LC
Leptodactylus fallax	CR
Leptodactylus flavopictus	LC
Leptodactylus fragilis	LC
Leptodactylus furnarius	LC
Leptodactylus fuscus	LC
Leptodactylus gracilis	LC
Leptodactylus griseigularis	LC
Leptodactylus hylodes	DD
Pristimantis vilcabambae	DD
Pristimantis vinhai	LC
Pristimantis viridicans	EN
Pristimantis viridis	NT
Pristimantis wagteri	DD
Pristimantis walkeri	LC
Pristimantis waoranii	DD
Pristimantis wiensi	DD
Pristimantis w-nigrum	LC
Pristimantis xeniolum	DD
Pristimantis xestus	DD
Pristimantis xylochobates	VU
Pristimantis yaviensis	DD
Pristimantis yukpa	LC
Pristimantis yustizi	DD
Pristimantis zeuctotylus	LC
Pristimantis zimmermanae	LC
Pristimantis zoilae	DD
Pristimantis zophus	EN
Proceratophrys appendiculata	LC
Proceratophrys avelinoi	LC
Proceratophrys bigibbosa	NT
Proceratophrys boiei	LC
Proceratophrys brauni	LC
Proceratophrys concavitympanum	DD
Proceratophrys cristiceps	LC
Proceratophrys cururu	DD
Proceratophrys goyana	LC
Proceratophrys laticeps	LC
Proceratophrys melanopogon	LC
Proceratophrys moehringi	DD
Proceratophrys moratoi	CR
Proceratophrys palustris	DD
Proceratophrys phyllostomus	DD
Proceratophrys schirchi	LC
Proceratophrys subguttata	LC
Proceratophrys vielliardi	DD
Prostherapis dunni	CR
Pseudis bolbodactyla	LC
Pseudis cardosoi	LC
Pseudis fusca	LC
Pseudis minuta	LC
Pseudis paradoxa	LC
Pseudis platensis	DD
Pseudis tocantins	LC
Pseudopaludicola boliviana	LC
Pseudopaludicola canga	DD
Pseudopaludicola falcipes	LC
Pseudopaludicola llanera	LC

Craugastor fitzingeri	LC
Craugastor fleischmanni	CR
Craugastor glaucus	CR
Craugastor gollmeri	LC
Craugastor greggi	CR
Craugastor guerreroensis	CR
Craugastor gulosus	CR
Craugastor hobartsmithi	EN
Craugastor inachus	EN
Craugastor jota	DD
Craugastor laevissimus	EN
Craugastor laticeps	NT
Craugastor lauraster	EN
Craugastor lineatus	CR
Craugastor loki	LC
Craugastor longirostris	LC
Craugastor matudai	VU
Craugastor megacephalus	LC
Craugastor megalotympanum	CR
Craugastor melanostictus	LC
Craugastor merendonensis	CR
Craugastor mexicanus	LC
Craugastor milesi	CR
Craugastor mimus	LC
Craugastor monnichorum	DD
Craugastor montanus	EN
Craugastor myllomyllon	DD
Craugastor nefrens	DD
Craugastor noblei	LC
Craugastor obesus	CR
Craugastor occidentalis	DD
Craugastor olanchano	CR
Craugastor omiltemanus	EN
Craugastor omoaensis	CR
Craugastor opimus	LC
Craugastor palenque	DD
Craugastor pechorum	EN
Craugastor pelorus	DD
Craugastor persimilis	VU
Craugastor phasma	DD
Craugastor podiciferus	NT
Craugastor polymniae	CR
Craugastor polyptychus	LC
Craugastor pozo	CR
Craugastor psephosypharus	VU
Craugastor punctariolus	EN
Craugastor pygmaeus	VU
Craugastor raniformis	LC
Craugastor ranoides	CR
Leptodactylus jolyi	DD
Leptodactylus knudseni	LC
Leptodactylus labrosus	LC
Leptodactylus labyrinthicus	LC
Leptodactylus laticeps	NT
Leptodactylus latinasus	LC
Leptodactylus latrans	LC
Leptodactylus lauramiriamae	DD
Leptodactylus leptodactyloides	LC
Leptodactylus lithonaetes	LC
Leptodactylus longirostris	LC
Leptodactylus magistris	CR
Leptodactylus marambaiae	LC
Leptodactylus melanonotus	LC
Leptodactylus myersi	LC
Leptodactylus mystaceus	LC
Leptodactylus mystacinus	LC
Leptodactylus natalensis	LC
Leptodactylus notoaktites	LC
Leptodactylus paraensis	LC
Leptodactylus pentadactylus	LC
Leptodactylus peritoaktites	VU
Leptodactylus petersii	LC
Leptodactylus plaumanni	LC
Leptodactylus podicipinus	LC
Leptodactylus poecilochilus	LC
Leptodactylus pustulatus	LC
Leptodactylus rhodomerus	LC
Leptodactylus rhodomystax	LC
Leptodactylus rhodonotus	LC
Leptodactylus riveroi	LC
Leptodactylus rugosus	LC
Leptodactylus sabanensis	LC
Leptodactylus savagei	LC
Leptodactylus sertanejo	LC
Leptodactylus silvanimbus	CR
Leptodactylus spixi	LC
Leptodactylus stenodema	LC
Leptodactylus syphax	LC
Leptodactylus tapiti	DD
Leptodactylus troglodytes	LC
Leptodactylus turimiquensis	NT
Leptodactylus validus	LC
Leptodactylus vastus	LC
Leptodactylus ventrimaculatus	LC
Leptodactylus viridis	DD
Leptodactylus wagneri	LC
Limnomedusa macroglossa	LC
Lithobates berlandieri	LC
Pseudopaludicola mineira	DD
Pseudopaludicola mystacalis	LC
Pseudopaludicola pusilla	LC
Pseudopaludicola saltica	LC
Pseudopaludicola ternetzi	LC
Psychrophrynella adenopleura	VU
Psychrophrynella ankohuma	VU
Psychrophrynella boettgeri	EN
Psychrophrynella chacaltaya	VU
Psychrophrynella guillei	CR
Psychrophrynella harveyi	DD
Psychrophrynella iani	DD
Psychrophrynella iatamasi	LC
Psychrophrynella illampu	VU
Psychrophrynella kallawaya	CR
Psychrophrynella katantika	LC
Psychrophrynella kempffi	VU
Psychrophrynella pinguis	VU
Psychrophrynella quimsacruzis	VU
Psychrophrynella saltator	CR
Psychrophrynella usurpator	EN
Psychrophrynella wettsteini	VU
Ptychohyla acrochorda	DD
Ptychohyla dendrophasma	CR
Ptychohyla erythromma	EN
Ptychohyla euthysanota	NT
Ptychohyla hypomykter	LC
Ptychohyla legleri	EN
Ptychohyla leonhardschultzei	EN
Ptychohyla macrotympanum	CR
Ptychohyla panchoi	EN
Ptychohyla salvadorensis	EN
Ptychohyla sanctaecrucis	CR
Ptychohyla spinipollex	EN
Ptychohyla zophodes	DD
Ranitomeya amazonica	DD
Ranitomeya benedicta	VU
Ranitomeya fantastica	NT
Ranitomeya flavovittata	LC
Ranitomeya imitator	LC
Ranitomeya reticulata	LC
Ranitomeya sirensis	LC
Ranitomeya summersi	EN
Ranitomeya uakarii	LC
Ranitomeya vanzolinii	LC
Ranitomeya variabilis	DD
Ranitomeya ventrimaculata	LC
Rhaebo blombergi	NT
Rhaebo caeruleostictus	EN

Craugastor rayo	DD
Craugastor rhodopis	VU
Craugastor rhyacobatrachus	EN
Craugastor rivulus	VU
Craugastor rostralis	NT
Craugastor rugosus	LC
Craugastor rugulosus	LC
Craugastor rupinius	LC
Craugastor sabrinus	EN
Craugastor saltuarius	CR
Craugastor sandersoni	EN
Craugastor silvicola	EN
Craugastor spatulatus	EN
Craugastor stadelmani	CR
Craugastor stejnegerianus	LC
Craugastor stuarti	EN
Craugastor tabasarae	CR
Craugastor talamancae	LC
Craugastor tarahumaraensis	VU
Craugastor taurus	CR
Craugastor taylori	DD
Craugastor trachydermus	CR
Craugastor underwoodi	LC
Craugastor uno	EN
Craugastor vocalis	LC
Craugastor vulcani	EN
Craugastor xucanebi	VU
Craugastor yucatanensis	NT
Crossodactylodes bokermanni	NT
Crossodactylodes izecksohni	NT
Crossodactylodes pintoi	DD
Crossodactylus aeneus	DD
Crossodactylus bokermanni	DD
Crossodactylus caramaschii	LC
Crossodactylus cyclospinus	DD
Crossodactylus dantei	DD
Crossodactylus dispar	DD
Crossodactylus gaudichaudii	LC
Crossodactylus grandis	DD
Crossodactylus lutzorum	DD
Crossodactylus schmidti	NT
Crossodactylus trachystomus	DD
Cruziohyla calcarifer	LC
Cruziohyla craspedopus	LC
Cryptobatrachus boulengeri	EN
Cryptobatrachus fuhrmanni	VU
Ctenophryne aequatorialis	LC
Ctenophryne aterrima	LC
Ctenophryne barbatula	VU
Lithobates bwana	VU
Lithobates chiricahuensis	VU
Lithobates dunni	EN
Lithobates forreri	LC
Lithobates grylio	LC
Lithobates johni	EN
Lithobates juliani	NT
Lithobates lemosespinali	DD
Lithobates macroglossa	VU
Lithobates maculatus	LC
Lithobates magnaocularis	LC
Lithobates megapoda	VU
Lithobates montezumae	LC
Lithobates neovolcanicus	NT
Lithobates omiltemanus	CR
Lithobates palmipes	LC
Lithobates pipiens	LC
Lithobates psilonota	DD
Lithobates pustulosus	LC
Lithobates sierramadrensis	VU
Lithobates spectabilis	LC
Lithobates tarahumarae	VU
Lithobates taylori	LC
Lithobates tlaloci	CR
Lithobates vaillanti	LC
Lithobates vibicarius	VU
Lithobates warszewitschii	LC
Lithobates yavapaiensis	LC
Lithobates zweifeli	LC
Lithodytes lineatus	LC
Lynchius flavomaculatus	VU
Lynchius nebulanastes	DD
Lynchius parkeri	EN
Lynchius simmonsi	VU
Lysapsus bolivianus	DD
Lysapsus caraya	LC
Lysapsus laevis	LC
Lysapsus limellum	LC
Macrogenioglottus alipioi	LC
Mannophryne caquetio	CR
Mannophryne collaris	EN
Mannophryne cordilleriana	CR
Mannophryne herminae	NT
Mannophryne lamarcai	CR
Mannophryne larandina	DD
Mannophryne leonardoi	EN
Mannophryne neblina	CR
Mannophryne oblitterata	DD
Mannophryne riveroi	EN
Rhaebo glaberrimus	LC
Rhaebo guttatus	LC
Rhaebo haematiticus	LC
Rhaebo hypomelas	NT
Rhaebo lynchi	DD
Rhaebo nasicus	LC
Rheobates palmatus	LC
Rheobates pseudopalmatus	DD
Rhinella abei	LC
Rhinella achalensis	NT
Rhinella achavali	LC
Rhinella acrolopha	DD
Rhinella acutirostris	LC
Rhinella alata	DD
Rhinella amboroensis	DD
Rhinella arborescandens	DD
Rhinella arenarum	LC
Rhinella arunco	LC
Rhinella atacamensis	LC
Rhinella bergi	LC
Rhinella castaneotica	LC
Rhinella ceratophrys	LC
Rhinella cerradensis	DD
Rhinella chavin	CR
Rhinella chrysophora	EN
Rhinella cristinae	DD
Rhinella crucifer	LC
Rhinella dapsilis	LC
Rhinella diptycha	DD
Rhinella dorbignyi	LC
Rhinella fernandezae	LC
Rhinella festae	NT
Rhinella fissipes	LC
Rhinella gallardoi	EN
Rhinella gnustae	DD
Rhinella granulosa	LC
Rhinella henseli	LC
Rhinella hoogmoedi	LC
Rhinella humboldti	LC
Rhinella icterica	LC
Rhinella inca	LC
Rhinella iserni	DD
Rhinella jimi	LC
Rhinella justinianoi	VU
Rhinella lescurei	DD
Rhinella limensis	LC
Rhinella lindae	DD
Rhinella macrorhina	EN
Rhinella magnussoni	LC

Ctenophryne carpish	EN
Ctenophryne geayi	LC
Ctenophryne minor	DD
Cycloramphus acangatan	VU
Cycloramphus asper	DD
Cycloramphus bandeirensis	DD
Cycloramphus bolitoglossus	DD
Cycloramphus boraceiensis	LC
Cycloramphus brasiliensis	NT
Cycloramphus carvalhoi	DD
Cycloramphus catarinensis	DD
Cycloramphus cedrensis	DD
Cycloramphus diringshofeni	DD
Cycloramphus dubius	LC
Cycloramphus duseni	DD
Cycloramphus eleutherodactylus	DD
Cycloramphus fuliginosus	LC
Cycloramphus granulosus	DD
Cycloramphus izecksohni	DD
Cycloramphus juimirim	DD
Cycloramphus lutzorum	DD
Cycloramphus migueli	DD
Cycloramphus mirandaribeiroi	DD
Cycloramphus ohausi	DD
Cycloramphus organensis	DD
Cycloramphus rhyakonastes	LC
Cycloramphus semipalmatus	NT
Cycloramphus stejnegeri	DD
Cycloramphus valae	DD
Dasypops schirchi	VU
Dendrobates auratus	LC
Dendrobates leucomelas	LC
Dendrobates nubeculosus	DD
Dendrobates tinctorius	LC
Dendrobates truncatus	LC
Dendrophryniscus berthalutzae	LC
Dendrophryniscus brevipollicatus	LC
Dendrophryniscus carvalhoi	EN
Dendrophryniscus krausae	DD
Dendrophryniscus leucomystax	LC
Dendrophryniscus proboscideus	DD
Dendrophryniscus stawiarskyi	DD
Dendropsophus acreanus	LC
Dendropsophus amicorum	CR
Dendropsophus anataliasiasi	LC
Dendropsophus anceps	LC
Dendropsophus aperomeus	LC
Dendropsophus araguaya	DD
Mannophryne trinitatis	VU
Mannophryne trujillensis	EN
Mannophryne venezuelensis	NT
Mannophryne yustizi	EN
Megaelosia apuana	DD
Megaelosia bocainensis	DD
Megaelosia boticariana	DD
Megaelosia goeldii	LC
Megaelosia jordanensis	DD
Megaelosia lutzae	DD
Megaelosia massarti	DD
Megastomatohyla mixomaculata	EN
Megastomatohyla nubicola	EN
Megastomatohyla pellita	CR
Melanophryniscus admirabilis	CR
Melanophryniscus alipioi	DD
Melanophryniscus atroluteus	LC
Melanophryniscus cambaraensis	DD
Melanophryniscus cupreuscapularis	NT
Melanophryniscus devincenzii	EN
Melanophryniscus dorsalis	VU
Melanophryniscus fulvoguttatus	LC
Melanophryniscus klappenbachi	LC
Melanophryniscus krauczuki	DD
Melanophryniscus langonei	CR
Melanophryniscus macrogranulosus	VU
Melanophryniscus montevidensis	VU
Melanophryniscus moreirae	NT
Melanophryniscus pachyrhynus	DD
Melanophryniscus peritus	CR
Melanophryniscus rubriventris	LC
Melanophryniscus sanmartini	NT
Melanophryniscus simplex	DD
Melanophryniscus stelzneri	LC
Melanophryniscus tumifrons	LC
Metaphryniscus sosai	VU
Minyobates steyermarki	CR
Myersiella microps	LC
Myersiohyla aromatica	DD
Myersiohyla inparquesi	DD
Myersiohyla kanaima	LC
Myersiohyla loveridgei	DD
Nannophryne apolobambica	DD
Nannophryne cophotis	LC
Nannophryne corynetes	VU
Nannophryne variegata	LC
Niceforonia adenobrachia	CR
Niceforonia columbiana	DD
Rhinella manu	VU
Rhinella margaritifera	LC
Rhinella marina	LC
Rhinella martyi	LC
Rhinella multiverrucosa	DD
Rhinella nesiotes	EN
Rhinella nicefori	EN
Rhinella ocellata	LC
Rhinella ornata	LC
Rhinella poeppigii	LC
Rhinella proboscidea	LC
Rhinella pygmaea	LC
Rhinella quechua	VU
Rhinella roqueana	LC
Rhinella rostrata	CR
Rhinella rubescens	LC
Rhinella rubropunctata	VU
Rhinella ruizi	DD
Rhinella rumbolli	VU
Rhinella schneideri	LC
Rhinella scitula	DD
Rhinella sclerocephala	EN
Rhinella spinulosa	LC
Rhinella stanlaii	LC
Rhinella sternosignata	NT
Rhinella tacana	DD
Rhinella tenrec	DD
Rhinella vellardi	DD
Rhinella veraguensis	LC
Rhinella veredas	LC
Rhinoderma darwinii	VU
Rhinoderma rufum	CR
Rhinophrynus dorsalis	LC
Rulyrana adiazeta	VU
Rulyrana flavopunctata	LC
Rulyrana mcdiarmidi	DD
Rulyrana saxiscandens	EN
Rulyrana spiculata	NT
Rulyrana susatamai	VU
Rupirana cardosoi	NT
Sachatamia albomaculata	LC
Sachatamia ilex	LC
Sachatamia orejuela	DD
Sachatamia punctulata	EN
Scaphiopus couchii	LC
Scarthyla goinorum	LC
Scarthyla vigilans	LC
Scinax acuminatus	LC

Dendropsophus battersbyi	DD
Dendropsophus berthalutzae	LC
Dendropsophus bifurcus	LC
Dendropsophus bipunctatus	LC
Dendropsophus bogerti	LC
Dendropsophus bokermanni	LC
Dendropsophus branneri	LC
Dendropsophus brevifrons	LC
Dendropsophus cachimbo	DD
Dendropsophus carnifex	LC
Dendropsophus cerradensis	DD
Dendropsophus coffeus	LC
Dendropsophus columbianus	LC
Dendropsophus cruzi	LC
Dendropsophus decipiens	LC
Dendropsophus delarivai	LC
Dendropsophus dutrai	DD
Dendropsophus ebraccatus	LC
Dendropsophus elegans	LC
Dendropsophus elianeae	LC
Dendropsophus garagoensis	LC
Dendropsophus gaucheri	LC
Dendropsophus giesleri	LC
Dendropsophus gryllatus	EN
Dendropsophus haddadi	LC
Dendropsophus haraldschultzi	LC
Dendropsophus jimi	LC
Dendropsophus juliani	LC
Dendropsophus koechlini	LC
Dendropsophus labialis	LC
Dendropsophus leali	LC
Dendropsophus leucophyllatus	LC
Dendropsophus luteoocellatus	LC
Dendropsophus marmoratus	LC
Dendropsophus mathiassoni	LC
Dendropsophus melanargyreus	LC
Dendropsophus meridensis	EN
Dendropsophus meridianus	LC
Dendropsophus microcephalus	LC
Dendropsophus microps	LC
Dendropsophus minimus	DD
Dendropsophus minusculus	LC
Dendropsophus minutus	LC
Dendropsophus miyatai	LC
Dendropsophus nahdereri	LC
Dendropsophus nanus	LC
Dendropsophus novaisi	DD
Dendropsophus oliveirai	LC
Dendropsophus padreluna	LC
Niceforonia nana	DD
Noblella carrascoicola	LC
Noblella duellmani	DD
Noblella heyeri	DD
Noblella lochites	NT
Noblella lynchi	DD
Noblella myrmecoides	LC
Noblella pygmaea	LC
Noblella ritarasquinae	DD
Nyctimantis rugiceps	LC
Nymphargus armatus	VU
Nymphargus bejaranoi	LC
Nymphargus buenaventura	DD
Nymphargus cariticommatus	DD
Nymphargus chami	DD
Nymphargus chancas	DD
Nymphargus cochranae	VU
Nymphargus cristinae	DD
Nymphargus garciae	VU
Nymphargus grandisonae	LC
Nymphargus griffithsi	VU
Nymphargus ignotus	NT
Nymphargus laurae	CR
Nymphargus luminosus	EN
Nymphargus luteopunctatus	DD
Nymphargus mariae	EN
Nymphargus megacheirus	EN
Nymphargus mixomaculatus	DD
Nymphargus nephelophila	DD
Nymphargus ocellatus	NT
Nymphargus oreonympha	DD
Nymphargus phenax	DD
Nymphargus pluvialis	DD
Nymphargus posadae	VU
Nymphargus prasinus	VU
Nymphargus rosada	VU
Nymphargus ruizi	VU
Nymphargus siren	VU
Nymphargus spilotus	DD
Nymphargus truebae	DD
Nymphargus vicenteruedai	DD
Nymphargus wileyi	DD
Odontophrynus achalensis	VU
Odontophrynus americanus	LC
Odontophrynus barrioi	DD
Odontophrynus carvalhoi	LC
Odontophrynus cordobae	LC
Odontophrynus cultripes	LC
Odontophrynus lavillai	LC
Scinax agilis	LC
Scinax albicans	LC
Scinax altae	LC
Scinax alter	LC
Scinax angrensis	LC
Scinax arduous	DD
Scinax argyreornatus	LC
Scinax ariadne	DD
Scinax aromothyella	DD
Scinax atratus	DD
Scinax auratus	LC
Scinax baumgardneri	DD
Scinax belloni	EN
Scinax berthae	LC
Scinax blairi	LC
Scinax boesemani	LC
Scinax boulengeri	LC
Scinax brieni	LC
Scinax cabralensis	DD
Scinax caldarum	LC
Scinax camposseabrai	DD
Scinax canastrensis	DD
Scinax cardosoi	LC
Scinax carnevallii	LC
Scinax castroviejoi	DD
Scinax catharinae	LC
Scinax centralis	LC
Scinax chiquitanus	LC
Scinax constrictus	LC
Scinax cretatus	LC
Scinax crospedospilus	LC
Scinax cruentommus	LC
Scinax curicica	DD
Scinax cuspidatus	LC
Scinax danae	DD
Scinax duartei	LC
Scinax elaeochrous	LC
Scinax eurydice	LC
Scinax exiguus	LC
Scinax flavoguttatus	LC
Scinax funereus	LC
Scinax fuscomarginatus	LC
Scinax fuscovarius	LC
Scinax garbei	LC
Scinax granulatus	LC
Scinax hayii	LC
Scinax heyeri	DD
Scinax hiemalis	LC
Scinax humilis	LC

Dendropsophus parviceps	LC
Dendropsophus pauiniensis	LC
Dendropsophus phlebodes	LC
Dendropsophus praestans	LC
Dendropsophus pseudomeridianus	LC
Dendropsophus reichlei	DD
Dendropsophus rhea	DD
Dendropsophus rhodopeplus	LC
Dendropsophus riveroi	LC
Dendropsophus robertmertensi	LC
Dendropsophus rossalleni	LC
Dendropsophus rubicundulus	LC
Dendropsophus ruschii	DD
Dendropsophus sanborni	LC
Dendropsophus sarayacuensis	LC
Dendropsophus sartori	LC
Dendropsophus schubarti	LC
Dendropsophus seniculus	LC
Dendropsophus soaresi	LC
Dendropsophus stingi	VU
Dendropsophus studerae	DD
Dendropsophus subocularis	LC
Dendropsophus timbeba	LC
Dendropsophus tintinnabulum	DD
Dendropsophus triangulum	LC
Dendropsophus tritaeniatus	LC
Dendropsophus virolinensis	LC
Dendropsophus walfordi	LC
Dendropsophus werneri	LC
Dendropsophus xapuriensis	LC
Dendropsophus yaracuyanus	DD
Dermatonotus muelleri	LC
Diaglena spatulata	LC
Diasporus anthrax	DD
Diasporus diastema	LC
Diasporus gularis	LC
Diasporus hylaeformis	LC
Diasporus quidditus	LC
Diasporus tigrillo	DD
Diasporus tinker	LC
Diasporus vocator	LC
Dischidodactylus colonnelloi	DD
Dischidodactylus duidensis	DD
Dryaderces pearsoni	LC
Duellmanohyla chamulae	EN
Duellmanohyla ignicolor	EN
Duellmanohyla lythrodes	EN
Duellmanohyla rufioculis	LC
Duellmanohyla salvavida	CR
Odontophrynus occidentalis	LC
Odontophrynus salvatori	DD
Oophaga arborea	EN
Oophaga granulifera	VU
Oophaga histrionica	LC
Oophaga lehmanni	CR
Oophaga occultator	DD
Oophaga pumilio	LC
Oophaga speciosa	EN
Oophaga sylvatica	NT
Oophaga vicentei	DD
Oreobates ayacucho	EN
Oreobates choristolemma	DD
Oreobates crepitans	DD
Oreobates cruralis	LC
Oreobates discoidalis	LC
Oreobates heterodactylus	DD
Oreobates ibischi	LC
Oreobates lehri	LC
Oreobates lundbergi	DD
Oreobates madidi	LC
Oreobates pereger	CR
Oreobates quixensis	LC
Oreobates sanctaecrucis	LC
Oreobates sanderi	LC
Oreobates saxatilis	DD
Oreobates zongoensis	CR
Oreophrynella cryptica	VU
Oreophrynella dendronastes	DD
Oreophrynella huberi	VU
Oreophrynella macconnelli	VU
Oreophrynella nigra	VU
Oreophrynella quelchii	VU
Oreophrynella vasquezi	VU
Oreophrynella weiassipuensis	DD
Osornophryne antisana	EN
Osornophryne bufoniformis	NT
Osornophryne guacamayo	EN
Osornophryne percrassa	EN
Osornophryne puruanta	EN
Osornophryne talipes	EN
Osteocephalus alboguttatus	LC
Osteocephalus buckleyi	LC
Osteocephalus cabrerai	LC
Osteocephalus castaneicola	LC
Osteocephalus deridens	LC
Osteocephalus fuscifacies	DD
Osteocephalus heyeri	LC
Osteocephalus leoniae	LC
Scinax ictericus	LC
Scinax insperatus	DD
Scinax iquitorum	LC
Scinax jolyi	DD
Scinax jureia	DD
Scinax karenanneae	LC
Scinax kennedyi	LC
Scinax lindsayi	LC
Scinax littoralis	LC
Scinax littoreus	LC
Scinax longilineus	LC
Scinax luizotavioi	LC
Scinax machadoi	LC
Scinax manriquei	LC
Scinax maracaya	DD
Scinax melloi	DD
Scinax nasicus	LC
Scinax nebulosus	LC
Scinax obtriangulatus	LC
Scinax oreites	NT
Scinax pachycrus	LC
Scinax pedromedinae	LC
Scinax perereca	LC
Scinax perpusillus	LC
Scinax pinima	DD
Scinax proboscideus	LC
Scinax quinquefasciatus	LC
Scinax ranki	DD
Scinax rizibilis	LC
Scinax rostratus	LC
Scinax ruber	LC
Scinax similis	LC
Scinax squalirostris	LC
Scinax staufferi	LC
Scinax sugillatus	LC
Scinax tigrinus	LC
Scinax trapicheiroi	NT
Scinax uruguayus	LC
Scinax v-signatus	LC
Scinax wandae	LC
Scinax x-signatus	LC
Scythrophrys sawayae	LC
Silverstoneia erasmios	DD
Silverstoneia flotator	LC
Silverstoneia nubicola	NT
Smilisca baudinii	LC
Smilisca cyanosticta	NT
Smilisca fodiens	LC
Smilisca phaeota	LC

Duellmanohyla schmidtorum	VU
Duellmanohyla soralia	EN
Duellmanohyla uranochroa	EN
Ecnomiohyla echinata	CR
Ecnomiohyla fimbrimembra	EN
Ecnomiohyla miliaria	VU
Ecnomiohyla minera	EN
Ecnomiohyla miotympanum	NT
Ecnomiohyla phantasmagoria	EN
Ecnomiohyla rabborum	CR
Ecnomiohyla salvaje	CR
Ecnomiohyla thysanota	DD
Ecnomiohyla tuberculosa	LC
Ecnomiohyla valancifer	CR
Edalorhina nasuta	DD
Edalorhina perezi	LC
Elachistocleis bicolor	LC
Elachistocleis bumbameuboi	DD
Elachistocleis carvalhoi	LC
Elachistocleis erythrogaster	NT
Elachistocleis helianneae	LC
Elachistocleis matogrosso	LC
Elachistocleis ovalis	LC
Elachistocleis panamensis	LC
Elachistocleis pearsei	LC
Elachistocleis piauiensis	LC
Elachistocleis skotogaster	DD
Elachistocleis surinamensis	LC
Elachistocleis surumu	DD
Eleutherodactylus abbotti	LC
Eleutherodactylus acmonis	EN
Eleutherodactylus adelus	EN
Eleutherodactylus albipes	CR
Eleutherodactylus albolabris	CR
Eleutherodactylus alcoae	EN
Eleutherodactylus alticola	DD
Eleutherodactylus amadeus	CR
Eleutherodactylus amplinympha	EN
Eleutherodactylus andrewsi	EN
Eleutherodactylus angustidigitorum	VU
Eleutherodactylus antillensis	LC
Eleutherodactylus apostates	CR
Eleutherodactylus armstrongi	EN
Eleutherodactylus atkinsi	LC
Eleutherodactylus audanti	VU
Eleutherodactylus auriculatoides	EN
Eleutherodactylus auriculatus	LC
Eleutherodactylus bakeri	CR
Eleutherodactylus barlagnei	EN
Osteocephalus leprieurii	LC
Osteocephalus mimeticus	LC
Osteocephalus mutabor	LC
Osteocephalus oophagus	LC
Osteocephalus planiceps	LC
Osteocephalus subtilis	LC
Osteocephalus taurinus	LC
Osteocephalus verruciger	LC
Osteocephalus yasuni	LC
Osteopilus crucialis	EN
Osteopilus dominicensis	LC
Osteopilus marianae	EN
Osteopilus ocellatus	LC
Osteopilus pulchrilineatus	VU
Osteopilus septentrionalis	LC
Osteopilus vastus	VU
Osteopilus wilderi	EN
Otophryne pyburni	LC
Otophryne robusta	LC
Otophryne steyermarki	LC
Paratelmatobius cardosoi	DD
Paratelmatobius gaigeae	DD
Paratelmatobius lutzii	DD
Paratelmatobius mantiqueira	DD
Paratelmatobius poecilogaster	DD
Peltophryne cataulaciceps	EN
Peltophryne empusa	VU
Peltophryne florentinoi	CR
Peltophryne fluviatica	CR
Peltophryne fracta	EN
Peltophryne fustiger	LC
Peltophryne guentheri	VU
Peltophryne gundlachi	VU
Peltophryne lemur	CR
Peltophryne longinasus	EN
Peltophryne peltocephala	LC
Peltophryne taladai	VU
Phasmahyla cochranae	LC
Phasmahyla exilis	LC
Phasmahyla guttata	LC
Phasmahyla jandaia	LC
Phasmahyla spectabilis	DD
Phasmahyla timbo	DD
Phrynomedusa appendiculata	NT
Phrynomedusa bokermanni	DD
Phrynomedusa fimbriata	EX
Phrynomedusa marginata	LC
Phrynomedusa vanzolinii	DD
Phrynopus auriculatus	DD
Smilisca puma	LC
Smilisca sila	LC
Smilisca sordida	LC
Spea bombifrons	LC
Spea multiplicata	LC
Sphaenorhynchus bromelicola	DD
Sphaenorhynchus caramaschii	LC
Sphaenorhynchus carneus	LC
Sphaenorhynchus dorisae	LC
Sphaenorhynchus lacteus	LC
Sphaenorhynchus mirim	DD
Sphaenorhynchus orophilus	LC
Sphaenorhynchus palustris	LC
Sphaenorhynchus pauloalvini	DD
Sphaenorhynchus planicola	LC
Sphaenorhynchus prasinus	LC
Sphaenorhynchus surdus	LC
Stefania ackawaio	LC
Stefania ayangannae	LC
Stefania breweri	DD
Stefania coxi	LC
Stefania evansi	LC
Stefania ginesi	LC
Stefania goini	DD
Stefania marahuaquensis	DD
Stefania oculosa	DD
Stefania percristata	DD
Stefania riae	DD
Stefania riveroi	VU
Stefania roraimae	DD
Stefania satelles	NT
Stefania scalae	LC
Stefania schuberti	VU
Stefania tamacuarina	DD
Stefania woodleyi	LC
Stereocyclops incrassatus	LC
Stereocyclops parkeri	LC
Strabomantis anatipes	VU
Strabomantis anomalus	LC
Strabomantis biporcatus	VU
Strabomantis bufoniformis	LC
Strabomantis cerastes	LC
Strabomantis cheiroplethus	VU
Strabomantis cornutus	VU
Strabomantis helonotus	CR
Strabomantis ingeri	VU
Strabomantis laticorpus	DD
Strabomantis necerus	VU
Strabomantis necopinus	VU

Eleutherodactylus bartonsmithi	CR
Eleutherodactylus bilineatus	LC
Eleutherodactylus blairhedgesi	CR
Eleutherodactylus brevirostris	CR
Eleutherodactylus brittoni	LC
Eleutherodactylus caribe	CR
Eleutherodactylus casparii	EN
Eleutherodactylus cavernicola	CR
Eleutherodactylus chlorophenax	CR
Eleutherodactylus cochranae	LC
Eleutherodactylus cooki	VU
Eleutherodactylus coqui	LC
Eleutherodactylus corona	CR
Eleutherodactylus counouspeus	EN
Eleutherodactylus cubanus	CR
Eleutherodactylus cundalli	NT
Eleutherodactylus cuneatus	LC
Eleutherodactylus cystignathoides	LC
Eleutherodactylus darlingtoni	CR
Eleutherodactylus dennisi	EN
Eleutherodactylus dilatus	EN
Eleutherodactylus dimidiatus	NT
Eleutherodactylus diplasius	EN
Eleutherodactylus dolomedes	CR
Eleutherodactylus eileenae	NT
Eleutherodactylus emiliae	EN
Eleutherodactylus eneidae	CR
Eleutherodactylus etheridgei	EN
Eleutherodactylus eunaster	CR
Eleutherodactylus flavescens	NT
Eleutherodactylus fowleri	CR
Eleutherodactylus furcyensis	CR
Eleutherodactylus fuscus	CR
Eleutherodactylus glamyrus	EN
Eleutherodactylus glandulifer	CR
Eleutherodactylus glanduliferoides	CR
Eleutherodactylus glaphycompus	EN
Eleutherodactylus glaucoreius	NT
Eleutherodactylus goini	VU
Eleutherodactylus gossei	LC
Eleutherodactylus grabhami	EN
Eleutherodactylus grahami	EN
Eleutherodactylus grandis	CR
Eleutherodactylus greyi	EN
Eleutherodactylus griphus	CR
Eleutherodactylus gryllus	EN
Eleutherodactylus guanahacabibes	EN
Eleutherodactylus guantanamera	VU
Phrynopus barthlenae	VU
Phrynopus bracki	EN
Phrynopus bufoides	DD
Phrynopus dagmarae	CR
Phrynopus heimorum	CR
Phrynopus horstpauli	VU
Phrynopus juninensis	CR
Phrynopus kauneorum	CR
Phrynopus kotosh	DD
Phrynopus montium	EN
Phrynopus nicoleae	DD
Phrynopus oblivius	DD
Phrynopus peruanus	CR
Phrynopus thompsoni	DD
Phrynopus tribulosus	DD
Phyllobates aurotaenia	NT
Phyllobates bicolor	NT
Phyllobates lugubris	LC
Phyllobates terribilis	EN
Phyllobates vittatus	EN
Phyllodytes acuminatus	LC
Phyllodytes brevirostris	DD
Phyllodytes edelmoi	DD
Phyllodytes gyrinaethes	DD
Phyllodytes kautskyi	LC
Phyllodytes luteolus	LC
Phyllodytes maculosus	DD
Phyllodytes melanomystax	LC
Phyllodytes punctatus	DD
Phyllodytes tuberculosus	DD
Phyllodytes wuchereri	DD
Phyllomedusa atelopoides	LC
Phyllomedusa ayeaye	CR
Phyllomedusa azurea	DD
Phyllomedusa bahiana	DD
Phyllomedusa baltea	EN
Phyllomedusa bicolor	LC
Phyllomedusa boliviana	LC
Phyllomedusa burmeisteri	LC
Phyllomedusa camba	LC
Phyllomedusa centralis	DD
Phyllomedusa coelestis	LC
Phyllomedusa distincta	LC
Phyllomedusa duellmani	DD
Phyllomedusa hypochondrialis	LC
Phyllomedusa iheringii	LC
Phyllomedusa megacephala	DD
Phyllomedusa neildi	DD
Strabomantis ruizi	EN
Strabomantis sulcatus	LC
Strabomantis zygodactylus	LC
Synapturanus mirandaribeiroi	LC
Synapturanus rabus	LC
Synapturanus salseri	LC
Telmatobius arequipensis	VU
Telmatobius atacamensis	CR
Telmatobius atahualpai	NT
Telmatobius bolivianus	NT
Telmatobius brachydactylus	EN
Telmatobius brevipes	EN
Telmatobius brevirostris	EN
Telmatobius carrillae	VU
Telmatobius ceiorum	EN
Telmatobius cirrhacelis	CR
Telmatobius colanensis	EN
Telmatobius contrerasi	DD
Telmatobius culeus	CR
Telmatobius dankoi	DD
Telmatobius degener	EN
Telmatobius edaphonastes	EN
Telmatobius espadai	CR
Telmatobius gigas	CR
Telmatobius halli	DD
Telmatobius hauthali	VU
Telmatobius hintoni	VU
Telmatobius hockingi	VU
Telmatobius huayra	VU
Telmatobius hypselocephalus	EN
Telmatobius ignavus	EN
Telmatobius intermedius	DD
Telmatobius jelskii	NT
Telmatobius laticeps	EN
Telmatobius latirostris	EN
Telmatobius macrostomus	EN
Telmatobius marmoratus	VU
Telmatobius mayoloi	EN
Telmatobius necopinus	EN
Telmatobius niger	CR
Telmatobius oxycephalus	VU
Telmatobius pefauri	CR
Telmatobius peruvianus	VU
Telmatobius philippii	DD
Telmatobius pinguiculus	DD
Telmatobius pisanoi	EN
Telmatobius platycephalus	EN
Telmatobius punctatus	CR

Eleutherodactylus gundlachi	EN
Eleutherodactylus guttilatus	LC
Eleutherodactylus haitianus	EN
Eleutherodactylus hedricki	EN
Eleutherodactylus heminota	EN
Eleutherodactylus hypostenor	EN
Eleutherodactylus iberia	CR
Eleutherodactylus inoptatus	LC
Eleutherodactylus intermedius	EN
Eleutherodactylus interorbitalis	DD
Eleutherodactylus ionthus	EN
Eleutherodactylus jamaicensis	EN
Eleutherodactylus jasperi	CR
Eleutherodactylus jaumei	CR
Eleutherodactylus johnstonei	LC
Eleutherodactylus jugans	CR
Eleutherodactylus junori	CR
Eleutherodactylus karlschmidti	CR
Eleutherodactylus klinikowskii	EN
Eleutherodactylus lamprotes	CR
Eleutherodactylus leberi	EN
Eleutherodactylus leoncei	CR
Eleutherodactylus leprus	VU
Eleutherodactylus limbatus	VU
Eleutherodactylus locustus	CR
Eleutherodactylus longipes	VU
Eleutherodactylus lucioi	CR
Eleutherodactylus luteolus	EN
Eleutherodactylus maestrensis	DD
Eleutherodactylus mariposa	CR
Eleutherodactylus marnockii	LC
Eleutherodactylus martinicensis	NT
Eleutherodactylus maurus	DD
Eleutherodactylus melacara	EN
Eleutherodactylus michaelschmidi	EN
Eleutherodactylus minutus	EN
Eleutherodactylus modestus	VU
Eleutherodactylus montanus	EN
Eleutherodactylus nitidus	LC
Eleutherodactylus nortoni	CR
Eleutherodactylus notidodes	EN
Eleutherodactylus nubicola	EN
Eleutherodactylus orcutti	CR
Eleutherodactylus orientalis	CR
Eleutherodactylus oxyrhyncus	CR
Eleutherodactylus pallidus	DD
Eleutherodactylus pantoni	NT
Eleutherodactylus parabates	CR
Eleutherodactylus paralius	NT
Phyllomedusa nordestina	DD
Phyllomedusa oreades	DD
Phyllomedusa palliata	LC
Phyllomedusa perinesos	DD
Phyllomedusa rohdei	LC
Phyllomedusa sauvagii	LC
Phyllomedusa tarsius	LC
Phyllomedusa tetraploidea	LC
Phyllomedusa tomopterna	LC
Phyllomedusa trinitatis	LC
Phyllomedusa vaillantii	LC
Phyllomedusa venusta	LC
Physalaemus aguirrei	LC
Physalaemus albifrons	LC
Physalaemus albonotatus	LC
Physalaemus angrensis	DD
Physalaemus barrioi	DD
Physalaemus biligonigerus	LC
Physalaemus caete	DD
Physalaemus centralis	LC
Physalaemus cicada	LC
Physalaemus crombiei	LC
Physalaemus cuqui	LC
Physalaemus cuvieri	LC
Physalaemus deimaticus	DD
Physalaemus ephippifer	LC
Physalaemus erikae	LC
Physalaemus erythros	DD
Physalaemus evangelistai	DD
Physalaemus fernandezae	LC
Physalaemus fischeri	LC
Physalaemus gracilis	LC
Physalaemus henselii	LC
Physalaemus insperatus	DD
Physalaemus irroratus	DD
Physalaemus jordanensis	DD
Physalaemus kroyeri	LC
Physalaemus lisei	LC
Physalaemus maculiventris	LC
Physalaemus marmoratus	LC
Physalaemus maximus	DD
Physalaemus moreirae	DD
Physalaemus nanus	LC
Physalaemus nattereri	LC
Physalaemus obtectus	DD
Physalaemus olfersii	LC
Physalaemus riograndensis	LC
Physalaemus rupestris	DD
Physalaemus santafecinus	LC
Telmatobius rimac	LC
Telmatobius sanborni	VU
Telmatobius schreiteri	EN
Telmatobius scrocchii	EN
Telmatobius sibiricus	EN
Telmatobius simonsi	NT
Telmatobius stephani	EN
Telmatobius thompsoni	EN
Telmatobius timens	CR
Telmatobius truebae	EN
Telmatobius vellardi	CR
Telmatobius verrucosus	VU
Telmatobius vilamensis	DD
Telmatobius yuracare	VU
Telmatobius zapahuirensis	CR
Telmatobufo australis	VU
Telmatobufo bullocki	CR
Telmatobufo venustus	EN
Tepuihyla aecii	DD
Tepuihyla edelcae	LC
Tepuihyla luteolabris	DD
Tepuihyla rimarum	VU
Tepuihyla rodriguezi	DD
Tepuihyla warreni	DD
Teratohyla adenocheira	DD
Teratohyla amelie	DD
Teratohyla midas	LC
Teratohyla pulverata	LC
Teratohyla spinosa	LC
Thoropa lutzi	EN
Thoropa megatympanum	LC
Thoropa miliaris	LC
Thoropa petropolitana	VU
Thoropa saxatilis	NT
Tlalocohyla godmani	VU
Tlalocohyla loquax	LC
Tlalocohyla picta	LC
Tlalocohyla smithii	LC
Trachycephalus atlas	LC
Trachycephalus coriaceus	LC
Trachycephalus dibernardoi	LC
Trachycephalus hadroceps	LC
Trachycephalus imitatrix	LC
Trachycephalus jordani	LC
Trachycephalus lepidus	DD
Trachycephalus mesophaeus	LC
Trachycephalus nigromaculatus	LC
Trachycephalus resinifictrix	LC
Triprion petasatus	LC

Eleutherodactylus parapelates	CR	*Physalaemus signifer*	LC	*Truebella skoptes*	DD
Eleutherodactylus patriciae	EN	*Physalaemus soaresi*	EN	*Truebella tothastes*	DD
Eleutherodactylus paulsoni	CR	*Physalaemus spiniger*	LC	*Vitreorana antisthenesi*	VU
Eleutherodactylus pentasyringos	VU	*Phytotriades auratus*	CR	*Vitreorana castroviejoi*	DD
Eleutherodactylus pezopetrus	CR	*Phyzelaphryne miriamae*	LC	*Vitreorana eurygnatha*	LC
Eleutherodactylus pictissimus	VU	*Pipa arrabali*	LC	*Vitreorana gorzulae*	DD
Eleutherodactylus pinarensis	EN	*Pipa aspera*	LC	*Vitreorana helenae*	DD
Eleutherodactylus pinchoni	EN	*Pipa carvalhoi*	LC	*Vitreorana parvula*	DD
Eleutherodactylus pipilans	LC	*Pipa myersi*	EN	*Vitreorana ritae*	DD
Eleutherodactylus pituinus	EN	*Pipa parva*	LC	*Vitreorana uranoscopa*	LC
Eleutherodactylus planirostris	LC	*Pipa*	LC	*Xenohyla eugenioi*	DD
Eleutherodactylus poolei	CR	*Pipa snethlageae*	LC	*Xenohyla truncata*	NT
Eleutherodactylus portoricensis	EN	*Plectrohyla acanthodes*	CR	*Yunganastes ashkapara*	VU
Eleutherodactylus principalis	EN	*Plectrohyla ameibothalame*	DD	*Yunganastes bisignatus*	EN
Eleutherodactylus probolaeus	EN	*Plectrohyla arborescandens*	EN	*Yunganastes fraudator*	LC
Eleutherodactylus rhodesi	CR	*Plectrohyla avia*	CR	*Yunganastes mercedesae*	DD
Eleutherodactylus richmondi	CR	*Plectrohyla bistincta*	LC	*Yunganastes pluvicanorus*	LC
Eleutherodactylus ricordii	VU	*Plectrohyla calthula*	CR	*Zachaenus parvulus*	LC
Eleutherodactylus riparius	LC	*Plectrohyla calvicollina*	CR		

Appendix A2

List of sample sizes of pseudo-occurrences generated within the species range map's polygons threated as real occurrences. We modeled 2669 species with at least three pseudo-occurrences to explore changes in spatial patterns of anuran β-diversity across the Neotropical region due to projected climate change. (a) Species modelled with sample sizes between three and 10 pseudo-occurrences, *n* = 398. (b) Species modelled with sample sizes between 11 and 100 pseudo-occurrences, *n* = 701. (c) Species modelled with sample sizes between 101 and 1000 pseudo-occurrences, *n* = 697 . (d) Species modelled with sample sizes between 1001 and 5000 pseudo-occurrences, *n* = 358. (e) Species modelled with more than 5000 pseudo-occurrences, *n* = 515.

(a) *Adelophryne maranguapensis, Adenomera coca, Allobates bromelicola, Allobates cepedai, Allobates nidicola, Alsodes igneus, Alsodes montanus, Alsodes pehuenche, Alsodes tumultuosus, Ameerega erythromos, Ameerega ingeri, Andinobates altobueyensis, Andinobates claudiae, Andinobates dorisswansonae, Andinobates tolimensis, Andinophryne olallai, Anomaloglossus atopoglossus, Anomaloglossus breweri, Anomaloglossus murisipanensis, Anomaloglossus triunfo, Anomaloglossus wothuja, Aparasphenodon bokermanni, Aplastodiscus weygoldti, Aromobates capurinensis, Aromobates leopardalis, Atelognathus nitoi, Atelopus angelito, Atelopus ardila, Atelopus arsyecue, Atelopus chrysocorallus, Atelopus dimorphus, Atelopus epikeisthos, Atelopus eusebiodiazi, Atelopus farci, Atelopus galactogaster, Atelopus guanujo, Atelopus guitarraensis, Atelopus halihelos, Atelopus lynchi, Atelopus minutulus, Atelopus monohernandezii, Atelopus mucubajiensis, Atelopus nanay, Atelopus nicefori, Atelopus palmatus, Atelopus patazensis, Atelopus pinangoi, Atelopus pyrodactylus, Atelopus reticulatus, Atelopus siranus, Atelopus tamaense, Atopophrynus syntomopus, Bokermannohyla ahenea, Bokermannohyla diamantina, Bokermannohyla ibitipoca, Bokermannohyla izecksohni, Bokermannohyla langei, Bokermannohyla ravida, Brachycephalus brunneus, Brachycephalus izecksohni, Brachycephalus nodoterga, Brachycephalus pernix, Bryophryne hanssaueri, Bryophryne zonalis, Celsiella vozmedianoi, Centrolene acanthidiocephalum, Centrolene azulae, Centrolene condor, Centrolene gemmatum, Centrolene guanacarum, Centrolene hesperium, Centrolene huilense, Centrolene lemniscatum, Centrolene sanchezi, Centrolene solitaria, Ceratophrys testudo, Ceuthomantis cavernibardus, Chaltenobatrachus grandisonae, Charadrahyla altipotens, Chiasmocleis devriesi, Chiasmocleis mantiqueira, Chiasmocleis sapiranga, Cochranella erminea, Cochranella geijskesi, Cochranella phryxa, Colostethus alacris, Colostethus dysprosium, Colostethus lynchi, Craugastor adamastus, Craugastor campbelli, Craugastor chrysozetetes, Craugastor cruzi, Craugastor cuaquero, Craugastor glaucus, Craugastor guerreroensis, Craugastor matudai, Craugastor megalotympanum, Craugastor merendonensis, Craugastor myllomyllon, Craugastor nefrens, Craugastor omoaensis, Craugastor phasma, Craugastor pozo, Craugastor tabasarae, Craugastor taylori, Craugastor trachydermus, Crossodactylodes izecksohni, Crossodactylodes pintoi, Crossodactylus dantei, Crossodactylus lutzorum, Ctenophryne minor, Cycloramphus bandeirensis, Cycloramphus catarinensis, Dendrobates nubeculosus, Dendrophryniscus krausae, Dendrophryniscus stawiarskyi, Dendropsophus amicorum, Dendropsophus battersbyi, Dendropsophus cachimbo, Dendropsophus coffeus, Dendropsophus minimus, Dendropsophus rhea, Dendropsophus stingi, Diasporus tigrillo, Ecnomiohyla echinata, Ecnomiohyla rabborum, Ecnomiohyla thysanota, Elachistocleis bumbameuboi, Elachistocleis skotogaster, Elachistocleis surumu, Eleutherodactylus adelus, Eleutherodactylus albipes, Eleutherodactylus alticola, Eleutherodactylus bartonsmithi, Eleutherodactylus blairhedgesi, Eleutherodactylus caribe, Eleutherodactylus cavernicola, Eleutherodactylus corona, Eleutherodactylus darlingtoni, Eleutherodactylus dolomedes, Eleutherodactylus glanduliferoides, Eleutherodactylus grandis, Eleutherodactylus iberia, Eleutherodactylus jaumei, Eleutherodactylus lucioi, Eleutherodactylus maestrensis, Eleutherodactylus orientalis, Eleutherodactylus pezopetrus, Eleutherodactylus poolei, Eleutherodactylus rhodesi, Eleutherodactylus rivularis, Eleutherodactylus sciagraphus, Eleutherodactylus sisyphodemus, Eleutherodactylus teretistes, Eleutherodactylus tetajulia, Eleutherodactylus thorectes, Eleutherodactylus tonyi, Eleutherodactylus ventrilineatus, Epipedobates narinensis, Euparkerella robusta, Eupsophus migueli, Exerodonta abdivita, Exerodonta perkinsi, Gastrophryne carolinensis, Gastrotheca atympana, Gastrotheca* *flamma, Gastrotheca ossilaginis, Gastrotheca pacchamama, Gastrotheca psychrophila, Gastrotheca rebeccae, Gastrotheca splendens, Gastrotheca zeugocystis, Holoaden pholeter, Hyalinobatrachium tatayoi, Hydrolaetare caparu, Hyla cinerea, Hyla nicefori, Hylodes amnicola, Hyloscirtus pacha, Hyloxalus aeruginosus, Hyloxalus chlorocraspedus, Hyloxalus craspedoceps, Hyloxalus edwardsi, Hyloxalus eleutherodactylus, Hyloxalus leucophaeus, Hyloxalus maculosus, Hyloxalus maquipucuna, Hyloxalus marmoreoventris, Hyloxalus mystax, Hyloxalus parcus, Hyloxalus pulcherrimus, Hyloxalus ruizi, Hyloxalus saltuarius, Hyloxalus spilotogaster, Hyloxalus whymperi, Hypodactylus adercus, Hypodactylus araiodactylus, Hypodactylus fallaciosus, Hypodactylus lucida, Hypsiboas beckeri, Hypsiboas cordobae, Hypsiboas ericae, Hypsiboas exastis, Hypsiboas latistriatus, Hypsiboas leucocheilus, Hypsiboas melanopleura, Hypsiboas pulidoi, Hypsiboas varelae, Ischnocnema gehrti, Ischnocnema paranaensis, Ischnocnema randorum, Isthmohyla infucata, Isthmohyla xanthosticta, Leptodactylus hylodes, Leptodactylus magistris, Leptodactylus marambaiae, Lynchius nebulanastes, Mannophryne cordilleriana, Mannophryne lamarcai, Mannophryne larandina, Mannophryne trujillensis, Megaelosia apuana, Megaelosia bocainensis, Megaelosia boticariana, Melanophryniscus admirabilis, Melanophryniscus alipioi, Melanophryniscus macrogranulosus, Melanophryniscus peritus, Metaphryniscus sosai, Minyobates steyermarki, Myersiohyla aromatica, Myersiohyla inparquesi, Nannophryne apolobambica, Nannophryne corynetes, Niceforonia adenobrachia, Niceforonia columbiana, Noblella duellmani, Noblella lynchi, Noblella pygmaea, Nymphargus armatus, Nymphargus buenaventura, Nymphargus cariticommatus, Nymphargus chancas, Nymphargus laurae, Nymphargus mariae, Nymphargus mixomaculatus, Nymphargus nephelophila, Nymphargus oreonympha, Nymphargus spilotus, Nymphargus wileyi, Odontophrynus barrioi, Oreobates choristolemma, Oreobates lundbergi, Oreobates pereger, Oreobates zongoensis, Oreophrynella dendronastes, Oreophrynella vasquezi, Oreophrynella weiassipuensis, Osornophryne puruanta, Paratelmatobius gaigeae, Paratelmatobius lutzii, Paratelmatobius mantiqueira, Peltophryne florentinoi, Phrynopus auriculatus, Phrynopus heimorum, Phrynopus kotosh, Phrynopus nicoleae, Phrynopus peruanus, Phrynopus thompsoni, Phrynopus tribulosus, Phyllodytes brevirostris, Phyllodytes punctatus, Phyllomedusa duellmani, Phyllomedusa neildi, Phyllomedusa perinesos, Physalaemus angrensis, Physalaemus erythros, Physalaemus insperatus, Physalaemus soaresi, Phytotriades auratus, Plectrohyla ameibothalame, Plectrohyla calthula, Plectrohyla calvicollina, Plectrohyla cyanomma, Plectrohyla ephemera, Plectrohyla labedactyla, Plectrohyla miahuatlanensis, Plectrohyla pachyderma, Plectrohyla pycnochila, Plectrohyla sabrina, Plectrohyla tecunumani, Plectrohyla teuchestes, Pristimantis acerus, Pristimantis actites, Pristimantis acutirostris, Pristimantis albericoi, Pristimantis anemerus, Pristimantis aniptopalmatus, Pristimantis anotis, Pristimantis aureoventris, Pristimantis avicuporum, Pristimantis avius, Pristimantis balionotus, Pristimantis bambu, Pristimantis batrachites, Pristimantis boconoensis, Pristimantis chimu, Pristimantis coronatus, Pristimantis cremnobates, Pristimantis cuneirostris, Pristimantis dendrobatoides, Pristimantis diaphonus, Pristimantis duende, Pristimantis epacrus, Pristimantis esmeraldas, Pristimantis euphronides, Pristimantis ganonotus, Pristimantis gentryi, Pristimantis huicundo, Pristimantis ixalus, Pristimantis jester, Pristimantis katoptroides, Pristimantis lassoalcalai, Pristimantis lichenoides, Pristimantis lividus, Pristimantis lucasi, Pristimantis marahuaka, Pristimantis mars, Pristimantis memorans, Pristimantis ocreatus, Pristimantis ortizi, Pristimantis paramerus, Pristimantis pardalinus, Pristimantis pastazensis, Pristimantis percultus, Pristimantis philipi, Pristimantis pirrensis, Pristimantis rivasi, Pristimantis salaputium, Pristimantis scitulus, Pristimantis shrevei, Pristimantis simonbolivari, Pristimantis simonsii, Pristimantis spilogaster, Pristimantis stenodiscus, Pristimantis sternothylax, Pristimantis telefericus, Pristimantis thymalopsoides, Pristimantis turik, Pristimantis wiensi, Pristimantis xestus, Proceratophrys moratoi, Psychrophrynella ankohuma, Psychrophrynella chacaltaya, Psychrophrynella guillei, Psychrophrynella harveyi, Psychrophrynella iani, Psychrophrynella iatamasi, Psychrophrynella illampu, Psychrophrynella kallawaya, Psychrophrynella saltator, Psychrophrynella wettsteini, Ptychohyla dendrophasma, Ptychohyla macrotympanum, Ptychohyla sanctaecrucis, Rheobates pseudopalmatus, Rhinella lindae, Rhinella nesiotes, Rhinella scitula, Rhinella tacana, Rhinella vellardi, Rulyrana saxiscandens, Scinax arduous, Scinax aromothyella, Scinax belloni, Scinax curicica, Scinax insperatus, Scinax jolyi, Sphaenorhynchus bromelicola, Sphaenorhynchus mirim, Stefania breweri, Stefania tamacuarina, Telmatobius atacamensis, Telmatobius cirrhacelis, Telmatobius dankoi, Telmatobius gigas, Telmatobius intermedius, Telmatobius latirostris, Telmatobius necopinus, Telmatobius punctatus, Telmatobius thompsoni, Tepuihyla luteolabris, Teratohyla adenocheira, Teratohyla amelie, Trachycephalus lepidus, Truebella skoptes, Truebella tothastes, Vitreorana castroviejoi.*

(b) Adelastes hylonomos, Adelophryne baturitensis, Adelophryne patamona, Adenomera ajurauna, Agalychnis danieli, Agalychnis medinae, Agalychnis psilopygion, Allobates alessandroi, Allobates fratisenescus, Allobates humilis, Allobates juanii, Allobates mandelorum, Allobates ornatus, Allobates picachos, Allobates sanmartini, Allobates subfolionidificans, Allobates undulatus, Allobates wayuu, Alsodes barrioi, Alsodes hugoi, Alsodes kaweshkari, Alsodes valdiviensis, Alsodes verrucosus, Alsodes vittatus, Ameerega andina, Ameerega boehmei, Ameerega cainarachi, Ameerega planipaleae, Ameerega silverstonei, Ameerega smaragdina, Ameerega yungicola, Andinobates bombetes, Andinobates daleswansoni, Andinophryne atelopoides, Andinophryne colomai, Anomaloglossus ayarzaguenai, Anomaloglossus beebei, Anomaloglossus guanayensis, Anomaloglossus parkerae, Anomaloglossus praderioi,

Anomaloglossus roraima, Anomaloglossus rufulus, Anomaloglossus tamacuarensis, Aplastodiscus flumineus, Aplastodiscus musicus, Aplastodiscus sibilatus, Aromobates alboguttatus, Aromobates duranti, Aromobates haydeeae, Aromobates mayorgai, Aromobates meridensis, Aromobates molinarii, Aromobates nocturnus, Aromobates orostoma, Aromobates saltuensis, Aromobates serranus, Atelognathus ceii, Atelognathus patagonicus, Atelognathus salai, Atelognathus solitarius, Atelopus arthuri, Atelopus balios, Atelopus carauta, Atelopus carbonerensis, Atelopus carrikeri, Atelopus certus, Atelopus chocoensis, Atelopus erythropus, Atelopus eusebianus, Atelopus exiguus, Atelopus famelicus, Atelopus flavescens, Atelopus glyphus, Atelopus laetissimus, Atelopus limosus, Atelopus longibrachius, Atelopus lozanoi, Atelopus mandingues, Atelopus muisca, Atelopus nahumae, Atelopus oxapampae, Atelopus oxyrhynchus, Atelopus pedimarmoratus, Atelopus petriruizi, Atelopus pictiventris, Atelopus podocarpus, Atelopus quimbaya, Atelopus sanjosei, Atelopus senex, Atelopus sernai, Atelopus simulatus, Atelopus sonsonensis, Atelopus sorianoi, Atelopus subornatus, Atelopus walkeri, Bokermannohyla gouveai, Bokermannohyla vulcaniae, Brachycephalus alipioi, Brachycephalus ferruginus, Brachycephalus pombali, Brachycephalus vertebralis, Bryophryne bustamantei, Bryophryne cophites, Bryophryne gymnotis, Bryophryne nubilosus, Centrolene altitudinale, Centrolene bacatum, Centrolene ballux, Centrolene petrophilum, Centrolene pipilatum, Centrolene quindianum, Centrolene scirtetes, Ceuthomantis aracamuni, Ceuthomantis duellmani, Charadrahyla chaneque, Charadrahyla trux, Chiasmocleis alagoana, Cochranella duidaeana, Cochranella euhystrix, Cochranella mache, Cochranella ramirezi, Cochranella riveroi, Colostethus brachistriatus, Colostethus fugax, Colostethus furviventris, Colostethus imbricolus, Colostethus latinasus, Colostethus mertensi, Colostethus poecilonotus, Colostethus ramirezi, Colostethus ruthveni, Colostethus yaguara, Craugastor anciano, Craugastor angelicus, Craugastor aphanus, Craugastor azueroensis, Craugastor batrachylus, Craugastor catalinae, Craugastor chingopetaca, Craugastor coffeus, Craugastor cyanochthebius, Craugastor emleni, Craugastor epochthidius, Craugastor escoces, Craugastor fecundus, Craugastor greggi, Craugastor inachus, Craugastor jota, Craugastor milesi, Craugastor monnichorum, Craugastor montanus, Craugastor olanchano, Craugastor polymniae, Craugastor rayo, Craugastor saltuarius, Craugastor silvicola, Craugastor spatulatus, Craugastor stadelmani, Craugastor uno, Crossodactylus bokermanni, Crossodactylus cyclospinus, Cryptobatrachus boulengeri, Ctenophryne barbatula, Cycloramphus carvalhoi, Cycloramphus cedrensis, Cycloramphus dubius, Cycloramphus duseni, Cycloramphus juimirim, Cycloramphus migueli, Cycloramphus mirandaribeiroi, Cycloramphus ohausi, Cycloramphus organensis, Cycloramphus rhyakonastes, Cycloramphus stejnegeri, Dendrophryniscus carvalhoi, Dendrophryniscus proboscideus, Dendropsophus araguaya, Dendropsophus carnifex, Dendropsophus cerradensis, Dendropsophus garagoensis, Dendropsophus gryllatus, Dendropsophus meridensis, Dendropsophus novaisi, Dendropsophus padreluna, Dendropsophus praestans, Dendropsophus ruschii, Dendropsophus studerae, Dendropsophus yaracuyanus, Diasporus anthrax, Dischidodactylus colonnelloi, Dischidodactylus duidensis, Duellmanohyla chamulae, Duellmanohyla ignicolor, Duellmanohyla lythrodes, Duellmanohyla salvavida, Duellmanohyla soralia, Ecnomiohyla fimbrimembra, Ecnomiohyla minera, Ecnomiohyla phantasmagoria, Ecnomiohyla salvaje, Ecnomiohyla valancifer, Elachistocleis erythrogaster, Eleutherodactylus albolabris, Eleutherodactylus amadeus, Eleutherodactylus amplinympha, Eleutherodactylus andrewsi, Eleutherodactylus apostates, Eleutherodactylus armstrongi, Eleutherodactylus bakeri, Eleutherodactylus barlagnei, Eleutherodactylus brevirostris, Eleutherodactylus casparii, Eleutherodactylus chlorophenax, Eleutherodactylus cooki, Eleutherodactylus cubanus, Eleutherodactylus dennisi, Eleutherodactylus dilatus, Eleutherodactylus diplasius, Eleutherodactylus emiliae, Eleutherodactylus etheridgei, Eleutherodactylus eunaster, Eleutherodactylus fowleri, Eleutherodactylus fuscus, Eleutherodactylus glamyrus, Eleutherodactylus glandulifer, Eleutherodactylus glaucoreius, Eleutherodactylus grahami, Eleutherodactylus griphus, Eleutherodactylus gryllus, Eleutherodactylus guanahacabibes, Eleutherodactylus interorbitalis, Eleutherodactylus jasperi, Eleutherodactylus jugans, Eleutherodactylus junori, Eleutherodactylus karlschmidti, Eleutherodactylus klinikowskii, Eleutherodactylus lamprotes, Eleutherodactylus leberi, Eleutherodactylus locustus, Eleutherodactylus mariposa, Eleutherodactylus marnockii, Eleutherodactylus maurus, Eleutherodactylus melacara, Eleutherodactylus michaelschmidi, Eleutherodactylus notidodes, Eleutherodactylus nubicola, Eleutherodactylus orcutti, Eleutherodactylus parabates, Eleutherodactylus parapelates, Eleutherodactylus pentasyringos, Eleutherodactylus pinchoni, Eleutherodactylus principalis, Eleutherodactylus richmondi, Eleutherodactylus rufifemoralis, Eleutherodactylus saxatilis, Eleutherodactylus semipalmatus, Eleutherodactylus symingtoni, Eleutherodactylus syristes, Eleutherodactylus turquinensis, Eleutherodactylus verruculatus, Eleutherodactylus wightmanae, Engystomops coloradorum, Espadarana callistomma, Eupsophus septentrionalis, Excidobates mysteriosus, Exerodonta bivocata, Exerodonta catracha, Exerodonta chimalapa, Exerodonta pinorum, Gastrotheca abdita, Gastrotheca antoniiochoai, Gastrotheca aratia, Gastrotheca carinaceps, Gastrotheca espeletia, Gastrotheca galeata, Gastrotheca helenae, Gastrotheca lateonota, Gastrotheca lauzuricae, Gastrotheca piperata, Gastrotheca ruizi, Gastrotheca stictopleura, Gastrotheca trachyceps, Gastrotheca walkeri, Gastrotheca williamsoni, *Geobatrachus walkeri, Haddadus aramunha, Holoaden bradei, Hyalinobatrachium esmeralda, Hyalinobatrachium guairarepanense, Hyalinobatrachium pallidum, Hyalinobatrachium pellucidum, Hyalinobatrachium vireovittatum, Hyla bocourti, Hylodes babax, Hylodes charadranaetes, Hylodes dactylocinus, Hylodes glaber, Hylodes magalhaesi, Hylodes mertensi, Hylodes pipilans, Hylodes regius, Hylodes vanzolinii, Hyloscirtus caucanus, Hyloscirtus charazani, Hyloscirtus chlorosteus, Hyloscirtus lynchi, Hyloscirtus pantostictus, Hyloscirtus piceigularis, Hyloscirtus ptychodactylus, Hyloscirtus sarampiona, Hyloscirtus staufferorum, Hyloxalus abditaurantius, Hyloxalus betancuri, Hyloxalus borjai, Hyloxalus breviquartus, Hyloxalus cevallosi, Hyloxalus delatorreae, Hyloxalus exasperatus, Hyloxalus excisus, Hyloxalus faciopunctulatus, Hyloxalus fallax, Hyloxalus fuliginosus, Hyloxalus mittermeieri, Hyloxalus pinguis, Hyloxalus sylvaticus, Hyloxalus utcubambensis, Hyloxalus vergeli, Hypodactylus brunneus, Hypodactylus latens, Hypodactylus peraccai, Hypsiboas buriti, Hypsiboas cymbalum, Hypsiboas fuentei, Hypsiboas jimenezi, Hypsiboas palaestes, Hypsiboas riojanus, Hypsiboas roraima, Hypsiboas secedens, Hypsiboas stenocephalus, Incilius cavifrons, Incilius chompipe, Incilius cristatus, Incilius epioticus, Incilius fastidiosus, Incilius gemmifer, Incilius guanacaste, Incilius holdridgei, Incilius periglenes, Incilius peripatetes, Incilius pisinnus, Incilius spiculatus, Incilius tacanensis, Insuetophrynus acarpicus, Ischnocnema erythromera, Ischnocnema gualteri, Ischnocnema holti, Ischnocnema nigriventris, Ischnocnema pusilla, Ischnocnema sambaqui, Isthmohyla calypsa, Isthmohyla insolita, Isthmohyla melacaena, Leptodactylus cupreus, Leptodactylus fallax, Leptodactylus jolyi, Leptodactylus lauramiriamae, Leptodactylus silvanimbus, Leptodactylus tapiti, Lithobates dunni, Lithobates grylio, Lithobates lemosespinali, Lithobates omiltemanus, Lithobates tlaloci, Lynchius flavomaculatus, Lynchius parkeri, Lynchius simmonsi, Mannophryne caquetio, Mannophryne collaris, Mannophryne neblina, Mannophryne riveroi, Mannophryne trinitatis, Mannophryne venezuelensis, Mannophryne yustizi, Megaelosia jordanensis, Megaelosia lutzae, Megaelosia massarti, Megastomatohyla mixomaculata, Megastomatohyla nubicola, Megastomatohyla pellita, Melanophryniscus cambaraensis, Melanophryniscus krauczuki, Melanophryniscus langonei, Melanophryniscus moreirae, Melanophryniscus pachyrhynus, Melanophryniscus simplex, Myersiohyla kanaima, Myersiohyla loveridgei, Niceforonia nana, Noblella heyeri, Nymphargus cristinae, Nymphargus luminosus, Nymphargus luteopunctatus, Nymphargus megacheirus, Nymphargus phenax, Nymphargus pluvialis, Nymphargus rosada, Nymphargus truebae, Nymphargus vicenteruedai, Oophaga arborea, Oophaga lehmanni, Oophaga occultator, Oophaga speciosa, Oophaga vicentei, Oreobates ayacucho, Oreobates madidi, Oreobates sanderi, Oreophrynella cryptica, Oreophrynella huberi, Oreophrynella macconnelli, Oreophrynella nigra, Oreophrynella quelchii, Osornophryne antisana, Osornophryne percrassa, Osornophryne talipes, Paratelmatobius cardosoi, Paratelmatobius poecilogaster, Peltophryne fluviatica, Peltophryne fracta, Peltophryne lemur, Phasmahyla spectabilis, Phasmahyla timbo, Phrynomedusa appendiculata, Phrynomedusa bokermanni, Phrynomedusa fimbriata, Phrynopus barthlenae, Phrynopus bracki, Phrynopus bufoides, Phrynopus dagmarae, Phrynopus horstpauli, Phrynopus juninensis, Phrynopus kauneorum, Phrynopus oblivius, Phyllobates terribilis, Phyllodytes gyrinaethes, Phyllodytes tuberculosus, Phyllomedusa ayeaye, Phyllomedusa baltea, Phyllomedusa centralis, Phyllomedusa oreades, Physalaemus barrioi, Physalaemus deimaticus, Physalaemus irroratus, Physalaemus rupestris, Pipa myersi, Plectrohyla acanthodes, Plectrohyla celata, Plectrohyla cembra, Plectrohyla chryses, Plectrohyla chrysopleura, Plectrohyla crassa, Plectrohyla dasypus, Plectrohyla exquisita, Plectrohyla hazelae, Plectrohyla ixil, Plectrohyla lacertosa, Plectrohyla mykter, Plectrohyla pokomchi, Plectrohyla psiloderma, Plectrohyla robertsorum, Plectrohyla thorectes, Pleurodema somuncurense, Pristimantis actinolaimus, Pristimantis adiastolus, Pristimantis aemulatus, Pristimantis affinis, Pristimantis albertus, Pristimantis amydrotus, Pristimantis angustilineatus, Pristimantis apiculatus, Pristimantis aquilonaris, Pristimantis atrabracus, Pristimantis aurantiguttatus, Pristimantis bacchus, Pristimantis baiotis, Pristimantis bellona, Pristimantis bernali, Pristimantis briceni, Pristimantis cabrerai, Pristimantis cacao, Pristimantis caeruleonotus, Pristimantis capitonis, Pristimantis carlossanchezi, Pristimantis carmelitae, Pristimantis carranguerorum, Pristimantis citriogaster, Pristimantis colomai, Pristimantis colonensis, Pristimantis colostichos, Pristimantis cordovae, Pristimantis cosnipatae, Pristimantis cristinae, Pristimantis cruciocularis, Pristimantis cuentasi, Pristimantis degener, Pristimantis delicatus, Pristimantis delius, Pristimantis devillei, Pristimantis diogenes, Pristimantis dissimulatus, Pristimantis divnae, Pristimantis eugeniae, Pristimantis fasciatus, Pristimantis fetosus, Pristimantis flabellidiscus, Pristimantis flavobracatus, Pristimantis ginesi, Pristimantis gladiator, Pristimantis glandulosus, Pristimantis grandiceps, Pristimantis hectus, Pristimantis helvolus, Pristimantis hernandezi, Pristimantis ignicolor, Pristimantis incanus, Pristimantis incertus, Pristimantis infraguttatus, Pristimantis insignitus, Pristimantis jaimei, Pristimantis jorgevelosai, Pristimantis jubatus, Pristimantis kareliae, Pristimantis kelephus, Pristimantis lancinii, Pristimantis lasalleorum, Pristimantis lentiginosus, Pristimantis leucopus, Pristimantis librarius, Pristimantis lindae, Pristimantis lirellus, Pristimantis loustes, Pristimantis luteolateralis, Pristimantis lutitus, Pristimantis lynchi, Pristimantis maculosus, Pristimantis meridionalis, Pristimantis merostictus, Pristimantis metabates, Pristimantis minutulus, Pristimantis mnionaetes, Pristimantis modipeplus, Pristimantis moro,* *Pristimantis nebulosus, Pristimantis ornatus, Pristimantis parectatus, Pristimantis peraticus, Pristimantis petrobardus, Pristimantis phalaroinguinis, Pristimantis phalarus, Pristimantis phragmipleuron, Pristimantis pinguis, Pristimantis pleurostriatus, Pristimantis pruinatus, Pristimantis pteridophilus, Pristimantis ptochus, Pristimantis quantus, Pristimantis reclusas, Pristimantis renjiforum, Pristimantis repens, Pristimantis reticulatus, Pristimantis rhabdocnemus, Pristimantis rhigophilus, Pristimantis rhodoplichus, Pristimantis riveroi, Pristimantis rozei, Pristimantis ruthveni, Pristimantis saltissimus, Pristimantis satagius, Pristimantis scoloblepharus, Pristimantis scopaeus, Pristimantis seorsus, Pristimantis signifer, Pristimantis simoteriscus, Pristimantis simoterus, Pristimantis siopelus, Pristimantis sobetes, Pristimantis spinosus, Pristimantis stictoboubonus, Pristimantis suetus, Pristimantis sulculus, Pristimantis taciturnus, Pristimantis tantanti, Pristimantis tanyrhynchus, Pristimantis thyellus, Pristimantis turumiquirensis, Pristimantis uisae, Pristimantis vanadise, Pristimantis veletis, Pristimantis versicolor, Pristimantis vidua, Pristimantis vilcabambae, Pristimantis viridicans, Pristimantis viridis, Pristimantis wagteri, Pristimantis waoranii, Pristimantis xeniolum, Pristimantis xylochobates, Pristimantis yaviensis, Pristimantis yukpa, Pristimantis zoilae, Pristimantis zophus, Proceratophrys concavitympanum, Proceratophrys cururu, Proceratophrys palustris, Proceratophrys phyllostomus, Prostherapis dunni, Psychrophrynella adenopleura, Psychrophrynella boettgeri, Psychrophrynella katantika, Psychrophrynella pinguis, Psychrophrynella quimsacruzis, Ptychohyla acrochorda, Ptychohyla legleri, Ptychohyla leonhardschultzei, Ptychohyla panchoi, Ptychohyla spinipollex, Ranitomeya summersi, Rhaebo lynchi, Rhinella acrolopha, Rhinella alata, Rhinella amboroensis, Rhinella arborescandens, Rhinella chavin, Rhinella chrysophora, Rhinella cristinae, Rhinella iserni, Rhinella macrorhina, Rhinella magnussoni, Rhinella manu, Rhinella multiverrucosa, Rhinella nicefori, Rhinella rostrata, Rhinella ruizi, Rhinella sclerocephala, Rhinella tenrec, Sachatamia orejuela, Scinax angrensis, Scinax ariadne, Scinax cabralensis, Scinax danae, Scinax heyeri, Scinax jureia, Scinax karenanneae, Scinax melloi, Scinax pinima, Silverstoneia erasmios, Stefania ackawaio, Stefania ayangannae, Stefania coxi, Stefania goini, Stefania marahuaquensis, Stefania riae, Stefania riveroi, Stefania roraimae, Stefania satelles, Stefania schuberti, Strabomantis helonotus, Strabomantis ingeri, Strabomantis laticorpus, Strabomantis ruizi, Telmatobius colanensis, Telmatobius contrerasi, Telmatobius degener, Telmatobius edaphonastes, Telmatobius halli, Telmatobius hauthali, Telmatobius hockingi, Telmatobius hypselocephalus, Telmatobius ignavus, Telmatobius laticeps, Telmatobius mayoloi, Telmatobius oxycephalus, Telmatobius pefauri, Telmatobius philippii, Telmatobius pinguiculus, Telmatobius pisanoi, Telmatobius platycephalus, Telmatobius scrocchii, Telmatobius stephani, Telmatobius timens, Telmatobius vellardi, Telmatobius vilamensis, Telmatobius zapahuirensis, Tepuihyla aecii, Tepuihyla rimarum, Tepuihyla rodriguezi, Tepuihyla warreni, Vitreorana gorzulae, Vitreorana helenae, Vitreorana parvula, Yunganastes ashkapara, Yunganastes bisignatus.*

(c) *Adelophryne pachydactyla, Adenomera araucaria, Adenomera lutzi, Adenomera nana, Adenomera thomei, Agalychnis annae, Agalychnis aspera, Agalychnis granulosa, Agalychnis lemur, Agalychnis saltator, Allobates algorei, Allobates caeruleodactylus, Allobates crombiei, Allobates insperatus, Allobates kingsburyi, Allobates masniger, Allobates melanolaemus, Allobates niputidea, Allobates paleovarzensis, Allobates pittieri, Allobates ranoides, Alsodes australis, Alsodes gargola, Alsodes nodosus, Amazophrynella bokermanni, Ameerega boliviana, Ameerega pongoensis, Ameerega pulchripecta, Ameerega rubriventris, Anaxyrus woodhousii, Andinobates opisthomelas, Andinobates viridis, Andinobates virolinensis, Anomaloglossus kaiei, Anomaloglossus lacrimosus, Anomaloglossus shrevei, Anomaloglossus tepuyensis, Anotheca spinosa, Aplastodiscus albofrenatus, Aplastodiscus callipygius, Aplastodiscus cochranae, Aplastodiscus eugenioi, Aplastodiscus ibirapitanga, Atelognathus praebasalticus, Atelognathus reverberii, Atelopus andinus, Atelopus bomolochos, Atelopus boulengeri, Atelopus chiriquiensis, Atelopus coynei, Atelopus cruciger, Atelopus ebenoides, Atelopus elegans, Atelopus ignescens, Atelopus longirostris, Atelopus mindoensis, Atelopus nepiozomus, Atelopus pachydermus, Atelopus pastuso, Atelopus petersi, Atelopus planispina, Atelopus pulcher, Atelopus seminiferus, Atelopus zeteki, Barycholos pulcher, Batrachyla nibaldoi, Bokermannohyla caramaschii, Bokermannohyla carvalhoi, Bokermannohyla claresignata, Bokermannohyla clepsydra, Bokermannohyla itapoty, Bokermannohyla luctuosa, Bokermannohyla nanuzae, Bokermannohyla oxente, Bokermannohyla sagarana, Bromeliohyla bromeliacia, Bromeliohyla dendroscarta, Celsiella revocata, Centrolene antioquiense, Centrolene daidaleum, Centrolene geckoideum, Centrolene heloderma, Centrolene hybrida, Centrolene lynchi, Centrolene medemi, Centrolene notostictum, Centrolene peristictum, Centrolene robledoi, Centrolene savagei, Centrolene venezuelense, Ceratophrys stolzmanni, Charadrahyla nephila, Charadrahyla taeniopus, Chiasmocleis capixaba, Chiasmocleis magnova, Chimerella mariaelenae, Cochranella balionota, Cochranella litoralis, Cochranella megista, Cochranella nola, Cochranella xanthocheridia, Colostethus agilis, Colostethus argyrogaster, Colostethus jacobuspetersi, Colostethus thorntoni, Colostethus ucumari, Craugastor amniscola, Craugastor andi, Craugastor aurilegulus, Craugastor bocourti, Craugastor brocchi, Craugastor chac, Craugastor charadra, Craugastor daryi,*

Craugastor decoratus, Craugastor emcelae, Craugastor fleischmanni, Craugastor gulosus, Craugastor hobartsmithi, Craugastor laticeps, Craugastor lauraster, Craugastor lineatus, Craugastor melanostictus, Craugastor obesus, Craugastor omiltemanus, Craugastor palenque, Craugastor pechorum, Craugastor pelorus, Craugastor persimilis, Craugastor podiciferus, Craugastor polyptychus, Craugastor psephosypharus, Craugastor punctariolus, Craugastor pygmaeus, Craugastor rhodopis, Craugastor rhyacobatrachus, Craugastor rivulus, Craugastor rostralis, Craugastor rugosus, Craugastor sabrinus, Craugastor sandersoni, Craugastor stejnegerianus, Craugastor stuarti, Craugastor tarahumaraensis, Craugastor taurus, Craugastor underwoodi, Craugastor vulcani, Craugastor xucanebi, Crossodactylodes bokermanni, Crossodactylus grandis, Crossodactylus trachystomus, Cryptobatrachus fuhrmanni, Ctenophryne aequatorialis, Ctenophryne carpish, Cycloramphus acangatan, Cycloramphus asper, Cycloramphus brasiliensis, Cycloramphus diringshofeni, Cycloramphus granulosus, Cycloramphus izecksohni, Cycloramphus semipalmatus, Cycloramphus valae, Dasypops schirchi, Dendrophryniscus berthalutzae, Dendropsophus bogerti, Dendropsophus columbianus, Dendropsophus dutrai, Dendropsophus gaucheri, Dendropsophus juliani, Dendropsophus meridianus, Dendropsophus nahdereri, Dendropsophus pseudomeridianus, Dendropsophus reichlei, Dendropsophus sartori, Dendropsophus virolinensis, Diasporus hylaeformis, Duellmanohyla schmidtorum, Duellmanohyla uranochroa, Ecnomiohyla miliaria, Edalorhina nasuta, Elachistocleis matogrosso, Eleutherodactylus acmonis, Eleutherodactylus alcoae, Eleutherodactylus angustidigitorum, Eleutherodactylus antillensis, Eleutherodactylus audanti, Eleutherodactylus auriculatoides, Eleutherodactylus brittoni, Eleutherodactylus cochranae, Eleutherodactylus coqui, Eleutherodactylus counouspeus, Eleutherodactylus cundalli, Eleutherodactylus cuneatus, Eleutherodactylus cystignathoides, Eleutherodactylus eneidae, Eleutherodactylus furcyensis, Eleutherodactylus glaphycompus, Eleutherodactylus goini, Eleutherodactylus gossei, Eleutherodactylus grabhami, Eleutherodactylus greyi, Eleutherodactylus guantanamera, Eleutherodactylus gundlachi, Eleutherodactylus guttilatus, Eleutherodactylus haitianus, Eleutherodactylus hedricki, Eleutherodactylus heminota, Eleutherodactylus hypostenor, Eleutherodactylus intermedius, Eleutherodactylus ionthus, Eleutherodactylus jamaicensis, Eleutherodactylus leoncei, Eleutherodactylus leprus, Eleutherodactylus limbatus, Eleutherodactylus longipes, Eleutherodactylus luteolus, Eleutherodactylus martinicensis, Eleutherodactylus minutus, Eleutherodactylus modestus, Eleutherodactylus montanus, Eleutherodactylus nortoni, Eleutherodactylus oxyrhyncus, Eleutherodactylus pallidus, Eleutherodactylus pantoni, Eleutherodactylus paralius, Eleutherodactylus patriciae, Eleutherodactylus paulsoni, Eleutherodactylus pinarensis, Eleutherodactylus pituinus, Eleutherodactylus portoricensis, Eleutherodactylus probolaeus, Eleutherodactylus ricordii, Eleutherodactylus ronaldi, Eleutherodactylus rubrimaculatus, Eleutherodactylus ruthae, Eleutherodactylus schmidti, Eleutherodactylus sommeri, Eleutherodactylus thomasi, Eleutherodactylus toa, Eleutherodactylus varians, Eleutherodactylus verrucipes, Eleutherodactylus wetmorei, Eleutherodactylus zeus, Eleutherodactylus zugi, Engystomops guayaco, Engystomops montubio, Engystomops randi, Epipedobates anthonyi, Epipedobates tricolor, Espadarana durrellorum, Euparkerella brasiliensis, Euparkerella cochranae, Eupsophus contulmoensis, Eupsophus nahuelbutensis, Excidobates captivus, Exerodonta juanitae, Exerodonta melanomma, Exerodonta xera, Flectonotus fitzgeraldi, Frostius erythrophthalmus, Gastrotheca aguaruna, Gastrotheca andaquiensis, Gastrotheca angustifrons, Gastrotheca antomia, Gastrotheca argenteovirens, Gastrotheca aureomaculata, Gastrotheca bufona, Gastrotheca christiani, Gastrotheca chrysosticta, Gastrotheca dendronastes, Gastrotheca dunni, Gastrotheca ernestoi, Gastrotheca excubitor, Gastrotheca fulvorufa, Gastrotheca gracilis, Gastrotheca griswoldi, Gastrotheca guentheri, Gastrotheca litonedis, Gastrotheca ochoai, Gastrotheca orophylax, Gastrotheca ovifera, Gastrotheca plumbea, Gastrotheca pseustes, Gastrotheca riobambae, Hamptophryne alios, Hemiphractus johnsoni, Holoaden luederwaldti, Hyalinobatrachium chirripoi, Hyalinobatrachium duranti, Hyalinobatrachium fragile, Hyalinobatrachium ibama, Hyalinobatrachium orientale, Hyalinobatrachium ruedai, Hyalinobatrachium talamancae, Hyla arboricola, Hyla euphorbiacea, Hyla squirella, Hyla walkeri, Hylodes cardosoi, Hylodes heyeri, Hylodes meridionalis, Hylodes ornatus, Hylodes otavioi, Hylodes perplicatus, Hylodes sazimai, Hylodes uai, Hyloscirtus bogotensis, Hyloscirtus callipeza, Hyloscirtus colymba, Hyloscirtus denticulentus, Hyloscirtus jahni, Hyloscirtus larinopygion, Hyloscirtus lascinius, Hyloscirtus lindae, Hyloscirtus platydactylus, Hyloscirtus psarolaimus, Hyloscirtus simmonsi, Hyloscirtus torrenticola, Hyloxalus anthracinus, Hyloxalus awa, Hyloxalus azureiventris, Hyloxalus chocoensis, Hyloxalus elachyhistus, Hyloxalus fascianigrus, Hyloxalus idiomelus, Hyloxalus insulatus, Hyloxalus littoralis, Hyloxalus pulchellus, Hyloxalus ramosi, Hyloxalus shuar, Hyloxalus sordidatus, Hyloxalus subpunctatus, Hyloxalus toachi, Hyloxalus vertebralis, Hypodactylus babax, Hypodactylus dolops, Hypodactylus elassodiscus, Hypopachus barberi, Hypsiboas alemani, Hypsiboas callipleura, Hypsiboas curupi, Hypsiboas joaquini, Hypsiboas liliae, Hypsiboas marginatus, Hypsiboas phaeopleura, Hypsiboas rhythmicus, Hypsiboas semiguttatus, Hypsiboas stellae, Ikakogi tayrona, Incilius aucoinae, Incilius bocourti, Incilius campbelli, Incilius canaliferus, Incilius cycladen, Incilius ibarrai, Incilius leucomyos, Incilius macrocristatus, Incilius melanochlorus, Incilius perplexus, Incilius porteri, Incilius signifer, Incilius tutelarius, Ischnocnema bolbodactyla, *Ischnocnema hoehnei, Ischnocnema izecksohni, Ischnocnema manezinho, Ischnocnema octavioi, Ischnocnema spanios, Ischnocnema venancioi, Isthmohyla angustilineata, Isthmohyla debilis, Isthmohyla graceae, Isthmohyla lancasteri, Isthmohyla picadoi, Isthmohyla pictipes, Isthmohyla pseudopuma, Isthmohyla rivularis, Isthmohyla tica, Isthmohyla zeteki, Leptodactylus albilabris, Leptodactylus camaquara, Leptodactylus peritoaktites, Leptodactylus sabanensis, Leptodactylus turimiquensis, Leptodactylus validus, Leptodactylus viridis, Lithobates bwana, Lithobates johni, Lithobates juliani, Lithobates macroglossa, Lithobates pipiens, Lithobates sierramadrensis, Lithobates vibicarius, Lithobates yavapaiensis, Mannophryne herminae, Mannophryne leonardoi, Mannophryne oblitterata, Megaelosia goeldii, Melanophryniscus devincenzii, Melanophryniscus dorsalis, Melanophryniscus montevidensis, Melanophryniscus sanmartini, Nannophryne cophotis, Noblella carrascoicola, Noblella lochites, Noblella ritarasquinae, Nymphargus chami, Nymphargus cochranae, Nymphargus garciae, Nymphargus griffithsi, Nymphargus ignotus, Nymphargus prasinus, Nymphargus ruizi, Nymphargus siren, Odontophrynus achalensis, Oophaga granulifera, Oreobates crepitans, Oreobates heterodactylus, Oreobates ibischi, Oreobates lehri, Oreobates sanctaecrucis, Oreobates saxatilis, Osornophryne guacamayo, Osteocephalus alboguttatus, Osteocephalus fuscifacies, Osteocephalus heyeri, Osteocephalus verruciger, Osteopilus crucialis, Osteopilus marianae, Osteopilus ocellatus, Osteopilus wilderi, Peltophryne cataulaciceps, Peltophryne longinasus, Peltophryne taladai, Phrynopus montium, Phyllobates aurotaenia, Phyllobates bicolor, Phyllobates vittatus, Phyllodytes edelmoi, Phyllodytes maculosus, Phyllodytes wuchereri, Phyllomedusa megacephala, Physalaemus caete, Physalaemus erikae, Physalaemus evangelistai, Physalaemus jordanensis, Physalaemus maximus, Physalaemus moreirae, Physalaemus spiniger, Plectrohyla arborescandens, Plectrohyla avia, Plectrohyla charadricola, Plectrohyla cyclada, Plectrohyla glandulosa, Plectrohyla hartwegi, Plectrohyla matudai, Plectrohyla pentheter, Plectrohyla quecchi, Plectrohyla sagorum, Pleurodema kriegi, Pristimantis acatallelus, Pristimantis alalocophus, Pristimantis altae, Pristimantis altamnis, Pristimantis anolirex, Pristimantis appendiculatus, Pristimantis ardalonychus, Pristimantis atratus, Pristimantis baryecuus, Pristimantis bearsei, Pristimantis bellator, Pristimantis bicolor, Pristimantis bicumulus, Pristimantis bogotensis, Pristimantis brevifrons, Pristimantis bromeliaceus, Pristimantis cajamarcensis, Pristimantis calcaratus, Pristimantis calcarulatus, Pristimantis cantitans, Pristimantis celator, Pristimantis ceuthospilus, Pristimantis chloronotus, Pristimantis chrysops, Pristimantis colodactylus, Pristimantis condor, Pristimantis corniger, Pristimantis corrugatus, Pristimantis crenunguis, Pristimantis crucifer, Pristimantis cryophilius, Pristimantis cryptomelas, Pristimantis culatensis, Pristimantis curtipes, Pristimantis deinops, Pristimantis dorsopictus, Pristimantis douglasi, Pristimantis duellmani, Pristimantis dundeei, Pristimantis elegans, Pristimantis eremitus, Pristimantis eriphus, Pristimantis exoristus, Pristimantis factiosus, Pristimantis fallax, Pristimantis floridus, Pristimantis frater, Pristimantis gracilis, Pristimantis hybotragus, Pristimantis illotus, Pristimantis incomptus, Pristimantis inusitatus, Pristimantis johannesdei, Pristimantis juanchoi, Pristimantis laticlavius, Pristimantis lemur, Pristimantis leoni, Pristimantis leptolophus, Pristimantis llojsintuta, Pristimantis luscombei, Pristimantis lythrodes, Pristimantis medemi, Pristimantis megalops, Pristimantis melanogaster, Pristimantis melanoproctus, Pristimantis miyatai, Pristimantis molybrignus, Pristimantis mondolfii, Pristimantis muricatus, Pristimantis muscosus, Pristimantis museosus, Pristimantis myersi, Pristimantis myops, Pristimantis nephophilus, Pristimantis nervicus, Pristimantis nicefori, Pristimantis nigrogriseus, Pristimantis nyctophylax, Pristimantis obmutescens, Pristimantis ocellatus, Pristimantis olivaceus, Pristimantis orcesi, Pristimantis orestes, Pristimantis ornatissimus, Pristimantis orpacobates, Pristimantis orphnolaimus, Pristimantis padrecarlosi, Pristimantis paisa, Pristimantis palmeri, Pristimantis pardalis, Pristimantis pataikos, Pristimantis pecki, Pristimantis pedimontanus, Pristimantis penelopus, Pristimantis permixtus, Pristimantis petersi, Pristimantis phoxocephalus, Pristimantis platychilus, Pristimantis polychrus, Pristimantis prolatus, Pristimantis proserpens, Pristimantis pugnax, Pristimantis pycnodermis, Pristimantis pyrrhomerus, Pristimantis quinquagesimus, Pristimantis racemus, Pristimantis restrepoi, Pristimantis rhodostichus, Pristimantis riveti, Pristimantis rosadoi, Pristimantis roseus, Pristimantis rubicundus, Pristimantis ruedai, Pristimantis rufioculis, Pristimantis samaipatae, Pristimantis sanctaemartae, Pristimantis sanguineus, Pristimantis savagei, Pristimantis schultei, Pristimantis scolodiscus, Pristimantis serendipitus, Pristimantis silverstonei, Pristimantis supernatis, Pristimantis surdus, Pristimantis susaguae, Pristimantis tamsitti, Pristimantis tayrona, Pristimantis tenebrionis, Pristimantis terraebolivaris, Pristimantis thectopternus, Pristimantis thymelensis, Pristimantis trachyblepharis, Pristimantis truebae, Pristimantis tubernasus, Pristimantis unistrigatus, Pristimantis uranobates, Pristimantis urichi, Pristimantis verecundus, Pristimantis vertebralis, Pristimantis vicarius, Pristimantis viejas, Pristimantis yustizi, Proceratophrys brauni, Proceratophrys melanopogon, Proceratophrys moehringi, Pseudis cardosoi, Pseudopaludicola canga, Pseudopaludicola mineira, Psychrophrynella kempffi, Psychrophrynella usurpator, Ptychohyla erythromma, Ptychohyla euthysanota, Ptychohyla salvadorensis, Ptychohyla zophodes, Ranitomeya amazonica, Ranitomeya benedicta, Ranitomeya fantastica, Ranitomeya flavovittata, Ranitomeya imitator, Ranitomeya variabilis, Rheobates palmatus, Rhinella atacamensis, Rhinella diptycha, Rhinella gallardoi, Rhinella gnustae, Rhinella justinianoi,* *Rhinella lescurei, Rhinella pygmaea, Rhinella quechua, Rhinella rubropunctata, Rhinella rumbolli, Rulyrana adiazeta, Rulyrana mcdiarmidi, Rulyrana spiculata, Rulyrana susatamai, Rupirana cardosoi, Sachatamia punctulata, Scinax albicans, Scinax altae, Scinax atratus, Scinax baumgardneri, Scinax canastrensis, Scinax exiguus, Scinax littoralis, Scinax littoreus, Scinax manriquei, Scinax maracaya, Scinax ranki, Scinax sugillatus, Scinax tigrinus, Scinax trapicheiroi, Scythrophrys sawayae, Smilisca puma, Stefania ginesi, Stefania oculosa, Stefania percristata, Stefania scalae, Stefania woodleyi, Stereocyclops parkeri, Strabomantis anatipes, Strabomantis biporcatus, Strabomantis cheiroplethus, Strabomantis necerus, Strabomantis necopinus, Telmatobius atahualpai, Telmatobius bolivianus, Telmatobius brachydactylus, Telmatobius brevipes, Telmatobius brevirostris, Telmatobius carrillae, Telmatobius ceiorum, Telmatobius culeus, Telmatobius espadai, Telmatobius huayra, Telmatobius macrostomus, Telmatobius niger, Telmatobius peruvianus, Telmatobius rimac, Telmatobius sanborni, Telmatobius schreiteri, Telmatobius sibiricus, Telmatobius truebae, Telmatobius verrucosus, Telmatobius yuracare, Telmatobufo australis, Telmatobufo bullocki, Tepuihyla edelcae, Thoropa petropolitana, Thoropa saxatilis, Tlalocohyla godmani, Vitreorana antisthenesi, Vitreorana ritae, Xenohyla eugenioi, Xenohyla truncata, Yunganastes fraudator, Yunganastes pluvicanorus, Zachaenus parvulus.*

(d) *Adelphobates castaneoticus, Agalychnis buckleyi, Agalychnis hulli, Agalychnis moreletii, Allobates gasconi, Allobates goianus, Allobates granti, Allobates mcdiarmidi, Allobates myersi, Allobates vanzolinius, Allobates zaparo, Ameerega bassleri, Ameerega berohoka, Ameerega bilinguis, Ameerega macero, Ameerega petersi, Ameerega simulans, Anaxyrus compactilis, Anaxyrus debilis, Anaxyrus kelloggi, Anaxyrus speciosus, Andinobates fulguritus, Andinobates minutus, Anomaloglossus stepheni, Aparasphenodon venezolanus, Aplastodiscus albosignatus, Aplastodiscus cavicola, Aplastodiscus ehrhardti, Arcovomer passarellii, Argenteohyla siemersi, Atelopus franciscus, Atelopus peruensis, Atelopus spurrelli, Atelopus tricolor, Atelopus varius, Bokermannohyla astartea, Bokermannohyla circumdata, Bokermannohyla hylax, Bokermannohyla martinsi, Bokermannohyla saxicola, Bokermannohyla sazimai, Brachycephalus didactylus, Brachycephalus hermogenesi, Ceratophrys joazeirensis, Chiasmocleis anatipes, Chiasmocleis atlantica, Chiasmocleis centralis, Chiasmocleis schubarti, Cochranella euknemos, Cochranella resplendens, Colostethus fraterdanieli, Colostethus inguinalis, Colostethus panamansis, Colostethus pratti, Craugastor alfredi, Craugastor berkenbuschii, Craugastor bransfordii, Craugastor crassidigitus, Craugastor gollmeri, Craugastor laevissimus, Craugastor mexicanus, Craugastor mimus, Craugastor occidentalis, Craugastor opimus, Craugastor ranoides, Craugastor rugulosus, Craugastor rupinius, Craugastor talamancae, Craugastor yucatanensis, Crossodactylus aeneus, Crossodactylus caramaschii, Crossodactylus dispar, Crossodactylus gaudichaudii, Crossodactylus schmidti, Cruziohyla calcarifer, Cycloramphus bolitoglossus, Cycloramphus boraceiensis, Cycloramphus lutzorum, Dendrobates truncatus, Dendrophryniscus brevipollicatus, Dendrophryniscus leucomystax, Dendropsophus aperomeus, Dendropsophus berthalutzae, Dendropsophus delarivai, Dendropsophus giesleri, Dendropsophus haddadi, Dendropsophus jimi, Dendropsophus labialis, Dendropsophus luteoocellatus, Dendropsophus mathiassoni, Dendropsophus robertmertensi, Dendropsophus subocularis, Dendropsophus tintinnabulum, Dendropsophus werneri, Diasporus gularis, Diasporus quidditus, Diasporus tinker, Diasporus vocator, Duellmanohyla rufioculis, Ecnomiohyla miotympanum, Elachistocleis carvalhoi, Eleutherodactylus abbotti, Eleutherodactylus atkinsi, Eleutherodactylus auriculatus, Eleutherodactylus bilineatus, Eleutherodactylus dimidiatus, Eleutherodactylus eileenae, Eleutherodactylus flavescens, Eleutherodactylus inoptatus, Eleutherodactylus johnstonei, Eleutherodactylus pictissimus, Eleutherodactylus pipilans, Eleutherodactylus planirostris, Eleutherodactylus riparius, Eleutherodactylus varleyi, Eleutherodactylus weinlandi, Engystomops pustulatus, Epipedobates boulengeri, Epipedobates machalilla, Espadarana andina, Eupsophus emiliopugini, Eupsophus roseus, Eupsophus vertebralis, Exerodonta sumichrasti, Flectonotus fissilis, Flectonotus pygmaeus, Fritziana ohausi, Frostius pernambucensis, Gastrotheca albolineata, Gastrotheca cornuta, Gastrotheca longipes, Gastrotheca monticola, Gastrotheca peruana, Gastrotheca weinlandii, Hemiphractus bubalus, Hemiphractus fasciatus, Hyalinobatrachium aureoguttatum, Hyalinobatrachium iaspidiense, Hyla plicata, Hyla wrightorum, Hylodes asper, Hylodes lateristrigatus, Hylodes phyllodes, Hylorina sylvatica, Hyloscirtus albopunctulatus, Hyloscirtus alytolylax, Hyloscirtus armatus, Hyloscirtus palmeri, Hyloxalus bocagei, Hyloxalus infraguttatus, Hyloxalus lehmanni, Hyloxalus nexipus, Hyloxalus sauli, Hypodactylus mantipus, Hypopachus pictiventris, Hypsiboas alboniger, Hypsiboas atlanticus, Hypsiboas balzani, Hypsiboas caingua, Hypsiboas cipoensis, Hypsiboas guentheri, Hypsiboas heilprini, Hypsiboas hutchinsi, Hypsiboas lemai, Hypsiboas marianitae, Hypsiboas pellucens, Hypsiboas picturatus, Hypsiboas pombali, Hypsiboas rubracylus, Hypsiboas rufitelus, Hypsiboas tepuianus, Incilius alvarius, Incilius mazatlanensis, Incilius nebulifer, Ischnocnema henselii, Ischnocnema penaxavantinho, Ischnocnema verrucosa, Leptodactylus flavopictus, Leptodactylus griseigularis, Leptodactylus labrosus, Leptodactylus rhodomerus, Lithobates chiricahuensis, Lithobates magnaocularis, Lithobates megapoda, Lithobates montezumae, Lithobates neovolcanicus, Lithobates psilonota, Lithobates pustulosus, Lithobates spectabilis, Lithobates tarahumarae, Lithobates taylori, Lithobates zweifeli, Lysapsus laevis, Melanophryniscus cupreuscapularis, Melanophryniscus fulvoguttatus, Melanophryniscus rubriventris, Melanophryniscus stelzneri, Myersiella microps, Nyctimantis rugiceps, Nymphargus bejaranoi, Nymphargus grandisonae, Nymphargus ocellatus, Nymphargus posadae, Odontophrynus cordobae,* *Odontophrynus salvatori, Oophaga histrionica, Oophaga pumilio, Oophaga sylvatica, Oreobates discoidalis, Osornophryne bufoniformis, Osteocephalus castaneicola, Osteocephalus deridens, Osteocephalus leoniae, Osteocephalus mutabor, Osteopilus dominicensis, Osteopilus pulchrilineatus, Osteopilus vastus, Otophryne robusta, Otophryne steyermarki, Peltophryne empusa, Peltophryne fustiger, Peltophryne guentheri, Peltophryne gundlachi, Peltophryne peltocephala, Phasmahyla cochranae, Phasmahyla exilis, Phasmahyla guttata, Phasmahyla jandaia, Phrynomedusa marginata, Phrynomedusa vanzolinii, Phyllobates lugubris, Phyllodytes acuminatus, Phyllodytes kautskyi, Phyllodytes melanomystax, Phyllomedusa bahiana, Phyllomedusa coelestis, Phyllomedusa trinitatis, Physalaemus aguirrei, Physalaemus crombiei, Physalaemus fernandezae, Physalaemus lisei, Physalaemus nanus, Physalaemus obtectus, Physalaemus santafecinus, Pipa aspera, Pipa parva, Plectrohyla guatemalensis, Pleurodema borellii, Pleurodema guayapae, Pristimantis aaptus, Pristimantis aureolineatus, Pristimantis boulengeri, Pristimantis buccinator, Pristimantis buckleyi, Pristimantis caprifer, Pristimantis caryophyllaceus, Pristimantis cerasinus, Pristimantis chalceus, Pristimantis cruentus, Pristimantis danae, Pristimantis erythropleura, Pristimantis galdi, Pristimantis imitatrix, Pristimantis kichwarum, Pristimantis labiosus, Pristimantis latidiscus, Pristimantis lymani, Pristimantis parvillus, Pristimantis paulodutrai, Pristimantis paululus, Pristimantis percnopterus, Pristimantis piceus, Pristimantis prolixodiscus, Pristimantis pseudoacuminatus, Pristimantis quaquaversus, Pristimantis subsigillatus, Pristimantis vinhai, Pristimantis walkeri, Pristimantis zimmermanae, Proceratophrys bigibbosa, Proceratophrys goyana, Proceratophrys laticeps, Proceratophrys subguttata, Proceratophrys vielliardi, Pseudis fusca, Pseudopaludicola pusilla, Ptychohyla hypomykter, Rhaebo blombergi, Rhaebo caeruleostictus, Rhaebo hypomelas, Rhaebo nasicus, Rhinella abei, Rhinella achalensis, Rhinella arunco, Rhinella festae, Rhinella fissipes, Rhinella inca, Rhinella limensis, Rhinella stanlaii, Rhinella sternosignata, Rhinoderma rufum, Rulyrana flavopunctata, Sachatamia albomaculata, Sachatamia ilex, Scinax agilis, Scinax brieni, Scinax caldarum, Scinax camposseabrai, Scinax cardosoi, Scinax carnevallii, Scinax castroviejoi, Scinax catharinae, Scinax centralis, Scinax constrictus, Scinax cretatus, Scinax crospedospilus, Scinax duartei, Scinax elaeochrous, Scinax hiemalis, Scinax humilis, Scinax ictericus, Scinax iquitorum, Scinax kennedyi, Scinax lindsayi, Scinax longilineus, Scinax machadoi, Scinax obtriangulatus, Scinax oreites, Scinax perpusillus, Scinax quinquefasciatus, Scinax similis, Scinax v_signatus, Silverstoneia flotator, Silverstoneia nubicola, Smilisca cyanosticta, Smilisca sordida, Spea bombifrons, Sphaenorhynchus caramaschii, Sphaenorhynchus orophilus, Sphaenorhynchus pauloalvini, Sphaenorhynchus planicola, Sphaenorhynchus surdus, Stefania evansi, Strabomantis anomalus, Strabomantis bufoniformis, Strabomantis cerastes, Strabomantis cornutus, Strabomantis zygodactylus, Telmatobius arequipensis, Telmatobius hintoni, Telmatobius jelskii, Telmatobius simonsi, Telmatobufo venustus, Thoropa lutzi, Thoropa megatympanum, Trachycephalus dibernardoi, Trachycephalus jordani, Yunganastes mercedesae.*

(e) Adelophryne adiastola, Adelophryne gutturosa, Adelphobates galactonotus, Adelphobates quinquevittatus, Adenomera andreae, Adenomera bokermanni, Adenomera diptyx, Adenomera heyeri, Adenomera hylaedactyla, Adenomera marmorata, Adenomera martinezi, Agalychnis callidryas, Agalychnis dacnicolor, Agalychnis spurrelli, Allobates brunneus, Allobates conspicuus, Allobates femoralis, Allobates fuscellus, Allobates marchesianus, Allobates olfersioides, Allobates sumtuosus, Allobates talamancae, Allobates trilineatus, Allophryne ruthveni, Amazophrynella minuta, Ameerega braccata, Ameerega flavopicta, Ameerega hahneli, Ameerega parvula, Ameerega picta, Ameerega trivittata, Anaxyrus cognatus, Anaxyrus mexicanus, Anaxyrus punctatus, Anomaloglossus baeobatrachus, Anomaloglossus degranvillei, Aparasphenodon brunoi, Aplastodiscus arildae, Aplastodiscus leucopygius, Aplastodiscus perviridis, Atelopus spumarius, Barycholos ternetzi, Batrachyla antartandica, Batrachyla leptopus, Batrachyla taeniata, Bokermannohyla alvarengai, Bokermannohyla pseudopseudis, Brachycephalus ephippium, Calyptocephalella gayi, Centrolene buckleyi, Ceratophrys aurita, Ceratophrys calcarata, Ceratophrys cornuta, Ceratophrys cranwelli, Ceratophrys ornata, Chacophrys pierottii, Chiasmocleis albopunctata, Chiasmocleis antenori, Chiasmocleis avilapiresae, Chiasmocleis bassleri, Chiasmocleis hudsoni, Chiasmocleis leucosticta, Chiasmocleis mehelyi, Chiasmocleis shudikarensis, Chiasmocleis tridactyla, Chiasmocleis ventrimaculata, Cochranella granulosa, Corythomantis greeningi, Craugastor augusti, Craugastor fitzingeri, Craugastor loki, Craugastor longirostris, Craugastor megacephalus, Craugastor noblei, Craugastor raniformis, Craugastor vocalis, Cruziohyla craspedopus, Ctenophryne aterrima, Ctenophryne geayi, Cycloramphus eleutherodactylus, Cycloramphus fuliginosus, Dendrobates auratus, Dendrobates leucomelas, Dendrobates tinctorius, Dendropsophus acreanus, Dendropsophus anataliasiasi, Dendropsophus anceps, Dendropsophus bifurcus, Dendropsophus bipunctatus, Dendropsophus bokermanni, Dendropsophus branneri, Dendropsophus brevifrons, Dendropsophus cruzi, Dendropsophus decipiens, Dendropsophus ebraccatus, Dendropsophus elegans, Dendropsophus elianeae, Dendropsophus haraldschultzi, Dendropsophus koechlini, Dendropsophus leali, Dendropsophus leucophyllatus, Dendropsophus marmoratus, Dendropsophus melanargyreus, Dendropsophus microcephalus, Dendropsophus microps, Dendropsophus minusculus, Dendropsophus minutus, Dendropsophus miyatai, Dendropsophus nanus, Dendropsophus oliveirai, Dendropsophus parviceps, Dendropsophus pauiniensis, Dendropsophus phlebodes, Dendropsophus rhodopeplus, Dendropsophus riveroi,

Dendropsophus rossalleni, Dendropsophus rubicundulus, Dendropsophus sanborni, Dendropsophus sarayacuensis, Dendropsophus schubarti, Dendropsophus seniculus, Dendropsophus soaresi, Dendropsophus timbeba, Dendropsophus triangulum, Dendropsophus tritaeniatus, Dendropsophus walfordi, Dendropsophus xapuriensis, Dermatonotus muelleri, Diaglena spatulata, Diasporus diastema, Dryaderces pearsoni, Ecnomiohyla tuberculosa, Edalorhina perezi, Elachistocleis bicolor, Elachistocleis helianneae, Elachistocleis ovalis, Elachistocleis panamensis, Elachistocleis pearsei, Elachistocleis piauiensis, Elachistocleis surinamensis, Eleutherodactylus nitidus, Engystomops freibergi, Engystomops petersi, Engystomops pustulosus, Eupsophus calcaratus, Exerodonta smaragdina, Fritziana goeldii, Gastrophryne elegans, Gastrophryne olivacea, Gastrotheca fissipes, Gastrotheca marsupiata, Gastrotheca microdiscus, Gastrotheca nicefori, Gastrotheca testudinea, Haddadus binotatus, Hamptophryne boliviana, Hemiphractus helioi, Hemiphractus proboscideus, Hemiphractus scutatus, Hyalinobatrachium colymbiphyllum, Hyalinobatrachium fleischmanni, Hyalinobatrachium taylori, Hyalinobatrachium valerioi, Hydrolaetare dantasi, Hydrolaetare schmidti, Hyla arenicolor, Hyla eximia, Hylodes nasus, Hyloscirtus phyllognathus, Hyloxalus peruvianus, Hypodactylus nigrovittatus, Hypopachus ustus, Hypopachus variolosus, Hypsiboas albomarginatus, Hypsiboas albopunctatus, Hypsiboas bischoffi, Hypsiboas boans, Hypsiboas calcaratus, Hypsiboas cinerascens, Hypsiboas crepitans, Hypsiboas dentei, Hypsiboas faber, Hypsiboas fasciatus, Hypsiboas geographicus, Hypsiboas goianus, Hypsiboas hobbsi, Hypsiboas lanciformis, Hypsiboas leptolineatus, Hypsiboas lundii, Hypsiboas microderma, Hypsiboas multifasciatus, Hypsiboas nympha, Hypsiboas ornatissimus, Hypsiboas pardalis, Hypsiboas polytaenius, Hypsiboas prasinus, Hypsiboas pugnax, Hypsiboas pulchellus, Hypsiboas punctatus, Hypsiboas raniceps, Hypsiboas rosenbergi, Hypsiboas semilineatus, Hypsiboas sibleszi, Hypsiboas wavrini, Incilius coccifer, Incilius coniferus, Incilius luetkenii, Incilius marmoreus, Incilius occidentalis, Incilius valliceps, Ischnocnema guentheri, Ischnocnema juipoca, Ischnocnema lactea, Ischnocnema nasuta, Ischnocnema parva, Itapotihyla langsdorffii, Lepidobatrachus asper, Lepidobatrachus laevis, Lepidobatrachus llanensis, Leptodactylus bolivianus, Leptodactylus bufonius, Leptodactylus caatingae, Leptodactylus chaquensis, Leptodactylus colombiensis, Leptodactylus cunicularius, Leptodactylus didymus, Leptodactylus diedrus, Leptodactylus discodactylus, Leptodactylus elenae, Leptodactylus fragilis, Leptodactylus furnarius, Leptodactylus fuscus, Leptodactylus gracilis, Leptodactylus knudseni, Leptodactylus labyrinthicus, Leptodactylus laticeps, Leptodactylus latinasus, Leptodactylus latrans, Leptodactylus leptodactyloides, Leptodactylus lithonaetes, Leptodactylus longirostris, Leptodactylus melanonotus, Leptodactylus myersi, Leptodactylus mystaceus, Leptodactylus mystacinus, Leptodactylus natalensis, Leptodactylus notoaktites, Leptodactylus paraensis, Leptodactylus pentadactylus, Leptodactylus petersii, Leptodactylus plaumanni, Leptodactylus podicipinus, Leptodactylus poecilochilus, Leptodactylus pustulatus, Leptodactylus rhodomystax, Leptodactylus rhodonotus, Leptodactylus riveroi, Leptodactylus rugosus, Leptodactylus savagei, Leptodactylus sertanejo, Leptodactylus spixi, Leptodactylus stenodema, Leptodactylus syphax, Leptodactylus troglodytes, Leptodactylus vastus, Leptodactylus ventrimaculatus, Leptodactylus wagneri, Limnomedusa macroglossa, Lithobates berlandieri, Lithobates forreri, Lithobates maculatus, Lithobates palmipes, Lithobates vaillanti, Lithobates warszewitschii, Lithodytes lineatus, Lysapsus bolivianus, Lysapsus caraya, Lysapsus limellum, Macrogenioglottus alipioi, Melanophryniscus atroluteus, Melanophryniscus klappenbachi, Melanophryniscus tumifrons, Nannophryne variegata, Noblella myrmecoides, Odontophrynus americanus, Odontophrynus carvalhoi, Odontophrynus cultripes, Odontophrynus lavillai, Odontophrynus occidentalis, Oreobates cruralis, Oreobates quixensis, Osteocephalus buckleyi, Osteocephalus cabrerai, Osteocephalus leprieurii, Osteocephalus mimeticus, Osteocephalus oophagus, Osteocephalus planiceps, Osteocephalus subtilis, Osteocephalus taurinus, Osteocephalus yasuni, Osteopilus septentrionalis, Otophryne pyburni, Phyllodytes luteolus, Phyllomedusa atelopoides, Phyllomedusa azurea, Phyllomedusa bicolor, Phyllomedusa boliviana, Phyllomedusa burmeisteri, Phyllomedusa camba, Phyllomedusa distincta, Phyllomedusa hypochondrialis, Phyllomedusa iheringii, Phyllomedusa nordestina, Phyllomedusa palliata, Phyllomedusa rohdei, Phyllomedusa sauvagii, Phyllomedusa tarsius, Phyllomedusa tetraploidea, Phyllomedusa tomopterna, Phyllomedusa vaillantii, Phyllomedusa venusta, Physalaemus albifrons, Physalaemus albonotatus, Physalaemus biligonigerus, Physalaemus centralis, Physalaemus cicada, Physalaemus cuqui, Physalaemus cuvieri, Physalaemus ephippifer, Physalaemus fischeri, Physalaemus gracilis, Physalaemus henselii, Physalaemus kroyeri, Physalaemus maculiventris, Physalaemus marmoratus, Physalaemus nattereri, Physalaemus olfersii, Physalaemus riograndensis, Physalaemus signifer, Phyzelaphryne miriamae, Pipa arrabali, Pipa carvalhoi, Pipa, Pipa snethlageae, Plectrohyla bistincta, Pleurodema bibroni, Pleurodema brachyops, Pleurodema bufoninum, Pleurodema cinereum, Pleurodema diplolister, Pleurodema marmoratum, Pleurodema nebulosum, Pleurodema thaul, Pleurodema tucumanum, Pristimantis achatinus, Pristimantis acuminatus, Pristimantis altamazonicus, Pristimantis carvalhoi, Pristimantis chiastonotus, Pristimantis conspicillatus, Pristimantis croceoinguinis, Pristimantis diadematus, Pristimantis eurydactylus, Pristimantis fenestratus, Pristimantis gaigei, Pristimantis gutturalis, Pristimantis inguinalis, Pristimantis lacrimosus, Pristimantis *lanthanites, Pristimantis malkini, Pristimantis marmoratus, Pristimantis martiae, Pristimantis mendax, Pristimantis ockendeni, Pristimantis orcus, Pristimantis peruvianus, Pristimantis platydactylus, Pristimantis pulvinatus, Pristimantis ramagii, Pristimantis rhabdolaemus, Pristimantis ridens, Pristimantis skydmainos, Pristimantis taeniatus, Pristimantis toftae, Pristimantis variabilis, Pristimantis ventrimarmoratus, Pristimantis vilarsi, Pristimantis w_nigrum, Pristimantis zeuctotylus, Proceratophrys appendiculata, Proceratophrys avelinoi, Proceratophrys boiei, Proceratophrys cristiceps, Proceratophrys schirchi, Pseudis bolbodactyla, Pseudis minuta, Pseudis paradoxa, Pseudis platensis, Pseudis tocantins, Pseudopaludicola boliviana, Pseudopaludicola falcipes, Pseudopaludicola llanera, Pseudopaludicola mystacalis, Pseudopaludicola saltica, Pseudopaludicola ternetzi, Ranitomeya reticulata, Ranitomeya sirensis, Ranitomeya uakarii, Ranitomeya vanzolinii, Ranitomeya ventrimaculata, Rhaebo glaberrimus, Rhaebo guttatus, Rhaebo haematiticus, Rhinella achavali, Rhinella acutirostris, Rhinella arenarum, Rhinella bergi, Rhinella castaneotica, Rhinella ceratophrys, Rhinella cerradensis, Rhinella crucifer, Rhinella dapsilis, Rhinella dorbignyi, Rhinella fernandezae, Rhinella granulosa, Rhinella henseli, Rhinella hoogmoedi, Rhinella humboldti, Rhinella icterica, Rhinella jimi, Rhinella margaritifera, Rhinella marina, Rhinella martyi, Rhinella ocellata, Rhinella ornata, Rhinella poeppigii, Rhinella proboscidea, Rhinella roqueana, Rhinella rubescens, Rhinella schneideri, Rhinella spinulosa, Rhinella veraguensis, Rhinella veredas, Rhinoderma darwinii, Rhinophrynus dorsalis, Scaphiopus couchii, Scarthyla goinorum, Scarthyla vigilans, Scinax acuminatus, Scinax alter, Scinax argyreornatus, Scinax auratus, Scinax berthae, Scinax blairi, Scinax boesemani, Scinax boulengeri, Scinax chiquitanus, Scinax cruentommus, Scinax cuspidatus, Scinax eurydice, Scinax flavoguttatus, Scinax funereus, Scinax fuscomarginatus, Scinax fuscovarius, Scinax garbei, Scinax granulatus, Scinax hayii, Scinax luizotavioi, Scinax nasicus, Scinax nebulosus, Scinax pachycrus, Scinax pedromedinae, Scinax perereca, Scinax proboscideus, Scinax rizibilis, Scinax rostratus, Scinax ruber, Scinax squalirostris, Scinax staufferi, Scinax uruguayus, Scinax wandae, Scinax x_signatus, Smilisca baudinii, Smilisca fodiens, Smilisca phaeota, Smilisca sila, Spea multiplicata, Sphaenorhynchus carneus, Sphaenorhynchus dorisae, Sphaenorhynchus lacteus, Sphaenorhynchus palustris, Sphaenorhynchus prasinus, Stereocyclops incrassatus, Strabomantis sulcatus, Synapturanus mirandaribeiroi, Synapturanus rabus, Synapturanus salseri, Telmatobius marmoratus, Teratohyla midas, Teratohyla pulverata, Teratohyla spinosa, Thoropa miliaris, Tlalocohyla loquax, Tlalocohyla picta, Tlalocohyla smithii, Trachycephalus atlas, Trachycephalus coriaceus, Trachycephalus hadroceps, Trachycephalus imitatrix, Trachycephalus mesophaeus, Trachycephalus nigromaculatus, Trachycephalus resinifictrix, Triprion petasatus, Vitreorana eurygnatha, Vitreorana uranoscopa.*

Appendix A3

Table A3.2. Ecoregions occupied by the studied 2669 species following the regionalisation of Morrone (2014)*. Ecoregions were used to calibrate models (see Methods). Abbreviations are as follow: Andean (A), Antillean Subregion (AS), Boreal Brazilian Dominion (BBD), Chacoan Subregion (CS), Mesoamerican Dominion (MD), Mexican Transition Zone (MTZ), Pacific Dominion (PD), South American Transition Zone (SATZ), South Brazilian Dominion (SBD). Number one (1) indicates presence and number cero (0) absence.

SPECIES	A	AS	BBD	CS	MD	MTZ	PD	SATZ	SBD
Adelastes hylonomos	0	0	1	0	0	0	0	0	0
Adelophryne adiastola	0	0	1	0	0	0	0	0	1
Adelophryne baturitensis	0	0	0	1	0	0	0	0	0
Adelophryne gutturosa	0	0	1	0	0	0	0	0	0
Adelophryne maranguapensis	0	0	0	1	0	0	0	0	0
Adelophryne pachydactyla	0	0	0	1	0	0	0	0	0
Adelophryne patamona	0	0	1	0	0	0	0	0	0
Adelphobates castaneoticus	0	0	0	1	0	0	0	0	1
Adelphobates galactonotus	0	0	1	1	0	0	0	0	0
Adelphobates quinquevittatus	0	0	1	1	0	0	0	0	1
Adenomera ajurauna	0	0	0	1	0	0	0	0	0
Adenomera andreae	0	0	1	1	0	0	1	1	1
Adenomera araucaria	0	0	0	1	0	0	0	0	0
Adenomera bokermanni	0	0	0	1	0	0	0	0	0
Adenomera coca	0	0	0	0	0	0	0	0	1
Adenomera diptyx	0	0	0	1	0	0	0	0	1
Adenomera heyeri	0	0	1	0	0	0	0	0	0
Adenomera hylaedactyla	0	0	1	1	0	0	1	1	1
Adenomera lutzi	0	0	1	0	0	0	0	0	0
Adenomera marmorata	0	0	0	1	0	0	0	0	0
Adenomera martinezi	0	0	0	1	0	0	0	0	0
Adenomera nana	0	0	0	1	0	0	0	0	0
Adenomera thomei	0	0	0	1	0	0	0	0	0
Agalychnis annae	0	0	0	0	0	0	1	0	0
Agalychnis aspera	0	0	0	1	0	0	0	0	0
Agalychnis buckleyi	0	0	1	0	0	0	1	1	0
Agalychnis callidryas	0	0	0	0	1	1	1	0	0
Agalychnis dacnicolor	0	0	0	0	1	1	0	0	0
Agalychnis danieli	0	0	0	0	0	0	1	0	0
Agalychnis granulosa	0	0	0	1	0	0	0	0	0
Agalychnis hulli	0	0	1	0	0	0	0	1	0
Agalychnis lemur	0	0	0	0	0	0	1	0	0
Agalychnis medinae	0	0	0	0	0	0	1	0	0
Agalychnis moreletii	0	0	0	0	1	1	0	0	0
Agalychnis psilopygion	0	0	0	0	0	0	1	0	0
Agalychnis saltator	0	0	0	0	1	0	1	0	0
Agalychnis spurrelli	0	0	0	0	0	0	1	0	0
Allobates alessandroi	0	0	0	0	0	0	0	0	1
Allobates algorei	0	0	0	0	0	0	1	1	0
Allobates bromelicola	0	0	0	0	0	0	1	0	0
Allobates brunneus	0	0	1	1	0	0	0	0	1
Allobates caeruleodactylus	0	0	0	0	0	0	0	0	1

Allobates cepedai	0	0	0	0	0	0	1	0	0
Allobates conspicuus	0	0	1	0	0	0	0	0	1
Allobates crombiei	0	0	0	1	0	0	0	0	0
Allobates femoralis	0	0	1	1	0	0	1	1	1
Allobates fratisenescus	0	0	0	0	0	0	0	1	0
Allobates fuscellus	0	0	1	0	0	0	0	0	1
Allobates gasconi	0	0	0	0	0	0	0	0	1
Allobates goianus	0	0	0	1	0	0	0	0	0
Allobates granti	0	0	1	0	0	0	0	0	0
Allobates humilis	0	0	0	0	0	0	1	0	0
Allobates insperatus	0	0	1	0	0	0	0	0	0
Allobates juanii	0	0	0	0	0	0	1	1	0
Allobates kingsburyi	0	0	1	0	0	0	0	1	0
Allobates mandelorum	0	0	0	0	0	0	1	0	0
Allobates marchesianus	0	0	1	1	0	0	0	0	1
Allobates masniger	0	0	0	1	0	0	0	0	1
Allobates mcdiarmidi	0	0	0	0	0	0	0	0	1
Allobates melanolaemus	0	0	1	0	0	0	0	0	1
Allobates myersi	0	0	1	0	0	0	0	0	0
Allobates nidicola	0	0	0	0	0	0	0	0	1
Allobates niputidea	0	0	0	0	0	0	1	0	0
Allobates olfersioides	0	0	0	1	0	0	0	0	0
Allobates ornatus	0	0	0	0	0	0	0	0	1
Allobates paleovarzensis	0	0	1	0	0	0	0	0	1
Allobates picachos	0	0	0	0	0	0	0	1	0
Allobates pittieri	0	0	0	0	0	0	1	0	0
Allobates ranoides	0	0	0	0	0	0	1	1	0
Allobates sanmartini	0	0	0	0	0	0	1	0	0
Allobates subfolionidificans	0	0	0	0	0	0	0	0	1
Allobates sumtuosus	0	0	1	1	0	0	0	0	1
Allobates talamancae	0	0	0	0	0	0	1	0	0
Allobates trilineatus	0	0	1	1	0	0	0	0	1
Allobates undulatus	0	0	1	0	0	0	0	0	0
Allobates vanzolinius	0	0	1	0	0	0	0	0	1
Allobates wayuu	0	0	0	0	0	0	1	0	0
Allobates zaparo	0	0	1	0	0	0	0	1	0
Allophryne ruthveni	0	0	1	1	0	0	1	0	1
Alsodes australis	1	0	0	0	0	0	0	0	0
Alsodes barrioi	1	0	0	0	0	0	0	1	0
Alsodes gargola	1	0	0	0	0	0	0	1	0
Alsodes hugoi	1	0	0	0	0	0	0	0	0
Alsodes igneus	1	0	0	0	0	0	0	0	0
Alsodes kaweshkari	1	0	0	0	0	0	0	0	0
Alsodes montanus	1	0	0	0	0	0	0	1	0
Alsodes nodosus	1	0	0	0	0	0	0	1	0
Alsodes pehuenche	1	0	0	0	0	0	0	1	0
Alsodes tumultuosus	0	0	0	0	0	0	0	1	0
Alsodes valdiviensis	1	0	0	0	0	0	0	0	0
Alsodes verrucosus	1	0	0	0	0	0	0	0	0
Alsodes vittatus	1	0	0	0	0	0	0	0	0
Amazophrynella bokermanni	0	0	1	0	0	0	0	0	1
Amazophrynella minuta	0	0	1	1	0	0	1	1	1
Ameerega andina	0	0	0	0	0	0	1	0	0
Ameerega bassleri	0	0	0	0	0	0	0	0	1
Ameerega berohoka	0	0	0	1	0	0	0	0	0
Ameerega bilinguis	0	0	1	0	0	0	0	1	0

Ameerega boehmei	0	0	0	0	0	0	0	0	1
Ameerega boliviana	0	0	0	0	0	0	0	0	1
Ameerega braccata	0	0	0	1	0	0	0	0	1
Ameerega cainarachi	0	0	0	0	0	0	0	0	1
Ameerega erythromos	0	0	0	0	0	0	1	0	0
Ameerega flavopicta	0	0	1	1	0	0	0	0	1
Ameerega hahneli	0	0	1	1	0	0	1	1	1
Ameerega ingeri	0	0	1	0	0	0	0	0	0
Ameerega macero	0	0	0	0	0	0	0	0	1
Ameerega parvula	0	0	1	0	0	0	0	1	1
Ameerega petersi	0	0	0	0	0	0	0	0	1
Ameerega picta	0	0	1	1	0	0	1	1	1
Ameerega planipaleae	0	0	0	0	0	0	0	0	1
Ameerega pongoensis	0	0	0	0	0	0	0	0	1
Ameerega pulchripecta	0	0	1	0	0	0	0	0	0
Ameerega rubriventris	0	0	0	0	0	0	0	0	1
Ameerega silverstonei	0	0	0	0	0	0	0	0	1
Ameerega simulans	0	0	0	0	0	0	0	0	1
Ameerega smaragdina	0	0	0	0	0	0	0	0	1
Ameerega trivittata	0	0	1	1	0	0	1	1	1
Ameerega yungicola	0	0	0	0	0	0	0	0	1
Anaxyrus cognatus	0	0	0	0	1	1	0	0	0
Anaxyrus compactilis	0	0	0	0	1	1	0	0	0
Anaxyrus debilis	0	0	0	0	1	1	0	0	0
Anaxyrus kelloggi	0	0	0	0	1	1	0	0	0
Anaxyrus mexicanus	0	0	0	0	1	1	0	0	0
Anaxyrus punctatus	0	0	0	0	1	1	0	0	0
Anaxyrus speciosus	0	0	0	0	1	1	0	0	0
Anaxyrus woodhousii	0	0	0	0	0	1	0	0	0
Andinobates altobueyensis	0	0	0	0	0	0	1	0	0
Andinobates bombetes	0	0	0	0	0	0	1	0	0
Andinobates claudiae	0	0	0	0	0	0	1	0	0
Andinobates daleswansoni	0	0	0	0	0	0	1	0	0
Andinobates dorisswansonae	0	0	0	0	0	0	1	0	0
Andinobates fulguritus	0	0	0	0	0	0	1	0	0
Andinobates minutus	0	0	0	0	0	0	1	0	0
Andinobates opisthomelas	0	0	0	0	0	0	1	0	0
Andinobates tolimensis	0	0	0	0	0	0	1	0	0
Andinobates viridis	0	0	0	0	0	0	1	0	0
Andinobates virolinensis	0	0	0	0	0	0	1	0	0
Andinophryne atelopoides	0	0	0	0	0	0	1	0	0
Andinophryne colomai	0	0	0	0	0	0	1	0	0
Andinophryne olallai	0	0	0	0	0	0	1	0	0
Anomaloglossus atopoglossus	0	0	0	0	0	0	1	0	0
Anomaloglossus ayarzaguenai	0	0	1	0	0	0	0	0	0
Anomaloglossus baeobatrachus	0	0	1	0	0	0	0	0	1
Anomaloglossus beebei	0	0	1	0	0	0	0	0	0
Anomaloglossus breweri	0	0	1	0	0	0	0	0	0
Anomaloglossus degranvillei	0	0	1	0	0	0	0	0	0
Anomaloglossus guanayensis	0	0	1	0	0	0	0	0	0
Anomaloglossus kaiei	0	0	1	0	0	0	0	0	0
Anomaloglossus lacrimosus	0	0	0	0	0	0	1	0	0
Anomaloglossus murisipanensis	0	0	1	0	0	0	0	0	0
Anomaloglossus parkerae	0	0	1	0	0	0	0	0	0
Anomaloglossus praderioi	0	0	1	0	0	0	0	0	0
Anomaloglossus roraima	0	0	1	0	0	0	0	0	0

Anomaloglossus rufulus	0	0	1	0	0	0	0	0	0
Anomaloglossus shrevei	0	0	1	0	0	0	0	0	0
Anomaloglossus stepheni	0	0	1	0	0	0	0	0	0
Anomaloglossus tamacuarensis	0	0	1	0	0	0	0	0	0
Anomaloglossus tepuyensis	0	0	1	0	0	0	0	0	0
Anomaloglossus triunfo	0	0	1	0	0	0	0	0	0
Anomaloglossus wothuja	0	0	1	0	0	0	0	0	0
Anotheca spinosa	0	0	0	0	1	1	1	0	0
Aparasphenodon bokermanni	0	0	0	1	0	0	0	0	0
Aparasphenodon brunoi	0	0	0	1	0	0	0	0	0
Aparasphenodon venezolanus	0	0	1	0	0	0	0	0	0
Aplastodiscus albofrenatus	0	0	0	1	0	0	0	0	0
Aplastodiscus albosignatus	0	0	0	1	0	0	0	0	0
Aplastodiscus arildae	0	0	0	1	0	0	0	0	0
Aplastodiscus callipygius	0	0	0	1	0	0	0	0	0
Aplastodiscus cavicola	0	0	0	1	0	0	0	0	0
Aplastodiscus cochranae	0	0	0	1	0	0	0	0	0
Aplastodiscus ehrhardti	0	0	0	1	0	0	0	0	0
Aplastodiscus eugenioi	0	0	0	1	0	0	0	0	0
Aplastodiscus flumineus	0	0	0	1	0	0	0	0	0
Aplastodiscus ibirapitanga	0	0	0	1	0	0	0	0	0
Aplastodiscus leucopygius	0	0	0	1	0	0	0	0	0
Aplastodiscus musicus	0	0	0	1	0	0	0	0	0
Aplastodiscus perviridis	0	0	0	1	0	0	0	0	0
Aplastodiscus sibilatus	0	0	0	1	0	0	0	0	0
Aplastodiscus weygoldti	0	0	0	1	0	0	0	0	0
Arcovomer passarellii	0	0	0	1	0	0	0	0	0
Argenteohyla siemersi	0	0	0	1	0	0	0	0	0
Aromobates alboguttatus	0	0	0	0	0	0	1	0	0
Aromobates capurinensis	0	0	0	0	0	0	1	0	0
Aromobates duranti	0	0	0	0	0	0	1	0	0
Aromobates haydeeae	0	0	0	0	0	0	1	0	0
Aromobates leopardalis	0	0	0	0	0	0	1	0	0
Aromobates mayorgai	0	0	0	0	0	0	1	0	0
Aromobates meridensis	0	0	0	0	0	0	1	0	0
Aromobates molinarii	0	0	0	0	0	0	1	0	0
Aromobates nocturnus	0	0	0	0	0	0	1	0	0
Aromobates orostoma	0	0	0	0	0	0	1	0	0
Aromobates saltuensis	0	0	0	0	0	0	1	0	0
Aromobates serranus	0	0	0	0	0	0	1	0	0
Atelognathus ceii	1	0	0	0	0	0	0	0	0
Atelognathus nitoi	1	0	0	0	0	0	0	0	0
Atelognathus patagonicus	1	0	0	0	0	0	0	0	0
Atelognathus praebasalticus	1	0	0	0	0	0	0	1	0
Atelognathus reverberii	1	0	0	0	0	0	0	1	0
Atelognathus salai	1	0	0	0	0	0	0	0	0
Atelognathus solitarius	1	0	0	0	0	0	0	0	0
Atelopus andinus	0	0	0	0	0	0	0	0	1
Atelopus angelito	0	0	0	0	0	0	1	0	0
Atelopus ardila	0	0	0	0	0	0	1	1	0
Atelopus arsyecue	0	0	0	0	0	0	1	0	0
Atelopus arthuri	0	0	0	0	0	0	1	0	0
Atelopus balios	0	0	0	0	0	0	1	0	0
Atelopus bomolochos	0	0	0	0	0	0	1	1	0
Atelopus boulengeri	0	0	0	0	0	0	1	1	0
Atelopus carauta	0	0	0	0	0	0	1	0	0

Atelopus carbonerensis	0	0	0	0	0	0	1	0	0
Atelopus carrikeri	0	0	0	0	0	0	1	0	0
Atelopus certus	0	0	0	0	0	0	1	0	0
Atelopus chiriquiensis	0	0	0	0	0	0	1	0	0
Atelopus chocoensis	0	0	0	0	0	0	1	0	0
Atelopus chrysocorallus	0	0	0	0	0	0	1	0	0
Atelopus coynei	0	0	0	0	0	0	1	0	0
Atelopus cruciger	0	0	0	0	0	0	1	0	0
Atelopus dimorphus	0	0	0	0	0	0	0	0	1
Atelopus ebenoides	0	0	0	0	0	0	1	0	0
Atelopus elegans	0	0	0	0	0	0	1	0	0
Atelopus epikeisthos	0	0	0	0	0	0	0	0	1
Atelopus erythropus	0	0	0	0	0	0	0	0	1
Atelopus eusebianus	0	0	0	0	0	0	1	0	0
Atelopus eusebiodiazi	0	0	0	0	0	0	1	0	0
Atelopus exiguus	0	0	0	0	0	0	1	0	0
Atelopus famelicus	0	0	0	0	0	0	1	0	0
Atelopus farci	0	0	0	0	0	0	1	0	0
Atelopus flavescens	0	0	1	0	0	0	0	0	0
Atelopus franciscus	0	0	1	0	0	0	0	0	0
Atelopus galactogaster	0	0	0	0	0	0	1	0	0
Atelopus glyphus	0	0	0	0	0	0	1	0	0
Atelopus guanujo	0	0	0	0	0	0	1	0	0
Atelopus guitarraensis	0	0	0	0	0	0	0	1	0
Atelopus halihelos	0	0	0	0	0	0	0	1	0
Atelopus ignescens	0	0	0	0	0	0	1	1	0
Atelopus laetissimus	0	0	0	0	0	0	1	0	0
Atelopus limosus	0	0	0	0	0	0	1	0	0
Atelopus longibrachius	0	0	0	0	0	0	1	0	0
Atelopus longirostris	0	0	0	0	0	0	1	0	0
Atelopus lozanoi	0	0	0	0	0	0	0	1	0
Atelopus lynchi	0	0	0	0	0	0	1	0	0
Atelopus mandingues	0	0	0	0	0	0	1	1	0
Atelopus mindoensis	0	0	0	0	0	0	1	0	0
Atelopus minutulus	0	0	0	0	0	0	1	1	0
Atelopus monohernandezii	0	0	0	0	0	0	1	0	0
Atelopus mucubajiensis	0	0	0	0	0	0	1	0	0
Atelopus muisca	0	0	0	0	0	0	0	1	0
Atelopus nahumae	0	0	0	0	0	0	1	0	0
Atelopus nanay	0	0	0	0	0	0	1	0	0
Atelopus nepiozomus	0	0	0	0	0	0	1	0	0
Atelopus nicefori	0	0	0	0	0	0	1	0	0
Atelopus oxapampae	0	0	0	0	0	0	0	0	1
Atelopus oxyrhynchus	0	0	0	0	0	0	1	0	0
Atelopus pachydermus	0	0	0	0	0	0	1	1	1
Atelopus palmatus	0	0	0	0	0	0	0	1	0
Atelopus pastuso	0	0	0	0	0	0	1	1	0
Atelopus patazensis	0	0	0	0	0	0	0	1	1
Atelopus pedimarmoratus	0	0	0	0	0	0	0	1	0
Atelopus peruensis	0	0	0	0	0	0	1	1	0
Atelopus petersi	0	0	0	0	0	0	1	1	0
Atelopus petriruizi	0	0	0	0	0	0	0	1	0
Atelopus pictiventris	0	0	0	0	0	0	1	0	0
Atelopus pinangoi	0	0	0	0	0	0	1	0	0
Atelopus planispina	0	0	1	0	0	0	0	1	0
Atelopus podocarpus	0	0	0	0	0	0	1	0	0

Atelopus pulcher	0	0	0	0	0	0	0	0	1
Atelopus pyrodactylus	0	0	0	0	0	0	0	0	1
Atelopus quimbaya	0	0	0	0	0	0	1	0	0
Atelopus reticulatus	0	0	0	0	0	0	0	0	1
Atelopus sanjosei	0	0	0	0	0	0	1	0	0
Atelopus seminiferus	0	0	0	0	0	0	0	0	1
Atelopus senex	0	0	0	0	0	0	1	0	0
Atelopus sernai	0	0	0	0	0	0	1	0	0
Atelopus simulatus	0	0	0	0	0	0	1	1	0
Atelopus siranus	0	0	0	0	0	0	0	0	1
Atelopus sonsonensis	0	0	0	0	0	0	1	0	0
Atelopus sorianoi	0	0	0	0	0	0	1	0	0
Atelopus spumarius	0	0	1	1	0	0	1	1	1
Atelopus spurrelli	0	0	0	0	0	0	1	0	0
Atelopus subornatus	0	0	0	0	0	0	1	0	0
Atelopus tamaense	0	0	0	0	0	0	0	1	0
Atelopus tricolor	0	0	0	0	0	0	0	0	1
Atelopus varius	0	0	0	0	0	0	1	0	0
Atelopus walkeri	0	0	0	0	0	0	1	0	0
Atelopus zeteki	0	0	0	0	0	0	1	0	0
Atopophrynus syntomopus	0	0	0	0	0	0	1	0	0
Barycholos pulcher	0	0	0	0	0	0	1	0	0
Barycholos ternetzi	0	0	0	1	0	0	0	0	0
Batrachyla antartandica	1	0	0	0	0	0	0	0	0
Batrachyla leptopus	1	0	0	0	0	0	0	0	0
Batrachyla nibaldoi	1	0	0	0	0	0	0	0	0
Batrachyla taeniata	1	0	0	0	0	0	0	0	0
Bokermannohyla ahenea	0	0	0	1	0	0	0	0	0
Bokermannohyla alvarengai	0	0	0	1	0	0	0	0	0
Bokermannohyla astartea	0	0	0	1	0	0	0	0	0
Bokermannohyla caramaschii	0	0	0	1	0	0	0	0	0
Bokermannohyla carvalhoi	0	0	0	1	0	0	0	0	0
Bokermannohyla circumdata	0	0	0	1	0	0	0	0	0
Bokermannohyla claresignata	0	0	0	1	0	0	0	0	0
Bokermannohyla clepsydra	0	0	0	1	0	0	0	0	0
Bokermannohyla diamantina	0	0	0	1	0	0	0	0	0
Bokermannohyla gouveai	0	0	0	1	0	0	0	0	0
Bokermannohyla hylax	0	0	0	1	0	0	0	0	0
Bokermannohyla ibitipoca	0	0	0	1	0	0	0	0	0
Bokermannohyla itapoty	0	0	0	1	0	0	0	0	0
Bokermannohyla izecksohni	0	0	0	1	0	0	0	0	0
Bokermannohyla langei	0	0	0	1	0	0	0	0	0
Bokermannohyla luctuosa	0	0	0	1	0	0	0	0	0
Bokermannohyla martinsi	0	0	0	1	0	0	0	0	0
Bokermannohyla nanuzae	0	0	0	1	0	0	0	0	0
Bokermannohyla oxente	0	0	0	1	0	0	0	0	0
Bokermannohyla pseudopseudis	0	0	0	1	0	0	0	0	0
Bokermannohyla ravida	0	0	0	1	0	0	0	0	0
Bokermannohyla sagarana	0	0	0	1	0	0	0	0	0
Bokermannohyla saxicola	0	0	0	1	0	0	0	0	0
Bokermannohyla sazimai	0	0	0	1	0	0	0	0	0
Bokermannohyla vulcaniae	0	0	0	1	0	0	0	0	0
Brachycephalus alipioi	0	0	0	1	0	0	0	0	0
Brachycephalus brunneus	0	0	0	1	0	0	0	0	0
Brachycephalus didactylus	0	0	0	1	0	0	0	0	0
Brachycephalus ephippium	0	0	0	1	0	0	0	0	0

Brachycephalus ferruginus	0	0	0	1	0	0	0	0	0
Brachycephalus hermogenesi	0	0	0	1	0	0	0	0	0
Brachycephalus izecksohni	0	0	0	1	0	0	0	0	0
Brachycephalus nodoterga	0	0	0	1	0	0	0	0	0
Brachycephalus pernix	0	0	0	1	0	0	0	0	0
Brachycephalus pombali	0	0	0	1	0	0	0	0	0
Brachycephalus vertebralis	0	0	0	1	0	0	0	0	0
Bromeliohyla bromeliacia	0	0	0	0	1	1	0	0	0
Bromeliohyla dendroscarta	0	0	0	0	1	1	0	0	0
Bryophryne bustamantei	0	0	0	0	0	0	0	0	1
Bryophryne cophites	0	0	0	0	0	0	0	0	1
Bryophryne gymnotis	0	0	0	0	0	0	0	0	1
Bryophryne hanssaueri	0	0	0	0	0	0	0	0	1
Bryophryne nubilosus	0	0	0	0	0	0	0	0	1
Bryophryne zonalis	0	0	0	0	0	0	0	0	1
Calyptocephalella gayi	1	0	0	0	0	0	0	1	0
Celsiella revocata	0	0	0	0	0	0	1	0	0
Celsiella vozmedianoi	0	0	0	0	0	0	1	0	0
Centrolene acanthidiocephalum	0	0	0	0	0	0	1	0	0
Centrolene altitudinale	0	0	0	0	0	0	1	0	0
Centrolene antioquiense	0	0	0	0	0	0	1	0	0
Centrolene azulae	0	0	0	0	0	0	0	0	1
Centrolene bacatum	0	0	1	0	0	0	1	1	0
Centrolene ballux	0	0	0	0	0	0	1	0	0
Centrolene buckleyi	0	0	0	0	0	0	1	1	0
Centrolene condor	0	0	0	0	0	0	1	0	0
Centrolene daidaleum	0	0	0	0	0	0	1	0	0
Centrolene geckoideum	0	0	0	0	0	0	1	1	0
Centrolene gemmatum	0	0	0	0	0	0	1	0	0
Centrolene guanacarum	0	0	0	0	0	0	1	0	0
Centrolene heloderma	0	0	0	0	0	0	1	0	0
Centrolene hesperium	0	0	0	0	0	0	0	1	0
Centrolene huilense	0	0	0	0	0	0	1	0	0
Centrolene hybrida	0	0	1	0	0	0	1	1	0
Centrolene lemniscatum	0	0	0	0	0	0	0	0	1
Centrolene lynchi	0	0	0	0	0	0	1	0	0
Centrolene medemi	0	0	1	0	0	0	1	1	0
Centrolene notostictum	0	0	0	0	0	0	1	1	0
Centrolene peristictum	0	0	0	0	0	0	1	0	0
Centrolene petrophilum	0	0	0	0	0	0	1	1	0
Centrolene pipilatum	0	0	0	0	0	0	0	1	0
Centrolene quindianum	0	0	0	0	0	0	1	0	0
Centrolene robledoi	0	0	0	0	0	0	1	0	0
Centrolene sanchezi	0	0	0	0	0	0	0	1	0
Centrolene savagei	0	0	0	0	0	0	1	0	0
Centrolene scirtetes	0	0	0	0	0	0	1	0	0
Centrolene solitaria	0	0	0	0	0	0	0	1	0
Centrolene venezuelense	0	0	0	0	0	0	1	1	0
Ceratophrys aurita	0	0	0	1	0	0	0	0	0
Ceratophrys calcarata	0	0	0	0	0	0	1	0	0
Ceratophrys cornuta	0	0	1	1	0	0	1	1	1
Ceratophrys cranwelli	0	0	0	1	0	0	0	0	1
Ceratophrys joazeirensis	0	0	0	1	0	0	0	0	0
Ceratophrys ornata	0	0	0	1	0	0	0	0	0
Ceratophrys stolzmanni	0	0	0	0	0	0	1	0	0
Ceratophrys testudo	0	0	0	0	0	0	0	1	0

Ceuthomantis aracamuni	0	0	1	0	0	0	0	0	0
Ceuthomantis cavernibardus	0	0	1	0	0	0	0	0	0
Ceuthomantis duellmani	0	0	1	0	0	0	0	0	0
Chacophrys pierottii	0	0	0	1	0	0	0	0	1
Chaltenobatrachus grandisonae	1	0	0	0	0	0	0	0	0
Charadrahyla altipotens	0	0	0	0	1	1	0	0	0
Charadrahyla chaneque	0	0	0	0	1	0	0	0	0
Charadrahyla nephila	0	0	0	0	1	1	0	0	0
Charadrahyla taeniopus	0	0	0	0	1	1	0	0	0
Charadrahyla trux	0	0	0	0	1	0	0	0	0
Chiasmocleis alagoana	0	0	0	1	0	0	0	0	0
Chiasmocleis albopunctata	0	0	0	1	0	0	0	0	1
Chiasmocleis anatipes	0	0	1	0	0	0	0	1	1
Chiasmocleis antenori	0	0	1	0	0	0	0	1	1
Chiasmocleis atlantica	0	0	0	1	0	0	0	0	0
Chiasmocleis avilapiresae	0	0	1	1	0	0	0	0	1
Chiasmocleis bassleri	0	0	1	0	0	0	0	0	1
Chiasmocleis capixaba	0	0	0	1	0	0	0	0	0
Chiasmocleis centralis	0	0	0	1	0	0	0	0	0
Chiasmocleis devriesi	0	0	1	0	0	0	0	0	0
Chiasmocleis hudsoni	0	0	1	0	0	0	1	0	1
Chiasmocleis leucosticta	0	0	0	1	0	0	0	0	0
Chiasmocleis magnova	0	0	1	0	0	0	0	0	1
Chiasmocleis mantiqueira	0	0	0	1	0	0	0	0	0
Chiasmocleis mehelyi	0	0	0	1	0	0	0	0	1
Chiasmocleis sapiranga	0	0	0	1	0	0	0	0	0
Chiasmocleis schubarti	0	0	0	1	0	0	0	0	0
Chiasmocleis shudikarensis	0	0	1	1	0	0	0	0	1
Chiasmocleis tridactyla	0	0	1	0	0	0	0	0	1
Chiasmocleis ventrimaculata	0	0	1	0	0	0	0	1	1
Chimerella mariaelenae	0	0	1	0	0	0	1	1	0
Cochranella balionota	0	0	0	0	0	0	1	0	0
Cochranella duidaeana	0	0	1	0	0	0	0	0	0
Cochranella erminea	0	0	0	0	0	0	0	0	1
Cochranella euhystrix	0	0	0	0	0	0	0	1	0
Cochranella euknemos	0	0	0	0	0	0	1	0	0
Cochranella geijskesi	0	0	1	0	0	0	0	0	0
Cochranella granulosa	0	0	0	0	1	1	1	0	0
Cochranella litoralis	0	0	0	0	0	0	1	0	0
Cochranella mache	0	0	0	0	0	0	1	0	0
Cochranella megista	0	0	0	0	0	0	1	0	0
Cochranella nola	0	0	0	1	0	0	0	0	1
Cochranella phryxa	0	0	0	0	0	0	0	0	1
Cochranella ramirezi	0	0	0	0	0	0	1	0	0
Cochranella resplendens	0	0	1	0	0	0	0	1	1
Cochranella riveroi	0	0	1	0	0	0	0	0	0
Cochranella xanthocheridia	0	0	0	0	0	0	1	0	0
Colostethus agilis	0	0	0	0	0	0	1	0	0
Colostethus alacris	0	0	0	0	0	0	1	0	0
Colostethus argyrogaster	0	0	0	0	0	0	1	0	1
Colostethus brachistriatus	0	0	0	0	0	0	1	0	0
Colostethus dysprosium	0	0	0	0	0	0	1	0	0
Colostethus fraterdanieli	0	0	0	0	0	0	1	0	0
Colostethus fugax	0	0	1	0	0	0	0	1	0
Colostethus furviventris	0	0	0	0	0	0	1	0	0
Colostethus imbricolus	0	0	0	0	0	0	1	0	0

Colostethus inguinalis	0	0	0	0	0	0	1	0	0
Colostethus jacobuspetersi	0	0	0	0	0	0	1	0	0
Colostethus latinasus	0	0	0	0	0	0	1	0	0
Colostethus lynchi	0	0	0	0	0	0	1	0	0
Colostethus mertensi	0	0	0	0	0	0	1	0	0
Colostethus panamansis	0	0	0	0	0	0	1	0	0
Colostethus poecilonotus	0	0	0	0	0	0	0	0	1
Colostethus pratti	0	0	0	0	0	0	1	0	0
Colostethus ramirezi	0	0	0	0	0	0	1	0	0
Colostethus ruthveni	0	0	0	0	0	0	1	0	0
Colostethus thorntoni	0	0	0	0	0	0	1	0	0
Colostethus ucumari	0	0	0	0	0	0	1	0	0
Colostethus yaguara	0	0	0	0	0	0	1	0	0
Corythomantis greeningi	0	0	1	1	0	0	0	0	0
Craugastor adamastus	0	0	0	0	1	0	0	0	0
Craugastor alfredi	0	0	0	0	1	1	0	0	0
Craugastor amniscola	0	0	0	0	1	1	0	0	0
Craugastor anciano	0	0	0	0	0	1	0	0	0
Craugastor andi	0	0	0	0	0	0	1	0	0
Craugastor angelicus	0	0	0	0	0	0	1	0	0
Craugastor aphanus	0	0	0	0	1	0	0	0	0
Craugastor augusti	0	0	0	0	1	1	0	0	0
Craugastor aurilegulus	0	0	0	0	1	0	0	0	0
Craugastor azueroensis	0	0	0	0	0	0	1	0	0
Craugastor batrachylus	0	0	0	0	1	1	0	0	0
Craugastor berkenbuschii	0	0	0	0	1	1	0	0	0
Craugastor bocourti	0	0	0	0	1	1	0	0	0
Craugastor bransfordii	0	0	0	0	1	0	1	0	0
Craugastor brocchi	0	0	0	0	1	1	0	0	0
Craugastor campbelli	0	0	0	0	1	0	0	0	0
Craugastor catalinae	0	0	0	0	0	0	1	0	0
Craugastor chac	0	0	0	0	1	1	0	0	0
Craugastor charadra	0	0	0	0	1	1	0	0	0
Craugastor chingopetaca	0	0	0	0	0	0	1	0	0
Craugastor chrysozetetes	0	0	0	0	1	0	0	0	0
Craugastor coffeus	0	0	0	0	1	1	0	0	0
Craugastor crassidigitus	0	0	0	0	0	0	1	0	0
Craugastor cruzi	0	0	0	0	1	0	0	0	0
Craugastor cuaquero	0	0	0	0	0	0	1	0	0
Craugastor cyanochthebius	0	0	0	0	1	1	0	0	0
Craugastor daryi	0	0	0	0	1	1	0	0	0
Craugastor decoratus	0	0	0	0	1	1	0	0	0
Craugastor emcelae	0	0	0	0	0	0	1	0	0
Craugastor emleni	0	0	0	0	0	1	0	0	0
Craugastor epochthidius	0	0	0	0	1	1	0	0	0
Craugastor escoces	0	0	0	0	0	0	1	0	0
Craugastor fecundus	0	0	0	0	1	0	0	0	0
Craugastor fitzingeri	0	0	0	0	1	1	1	0	0
Craugastor fleischmanni	0	0	0	0	0	0	1	0	0
Craugastor glaucus	0	0	0	0	0	1	0	0	0
Craugastor gollmeri	0	0	0	0	0	0	1	0	0
Craugastor greggi	0	0	0	0	1	1	0	0	0
Craugastor guerreroensis	0	0	0	0	1	0	0	0	0
Craugastor gulosus	0	0	0	0	0	0	1	0	0
Craugastor hobartsmithi	0	0	0	0	1	1	0	0	0
Craugastor inachus	0	0	0	0	1	1	0	0	0

Craugastor jota	0	0	0	0	0	0	1	0	0
Craugastor laevissimus	0	0	0	0	1	1	0	0	0
Craugastor laticeps	0	0	0	0	1	1	0	0	0
Craugastor lauraster	0	0	0	0	1	1	0	0	0
Craugastor lineatus	0	0	0	0	1	1	0	0	0
Craugastor loki	0	0	0	0	1	1	0	0	0
Craugastor longirostris	0	0	0	0	0	0	1	0	0
Craugastor matudai	0	0	0	0	1	1	0	0	0
Craugastor megacephalus	0	0	0	0	1	1	1	0	0
Craugastor megalotympanum	0	0	0	0	1	0	0	0	0
Craugastor melanostictus	0	0	0	0	0	0	1	0	0
Craugastor merendonensis	0	0	0	0	1	0	0	0	0
Craugastor mexicanus	0	0	0	0	1	1	0	0	0
Craugastor milesi	0	0	0	0	1	1	0	0	0
Craugastor mimus	0	0	0	0	1	0	1	0	0
Craugastor monnichorum	0	0	0	0	0	0	1	0	0
Craugastor montanus	0	0	0	0	1	0	0	0	0
Craugastor myllomyllon	0	0	0	0	0	1	0	0	0
Craugastor nefrens	0	0	0	0	1	0	0	0	0
Craugastor noblei	0	0	0	0	1	1	1	0	0
Craugastor obesus	0	0	0	0	0	0	1	0	0
Craugastor occidentalis	0	0	0	0	1	1	0	0	0
Craugastor olanchano	0	0	0	0	1	0	0	0	0
Craugastor omiltemanus	0	0	0	0	1	0	0	0	0
Craugastor omoaensis	0	0	0	0	1	0	0	0	0
Craugastor opimus	0	0	0	0	0	0	1	0	0
Craugastor palenque	0	0	0	0	1	0	0	0	0
Craugastor pechorum	0	0	0	0	1	0	0	0	0
Craugastor pelorus	0	0	0	0	1	1	0	0	0
Craugastor persimilis	0	0	0	0	0	0	1	0	0
Craugastor phasma	0	0	0	0	0	0	1	0	0
Craugastor podiciferus	0	0	0	0	0	0	1	0	0
Craugastor polymniae	0	0	0	0	1	1	0	0	0
Craugastor polyptychus	0	0	0	0	0	0	1	0	0
Craugastor pozo	0	0	0	0	1	0	0	0	0
Craugastor psephosypharus	0	0	0	0	1	0	0	0	0
Craugastor punctariolus	0	0	0	0	0	0	1	0	0
Craugastor pygmaeus	0	0	0	0	1	1	0	0	0
Craugastor raniformis	0	0	0	0	0	0	1	0	0
Craugastor ranoides	0	0	0	0	0	0	1	0	0
Craugastor rayo	0	0	0	0	0	0	1	0	0
Craugastor rhodopis	0	0	0	0	1	1	0	0	0
Craugastor rhyacobatrachus	0	0	0	0	0	0	1	0	0
Craugastor rivulus	0	0	0	0	1	1	0	0	0
Craugastor rostralis	0	0	0	0	1	1	0	0	0
Craugastor rugosus	0	0	0	0	0	0	1	0	0
Craugastor rugulosus	0	0	0	0	1	1	0	0	0
Craugastor rupinius	0	0	0	0	1	1	0	0	0
Craugastor sabrinus	0	0	0	0	1	0	0	0	0
Craugastor saltuarius	0	0	0	0	1	0	0	0	0
Craugastor sandersoni	0	0	0	0	1	1	0	0	0
Craugastor silvicola	0	0	0	0	1	0	0	0	0
Craugastor spatulatus	0	0	0	0	1	1	0	0	0
Craugastor stadelmani	0	0	0	0	1	0	0	0	0
Craugastor stejnegerianus	0	0	0	0	0	0	1	0	0
Craugastor stuarti	0	0	0	0	1	1	0	0	0

Craugastor tabasarae	0	0	0	0	0	0	1	0	0
Craugastor talamancae	0	0	0	0	1	0	1	0	0
Craugastor tarahumaraensis	0	0	0	0	0	1	0	0	0
Craugastor taurus	0	0	0	0	0	0	1	0	0
Craugastor taylori	0	0	0	0	1	0	0	0	0
Craugastor trachydermus	0	0	0	0	1	0	0	0	0
Craugastor underwoodi	0	0	0	0	0	0	1	0	0
Craugastor uno	0	0	0	0	1	1	0	0	0
Craugastor vocalis	0	0	0	0	1	1	0	0	0
Craugastor vulcani	0	0	0	0	1	0	0	0	0
Craugastor xucanebi	0	0	0	0	1	1	0	0	0
Craugastor yucatanensis	0	0	0	0	1	0	0	0	0
Crossodactylodes bokermanni	0	0	0	1	0	0	0	0	0
Crossodactylodes izecksohni	0	0	0	1	0	0	0	0	0
Crossodactylodes pintoi	0	0	0	1	0	0	0	0	0
Crossodactylus aeneus	0	0	0	1	0	0	0	0	0
Crossodactylus bokermanni	0	0	0	1	0	0	0	0	0
Crossodactylus caramaschii	0	0	0	1	0	0	0	0	0
Crossodactylus cyclospinus	0	0	0	1	0	0	0	0	0
Crossodactylus dantei	0	0	0	1	0	0	0	0	0
Crossodactylus dispar	0	0	0	1	0	0	0	0	0
Crossodactylus gaudichaudii	0	0	0	1	0	0	0	0	0
Crossodactylus grandis	0	0	0	1	0	0	0	0	0
Crossodactylus lutzorum	0	0	0	1	0	0	0	0	0
Crossodactylus schmidti	0	0	0	1	0	0	0	0	0
Crossodactylus trachystomus	0	0	0	1	0	0	0	0	0
Cruziohyla calcarifer	0	0	0	0	1	0	1	0	0
Cruziohyla craspedopus	0	0	1	0	0	0	0	1	1
Cryptobatrachus boulengeri	0	0	0	0	0	0	1	0	0
Cryptobatrachus fuhrmanni	0	0	0	0	0	0	1	0	0
Ctenophryne aequatorialis	0	0	0	0	0	0	1	0	0
Ctenophryne aterrima	0	0	0	0	0	0	1	0	0
Ctenophryne barbatula	0	0	0	0	0	0	0	0	1
Ctenophryne carpish	0	0	0	0	0	0	0	0	1
Ctenophryne geayi	0	0	1	1	0	0	1	1	1
Ctenophryne minor	0	0	0	0	0	0	1	0	0
Cycloramphus acangatan	0	0	0	1	0	0	0	0	0
Cycloramphus asper	0	0	0	1	0	0	0	0	0
Cycloramphus bandeirensis	0	0	0	1	0	0	0	0	0
Cycloramphus bolitoglossus	0	0	0	1	0	0	0	0	0
Cycloramphus boraceiensis	0	0	0	1	0	0	0	0	0
Cycloramphus brasiliensis	0	0	0	1	0	0	0	0	0
Cycloramphus carvalhoi	0	0	0	1	0	0	0	0	0
Cycloramphus catarinensis	0	0	0	1	0	0	0	0	0
Cycloramphus cedrensis	0	0	0	1	0	0	0	0	0
Cycloramphus diringshofeni	0	0	0	1	0	0	0	0	0
Cycloramphus dubius	0	0	0	1	0	0	0	0	0
Cycloramphus duseni	0	0	0	1	0	0	0	0	0
Cycloramphus eleutherodactylus	0	0	0	1	0	0	0	0	0
Cycloramphus fuliginosus	0	0	0	1	0	0	0	0	0
Cycloramphus granulosus	0	0	0	1	0	0	0	0	0
Cycloramphus izecksohni	0	0	0	1	0	0	0	0	0
Cycloramphus juimirim	0	0	0	1	0	0	0	0	0
Cycloramphus lutzorum	0	0	0	1	0	0	0	0	0
Cycloramphus migueli	0	0	0	1	0	0	0	0	0
Cycloramphus mirandaribeiroi	0	0	0	1	0	0	0	0	0

Cycloramphus ohausi	0	0	0	1	0	0	0	0	0
Cycloramphus organensis	0	0	0	1	0	0	0	0	0
Cycloramphus rhyakonastes	0	0	0	1	0	0	0	0	0
Cycloramphus semipalmatus	0	0	0	1	0	0	0	0	0
Cycloramphus stejnegeri	0	0	0	1	0	0	0	0	0
Cycloramphus valae	0	0	0	1	0	0	0	0	0
Dasypops schirchi	0	0	0	1	0	0	0	0	0
Dendrobates auratus	0	0	0	0	1	0	1	0	0
Dendrobates leucomelas	0	0	1	0	0	0	1	0	0
Dendrobates nubeculosus	0	0	1	0	0	0	0	0	0
Dendrobates tinctorius	0	0	1	0	0	0	0	0	1
Dendrobates truncatus	0	0	0	0	0	0	1	1	0
Dendrophryniscus berthalutzae	0	0	0	1	0	0	0	0	0
Dendrophryniscus brevipollicatus	0	0	0	1	0	0	0	0	0
Dendrophryniscus carvalhoi	0	0	0	1	0	0	0	0	0
Dendrophryniscus krausae	0	0	0	1	0	0	0	0	0
Dendrophryniscus leucomystax	0	0	0	1	0	0	0	0	0
Dendrophryniscus proboscideus	0	0	0	1	0	0	0	0	0
Dendrophryniscus stawiarskyi	0	0	0	1	0	0	0	0	0
Dendropsophus acreanus	0	0	0	1	0	0	0	0	1
Dendropsophus amicorum	0	0	0	0	0	0	1	0	0
Dendropsophus anataliasiasi	0	0	0	1	0	0	0	0	0
Dendropsophus anceps	0	0	0	1	0	0	0	0	0
Dendropsophus aperomeus	0	0	0	0	0	0	0	0	1
Dendropsophus araguaya	0	0	0	1	0	0	0	0	0
Dendropsophus battersbyi	0	0	0	0	0	0	1	0	0
Dendropsophus berthalutzae	0	0	0	1	0	0	0	0	0
Dendropsophus bifurcus	0	0	1	1	0	0	0	1	1
Dendropsophus bipunctatus	0	0	0	1	0	0	0	0	0
Dendropsophus bogerti	0	0	0	0	0	0	1	0	0
Dendropsophus bokermanni	0	0	1	0	0	0	0	1	1
Dendropsophus branneri	0	0	1	1	0	0	0	0	0
Dendropsophus brevifrons	0	0	1	0	0	0	1	1	1
Dendropsophus cachimbo	0	0	0	1	0	0	0	0	0
Dendropsophus carnifex	0	0	0	0	0	0	1	0	0
Dendropsophus cerradensis	0	0	0	1	0	0	0	0	0
Dendropsophus coffeus	0	0	0	0	0	0	0	0	1
Dendropsophus columbianus	0	0	0	0	0	0	1	0	0
Dendropsophus cruzi	0	0	0	1	0	0	0	0	0
Dendropsophus decipiens	0	0	1	1	0	0	0	0	0
Dendropsophus delarivai	0	0	0	0	0	0	0	0	1
Dendropsophus dutrai	0	0	0	1	0	0	0	0	0
Dendropsophus ebraccatus	0	0	0	0	1	1	1	0	0
Dendropsophus elegans	0	0	0	1	0	0	0	0	0
Dendropsophus elianeae	0	0	0	1	0	0	0	0	0
Dendropsophus garagoensis	0	0	0	0	0	0	0	1	0
Dendropsophus gaucheri	0	0	1	0	0	0	0	0	0
Dendropsophus giesleri	0	0	0	1	0	0	0	0	0
Dendropsophus gryllatus	0	0	0	0	0	0	1	0	0
Dendropsophus haddadi	0	0	0	1	0	0	0	0	0
Dendropsophus haraldschultzi	0	0	1	0	0	0	0	0	1
Dendropsophus jimi	0	0	0	1	0	0	0	0	0
Dendropsophus juliani	0	0	0	0	0	0	0	0	1
Dendropsophus koechlini	0	0	1	1	0	0	0	0	1
Dendropsophus labialis	0	0	0	0	0	0	1	1	0
Dendropsophus leali	0	0	1	1	0	0	0	0	1

Dendropsophus leucophyllatus	0	0	1	1	0	0	0	1	1
Dendropsophus luteoocellatus	0	0	0	0	0	0	1	0	0
Dendropsophus marmoratus	0	0	1	1	0	0	1	0	1
Dendropsophus mathiassoni	0	0	1	0	0	0	1	1	0
Dendropsophus melanargyreus	0	0	1	1	0	0	0	0	1
Dendropsophus meridensis	0	0	0	0	0	0	1	0	0
Dendropsophus meridianus	0	0	0	1	0	0	0	0	0
Dendropsophus microcephalus	0	0	1	1	1	1	1	1	1
Dendropsophus microps	0	0	0	1	0	0	0	0	0
Dendropsophus minimus	0	0	0	1	0	0	0	0	0
Dendropsophus minusculus	0	0	1	0	0	0	1	1	0
Dendropsophus minutus	0	0	1	1	0	0	1	1	1
Dendropsophus miyatai	0	0	1	0	0	0	0	0	1
Dendropsophus nahdereri	0	0	0	1	0	0	0	0	0
Dendropsophus nanus	0	0	1	1	0	0	0	0	1
Dendropsophus novaisi	0	0	0	1	0	0	0	0	0
Dendropsophus oliveirai	0	0	0	1	0	0	0	0	0
Dendropsophus padreluna	0	0	0	0	0	0	1	0	0
Dendropsophus parviceps	0	0	1	1	0	0	1	0	1
Dendropsophus pauiniensis	0	0	0	0	0	0	0	0	1
Dendropsophus phlebodes	0	0	0	0	1	0	1	0	0
Dendropsophus praestans	0	0	0	0	0	0	1	0	0
Dendropsophus pseudomeridianus	0	0	0	1	0	0	0	0	0
Dendropsophus reichlei	0	0	0	0	0	0	0	0	1
Dendropsophus rhea	0	0	0	1	0	0	0	0	0
Dendropsophus rhodopeplus	0	0	1	1	0	0	0	1	1
Dendropsophus riveroi	0	0	1	0	0	0	0	0	1
Dendropsophus robertmertensi	0	0	0	0	1	1	0	0	0
Dendropsophus rossalleni	0	0	1	0	0	0	0	0	1
Dendropsophus rubicundulus	0	0	0	1	0	0	0	0	1
Dendropsophus ruschii	0	0	0	1	0	0	0	0	0
Dendropsophus sanborni	0	0	0	1	0	0	0	0	0
Dendropsophus sarayacuensis	0	0	1	0	0	0	1	1	1
Dendropsophus sartori	0	0	0	0	1	1	0	0	0
Dendropsophus schubarti	0	0	0	1	0	0	0	0	1
Dendropsophus seniculus	0	0	0	1	0	0	0	0	0
Dendropsophus soaresi	0	0	1	1	0	0	0	0	0
Dendropsophus stingi	0	0	0	0	0	0	0	1	0
Dendropsophus studerae	0	0	0	1	0	0	0	0	0
Dendropsophus subocularis	0	0	0	0	0	0	1	0	0
Dendropsophus timbeba	0	0	0	0	0	0	0	0	1
Dendropsophus tintinnabulum	0	0	1	0	0	0	0	0	0
Dendropsophus triangulum	0	0	1	1	0	0	1	1	1
Dendropsophus tritaeniatus	0	0	0	1	0	0	0	0	1
Dendropsophus virolinensis	0	0	0	0	0	0	1	0	0
Dendropsophus walfordi	0	0	1	1	0	0	0	0	1
Dendropsophus werneri	0	0	0	1	0	0	0	0	0
Dendropsophus xapuriensis	0	0	0	0	0	0	0	0	1
Dendropsophus yaracuyanus	0	0	0	0	0	0	1	0	0
Dermatonotus muelleri	0	0	1	1	0	0	0	0	1
Diaglena spatulata	0	0	0	0	1	1	0	0	0
Diasporus anthrax	0	0	0	0	0	0	1	0	0
Diasporus diastema	0	0	0	0	1	0	1	0	0
Diasporus gularis	0	0	0	0	0	0	1	0	0
Diasporus hylaeformis	0	0	0	0	0	0	1	0	0
Diasporus quidditus	0	0	0	0	0	0	1	0	0

Diasporus tigrillo	0	0	0	0	0	0	1	0	0
Diasporus tinker	0	0	0	0	0	0	1	0	0
Diasporus vocator	0	0	0	0	0	0	1	0	0
Dischidodactylus colonnelloi	0	0	1	0	0	0	0	0	0
Dischidodactylus duidensis	0	0	1	0	0	0	0	0	0
Dryaderces pearsoni	0	0	0	0	0	0	0	0	1
Duellmanohyla chamulae	0	0	0	0	1	0	0	0	0
Duellmanohyla ignicolor	0	0	0	0	0	1	0	0	0
Duellmanohyla lythrodes	0	0	0	0	0	0	1	0	0
Duellmanohyla rufioculis	0	0	0	0	0	0	1	0	0
Duellmanohyla salvavida	0	0	0	0	1	0	0	0	0
Duellmanohyla schmidtorum	0	0	0	0	1	1	0	0	0
Duellmanohyla soralia	0	0	0	0	1	1	0	0	0
Duellmanohyla uranochroa	0	0	0	0	0	0	1	0	0
Ecnomiohyla echinata	0	0	0	0	0	1	0	0	0
Ecnomiohyla fimbrimembra	0	0	0	0	0	0	1	0	0
Ecnomiohyla miliaria	0	0	0	0	1	0	1	0	0
Ecnomiohyla minera	0	0	0	0	1	1	0	0	0
Ecnomiohyla miotympanum	0	0	0	0	1	1	0	0	0
Ecnomiohyla phantasmagoria	0	0	0	0	0	0	1	0	0
Ecnomiohyla rabborum	0	0	0	0	0	0	1	0	0
Ecnomiohyla salvaje	0	0	0	0	1	1	0	0	0
Ecnomiohyla thysanota	0	0	0	0	0	0	1	0	0
Ecnomiohyla tuberculosa	0	0	1	0	0	0	0	1	1
Ecnomiohyla valancifer	0	0	0	0	1	0	0	0	0
Edalorhina nasuta	0	0	0	0	0	0	0	0	1
Edalorhina perezi	0	0	1	0	0	0	0	0	1
Elachistocleis bicolor	0	0	0	1	0	0	0	0	1
Elachistocleis bumbameuboi	0	0	0	1	0	0	0	0	0
Elachistocleis carvalhoi	0	0	0	1	0	0	0	0	0
Elachistocleis erythrogaster	0	0	0	1	0	0	0	0	0
Elachistocleis helianneae	0	0	1	1	0	0	0	0	1
Elachistocleis matogrosso	0	0	0	1	0	0	0	0	1
Elachistocleis ovalis	0	0	1	1	0	0	1	1	1
Elachistocleis panamensis	0	0	0	0	0	0	1	0	0
Elachistocleis pearsei	0	0	0	0	0	0	1	1	0
Elachistocleis piauiensis	0	0	0	1	0	0	0	0	0
Elachistocleis skotogaster	0	0	0	0	0	0	0	0	1
Elachistocleis surinamensis	0	0	1	0	0	0	1	0	0
Elachistocleis surumu	0	0	1	0	0	0	0	0	0
Eleutherodactylus abbotti	0	1	0	0	0	0	0	0	0
Eleutherodactylus acmonis	0	1	0	0	0	0	0	0	0
Eleutherodactylus adelus	0	1	0	0	0	0	0	0	0
Eleutherodactylus albipes	0	1	0	0	0	0	0	0	0
Eleutherodactylus albolabris	0	0	0	0	1	0	0	0	0
Eleutherodactylus alcoae	0	1	0	0	0	0	0	0	0
Eleutherodactylus alticola	0	1	0	0	0	0	0	0	0
Eleutherodactylus amadeus	0	1	0	0	0	0	0	0	0
Eleutherodactylus amplinympha	0	1	0	0	0	0	0	0	0
Eleutherodactylus andrewsi	0	1	0	0	0	0	0	0	0
Eleutherodactylus angustidigitorum	0	0	0	0	1	1	0	0	0
Eleutherodactylus antillensis	0	1	0	0	0	0	0	0	0
Eleutherodactylus apostates	0	1	0	0	0	0	0	0	0
Eleutherodactylus armstrongi	0	1	0	0	0	0	0	0	0
Eleutherodactylus atkinsi	0	1	0	0	0	0	0	0	0
Eleutherodactylus audanti	0	1	0	0	0	0	0	0	0

Eleutherodactylus auriculatoides	0	1	0	0	0	0	0	0	0
Eleutherodactylus auriculatus	0	1	0	0	0	0	0	0	0
Eleutherodactylus bakeri	0	1	0	0	0	0	0	0	0
Eleutherodactylus barlagnei	0	1	0	0	0	0	0	0	0
Eleutherodactylus bartonsmithi	0	1	0	0	0	0	0	0	0
Eleutherodactylus bilineatus	0	0	0	1	0	0	0	0	0
Eleutherodactylus blairhedgesi	0	1	0	0	0	0	0	0	0
Eleutherodactylus brevirostris	0	1	0	0	0	0	0	0	0
Eleutherodactylus brittoni	0	1	0	0	0	0	0	0	0
Eleutherodactylus caribe	0	1	0	0	0	0	0	0	0
Eleutherodactylus casparii	0	1	0	0	0	0	0	0	0
Eleutherodactylus cavernicola	0	1	0	0	0	0	0	0	0
Eleutherodactylus chlorophenax	0	1	0	0	0	0	0	0	0
Eleutherodactylus cochranae	0	1	0	0	0	0	0	0	0
Eleutherodactylus cooki	0	1	0	0	0	0	0	0	0
Eleutherodactylus coqui	0	1	0	0	0	0	0	0	0
Eleutherodactylus corona	0	1	0	0	0	0	0	0	0
Eleutherodactylus counouspeus	0	1	0	0	0	0	0	0	0
Eleutherodactylus cubanus	0	1	0	0	0	0	0	0	0
Eleutherodactylus cundalli	0	1	0	0	0	0	0	0	0
Eleutherodactylus cuneatus	0	1	0	0	0	0	0	0	0
Eleutherodactylus cystignathoides	0	0	0	0	1	1	0	0	0
Eleutherodactylus darlingtoni	0	1	0	0	0	0	0	0	0
Eleutherodactylus dennisi	0	0	0	0	1	0	0	0	0
Eleutherodactylus dilatus	0	0	0	0	1	0	0	0	0
Eleutherodactylus dimidiatus	0	1	0	0	0	0	0	0	0
Eleutherodactylus diplasius	0	1	0	0	0	0	0	0	0
Eleutherodactylus dolomedes	0	1	0	0	0	0	0	0	0
Eleutherodactylus eileenae	0	1	0	0	0	0	0	0	0
Eleutherodactylus emiliae	0	1	0	0	0	0	0	0	0
Eleutherodactylus eneidae	0	1	0	0	0	0	0	0	0
Eleutherodactylus etheridgei	0	1	0	0	0	0	0	0	0
Eleutherodactylus eunaster	0	1	0	0	0	0	0	0	0
Eleutherodactylus flavescens	0	1	0	0	0	0	0	0	0
Eleutherodactylus fowleri	0	1	0	0	0	0	0	0	0
Eleutherodactylus furcyensis	0	1	0	0	0	0	0	0	0
Eleutherodactylus fuscus	0	1	0	0	0	0	0	0	0
Eleutherodactylus glamyrus	0	1	0	0	0	0	0	0	0
Eleutherodactylus glandulifer	0	1	0	0	0	0	0	0	0
Eleutherodactylus glanduliferoides	0	1	0	0	0	0	0	0	0
Eleutherodactylus glaphycompus	0	1	0	0	0	0	0	0	0
Eleutherodactylus glaucoreius	0	1	0	0	0	0	0	0	0
Eleutherodactylus goini	0	1	0	0	0	0	0	0	0
Eleutherodactylus gossei	0	1	0	0	0	0	0	0	0
Eleutherodactylus grabhami	0	1	0	0	0	0	0	0	0
Eleutherodactylus grahami	0	1	0	0	0	0	0	0	0
Eleutherodactylus grandis	0	0	0	0	0	1	0	0	0
Eleutherodactylus greyi	0	1	0	0	0	0	0	0	0
Eleutherodactylus griphus	0	1	0	0	0	0	0	0	0
Eleutherodactylus gryllus	0	1	0	0	0	0	0	0	0
Eleutherodactylus guanahacabibes	0	1	0	0	0	0	0	0	0
Eleutherodactylus guantanamera	0	1	0	0	0	0	0	0	0
Eleutherodactylus gundlachi	0	1	0	0	0	0	0	0	0
Eleutherodactylus guttilatus	0	0	0	0	1	1	0	0	0
Eleutherodactylus haitianus	0	1	0	0	0	0	0	0	0
Eleutherodactylus hedricki	0	1	0	0	0	0	0	0	0

Eleutherodactylus heminota	0	1	0	0	0	0	0	0	0
Eleutherodactylus hypostenor	0	1	0	0	0	0	0	0	0
Eleutherodactylus iberia	0	1	0	0	0	0	0	0	0
Eleutherodactylus inoptatus	0	1	0	0	0	0	0	0	0
Eleutherodactylus intermedius	0	1	0	0	0	0	0	0	0
Eleutherodactylus interorbitalis	0	0	0	0	1	0	0	0	0
Eleutherodactylus ionthus	0	1	0	0	0	0	0	0	0
Eleutherodactylus jamaicensis	0	1	0	0	0	0	0	0	0
Eleutherodactylus jasperi	0	1	0	0	0	0	0	0	0
Eleutherodactylus jaumei	0	1	0	0	0	0	0	0	0
Eleutherodactylus johnstonei	0	1	1	0	0	0	1	0	0
Eleutherodactylus jugans	0	1	0	0	0	0	0	0	0
Eleutherodactylus junori	0	1	0	0	0	0	0	0	0
Eleutherodactylus karlschmidti	0	1	0	0	0	0	0	0	0
Eleutherodactylus klinikowskii	0	1	0	0	0	0	0	0	0
Eleutherodactylus lamprotes	0	1	0	0	0	0	0	0	0
Eleutherodactylus leberi	0	1	0	0	0	0	0	0	0
Eleutherodactylus leoncei	0	1	0	0	0	0	0	0	0
Eleutherodactylus leprus	0	0	0	0	1	0	0	0	0
Eleutherodactylus limbatus	0	1	0	0	0	0	0	0	0
Eleutherodactylus locustus	0	1	0	0	0	0	0	0	0
Eleutherodactylus longipes	0	0	0	0	1	1	0	0	0
Eleutherodactylus lucioi	0	1	0	0	0	0	0	0	0
Eleutherodactylus luteolus	0	1	0	0	0	0	0	0	0
Eleutherodactylus maestrensis	0	1	0	0	0	0	0	0	0
Eleutherodactylus mariposa	0	1	0	0	0	0	0	0	0
Eleutherodactylus marnockii	0	0	0	0	0	1	0	0	0
Eleutherodactylus martinicensis	0	1	0	0	0	0	0	0	0
Eleutherodactylus maurus	0	0	0	0	1	1	0	0	0
Eleutherodactylus melacara	0	1	0	0	0	0	0	0	0
Eleutherodactylus michaelschmidi	0	1	0	0	0	0	0	0	0
Eleutherodactylus minutus	0	1	0	0	0	0	0	0	0
Eleutherodactylus modestus	0	0	0	0	1	1	0	0	0
Eleutherodactylus montanus	0	1	0	0	0	0	0	0	0
Eleutherodactylus nitidus	0	0	0	0	1	1	0	0	0
Eleutherodactylus nortoni	0	1	0	0	0	0	0	0	0
Eleutherodactylus notidodes	0	1	0	0	0	0	0	0	0
Eleutherodactylus nubicola	0	1	0	0	0	0	0	0	0
Eleutherodactylus orcutti	0	1	0	0	0	0	0	0	0
Eleutherodactylus orientalis	0	1	0	0	0	0	0	0	0
Eleutherodactylus oxyrhyncus	0	1	0	0	0	0	0	0	0
Eleutherodactylus pallidus	0	0	0	0	1	1	0	0	0
Eleutherodactylus pantoni	0	1	0	0	0	0	0	0	0
Eleutherodactylus parabates	0	1	0	0	0	0	0	0	0
Eleutherodactylus paralius	0	1	0	0	0	0	0	0	0
Eleutherodactylus parapelates	0	1	0	0	0	0	0	0	0
Eleutherodactylus patriciae	0	1	0	0	0	0	0	0	0
Eleutherodactylus paulsoni	0	1	0	0	0	0	0	0	0
Eleutherodactylus pentasyringos	0	1	0	0	0	0	0	0	0
Eleutherodactylus pezopetrus	0	1	0	0	0	0	0	0	0
Eleutherodactylus pictissimus	0	1	0	0	0	0	0	0	0
Eleutherodactylus pinarensis	0	1	0	0	0	0	0	0	0
Eleutherodactylus pinchoni	0	1	0	0	0	0	0	0	0
Eleutherodactylus pipilans	0	0	0	0	1	1	0	0	0
Eleutherodactylus pituinus	0	1	0	0	0	0	0	0	0
Eleutherodactylus planirostris	0	1	0	0	0	0	0	0	0

Eleutherodactylus poolei	0	1	0	0	0	0	0	0	0
Eleutherodactylus portoricensis	0	1	0	0	0	0	0	0	0
Eleutherodactylus principalis	0	1	0	0	0	0	0	0	0
Eleutherodactylus probolaeus	0	1	0	0	0	0	0	0	0
Eleutherodactylus rhodesi	0	1	0	0	0	0	0	0	0
Eleutherodactylus richmondi	0	1	0	0	0	0	0	0	0
Eleutherodactylus ricordii	0	1	0	0	0	0	0	0	0
Eleutherodactylus riparius	0	1	0	0	0	0	0	0	0
Eleutherodactylus rivularis	0	1	0	0	0	0	0	0	0
Eleutherodactylus ronaldi	0	1	0	0	0	0	0	0	0
Eleutherodactylus rubrimaculatus	0	0	0	0	1	1	0	0	0
Eleutherodactylus rufifemoralis	0	1	0	0	0	0	0	0	0
Eleutherodactylus ruthae	0	1	0	0	0	0	0	0	0
Eleutherodactylus saxatilis	0	0	0	0	0	1	0	0	0
Eleutherodactylus schmidti	0	1	0	0	0	0	0	0	0
Eleutherodactylus sciagraphus	0	1	0	0	0	0	0	0	0
Eleutherodactylus semipalmatus	0	1	0	0	0	0	0	0	0
Eleutherodactylus sisyphodemus	0	1	0	0	0	0	0	0	0
Eleutherodactylus sommeri	0	1	0	0	0	0	0	0	0
Eleutherodactylus symingtoni	0	1	0	0	0	0	0	0	0
Eleutherodactylus syristes	0	0	0	0	1	0	0	0	0
Eleutherodactylus teretistes	0	0	0	0	1	0	0	0	0
Eleutherodactylus tetajulia	0	1	0	0	0	0	0	0	0
Eleutherodactylus thomasi	0	1	0	0	0	0	0	0	0
Eleutherodactylus thorectes	0	1	0	0	0	0	0	0	0
Eleutherodactylus toa	0	1	0	0	0	0	0	0	0
Eleutherodactylus tonyi	0	1	0	0	0	0	0	0	0
Eleutherodactylus turquinensis	0	1	0	0	0	0	0	0	0
Eleutherodactylus varians	0	1	0	0	0	0	0	0	0
Eleutherodactylus varleyi	0	1	0	0	0	0	0	0	0
Eleutherodactylus ventrilineatus	0	1	0	0	0	0	0	0	0
Eleutherodactylus verrucipes	0	0	0	0	1	1	0	0	0
Eleutherodactylus verruculatus	0	0	0	0	1	1	0	0	0
Eleutherodactylus weinlandi	0	1	0	0	0	0	0	0	0
Eleutherodactylus wetmorei	0	1	0	0	0	0	0	0	0
Eleutherodactylus wightmanae	0	1	0	0	0	0	0	0	0
Eleutherodactylus zeus	0	1	0	0	0	0	0	0	0
Eleutherodactylus zugi	0	1	0	0	0	0	0	0	0
Engystomops coloradorum	0	0	0	0	0	0	1	0	0
Engystomops freibergi	0	0	1	1	0	0	0	0	1
Engystomops guayaco	0	0	0	0	0	0	1	0	0
Engystomops montubio	0	0	0	0	0	0	1	0	0
Engystomops petersi	0	0	1	0	0	0	1	1	1
Engystomops pustulatus	0	0	0	0	0	0	1	0	0
Engystomops pustulosus	0	0	1	0	1	1	1	1	0
Engystomops randi	0	0	0	0	0	0	1	0	0
Epipedobates anthonyi	0	0	0	0	0	0	1	0	0
Epipedobates boulengeri	0	0	0	0	0	0	1	0	0
Epipedobates machalilla	0	0	0	0	0	0	1	0	0
Epipedobates narinensis	0	0	0	0	0	0	1	0	0
Epipedobates tricolor	0	0	0	0	0	0	1	0	0
Espadarana andina	0	0	0	0	0	0	1	1	0
Espadarana callistomma	0	0	0	0	0	0	1	0	0
Espadarana durrellorum	0	0	1	0	0	0	1	1	0
Euparkerella brasiliensis	0	0	0	1	0	0	0	0	0
Euparkerella cochranae	0	0	0	1	0	0	0	0	0

Euparkerella robusta	0	0	0	1	0	0	0	0	0
Eupsophus calcaratus	1	0	0	0	0	0	0	0	0
Eupsophus contulmoensis	1	0	0	0	0	0	0	0	0
Eupsophus emiliopugini	1	0	0	0	0	0	0	0	0
Eupsophus migueli	1	0	0	0	0	0	0	0	0
Eupsophus nahuelbutensis	1	0	0	0	0	0	0	0	0
Eupsophus roseus	1	0	0	0	0	0	0	0	0
Eupsophus septentrionalis	1	0	0	0	0	0	0	0	0
Eupsophus vertebralis	1	0	0	0	0	0	0	0	0
Excidobates captivus	0	0	1	0	0	0	1	0	1
Excidobates mysteriosus	0	0	0	0	0	0	1	0	0
Exerodonta abdivita	0	0	0	0	1	0	0	0	0
Exerodonta bivocata	0	0	0	0	1	1	0	0	0
Exerodonta catracha	0	0	0	0	0	1	0	0	0
Exerodonta chimalapa	0	0	0	0	1	0	0	0	0
Exerodonta juanitae	0	0	0	0	1	1	0	0	0
Exerodonta melanomma	0	0	0	0	1	1	0	0	0
Exerodonta perkinsi	0	0	0	0	1	0	0	0	0
Exerodonta pinorum	0	0	0	0	1	1	0	0	0
Exerodonta smaragdina	0	0	0	0	1	1	0	0	0
Exerodonta sumichrasti	0	0	0	0	1	1	0	0	0
Exerodonta xera	0	0	0	0	1	1	0	0	0
Flectonotus fissilis	0	0	0	1	0	0	0	0	0
Flectonotus fitzgeraldi	0	0	0	0	0	0	1	0	0
Flectonotus pygmaeus	0	0	0	0	0	0	1	1	0
Fritziana goeldii	0	0	0	1	0	0	0	0	0
Fritziana ohausi	0	0	0	1	0	0	0	0	0
Frostius erythrophthalmus	0	0	0	1	0	0	0	0	0
Frostius pernambucensis	0	0	0	1	0	0	0	0	0
Gastrophryne carolinensis	0	1	0	0	0	0	0	0	0
Gastrophryne elegans	0	0	0	0	1	1	0	0	0
Gastrophryne olivacea	0	0	0	0	1	1	0	0	0
Gastrotheca abdita	0	0	0	0	0	0	0	0	1
Gastrotheca aguaruna	0	0	0	0	0	0	0	0	1
Gastrotheca albolineata	0	0	0	1	0	0	0	0	0
Gastrotheca andaquiensis	0	0	1	0	0	0	1	1	0
Gastrotheca angustifrons	0	0	0	0	0	0	1	0	0
Gastrotheca antomia	0	0	0	0	0	0	1	0	0
Gastrotheca antoniiochoai	0	0	0	0	0	0	0	0	1
Gastrotheca aratia	0	0	0	0	0	0	1	1	0
Gastrotheca argenteovirens	0	0	0	0	0	0	1	0	0
Gastrotheca atympana	0	0	0	0	0	0	0	0	1
Gastrotheca aureomaculata	0	0	0	0	0	0	1	0	0
Gastrotheca bufona	0	0	0	0	0	0	1	0	0
Gastrotheca carinaceps	0	0	0	0	0	0	0	0	1
Gastrotheca christiani	0	0	0	0	0	0	0	1	1
Gastrotheca chrysosticta	0	0	0	0	0	0	0	1	1
Gastrotheca cornuta	0	0	0	0	0	0	1	0	0
Gastrotheca dendronastes	0	0	0	0	0	0	1	0	0
Gastrotheca dunni	0	0	0	0	0	0	1	0	0
Gastrotheca ernestoi	0	0	0	1	0	0	0	0	0
Gastrotheca espeletia	0	0	0	0	0	0	1	1	0
Gastrotheca excubitor	0	0	0	0	0	0	0	0	1
Gastrotheca fissipes	0	0	0	1	0	0	0	0	0
Gastrotheca flamma	0	0	0	1	0	0	0	0	0
Gastrotheca fulvorufa	0	0	0	1	0	0	0	0	0

Gastrotheca galeata	0	0	0	0	0	0	1	0	0
Gastrotheca gracilis	0	0	0	1	0	0	0	0	0
Gastrotheca griswoldi	0	0	0	0	0	0	0	1	1
Gastrotheca guentheri	0	0	0	0	0	0	1	0	0
Gastrotheca helenae	0	0	0	0	0	0	0	1	0
Gastrotheca lateonota	0	0	0	0	0	0	1	0	0
Gastrotheca lauzuricae	0	0	0	0	0	0	0	0	1
Gastrotheca litonedis	0	0	0	0	0	0	1	0	0
Gastrotheca longipes	0	0	1	0	0	0	1	1	1
Gastrotheca marsupiata	0	0	0	0	0	0	0	1	1
Gastrotheca microdiscus	0	0	0	1	0	0	0	0	0
Gastrotheca monticola	0	0	0	0	0	0	1	1	1
Gastrotheca nicefori	0	0	1	0	0	0	1	1	0
Gastrotheca ochoai	0	0	0	0	0	0	0	0	1
Gastrotheca orophylax	0	0	0	0	0	0	0	1	0
Gastrotheca ossilaginis	0	0	0	0	0	0	0	0	1
Gastrotheca ovifera	0	0	0	0	0	0	1	0	0
Gastrotheca pacchamama	0	0	0	0	0	0	0	0	1
Gastrotheca peruana	0	0	0	0	0	0	0	1	1
Gastrotheca piperata	0	0	0	1	0	0	0	0	1
Gastrotheca plumbea	0	0	0	0	0	0	1	0	0
Gastrotheca pseustes	0	0	0	0	0	0	1	1	0
Gastrotheca psychrophila	0	0	0	0	0	0	1	0	0
Gastrotheca rebeccae	0	0	0	0	0	0	0	0	1
Gastrotheca riobambae	0	0	0	0	0	0	1	1	0
Gastrotheca ruizi	0	0	0	0	0	0	0	1	0
Gastrotheca splendens	0	0	0	0	0	0	0	0	1
Gastrotheca stictopleura	0	0	0	0	0	0	0	0	1
Gastrotheca testudinea	0	0	1	0	0	0	1	1	1
Gastrotheca trachyceps	0	0	0	0	0	0	1	0	0
Gastrotheca walkeri	0	0	0	0	0	0	1	0	0
Gastrotheca weinlandii	0	0	1	0	0	0	1	1	0
Gastrotheca williamsoni	0	0	0	0	0	0	1	0	0
Gastrotheca zeugocystis	0	0	0	0	0	0	0	0	1
Geobatrachus walkeri	0	0	0	0	0	0	1	0	0
Haddadus aramunha	0	0	0	1	0	0	0	0	0
Haddadus binotatus	0	0	0	1	0	0	0	0	0
Hamptophryne alios	0	0	0	0	0	0	0	0	1
Hamptophryne boliviana	0	0	1	1	0	0	1	0	1
Hemiphractus bubalus	0	0	1	0	0	0	1	1	0
Hemiphractus fasciatus	0	0	0	0	0	0	1	0	0
Hemiphractus helioi	0	0	1	0	0	0	0	1	1
Hemiphractus johnsoni	0	0	1	0	0	0	1	1	1
Hemiphractus proboscideus	0	0	1	0	0	0	0	1	1
Hemiphractus scutatus	0	0	1	0	0	0	1	1	1
Holoaden bradei	0	0	0	1	0	0	0	0	0
Holoaden luederwaldti	0	0	0	1	0	0	0	0	0
Holoaden pholeter	0	0	0	1	0	0	0	0	0
Hyalinobatrachium aureoguttatum	0	0	0	0	0	0	1	0	0
Hyalinobatrachium chirripoi	0	0	0	0	0	0	1	0	0
Hyalinobatrachium colymbiphyllum	0	0	0	0	0	0	1	0	0
Hyalinobatrachium duranti	0	0	0	0	0	0	1	0	0
Hyalinobatrachium esmeralda	0	0	0	0	0	0	1	0	0
Hyalinobatrachium fleischmanni	0	0	1	0	1	1	1	0	0
Hyalinobatrachium fragile	0	0	0	0	0	0	1	0	0
Hyalinobatrachium guairarepanense	0	0	0	0	0	0	1	0	0

Hyalinobatrachium iaspidiense	0	0	1	0	0	0	0	0	0
Hyalinobatrachium ibama	0	0	0	0	0	0	1	1	0
Hyalinobatrachium orientale	0	0	0	0	0	0	1	0	0
Hyalinobatrachium pallidum	0	0	0	0	0	0	1	0	0
Hyalinobatrachium pellucidum	0	0	0	0	0	0	0	1	1
Hyalinobatrachium ruedai	0	0	1	0	0	0	0	1	0
Hyalinobatrachium talamancae	0	0	0	0	0	0	1	0	0
Hyalinobatrachium tatayoi	0	0	0	0	0	0	1	0	0
Hyalinobatrachium taylori	0	0	1	0	0	0	0	0	0
Hyalinobatrachium valerioi	0	0	0	0	0	0	1	0	0
Hyalinobatrachium vireovittatum	0	0	0	0	0	0	1	0	0
Hydrolaetare caparu	0	0	0	0	0	0	0	0	1
Hydrolaetare dantasi	0	0	0	0	0	0	0	0	1
Hydrolaetare schmidti	0	0	1	1	0	0	0	0	1
Hyla arboricola	0	0	0	0	1	1	0	0	0
Hyla arenicolor	0	0	0	0	1	1	0	0	0
Hyla bocourti	0	0	0	0	1	1	0	0	0
Hyla cinerea	0	1	0	0	0	0	0	0	0
Hyla euphorbiacea	0	0	0	0	1	1	0	0	0
Hyla eximia	0	0	0	0	1	1	0	0	0
Hyla nicefori	0	0	0	0	0	0	0	1	0
Hyla plicata	0	0	0	0	1	1	0	0	0
Hyla squirella	0	1	0	0	0	0	0	0	0
Hyla walkeri	0	0	0	0	1	1	0	0	0
Hyla wrightorum	0	0	0	0	1	1	0	0	0
Hylodes amnicola	0	0	0	1	0	0	0	0	0
Hylodes asper	0	0	0	1	0	0	0	0	0
Hylodes babax	0	0	0	1	0	0	0	0	0
Hylodes cardosoi	0	0	0	1	0	0	0	0	0
Hylodes charadranaetes	0	0	0	1	0	0	0	0	0
Hylodes dactylocinus	0	0	0	1	0	0	0	0	0
Hylodes glaber	0	0	0	1	0	0	0	0	0
Hylodes heyeri	0	0	0	1	0	0	0	0	0
Hylodes lateristrigatus	0	0	0	1	0	0	0	0	0
Hylodes magalhaesi	0	0	0	1	0	0	0	0	0
Hylodes meridionalis	0	0	0	1	0	0	0	0	0
Hylodes mertensi	0	0	0	1	0	0	0	0	0
Hylodes nasus	0	0	0	1	0	0	0	0	0
Hylodes ornatus	0	0	0	1	0	0	0	0	0
Hylodes otavioi	0	0	0	1	0	0	0	0	0
Hylodes perplicatus	0	0	0	1	0	0	0	0	0
Hylodes phyllodes	0	0	0	1	0	0	0	0	0
Hylodes pipilans	0	0	0	1	0	0	0	0	0
Hylodes regius	0	0	0	1	0	0	0	0	0
Hylodes sazimai	0	0	0	1	0	0	0	0	0
Hylodes uai	0	0	0	1	0	0	0	0	0
Hylodes vanzolinii	0	0	0	1	0	0	0	0	0
Hylorina sylvatica	1	0	0	0	0	0	0	0	0
Hyloscirtus albopunctulatus	0	0	1	0	0	0	0	0	0
Hyloscirtus alytolylax	0	0	0	0	0	0	1	0	0
Hyloscirtus armatus	0	0	0	0	0	0	0	0	1
Hyloscirtus bogotensis	0	0	0	0	0	0	1	1	0
Hyloscirtus callipeza	0	0	0	0	0	0	1	1	0
Hyloscirtus caucanus	0	0	0	0	0	0	1	0	0
Hyloscirtus charazani	0	0	0	0	0	0	0	0	1
Hyloscirtus chlorosteus	0	0	0	0	0	0	0	0	1

Hyloscirtus colymba	0	0	0	0	0	0	1	0	0
Hyloscirtus denticulentus	0	0	0	0	0	0	1	0	0
Hyloscirtus jahni	0	0	0	0	0	0	1	0	0
Hyloscirtus larinopygion	0	0	0	0	0	0	1	1	0
Hyloscirtus lascinius	0	0	0	0	0	0	1	1	0
Hyloscirtus lindae	0	0	0	0	0	0	1	1	0
Hyloscirtus lynchi	0	0	0	0	0	0	1	0	0
Hyloscirtus pacha	0	0	0	0	0	0	1	0	0
Hyloscirtus palmeri	0	0	0	0	0	0	1	0	0
Hyloscirtus pantostictus	0	0	0	0	0	0	0	1	0
Hyloscirtus phyllognathus	0	0	1	0	0	0	1	1	1
Hyloscirtus piceigularis	0	0	0	0	0	0	1	0	0
Hyloscirtus platydactylus	0	0	0	0	0	0	1	1	0
Hyloscirtus psarolaimus	0	0	1	0	0	0	0	1	0
Hyloscirtus ptychodactylus	0	0	0	0	0	0	1	0	0
Hyloscirtus sarampiona	0	0	0	0	0	0	1	0	0
Hyloscirtus simmonsi	0	0	0	0	0	0	1	0	0
Hyloscirtus staufferorum	0	0	0	0	0	0	0	1	0
Hyloscirtus torrenticola	0	0	1	0	0	0	0	1	0
Hyloxalus abditaurantius	0	0	0	0	0	0	1	0	0
Hyloxalus aeruginosus	0	0	0	0	0	0	0	0	1
Hyloxalus anthracinus	0	0	0	0	0	0	1	0	0
Hyloxalus awa	0	0	0	0	0	0	1	0	0
Hyloxalus azureiventris	0	0	0	0	0	0	0	0	1
Hyloxalus betancuri	0	0	0	0	0	0	1	0	0
Hyloxalus bocagei	0	0	1	0	0	0	1	1	0
Hyloxalus borjai	0	0	0	0	0	0	1	0	0
Hyloxalus breviquartus	0	0	0	0	0	0	1	0	0
Hyloxalus cevallosi	0	0	1	0	0	0	1	1	0
Hyloxalus chlorocraspedus	0	0	0	0	0	0	0	0	1
Hyloxalus chocoensis	0	0	0	0	0	0	1	0	0
Hyloxalus craspedoceps	0	0	0	0	0	0	0	0	1
Hyloxalus delatorreae	0	0	0	0	0	0	1	0	0
Hyloxalus edwardsi	0	0	0	0	0	0	0	1	0
Hyloxalus elachyhistus	0	0	0	0	0	0	1	1	0
Hyloxalus eleutherodactylus	0	0	0	0	0	0	0	0	1
Hyloxalus exasperatus	0	0	0	0	0	0	1	1	0
Hyloxalus excisus	0	0	0	0	0	0	1	0	0
Hyloxalus faciopunctulatus	0	0	1	0	0	0	0	0	0
Hyloxalus fallax	0	0	0	0	0	0	1	0	0
Hyloxalus fascianigrus	0	0	0	0	0	0	1	0	0
Hyloxalus fuliginosus	0	0	0	0	0	0	0	1	0
Hyloxalus idiomelus	0	0	0	0	0	0	0	0	1
Hyloxalus infraguttatus	0	0	0	0	0	0	1	0	0
Hyloxalus insulatus	0	0	0	0	0	0	0	1	1
Hyloxalus lehmanni	0	0	0	0	0	0	1	1	0
Hyloxalus leucophaeus	0	0	0	0	0	0	0	0	1
Hyloxalus littoralis	0	0	0	0	0	0	0	1	1
Hyloxalus maculosus	0	0	0	0	0	0	0	1	0
Hyloxalus maquipucuna	0	0	0	0	0	0	1	0	0
Hyloxalus marmoreoventris	0	0	0	0	0	0	0	1	0
Hyloxalus mittermeieri	0	0	0	0	0	0	0	0	1
Hyloxalus mystax	0	0	0	0	0	0	1	0	0
Hyloxalus nexipus	0	0	1	0	0	0	1	1	1
Hyloxalus parcus	0	0	0	0	0	0	1	0	0
Hyloxalus peruvianus	0	0	1	0	0	0	0	0	1

Hyloxalus pinguis	0	0	0	0	0	0	1	0	0
Hyloxalus pulchellus	0	0	1	0	0	0	1	1	0
Hyloxalus pulcherrimus	0	0	0	0	0	0	0	1	0
Hyloxalus ramosi	0	0	0	0	0	0	1	0	0
Hyloxalus ruizi	0	0	0	0	0	0	1	1	0
Hyloxalus saltuarius	0	0	0	0	0	0	0	1	0
Hyloxalus sauli	0	0	1	0	0	0	0	1	0
Hyloxalus shuar	0	0	1	0	0	0	1	1	0
Hyloxalus sordidatus	0	0	0	0	0	0	0	0	1
Hyloxalus spilotogaster	0	0	0	0	0	0	0	0	1
Hyloxalus subpunctatus	0	0	0	0	0	0	1	1	0
Hyloxalus sylvaticus	0	0	0	0	0	0	1	0	0
Hyloxalus toachi	0	0	0	0	0	0	1	0	0
Hyloxalus utcubambensis	0	0	0	0	0	0	0	0	1
Hyloxalus vergeli	0	0	0	0	0	0	1	0	0
Hyloxalus vertebralis	0	0	0	0	0	0	1	0	0
Hyloxalus whymperi	0	0	0	0	0	0	1	0	0
Hypodactylus adercus	0	0	0	0	0	0	1	0	0
Hypodactylus araiodactylus	0	0	0	0	0	0	0	0	1
Hypodactylus babax	0	0	0	0	0	0	1	0	0
Hypodactylus brunneus	0	0	0	0	0	0	1	1	0
Hypodactylus dolops	0	0	1	0	0	0	0	1	0
Hypodactylus elassodiscus	0	0	0	0	0	0	0	1	0
Hypodactylus fallaciosus	0	0	0	0	0	0	0	0	1
Hypodactylus latens	0	0	0	0	0	0	1	0	0
Hypodactylus lucida	0	0	0	0	0	0	0	0	1
Hypodactylus mantipus	0	0	0	0	0	0	1	0	0
Hypodactylus nigrovittatus	0	0	1	0	0	0	1	1	1
Hypodactylus peraccai	0	0	0	0	0	0	1	1	0
Hypopachus barberi	0	0	0	0	1	1	0	0	0
Hypopachus pictiventris	0	0	0	0	1	0	1	0	0
Hypopachus ustus	0	0	0	0	1	1	0	0	0
Hypopachus variolosus	0	0	0	0	1	1	1	0	0
Hypsiboas albomarginatus	0	0	0	1	0	0	0	0	0
Hypsiboas alboniger	0	0	0	0	0	0	0	1	1
Hypsiboas albopunctatus	0	0	0	1	0	0	0	0	1
Hypsiboas alemani	0	0	0	0	0	0	1	0	0
Hypsiboas atlanticus	0	0	0	1	0	0	0	0	0
Hypsiboas balzani	0	0	0	1	0	0	0	0	1
Hypsiboas beckeri	0	0	0	1	0	0	0	0	0
Hypsiboas bischoffi	0	0	0	1	0	0	0	0	0
Hypsiboas boans	0	0	1	1	0	0	1	0	1
Hypsiboas buriti	0	0	0	1	0	0	0	0	0
Hypsiboas caingua	0	0	0	1	0	0	0	0	0
Hypsiboas calcaratus	0	0	1	1	0	0	1	0	1
Hypsiboas callipleura	0	0	0	0	0	0	0	0	1
Hypsiboas cinerascens	0	0	1	1	0	0	1	1	1
Hypsiboas cipoensis	0	0	0	1	0	0	0	0	0
Hypsiboas cordobae	0	0	0	1	0	0	0	0	0
Hypsiboas crepitans	0	0	1	1	0	0	1	1	0
Hypsiboas curupi	0	0	0	1	0	0	0	0	0
Hypsiboas cymbalum	0	0	0	1	0	0	0	0	0
Hypsiboas dentei	0	0	1	0	0	0	0	0	0
Hypsiboas ericae	0	0	0	1	0	0	0	0	0
Hypsiboas exastis	0	0	0	1	0	0	0	0	0
Hypsiboas faber	0	0	0	1	0	0	0	0	0

Hypsiboas fasciatus	0	0	1	1	0	0	0	0	1
Hypsiboas fuentei	0	0	1	0	0	0	0	0	0
Hypsiboas geographicus	0	0	1	1	0	0	1	1	1
Hypsiboas goianus	0	0	0	1	0	0	0	0	0
Hypsiboas guentheri	0	0	0	1	0	0	0	0	0
Hypsiboas heilprini	0	1	0	0	0	0	0	0	0
Hypsiboas hobbsi	0	0	1	0	0	0	0	0	0
Hypsiboas hutchinsi	0	0	1	0	0	0	0	0	0
Hypsiboas jimenezi	0	0	1	0	0	0	0	0	0
Hypsiboas joaquini	0	0	0	1	0	0	0	0	0
Hypsiboas lanciformis	0	0	1	1	0	0	1	1	1
Hypsiboas latistriatus	0	0	0	1	0	0	0	0	0
Hypsiboas lemai	0	0	1	0	0	0	0	0	0
Hypsiboas leptolineatus	0	0	0	1	0	0	0	0	0
Hypsiboas leucocheilus	0	0	0	0	0	0	0	0	1
Hypsiboas liliae	0	0	1	0	0	0	0	0	0
Hypsiboas lundii	0	0	0	1	0	0	0	0	0
Hypsiboas marginatus	0	0	0	1	0	0	0	0	0
Hypsiboas marianitae	0	0	0	1	0	0	0	1	1
Hypsiboas melanopleura	0	0	0	0	0	0	0	0	1
Hypsiboas microderma	0	0	1	0	0	0	0	0	1
Hypsiboas multifasciatus	0	0	1	1	0	0	1	0	1
Hypsiboas nympha	0	0	1	0	0	0	0	1	1
Hypsiboas ornatissimus	0	0	1	0	0	0	0	0	0
Hypsiboas palaestes	0	0	0	0	0	0	0	0	1
Hypsiboas pardalis	0	0	0	1	0	0	0	0	0
Hypsiboas pellucens	0	0	0	0	0	0	1	0	0
Hypsiboas phaeopleura	0	0	0	1	0	0	0	0	0
Hypsiboas picturatus	0	0	0	0	0	0	1	0	0
Hypsiboas polytaenius	0	0	0	1	0	0	0	0	0
Hypsiboas pombali	0	0	0	1	0	0	0	0	0
Hypsiboas prasinus	0	0	0	1	0	0	0	0	0
Hypsiboas pugnax	0	0	0	0	0	0	1	1	0
Hypsiboas pulchellus	0	0	0	1	0	0	0	0	0
Hypsiboas pulidoi	0	0	1	0	0	0	0	0	0
Hypsiboas punctatus	0	0	1	1	0	0	1	1	1
Hypsiboas raniceps	0	0	1	1	0	0	0	0	1
Hypsiboas rhythmicus	0	0	1	0	0	0	0	0	0
Hypsiboas riojanus	0	0	0	1	0	0	0	1	0
Hypsiboas roraima	0	0	1	0	0	0	0	0	0
Hypsiboas rosenbergi	0	0	0	0	0	0	1	0	0
Hypsiboas rubracylus	0	0	0	0	0	0	1	0	0
Hypsiboas rufitelus	0	0	0	0	1	0	1	0	0
Hypsiboas secedens	0	0	0	1	0	0	0	0	0
Hypsiboas semiguttatus	0	0	0	1	0	0	0	0	0
Hypsiboas semilineatus	0	0	0	1	0	0	0	0	0
Hypsiboas sibleszi	0	0	1	0	0	0	0	0	0
Hypsiboas stellae	0	0	0	1	0	0	0	0	0
Hypsiboas stenocephalus	0	0	0	1	0	0	0	0	0
Hypsiboas tepuianus	0	0	1	0	0	0	0	0	0
Hypsiboas varelae	0	0	0	1	0	0	0	0	0
Hypsiboas wavrini	0	0	1	1	0	0	0	0	1
Ikakogi tayrona	0	0	0	0	0	0	1	0	0
Incilius alvarius	0	0	0	0	1	1	0	0	0
Incilius aucoinae	0	0	0	0	0	0	1	0	0
Incilius bocourti	0	0	0	0	0	1	0	0	0

Incilius campbelli	0	0	0	0	1	1	0	0	0
Incilius canaliferus	0	0	0	0	1	1	0	0	0
Incilius cavifrons	0	0	0	0	1	0	0	0	0
Incilius chompipe	0	0	0	0	0	0	1	0	0
Incilius coccifer	0	0	0	0	1	1	1	0	0
Incilius coniferus	0	0	0	0	1	0	1	0	0
Incilius cristatus	0	0	0	0	1	1	0	0	0
Incilius cycladen	0	0	0	0	1	1	0	0	0
Incilius epioticus	0	0	0	0	0	0	1	0	0
Incilius fastidiosus	0	0	0	0	0	0	1	0	0
Incilius gemmifer	0	0	0	0	1	0	0	0	0
Incilius guanacaste	0	0	0	0	0	0	1	0	0
Incilius holdridgei	0	0	0	0	0	0	1	0	0
Incilius ibarrai	0	0	0	0	1	1	0	0	0
Incilius leucomyos	0	0	0	0	1	1	0	0	0
Incilius luetkenii	0	0	0	0	1	1	1	0	0
Incilius macrocristatus	0	0	0	0	1	1	0	0	0
Incilius marmoreus	0	0	0	0	1	1	0	0	0
Incilius mazatlanensis	0	0	0	0	1	1	0	0	0
Incilius melanochlorus	0	0	0	0	0	0	1	0	0
Incilius nebulifer	0	0	0	0	1	1	0	0	0
Incilius occidentalis	0	0	0	0	1	1	0	0	0
Incilius periglenes	0	0	0	0	0	0	1	0	0
Incilius peripatetes	0	0	0	0	0	0	1	0	0
Incilius perplexus	0	0	0	0	1	1	0	0	0
Incilius pisinnus	0	0	0	0	1	0	0	0	0
Incilius porteri	0	0	0	0	1	1	0	0	0
Incilius signifer	0	0	0	0	0	0	1	0	0
Incilius spiculatus	0	0	0	0	0	1	0	0	0
Incilius tacanensis	0	0	0	0	1	1	0	0	0
Incilius tutelarius	0	0	0	0	1	1	0	0	0
Incilius valliceps	0	0	0	0	1	1	1	0	0
Insuetophrynus acarpicus	1	0	0	0	0	0	0	0	0
Ischnocnema bolbodactyla	0	0	0	1	0	0	0	0	0
Ischnocnema erythromera	0	0	0	1	0	0	0	0	0
Ischnocnema gehrti	0	0	0	1	0	0	0	0	0
Ischnocnema gualteri	0	0	0	1	0	0	0	0	0
Ischnocnema guentheri	0	0	0	1	0	0	0	0	0
Ischnocnema henselii	0	0	0	1	0	0	0	0	0
Ischnocnema hoehnei	0	0	0	1	0	0	0	0	0
Ischnocnema holti	0	0	0	1	0	0	0	0	0
Ischnocnema izecksohni	0	0	0	1	0	0	0	0	0
Ischnocnema juipoca	0	0	0	1	0	0	0	0	0
Ischnocnema lactea	0	0	0	1	0	0	0	0	0
Ischnocnema manezinho	0	0	0	1	0	0	0	0	0
Ischnocnema nasuta	0	0	0	1	0	0	0	0	0
Ischnocnema nigriventris	0	0	0	1	0	0	0	0	0
Ischnocnema octavioi	0	0	0	1	0	0	0	0	0
Ischnocnema paranaensis	0	0	0	1	0	0	0	0	0
Ischnocnema parva	0	0	0	1	0	0	0	0	0
Ischnocnema penaxavantinho	0	0	0	1	0	0	0	0	0
Ischnocnema pusilla	0	0	0	1	0	0	0	0	0
Ischnocnema randorum	0	0	0	1	0	0	0	0	0
Ischnocnema sambaqui	0	0	0	1	0	0	0	0	0
Ischnocnema spanios	0	0	0	1	0	0	0	0	0
Ischnocnema venancioi	0	0	0	1	0	0	0	0	0

Ischnocnema verrucosa	0	0	0	1	0	0	0	0	0
Isthmohyla angustilineata	0	0	0	0	0	0	1	0	0
Isthmohyla calypsa	0	0	0	0	0	0	1	0	0
Isthmohyla debilis	0	0	0	0	0	0	1	0	0
Isthmohyla graceae	0	0	0	0	0	0	1	0	0
Isthmohyla infucata	0	0	0	0	0	0	1	0	0
Isthmohyla insolita	0	0	0	0	1	0	0	0	0
Isthmohyla lancasteri	0	0	0	0	0	0	1	0	0
Isthmohyla melacaena	0	0	0	0	1	0	0	0	0
Isthmohyla picadoi	0	0	0	0	0	0	1	0	0
Isthmohyla pictipes	0	0	0	0	0	0	1	0	0
Isthmohyla pseudopuma	0	0	0	0	0	0	1	0	0
Isthmohyla rivularis	0	0	0	0	0	0	1	0	0
Isthmohyla tica	0	0	0	0	0	0	1	0	0
Isthmohyla xanthosticta	0	0	0	0	0	0	1	0	0
Isthmohyla zeteki	0	0	0	0	0	0	1	0	0
Itapotihyla langsdorffii	0	0	0	1	0	0	0	0	0
Lepidobatrachus asper	0	0	0	1	0	0	0	0	1
Lepidobatrachus laevis	0	0	0	1	0	0	0	0	1
Lepidobatrachus llanensis	0	0	0	1	0	0	0	0	0
Leptodactylus albilabris	0	1	0	0	0	0	0	0	0
Leptodactylus bolivianus	0	0	1	1	0	0	1	1	1
Leptodactylus bufonius	0	0	0	1	0	0	0	1	1
Leptodactylus caatingae	0	0	0	1	0	0	0	0	0
Leptodactylus camaquara	0	0	0	1	0	0	0	0	0
Leptodactylus chaquensis	0	0	0	1	0	0	0	0	1
Leptodactylus colombiensis	0	0	1	0	0	0	1	1	0
Leptodactylus cunicularius	0	0	0	1	0	0	0	0	0
Leptodactylus cupreus	0	0	0	1	0	0	0	0	0
Leptodactylus didymus	0	0	0	1	0	0	0	0	1
Leptodactylus diedrus	0	0	1	0	0	0	0	0	1
Leptodactylus discodactylus	0	0	1	0	0	0	1	1	1
Leptodactylus elenae	0	0	0	1	0	0	0	1	1
Leptodactylus fallax	0	1	0	0	0	0	0	0	0
Leptodactylus flavopictus	0	0	0	1	0	0	0	0	0
Leptodactylus fragilis	0	0	1	0	1	1	1	1	0
Leptodactylus furnarius	0	0	0	1	0	0	0	0	1
Leptodactylus fuscus	0	0	1	1	0	0	1	1	1
Leptodactylus gracilis	0	0	0	1	0	0	0	1	1
Leptodactylus griseigularis	0	0	0	0	0	0	0	0	1
Leptodactylus hylodes	0	0	0	1	0	0	0	0	0
Leptodactylus jolyi	0	0	0	1	0	0	0	0	0
Leptodactylus knudseni	0	0	1	1	0	0	1	0	1
Leptodactylus labrosus	0	0	0	0	0	0	1	1	0
Leptodactylus labyrinthicus	0	0	0	1	0	0	0	0	1
Leptodactylus laticeps	0	0	0	1	0	0	0	0	1
Leptodactylus latinasus	0	0	0	1	0	0	0	0	1
Leptodactylus latrans	0	0	1	1	0	0	1	1	1
Leptodactylus lauramiriamae	0	0	0	1	0	0	0	0	0
Leptodactylus leptodactyloides	0	0	1	1	0	0	1	1	1
Leptodactylus lithonaetes	0	0	1	0	0	0	1	0	0
Leptodactylus longirostris	0	0	1	1	0	0	1	0	0
Leptodactylus magistris	0	0	0	0	0	0	1	0	0
Leptodactylus marambaiae	0	0	0	1	0	0	0	0	0
Leptodactylus melanonotus	0	0	0	0	1	1	1	0	0
Leptodactylus myersi	0	0	1	1	0	0	0	0	1

Leptodactylus mystaceus	0	0	1	1	0	0	1	1	1
Leptodactylus mystacinus	1	0	1	1	0	0	0	1	1
Leptodactylus natalensis	0	0	0	1	0	0	0	0	0
Leptodactylus notoaktites	0	0	0	1	0	0	0	0	0
Leptodactylus paraensis	0	0	1	1	0	0	0	0	1
Leptodactylus pentadactylus	0	0	1	1	0	0	1	1	1
Leptodactylus peritoaktites	0	0	0	0	0	0	1	0	0
Leptodactylus petersii	0	0	1	1	0	0	1	0	1
Leptodactylus plaumanni	0	0	0	1	0	0	0	0	0
Leptodactylus podicipinus	0	0	1	1	0	0	0	0	1
Leptodactylus poecilochilus	0	0	0	0	0	0	1	0	0
Leptodactylus pustulatus	0	0	1	1	0	0	0	0	1
Leptodactylus rhodomerus	0	0	0	0	0	0	1	0	0
Leptodactylus rhodomystax	0	0	1	1	0	0	0	0	1
Leptodactylus rhodonotus	0	0	1	1	0	0	0	0	1
Leptodactylus riveroi	0	0	1	0	0	0	0	0	1
Leptodactylus rugosus	0	0	1	0	0	0	0	0	0
Leptodactylus sabanensis	0	0	1	0	0	0	0	0	0
Leptodactylus savagei	0	0	0	0	1	1	1	0	0
Leptodactylus sertanejo	0	0	0	1	0	0	0	0	0
Leptodactylus silvanimbus	0	0	0	0	1	1	0	0	0
Leptodactylus spixi	0	0	0	1	0	0	0	0	0
Leptodactylus stenodema	0	0	1	1	0	0	0	0	1
Leptodactylus syphax	0	0	1	1	0	0	0	0	1
Leptodactylus tapiti	0	0	0	1	0	0	0	0	0
Leptodactylus troglodytes	0	0	1	1	0	0	0	0	0
Leptodactylus turimiquensis	0	0	0	0	0	0	1	0	0
Leptodactylus validus	0	1	0	0	0	0	1	0	0
Leptodactylus vastus	0	0	1	1	0	0	0	0	0
Leptodactylus ventrimaculatus	0	0	0	0	0	0	1	0	0
Leptodactylus viridis	0	0	0	1	0	0	0	0	0
Leptodactylus wagneri	0	0	1	0	0	0	1	1	1
Limnomedusa macroglossa	0	0	0	1	0	0	0	0	0
Lithobates berlandieri	0	0	0	0	1	1	0	0	0
Lithobates bwana	0	0	0	0	0	0	1	0	0
Lithobates chiricahuensis	0	0	0	0	0	1	0	0	0
Lithobates dunni	0	0	0	0	1	1	0	0	0
Lithobates forreri	0	0	0	0	1	1	1	0	0
Lithobates grylio	0	1	0	0	0	0	0	0	0
Lithobates johni	0	0	0	0	1	0	0	0	0
Lithobates juliani	0	0	0	0	1	0	0	0	0
Lithobates lemosespinali	0	0	0	0	0	1	0	0	0
Lithobates macroglossa	0	0	0	0	0	1	0	0	0
Lithobates maculatus	0	0	0	0	1	1	0	0	0
Lithobates magnaocularis	0	0	0	0	1	1	0	0	0
Lithobates megapoda	0	0	0	0	1	1	0	0	0
Lithobates montezumae	0	0	0	0	1	1	0	0	0
Lithobates neovolcanicus	0	0	0	0	1	1	0	0	0
Lithobates omiltemanus	0	0	0	0	1	1	0	0	0
Lithobates palmipes	0	0	1	1	0	0	1	1	1
Lithobates pipiens	0	0	0	0	0	0	1	0	0
Lithobates psilonota	0	0	0	0	1	1	0	0	0
Lithobates pustulosus	0	0	0	0	1	1	0	0	0
Lithobates sierramadrensis	0	0	0	0	1	1	0	0	0
Lithobates spectabilis	0	0	0	0	1	1	0	0	0
Lithobates tarahumarae	0	0	0	0	1	1	0	0	0

Lithobates taylori	0	0	0	0	1	0	1	0	0
Lithobates tlaloci	0	0	0	0	0	1	0	0	0
Lithobates vaillanti	0	0	0	0	1	1	1	0	0
Lithobates vibicarius	0	0	0	0	0	0	1	0	0
Lithobates warszewitschii	0	0	0	0	1	1	1	0	0
Lithobates yavapaiensis	0	0	0	0	0	1	0	0	0
Lithobates zweifeli	0	0	0	0	1	1	0	0	0
Lithodytes lineatus	0	0	1	1	0	0	1	1	1
Lynchius flavomaculatus	0	0	0	0	0	0	1	0	0
Lynchius nebulanastes	0	0	0	0	0	0	1	0	0
Lynchius parkeri	0	0	0	0	0	0	1	0	0
Lynchius simmonsi	0	0	0	0	0	0	1	0	0
Lysapsus bolivianus	0	0	1	1	0	0	0	0	1
Lysapsus caraya	0	0	0	1	0	0	0	0	1
Lysapsus laevis	0	0	1	0	0	0	0	0	1
Lysapsus limellum	0	0	0	1	0	0	0	0	1
Macrogenioglottus alipioi	0	0	0	1	0	0	0	0	0
Mannophryne caquetio	0	0	0	0	0	0	1	0	0
Mannophryne collaris	0	0	0	0	0	0	1	0	0
Mannophryne cordilleriana	0	0	0	0	0	0	1	0	0
Mannophryne herminae	0	0	0	0	0	0	1	0	0
Mannophryne lamarcai	0	0	0	0	0	0	1	0	0
Mannophryne larandina	0	0	0	0	0	0	1	0	0
Mannophryne leonardoi	0	0	0	0	0	0	1	0	0
Mannophryne neblina	0	0	0	0	0	0	1	0	0
Mannophryne oblitterata	0	0	0	0	0	0	1	0	0
Mannophryne riveroi	0	0	0	0	0	0	1	0	0
Mannophryne trinitatis	0	0	0	0	0	0	1	0	0
Mannophryne trujillensis	0	0	0	0	0	0	1	0	0
Mannophryne venezuelensis	0	0	0	0	0	0	1	0	0
Mannophryne yustizi	0	0	0	0	0	0	1	0	0
Megaelosia apuana	0	0	0	1	0	0	0	0	0
Megaelosia bocainensis	0	0	0	1	0	0	0	0	0
Megaelosia boticariana	0	0	0	1	0	0	0	0	0
Megaelosia goeldii	0	0	0	1	0	0	0	0	0
Megaelosia jordanensis	0	0	0	1	0	0	0	0	0
Megaelosia lutzae	0	0	0	1	0	0	0	0	0
Megaelosia massarti	0	0	0	1	0	0	0	0	0
Megastomatohyla mixomaculata	0	0	0	0	1	1	0	0	0
Megastomatohyla nubicola	0	0	0	0	1	0	0	0	0
Megastomatohyla pellita	0	0	0	0	1	1	0	0	0
Melanophryniscus admirabilis	0	0	0	1	0	0	0	0	0
Melanophryniscus alipioi	0	0	0	1	0	0	0	0	0
Melanophryniscus atroluteus	0	0	0	1	0	0	0	0	0
Melanophryniscus cambaraensis	0	0	0	1	0	0	0	0	0
Melanophryniscus cupreuscapularis	0	0	0	1	0	0	0	0	0
Melanophryniscus devincenzii	0	0	0	1	0	0	0	0	0
Melanophryniscus dorsalis	0	0	0	1	0	0	0	0	0
Melanophryniscus fulvoguttatus	0	0	0	1	0	0	0	0	0
Melanophryniscus klappenbachi	0	0	0	1	0	0	0	0	1
Melanophryniscus krauczuki	0	0	0	1	0	0	0	0	0
Melanophryniscus langonei	0	0	0	1	0	0	0	0	0
Melanophryniscus macrogranulosus	0	0	0	1	0	0	0	0	0
Melanophryniscus montevidensis	0	0	0	1	0	0	0	0	0
Melanophryniscus moreirae	0	0	0	1	0	0	0	0	0
Melanophryniscus pachyrhynus	0	0	0	1	0	0	0	0	0

Melanophryniscus peritus	0	0	0	1	0	0	0	0	0
Melanophryniscus rubriventris	0	0	0	1	0	0	0	1	1
Melanophryniscus sanmartini	0	0	0	1	0	0	0	0	0
Melanophryniscus simplex	0	0	0	1	0	0	0	0	0
Melanophryniscus stelzneri	0	0	0	1	0	0	0	1	1
Melanophryniscus tumifrons	0	0	0	1	0	0	0	0	0
Metaphryniscus sosai	0	0	1	0	0	0	0	0	0
Minyobates steyermarki	0	0	1	0	0	0	0	0	0
Myersiella microps	0	0	0	1	0	0	0	0	0
Myersiohyla aromatica	0	0	1	0	0	0	0	0	0
Myersiohyla inparquesi	0	0	1	0	0	0	0	0	0
Myersiohyla kanaima	0	0	1	0	0	0	0	0	0
Myersiohyla loveridgei	0	0	1	0	0	0	0	0	0
Nannophryne apolobambica	0	0	0	0	0	0	0	0	1
Nannophryne cophotis	0	0	0	0	0	0	0	1	0
Nannophryne corynetes	0	0	0	0	0	0	0	0	1
Nannophryne variegata	1	0	0	0	0	0	0	0	0
Niceforonia adenobrachia	0	0	0	0	0	0	1	0	0
Niceforonia columbiana	0	0	0	0	0	0	1	1	0
Niceforonia nana	0	0	0	0	0	0	1	1	0
Noblella carrascoicola	0	0	0	0	0	0	0	0	1
Noblella duellmani	0	0	0	0	0	0	0	0	1
Noblella heyeri	0	0	0	0	0	0	1	0	0
Noblella lochites	0	0	1	0	0	0	1	1	0
Noblella lynchi	0	0	0	0	0	0	0	0	1
Noblella myrmecoides	0	0	1	0	0	0	0	0	1
Noblella pygmaea	0	0	0	0	0	0	0	0	1
Noblella ritarasquinae	0	0	0	0	0	0	0	0	1
Nyctimantis rugiceps	0	0	1	0	0	0	0	1	1
Nymphargus armatus	0	0	0	0	0	0	1	0	0
Nymphargus bejaranoi	0	0	0	1	0	0	0	1	1
Nymphargus buenaventura	0	0	0	0	0	0	1	0	0
Nymphargus cariticommatus	0	0	0	0	0	0	1	1	0
Nymphargus chami	0	0	0	0	0	0	1	0	0
Nymphargus chancas	0	0	0	0	0	0	0	0	1
Nymphargus cochranae	0	0	1	0	0	0	1	1	0
Nymphargus cristinae	0	0	0	0	0	0	1	0	0
Nymphargus garciae	0	0	0	0	0	0	1	1	0
Nymphargus grandisonae	0	0	0	0	0	0	1	0	0
Nymphargus griffithsi	0	0	0	0	0	0	1	0	0
Nymphargus ignotus	0	0	0	0	0	0	1	0	0
Nymphargus laurae	0	0	1	0	0	0	0	0	0
Nymphargus luminosus	0	0	0	0	0	0	1	0	0
Nymphargus luteopunctatus	0	0	0	0	0	0	1	0	0
Nymphargus mariae	0	0	0	0	0	0	0	0	1
Nymphargus megacheirus	0	0	0	0	0	0	0	1	0
Nymphargus mixomaculatus	0	0	0	0	0	0	0	0	1
Nymphargus nephelophila	0	0	0	0	0	0	0	1	0
Nymphargus ocellatus	0	0	0	0	0	0	0	0	1
Nymphargus oreonympha	0	0	0	0	0	0	0	1	0
Nymphargus phenax	0	0	0	0	0	0	0	0	1
Nymphargus pluvialis	0	0	0	0	0	0	0	0	1
Nymphargus posadae	0	0	1	0	0	0	1	1	0
Nymphargus prasinus	0	0	0	0	0	0	1	0	0
Nymphargus rosada	0	0	0	0	0	0	1	0	0
Nymphargus ruizi	0	0	0	0	0	0	1	0	0

Nymphargus siren	0	0	1	0	0	0	0	1	1
Nymphargus spilotus	0	0	0	0	0	0	1	0	0
Nymphargus truebae	0	0	0	0	0	0	0	0	1
Nymphargus vicenteruedai	0	0	0	0	0	0	1	0	0
Nymphargus wileyi	0	0	0	0	0	0	0	1	0
Odontophrynus achalensis	0	0	0	1	0	0	0	0	0
Odontophrynus americanus	0	0	0	1	0	0	0	1	1
Odontophrynus barrioi	0	0	0	0	0	0	0	1	0
Odontophrynus carvalhoi	0	0	1	1	0	0	0	0	0
Odontophrynus cordobae	0	0	0	1	0	0	0	0	0
Odontophrynus cultripes	0	0	0	1	0	0	0	0	0
Odontophrynus lavillai	0	0	0	1	0	0	0	1	1
Odontophrynus occidentalis	1	0	0	1	0	0	0	1	0
Odontophrynus salvatori	0	0	0	1	0	0	0	0	0
Oophaga arborea	0	0	0	0	0	0	1	0	0
Oophaga granulifera	0	0	0	0	0	0	1	0	0
Oophaga histrionica	0	0	0	0	0	0	1	0	0
Oophaga lehmanni	0	0	0	0	0	0	1	0	0
Oophaga occultator	0	0	0	0	0	0	1	0	0
Oophaga pumilio	0	0	0	0	1	0	1	0	0
Oophaga speciosa	0	0	0	0	0	0	1	0	0
Oophaga sylvatica	0	0	0	0	0	0	1	0	0
Oophaga vicentei	0	0	0	0	0	0	1	0	0
Oreobates ayacucho	0	0	0	0	0	0	0	0	1
Oreobates choristolemma	0	0	0	0	0	0	0	0	1
Oreobates crepitans	0	0	0	1	0	0	0	0	0
Oreobates cruralis	0	0	0	1	0	0	0	0	1
Oreobates discoidalis	0	0	0	1	0	0	0	1	1
Oreobates heterodactylus	0	0	0	1	0	0	0	0	1
Oreobates ibischi	0	0	0	1	0	0	0	0	1
Oreobates lehri	0	0	0	0	0	0	0	0	1
Oreobates lundbergi	0	0	0	0	0	0	0	0	1
Oreobates madidi	0	0	0	0	0	0	0	0	1
Oreobates pereger	0	0	0	0	0	0	0	0	1
Oreobates quixensis	0	0	1	0	0	0	0	1	1
Oreobates sanctaecrucis	0	0	0	0	0	0	0	0	1
Oreobates sanderi	0	0	0	0	0	0	0	0	1
Oreobates saxatilis	0	0	0	0	0	0	0	0	1
Oreobates zongoensis	0	0	0	0	0	0	0	0	1
Oreophrynella cryptica	0	0	1	0	0	0	0	0	0
Oreophrynella dendronastes	0	0	1	0	0	0	0	0	0
Oreophrynella huberi	0	0	1	0	0	0	0	0	0
Oreophrynella macconnelli	0	0	1	0	0	0	0	0	0
Oreophrynella nigra	0	0	1	0	0	0	0	0	0
Oreophrynella quelchii	0	0	1	0	0	0	0	0	0
Oreophrynella vasquezi	0	0	1	0	0	0	0	0	0
Oreophrynella weiassipuensis	0	0	1	0	0	0	0	0	0
Osornophryne antisana	0	0	0	0	0	0	0	1	0
Osornophryne bufoniformis	0	0	0	0	0	0	1	1	0
Osornophryne guacamayo	0	0	0	0	0	0	0	1	0
Osornophryne percrassa	0	0	0	0	0	0	1	0	0
Osornophryne puruanta	0	0	0	0	0	0	1	1	0
Osornophryne talipes	0	0	0	0	0	0	1	1	0
Osteocephalus alboguttatus	0	0	1	0	0	0	0	1	0
Osteocephalus buckleyi	0	0	1	1	0	0	1	1	1
Osteocephalus cabrerai	0	0	1	0	0	0	1	1	1

Osteocephalus castaneicola	0	0	0	0	0	0	0	0	1
Osteocephalus deridens	0	0	1	0	0	0	0	0	1
Osteocephalus fuscifacies	0	0	1	0	0	0	0	1	0
Osteocephalus heyeri	0	0	1	0	0	0	0	0	0
Osteocephalus leoniae	0	0	0	0	0	0	0	0	1
Osteocephalus leprieurii	0	0	1	1	0	0	0	0	1
Osteocephalus mimeticus	0	0	1	0	0	0	1	1	1
Osteocephalus mutabor	0	0	1	0	0	0	0	1	0
Osteocephalus oophagus	0	0	1	0	0	0	0	0	1
Osteocephalus planiceps	0	0	1	0	0	0	1	1	1
Osteocephalus subtilis	0	0	0	0	0	0	0	0	1
Osteocephalus taurinus	0	0	1	1	0	0	1	0	1
Osteocephalus verruciger	0	0	1	0	0	0	0	1	0
Osteocephalus yasuni	0	0	1	0	0	0	0	0	1
Osteopilus crucialis	0	1	0	0	0	0	0	0	0
Osteopilus dominicensis	0	1	0	0	0	0	0	0	0
Osteopilus marianae	0	1	0	0	0	0	0	0	0
Osteopilus ocellatus	0	1	0	0	0	0	0	0	0
Osteopilus pulchrilineatus	0	1	0	0	0	0	0	0	0
Osteopilus septentrionalis	0	1	0	0	0	0	1	0	0
Osteopilus vastus	0	1	0	0	0	0	0	0	0
Osteopilus wilderi	0	1	0	0	0	0	0	0	0
Otophryne pyburni	0	0	1	0	0	0	0	0	0
Otophryne robusta	0	0	1	0	0	0	0	0	0
Otophryne steyermarki	0	0	1	0	0	0	0	0	0
Paratelmatobius cardosoi	0	0	0	1	0	0	0	0	0
Paratelmatobius gaigeae	0	0	0	1	0	0	0	0	0
Paratelmatobius lutzii	0	0	0	1	0	0	0	0	0
Paratelmatobius mantiqueira	0	0	0	1	0	0	0	0	0
Paratelmatobius poecilogaster	0	0	0	1	0	0	0	0	0
Peltophryne cataulaciceps	0	1	0	0	0	0	0	0	0
Peltophryne empusa	0	1	0	0	0	0	0	0	0
Peltophryne florentinoi	0	1	0	0	0	0	0	0	0
Peltophryne fluviatica	0	1	0	0	0	0	0	0	0
Peltophryne fracta	0	1	0	0	0	0	0	0	0
Peltophryne fustiger	0	1	0	0	0	0	0	0	0
Peltophryne guentheri	0	1	0	0	0	0	0	0	0
Peltophryne gundlachi	0	1	0	0	0	0	0	0	0
Peltophryne lemur	0	1	0	0	0	0	0	0	0
Peltophryne longinasus	0	1	0	0	0	0	0	0	0
Peltophryne peltocephala	0	1	0	0	0	0	0	0	0
Peltophryne taladai	0	1	0	0	0	0	0	0	0
Phasmahyla cochranae	0	0	0	1	0	0	0	0	0
Phasmahyla exilis	0	0	0	1	0	0	0	0	0
Phasmahyla guttata	0	0	0	1	0	0	0	0	0
Phasmahyla jandaia	0	0	0	1	0	0	0	0	0
Phasmahyla spectabilis	0	0	0	1	0	0	0	0	0
Phasmahyla timbo	0	0	0	1	0	0	0	0	0
Phrynomedusa appendiculata	0	0	0	1	0	0	0	0	0
Phrynomedusa bokermanni	0	0	0	1	0	0	0	0	0
Phrynomedusa fimbriata	0	0	0	1	0	0	0	0	0
Phrynomedusa marginata	0	0	0	1	0	0	0	0	0
Phrynomedusa vanzolinii	0	0	0	1	0	0	0	0	0
Phrynopus auriculatus	0	0	0	0	0	0	0	0	1
Phrynopus barthlenae	0	0	0	0	0	0	0	0	1
Phrynopus bracki	0	0	0	0	0	0	0	0	1

Phrynopus bufoides	0	0	0	0	0	0	0	0	1
Phrynopus dagmarae	0	0	0	0	0	0	0	0	1
Phrynopus heimorum	0	0	0	0	0	0	0	0	1
Phrynopus horstpauli	0	0	0	0	0	0	0	0	1
Phrynopus juninensis	0	0	0	0	0	0	0	0	1
Phrynopus kauneorum	0	0	0	0	0	0	0	0	1
Phrynopus kotosh	0	0	0	0	0	0	0	1	1
Phrynopus montium	0	0	0	0	0	0	0	1	1
Phrynopus nicoleae	0	0	0	0	0	0	0	0	1
Phrynopus oblivius	0	0	0	0	0	0	0	0	1
Phrynopus peruanus	0	0	0	0	0	0	0	0	1
Phrynopus thompsoni	0	0	0	0	0	0	0	1	0
Phrynopus tribulosus	0	0	0	0	0	0	0	0	1
Phyllobates aurotaenia	0	0	0	0	0	0	1	0	0
Phyllobates bicolor	0	0	0	0	0	0	1	0	0
Phyllobates lugubris	0	0	0	0	0	0	1	0	0
Phyllobates terribilis	0	0	0	0	0	0	1	0	0
Phyllobates vittatus	0	0	0	0	0	0	1	0	0
Phyllodytes acuminatus	0	0	0	1	0	0	0	0	0
Phyllodytes brevirostris	0	0	0	1	0	0	0	0	0
Phyllodytes edelmoi	0	0	0	1	0	0	0	0	0
Phyllodytes gyrinaethes	0	0	0	1	0	0	0	0	0
Phyllodytes kautskyi	0	0	0	1	0	0	0	0	0
Phyllodytes luteolus	0	0	0	1	0	0	0	0	0
Phyllodytes maculosus	0	0	0	1	0	0	0	0	0
Phyllodytes melanomystax	0	0	0	1	0	0	0	0	0
Phyllodytes punctatus	0	0	0	1	0	0	0	0	0
Phyllodytes tuberculosus	0	0	0	1	0	0	0	0	0
Phyllodytes wuchereri	0	0	0	1	0	0	0	0	0
Phyllomedusa atelopoides	0	0	1	0	0	0	0	0	1
Phyllomedusa ayeaye	0	0	0	1	0	0	0	0	0
Phyllomedusa azurea	0	0	0	1	0	0	0	1	1
Phyllomedusa bahiana	0	0	0	1	0	0	0	0	0
Phyllomedusa baltea	0	0	0	0	0	0	0	0	1
Phyllomedusa bicolor	0	0	1	1	0	0	1	0	1
Phyllomedusa boliviana	0	0	0	1	0	0	0	1	1
Phyllomedusa burmeisteri	0	0	0	1	0	0	0	0	0
Phyllomedusa camba	0	0	0	1	0	0	0	0	1
Phyllomedusa centralis	0	0	0	1	0	0	0	0	0
Phyllomedusa coelestis	0	0	1	0	0	0	0	0	1
Phyllomedusa distincta	0	0	0	1	0	0	0	0	0
Phyllomedusa duellmani	0	0	0	0	0	0	0	0	1
Phyllomedusa hypochondrialis	0	0	1	1	0	0	1	0	1
Phyllomedusa iheringii	0	0	0	1	0	0	0	0	0
Phyllomedusa megacephala	0	0	0	1	0	0	0	0	0
Phyllomedusa neildi	0	0	0	0	0	0	1	0	0
Phyllomedusa nordestina	0	0	1	1	0	0	0	0	0
Phyllomedusa oreades	0	0	0	1	0	0	0	0	0
Phyllomedusa palliata	0	0	1	0	0	0	0	0	1
Phyllomedusa perinesos	0	0	0	0	0	0	0	1	0
Phyllomedusa rohdei	0	0	0	1	0	0	0	0	0
Phyllomedusa sauvagii	0	0	0	1	0	0	0	0	1
Phyllomedusa tarsius	0	0	1	1	0	0	1	1	1
Phyllomedusa tetraploidea	0	0	0	1	0	0	0	0	0
Phyllomedusa tomopterna	0	0	1	1	0	0	0	1	1
Phyllomedusa trinitatis	0	0	0	0	0	0	1	0	0

Phyllomedusa vaillantii	0	0	1	1	0	0	0	0	1
Phyllomedusa venusta	0	0	0	0	0	0	1	0	0
Physalaemus aguirrei	0	0	0	1	0	0	0	0	0
Physalaemus albifrons	0	0	1	1	0	0	0	0	0
Physalaemus albonotatus	0	0	0	1	0	0	0	0	1
Physalaemus angrensis	0	0	0	1	0	0	0	0	0
Physalaemus barrioi	0	0	0	1	0	0	0	0	0
Physalaemus biligonigerus	0	0	0	1	0	0	0	0	1
Physalaemus caete	0	0	0	1	0	0	0	0	0
Physalaemus centralis	0	0	0	1	0	0	0	0	1
Physalaemus cicada	0	0	0	1	0	0	0	0	0
Physalaemus crombiei	0	0	0	1	0	0	0	0	0
Physalaemus cuqui	0	0	0	1	0	0	0	1	1
Physalaemus cuvieri	0	0	1	1	0	0	0	0	1
Physalaemus deimaticus	0	0	0	1	0	0	0	0	0
Physalaemus ephippifer	0	0	1	1	0	0	1	0	1
Physalaemus erikae	0	0	0	1	0	0	0	0	0
Physalaemus erythros	0	0	0	1	0	0	0	0	0
Physalaemus evangelistai	0	0	0	1	0	0	0	0	0
Physalaemus fernandezae	0	0	0	1	0	0	0	0	0
Physalaemus fischeri	0	0	1	0	0	0	1	1	0
Physalaemus gracilis	0	0	0	1	0	0	0	0	0
Physalaemus henselii	0	0	0	1	0	0	0	0	0
Physalaemus insperatus	0	0	0	1	0	0	0	0	0
Physalaemus irroratus	0	0	0	1	0	0	0	0	0
Physalaemus jordanensis	0	0	0	1	0	0	0	0	0
Physalaemus kroyeri	0	0	0	1	0	0	0	0	0
Physalaemus lisei	0	0	0	1	0	0	0	0	0
Physalaemus maculiventris	0	0	0	1	0	0	0	0	0
Physalaemus marmoratus	0	0	0	1	0	0	0	0	1
Physalaemus maximus	0	0	0	1	0	0	0	0	0
Physalaemus moreirae	0	0	0	1	0	0	0	0	0
Physalaemus nanus	0	0	0	1	0	0	0	0	0
Physalaemus nattereri	0	0	0	1	0	0	0	0	1
Physalaemus obtectus	0	0	0	1	0	0	0	0	0
Physalaemus olfersii	0	0	0	1	0	0	0	0	0
Physalaemus riograndensis	0	0	0	1	0	0	0	0	0
Physalaemus rupestris	0	0	0	1	0	0	0	0	0
Physalaemus santafecinus	0	0	0	1	0	0	0	0	0
Physalaemus signifer	0	0	0	1	0	0	0	0	0
Physalaemus soaresi	0	0	0	1	0	0	0	0	0
Physalaemus spiniger	0	0	0	1	0	0	0	0	0
Phytotriades auratus	0	0	0	0	0	0	1	0	0
Phyzelaphryne miriamae	0	0	1	1	0	0	0	0	1
Pipa arrabali	0	0	1	1	0	0	1	0	1
Pipa aspera	0	0	1	0	0	0	0	0	0
Pipa carvalhoi	0	0	0	1	0	0	0	0	0
Pipa myersi	0	0	0	0	0	0	1	0	0
Pipa parva	0	0	0	0	0	0	1	1	0
Pipa	0	0	1	1	0	0	1	1	1
Pipa snethlageae	0	0	1	1	0	0	0	0	1
Plectrohyla acanthodes	0	0	0	0	1	1	0	0	0
Plectrohyla ameibothalame	0	0	0	0	0	1	0	0	0
Plectrohyla arborescandens	0	0	0	0	1	1	0	0	0
Plectrohyla avia	0	0	0	0	1	1	0	0	0
Plectrohyla bistincta	0	0	0	0	1	1	0	0	0

Plectrohyla calthula	0	0	0	0	0	1	0	0	0
Plectrohyla calvicollina	0	0	0	0	0	1	0	0	0
Plectrohyla celata	0	0	0	0	0	1	0	0	0
Plectrohyla cembra	0	0	0	0	0	1	0	0	0
Plectrohyla charadricola	0	0	0	0	1	1	0	0	0
Plectrohyla chryses	0	0	0	0	1	0	0	0	0
Plectrohyla chrysopleura	0	0	0	0	1	0	0	0	0
Plectrohyla crassa	0	0	0	0	0	1	0	0	0
Plectrohyla cyanomma	0	0	0	0	0	1	0	0	0
Plectrohyla cyclada	0	0	0	0	1	1	0	0	0
Plectrohyla dasypus	0	0	0	0	1	0	0	0	0
Plectrohyla ephemera	0	0	0	0	1	0	0	0	0
Plectrohyla exquisita	0	0	0	0	1	0	0	0	0
Plectrohyla glandulosa	0	0	0	0	1	1	0	0	0
Plectrohyla guatemalensis	0	0	0	0	1	1	0	0	0
Plectrohyla hartwegi	0	0	0	0	1	1	0	0	0
Plectrohyla hazelae	0	0	0	0	1	1	0	0	0
Plectrohyla ixil	0	0	0	0	1	1	0	0	0
Plectrohyla labedactyla	0	0	0	0	0	1	0	0	0
Plectrohyla lacertosa	0	0	0	0	1	0	0	0	0
Plectrohyla matudai	0	0	0	0	1	1	0	0	0
Plectrohyla miahuatlanensis	0	0	0	0	0	1	0	0	0
Plectrohyla mykter	0	0	0	0	1	0	0	0	0
Plectrohyla pachyderma	0	0	0	0	1	0	0	0	0
Plectrohyla pentheter	0	0	0	0	1	1	0	0	0
Plectrohyla pokomchi	0	0	0	0	1	1	0	0	0
Plectrohyla psiloderma	0	0	0	0	1	1	0	0	0
Plectrohyla pycnochila	0	0	0	0	1	0	0	0	0
Plectrohyla quecchi	0	0	0	0	1	1	0	0	0
Plectrohyla robertsorum	0	0	0	0	1	1	0	0	0
Plectrohyla sabrina	0	0	0	0	0	1	0	0	0
Plectrohyla sagorum	0	0	0	0	1	1	0	0	0
Plectrohyla tecunumani	0	0	0	0	0	1	0	0	0
Plectrohyla teuchestes	0	0	0	0	1	1	0	0	0
Plectrohyla thorectes	0	0	0	0	1	1	0	0	0
Pleurodema bibroni	0	0	0	1	0	0	0	0	0
Pleurodema borellii	0	0	0	1	0	0	0	0	1
Pleurodema brachyops	0	0	1	0	0	0	1	1	0
Pleurodema bufoninum	1	0	0	0	0	0	0	1	0
Pleurodema cinereum	0	0	0	0	0	0	0	1	1
Pleurodema diplolister	0	0	1	1	0	0	0	0	0
Pleurodema guayapae	0	0	0	1	0	0	0	0	0
Pleurodema kriegi	0	0	0	1	0	0	0	0	0
Pleurodema marmoratum	0	0	0	0	0	0	0	1	1
Pleurodema nebulosum	0	0	0	1	0	0	0	1	0
Pleurodema somuncurense	1	0	0	0	0	0	0	0	0
Pleurodema thaul	1	0	0	0	0	0	0	1	0
Pleurodema tucumanum	0	0	0	1	0	0	0	1	1
Pristimantis aaptus	0	0	1	0	0	0	0	0	1
Pristimantis acatallelus	0	0	0	0	0	0	1	0	0
Pristimantis acerus	0	0	0	0	0	0	0	1	0
Pristimantis achatinus	0	0	0	0	0	0	1	0	0
Pristimantis actinolaimus	0	0	0	0	0	0	1	0	0
Pristimantis actites	0	0	0	0	0	0	1	0	0
Pristimantis acuminatus	0	0	1	0	0	0	1	1	1
Pristimantis acutirostris	0	0	0	0	0	0	1	0	0

Pristimantis adiastolus	0	0	0	0	0	0	0	0	1
Pristimantis aemulatus	0	0	0	0	0	0	1	0	0
Pristimantis affinis	0	0	0	0	0	0	0	1	0
Pristimantis alalocophus	0	0	0	0	0	0	1	0	0
Pristimantis albericoi	0	0	0	0	0	0	1	0	0
Pristimantis albertus	0	0	0	0	0	0	0	0	1
Pristimantis altae	0	0	0	0	0	0	1	0	0
Pristimantis altamazonicus	0	0	1	0	0	0	0	1	1
Pristimantis altamnis	0	0	1	0	0	0	0	1	0
Pristimantis amydrotus	0	0	0	0	0	0	0	1	0
Pristimantis anemerus	0	0	0	0	0	0	1	0	0
Pristimantis angustilineatus	0	0	0	0	0	0	1	0	0
Pristimantis aniptopalmatus	0	0	0	0	0	0	0	0	1
Pristimantis anolirex	0	0	0	0	0	0	0	1	0
Pristimantis anotis	0	0	0	0	0	0	1	0	0
Pristimantis apiculatus	0	0	0	0	0	0	1	0	0
Pristimantis appendiculatus	0	0	0	0	0	0	1	0	0
Pristimantis aquilonaris	0	0	0	0	0	0	1	0	0
Pristimantis ardalonychus	0	0	0	0	0	0	0	0	1
Pristimantis atrabracus	0	0	0	0	0	0	0	0	1
Pristimantis atratus	0	0	0	0	0	0	1	1	0
Pristimantis aurantiguttatus	0	0	0	0	0	0	1	0	0
Pristimantis aureolineatus	0	0	1	0	0	0	0	1	1
Pristimantis aureoventris	0	0	1	0	0	0	0	0	0
Pristimantis avicuporum	0	0	0	0	0	0	0	0	1
Pristimantis avius	0	0	1	0	0	0	0	0	0
Pristimantis bacchus	0	0	0	0	0	0	1	0	0
Pristimantis baiotis	0	0	0	0	0	0	1	0	0
Pristimantis balionotus	0	0	0	0	0	0	1	0	0
Pristimantis bambu	0	0	0	0	0	0	1	0	0
Pristimantis baryecuus	0	0	0	0	0	0	1	1	0
Pristimantis batrachites	0	0	0	0	0	0	1	1	0
Pristimantis bearsei	0	0	0	0	0	0	0	0	1
Pristimantis bellator	0	0	0	0	0	0	1	0	0
Pristimantis bellona	0	0	0	0	0	0	1	0	0
Pristimantis bernali	0	0	0	0	0	0	1	0	0
Pristimantis bicolor	0	0	0	0	0	0	1	0	0
Pristimantis bicumulus	0	0	0	0	0	0	1	0	0
Pristimantis boconoensis	0	0	0	0	0	0	1	0	0
Pristimantis bogotensis	0	0	0	0	0	0	1	1	0
Pristimantis boulengeri	0	0	0	0	0	0	1	0	0
Pristimantis brevifrons	0	0	0	0	0	0	1	0	0
Pristimantis briceni	0	0	0	0	0	0	1	0	0
Pristimantis bromeliaceus	0	0	0	0	0	0	1	1	1
Pristimantis buccinator	0	0	0	0	0	0	0	0	1
Pristimantis buckleyi	0	0	0	0	0	0	1	1	0
Pristimantis cabrerai	0	0	0	0	0	0	1	0	0
Pristimantis cacao	0	0	0	0	0	0	1	0	0
Pristimantis caeruleonotus	0	0	0	0	0	0	1	0	0
Pristimantis cajamarcensis	0	0	0	0	0	0	1	1	0
Pristimantis calcaratus	0	0	0	0	0	0	1	0	0
Pristimantis calcarulatus	0	0	0	0	0	0	1	0	0
Pristimantis cantitans	0	0	1	0	0	0	0	0	0
Pristimantis capitonis	0	0	0	0	0	0	1	0	0
Pristimantis caprifer	0	0	0	0	0	0	1	0	0
Pristimantis carlossanchezi	0	0	0	0	0	0	1	1	0

Pristimantis carmelitae	0	0	0	0	0	0	1	0	0
Pristimantis carranguerorum	0	0	0	0	0	0	0	1	0
Pristimantis carvalhoi	0	0	1	0	0	0	0	0	1
Pristimantis caryophyllaceus	0	0	0	0	0	0	1	0	0
Pristimantis celator	0	0	0	0	0	0	1	1	0
Pristimantis cerasinus	0	0	0	0	1	0	1	0	0
Pristimantis ceuthospilus	0	0	0	0	0	0	1	1	0
Pristimantis chalceus	0	0	0	0	0	0	1	0	0
Pristimantis chiastonotus	0	0	1	0	0	0	0	0	0
Pristimantis chimu	0	0	0	0	0	0	1	0	0
Pristimantis chloronotus	0	0	1	0	0	0	1	1	0
Pristimantis chrysops	0	0	0	0	0	0	1	0	0
Pristimantis citriogaster	0	0	0	0	0	0	0	0	1
Pristimantis colodactylus	0	0	0	0	0	0	1	1	0
Pristimantis colomai	0	0	0	0	0	0	1	0	0
Pristimantis colonensis	0	0	1	0	0	0	0	1	0
Pristimantis colostichos	0	0	0	0	0	0	1	0	0
Pristimantis condor	0	0	0	0	0	0	1	1	0
Pristimantis conspicillatus	0	0	1	0	0	0	0	1	1
Pristimantis cordovae	0	0	0	0	0	0	0	1	0
Pristimantis corniger	0	0	0	0	0	0	1	1	0
Pristimantis coronatus	0	0	0	0	0	0	1	0	0
Pristimantis corrugatus	0	0	0	0	0	0	0	0	1
Pristimantis cosnipatae	0	0	0	0	0	0	0	0	1
Pristimantis cremnobates	0	0	0	0	0	0	0	1	0
Pristimantis crenunguis	0	0	0	0	0	0	1	0	0
Pristimantis cristinae	0	0	0	0	0	0	1	0	0
Pristimantis croceoinguinis	0	0	1	0	0	0	0	1	1
Pristimantis crucifer	0	0	0	0	0	0	1	0	0
Pristimantis cruciocularis	0	0	0	0	0	0	0	0	1
Pristimantis cruentus	0	0	0	0	0	0	1	0	0
Pristimantis cryophilius	0	0	0	0	0	0	1	1	0
Pristimantis cryptomelas	0	0	0	0	0	0	1	0	0
Pristimantis cuentasi	0	0	0	0	0	0	1	0	0
Pristimantis culatensis	0	0	0	0	0	0	1	0	0
Pristimantis cuneirostris	0	0	0	0	0	0	0	0	1
Pristimantis curtipes	0	0	0	0	0	0	1	1	0
Pristimantis danae	0	0	0	0	0	0	0	0	1
Pristimantis degener	0	0	0	0	0	0	1	0	0
Pristimantis deinops	0	0	0	0	0	0	1	0	0
Pristimantis delicatus	0	0	0	0	0	0	1	0	0
Pristimantis delius	0	0	1	0	0	0	0	0	0
Pristimantis dendrobatoides	0	0	1	0	0	0	0	0	0
Pristimantis devillei	0	0	0	0	0	0	1	1	0
Pristimantis diadematus	0	0	1	0	0	0	1	1	1
Pristimantis diaphonus	0	0	0	0	0	0	1	0	0
Pristimantis diogenes	0	0	0	0	0	0	1	0	0
Pristimantis dissimulatus	0	0	0	0	0	0	1	0	0
Pristimantis divnae	0	0	0	0	0	0	0	0	1
Pristimantis dorsopictus	0	0	0	0	0	0	1	0	0
Pristimantis douglasi	0	0	0	0	0	0	1	1	0
Pristimantis duellmani	0	0	0	0	0	0	1	1	0
Pristimantis duende	0	0	0	0	0	0	1	0	0
Pristimantis dundeei	0	0	0	1	0	0	0	0	1
Pristimantis elegans	0	0	0	0	0	0	1	1	0
Pristimantis epacrus	0	0	1	0	0	0	0	1	0

Pristimantis eremitus	0	0	0	0	0	0	1	0	0
Pristimantis eriphus	0	0	0	0	0	0	0	1	0
Pristimantis erythropleura	0	0	0	0	0	0	1	0	0
Pristimantis esmeraldas	0	0	0	0	0	0	1	0	0
Pristimantis eugeniae	0	0	0	0	0	0	1	0	0
Pristimantis euphronides	0	1	0	0	0	0	0	0	0
Pristimantis eurydactylus	0	0	1	0	0	0	0	0	1
Pristimantis exoristus	0	0	1	0	0	0	1	0	0
Pristimantis factiosus	0	0	0	0	0	0	1	0	0
Pristimantis fallax	0	0	0	0	0	0	1	0	0
Pristimantis fasciatus	0	0	0	0	0	0	1	0	0
Pristimantis fenestratus	0	0	1	1	0	0	0	0	1
Pristimantis fetosus	0	0	0	0	0	0	1	0	0
Pristimantis flabellidiscus	0	0	0	0	0	0	1	0	0
Pristimantis flavobracatus	0	0	0	0	0	0	0	0	1
Pristimantis floridus	0	0	0	0	0	0	1	0	0
Pristimantis frater	0	0	1	0	0	0	1	1	0
Pristimantis gaigei	0	0	0	0	0	0	1	0	0
Pristimantis galdi	0	0	1	0	0	0	1	1	1
Pristimantis ganonotus	0	0	0	0	0	0	0	1	0
Pristimantis gentryi	0	0	0	0	0	0	1	0	0
Pristimantis ginesi	0	0	0	0	0	0	1	0	0
Pristimantis gladiator	0	0	0	0	0	0	0	1	0
Pristimantis glandulosus	0	0	0	0	0	0	0	1	0
Pristimantis gracilis	0	0	0	0	0	0	1	0	0
Pristimantis grandiceps	0	0	0	0	0	0	1	0	0
Pristimantis gutturalis	0	0	1	0	0	0	0	0	0
Pristimantis hectus	0	0	0	0	0	0	1	0	0
Pristimantis helvolus	0	0	0	0	0	0	1	0	0
Pristimantis hernandezi	0	0	0	0	0	0	1	1	0
Pristimantis huicundo	0	0	0	0	0	0	0	1	0
Pristimantis hybotragus	0	0	0	0	0	0	1	0	0
Pristimantis ignicolor	0	0	0	0	0	0	0	1	0
Pristimantis illotus	0	0	0	0	0	0	1	0	0
Pristimantis imitatrix	0	0	0	0	0	0	0	0	1
Pristimantis incanus	0	0	0	0	0	0	0	1	0
Pristimantis incertus	0	0	0	0	0	0	1	0	0
Pristimantis incomptus	0	0	0	0	0	0	1	1	0
Pristimantis infraguttatus	0	0	0	0	0	0	0	0	1
Pristimantis inguinalis	0	0	1	0	0	0	0	0	0
Pristimantis insignitus	0	0	0	0	0	0	1	0	0
Pristimantis inusitatus	0	0	1	0	0	0	0	1	0
Pristimantis ixalus	0	0	0	0	0	0	1	0	0
Pristimantis jaimei	0	0	0	0	0	0	1	0	0
Pristimantis jester	0	0	1	0	0	0	0	0	0
Pristimantis johannesdei	0	0	0	0	0	0	1	0	0
Pristimantis jorgevelosai	0	0	0	0	0	0	1	0	0
Pristimantis juanchoi	0	0	0	0	0	0	1	0	0
Pristimantis jubatus	0	0	0	0	0	0	1	0	0
Pristimantis kareliae	0	0	0	0	0	0	1	0	0
Pristimantis katoptroides	0	0	0	0	0	0	1	1	0
Pristimantis kelephus	0	0	0	0	0	0	1	0	0
Pristimantis kichwarum	0	0	1	0	0	0	0	1	0
Pristimantis labiosus	0	0	0	0	0	0	1	0	0
Pristimantis lacrimosus	0	0	1	0	0	0	1	1	1
Pristimantis lancinii	0	0	0	0	0	0	1	0	0

Pristimantis lanthanites	0	0	1	0	0	0	0	1	1
Pristimantis lasalleorum	0	0	0	0	0	0	1	0	0
Pristimantis lassoalcalai	0	0	0	0	0	0	1	0	0
Pristimantis laticlavius	0	0	0	0	0	0	1	0	0
Pristimantis latidiscus	0	0	0	0	0	0	1	0	0
Pristimantis lemur	0	0	0	0	0	0	1	0	0
Pristimantis lentiginosus	0	0	0	0	0	0	1	1	0
Pristimantis leoni	0	0	0	0	0	0	1	1	0
Pristimantis leptolophus	0	0	0	0	0	0	1	0	0
Pristimantis leucopus	0	0	0	0	0	0	1	1	0
Pristimantis librarius	0	0	1	0	0	0	0	1	0
Pristimantis lichenoides	0	0	0	0	0	0	1	0	0
Pristimantis lindae	0	0	0	0	0	0	0	0	1
Pristimantis lirellus	0	0	0	0	0	0	0	0	1
Pristimantis lividus	0	0	0	0	0	0	0	1	0
Pristimantis llojsintuta	0	0	0	0	0	0	0	0	1
Pristimantis loustes	0	0	0	0	0	0	1	0	0
Pristimantis lucasi	0	0	0	0	0	0	0	0	1
Pristimantis luscombei	0	0	1	0	0	0	0	0	0
Pristimantis luteolateralis	0	0	0	0	0	0	1	0	0
Pristimantis lutitus	0	0	0	0	0	0	1	1	0
Pristimantis lymani	0	0	0	0	0	0	1	1	1
Pristimantis lynchi	0	0	0	0	0	0	1	1	0
Pristimantis lythrodes	0	0	1	0	0	0	0	0	0
Pristimantis maculosus	0	0	0	0	0	0	1	0	0
Pristimantis malkini	0	0	1	0	0	0	0	1	1
Pristimantis marahuaka	0	0	1	0	0	0	0	0	0
Pristimantis marmoratus	0	0	1	0	0	0	0	0	1
Pristimantis mars	0	0	0	0	0	0	1	0	0
Pristimantis martiae	0	0	1	0	0	0	0	0	1
Pristimantis medemi	0	0	0	0	0	0	1	1	0
Pristimantis megalops	0	0	0	0	0	0	1	0	0
Pristimantis melanogaster	0	0	0	0	0	0	0	0	1
Pristimantis melanoproctus	0	0	0	0	0	0	1	1	0
Pristimantis memorans	0	0	1	0	0	0	0	0	0
Pristimantis mendax	0	0	0	0	0	0	0	0	1
Pristimantis meridionalis	0	0	0	0	0	0	0	1	0
Pristimantis merostictus	0	0	0	0	0	0	1	0	0
Pristimantis metabates	0	0	0	0	0	0	0	0	1
Pristimantis minutulus	0	0	0	0	0	0	0	0	1
Pristimantis miyatai	0	0	0	0	0	0	1	0	0
Pristimantis mnionaetes	0	0	0	0	0	0	0	1	0
Pristimantis modipeplus	0	0	0	0	0	0	1	0	0
Pristimantis molybrignus	0	0	0	0	0	0	1	0	0
Pristimantis mondolfii	0	0	0	0	0	0	1	1	0
Pristimantis moro	0	0	0	0	0	0	1	0	0
Pristimantis muricatus	0	0	0	0	0	0	1	0	0
Pristimantis muscosus	0	0	0	0	0	0	1	0	1
Pristimantis museosus	0	0	0	0	0	0	1	0	0
Pristimantis myersi	0	0	0	0	0	0	1	1	0
Pristimantis myops	0	0	0	0	0	0	1	0	0
Pristimantis nebulosus	0	0	0	0	0	0	0	0	1
Pristimantis nephophilus	0	0	0	0	0	0	1	0	1
Pristimantis nervicus	0	0	0	0	0	0	1	1	0
Pristimantis nicefori	0	0	0	0	0	0	0	1	0
Pristimantis nigrogriseus	0	0	0	0	0	0	1	1	0

Pristimantis nyctophylax	0	0	0	0	0	0	1	0	0
Pristimantis obmutescens	0	0	0	0	0	0	1	0	0
Pristimantis ocellatus	0	0	0	0	0	0	1	0	0
Pristimantis ockendeni	0	0	1	0	0	0	1	1	1
Pristimantis ocreatus	0	0	0	0	0	0	1	1	0
Pristimantis olivaceus	0	0	0	0	0	0	0	0	1
Pristimantis orcesi	0	0	0	0	0	0	1	1	0
Pristimantis orcus	0	0	1	0	0	0	0	0	1
Pristimantis orestes	0	0	0	0	0	0	1	0	0
Pristimantis ornatissimus	0	0	0	0	0	0	1	0	0
Pristimantis ornatus	0	0	0	0	0	0	0	0	1
Pristimantis orpacobates	0	0	0	0	0	0	1	0	0
Pristimantis orphnolaimus	0	0	1	0	0	0	0	0	0
Pristimantis ortizi	0	0	0	0	0	0	1	1	0
Pristimantis padrecarlosi	0	0	0	0	0	0	1	0	0
Pristimantis paisa	0	0	0	0	0	0	1	0	0
Pristimantis palmeri	0	0	0	0	0	0	1	0	0
Pristimantis paramerus	0	0	0	0	0	0	1	0	0
Pristimantis pardalinus	0	0	0	0	0	0	0	0	1
Pristimantis pardalis	0	0	0	0	0	0	1	0	0
Pristimantis parectatus	0	0	0	0	0	0	1	0	0
Pristimantis parvillus	0	0	0	0	0	0	1	0	0
Pristimantis pastazensis	0	0	0	0	0	0	1	1	0
Pristimantis pataikos	0	0	0	0	0	0	1	1	1
Pristimantis paulodutrai	0	0	0	1	0	0	0	0	0
Pristimantis paululus	0	0	1	0	0	0	0	1	0
Pristimantis pecki	0	0	0	0	0	0	1	1	0
Pristimantis pedimontanus	0	0	0	0	0	0	1	1	0
Pristimantis penelopus	0	0	0	0	0	0	1	0	0
Pristimantis peraticus	0	0	0	0	0	0	1	0	0
Pristimantis percnopterus	0	0	0	0	0	0	1	0	1
Pristimantis percultus	0	0	0	0	0	0	1	0	0
Pristimantis permixtus	0	0	0	0	0	0	1	0	0
Pristimantis peruvianus	0	0	1	0	0	0	0	1	1
Pristimantis petersi	0	0	1	0	0	0	1	1	0
Pristimantis petrobardus	0	0	0	0	0	0	0	1	0
Pristimantis phalaroinguinis	0	0	0	0	0	0	0	1	0
Pristimantis phalarus	0	0	0	0	0	0	1	0	0
Pristimantis philipi	0	0	0	0	0	0	1	0	0
Pristimantis phoxocephalus	0	0	0	0	0	0	1	1	0
Pristimantis phragmipleuron	0	0	0	0	0	0	1	0	0
Pristimantis piceus	0	0	0	0	0	0	1	0	0
Pristimantis pinguis	0	0	0	0	0	0	0	1	0
Pristimantis pirrensis	0	0	0	0	0	0	1	0	0
Pristimantis platychilus	0	0	0	0	0	0	1	0	0
Pristimantis platydactylus	0	0	0	0	0	0	0	0	1
Pristimantis pleurostriatus	0	0	0	0	0	0	1	0	0
Pristimantis polychrus	0	0	0	0	0	0	1	0	0
Pristimantis prolatus	0	0	1	0	0	0	0	1	0
Pristimantis prolixodiscus	0	0	0	0	0	0	1	1	0
Pristimantis proserpens	0	0	0	0	0	0	1	1	0
Pristimantis pruinatus	0	0	1	0	0	0	0	0	0
Pristimantis pseudoacuminatus	0	0	1	0	0	0	0	1	0
Pristimantis pteridophilus	0	0	0	0	0	0	1	0	0
Pristimantis ptochus	0	0	0	0	0	0	1	0	0
Pristimantis pugnax	0	0	1	0	0	0	0	1	0

Pristimantis pulvinatus	0	0	1	0	0	0	0	0	0
Pristimantis pycnodermis	0	0	0	0	0	0	1	1	0
Pristimantis pyrrhomerus	0	0	0	0	0	0	1	0	0
Pristimantis quantus	0	0	0	0	0	0	1	0	0
Pristimantis quaquaversus	0	0	1	0	0	0	1	1	0
Pristimantis quinquagesimus	0	0	0	0	0	0	1	0	0
Pristimantis racemus	0	0	0	0	0	0	1	0	0
Pristimantis ramagii	0	0	0	1	0	0	0	0	0
Pristimantis reclusas	0	0	0	0	0	0	1	0	0
Pristimantis renjiforum	0	0	0	0	0	0	1	1	0
Pristimantis repens	0	0	0	0	0	0	1	0	0
Pristimantis restrepoi	0	0	0	0	0	0	1	0	0
Pristimantis reticulatus	0	0	0	0	0	0	1	0	0
Pristimantis rhabdocnemus	0	0	0	0	0	0	0	0	1
Pristimantis rhabdolaemus	0	0	0	0	0	0	0	0	1
Pristimantis rhigophilus	0	0	0	0	0	0	1	0	0
Pristimantis rhodoplichus	0	0	0	0	0	0	1	0	0
Pristimantis rhodostichus	0	0	0	0	0	0	1	0	1
Pristimantis ridens	0	0	0	0	1	0	1	0	0
Pristimantis rivasi	0	0	0	0	0	0	1	0	0
Pristimantis riveroi	0	0	0	0	0	0	1	0	0
Pristimantis riveti	0	0	0	0	0	0	1	1	0
Pristimantis rosadoi	0	0	0	0	0	0	1	0	0
Pristimantis roseus	0	0	0	0	0	0	1	0	0
Pristimantis rozei	0	0	0	0	0	0	1	0	0
Pristimantis rubicundus	0	0	0	0	0	0	0	1	0
Pristimantis ruedai	0	0	0	0	0	0	1	0	0
Pristimantis rufioculis	0	0	0	0	0	0	1	0	1
Pristimantis ruthveni	0	0	0	0	0	0	1	0	0
Pristimantis salaputium	0	0	0	0	0	0	0	0	1
Pristimantis saltissimus	0	0	1	0	0	0	0	0	0
Pristimantis samaipatae	0	0	0	1	0	0	0	0	1
Pristimantis sanctaemartae	0	0	0	0	0	0	1	0	0
Pristimantis sanguineus	0	0	0	0	0	0	1	0	0
Pristimantis satagius	0	0	0	0	0	0	1	0	0
Pristimantis savagei	0	0	1	0	0	0	1	1	0
Pristimantis schultei	0	0	0	0	0	0	1	0	1
Pristimantis scitulus	0	0	0	0	0	0	0	0	1
Pristimantis scoloblepharus	0	0	0	0	0	0	1	0	0
Pristimantis scolodiscus	0	0	0	0	0	0	1	0	0
Pristimantis scopaeus	0	0	0	0	0	0	1	0	0
Pristimantis seorsus	0	0	0	0	0	0	0	0	1
Pristimantis serendipitus	0	0	0	0	0	0	1	0	1
Pristimantis shrevei	0	1	0	0	0	0	0	0	0
Pristimantis signifer	0	0	0	0	0	0	1	0	0
Pristimantis silverstonei	0	0	0	0	0	0	1	0	0
Pristimantis simonbolivari	0	0	0	0	0	0	1	0	0
Pristimantis simonsii	0	0	0	0	0	0	0	1	0
Pristimantis simoteriscus	0	0	0	0	0	0	1	0	0
Pristimantis simoterus	0	0	0	0	0	0	1	0	0
Pristimantis siopelus	0	0	0	0	0	0	1	0	0
Pristimantis skydmainos	0	0	1	0	0	0	0	0	1
Pristimantis sobetes	0	0	0	0	0	0	1	0	0
Pristimantis spilogaster	0	0	0	0	0	0	1	0	0
Pristimantis spinosus	0	0	0	0	0	0	1	0	0
Pristimantis stenodiscus	0	0	0	0	0	0	1	0	0

Pristimantis sternothylax	0	0	0	0	0	0	1	0	0
Pristimantis stictoboubonus	0	0	0	0	0	0	0	0	1
Pristimantis subsigillatus	0	0	0	0	0	0	1	0	0
Pristimantis suetus	0	0	0	0	0	0	1	0	0
Pristimantis sulculus	0	0	0	0	0	0	1	0	0
Pristimantis supernatis	0	0	0	0	0	0	1	1	0
Pristimantis surdus	0	0	0	0	0	0	1	0	0
Pristimantis susaguae	0	0	0	0	0	0	1	1	0
Pristimantis taciturnus	0	0	0	0	0	0	1	0	0
Pristimantis taeniatus	0	0	0	0	0	0	1	0	0
Pristimantis tamsitti	0	0	1	0	0	0	1	1	0
Pristimantis tantanti	0	0	0	0	0	0	0	0	1
Pristimantis tanyrhynchus	0	0	0	0	0	0	0	0	1
Pristimantis tayrona	0	0	0	0	0	0	1	0	0
Pristimantis telefericus	0	0	0	0	0	0	1	0	0
Pristimantis tenebrionis	0	0	0	0	0	0	1	0	0
Pristimantis terraebolivaris	0	0	0	0	0	0	1	0	0
Pristimantis thectopternus	0	0	0	0	0	0	1	0	0
Pristimantis thyellus	0	0	0	0	0	0	1	0	0
Pristimantis thymalopsoides	0	0	0	0	0	0	1	0	0
Pristimantis thymelensis	0	0	0	0	0	0	1	1	0
Pristimantis toftae	0	0	0	0	0	0	0	0	1
Pristimantis trachyblepharis	0	0	0	0	0	0	1	1	0
Pristimantis truebae	0	0	0	0	0	0	1	0	0
Pristimantis tubernasus	0	0	0	0	0	0	1	1	0
Pristimantis turik	0	0	0	0	0	0	1	0	0
Pristimantis turumiquirensis	0	0	0	0	0	0	1	0	0
Pristimantis uisae	0	0	0	0	0	0	1	0	0
Pristimantis unistrigatus	0	0	0	0	0	0	1	1	0
Pristimantis uranobates	0	0	0	0	0	0	1	0	0
Pristimantis urichi	0	0	0	0	0	0	1	0	0
Pristimantis vanadise	0	0	0	0	0	0	1	0	0
Pristimantis variabilis	0	0	1	0	0	0	0	1	1
Pristimantis veletis	0	0	0	0	0	0	1	0	0
Pristimantis ventrimarmoratus	0	0	1	0	0	0	0	1	1
Pristimantis verecundus	0	0	0	0	0	0	1	0	0
Pristimantis versicolor	0	0	0	0	0	0	1	0	0
Pristimantis vertebralis	0	0	0	0	0	0	1	0	0
Pristimantis vicarius	0	0	0	0	0	0	1	1	0
Pristimantis vidua	0	0	0	0	0	0	1	0	0
Pristimantis viejas	0	0	0	0	0	0	1	0	0
Pristimantis vilarsi	0	0	1	0	0	0	1	0	1
Pristimantis vilcabambae	0	0	0	0	0	0	0	0	1
Pristimantis vinhai	0	0	0	1	0	0	0	0	0
Pristimantis viridicans	0	0	0	0	0	0	1	0	0
Pristimantis viridis	0	0	0	0	0	0	1	0	0
Pristimantis wagteri	0	0	0	0	0	0	0	0	1
Pristimantis walkeri	0	0	0	0	0	0	1	0	0
Pristimantis waoranii	0	0	1	0	0	0	0	0	0
Pristimantis wiensi	0	0	0	0	0	0	1	0	0
Pristimantis w-nigrum	0	0	1	0	0	0	1	1	0
Pristimantis xeniolum	0	0	0	0	0	0	1	0	0
Pristimantis xestus	0	0	0	0	0	0	1	0	0
Pristimantis xylochobates	0	0	0	0	0	0	1	0	0
Pristimantis yaviensis	0	0	1	0	0	0	0	0	0
Pristimantis yukpa	0	0	0	0	0	0	1	0	0

Pristimantis yustizi	0	0	0	0	0	0	1	1	0
Pristimantis zeuctotylus	0	0	1	0	0	0	0	0	0
Pristimantis zimmermanae	0	0	1	0	0	0	0	0	0
Pristimantis zoilae	0	0	1	0	0	0	0	1	0
Pristimantis zophus	0	0	0	0	0	0	1	0	0
Proceratophrys appendiculata	0	0	0	1	0	0	0	0	0
Proceratophrys avelinoi	0	0	0	1	0	0	0	0	0
Proceratophrys bigibbosa	0	0	0	1	0	0	0	0	0
Proceratophrys boiei	0	0	0	1	0	0	0	0	0
Proceratophrys brauni	0	0	0	1	0	0	0	0	0
Proceratophrys concavitympanum	0	0	0	0	0	0	0	0	1
Proceratophrys cristiceps	0	0	1	1	0	0	0	0	0
Proceratophrys cururu	0	0	0	1	0	0	0	0	0
Proceratophrys goyana	0	0	0	1	0	0	0	0	0
Proceratophrys laticeps	0	0	0	1	0	0	0	0	0
Proceratophrys melanopogon	0	0	0	1	0	0	0	0	0
Proceratophrys moehringi	0	0	0	1	0	0	0	0	0
Proceratophrys moratoi	0	0	0	1	0	0	0	0	0
Proceratophrys palustris	0	0	0	1	0	0	0	0	0
Proceratophrys phyllostomus	0	0	0	1	0	0	0	0	0
Proceratophrys schirchi	0	0	0	1	0	0	0	0	0
Proceratophrys subguttata	0	0	0	1	0	0	0	0	0
Proceratophrys vielliardi	0	0	0	1	0	0	0	0	0
Prostherapis dunni	0	0	0	0	0	0	1	0	0
Pseudis bolbodactyla	0	0	0	1	0	0	0	0	0
Pseudis cardosoi	0	0	0	1	0	0	0	0	0
Pseudis fusca	0	0	0	1	0	0	0	0	0
Pseudis minuta	0	0	0	1	0	0	0	0	0
Pseudis paradoxa	0	0	1	1	0	0	1	1	1
Pseudis platensis	0	0	0	1	0	0	0	0	1
Pseudis tocantins	0	0	0	1	0	0	0	0	0
Pseudopaludicola boliviana	0	0	1	1	0	0	1	0	1
Pseudopaludicola canga	0	0	0	1	0	0	0	0	0
Pseudopaludicola falcipes	0	0	0	1	0	0	0	0	0
Pseudopaludicola llanera	0	0	1	0	0	0	1	0	0
Pseudopaludicola mineira	0	0	0	1	0	0	0	0	0
Pseudopaludicola mystacalis	0	0	0	1	0	0	0	0	1
Pseudopaludicola pusilla	0	0	0	0	0	0	1	0	0
Pseudopaludicola saltica	0	0	0	1	0	0	0	0	1
Pseudopaludicola ternetzi	0	0	0	1	0	0	0	0	0
Psychrophrynella adenopleura	0	0	0	0	0	0	0	0	1
Psychrophrynella ankohuma	0	0	0	0	0	0	0	0	1
Psychrophrynella boettgeri	0	0	0	0	0	0	0	0	1
Psychrophrynella chacaltaya	0	0	0	0	0	0	0	0	1
Psychrophrynella guillei	0	0	0	0	0	0	0	0	1
Psychrophrynella harveyi	0	0	0	0	0	0	0	0	1
Psychrophrynella iani	0	0	0	0	0	0	0	0	1
Psychrophrynella iatamasi	0	0	0	0	0	0	0	0	1
Psychrophrynella illampu	0	0	0	0	0	0	0	0	1
Psychrophrynella kallawaya	0	0	0	0	0	0	0	0	1
Psychrophrynella katantika	0	0	0	0	0	0	0	0	1
Psychrophrynella kempffi	0	0	0	0	0	0	0	0	1
Psychrophrynella pinguis	0	0	0	0	0	0	0	0	1
Psychrophrynella quimsacruzis	0	0	0	0	0	0	0	0	1
Psychrophrynella saltator	0	0	0	0	0	0	0	0	1
Psychrophrynella usurpator	0	0	0	0	0	0	0	0	1

Psychrophrynella wettsteini	0	0	0	0	0	0	0	0	1
Ptychohyla acrochorda	0	0	0	0	1	1	0	0	0
Ptychohyla dendrophasma	0	0	0	0	0	1	0	0	0
Ptychohyla erythromma	0	0	0	0	1	1	0	0	0
Ptychohyla euthysanota	0	0	0	0	1	1	0	0	0
Ptychohyla hypomykter	0	0	0	0	1	1	0	0	0
Ptychohyla legleri	0	0	0	0	0	0	1	0	0
Ptychohyla leonhardschultzei	0	0	0	0	1	1	0	0	0
Ptychohyla macrotympanum	0	0	0	0	1	1	0	0	0
Ptychohyla panchoi	0	0	0	0	1	1	0	0	0
Ptychohyla salvadorensis	0	0	0	0	1	1	0	0	0
Ptychohyla sanctaecrucis	0	0	0	0	1	0	0	0	0
Ptychohyla spinipollex	0	0	0	0	1	0	0	0	0
Ptychohyla zophodes	0	0	0	0	1	1	0	0	0
Ranitomeya amazonica	0	0	1	0	0	0	0	0	1
Ranitomeya benedicta	0	0	0	0	0	0	0	0	1
Ranitomeya fantastica	0	0	0	0	0	0	0	0	1
Ranitomeya flavovittata	0	0	1	0	0	0	0	0	1
Ranitomeya imitator	0	0	0	0	0	0	0	0	1
Ranitomeya reticulata	0	0	1	0	0	0	0	0	1
Ranitomeya sirensis	0	0	0	0	0	0	0	0	1
Ranitomeya summersi	0	0	0	0	0	0	0	0	1
Ranitomeya uakarii	0	0	1	0	0	0	0	0	1
Ranitomeya vanzolinii	0	0	0	0	0	0	0	0	1
Ranitomeya variabilis	0	0	0	0	0	0	0	0	1
Ranitomeya ventrimaculata	0	0	1	1	0	0	0	0	1
Rhaebo blombergi	0	0	0	0	0	0	1	0	0
Rhaebo caeruleostictus	0	0	0	0	0	0	1	0	0
Rhaebo glaberrimus	0	0	1	0	0	0	1	0	1
Rhaebo guttatus	0	0	1	1	0	0	1	0	1
Rhaebo haematiticus	0	0	0	0	1	1	1	1	0
Rhaebo hypomelas	0	0	0	0	0	0	1	0	0
Rhaebo lynchi	0	0	0	0	0	0	1	0	0
Rhaebo nasicus	0	0	1	0	0	0	0	0	0
Rheobates palmatus	0	0	1	0	0	0	1	1	0
Rheobates pseudopalmatus	0	0	0	0	0	0	1	0	0
Rhinella abei	0	0	0	1	0	0	0	0	0
Rhinella achalensis	0	0	0	1	0	0	0	0	0
Rhinella achavali	0	0	0	1	0	0	0	0	0
Rhinella acrolopha	0	0	0	0	0	0	1	0	0
Rhinella acutirostris	0	0	1	0	0	0	1	1	0
Rhinella alata	0	0	0	0	0	0	1	0	0
Rhinella amboroensis	0	0	0	0	0	0	0	0	1
Rhinella arborescandens	0	0	0	0	0	0	0	0	1
Rhinella arenarum	1	0	0	1	0	0	0	1	1
Rhinella arunco	1	0	0	0	0	0	0	1	0
Rhinella atacamensis	1	0	0	0	0	0	0	1	0
Rhinella bergi	0	0	0	1	0	0	0	0	1
Rhinella castaneotica	0	0	1	1	0	0	0	0	1
Rhinella ceratophrys	0	0	1	0	0	0	0	1	1
Rhinella cerradensis	0	0	0	1	0	0	0	0	0
Rhinella chavin	0	0	0	0	0	0	0	0	1
Rhinella chrysophora	0	0	0	0	1	0	0	0	0
Rhinella cristinae	0	0	1	0	0	0	0	0	0
Rhinella crucifer	0	0	0	1	0	0	0	0	0
Rhinella dapsilis	0	0	1	0	0	0	0	0	1

Rhinella diptycha	0	0	0	1	0	0	0	0	0
Rhinella dorbignyi	0	0	0	1	0	0	0	0	0
Rhinella fernandezae	0	0	0	1	0	0	0	0	0
Rhinella festae	0	0	1	0	0	0	1	1	0
Rhinella fissipes	0	0	0	0	0	0	0	0	1
Rhinella gallardoi	0	0	0	1	0	0	0	0	1
Rhinella gnustae	0	0	0	0	0	0	0	1	0
Rhinella granulosa	0	0	1	1	0	0	1	1	1
Rhinella henseli	0	0	0	1	0	0	0	0	0
Rhinella hoogmoedi	0	0	0	1	0	0	0	0	0
Rhinella humboldti	0	0	1	0	0	0	1	0	0
Rhinella icterica	0	0	0	1	0	0	0	0	0
Rhinella inca	0	0	0	0	0	0	0	0	1
Rhinella iserni	0	0	0	0	0	0	0	0	1
Rhinella jimi	0	0	1	1	0	0	0	0	0
Rhinella justinianoi	0	0	0	0	0	0	0	0	1
Rhinella lescurei	0	0	1	0	0	0	0	0	0
Rhinella limensis	0	0	0	0	0	0	0	1	0
Rhinella lindae	0	0	0	0	0	0	1	0	0
Rhinella macrorhina	0	0	0	0	0	0	1	0	0
Rhinella magnussoni	0	0	0	1	0	0	0	0	1
Rhinella manu	0	0	0	0	0	0	0	0	1
Rhinella margaritifera	0	0	1	1	0	0	1	1	1
Rhinella marina	0	1	1	1	1	1	1	1	1
Rhinella martyi	0	0	1	0	0	0	0	0	0
Rhinella multiverrucosa	0	0	0	0	0	0	0	1	1
Rhinella nesiotes	0	0	0	0	0	0	0	0	1
Rhinella nicefori	0	0	0	0	0	0	1	0	0
Rhinella ocellata	0	0	0	1	0	0	0	0	1
Rhinella ornata	0	0	0	1	0	0	0	0	0
Rhinella poeppigii	0	0	0	1	0	0	0	0	1
Rhinella proboscidea	0	0	1	0	0	0	0	0	1
Rhinella pygmaea	0	0	0	1	0	0	0	0	0
Rhinella quechua	0	0	0	0	0	0	0	0	1
Rhinella roqueana	0	0	1	0	0	0	1	1	1
Rhinella rostrata	0	0	0	0	0	0	1	0	0
Rhinella rubescens	0	0	0	1	0	0	0	0	0
Rhinella rubropunctata	1	0	0	0	0	0	0	0	0
Rhinella ruizi	0	0	0	0	0	0	1	0	0
Rhinella rumbolli	0	0	0	1	0	0	0	1	1
Rhinella schneideri	0	0	1	1	0	0	0	0	1
Rhinella scitula	0	0	0	1	0	0	0	0	0
Rhinella sclerocephala	0	0	0	0	0	0	1	0	0
Rhinella spinulosa	1	0	0	1	0	0	0	1	1
Rhinella stanlaii	0	0	0	0	0	0	0	0	1
Rhinella sternosignata	0	0	0	0	0	0	1	0	0
Rhinella tacana	0	0	0	0	0	0	0	0	1
Rhinella tenrec	0	0	0	0	0	0	1	0	0
Rhinella vellardi	0	0	0	0	0	0	1	0	0
Rhinella veraguensis	0	0	0	1	0	0	0	1	1
Rhinella veredas	0	0	0	1	0	0	0	0	0
Rhinoderma darwinii	1	0	0	0	0	0	0	0	0
Rhinoderma rufum	1	0	0	0	0	0	0	0	0
Rhinophrynus dorsalis	0	0	0	0	1	1	1	0	0
Rulyrana adiazeta	0	0	0	0	0	0	1	0	0
Rulyrana flavopunctata	0	0	1	0	0	0	1	1	0

Rulyrana mcdiarmidi	0	0	0	0	0	0	1	0	1
Rulyrana saxiscandens	0	0	0	0	0	0	0	0	1
Rulyrana spiculata	0	0	0	0	0	0	0	0	1
Rulyrana susatamai	0	0	0	0	0	0	1	0	0
Rupirana cardosoi	0	0	0	1	0	0	0	0	0
Sachatamia albomaculata	0	0	0	0	1	1	1	0	0
Sachatamia ilex	0	0	0	0	0	0	1	0	0
Sachatamia orejuela	0	0	0	0	0	0	1	0	0
Sachatamia punctulata	0	0	0	0	0	0	1	0	0
Scaphiopus couchii	0	0	0	0	1	1	0	0	0
Scarthyla goinorum	0	0	1	0	0	0	0	0	1
Scarthyla vigilans	0	0	0	0	0	0	1	1	0
Scinax acuminatus	0	0	0	1	0	0	0	0	1
Scinax agilis	0	0	0	1	0	0	0	0	0
Scinax albicans	0	0	0	1	0	0	0	0	0
Scinax altae	0	0	0	0	0	0	1	0	0
Scinax alter	0	0	0	1	0	0	0	0	0
Scinax angrensis	0	0	0	1	0	0	0	0	0
Scinax arduous	0	0	0	1	0	0	0	0	0
Scinax argyreornatus	0	0	0	1	0	0	0	0	0
Scinax ariadne	0	0	0	1	0	0	0	0	0
Scinax aromothyella	0	0	0	1	0	0	0	0	0
Scinax atratus	0	0	0	1	0	0	0	0	0
Scinax auratus	0	0	0	1	0	0	0	0	0
Scinax baumgardneri	0	0	1	0	0	0	0	0	0
Scinax belloni	0	0	0	1	0	0	0	0	0
Scinax berthae	0	0	0	1	0	0	0	0	0
Scinax blairi	0	0	1	0	0	0	1	0	0
Scinax boesemani	0	0	1	1	0	0	1	0	1
Scinax boulengeri	0	0	0	0	1	0	1	0	0
Scinax brieni	0	0	0	1	0	0	0	0	0
Scinax cabralensis	0	0	0	1	0	0	0	0	0
Scinax caldarum	0	0	0	1	0	0	0	0	0
Scinax camposseabrai	0	0	0	1	0	0	0	0	0
Scinax canastrensis	0	0	0	1	0	0	0	0	0
Scinax cardosoi	0	0	0	1	0	0	0	0	0
Scinax carnevallii	0	0	0	1	0	0	0	0	0
Scinax castroviejoi	0	0	0	1	0	0	0	1	1
Scinax catharinae	0	0	0	1	0	0	0	0	0
Scinax centralis	0	0	0	1	0	0	0	0	0
Scinax chiquitanus	0	0	0	1	0	0	0	0	1
Scinax constrictus	0	0	0	1	0	0	0	0	0
Scinax cretatus	0	0	0	1	0	0	0	0	0
Scinax crospedospilus	0	0	0	1	0	0	0	0	0
Scinax cruentommus	0	0	1	1	0	0	0	0	1
Scinax curicica	0	0	0	1	0	0	0	0	0
Scinax cuspidatus	0	0	0	1	0	0	0	0	0
Scinax danae	0	0	1	0	0	0	0	0	0
Scinax duartei	0	0	0	1	0	0	0	0	0
Scinax elaeochrous	0	0	0	0	1	0	1	0	0
Scinax eurydice	0	0	1	1	0	0	0	0	0
Scinax exiguus	0	0	1	0	0	0	0	0	0
Scinax flavoguttatus	0	0	0	1	0	0	0	0	0
Scinax funereus	0	0	1	0	0	0	1	1	1
Scinax fuscomarginatus	0	0	1	1	0	0	0	0	1
Scinax fuscovarius	0	0	0	1	0	0	0	1	1

Scinax garbei	0	0	1	1	0	0	1	1	1
Scinax granulatus	0	0	0	1	0	0	0	0	0
Scinax hayii	0	0	0	1	0	0	0	0	0
Scinax heyeri	0	0	0	1	0	0	0	0	0
Scinax hiemalis	0	0	0	1	0	0	0	0	0
Scinax humilis	0	0	0	1	0	0	0	0	0
Scinax ictericus	0	0	1	0	0	0	0	0	1
Scinax insperatus	0	0	0	1	0	0	0	0	0
Scinax iquitorum	0	0	1	0	0	0	0	0	1
Scinax jolyi	0	0	1	0	0	0	0	0	0
Scinax jureia	0	0	0	1	0	0	0	0	0
Scinax karenanneae	0	0	1	0	0	0	0	0	0
Scinax kennedyi	0	0	1	0	0	0	1	0	0
Scinax lindsayi	0	0	1	0	0	0	0	0	0
Scinax littoralis	0	0	0	1	0	0	0	0	0
Scinax littoreus	0	0	0	1	0	0	0	0	0
Scinax longilineus	0	0	0	1	0	0	0	0	0
Scinax luizotavioi	0	0	0	1	0	0	0	0	0
Scinax machadoi	0	0	0	1	0	0	0	0	0
Scinax manriquei	0	0	0	0	0	0	1	1	0
Scinax maracaya	0	0	0	1	0	0	0	0	0
Scinax melloi	0	0	0	1	0	0	0	0	0
Scinax nasicus	0	0	0	1	0	0	0	0	1
Scinax nebulosus	0	0	1	1	0	0	0	0	1
Scinax obtriangulatus	0	0	0	1	0	0	0	0	0
Scinax oreites	0	0	0	0	0	0	0	0	1
Scinax pachycrus	0	0	0	1	0	0	0	0	0
Scinax pedromedinae	0	0	0	0	0	0	0	0	1
Scinax perereca	0	0	0	1	0	0	0	0	0
Scinax perpusillus	0	0	0	1	0	0	0	0	0
Scinax pinima	0	0	0	1	0	0	0	0	0
Scinax proboscideus	0	0	1	0	0	0	0	0	0
Scinax quinquefasciatus	0	0	0	0	0	0	1	0	0
Scinax ranki	0	0	0	1	0	0	0	0	0
Scinax rizibilis	0	0	0	1	0	0	0	0	0
Scinax rostratus	0	0	1	0	0	0	1	1	0
Scinax ruber	0	1	1	1	0	0	1	1	1
Scinax similis	0	0	0	1	0	0	0	0	0
Scinax squalirostris	0	0	0	1	0	0	0	0	1
Scinax staufferi	0	0	0	0	1	1	1	0	0
Scinax sugillatus	0	0	0	0	0	0	1	0	0
Scinax tigrinus	0	0	0	1	0	0	0	0	0
Scinax trapicheiroi	0	0	0	1	0	0	0	0	0
Scinax uruguayus	0	0	0	1	0	0	0	0	0
Scinax v-signatus	0	0	0	1	0	0	0	0	0
Scinax wandae	0	0	1	0	0	0	1	0	0
Scinax x-signatus	0	0	1	1	0	0	1	1	1
Scythrophrys sawayae	0	0	0	1	0	0	0	0	0
Silverstoneia erasmios	0	0	0	0	0	0	1	0	0
Silverstoneia flotator	0	0	0	0	0	0	1	0	0
Silverstoneia nubicola	0	0	0	0	0	0	1	0	0
Smilisca baudinii	0	0	0	0	1	1	1	0	0
Smilisca cyanosticta	0	0	0	0	1	1	0	0	0
Smilisca fodiens	0	0	0	0	1	1	0	0	0
Smilisca phaeota	0	0	0	0	1	1	1	0	0
Smilisca puma	0	0	0	0	0	0	1	0	0

Smilisca sila	0	0	0	0	0	0	1	0	0
Smilisca sordida	0	0	0	0	1	0	1	0	0
Spea bombifrons	0	0	0	0	0	1	0	0	0
Spea multiplicata	0	0	0	0	1	1	0	0	0
Sphaenorhynchus bromelicola	0	0	0	1	0	0	0	0	0
Sphaenorhynchus caramaschii	0	0	0	1	0	0	0	0	0
Sphaenorhynchus carneus	0	0	1	0	0	0	0	1	1
Sphaenorhynchus dorisae	0	0	1	0	0	0	0	0	1
Sphaenorhynchus lacteus	0	0	1	1	0	0	1	0	1
Sphaenorhynchus mirim	0	0	0	1	0	0	0	0	0
Sphaenorhynchus orophilus	0	0	0	1	0	0	0	0	0
Sphaenorhynchus palustris	0	0	0	1	0	0	0	0	0
Sphaenorhynchus pauloalvini	0	0	0	1	0	0	0	0	0
Sphaenorhynchus planicola	0	0	0	1	0	0	0	0	0
Sphaenorhynchus prasinus	0	0	0	1	0	0	0	0	0
Sphaenorhynchus surdus	0	0	0	1	0	0	0	0	0
Stefania ackawaio	0	0	1	0	0	0	0	0	0
Stefania ayangannae	0	0	1	0	0	0	0	0	0
Stefania breweri	0	0	1	0	0	0	0	0	0
Stefania coxi	0	0	1	0	0	0	0	0	0
Stefania evansi	0	0	1	0	0	0	0	0	0
Stefania ginesi	0	0	1	0	0	0	0	0	0
Stefania goini	0	0	1	0	0	0	0	0	0
Stefania marahuaquensis	0	0	1	0	0	0	0	0	0
Stefania oculosa	0	0	1	0	0	0	0	0	0
Stefania percristata	0	0	1	0	0	0	0	0	0
Stefania riae	0	0	1	0	0	0	0	0	0
Stefania riveroi	0	0	1	0	0	0	0	0	0
Stefania roraimae	0	0	1	0	0	0	0	0	0
Stefania satelles	0	0	1	0	0	0	0	0	0
Stefania scalae	0	0	1	0	0	0	0	0	0
Stefania schuberti	0	0	1	0	0	0	0	0	0
Stefania tamacuarina	0	0	1	0	0	0	0	0	0
Stefania woodleyi	0	0	1	0	0	0	0	0	0
Stereocyclops incrassatus	0	0	0	1	0	0	0	0	0
Stereocyclops parkeri	0	0	0	1	0	0	0	0	0
Strabomantis anatipes	0	0	0	0	0	0	1	0	0
Strabomantis anomalus	0	0	0	0	0	0	1	0	0
Strabomantis biporcatus	0	0	0	0	0	0	1	0	0
Strabomantis bufoniformis	0	0	0	0	0	0	1	0	0
Strabomantis cerastes	0	0	0	0	0	0	1	0	0
Strabomantis cheiroplethus	0	0	0	0	0	0	1	0	0
Strabomantis cornutus	0	0	1	0	0	0	1	1	0
Strabomantis helonotus	0	0	0	0	0	0	1	0	0
Strabomantis ingeri	0	0	0	0	0	0	1	1	0
Strabomantis laticorpus	0	0	0	0	0	0	1	0	0
Strabomantis necerus	0	0	0	0	0	0	1	0	0
Strabomantis necopinus	0	0	0	0	0	0	1	0	0
Strabomantis ruizi	0	0	0	0	0	0	1	0	0
Strabomantis sulcatus	0	0	1	0	0	0	1	1	1
Strabomantis zygodactylus	0	0	0	0	0	0	1	0	0
Synapturanus mirandaribeiroi	0	0	1	0	0	0	0	0	1
Synapturanus rabus	0	0	1	0	0	0	0	1	0
Synapturanus salseri	0	0	1	0	0	0	1	0	1
Telmatobius arequipensis	0	0	0	0	0	0	0	1	1
Telmatobius atacamensis	0	0	0	0	0	0	0	1	0

Telmatobius atahualpai	0	0	0	0	0	0	0	1	1
Telmatobius bolivianus	0	0	0	0	0	0	0	0	1
Telmatobius brachydactylus	0	0	0	0	0	0	0	1	1
Telmatobius brevipes	0	0	0	0	0	0	0	1	0
Telmatobius brevirostris	0	0	0	0	0	0	0	0	1
Telmatobius carrillae	0	0	0	0	0	0	0	1	0
Telmatobius ceiorum	0	0	0	1	0	0	0	0	0
Telmatobius cirrhacelis	0	0	0	0	0	0	1	0	0
Telmatobius colanensis	0	0	0	0	0	0	0	0	1
Telmatobius contrerasi	0	0	0	0	0	0	0	1	0
Telmatobius culeus	0	0	0	0	0	0	0	1	1
Telmatobius dankoi	0	0	0	0	0	0	0	1	0
Telmatobius degener	0	0	0	0	0	0	0	1	0
Telmatobius edaphonastes	0	0	0	0	0	0	0	0	1
Telmatobius espadai	0	0	0	0	0	0	0	1	1
Telmatobius gigas	0	0	0	0	0	0	0	1	0
Telmatobius halli	0	0	0	0	0	0	0	1	0
Telmatobius hauthali	0	0	0	0	0	0	0	1	0
Telmatobius hintoni	0	0	0	0	0	0	0	1	1
Telmatobius hockingi	0	0	0	0	0	0	0	1	0
Telmatobius huayra	0	0	0	0	0	0	0	1	0
Telmatobius hypselocephalus	0	0	0	0	0	0	0	1	0
Telmatobius ignavus	0	0	0	0	0	0	1	0	0
Telmatobius intermedius	0	0	0	0	0	0	0	1	0
Telmatobius jelskii	0	0	0	0	0	0	0	1	1
Telmatobius laticeps	0	0	0	1	0	0	0	0	0
Telmatobius latirostris	0	0	0	0	0	0	0	1	0
Telmatobius macrostomus	0	0	0	0	0	0	0	1	1
Telmatobius marmoratus	0	0	0	0	0	0	0	1	1
Telmatobius mayoloi	0	0	0	0	0	0	0	1	0
Telmatobius necopinus	0	0	0	0	0	0	0	0	1
Telmatobius niger	0	0	0	0	0	0	1	0	0
Telmatobius oxycephalus	0	0	0	0	0	0	0	0	1
Telmatobius pefauri	0	0	0	0	0	0	0	1	0
Telmatobius peruvianus	0	0	0	0	0	0	0	1	0
Telmatobius philippii	0	0	0	0	0	0	0	1	0
Telmatobius pinguiculus	0	0	0	0	0	0	0	1	0
Telmatobius pisanoi	0	0	0	1	0	0	0	1	0
Telmatobius platycephalus	0	0	0	0	0	0	0	1	0
Telmatobius punctatus	0	0	0	0	0	0	0	0	1
Telmatobius rimac	0	0	0	0	0	0	0	1	0
Telmatobius sanborni	0	0	0	0	0	0	0	0	1
Telmatobius schreiteri	0	0	0	1	0	0	0	1	0
Telmatobius scrocchii	0	0	0	0	0	0	0	1	0
Telmatobius sibiricus	0	0	0	0	0	0	0	0	1
Telmatobius simonsi	0	0	0	1	0	0	0	1	1
Telmatobius stephani	0	0	0	1	0	0	0	0	0
Telmatobius thompsoni	0	0	0	0	0	0	0	1	0
Telmatobius timens	0	0	0	0	0	0	0	0	1
Telmatobius truebae	0	0	0	0	0	0	0	0	1
Telmatobius vellardi	0	0	0	0	0	0	1	0	0
Telmatobius verrucosus	0	0	0	0	0	0	0	1	1
Telmatobius vilamensis	0	0	0	0	0	0	0	1	0
Telmatobius yuracare	0	0	0	0	0	0	0	0	1
Telmatobius zapahuirensis	0	0	0	0	0	0	0	1	0
Telmatobufo australis	1	0	0	0	0	0	0	0	0

Telmatobufo bullocki	1	0	0	0	0	0	0	0	0
Telmatobufo venustus	1	0	0	0	0	0	0	0	0
Tepuihyla aecii	0	0	1	0	0	0	0	0	0
Tepuihyla edelcae	0	0	1	0	0	0	0	0	0
Tepuihyla luteolabris	0	0	1	0	0	0	0	0	0
Tepuihyla rimarum	0	0	1	0	0	0	0	0	0
Tepuihyla rodriguezi	0	0	1	0	0	0	0	0	0
Tepuihyla warreni	0	0	1	0	0	0	0	0	0
Teratohyla adenocheira	0	0	0	0	0	0	0	0	1
Teratohyla amelie	0	0	1	0	0	0	0	0	0
Teratohyla midas	0	0	1	0	0	0	0	1	1
Teratohyla pulverata	0	0	0	0	1	1	1	0	0
Teratohyla spinosa	0	0	0	0	1	1	1	0	0
Thoropa lutzi	0	0	0	1	0	0	0	0	0
Thoropa megatympanum	0	0	0	1	0	0	0	0	0
Thoropa miliaris	0	0	0	1	0	0	0	0	0
Thoropa petropolitana	0	0	0	1	0	0	0	0	0
Thoropa saxatilis	0	0	0	1	0	0	0	0	0
Tlalocohyla godmani	0	0	0	0	1	1	0	0	0
Tlalocohyla loquax	0	0	0	0	1	1	1	0	0
Tlalocohyla picta	0	0	0	0	1	1	0	0	0
Tlalocohyla smithii	0	0	0	0	1	1	0	0	0
Trachycephalus atlas	0	0	0	1	0	0	0	0	0
Trachycephalus coriaceus	0	0	1	1	0	0	0	0	1
Trachycephalus dibernardoi	0	0	0	1	0	0	0	0	0
Trachycephalus hadroceps	0	0	1	0	0	0	0	0	0
Trachycephalus imitatrix	0	0	0	1	0	0	0	0	0
Trachycephalus jordani	0	0	0	0	0	0	1	0	0
Trachycephalus lepidus	0	0	0	1	0	0	0	0	0
Trachycephalus mesophaeus	0	0	0	1	0	0	0	0	0
Trachycephalus nigromaculatus	0	0	0	1	0	0	0	0	0
Trachycephalus resinifictrix	0	0	1	1	0	0	1	0	1
Triprion petasatus	0	0	0	0	1	0	0	0	0
Truebella skoptes	0	0	0	0	0	0	0	0	1
Truebella tothastes	0	0	0	0	0	0	0	0	1
Vitreorana antisthenesi	0	0	0	0	0	0	1	0	0
Vitreorana castroviejoi	0	0	0	0	0	0	1	0	0
Vitreorana eurygnatha	0	0	0	1	0	0	0	0	0
Vitreorana gorzulae	0	0	1	0	0	0	0	0	0
Vitreorana helenae	0	0	1	0	0	0	0	0	0
Vitreorana parvula	0	0	0	1	0	0	0	0	0
Vitreorana ritae	0	0	1	0	0	0	0	0	1
Vitreorana uranoscopa	0	0	0	1	0	0	0	0	0
Xenohyla eugenioi	0	0	0	1	0	0	0	0	0
Xenohyla truncata	0	0	0	1	0	0	0	0	0
Yunganastes ashkapara	0	0	0	0	0	0	0	0	1
Yunganastes bisignatus	0	0	0	0	0	0	0	0	1
Yunganastes fraudator	0	0	0	0	0	0	0	0	1
Yunganastes mercedesae	0	0	0	0	0	0	0	0	1
Yunganastes pluvicanorus	0	0	0	0	0	0	0	0	1
Zachaenus parvulus	0	0	0	1	0	0	0	0	0

*Morrone, J. J. 2014. Biogeographical regionalisation of the Neotropical region. *Zootaxa*, **3782**, 1–110.

Appendix A4

Uncertainties in forecasts of SDM: To evaluate the effect of five different uncertainties of SDM (i.e. grain size, number of predictors, extent of calibration area, thresholding and, dispersion; see main Methods) on the robustness of our estimates of shifts in β-diversity predictions, we fitted five sets of SDM's using different combinations of these uncertainty sources.

Set one: We used some of the parameters as described in Methods (main text) to model the species distributions of 2669 species (Appendix A1, Table A1.1), except that only eight climate data were drawn from WorlClim database (www.worldclim.org, Hijmans et al. 2005). The selected variables are recognised as biological appropriate (Menéndez-Guerrero and Graham 2013) and have been previously identified as important limiting factors of amphibian species distributions in several highly cited papers (e.g. Wiens et al. 2006, Sodhi et al. 2008, Munguía et al. 2012), and were not highly correlated (rho| <0.75). The variables chosen were Annual Mean Temperature, Mean Diurnal Range, Temperature Seasonality, Max Temperature of Warmest Month, Min Temperature of Coldest Month, Annual Precipitation, Precipitation of Wettest Month, and Precipitation of Driest Month. Additionally, we generated pseudo-absences (or background data) within a maximum arbitrary distance of 2 degrees from the species' range boundaries following Barbet-Massin et al. (2012), instead of generating pseudoabsences across the entire ecoregion(s) where species occur (see main Methods). Pseudo-absences were generated using the "Disk" strategy of Biomod2 (Thuiller et al. 2014). To transform continuous SDM outputs of suitability into presence/absence models, we selected the threshold corresponding to the 10th percentile (P10; Peterson et al. 2007) of suitability at model-fitting presences, instead of TSS-max used in the main Methods. The final models calculated for baseline (i.e. current) climate conditions were trimmed to the extent of the species' ocupied ecoregion(s) following the regionalisation of Morrone (2014; see Appendix A3, Table A3.2).

Under this set, β-diversity is predicted to decrease in approximately 78% of the Neotropical highlands, (i.e., there is a trend towards biotic homogenization; $\overline{X}$ β-diversity change = -10.4% ±18.87; Fig. A4.1). In contrast, in lowlands of the Neotropics β-diversity is predicted to increase in approximately 63% of assemblages ($\overline{X}$ β-diversity change = 20.49% ±40.64; Fig. A4.1), showing a general trend towards biotic differentiation.

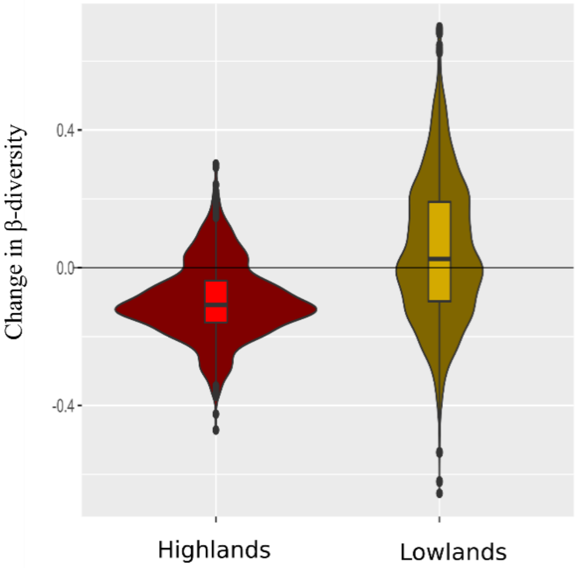

Figure A4.1 Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) of β-diversity changes in Neotropical highlands (red) or lowlands (yellow). This plot is based on results obtained from Set One.

Set two: We used the same parameters as described on Set one to model the species distributions of 2669 species (Appendix A1, Table A1.1). However, here we implemented a dispersal scenario of 16.9 km per decade*, following Chen et al. (2011) instead of the full-dispersal scenario used in Set one.

Under this set, the majority (~80%) of highland species assemblages are predicted to become increasingly homogeneous under climate change ($\overline{X}$ β-diversity change = -11.21% ±14.77; Fig. A4.2). On the other hand, approximately 58% of lowlands will face the increasing differentiation of species assemblages, and ~42% of assemblages will become more homogeneous ($\overline{X}$ β-diversity change = 9.39% ±40.71; Fig. A4.2).

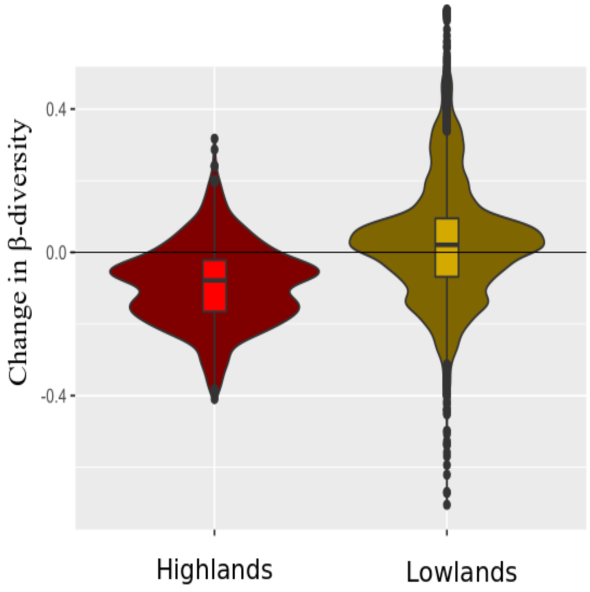

Figure A4.2 Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) of β-diversity changes in Neotropical highlands (red) or lowlands (yellow). This plot is based on results obtained from Set Two.

***Dispersal scenario methodology:** We incorporated a simple model of dispersal limitation (see Bateman et al. 2013) by generating a buffer representing a maximum dispersal capability of 16.9 km/decade around the current distribution of each species, and then identifying the buffered areas within the projected potential future distribution of species assuming no dispersal limits, as occupied. Analyses were performed in R using the package KISSMig (Nobis and Normand 2014, R Development Core Team 2015).

Set three: We used the same approach to model species distributions of 2669 species as described in Methods of the main text, however, here we implemented a dispersal scenario of 16.9 km per decade, following Chen et al. (2011) instead of a full-dispersal scenario.

Under this set, β-diversity is predicted to decrease in approximately 67% of the Neotropical highlands (showing a trend towards biotic homogenization; $\overline{X}$ β-diversity change = -5.56% ±16.91; Fig. A4.3). However, the geographic patterns of shifts of β-diversity in the Neotropical lowlands were less clear that those observed in the highlands. Approximately 49% of the lowland assemblages are predicted to become more heterogenous, whereas 51% were predicted to decrease in β-diversity (i.e. become more homogeneous; Fig. A4.3).

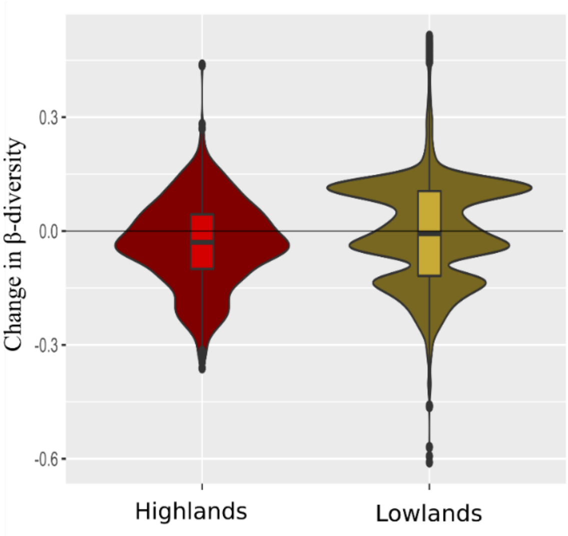

Figure A4.3. Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) of β-diversity changes in Neotropical highlands (red) or lowlands (yellow). This plot is based on results obtained from Set Three.

Set four: We used the same parameters described in Set One to model species distributions of 1997 species, nevertheless here we fitted SDM's with the same 8 bioclimatic variables mentioned above, but at a spatial resolution of 10 arc-minutes (i.e., ~ 20km). As in Set One, we implemented a full-dispersal scenario.

Under this set, β-diversity is predicted to decrease in approximately 80% of the Neotropical highlands, (i.e., there is a trend towards biotic homogenization; $\overline{X}$ β-diversity change = -10.25% ±16.51; Fig. A4.4). In contrast, in lowlands of the Neotropics β-diversity is predicted to increase in approximately 79% of assemblages ($\overline{X}$ β-diversity change = 55.65% ±74.98; Fig. A4.4), showing a general trend towards biotic differentiation.

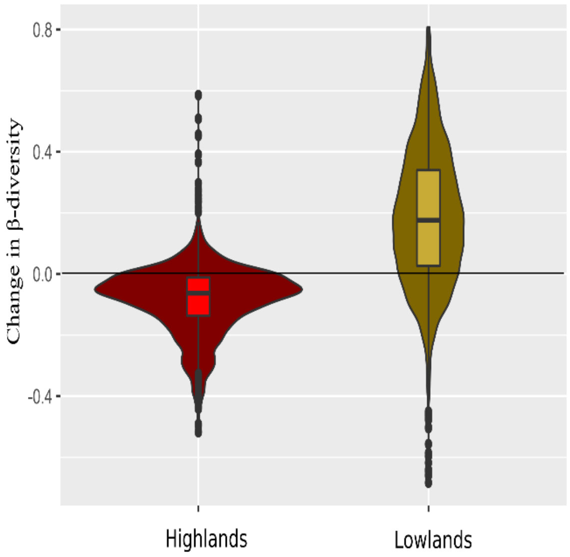

Figure A4.4. Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) of β-diversity changes in Neotropical highlands (red) or lowlands (yellow). This plot is based on results obtained from Set Four.

Set five: We modeled 1997 species distributions as described in Set four, however, here we implemented a dispersal scenario of 16.9 km per decade, following Chen et al. (2011) instead of the full-dispersal scenario.

Under this set, the majority (~68%) of highland species assemblages are predicted to become increasingly homogeneous under climate change ($\overline{X}$ β-diversity change = -10.02% ±7.07; Fig. A4.5). On the other hand, approximately 88% of lowlands will face the increasing differentiation of species assemblages, ($\overline{X}$ β-diversity change = 48.57% ±49.42; Fig. A4.5).

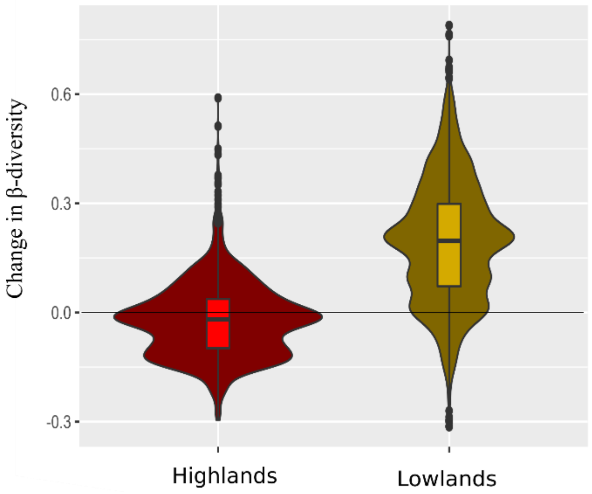

Figure A4.5. Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) of β-diversity changes in Neotropical highlands (red) or lowlands (yellow). This plot is based on results obtained from Set five.

Set six: We used the same suite of parameters as described in the Methods (main text) to model species distributions (Appendix A1, Table A1.1), and evaluated their fit using the true skill statistic (TSS, Allouche et al. 2006). However, instead of using the standard procedure of randomly partitioning (pseudo) occurrence data (see Main Methods), we used two schemes to spatially partition the data to conduct spatially independent cross-validation tests (e.g. Muscarella et al. 2014). Spatial partitions are especially important to evaluate transferability of SDMs in new scenarios (Hijmans 2012). We first used the “block” partition scheme that partitions data drawing latitudinal and longitudinal lines to divide occurrence localities into four spatially “independent” groups (i.e. k=4, Muscarella et al. 2014). For this scheme we modelled only species with at least 10 unique (pseudo) occurrence localities. Second, we applied a “Y” scheme, that partitions the occurrences through latitudinal lines that divide occurrence localities into two (in our case) equal-sized spatially “independent” groups (Wenger and Olden 2012). All analyses were implemented in the “BIOMOD_cv” function of BIOMOD2 (Thuiller et al. 2014).

Implementing “Block” partitioning, the majority (~69%) of highland species assemblages are predicted to become increasingly homogeneous with climate change ($\overline{X}$ β-diversity change = -11.94% ±8.28; Fig. A4.6a). In contrast, approximately 55% of lowlands will experience increasing differentiation of species assemblages, ($\overline{X}$ β-diversity change = 13.81% ±13.44; Fig. A4.6a). We modeled 1384 species.

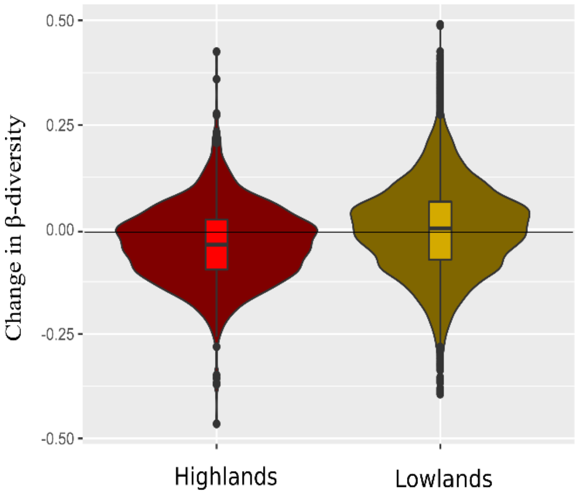

Figure A4.6a. Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) of β-diversity changes in Neotropical highlands (red) and lowlands (yellow). This plot is based on results obtained from implementing “Block” partitioning (Set six).

Implementing “Y” partition, the majority (~74%) of highland species assemblages are predicted to become increasingly homogeneous with climate change ($\overline{X}$ β-diversity change = -10.81% ±6.79; Fig. A4.6b). In contrast, approximately 73% of lowlands will experience increasing differentiation of species assemblages, ($\overline{X}$ β-diversity change = 14.54% ±11.59; Fig. A4.6b). We modeled 1856 species.

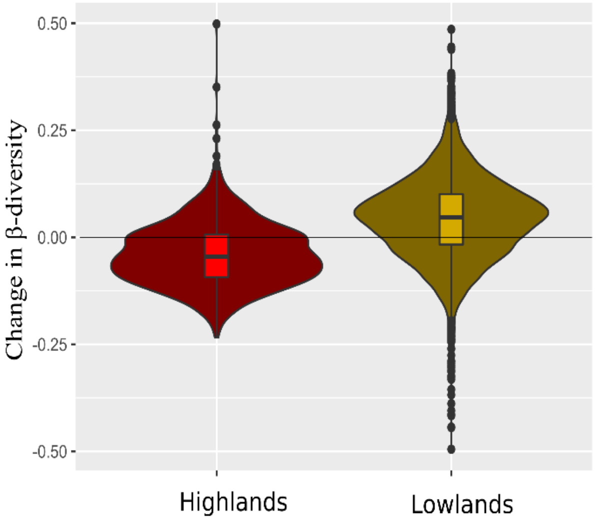

Figure A4.6b. Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) of β-diversity changes in Neotropical highlands (red) or lowlands (yellow). This plot is based on results obtained from implementing “Y” partition (Set six).

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Appendix A5

Niche breadth as surrogate of ecological generalism (Brown 1984).

We used the inverse concentration metrics of Levin (1968) to estimate niche breath of species (see Methods in main text). Levin's concentration metric ranges from 0–1, where 0 indicates minimum niche breadth (only one grid cell has a nonzero suitability) and 1 indicates the maximum (all grid cells are equally suitable (Mandle et al. 2010). We derived the mean of the niche breadths for the species present in each grid cell (under both current and future climate scenarios) and calculated their difference. Here, positive values represent assemblages that are predicted to become composed of a greater proportion of generalists, whereas negative values represent assemblages that are predicted to become composed of a greater proportion of specialists. We used the ENMTools R package (Warren 2016) to calculate this index.

GAM results showed that change in the average level of ecological generalism of the species (ΔEG; as measured by NICHE BREADTH) is negatively correlated with β-diversity change (Fig. A5.6).

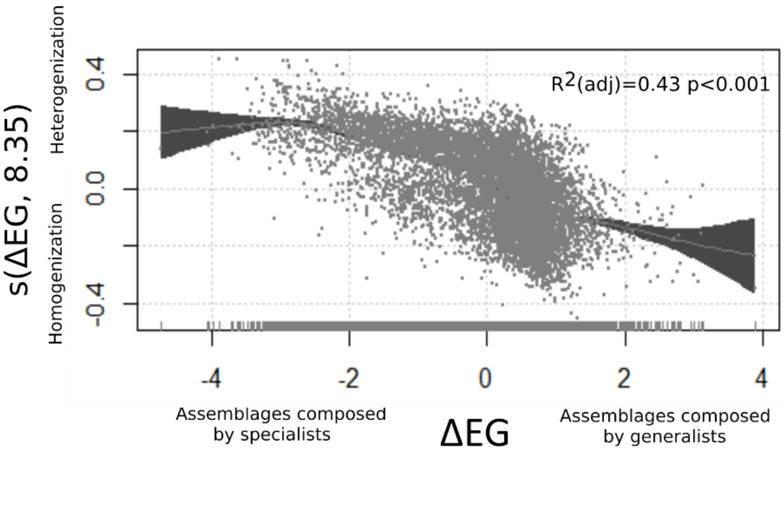

Figure A5.6 Plot of the relationships between change in β-diversity of frogs (homogenization vs. heterogenization) and change in the average level of ecological generalism of the species (ΔEG; assemblages composed by specialists vs. assemblages composed by generalists) as measured by **NICHE BREADTH**. An univariate generalized additive model (GAM) was used to predict this relationship (light gray line), showing 95% confidence interval of the prediction shaded in dark gray, and residuals (light gray points). Rug on the x axis (i.e., vertical lines that stick up from x axes) shows the distributions of predictor values. The Label on the y-axis of plot allude to the smoothed function (s) for the term of interest (ΔEG), and the estimated degrees of freedom (following the term). Additionally, as measures of overall fit we present adjusted R^2 and the significance of predictor (p).

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Appendix A6

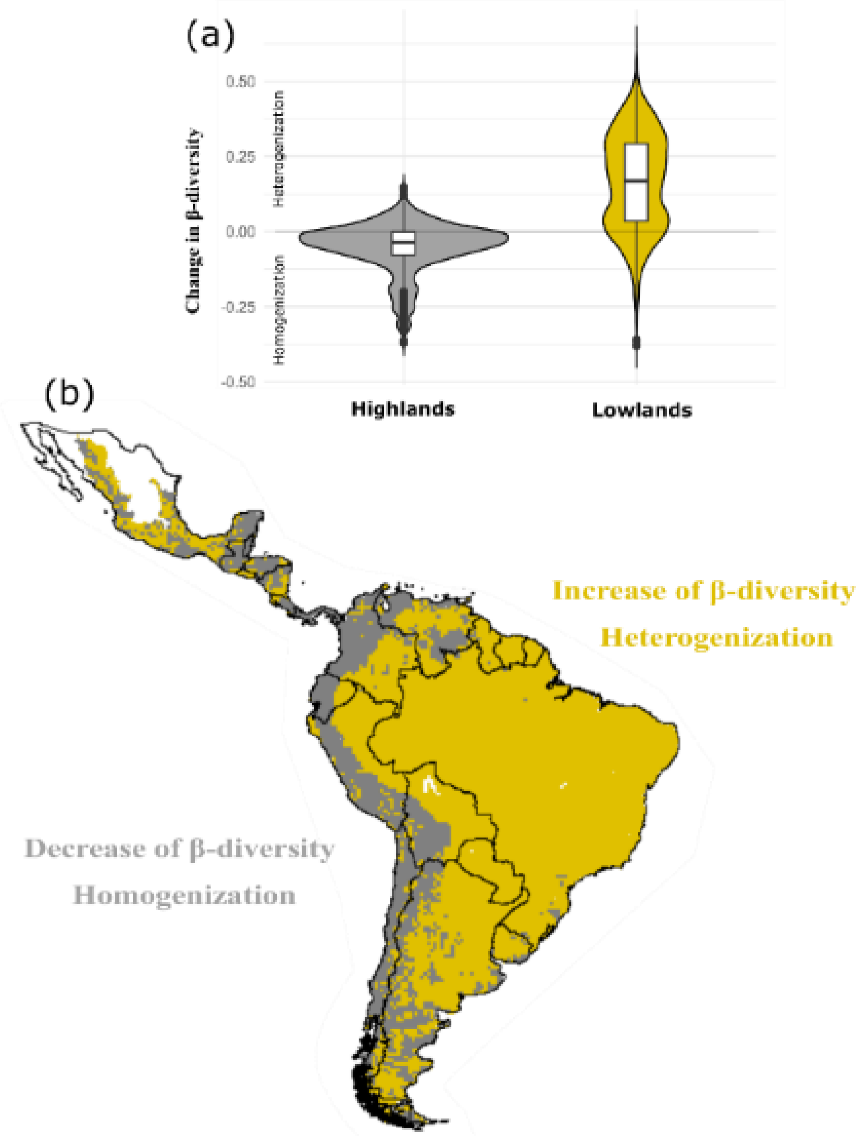


Figure A6.7. Projected changes in β-diversity (reflecting how differences in frogs' spatial composition changes over time) by 2070 in the Neotropical Region. We used the same approach to model species distributions described in Methods of the main text, however projections were made under the GISS-E2-R global climate model (i.e., moderate scenario; see Methods). (a) Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) of β diversity changes in Neotropical highlands (gray) or lowlands (yellow). (b) Map showing areas where biotic homogenization (i.e., decrease of β-diversity; gray areas) and biotic heterogenization (i.e., increase of β-diversity; yellow areas) are predicted to occur. The majority of highland assemblages are predicted to become more homogeneous, whereas the majority of lowland assemblages are predicted to become more heterogenous (see violin plot). Analyses were performed under the assumption that a species can reach any area with suitable environmental conditions (universal dispersion). Highlands refer to altitudes above 1300 m.a.s.l.

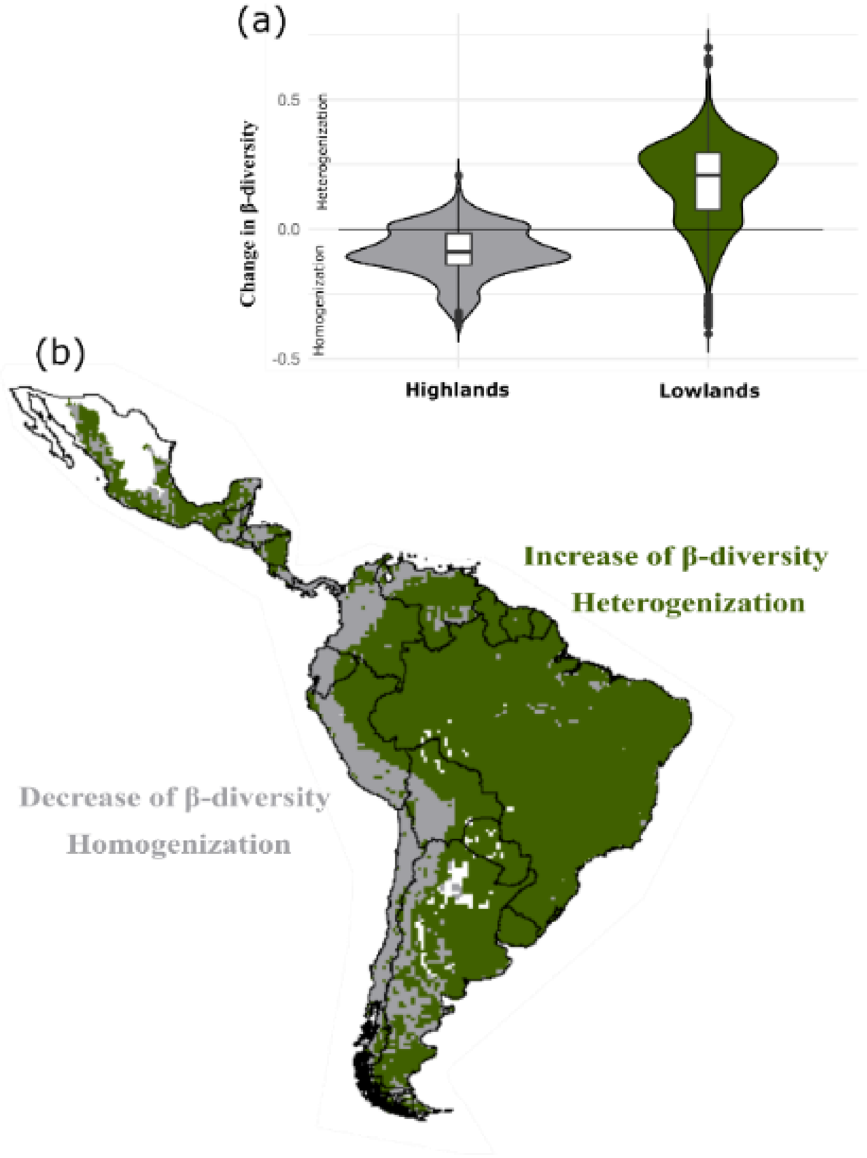


Figure A6.8. Projected changes in β-diversity (reflecting how differences in frogs' spatial composition changes over time) by 2070 in the Neotropical Region. We used the same approach to model species distributions described in Methods of the main text, however projections were made under the HadGEM2-ES global climate model (i.e., hotter/drier scenario; see Methods). (a) Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) of β diversity changes in Neotropical highlands (gray) or lowlands (green). (b) Map showing areas where biotic homogenization (i.e., decrease of β-diversity; gray areas) and biotic heterogenization (i.e., increase of β-diversity; green areas) are predicted to occur. The majority of highland assemblages are predicted to become more homogeneous, whereas the majority of lowland assemblages are predicted to become more heterogenous (see violin plot). Analyses were performed under the assumption that a species can reach any area with suitable environmental conditions (universal dispersion). Highlands refer to altitudes above 1300 m.a.s.l.

Appendix A7

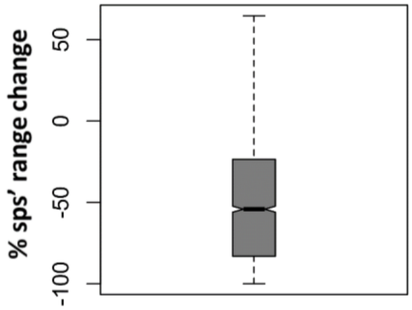


Figure A7.9. Percentage of species' range change between baseline conditions (see methods) and 2070 year due to climate change. The median of range change is shown (black horizontal line) with their respective 95% confidence interval (notches of box). The core boxes of boxplots indicate the interquartile range of data whereas the whisker lines extend to at most 1.5 the interquartile range from both ends of the box. Projections to calculate range changes were performed using 2669 neotropical frog species under the IPSL-CM5a-LR global climate model (i.e., warmer/dryer scenario; see methods).

Appendix A8

Table A8.3. Generalized additive models (GAMs) explaining changes in β-diversity, including degrees of freedom (df), Akaike Information Criterion (AIC), Log Likelihood (logLik), and AIC values relative to the lowest value (ΔAIC). Predictors include change in species richness (ΔSR), elevation, change in the average level of ecological generalism (ΔEG), and change in phylogenetic diversity (ΔPD).

Model (fixed variables)	df	AIC	ΔAIC	logLik
ΔSR+Elevation+ΔEG+ΔPD	31	-19699.8	0	9881.256
ΔSR+Elevation+ΔEG	26	-19559.806	139.9945	9806.557
ΔSR+ΔEG+ΔPD	23	-18625.306	1074.4936	9336.325
ΔSR+ΔEG	18	-18463.072	1236.7278	9250.199
Elevation+ΔEG+ΔPD	24	-18080.382	1619.4177	9064.474
Elevation+ΔEG	19	-17746.534	1953.266	8892.43
ΔEG+ΔPD	16	-16907.718	2792.0816	8470.353
ΔEG	10	-16539.246	3160.5535	8280.616
ΔSR+Elevation+ΔPD	23	-16241.572	3458.2281	8143.95
ΔSR+Elevation	18	-15800.774	3899.0261	7918.938
ΔSR+ΔPD	14	-14420.385	5279.4148	7225.13
ΔSR	9	-13881.207	5818.5928	6950.229
Elevation+ΔPD	16	-13802.364	5897.4359	6917.348
Elevation	10	-12635.102	7064.6981	6328.278
ΔPD	7	-11098.395	8601.4045	5557.086
(Null)	2	-9440.505	10259.296	4722.252

Appendix A9

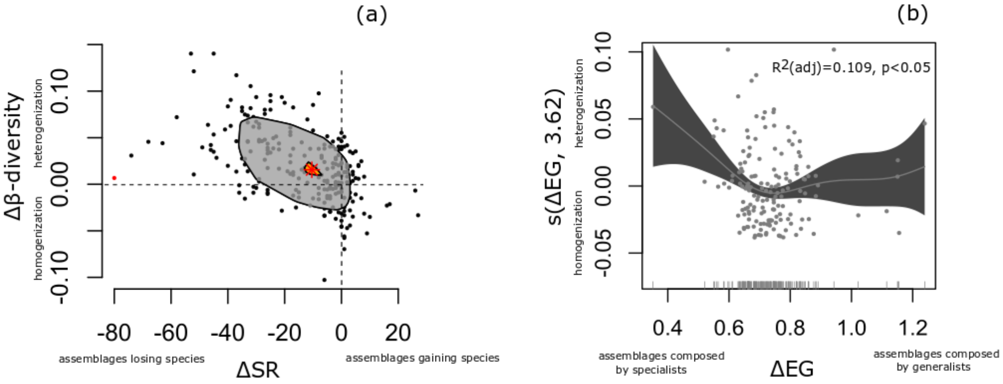


Figure A9.10. Plots of the relationships between change in β-diversity of frogs (homogenization vs. heterogenization) and two predictors in the Mesoamerican highlands: change in species richness (ΔSR; species gains vs. species loss) and change in the average level of ecological generalism of the species (ΔEG; assemblages composed by specialists vs. assemblages composed by generalists). (a) Bagplot of the relationship between change in β-diversity and ΔSR. Median is shown as red asterisk, and outliers are shown on red. The light gray polygon (i.e., the bag) contains 50% of the data points. (b) Biplot showing the predicted relationship between change in β-diversity and ΔEG. An univariate generalized additive model (GAM) was used to predict this relationship (light gray line), showing 95% confidence interval of the prediction shaded in dark gray, and residuals (light gray points). Rug on the x axis (i.e., vertical lines that stick up from x axes) shows the distributions of predictor values. The Label on the y-axis of plot allude to the smoothed function (s) for the term of interest (ΔEG), and the estimated degrees of freedom (following the term). Additionally, as measures of overall fit we present adjusted R^2 and the significance of predictor (p).

Appendix A10

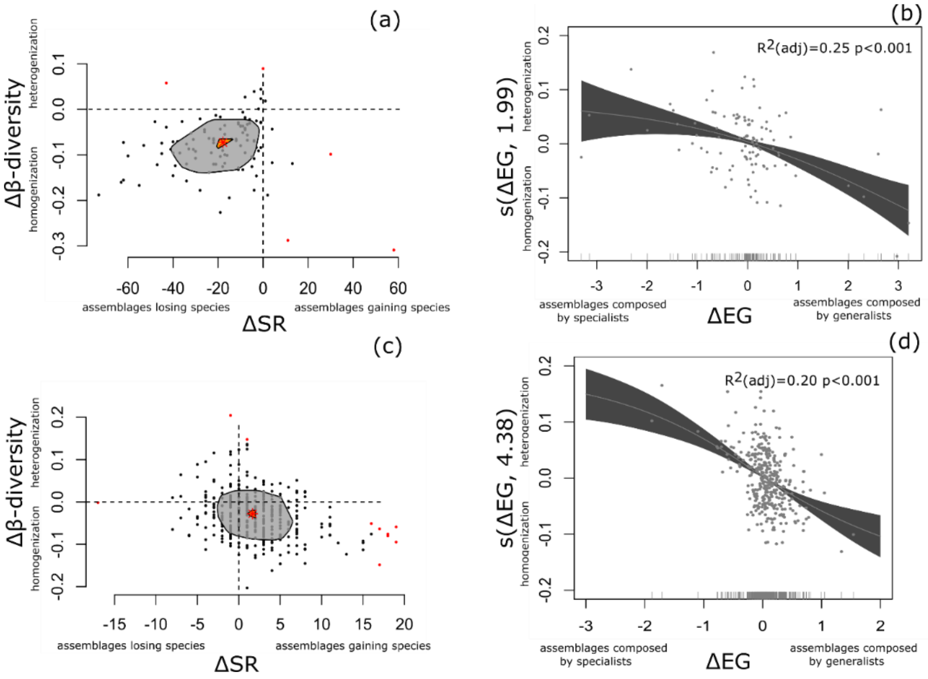


Figure A10.11. Plots of the relationships between change in β-diversity of frogs (homogenization vs. heterogenization) and two predictors in the Pacific lowlands of South America: change in species richness (ΔSR; species gains vs. species loss) and change in the average level of ecological generalism of the species (ΔEG; assemblages composed by specialists vs. assemblages composed by generalists). (a) Bagplot of the relationship between change in β-diversity and ΔSR in the northern Pacific lowlands of South America. (c) Bagplot of the relationship between change in β-diversity and ΔSR in the southern Pacific lowlands of South America. Median is shown as red asterisk, and outliers are shown on red. The light gray polygon (i.e., the bag) contains 50% of the data points. (b) Biplot showing the predicted relationship between change in β-diversity and ΔEG in the northern Pacific lowlands of South America. (d) Biplot showing the predicted relationship between change in β-diversity and ΔEG in the southern Pacific lowlands of South America. Univariate generalized additive models (GAMs) were used to predict these relationships (light gray line), showing 95% confidence interval of the prediction shaded in dark gray and residuals (light gray points). Rugs on the x axes (i.e., vertical lines that stick up from x axes) show the predictors values, and how they are distributed. Labels on the y-axes of plots allude to the smoothed function (s) for the term of interest (ΔEG), and the estimated degrees of freedom (following the term). As measures of overall fit we present adjusted R^2 and the significance of predictors (p).

Appendix A11

Geographically Weighted Regressions

To explore potential spatial nonstationarity in the relationships between response and predictor variables, (i.e., spatial variability of the relationships), we used geographically weighted regressions (GWR) to allow modelled parameters to vary in space, rather than assume a single global parameter for each predictor variable (Fotheringham et al. 2002).

The relationship between change in β-diversity and ΔSR, ΔEG and ΔPD showed little geographic variation, with the sign of modelled coefficients relatively consistent across space.

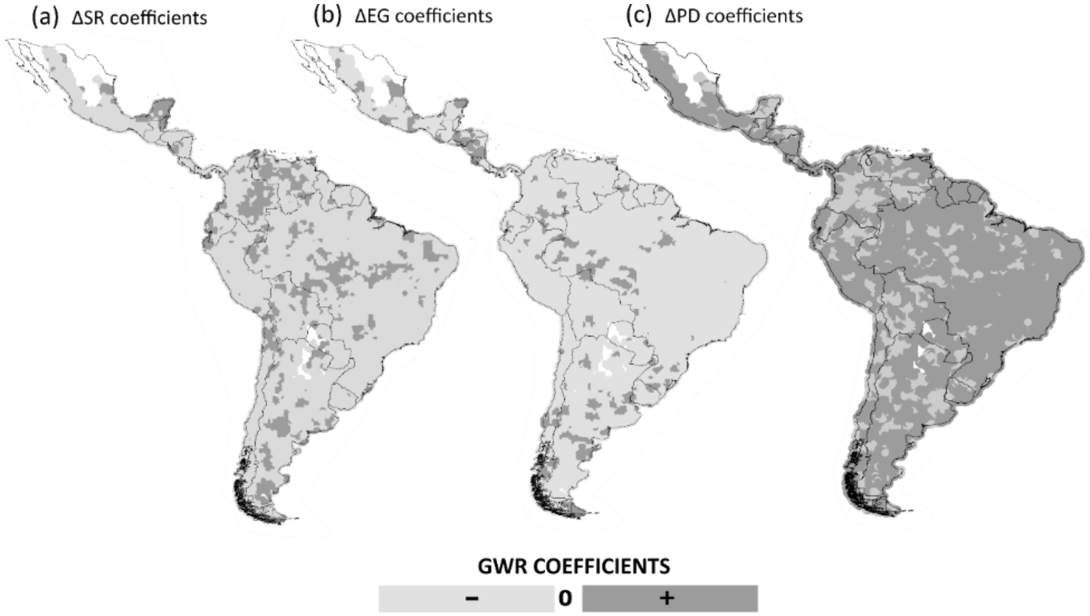


Figure A11.12. Maps of the predictor coefficients from univariate geographically weighted regressions (GWR): (a) Change in species richness (ΔSR); (b) change in ecological generalism (ΔEG), and (c) change in phylogenetic diversity (ΔPD).

Literature Cited

Fotheringham, A.S., Brunsdon, C. and Charlton, M. (2002) *Geographically Weighted Regression: The Analysis of Spatially Varying Relationships/cA. Stewart Fotherington, Chris Brunsdon, and Martin Charlton*. Wiley.

Appendix A12

Table A12.4. Multiple linear regression evaluating drivers of change in β-diversity. Predictors include change in species richness (ΔSR), change in phylogenetic diversity (ΔPD), change in the average level of ecological generalism (ΔEG), longitude (X), latitude (Y), elevation and the spatial term (X*Y). The standardized coefficients (z), standard errors, confidence intervals in parentheses (CI) and their associated probabilities (p) are shown as well. As measures of overall fit, the adjusted R^2 and probability are also presented.

Predictor variable	**Coefficient (z)**	**Standard error**	**95% CI**	***p* values**
ΔSR	-0.047	1.04E-03	(-0.049-0.045)	<0.001
ΔPD	0.008	9.20E-04	(0.006-0.010)	<0.001
ΔEG	-0.061	9.80E-04	(-0.062-0.058)	<0.001
X	0.004	6.76E-05	(0.003-0.004)	<0.001
Y	-0.005	2.94E-04	(-0.005-0.003)	<0.001
Elevation	0.000	1.00E-06	(-0.000-0.000)	<0.001
X*Y	0.000	3.98E-06	(-0.000-0.000)	<0.001
R^2(adj)	0.700			
***p* value**	<0.001			

Appendix A13

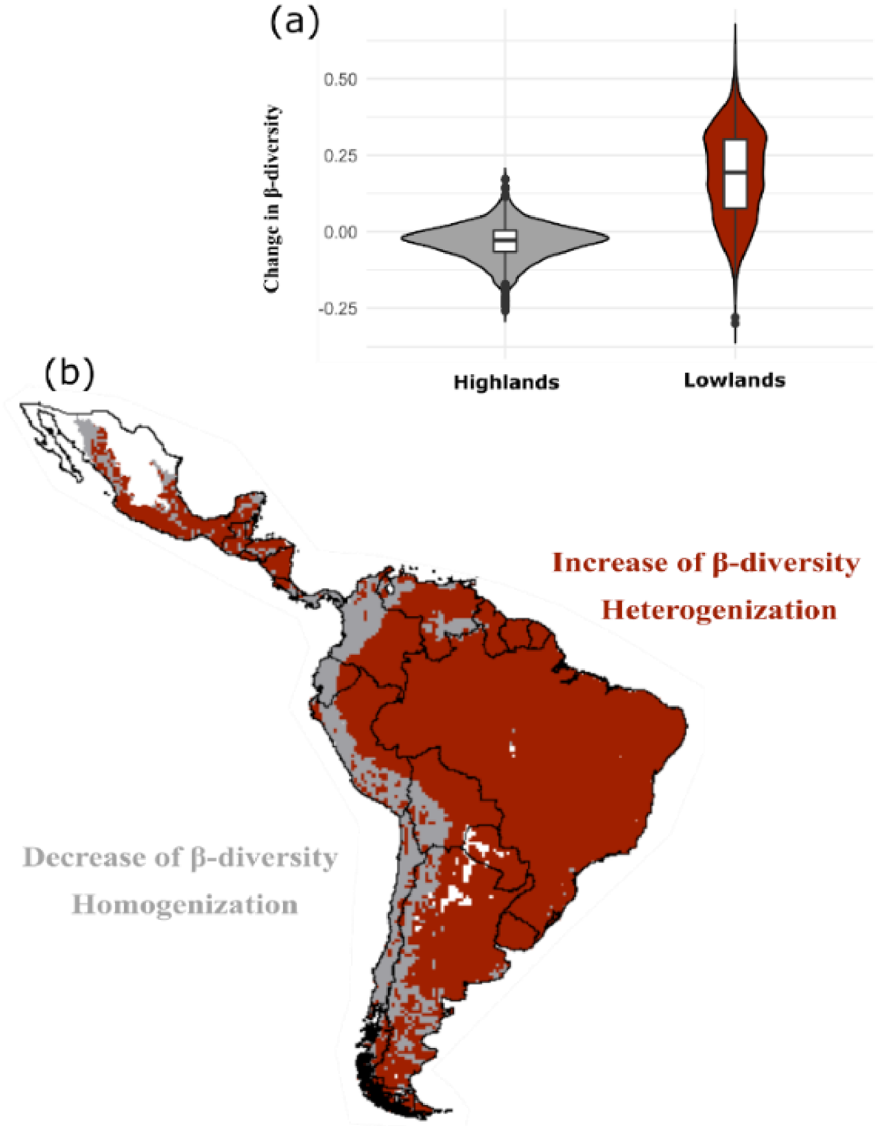


Figure A13.13. Projected changes in β-diversity (reflecting how differences in frogs' spatial composition changes over time) by 2070 in the Neotropical Region. We used the same approach to model species distributions (*n* = 2025) described in Methods of the main text, however projections were performed without species in the "data deficient" (DD) category of the IUCN Red List (http://www.redlist.org/), and under the IPSL-CM5a-LR global climate model (i.e., warmer/dryer scenario; see methods). (a) Violin plot showing the variation (median, range, kernel density, 25th-75th percentiles) of β diversity changes in Neotropical highlands (gray) or lowlands (red). (b) Map showing areas where biotic homogenization (i.e., decrease of β-diversity; gray areas) and biotic heterogenization (i.e., increase of β-diversity; red areas) are predicted to occur. The majority of highland assemblages are predicted to become more homogeneous, whereas the majority of lowland assemblages are predicted to become more heterogenous (see violin plot). Analyses were performed under the assumption that a species can reach any area with suitable environmental conditions (universal dispersion). Highlands refer to altitudes above 1300 m.a.s.l.

Appendix A14

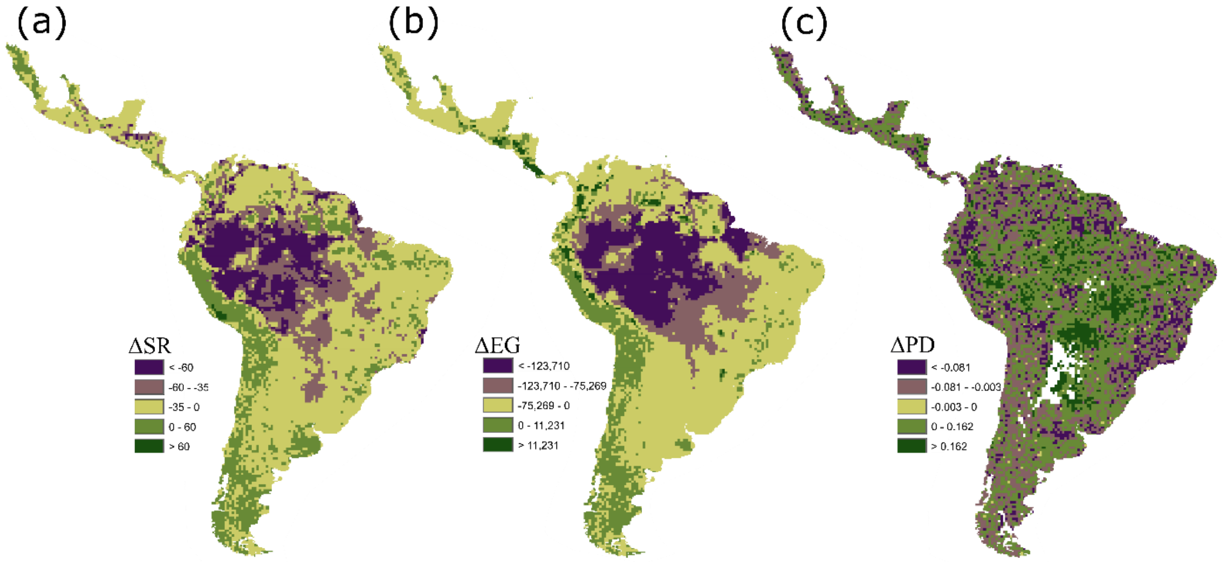


Figure A14.14. Maps of the projected changes by 2070 in the Neotropical Region due to climate change. (a) Changes in species richness – ΔSR (negative values represented projected species losses, while positive values represent projected species gains); (b) Changes in ecological generalism – ΔEG (positive values represent assemblages that are predicted to become composed of a greater proportion of generalists, whereas negative values represent assemblages that are predicted to become composed of a greater proportion of specialists; see Methods in the main text); (c) Changes in phylogenetic diversity – ΔPD (negative values indicate a trend towards decreased PD, while positive values indicate a trend towards increased PD; see Methods in the main text). Raw values are presented in the legends of maps. We used the Jenks Natural Breaks method, which identifies break points that best group similar values and maximize the differences between classes (Jenks 1967), to scale color shading.

Literature Cited

Jenks, G. F. 1967. The data model concept in statistical mapping. – Int. Yearbook Cartogr. 7: 186–190.

Appendix A15

R code to model species distributions, both under present and future conditions. Depending on the number of species, this code could take many hours to process (e.g., some species had many of points). This code was developed using different sources: Code of Laura Graham available at: “https://github.com/bw4sz/FutureAnalog/blob/master/fnSDM.R”, and information available on the R-Forge platform: “https://r-forge.r-project.org/scm/viewvc.php/*checkout*/pkg/biomod2/inst/doc/Simple_species_modelling.pdf?root=biomod”, and “https://r-forge.r-project.org/scm/viewvc.php/*checkout*/pkg/biomod2/inst/doc/Multi_species_computation.pdf?revision=598&root=biomod&pathrev=598”.

```
#### Code to run the SDMs ON BIOMOD2 ####

#Load packages
library("biomod2")

#DIR TO store temp files (this process will generate many tempfiles)
rasterOptions(tmpdir="/TEMP_FILES")
rasterTmpFile()

#Input: A1: (list of points with lat and long and species names in Ecoregion A1
following the #regionalisation of Morrone (2014). These points were generated in
GEOSPATIAL MODELLING #ENVIRONMENT).
#A1back: (list of random or background points with lat and long in Ecoregion A1.
#Points generated in GEOSPATIAL MODELLING ENVIRONMENT)

#Load data points
A1<-read.csv("A1_points00.csv")
SPECIES<-gsub('([[:punct:]])|\\s+','_',A1$FROST)
A1["SPECIES"] <- SPECIES
A1 <- A1[,-4]
A1count<-data.frame(table(A1$SPECIES))
write.csv(A1count, "A1count.csv")
A1<-A1[A1$SPECIES %in% A1count$Var1[A1count$Freq>2],]
A1back<-read.csv("A1_randomback00.csv")
colnames(A1back)[colnames(A1back)=="FROST"] <- "SPECIES"
#Joining species points with random points
loc_clean<- rbind(A1, A1back)
spec<-unique(loc_clean[("SPECIES")])
spec<-as.vector(spec$SPECIES)
spec <- spec[-length(spec)]
class(spec)

#Load Environmental data from Worldclim
require(raster)
myExpl = stack("/bio1.grd",
               "/bio2.grd")#.......

#loop on species to model one by one
for(sp.n in spec){
```

```
myRespName = sp.n
cat('\n',myRespName,'modeling...')


### definition of data:
#Defining Prescences and pseudo absences
myResp1 <- as.numeric(loc_clean$RESPONSE[loc_clean$SPECIES==myRespName])
random<- as.vector(loc_clean$RESPONSE[loc_clean$SPECIES=="randomback"])
myResp<-c(myResp1,random)
#Definiting coordinates of Prescences and pseudo absences
myRespCoord1 = as.numeric(loc_clean$LATDECDEG[loc_clean$SPECIES==myRespName])
myRespCoord2=as.numeric(loc_clean$LATDECDEG[loc_clean$SPECIES=="randomback"])
myReslat<-c(myRespCoord1,myRespCoord2)
myRespCoord3 = as.numeric(loc_clean$LONGDECDEG[loc_clean$SPECIES==myRespName])
myRespCoord4=as.numeric(loc_clean$LONGDECDEG[loc_clean$SPECIES=="randomback"])
myReslong<-c(myRespCoord3,myRespCoord4)
myRespCoord<-as.data.frame(cbind(myReslong,myReslat))

### Initialisation
myBiomodData <- BIOMOD_FormatingData(resp.var = myResp,
                                     expl.var = myExpl,
                                     resp.xy = myRespCoord,
                                     resp.name = myRespName,
                                     PA.nb.rep=1,
                                     PA.nb.absences=10000)

#PRINT PROJECT
#myBiomodData
#plot(myBiomodData)

#Give current project a name
projnam <- 'current'

# Individual model outputs ------------------------
#Definition of options
myBiomodOption <- BIOMOD_ModelingOptions()
# Modelling
myBiomodModelOut<-BIOMOD_Modeling( myBiomodData,
                                   models = c("RF"),
                                   models.options = myBiomodOption,
                                   NbRunEval=1,
                                   DataSplit=80,
                                   Prevalence=0.5,
                                   Yweights=NULL,
                                   VarImport=3,
                                   models.eval.meth = c('ROC',"TSS"),
                                   SaveObj = TRUE,
                                   modeling.id = paste(myRespName,"Final",sep=""))

# get all models evaluation
myBiomodModelEval <- get_evaluations(myBiomodModelOut)

# get ROC and TSS scores of all selected models and write to file
stat <- myBiomodModelEval[c("ROC","TSS"), "Testing.data",,,]
stat<-as.data.frame(stat)
filename <- paste(gsub("_",".",myRespName), "ModelEval.csv", sep="/")
write.csv(cbind(myRespName,stat),filename)
# get cutoffs
threshold<-myBiomodModelEval[c("ROC","TSS"), "Cutoff",,,]
threshold<-as.data.frame(threshold)
filename <- paste(gsub("_",".",myRespName), "Cutoffs.csv", sep="/")
write.csv(cbind(myRespName, threshold),filename)
#get specificity values
```

```
  Specifi<-myBiomodModelEval[c("ROC","TSS"), "Specificity",,,]
  Specifi<-as.data.frame(Specifi)
  filename <- paste(gsub("_",".",myRespName), "Specificity.csv", sep="/")
  write.csv(cbind(myRespName, Specifi),filename)
  #get sensitivity values
  sensit<-myBiomodModelEval[c("ROC","TSS"), "Sensitivity",,,]
  sensit<-as.data.frame(sensit)
  filename <- paste(gsub("_",".",myRespName), "Sensitivity.csv", sep="/")
  write.csv(cbind(myRespName, sensit),filename)

  # get variable importance and write to file
  m.var <- melt(get_variables_importance(myBiomodModelOut)[,,"RUN1",])
  filename <- paste(gsub("_",".",myRespName),"VarImportance.csv",sep="/")
  write.csv(cbind(m.var,myRespName),filename)

  # save modelling outputs for use in env projections
  save(myBiomodModelOut, file = paste(gsub("_", ".", myRespName),
"myBiomodModelOut.rda", sep="/"))

  ## Project SDM into current env projections##

  # DECISION
  myBiomodProjection <- BIOMOD_Projection(
    modeling.output = myBiomodModelOut,
    new.env = myExpl,
    proj.name = "current",
    selected.models = 'all',
    binary.meth = c("TSS", "ROC"),
    compress = "xz",
    clamping.mask = T,
    do.stack = F,
    output.format = ".grd")

  #REMOVE TEM FILES
  removeTmpFiles(h=0)
  (unlink("/TEMP_FILES/*", TRUE ))
}

#################################################################
## Project SDM into future env projections ##

rasterOptions(tmpdir="/TEMP_FILES4")
rasterTmpFile()

#Load future enviromental layers, with the same name tha current layers
GCM  = stack("/INMCM4-rcp45(70)/bio1.grd",
             "/INMCM4-rcp45(70)/bio2.grd")
#loop on species to model one by one. First load the current models
for(sp.n in spec){
  load(file.path(sp.n,"myBiomodModelOut.rda"))

  #Give future project a name
  projnam <- "IM45_70"

  # DECISION
  myBiomodProjection <- BIOMOD_Projection(
    modeling.output = myBiomodModelOut,
    new.env = GCM,
    proj.name = "IM45_70",
    selected.models = 'all',
    binary.meth = c("TSS", "ROC"),
    compress = 'xz',
    clamping.mask = T,
```

```
    do.stack = F,
    output.format = '.grd')

  # Binary transformation using a 500 fixed threshold
  #This is only another option to convert continous maps into binary
  all_proj <- get_predictions(myBiomodProjection)
  bin500<<-BinaryTransformation(all_proj, 500)
  writeRaster(bin500[[1]],(file.path(sp.n, "proj_IM45_70", "individual_projections",
                                     (paste(sp.n, "RUN1_IM_500.asc", sep=""))))) 
  writeRaster(bin500[[2]],(file.path(sp.n, "proj_IM45_70", "individual_projections",
                                     (paste(sp.n, "Full_IM_500.asc", sep=""))))) 
  #remove temp files
  removeTmpFiles(h=0)
  (unlink("/TEMP_FILES4/*", TRUE ))
  }


######################################################################################
#

  # 10th percentile threshold (P10, Peterson et al. 2007)
   # **DECISION**
  myBiomodProjection <- BIOMOD_Projection(
    modeling.output = myBiomodModelOut,
    new.env = myExpl,
    proj.name = "current",
    selected.models = 'all',
    binary.meth = c("TSS", "ROC"),
    compress = "xz",
    clamping.mask = T,
    do.stack = F,
    output.format = ".grd")

  removeTmpFiles(h=0)
  (unlink("E:/TEM_FILES/*", TRUE ))


  #GET_PREDICTIONS MAPS (FULL AND RUN)

  continuos_model <- get_predictions(myBiomodProjection)

  #Apply 10 percentile training presence threshold
  values<-loc_clean[loc_clean$SPECIES==myRespName,]
  values1<-values[,-c(1,4,5)]
  extracted_predictions<-raster::extract( continuos_model, values1)

  thresh <- function(modOccVals, type) {
    # remove all NA
    modOccVals <- na.omit(modOccVals)
    if (type == 'mtp') {re
      # apply minimum training presence threshold
      x <- min(modOccVals)
    } else if (type == 'p10') {
      # Define 10% training presence threshold
      if (length(modOccVals) < 10) {   # if less than 10 occ values, find 90% of total
and round down
        n90 <- floor(length(modOccVals) * 0.9)
      } else {  # if greater than or equal to 10 occ values, round up
        n90 <- ceiling(length(modOccVals) * 0.9)
      }
      x <- rev(sort(modOccVals))[n90]  # apply 10% training presence threshold over
all models
    }
```

```
    return(x)
  }

  #Apply threshold
  thr <- thresh(extracted_predictions[,2], "p10")
  binary_model<- continuos_model>thr

  #Croprop model with extension of Ecoregion
  shape_crop <- readOGR("A1_crop.shp")

  binary_model_crop<-raster::crop(binary_model, shape_crop)

  #Change extension of model to Neotropics
  alphaMap <- reclassify(subset(myExpl,1), c(-Inf,Inf,0))
  binary_model_crop00<-merge(alphaMap, binary_model_crop)


  writeRaster(binary_model_crop00[[2]],(file.path("B5_p10_5km",
                                                  (paste(sp.n, "FULL_10percent.grd",
sep=""))))) 

  removeTmpFiles(h=0)
  (unlink("E:/TEM_FILES3/*", TRUE ))

}
```

Supplementary Material Chapter 2

List of contents

Appendix S1

Appendix S1

Table S1. List of the 539 species used to analyze changes in spatial patterns of anuran β-diversity due to extinction of species. The IUCN extinction risk 37 categories are as follows: Critically Endangered (CR), Endangered (EN), Vulnerable (VU), Near Threatened (NT), Least Concern (LC), Data Deficient (DD), and NE (Not-Evaluated).

SPECIES	IUCN STATUS	SPECIES	IUCN STATUS	SPECIES	IUCN STATUS
Adelophryne adiastola	NE	*Atelopus mindoensis*	EN	*Centrolene condor*	DD
Adenomera andreae	LC	*Atelopus nanay*	CR	*Centrolene geckoideum*	CR
Adenomera hylaedactyla	LC	*Atelopus nepiozomus*	DD	*Centrolene gemmatum*	CR
Agalychnis buckleyi	NT	*Atelopus orcesi*	CR	*Centrolene heloderma*	CR
Agalychnis hulli	DD	*Atelopus pachydermus*	CR	*Centrolene lynchi*	CR
Agalychnis psilopygion	DD	*Atelopus palmatus*	DD	*Centrolene peristictum*	NT
Agalychnis spurrelli	LC	*Atelopus pastuso*	CR	*Centrolene pipilatum*	CR
Allobates femoralis	LC	*Atelopus petersi*	CR	*Centrolene scirtetes*	NE
Allobates fratisenescus	DD	*Atelopus planispina*	EN	*Ceratophrys cornuta*	DD
Allobates insperatus	NT	*Atelopus podocarpus*	CR	*Ceratophrys stolzmanni*	VU
Allobates kingsburyi	DD	*Atelopus spumarius*	VU	*Ceratophrys testudo*	DD
Allobates talamancae	DD	*Barycholos pulcher*	LC	*Chiasmocleis anatipes*	DD
Allobates trilineatus	LC	*Boana alfaroi*	LC	*Chiasmocleis antenori*	DD
Allobates zaparo	LC	*Boana almendarizae*	NT	*Chiasmocleis bassleri*	LC
Amazophrynella siona	LC	*Boana boans*	LC	*Chiasmocleis parkeri*	DD
Ameerega bilinguis	LC	*Boana calcarata*	LC	*Chiasmocleis ventrimaculata*	DD
Ameerega hahneli	LC	*Boana cinerascens*	LC	*Chimerella mariaelenae*	DD
Ameerega parvula	LC	*Boana fasciata*	NT	*Cochranella balionota*	CR
Atelopus angelito	CR	*Boana geographica*	LC	*Cochranella litoralis*	DD
Atelopus arthuri	CR	*Boana lanciformis*	LC	*Cochranella mache*	CR
Atelopus balios	CR	*Boana maculateralis*	LC	*Cochranella resplendens*	DD
Atelopus bomolochos	CR	*Boana nympha*	NT	*Craugastor longirostris*	LC
Atelopus boulengeri	DD	*Boana pellucens*	LC	*Cruziohyla calcarifer*	NT
Atelopus coynei	EN	*Boana picturata*	VU	*Cruziohyla craspedopus*	DD
Atelopus elegans	CR	*Boana punctata*	LC	*Ctenophryne aequatorialis*	EN
Atelopus exiguus	CR	*Boana rosenbergi*	LC	*Ctenophryne aterrima*	VU
Atelopus guanujo	CR	*Boana rubracyla*	NE	*Ctenophryne geayi*	DD
Atelopus halihelos	DD	*Centrolene bacatum*	DD	*Dendropsophus bifurcus*	LC
Atelopus ignescens	CR	*Centrolene ballux*	CR	*Dendropsophus bokermanni*	LC
Atelopus longirostris	CR	*Centrolene buckleyi*	CR	*Dendropsophus brevifrons*	LC
Atelopus lynchi	EN	*Centrolene charapita*	DD	*Dendropsophus carnifex*	LC

SPECIES	IUCN STATUS	SPECIES	IUCN STATUS	SPECIES	IUCN STATUS
Dendropsophus ebraccatus	LC	*Gastrotheca guentheri*	CR	*Hyloscirtus ptychodactylus*	EN
Dendropsophus gryllatus	VU	*Gastrotheca lateonota*	NE	*Hyloscirtus staufferorum*	EN
Dendropsophus marmoratus	LC	*Gastrotheca litonedis*	EN	*Hyloscirtus tigrinus*	CR
Dendropsophus minutus	NT	*Gastrotheca lojana*	VU	*Hyloscirtus torrenticola*	NT
Dendropsophus miyatai	NT	*Gastrotheca longipes*	DD	*Hyloxalus anthracinus*	CR
Dendropsophus parviceps	LC	*Gastrotheca orophylax*	VU	*Hyloxalus awa*	VU
Dendropsophus reticulatus	LC	*Gastrotheca plumbea*	VU	*Hyloxalus bocagei*	CR
Dendropsophus rhodopeplus	LC	*Gastrotheca pseustes*	LC	*Hyloxalus breviquartus*	DD
Dendropsophus riveroi	LC	*Gastrotheca psychrophila*	EN	*Hyloxalus cevallosi*	DD
Dendropsophus sarayacuensis	LC	*Gastrotheca riobambae*	VU	*Hyloxalus delatorreae*	CR
Dendropsophus shiwiarum	NT	*Gastrotheca testudinea*	NT	*Hyloxalus elachyhistus*	VU
Dendropsophus triangulum	LC	*Gastrotheca weinlandii*	DD	*Hyloxalus exasperatus*	DD
Diasporus gularis	NT	*Hamptophryne boliviana*	DD	*Hyloxalus fallax*	DD
Ecnomiohyla phantasmagoria	DD	*Hemiphractus bubalus*	NT	*Hyloxalus fuliginosus*	EN
Ectopoglossus confusus	CR	*Hemiphractus fasciatus*	DD	*Hyloxalus infraguttatus*	VU
Edalorhina perezi	LC	*Hemiphractus helioi*	NT	*Hyloxalus italoi*	NT
Engystomops coloradorum	NT	*Hemiphractus proboscideus*	NT	*Hyloxalus jacobuspetersi*	CR
Engystomops guayaco	LC	*Hemiphractus scutatus*	DD	*Hyloxalus lehmanni*	EN
Engystomops montubio	LC	*Hyalinobatrachium aureoguttatum*	DD	*Hyloxalus maculosus*	CR
Engystomops petersi	LC	*Hyalinobatrachium chirripoi*	NE	*Hyloxalus maquipucuna*	DD
Engystomops pustulatus	LC	*Hyalinobatrachium fleischmanni*	DD	*Hyloxalus marmoreoventris*	EN
Engystomops puyango	NE	*Hyalinobatrachium iaspidiense*	DD	*Hyloxalus mystax*	EN
Engystomops randi	LC	*Hyalinobatrachium munozorum*	LC	*Hyloxalus nexipus*	NT
Epipedobates anthonyi	LC	*Hyalinobatrachium pellucidum*	CR	*Hyloxalus peculiaris*	VU
Epipedobates boulengeri	LC	*Hyalinobatrachium ruedai*	DD	*Hyloxalus pulchellus*	EN
Epipedobates darwinwallacei	EN	*Hyalinobatrachium valerioi*	VU	*Hyloxalus sauli*	NT
Epipedobates espinosai	DD	*Hyalinobatrachium yaku*	DD	*Hyloxalus shuar*	NT
Epipedobates machalilla	NT	*Hyloscirtus albopunctulatus*	DD	*Hyloxalus toachi*	EN
Epipedobates tricolor	NT	*Hyloscirtus alytolylax*	NT	*Hyloxalus vertebralis*	EN
Espadarana audax	EN	*Hyloscirtus condor*	DD	*Hyloxalus yasuni*	NT
Espadarana callistomma	DD	*Hyloscirtus criptico*	EN	*Incilius coniferus*	LC
Espadarana durrellorum	DD	*Hyloscirtus larinopygion*	NT	*Leptodactylus discodactylus*	LC
Espadarana prosoblepon	LC	*Hyloscirtus lindae*	NT	*Leptodactylus knudseni*	DD
Excidobates captivus	DD	*Hyloscirtus mashpi*	DD	*Leptodactylus labrosus*	LC
Excidobates condor	DD	*Hyloscirtus pacha*	DD	*Leptodactylus leptodactyloides*	LC
Gastrotheca andaquiensis	NT	*Hyloscirtus palmeri*	DD	*Leptodactylus melanonotus*	LC
Gastrotheca angustifrons	DD	*Hyloscirtus pantostictus*	VU	*Leptodactylus mystaceus*	LC
Gastrotheca cornuta	DD	*Hyloscirtus phyllognathus*	VU	*Leptodactylus pentadactylus*	LC
Gastrotheca dendronastes	VU	*Hyloscirtus princecharlesi*	EN	*Leptodactylus peritoaktites*	EN
Gastrotheca espeletia	VU	*Hyloscirtus psarolaimus*	NT	*Leptodactylus petersii*	DD

SPECIES	IUCN STATUS	SPECIES	IUCN STATUS	SPECIES	IUCN STATUS
Leptodactylus rhodomerus	DD	*Osornophryne guacamayo*	EN	*Pristimantis aureolineatus*	DD
Leptodactylus rhodomystax	LC	*Osornophryne occidentalis*	EN	*Pristimantis balionotus*	EN
Leptodactylus stenodema	VU	*Osornophryne talipes*	CR	*Pristimantis bambu*	NE
Leptodactylus ventrimaculatus	LC	*Osteocephalus alboguttatus*	LC	*Pristimantis baryecuus*	EN
Leptodactylus wagneri	LC	*Osteocephalus buckleyi*	LC	*Pristimantis bellae*	NE
Leucostethus fugax	NT	*Osteocephalus cabrerai*	LC	*Pristimantis bicantus*	NE
Lithodytes lineatus	LC	*Osteocephalus cannatellai*	LC	*Pristimantis brevicrus*	LC
Lynchius flavomaculatus	DD	*Osteocephalus deridens*	DD	*Pristimantis bromeliaceus*	NT
Lynchius simmonsi	EN	*Osteocephalus duellmani*	DD	*Pristimantis buckleyi*	LC
Niceforonia babax	DD	*Osteocephalus festae*	NE	*Pristimantis buenaventura*	VU
Niceforonia brunnea	DD	*Osteocephalus fuscifacies*	DD	*Pristimantis caeruleonotus*	DD
Niceforonia dolops	DD	*Osteocephalus mutabor*	VU	*Pristimantis cajamarcensis*	LC
Niceforonia elassodisca	NT	*Osteocephalus planiceps*	LC	*Pristimantis calcarulatus*	LC
Niceforonia nigrovittata	LC	*Osteocephalus taurinus*	LC	*Pristimantis caprifer*	EN
Niceforonia peraccai	DD	*Osteocephalus verruciger*	LC	*Pristimantis carlosceroni*	DD
Noblella coloma	NE	*Osteocephalus vilmae*	DD	*Pristimantis carvalhoi*	DD
Noblella heyeri	NT	*Osteocephalus yasuni*	LC	*Pristimantis cedros*	EN
Noblella lochites	EN	*Paruwrobates erythromos*	CR	*Pristimantis celator*	NT
Noblella myrmecoides	DD	*Paruwrobates whymperi*	DD	*Pristimantis chalceus*	NT
Noblella personina	DD	*Phyllomedusa coelestis*	DD	*Pristimantis chloronotus*	LC
Nyctimantis rugiceps	LC	*Phyllomedusa ecuatoriana*	EN	*Pristimantis churuwiai*	NE
Nymphargus anomalus	CR	*Phyllomedusa tarsius*	LC	*Pristimantis citriogaster*	NE
Nymphargus cariticommatus	DD	*Phyllomedusa tomopterna*	LC	*Pristimantis colodactylus*	LC
Nymphargus chancas	NE	*Phyllomedusa vaillantii*	LC	*Pristimantis colomai*	DD
Nymphargus cochranae	LC	*Pipa*	LC	*Pristimantis colonensis*	NE
Nymphargus grandisonae	LC	*Pristimantis acerus*	EN	*Pristimantis condor*	VU
Nymphargus griffithsi	VU	*Pristimantis achatinus*	LC	*Pristimantis conspicillatus*	LC
Nymphargus lasgralarias	DD	*Pristimantis actites*	NT	*Pristimantis cremnobates*	EN
Nymphargus laurae	DD	*Pristimantis acuminatus*	LC	*Pristimantis crenunguis*	EN
Nymphargus mariae	LC	*Pristimantis albujai*	NE	*Pristimantis croceoinguinis*	LC
Nymphargus megacheirus	CR	*Pristimantis allpapuyu*	NE	*Pristimantis crucifer*	EN
Nymphargus posadae	DD	*Pristimantis almendariz*	DD	*Pristimantis cryophilius*	EN
Nymphargus siren	DD	*Pristimantis altamazonicus*	LC	*Pristimantis cryptomelas*	LC
Nymphargus sucre	DD	*Pristimantis altamnis*	VU	*Pristimantis curtipes*	LC
Oophaga sylvatica	LC	*Pristimantis andinognomus*	NE	*Pristimantis degener*	DD
Oreobates quixensis	LC	*Pristimantis anemerus*	DD	*Pristimantis delius*	NE
Osornophryne angel	DD	*Pristimantis apiculatus*	DD	*Pristimantis devillei*	NT
Osornophryne antisana	EN	*Pristimantis appendiculatus*	NT	*Pristimantis diadematus*	LC
Osornophryne bufoniformis	VU	*Pristimantis ardyae*	DD	*Pristimantis dissimulatus*	EN
Osornophryne cofanorum	NE	*Pristimantis atratus*	EN	*Pristimantis duellmani*	NT

SPECIES	IUCN STATUS	SPECIES	IUCN STATUS	SPECIES	IUCN STATUS
Pristimantis ecuadorensis	EN	*Pristimantis llanganati*	DD	*Pristimantis pataikos*	NE
Pristimantis enigmaticus	LC	*Pristimantis loujosti*	NE	*Pristimantis paululus*	LC
Pristimantis eremitus	NT	*Pristimantis loustes*	NT	*Pristimantis pecki*	NT
Pristimantis eriphus	DD	*Pristimantis lucidosignatus*	NE	*Pristimantis percultus*	EN
Pristimantis ernesti	DD	*Pristimantis luscombei*	NT	*Pristimantis peruvianus*	LC
Pristimantis erythros	EN	*Pristimantis luteolateralis*	NT	*Pristimantis petersi*	VU
Pristimantis esmeraldas	DD	*Pristimantis lymani*	NT	*Pristimantis philipi*	DD
Pristimantis eugeniae	EN	*Pristimantis malkini*	LC	*Pristimantis phoxocephalus*	VU
Pristimantis exoristus	DD	*Pristimantis marcoreyesi*	NE	*Pristimantis pichincha*	DD
Pristimantis festae	LC	*Pristimantis martiae*	NT	*Pristimantis pinchaque*	DD
Pristimantis floridus	EN	*Pristimantis matidiktyo*	VU	*Pristimantis prolatus*	EN
Pristimantis galdi	LC	*Pristimantis mazar*	DD	*Pristimantis prometeii*	DD
Pristimantis ganonotus	DD	*Pristimantis metabates*	NE	*Pristimantis proserpens*	EN
Pristimantis gentryi	EN	*Pristimantis miktos*	NT	*Pristimantis pseudoacuminatus*	LC
Pristimantis gladiator	EN	*Pristimantis mindo*	VU	*Pristimantis pteridophilus*	EN
Pristimantis glandulosus	EN	*Pristimantis minimus*	NE	*Pristimantis pugnax*	NT
Pristimantis gualacenio	DD	*Pristimantis modipeplus*	EN	*Pristimantis punzan*	NE
Pristimantis hamiotae	DD	*Pristimantis munozi*	DD	*Pristimantis puruscafeum*	NE
Pristimantis hampatusami	NE	*Pristimantis muranunka*	NE	*Pristimantis pycnodermis*	EN
Pristimantis hectus	DD	*Pristimantis muricatus*	VU	*Pristimantis pyrrhomerus*	VU
Pristimantis huicundo	DD	*Pristimantis muscosus*	NE	*Pristimantis quaquaversus*	LC
Pristimantis ignicolor	EN	*Pristimantis mutabilis*	DD	*Pristimantis quinquagesimus*	NT
Pristimantis illotus	DD	*Pristimantis nephophilus*	NE	*Pristimantis rhodoplichus*	NE
Pristimantis incanus	EN	*Pristimantis nietoi*	VU	*Pristimantis rhodostichus*	NE
Pristimantis incomptus	NT	*Pristimantis nigrogriseus*	NT	*Pristimantis riveti*	NT
Pristimantis inusitatus	EN	*Pristimantis nimbus*	DD	*Pristimantis romanorum*	NE
Pristimantis katoptroides	EN	*Pristimantis nyctophylax*	VU	*Pristimantis roni*	NE
Pristimantis kichwarum	LC	*Pristimantis ocellatus*	DD	*Pristimantis rosadoi*	VU
Pristimantis kuri	NE	*Pristimantis ocreatus*	VU	*Pristimantis rubicundus*	EN
Pristimantis labiosus	NT	*Pristimantis omeviridis*	LC	*Pristimantis rufoviridis*	NE
Pristimantis lacrimosus	LC	*Pristimantis onorei*	DD	*Pristimantis ruidus*	DD
Pristimantis lanthanites	LC	*Pristimantis orcesi*	VU	*Pristimantis sacharuna*	DD
Pristimantis latericius	DD	*Pristimantis orestes*	EN	*Pristimantis sambalan*	NE
Pristimantis laticlavius	DD	*Pristimantis ornatissimus*	VU	*Pristimantis saturninoi*	NE
Pristimantis latidiscus	VU	*Pristimantis orphnolaimus*	DD	*Pristimantis schultei*	NE
Pristimantis leoni	LC	*Pristimantis ortizi*	DD	*Pristimantis scolodiscus*	DD
Pristimantis leucopus	DD	*Pristimantis pahuma*	EN	*Pristimantis serendipitus*	DD
Pristimantis librarius	DD	*Pristimantis paquishae*	NE	*Pristimantis simonbolivari*	EN
Pristimantis limoncochensis	LC	*Pristimantis parvillus*	NT	*Pristimantis sirnigeli*	NE
Pristimantis lividus	EN	*Pristimantis pastazensis*	EN	*Pristimantis skydmainos*	DD

SPECIES	IUCN STATUS	SPECIES	IUCN STATUS	SPECIES	IUCN STATUS
Pristimantis sobetes	DD	*Rhinella alata*	NE	*Trachycephalus coriaceus*	LC
Pristimantis spinosus	EN	*Rhinella amabilis*	CR	*Trachycephalus cunauaru*	LC
Pristimantis sternothylax	NE	*Rhinella ceratophrys*	DD	*Trachycephalus jordani*	LC
Pristimantis subsigillatus	NT	*Rhinella dapsilis*	DD	*Trachycephalus macrotis*	LC
Pristimantis supernatis	DD	*Rhinella festae*	DD	*Trachycephalus quadrangulum*	LC
Pristimantis surdus	VU	*Rhinella horribilis*	LC	*Vitreorana ritae*	DD
Pristimantis tenebrionis	VU	*Rhinella margaritifera*	LC		
Pristimantis thymalopsoides	VU	*Rhinella marina*	LC		
Pristimantis thymelensis	NT	*Rhinella poeppigii*	DD		
Pristimantis tinajillas	DD	*Rhinella roqueana*	DD		
Pristimantis tinguichaca	NE	*Rulyrana flavopunctata*	LC		
Pristimantis trachyblepharis	LC	*Rulyrana mcdiarmidi*	NE		
Pristimantis truebae	EN	*Sachatamia albomaculata*	DD		
Pristimantis tungurahua	NE	*Sachatamia ilex*	DD		
Pristimantis unistrigatus	LC	*Sachatamia orejuela*	DD		
Pristimantis variabilis	LC	*Scinax cruentomma*	LC		
Pristimantis ventrimarmoratus	LC	*Scinax funereus*	LC		
Pristimantis verecundus	NT	*Scinax garbei*	LC		
Pristimantis versicolor	EN	*Scinax quinquefasciatus*	LC		
Pristimantis vertebralis	VU	*Scinax ruber*	LC		
Pristimantis vidua	EN	*Scinax sugillatus*	LC		
Pristimantis walkeri	LC	*Smilisca phaeota*	LC		
Pristimantis waoranii	DD	*Sphaenorhynchus carneus*	DD		
Pristimantis w-nigrum	EN	*Sphaenorhynchus lacteus*	DD		
Pristimantis yanezi	DD	*Strabomantis anatipes*	VU		
Pristimantis yumbo	NE	*Strabomantis anomalus*	NT		
Rana bwana	NT	*Strabomantis cerastes*	NT		
Rana palmipes	NT	*Strabomantis cornutus*	LC		
Rana vaillanti	LC	*Strabomantis helonotus*	DD		
Ranitomeya reticulata	DD	*Strabomantis necerus*	VU		
Ranitomeya variabilis	LC	*Strabomantis sulcatus*	LC		
Ranitomeya ventrimaculata	LC	*Synapturanus rabus*	DD		
Rhaebo andinophrynoides	EN	*Telmatobius cirrhacelis*	CR		
Rhaebo blombergi	EN	*Telmatobius niger*	CR		
Rhaebo caeruleostictus	VU	*Telmatobius vellardi*	DD		
Rhaebo colomai	EN	*Tepuihyla tuberculosa*	DD		
Rhaebo ecuadorensis	DD	*Teratohyla amelie*	DD		
Rhaebo guttatus	VU	*Teratohyla midas*	LC		
Rhaebo haematiticus	LC	*Teratohyla pulverata*	DD		
Rhaebo olallai	CR	*Teratohyla spinosa*	DD		

Table S2. Trait data used to measure functional distinctiveness and functional β-diversity in this study. All data were obtained from the portal BIOWEB (http://bioweb.bio) and complemented with information from Oliveira et al (2017)*.

Trait	**Description – Range or Categories**
Body-size (snout–vent length)	Males (11.1 – 160 mm), Females (13 – 194 mm)
Overall diel period as active	Diurnal, Nocturnal and Crepuscular
Habitat	Aquatic, Arboreal, Fossorial and Terrestrial
Breeding strategy	Direct reproduction and Larval development

* Oliveira, B.F., V.A. São-Pedro, G. Santos-Barrera, C. Penone, and G.C. Costa. 2017. AmphiBIO, a global database for amphibian ecological traits. Scientific data 4:170123.

Table S3. List of sample sizes of occurrences (***n***) used in species distribution modeling; we modeled species with at least five unique records. It also includes information on metrics used to evaluate the models: Area Under the Curve (AUC) of the receiver of a Receiver Operating Characteristic plot for test occurrences (i.e., the mean of the *k* test AUCs [**avg.test.AUC**]); omission rates implemented at the10 percentile training presence threshold (10pct; i.e., mean of all *k* test 10pct omission rates [**avg.test.or10pct**]), and Akaike Information Criterion corrected for finite sample sizes (**AICc**). Species models with avg.test.AUC scores of < 0.70 were assigned as NM_1 (i.e., first set of species not modeled), whereas species with less than five unique records were assigned as NM_2 (i.e., second set of species not modeled (see main text)*****.

Species	***n***	**avg.test.AUC**	**avg.test.or10pct**	**AICc**
Adelophryne adiastola	1	NM_2	NM_2	NM_2
Adenomera andreae	232	0.823	0.18	4061.79
Adenomera hylaedactyla	26	0.748	0.50	521.74
Agalychnis buckleyi	10	NM_1	NM_1	NM_1
Agalychnis hulli	33	0.829	0.21	586.87
Agalychnis psilopygion	5	0.914	0.60	117.54
Agalychnis spurrelli	44	0.902	0.26	675.61
Allobates femoralis	95	0.696	0.36	1623.95
Allobates fratisenescus	15	0.815	0.53	273.86
Allobates insperatus	149	0.806	0.14	2635.91
Allobates kingsburyi	57	0.882	0.16	812.36
Allobates talamancae	10	0.806	0.50	178.12
Allobates trilineatus	11	0.753	0.30	257.50
Allobates zaparo	70	0.830	0.06	1155.10
Amazophrynella minuta	84	0.740	0.23	1594.27
Ameerega bilinguis	118	0.775	0.15	1769.14
Ameerega hahneli	89	0.857	0.13	1450.47
Ameerega parvula	105	0.778	0.10	1699.48
Atelopus angelito	2	NM_2	NM_2	NM_2
Atelopus arthuri	1	NM_2	NM_2	NM_2
Atelopus balios	6	0.930	0.83	131.95
Atelopus bomolochos	26	0.883	0.29	524.73
Atelopus boulengeri	6	0.764	0.50	136.79
Atelopus coynei	5	0.794	0.40	117.02

Atelopus elegans	24	0.908	0.19	477.45
Atelopus exiguus	8	0.904	0.25	175.44
Atelopus guanujo	2	NM_2	NM_2	NM_2
Atelopus halihelos	1	NM_2	NM_2	NM_2
Atelopus ignescens	19	0.868	0.24	375.75
Atelopus longirostris	17	0.795	0.25	357.32
Atelopus lynchi	1	NM_2	NM_2	NM_2
Atelopus mindoensis	6	0.959	0.50	138.16
Atelopus nanay	8	0.975	0.33	126.26
Atelopus nepiozomus	4	NM_2	NM_2	NM_2
Atelopus orcesi	1	NM_2	NM_2	NM_2
Atelopus pachydermus	1	NM_2	NM_2	NM_2
Atelopus palmatus	11	0.818	0.38	196.38
Atelopus pastuso	11	0.915	0.27	224.84
Atelopus petersi	7	0.943	0.40	131.33
Atelopus planispina	3	NM_2	NM_2	NM_2
Atelopus podocarpus	11	0.845	0.50	241.79
Atelopus spumarius	32	0.851	0.27	652.82
Barycholos pulcher	59	0.855	0.16	1276.77
Boana alfaroi	84	0.762	0.12	1595.44
Boana almendarizae	140	0.930	0.13	1479.36
Boana boans	59	0.795	0.21	1320.60
Boana calcarata	102	0.763	0.12	1832.26
Boana cinerascens	191	0.891	0.11	3320.53
Boana fasciata	74	0.894	0.13	1245.46
Boana geographica	238	0.792	0.14	4119.61
Boana lanciformis	226	0.791	0.08	4158.74
Boana maculateralis	38	NM_1	NM_1	NM_1
Boana nympha	36	0.715	0.39	800.43
Boana pellucens	138	0.885	0.11	2383.55
Boana picturata	61	0.909	0.53	840.24
Boana punctata	47	0.765	0.05	937.21
Boana rosenbergi	110	0.884	0.14	1925.41
Boana rubracyla	1	NM_2	NM_2	NM_2
Centrolene bacatum	9	0.687	0.60	123.25
Centrolene ballux	9	0.942	0.25	163.72
Centrolene buckleyi	34	0.909	0.15	614.41
Centrolene charapita	7	NM_1	NM_1	NM_1
Centrolene condor	9	0.705	0.80	110.80
Centrolene geckoideum	3	NM_2	NM_2	NM_2
Centrolene gemmatum	1	NM_2	NM_2	NM_2
Centrolene heloderma	8	0.965	0.43	187.72
Centrolene lynchi	11	0.988	0.40	168.22
Centrolene peristictum	10	0.955	0.53	221.98

Centrolene pipilatum	7	0.935	0.50	144.63
Centrolene scirtetes	1	NM_2	NM_2	NM_2
Ceratophrys cornuta	9	0.777	0.38	223.71
Ceratophrys stolzmanni	14	0.723	0.50	206.60
Ceratophrys testudo	1	NM_2	NM_2	NM_2
Chiasmocleis anatipes	6	0.775	0.33	146.19
Chiasmocleis antenori	22	0.767	0.25	372.71
Chiasmocleis bassleri	60	0.775	0.20	930.90
Chiasmocleis parkeri	23	0.893	0.46	282.75
Chiasmocleis ventrimaculata	10	0.688	0.50	304.77
Chimerella mariaelenae	47	0.900	0.11	609.05
Cochranella balionota	2	NM_2	NM_2	NM_2
Cochranella litoralis	1	NM_2	NM_2	NM_2
Cochranella mache	10	0.916	0.78	300.80
Cochranella resplendens	7	NM_1	NM_1	NM_1
Craugastor longirostris	104	0.953	0.13	1744.32
Cruziohyla calcarifer	9	0.984	0.38	166.17
Cruziohyla craspedopus	22	0.771	0.11	419.58
Ctenophryne aequatorialis	6	0.909	1.00	88.86
Ctenophryne aterrima	2	NM_2	NM_2	NM_2
Ctenophryne geayi	1	NM_2	NM_2	NM_2
Dendropsophus bifurcus	205	0.843	0.13	3480.70
Dendropsophus bokermanni	25	0.748	0.13	582.48
Dendropsophus brevifrons	60	0.734	0.10	1222.23
Dendropsophus carnifex	86	0.937	0.09	1103.51
Dendropsophus ebraccatus	25	0.859	0.28	404.69
Dendropsophus gryllatus	1	NM_2	NM_2	NM_2
Dendropsophus marmoratus	71	0.914	0.10	1428.89
Dendropsophus minutus	75	0.947	0.12	1168.66
Dendropsophus miyatai	17	NM_1	NM_1	NM_1
Dendropsophus parviceps	179	0.917	0.14	3296.24
Dendropsophus reticulatus	99	0.902	0.17	2141.65
Dendropsophus rhodopeplus	110	0.931	0.12	2294.78
Dendropsophus riveroi	6	NM_1	NM_1	NM_1
Dendropsophus sarayacuensis	129	0.927	0.08	2420.05
Dendropsophus shiwiarum	25	NM_1	NM_1	NM_1
Dendropsophus triangulum	31	0.734	0.19	439.59
Diasporus gularis	19	0.957	0.21	280.34
Ecnomiohyla phantasmagoria	1	NM_2	NM_2	NM_2
Ectopoglossus confusus	6	0.976	0.50	137.18
Edalorhina perezi	68	0.768	0.12	1231.99
Engystomops coloradorum	31	0.981	0.14	262.90
Engystomops guayaco	24	0.826	0.58	414.12

Engystomops montubio	43	0.891	0.09	721.83
Engystomops petersi	223	0.948	0.13	2931.30
Engystomops pustulatus	66	0.856	0.20	1159.43
Engystomops puyango	21	0.938	0.53	328.14
Engystomops randi	43	0.895	0.30	658.39
Epipedobates anthonyi	142	0.910	0.17	2117.60
Epipedobates boulengeri	167	0.913	0.17	2293.51
Epipedobates darwinwallacei	34	0.948	0.32	289.13
Epipedobates espinosai	42	0.911	0.14	466.89
Epipedobates machalilla	101	0.839	0.22	1499.21
Epipedobates tricolor	52	0.973	0.08	446.26
Espadarana audax	22	0.925	0.33	476.21
Espadarana callistomma	28	0.924	0.28	360.65
Espadarana durrellorum	28	0.748	0.40	420.15
Espadarana prosoblepon	177	0.909	0.16	2140.64
Excidobates captivus	5	NM_1	NM_1	NM_1
Excidobates condor	10	0.873	0.88	251.47
Gastrotheca andaquiensis	2	NM_2	NM_2	NM_2
Gastrotheca angustifrons	2	NM_2	NM_2	NM_2
Gastrotheca cornuta	2	NM_2	NM_2	NM_2
Gastrotheca dendronastes	1	NM_2	NM_2	NM_2
Gastrotheca espeletia	6	0.868	0.33	164.77
Gastrotheca guentheri	5	0.961	0.40	114.74
Gastrotheca lateonota	9	0.977	0.50	102.97
Gastrotheca litonedis	25	0.884	0.15	388.42
Gastrotheca lojana	31	0.915	0.08	569.77
Gastrotheca longipes	11	NM_1	NM_1	NM_1
Gastrotheca orophylax	13	0.965	0.33	209.62
Gastrotheca plumbea	15	0.888	0.67	316.39
Gastrotheca pseustes	125	0.891	0.12	2545.79
Gastrotheca psychrophila	5	0.877	0.50	89.16
Gastrotheca riobambae	105	0.934	0.09	1826.35
Gastrotheca testudinea	14	0.883	0.21	343.26
Gastrotheca weinlandii	4	NM_2	NM_2	NM_2
Hamptophryne boliviana	17	0.686	0.36	318.13
Hemiphractus bubalus	21	0.881	0.25	460.34
Hemiphractus fasciatus	3	NM_2	NM_2	NM_2
Hemiphractus helioi	2	NM_2	NM_2	NM_2
Hemiphractus proboscideus	25	0.798	0.27	550.46
Hemiphractus scutatus	34	0.729	0.18	799.50
Hyalinobatrachium aureoguttatum	17	0.855	0.23	310.36
Hyalinobatrachium chirripoi	9	0.825	0.40	117.91
Hyalinobatrachium fleischmanni	35	0.825	0.17	603.30

Hyalinobatrachium iaspidiense	5	0.741	0.50	102.01
Hyalinobatrachium munozorum	9	0.703	0.33	238.59
Hyalinobatrachium pellucidum	18	0.888	0.58	494.61
Hyalinobatrachium ruedai	5	NM_1	NM_1	NM_1
Hyalinobatrachium valerioi	11	0.890	0.50	246.73
Hyalinobatrachium yaku	6	0.762	0.75	101.95
Hyloscirtus albopunctulatus	16	NM_1	NM_1	NM_1
Hyloscirtus alytolylax	103	0.874	0.26	1292.06
Hyloscirtus condor	6	NM_1	NM_1	NM_1
Hyloscirtus criptico	14	0.776	0.50	157.23
Hyloscirtus larinopygion	12	0.928	0.63	185.87
Hyloscirtus lindae	10	0.754	0.78	242.69
Hyloscirtus mashpi	3	NM_2	NM_2	NM_2
Hyloscirtus pacha	6	0.972	0.40	115.90
Hyloscirtus palmeri	23	0.850	0.69	340.79
Hyloscirtus pantostictus	19	0.924	0.40	188.79
Hyloscirtus phyllognathus	91	0.923	0.10	1177.30
Hyloscirtus princecharlesi	1	NM_2	NM_2	NM_2
Hyloscirtus psarolaimus	18	0.896	0.60	361.28
Hyloscirtus ptychodactylus	6	0.770	0.40	121.31
Hyloscirtus staufferorum	9	0.952	0.43	190.33
Hyloscirtus tigrinus	5	NM_1	NM_1	NM_1
Hyloscirtus torrenticola	1	NM_2	NM_2	NM_2
Hyloxalus anthracinus	12	0.924	0.50	233.94
Hyloxalus awa	102	0.906	0.12	1624.14
Hyloxalus bocagei	42	0.819	0.11	666.39
Hyloxalus breviquartus	2	NM_2	NM_2	NM_2
Hyloxalus cevallosi	42	0.932	0.41	468.40
Hyloxalus delatorreae	9	0.865	0.43	149.41
Hyloxalus elachyhistus	43	0.833	0.25	806.39
Hyloxalus exasperatus	3	NM_2	NM_2	NM_2
Hyloxalus fallax	1	NM_2	NM_2	NM_2
Hyloxalus fuliginosus	5	0.966	0.60	115.38
Hyloxalus infraguttatus	95	0.904	0.16	1410.19
Hyloxalus italoi	40	0.859	0.10	667.02
Hyloxalus jacobuspetersi	45	0.893	0.13	828.83
Hyloxalus lehmanni	9	0.885	0.38	189.78
Hyloxalus maculosus	21	0.909	0.26	308.92
Hyloxalus maquipucuna	1	NM_2	NM_2	NM_2
Hyloxalus marmoreoventris	1	NM_2	NM_2	NM_2
Hyloxalus mystax	9	0.819	0.43	158.36
Hyloxalus nexipus	26	0.906	0.19	445.42

Hyloxalus peculiaris	1	NM_2	NM_2	NM_2
Hyloxalus pulchellus	47	0.927	0.13	667.51
Hyloxalus sauli	63	0.838	0.21	948.71
Hyloxalus shuar	13	0.932	0.58	483.45
Hyloxalus toachi	30	0.936	0.19	510.89
Hyloxalus vertebralis	79	0.903	0.14	1307.32
Hyloxalus yasuni	71	0.752	0.19	1254.22
Incilius coniferus	21	0.964	0.50	199.92
Leptodactylus discodactylus	92	0.709	0.23	1554.01
Leptodactylus knudseni	37	0.812	0.13	776.12
Leptodactylus labrosus	79	0.860	0.18	1579.22
Leptodactylus leptodactyloides	52	0.751	0.13	1207.54
Leptodactylus melanonotus	19	0.824	0.33	455.99
Leptodactylus mystaceus	47	0.688	0.19	1019.58
Leptodactylus pentadactylus	73	0.749	0.07	1466.43
Leptodactylus peritoaktites	3	NM_2	NM_2	NM_2
Leptodactylus petersii	6	0.711	0.50	148.82
Leptodactylus rhodomerus	8	0.721	0.43	186.13
Leptodactylus rhodomystax	57	0.919	0.17	1141.58
Leptodactylus stenodema	8	0.721	0.25	193.87
Leptodactylus ventrimaculatus	102	0.893	0.18	1870.62
Leptodactylus wagneri	228	0.793	0.12	4045.71
Leucostethus fugax	14	0.771	0.27	299.05
Lithodytes lineatus	134	0.774	0.12	2412.57
Lynchius flavomaculatus	9	0.867	0.43	160.64
Lynchius simmonsi	10	0.729	1.00	260.77
Niceforonia babax	2	NM_2	NM_2	NM_2
Niceforonia brunneus	6	0.962	0.67	154.22
Niceforonia dolops	4	NM_2	NM_2	NM_2
Niceforonia elassodiscus	17	0.892	0.36	368.90
Niceforonia nigrovittatus	121	0.832	0.10	2160.99
Niceforonia peraccai	6	0.971	0.33	153.88
Noblella coloma	1	NM_2	NM_2	NM_2
Noblella heyeri	9	NM_1	NM_1	NM_1
Noblella lochites	24	0.810	0.42	573.00
Noblella myrmecoides	23	0.734	0.49	411.58
Noblella personina	17	0.950	0.75	166.95
Nyctimantis rugiceps	18	0.741	0.23	401.41
Nymphargus anomalus	1	NM_2	NM_2	NM_2
Nymphargus cariticommatus	6	0.893	0.33	144.48
Nymphargus chancas	1	NM_2	NM_2	NM_2
Nymphargus cochranae	52	0.899	0.16	692.87
Nymphargus grandisonae	45	0.937	0.15	662.32

Nymphargus griffithsi	32	0.929	0.21	607.28
Nymphargus lasgralarias	1	NM_2	NM_2	NM_2
Nymphargus laurae	1	NM_2	NM_2	NM_2
Nymphargus mariae	22	0.871	0.17	386.57
Nymphargus megacheirus	4	NM_2	NM_2	NM_2
Nymphargus posadae	12	0.848	0.63	271.08
Nymphargus siren	26	0.941	0.20	405.37
Nymphargus sucre	1	NM_2	NM_2	NM_2
Oophaga sylvatica	115	0.894	0.18	1461.00
Oreobates quixensis	163	0.865	0.13	2951.10
Osornophryne angel	5	NM_1	NM_1	NM_1
Osornophryne antisana	11	0.873	0.40	214.16
Osornophryne bufoniformis	13	0.907	0.30	207.73
Osornophryne cofanorum	3	NM_2	NM_2	NM_2
Osornophryne guacamayo	37	0.936	0.18	461.35
Osornophryne occidentalis	13	0.937	0.33	293.80
Osornophryne talipes	1	NM_2	NM_2	NM_2
Osteocephalus alboguttatus	16	0.876	0.15	295.33
Osteocephalus buckleyi	80	0.800	0.11	1544.59
Osteocephalus cabrerai	7	0.741	0.33	145.80
Osteocephalus cannatellai	29	0.767	0.29	587.46
Osteocephalus deridens	44	0.818	0.16	810.12
Osteocephalus duellmani	6	0.820	0.60	116.77
Osteocephalus festae	17	0.697	0.69	563.41
Osteocephalus fuscifacies	56	0.856	0.22	1103.87
Osteocephalus mutabor	48	0.867	0.11	846.44
Osteocephalus planiceps	189	0.844	0.16	2754.64
Osteocephalus taurinus	98	0.908	0.11	2090.80
Osteocephalus verruciger	97	0.934	0.13	1238.57
Osteocephalus vilmae	5	NM_1	NM_1	NM_1
Osteocephalus yasuni	69	0.878	0.19	958.38
Paruwrobates erythromos	1	NM_2	NM_2	NM_2
Paruwrobates whymperi	2	NM_2	NM_2	NM_2
Phyllomedusa coelestis	5	0.824	0.50	100.95
Phyllomedusa ecuatoriana	9	0.853	0.44	237.20
Phyllomedusa tarsius	61	0.825	0.19	1118.93
Phyllomedusa tomopterna	72	0.747	0.14	1436.80
Phyllomedusa vaillantii	93	0.799	0.18	1626.61
Pipa	15	0.739	0.07	328.71
Pristimantis acerus	5	0.898	0.75	98.34
Pristimantis achatinus	597	0.914	0.11	8964.24
Pristimantis actites	68	0.937	0.09	449.56
Pristimantis acuminatus	56	0.708	0.23	1093.08
Pristimantis albujai	1	NM_2	NM_2	NM_2

Pristimantis allpapuyu	1	NM_2	NM_2	NM_2
Pristimantis almendariz	2	NM_2	NM_2	NM_2
Pristimantis altamazonicus	138	0.798	0.12	2417.75
Pristimantis altamnis	86	0.943	0.15	1038.69
Pristimantis andinognomus	22	0.905	0.50	300.30
Pristimantis anemerus	1	NM_2	NM_2	NM_2
Pristimantis apiculatus	3	NM_2	NM_2	NM_2
Pristimantis appendiculatus	89	0.953	0.14	1026.29
Pristimantis ardyae	8	0.917	0.75	91.28
Pristimantis atratus	29	0.869	0.19	455.66
Pristimantis aureolineatus	11	0.738	0.20	235.92
Pristimantis balionotus	1	NM_2	NM_2	NM_2
Pristimantis bambu	43	0.911	0.54	149.38
Pristimantis baryecuus	8	0.877	0.38	256.95
Pristimantis bellae	20	0.865	0.58	299.37
Pristimantis bicantus	152	0.935	0.14	1026.09
Pristimantis brevicrus	43	0.900	0.21	642.36
Pristimantis bromeliaceus	21	0.855	0.24	484.39
Pristimantis buckleyi	41	0.913	0.06	717.39
Pristimantis buenaventura	6	0.940	0.50	128.08
Pristimantis caeruleonotus	11	0.951	0.75	164.68
Pristimantis cajamarcensis	13	0.778	0.63	280.78
Pristimantis calcarulatus	99	0.934	0.21	1130.32
Pristimantis caprifer	8	0.848	0.29	156.78
Pristimantis carlosceroni	1	NM_2	NM_2	NM_2
Pristimantis carvalhoi	34	0.824	0.14	725.92
Pristimantis cedros	10	0.873	0.50	190.89
Pristimantis celator	9	0.888	0.33	239.86
Pristimantis chalceus	41	0.894	0.14	772.88
Pristimantis chloronotus	24	0.947	0.21	477.46
Pristimantis churuwiai	30	0.934	0.29	391.60
Pristimantis citriogaster	36	0.886	0.85	308.59
Pristimantis colodactylus	31	0.821	0.36	505.87
Pristimantis colomai	15	0.936	0.50	174.97
Pristimantis colonensis	16	0.899	0.65	294.15
Pristimantis condor	50	0.886	0.12	739.38
Pristimantis conspicillatus	272	0.845	0.17	4396.82
Pristimantis cremnobates	42	0.886	0.25	652.04
Pristimantis crenunguis	62	0.921	0.14	866.09
Pristimantis croceoinguinis	118	0.840	0.13	2164.89
Pristimantis crucifer	36	0.920	0.15	552.30
Pristimantis cryophilius	37	0.905	0.14	594.53
Pristimantis cryptomelas	18	0.847	0.57	304.70
Pristimantis curtipes	191	0.907	0.11	3101.93

Pristimantis degener	13	0.905	0.53	296.83
Pristimantis delius	56	0.801	0.13	1131.87
Pristimantis devillei	74	0.919	0.18	1145.24
Pristimantis diadematus	130	0.789	0.11	2262.74
Pristimantis dissimulatus	3	NM_2	NM_2	NM_2
Pristimantis duellmani	18	0.838	0.34	332.50
Pristimantis ecuadorensis	5	0.983	0.60	129.50
Pristimantis enigmaticus	25	0.842	0.28	489.64
Pristimantis eremitus	38	0.948	0.21	530.21
Pristimantis eriphus	65	0.891	0.32	649.51
Pristimantis ernesti	6	0.998	1.00	86.85
Pristimantis erythros	1	NM_2	NM_2	NM_2
Pristimantis esmeraldas	50	0.924	0.14	610.21
Pristimantis eugeniae	41	0.963	0.10	585.27
Pristimantis exoristus	6	0.887	0.60	124.87
Pristimantis festae	38	0.922	0.18	566.57
Pristimantis floridus	43	0.873	0.21	616.69
Pristimantis galdi	70	0.899	0.23	1081.21
Pristimantis ganonotus	17	0.940	0.13	359.25
Pristimantis gentryi	12	0.963	0.42	209.46
Pristimantis gladiator	25	0.894	0.15	433.87
Pristimantis glandulosus	23	0.961	0.15	391.91
Pristimantis gualacenio	1	NM_2	NM_2	NM_2
Pristimantis hamiotae	3	NM_2	NM_2	NM_2
Pristimantis hampatusami	6	0.910	0.50	144.48
Pristimantis hectus	6	0.833	1.00	115.19
Pristimantis huicundo	23	0.920	0.40	223.78
Pristimantis ignicolor	7	0.904	0.33	167.20
Pristimantis illotus	26	0.933	0.30	391.92
Pristimantis incanus	18	0.945	0.07	307.41
Pristimantis incomptus	173	0.886	0.13	2224.25
Pristimantis inusitatus	20	0.962	0.33	214.02
Pristimantis katoptroides	30	0.886	0.15	585.55
Pristimantis kichwarum	321	0.781	0.11	2151.51
Pristimantis kuri	2	NM_2	NM_2	NM_2
Pristimantis labiosus	105	0.916	0.22	1036.77
Pristimantis lacrimosus	24	NM_1	NM_1	NM_1
Pristimantis lanthanites	163	0.800	0.12	2700.98
Pristimantis latericius	1	NM_2	NM_2	NM_2
Pristimantis laticlavius	36	0.904	0.17	409.28
Pristimantis latidiscus	120	0.913	0.09	1270.17
Pristimantis leoni	148	0.895	0.24	1233.72
Pristimantis leucopus	8	0.918	0.86	200.42
Pristimantis librarius	45	NM_1	NM_1	NM_1

Pristimantis limoncochensis	29	0.790	0.19	604.01
Pristimantis lividus	13	0.947	0.50	178.07
Pristimantis llanganati	16	0.916	0.67	148.22
Pristimantis loujosti	1	NM_2	NM_2	NM_2
Pristimantis loustes	1	NM_2	NM_2	NM_2
Pristimantis lucidosignatus	2	NM_2	NM_2	NM_2
Pristimantis luscombei	62	0.699	0.20	1106.68
Pristimantis luteolateralis	62	0.954	0.13	868.69
Pristimantis lymani	84	0.823	0.23	1580.47
Pristimantis malkini	107	0.869	0.13	1989.63
Pristimantis marcoreyesi	5	0.986	0.80	126.60
Pristimantis martiae	66	0.811	0.10	1222.50
Pristimantis matidiktyo	36	0.779	0.11	684.46
Pristimantis mazar	30	0.911	0.38	182.31
Pristimantis metabates	1	NM_2	NM_2	NM_2
Pristimantis miktos	26	0.748	0.17	602.46
Pristimantis mindo	24	0.972	0.28	324.13
Pristimantis minimus	1	NM_2	NM_2	NM_2
Pristimantis modipeplus	11	0.935	0.43	217.88
Pristimantis munozi	1	NM_2	NM_2	NM_2
Pristimantis muranunka	7	0.986	0.50	88.23
Pristimantis muricatus	11	0.806	0.58	207.48
Pristimantis muscosus	10	0.867	1.00	172.53
Pristimantis mutabilis	8	0.752	1.00	93.39
Pristimantis nephophilus	1	NM_2	NM_2	NM_2
Pristimantis nietoi	14	0.890	0.83	131.05
Pristimantis nigrogriseus	29	0.907	0.18	515.94
Pristimantis nimbus	1	NM_2	NM_2	NM_2
Pristimantis nyctophylax	41	0.909	0.16	612.78
Pristimantis ocellatus	2	NM_2	NM_2	NM_2
Pristimantis ocreatus	58	0.868	0.43	378.07
Pristimantis omeviridis	18	0.780	0.14	336.53
Pristimantis onorei	3	NM_2	NM_2	NM_2
Pristimantis orcesi	12	0.846	0.48	242.55
Pristimantis orestes	91	0.869	0.13	1230.46
Pristimantis ornatissimus	12	0.888	0.58	333.10
Pristimantis orphnolaimus	9	0.728	0.22	220.92
Pristimantis ortizi	11	0.869	0.63	148.38
Pristimantis pahuma	1	NM_2	NM_2	NM_2
Pristimantis paquishae	1	NM_2	NM_2	NM_2
Pristimantis parvillus	138	0.943	0.12	1179.51
Pristimantis pastazensis	2	NM_2	NM_2	NM_2
Pristimantis pataikos	1	NM_2	NM_2	NM_2
Pristimantis paululus	19	0.767	0.39	431.09

Pristimantis pecki	13	NM_1	NM_1	NM_1
Pristimantis percultus	1	NM_2	NM_2	NM_2
Pristimantis peruvianus	27	0.853	0.22	614.58
Pristimantis petersi	31	0.937	0.28	356.10
Pristimantis philipi	5	0.955	0.50	
Pristimantis phoxocephalus	90	0.889	0.25	1433.37
Pristimantis pichincha	5	0.770	0.60	110.13
Pristimantis pinchaque	1	NM_2	NM_2	NM_2
Pristimantis prolatus	122	0.939	0.09	1108.39
Pristimantis prometeii	9	0.981	0.50	69.23
Pristimantis proserpens	10	0.905	0.40	268.30
Pristimantis pseudoacuminatus	7	0.779	0.33	141.12
Pristimantis pteridophilus	93	0.916	0.16	797.27
Pristimantis pugnax	6	0.915	0.33	139.28
Pristimantis punzan	2	NM_2	NM_2	NM_2
Pristimantis puruscafeum	1	NM_2	NM_2	NM_2
Pristimantis pycnodermis	40	0.884	0.31	409.89
Pristimantis pyrrhomerus	38	0.906	0.27	604.49
Pristimantis quaquaversus	163	0.895	0.14	1910.76
Pristimantis quinquagesimus	30	0.958	0.32	449.04
Pristimantis rhodoplichus	15	0.965	0.83	102.29
Pristimantis rhodostichus	11	0.767	0.50	250.20
Pristimantis riveti	84	0.911	0.14	1279.79
Pristimantis romanorum	12	0.944	0.83	199.83
Pristimantis roni	1	NM_2	NM_2	NM_2
Pristimantis rosadoi	19	0.907	0.18	408.02
Pristimantis rubicundus	29	0.925	0.27	478.61
Pristimantis rufoviridis	6	0.928	0.50	90.45
Pristimantis ruidus	1	NM_2	NM_2	NM_2
Pristimantis sacharuna	1	NM_2	NM_2	NM_2
Pristimantis sambalan	1	NM_2	NM_2	NM_2
Pristimantis saturninoi	1	NM_2	NM_2	NM_2
Pristimantis schultei	9	0.849	0.33	222.26
Pristimantis scolodiscus	16	0.882	0.37	281.46
Pristimantis serendipitus	24	0.828	0.32	481.43
Pristimantis simonbolivari	16	0.945	0.67	167.62
Pristimantis sirnigeli	11	0.901	0.53	224.36
Pristimantis skydmainos	7	0.818	0.43	243.39
Pristimantis sobetes	66	0.949	0.14	716.29
Pristimantis spinosus	14	0.864	0.54	316.76
Pristimantis sternothylax	2	NM_2	NM_2	NM_2
Pristimantis subsigillatus	49	0.903	0.22	924.65
Pristimantis supernatis	1	NM_2	NM_2	NM_2

Pristimantis surdus	28	0.920	0.17	492.99
Pristimantis tenebrionis	13	0.910	0.33	277.30
Pristimantis thymalopsoides	1	NM_2	NM_2	NM_2
Pristimantis thymelensis	67	0.944	0.15	706.05
Pristimantis tinajillas	1	NM_2	NM_2	NM_2
Pristimantis tinguichaca	7	0.984	0.29	186.34
Pristimantis trachyblepharis	229	0.872	0.15	2344.27
Pristimantis truebae	31	0.906	0.19	566.62
Pristimantis tungurahua	2	NM_2	NM_2	NM_2
Pristimantis unistrigatus	229	0.915	0.10	4136.22
Pristimantis variabilis	77	0.807	0.12	1578.52
Pristimantis ventrimarmoratus	86	0.923	0.19	1021.89
Pristimantis verecundus	44	0.914	0.09	643.08
Pristimantis versicolor	35	0.863	0.27	551.57
Pristimantis vertebralis	84	0.900	0.16	1090.00
Pristimantis vidua	5	NM_1	NM_1	NM_1
Pristimantis walkeri	110	0.907	0.14	1931.94
Pristimantis waoranii	1	NM_2	NM_2	NM_2
Pristimantis w-nigrum	297	0.896	0.12	5258.46
Pristimantis yanezi	6	0.970	0.50	89.10
Pristimantis yumbo	14	0.851	0.72	409.51
Rana bwana	16	0.887	0.36	315.19
Rana palmipes	53	0.796	0.18	1027.05
Rana vaillanti	12	0.848	0.50	257.36
Ranitomeya reticulata	5	0.685	0.60	113.92
Ranitomeya variabilis	55	0.879	0.13	1099.76
Ranitomeya ventrimaculata	48	0.840	0.13	700.34
Rhaebo andinophrynoides	2	NM_2	NM_2	NM_2
Rhaebo blombergi	8	0.955	0.25	159.00
Rhaebo caeruleostictus	5	0.735	1.00	120.92
Rhaebo colomai	2	NM_2	NM_2	NM_2
Rhaebo ecuadorensis	36	0.859	0.12	811.15
Rhaebo guttatus	9	0.760	0.43	165.09
Rhaebo haematiticus	69	0.947	0.23	1032.12
Rhaebo olallai	5	NM_1	NM_1	NM_1
Rhinella alata	57	0.945	0.28	1062.37
Rhinella amabilis	1	NM_2	NM_2	NM_2
Rhinella ceratophrys	15	0.699	0.20	374.45
Rhinella dapsilis	84	0.746	0.15	1260.15
Rhinella festae	115	0.868	0.06	1683.99
Rhinella horribilis	178	0.831	0.17	3593.46
Rhinella margaritifera	175	0.874	0.14	3575.56
Rhinella marina	167	0.794	0.12	3486.10

Rhinella poeppigii	25	0.833	0.23	519.58
Rhinella roqueana	6	0.750	0.40	143.68
Rulyrana flavopunctata	38	0.887	0.14	644.36
Rulyrana mcdiarmidi	81	0.902	0.17	799.96
Sachatamia albomaculata	10	0.936	0.53	293.75
Sachatamia ilex	25	0.893	0.22	469.39
Sachatamia orejuela	9	0.942	0.38	181.38
Scinax cruentommus	41	0.764	0.11	867.03
Scinax funereus	23	0.775	0.18	524.78
Scinax garbei	118	0.815	0.10	2292.06
Scinax quinquefasciatus	79	0.886	0.13	1588.80
Scinax ruber	267	0.819	0.10	4698.71
Scinax sugillatus	21	0.925	0.32	414.43
Smilisca phaeota	137	0.885	0.14	2535.03
Sphaenorhynchus carneus	1	NM_2	NM_2	NM_2
Sphaenorhynchus lacteus	14	0.728	0.36	330.60
Strabomantis anatipes	3	NM_2	NM_2	NM_2
Strabomantis anomalus	14	0.892	0.36	297.47
Strabomantis cerastes	6	0.802	0.67	143.35
Strabomantis cornutus	14	0.744	0.64	411.58
Strabomantis helonotus	3	NM_2	NM_2	NM_2
Strabomantis necerus	16	0.965	0.31	295.17
Strabomantis sulcatus	58	0.817	0.11	1077.85
Synapturanus rabus	9	0.777	0.33	203.47
Telmatobius cirrhacelis	2	NM_2	NM_2	NM_2
Telmatobius niger	28	0.879	0.19	601.89
Telmatobius vellardi	6	0.852	0.67	145.05
Tepuihyla tuberculosa	12	NM_1	NM_1	NM_1
Teratohyla amelie	13	0.835	0.30	226.66
Teratohyla midas	79	0.879	0.10	1477.66
Teratohyla pulverata	14	0.937	0.25	263.77
Teratohyla spinosa	25	0.901	0.17	379.24
Trachycephalus coriaceus	7	0.752	0.00	125.44
Trachycephalus cunauaru	16	NM_1	NM_1	NM_1
Trachycephalus jordani	75	0.868	0.20	1455.69
Trachycephalus macrotis	18	0.826	0.36	306.10
Trachycephalus quadrangulum	41	0.867	0.32	715.93
Vitreorana ritae	10	0.741	0.40	244.84

**** Records of NM_1 and NM_2 species were also used to calculate β-diversity metrics.***

Table S4 Results of linear models (ANOVA) to determine if differences in mean functional distinctiveness (D_i) between CR species and species in other extinction risk (IUCN) categories were statistically significant. Results are presented separately for Highlands and Lowlands of Ecuador. IUCN categories are as follows: Critically Endangered (CR), Endangered (EN), Vulnerable (VU), Near Threatened (NT), Least Concern (LC). Standard error of estimates (SE), t-values (*t*) and their associated probabilities (*P*) are shown. Significant *P*-values in bold.

REGION	**Extinction risk category**	**Extinction risk category**	**SE**	***t***	***P*-value**
HIGHLANDS	CR	EN	0.027	−1.944	**0.05***
		VU	0.027	−2.768	**<0.01**
		NT	0.024	−3.211	**<0.01**
		LC	0.018	-3.88	**<0.001**
LOWLANDS	CR	EN	0.038	-0.893	>0.05
		VU	0.037	-0.261	>0.05
		NT	0.032	-0.227	>0.05
		LC	0.023	-0.969	>0.05

*marginally significant *P*-value

Table S5 Number of assemblages of Ecuadorian anurans that are expected to become taxonomically, phylogenetically and functionally more similar under two scenarios of species extinctions: Critically endangered (CR) species extinction scenario (CR extinction) and CR and endangered (EN) species extinction scenario (CR-EN extinction).

Diversity Facet	**Scenario**	**no. assemblages**
Taxonomic homogenization	CR extinction	918
	CR–EN extinction	1706
Phylogenetic homogenization	CR extinction	1089
	CR–EN extinction	2080
Functional homogenization	CR extinction	476
	CR–EN extinction	2132

Table S6 Results of separate linear mixed models analyzing the further effect of the sequential removal of endangered species (EN) on taxonomic, phylogenetic and functional homogenization. Categorical coefficient estimates represent departures from the predicted homogenization due to the extinction of critically endangered species (CR). Standard error (SE), *t* values and *P*-values are shown. All *P*-values were significant. Altitude (i.e., lowlands = areas < 1000 m and highlands [Andes] = areas > 1000 m) was included as random categorical factor. Homogenization was calculated as the percentage of negative change in β-diversity.

Effect	**Metric**	**Estimate**	**SE**	***t* value**	***P*-value**
Extinction of CR and EN species	Taxonomic homogenization	–5.14	0.38	–13.53	<0.01
Extinction of CR and EN species	Phylogenetic homogenization	–5.64	0.36	–15.88	<0.01
Extinction of CR and EN species	Functional homogenization	–14.05	1.47	–9.59	<0.01

Figure S1. Bar chart showing the percentage of critically endangered species (**CR**) and non-critically endangered species (**NO CR**) with different breeding strategies: Direct development (yellow color) or Larval development (gray color).

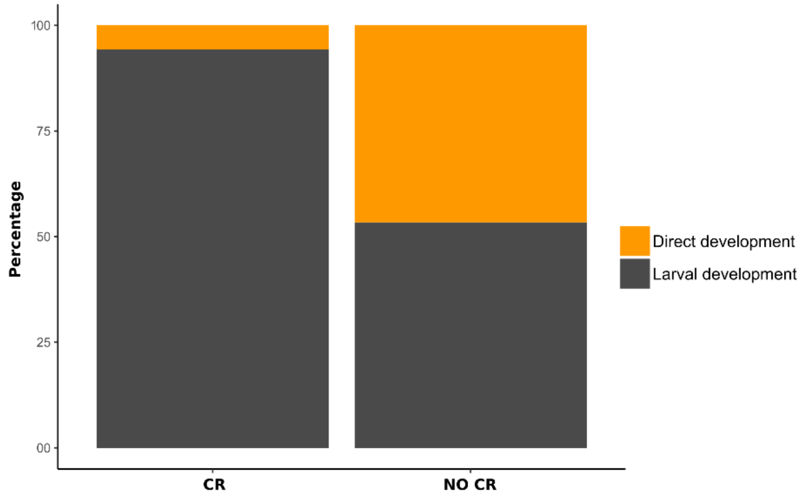


Figure S2. Boxplot showing variation (medians and 25th-75th percentiles) in body size of critically endangered species (CR) vs. non-critically endangered species (NO CR). Species are also classified by sex. Outliers were removed.

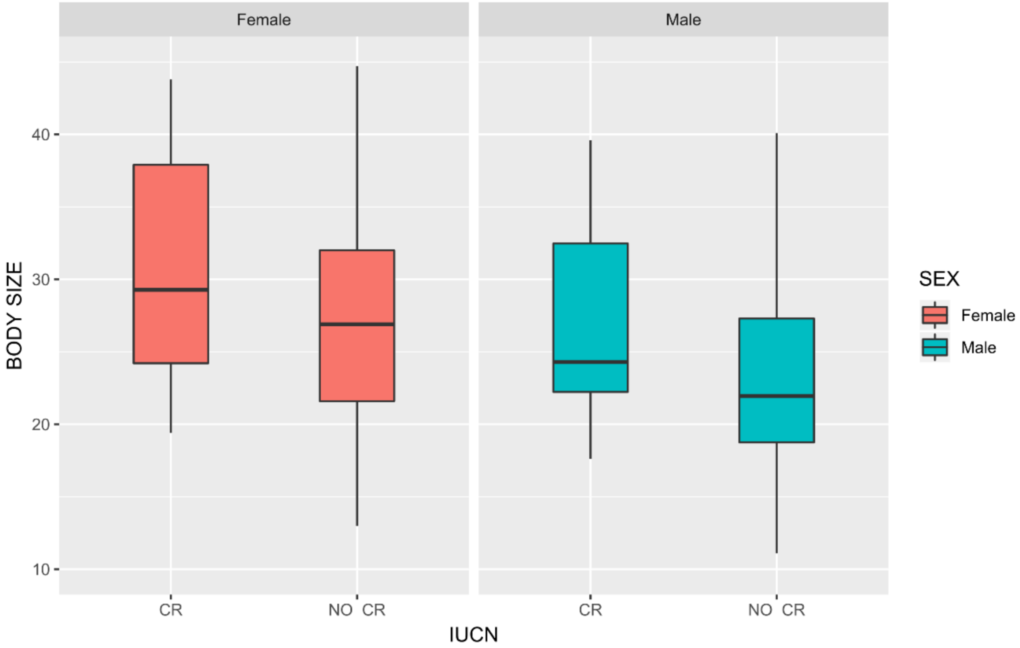


Figure S3. Spatial patterns of IUCN categories in the Ecuadorian anuran assemblages. Critically endangered species (CR) are dominant (i.e., more abundant) in red coloured assemblages, endangered species (EN) in orange coloured assemblages, vulnerable species (VU) in light green coloured assemblages, near threatened species (NT) in dark green coloured assemblages, least concern species (LC) in gray coloured assemblages, and data deficient species (DD) in black coloured assemblages. Dominant species refers to those that, classified under the IUCN categories, are the most numerous within assemblages.

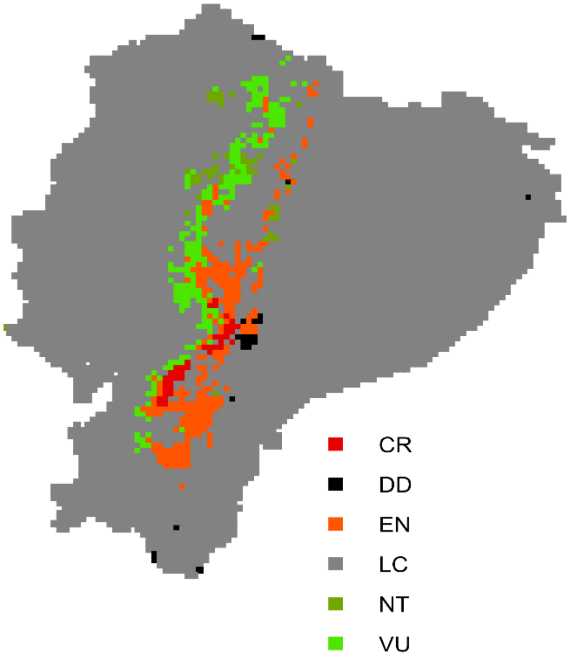


Figure S4 Number of assemblages predicted to become more homogenous under two scenarios of species extinctions: *CR loss* scenario in which critically endangered species (CR) become extinct; *CR-EN loss* scenario in which both CR and endangered species (EN) become extinct. Blue bars show the number of assemblages showing increasing taxonomic homogeneity (TH); gray bars show the number of assemblages showing increasing phylogenetic homogeneity (PH); red bars show the number of assemblages showing increasing functional homogeneity (FH).

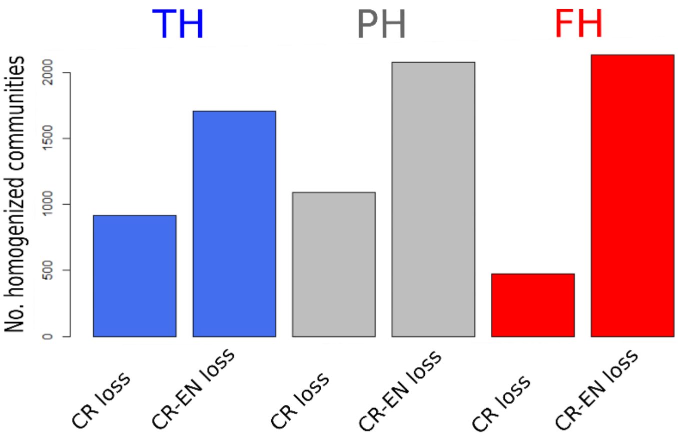
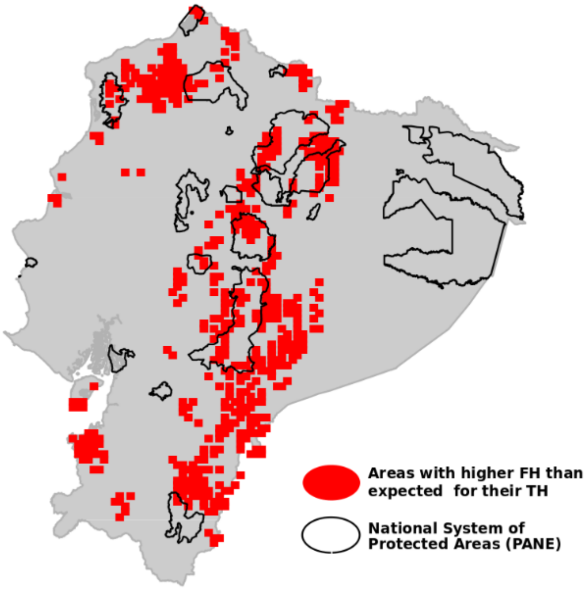


Figure S5 Map of the positive residuals (in red) of the linear regression between functional homogenization (FH) values and taxonomic homogenization (TH) values. The overlap between these residuals and the National System of Protected Areas of Ecuador (PANE) is shown.



Supplementary Material Chapter 3

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Table S1 Sampling efforts of surveys (i.e., hours per person) for each period time (T1, T2, T3) per locality. Time periods are as follow: T1 (1967-1987), T2 (2000-2003) and T3 (2016-2018). Localities are as follow: Bosque Protector Cashca Totoras (BPCT; P1), Pilaló (P2), Paramo of Antisana (P3), Paramo of Guamaní (P4), Quebrada Zapadores (P5), Río Azuela (P6) and Río Faisanes (P7). ND = no data.

LOCALITY/TIME PERIOD	**T1 hours/per.**	**T2 hours/per.**	**T3 hours/per.**
BPCT	ND	537.47	36
Paramo Antisana	ND	40.93	42
Paramo Guamaní	2	45.12	45
Pilaló	25	36.6	48
Quebrada Zapadores	40	58	50
Río Azuela	72	90.82	90
Rio Faisanes	32	39	50
Total	171	847.94	361

Table S2 List of species recorded at the seven sampling localities during the three time periods (T1, T2, T3). Time periods are as follow: T1 (1967-1987), T2 (2000-2003) and T3 (2016-2018). Localities are as follow: Bosque Protector Cashca Totoras (BPCT; P1), Pilaló (P2), Paramo of Antisana (P3), Paramo of Guamaní (P4), Quebrada Zapadores (P5), Río Azuela (P6) and Río Faisanes (P7). Number 1 means presence, 0 means absence.

Species	Locality	T1	T2	T3
Agalychnis buckleyi	Río Azuela	1	1	0
Andinobates abditus	Río Azuela	1	0	0
Atelopus arthuri	BPCT	1	0	0
Atelopus coynei	Pilaló	1	0	0
Atelopus ignescens	Paramo Antisana	1	0	0
Atelopus ignescens	Paramo Guamaní	1	0	0
Atelopus longirostris	Río Faisanes	1	0	0
Atelopus mindoensis	Quebrada Zapadores	1	0	0
Atelopus planispina	Río Azuela	1	0	0
Boana pellucens	Río Faisanes	0	1	0
Boana picturata	Río Faisanes	1	0	0
Centrolene buckleyi	BPCT	1	1	0
Centrolene buckleyi	Pilaló	1	0	0
Centrolene geckoideum	Quebrada Zapadores	1	0	0
Centrolene heloderma	Quebrada Zapadores	1	1	1
Centrolene lynchi	Río Faisanes	1	0	0
Dendropsophus carnifex	Quebrada Zapadores	1	1	1
Dendropsophus carnifex	Río Faisanes	1	1	1
Dendropsophus minutus	Río Azuela	0	1	0
Dendropsophus sarayacuensis	Río Azuela	0	1	1
Epipedobates darwinwallacei	Río Faisanes	1	1	1
Espadarana prosoblepon	Río Faisanes	1	1	1
Gastrotheca guentheri	Quebrada Zapadores	1	0	0
Gastrotheca plumbea	BPCT	1	1	0
Gastrotheca plumbea	Pilaló	1	1	0
Gastrotheca plumbea	Quebrada Zapadores	1	0	0
Gastrotheca pseustes	BPCT	1	1	1
Gastrotheca pseustes	Paramo Antisana	1	1	1
Gastrotheca pseustes	Paramo Guamaní	1	0	0
Gastrotheca weinlandii	Río Azuela	1	0	0
Hemiphractus bubalus	Río Azuela	1	0	0

Hyalinobatrachium pellucidum	Río Azuela	1	0	0
Hyalinobatrachium valerioi	Río Faisanes	1	0	0
Hyloscirtus alytolylax	Río Faisanes	1	1	1
Hyloscirtus phyllognathus	Río Azuela	1	1	1
Hyloscirtus ptychodactylus	Pilaló	1	1	1
Hyloxalus awa	Río Faisanes	1	0	0
Hyloxalus jacobuspetersi	Pilaló	1	0	0
Hyloxalus pulchellus	Río Azuela	1	1	1
Hypodactylus dolops	Río Azuela	1	0	0
Nymphargus anomalus	Río Azuela	1	0	0
Nymphargus grandisonae	Quebrada Zapadores	0	1	1
Nymphargus grandisonae	Río Faisanes	0	1	0
Nymphargus griffithsi	Quebrada Zapadores	1	1	1
Nymphargus megacheirus	Río Azuela	1	0	0
Nymphargus siren	Río Azuela	1	1	1
Osteocephalus verruciger	Río Azuela	1	1	1
Pristimantis achatinus	Río Faisanes	1	1	1
Pristimantis actites	Pilaló	1	1	1
Pristimantis actites	Quebrada Zapadores	0	0	1
Pristimantis appendiculatus	Quebrada Zapadores	1	1	1
Pristimantis calcarulatus	Quebrada Zapadores	0	1	0
Pristimantis calcarulatus	Río Faisanes	1	0	0
Pristimantis crenunguis	Río Faisanes	0	1	0
Pristimantis curtipes	Paramo Antisana	1	1	1
Pristimantis curtipes	Paramo Guamaní	1	1	1
Pristimantis dissimulatus	Quebrada Zapadores	1	0	0
Pristimantis duellmani	Quebrada Zapadores	1	0	0
Pristimantis eugeniae	Quebrada Zapadores	1	1	1
Pristimantis festae	Paramo Guamaní	0	1	1
Pristimantis floridus	Quebrada Zapadores	0	1	0
Pristimantis galdi	Río Azuela	1	0	0
Pristimantis incanus	Río Azuela	1	1	1
Pristimantis incomptus	Río Azuela	1	1	1
Pristimantis kirklandi	Río Azuela	0	1	0
Pristimantis lacrimosus	Río Azuela	0	1	1
Pristimantis lanthanites	Río Azuela	0	0	1
Pristimantis luteolateralis	Río Faisanes	1	1	1
Pristimantis new species	Pilaló	0	0	1
Pristimantis new species2	Río Azuela	0	0	1
Pristimantis nigrogriseus	Río Azuela	0	1	0
Pristimantis nyctophylax	Río Faisanes	1	1	1

Pristimantis orcesi	BPCT	1	0	0
Pristimantis peruvianus	Río Azuela	1	0	0
Pristimantis petersi	Río Azuela	1	1	1
Pristimantis phoxocephalus	Pilaló	1	1	1
Pristimantis phoxocephalus	Quebrada Zapadores	1	0	0
Pristimantis prolatus	Río Azuela	0	0	1
Pristimantis pyrrhomerus	BPCT	1	1	1
Pristimantis pyrrhomerus	Pilaló	0	1	0
Pristimantis quaquaversus	Río Azuela	1	1	1
Pristimantis simonbolivari	BPCT	1	1	1
Pristimantis sobetes	Pilaló	0	1	1
Pristimantis sobetes	Quebrada Zapadores	0	1	0
Pristimantis thymalopsoides	Pilaló	1	0	0
Pristimantis thymelensis	Paramo Guamaní	0	1	1
Pristimantis totoroi	BPCT	1	1	1
Pristimantis totoroi	Pilaló	0	0	1
Pristimantis truebae	BPCT	1	1	1
Pristimantis unistrigatus	Pilaló	1	1	1
Pristimantis vertebralis	BPCT	0	1	0
Pristimantis vertebralis	Pilaló	1	1	1
Pristimantis yumbo	Pilaló	0	0	1
Rhinella margaritifer	Río Azuela	1	1	1
Strabomantis cornutus	Río Azuela	1	0	0
Strabomantis necerus	Río Faisanes	1	0	0

Table S3 Changes in community composition between different time periods. First column is the time period. Second column is the site location. Third column represents the scaled number of species losses between time periods. Fourth column represents the scaled number of species gains between time periods. Fifth column is the temporal beta-diversity index used to characterize changes in species composition (i.e., dissimilarity) between sampling time periods. Sixth column shows the direction of change, minus sign indicates species losses dominate species gains, and plus sign indicates species gains dominate species losses. BPCT refers to Bosque Protector Cashca Totoras.

Time period	**Locality**	**Scaled losses**	**Scaled gains**	**$D_{\%diff}$**	**Change**
T1-T3	BPCT	0.29	0.00	0.29	-
T1-T3	Pilaló	0.26	0.21	0.47	-
T1-T3	Paramo Antisana	0.20	0.00	0.20	-
T1-T3	Paramo Guamaní	0.33	0.33	0.67	0
T1-T3	Quebrada Zapadores	0.37	0.11	0.47	-
T1-T3	Río Azuela	0.33	0.17	0.50	-
T1-T3	Río Faisanes	0.33	0.00	0.33	-
T1-T2	BPCT	0.12	0.06	0.18	-
T1-T2	Pilaló	0.22	0.11	0.33	-
T1-T2	Paramo Antisana	0.20	0.00	0.20	-
T1-T2	Paramo Guamaní	0.33	0.33	0.67	0
T1-T2	Quebrada Zapadores	0.33	0.19	0.52	-
T1-T2	Río Azuela	0.30	0.16	0.46	-
T1-T2	Río Faisanes	0.29	0.13	0.42	-
T2-T3	BPCT	0.23	0.00	0.23	-
T2-T3	Pilaló	0.12	0.18	0.29	+
T2-T3	Paramo Antisana	0.00	0.00	0.00	0
T2-T3	Paramo Guamaní	0.00	0.00	0.00	0
T2-T3	Quebrada Zapadores	0.19	0.06	0.25	-
T2-T3	Río Azuela	0.16	0.13	0.29	-
T2-T3	Río Faisanes	0.18	0.00	0.18	-

Figure S1 Time periods during which data on anuran composition were obtained. T1 (1967-1987), T2 (2000-2003) and T3 (2016-2018). Also shown are the time periods used for the calculation of maximum temperatures and other climatic variables (see main text),. For instance, extreme warm temperature events (i.e., maximum temperature values) before T2 were correlated with changes in community changes from T1 to T2, and maximum temperature values before T3 (and after T2) were correlated with community changes from T2 to T3. Other climatic variables were estimated similarly.

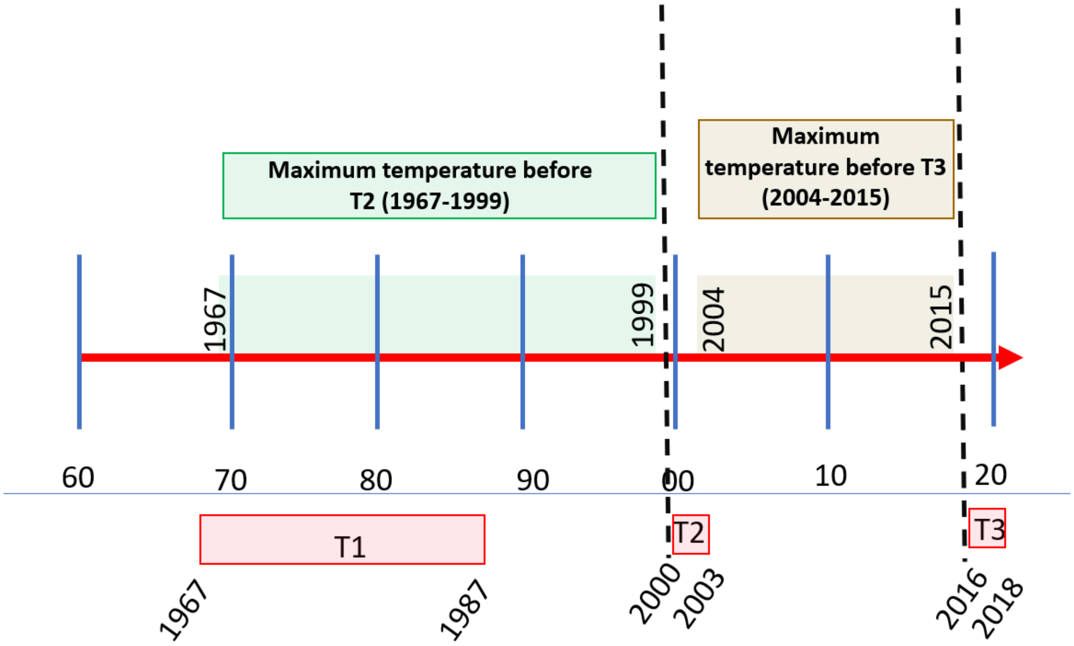


Figure S2 Pairwise correlations between predictors of local species extinctions. Values refer to the Pearson correlation (*r*). **$p < 0.05$, ***$p < 0.01$.

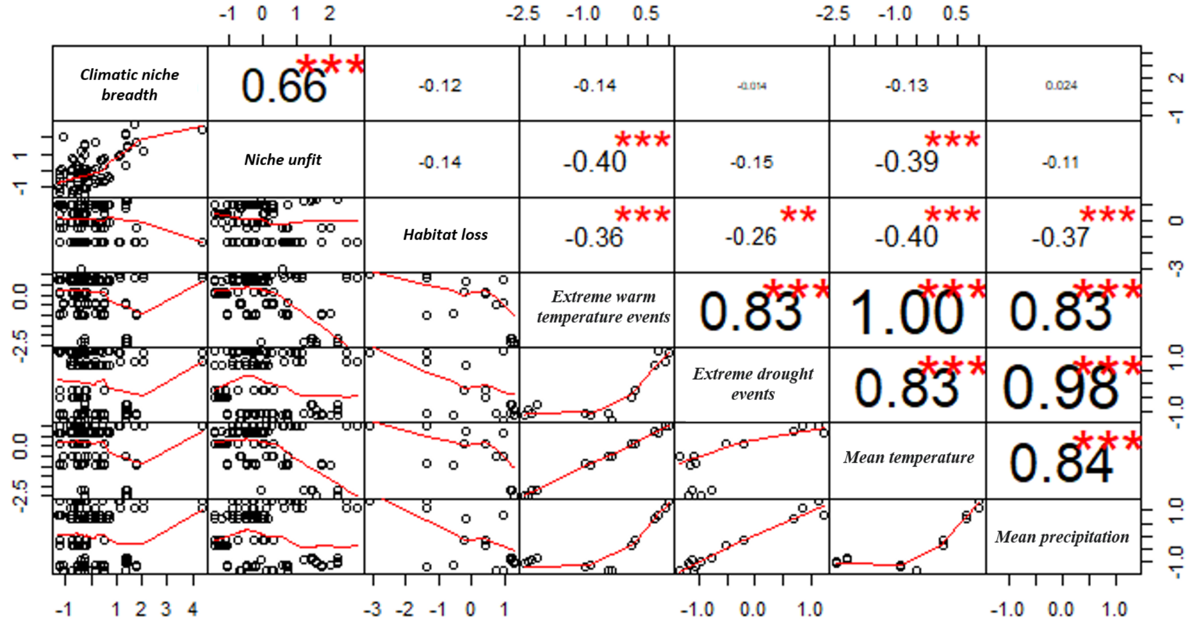


Figure S3. Bayesian regression coefficients for predictors of extinctions. Blue circles represent posterior means; dark red horizontal bars represent 50% credible intervals; dark gray horizontal lines represent 95% credible intervals. In (A) mean temperature was included instead of maximum temperature (i.e., extreme warm temperature events), in (B) mean precipitation and in (C) minimum precipitation (i.e., extreme drought events).

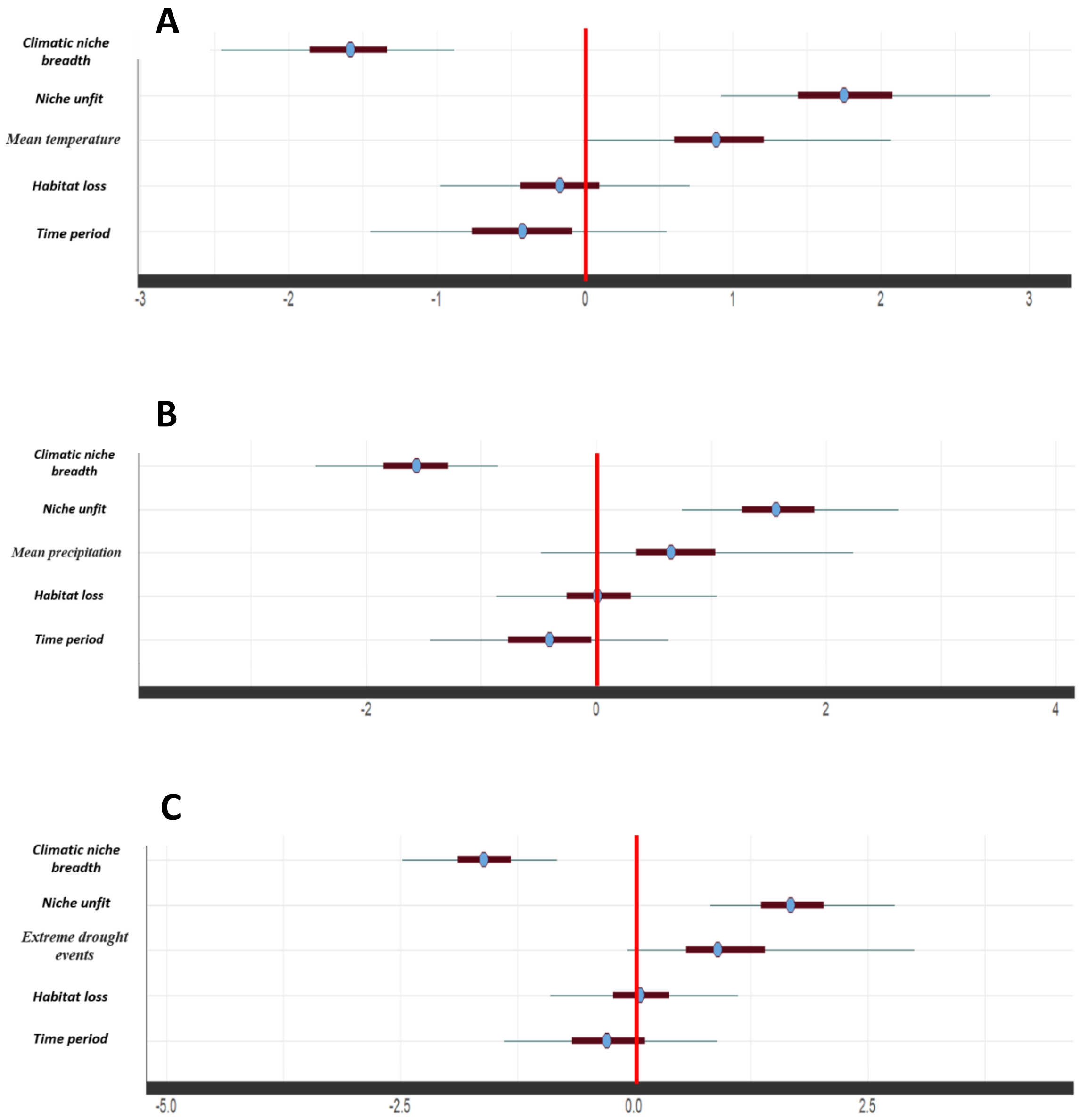
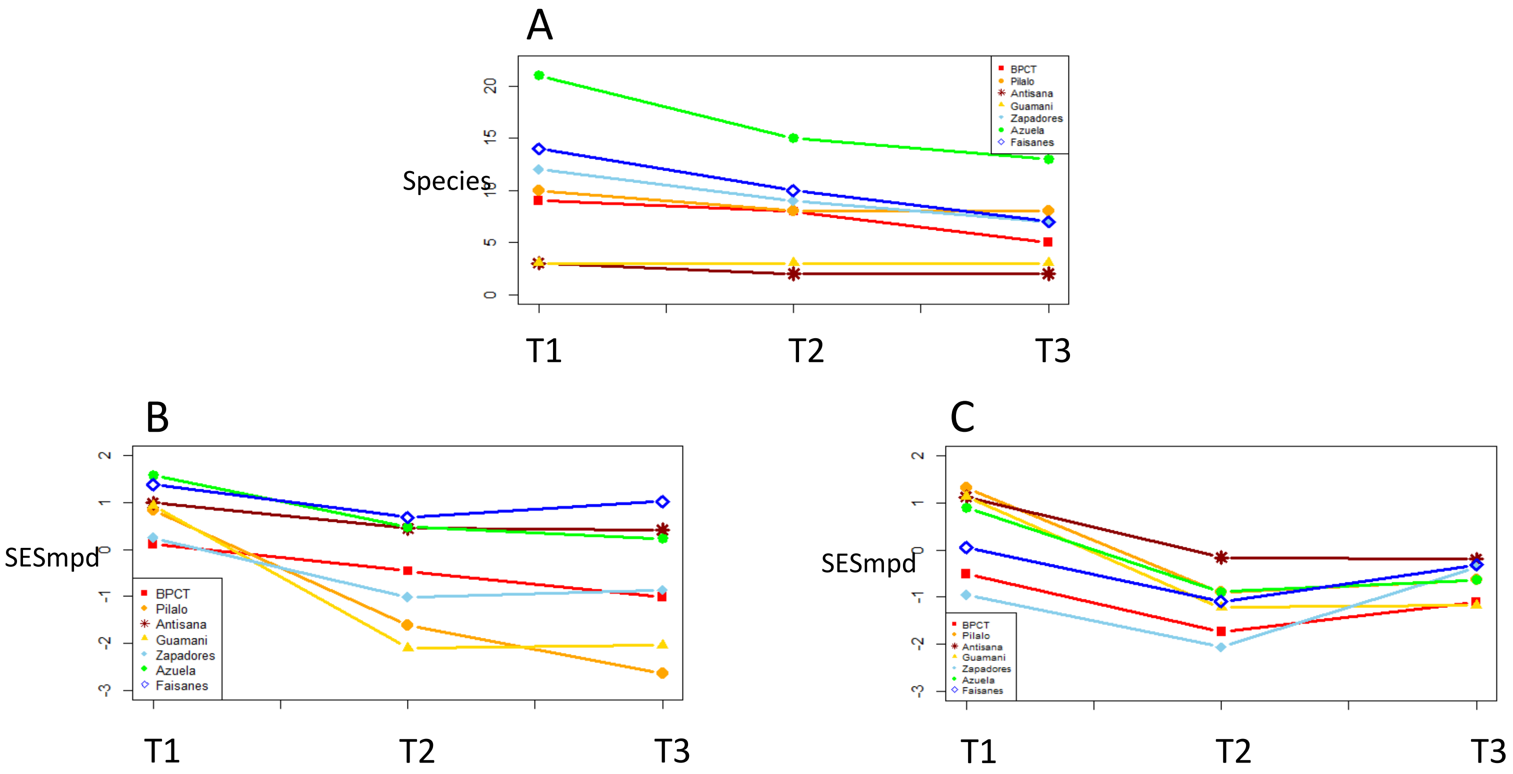


Figure S4. Changes in taxonomic, phylogenetic and functional diversity through time. Taxonomic diversity is measured as species richness (A), phylogenetic diversity as the standard effect size of the mean pairwise phylogenetic distance (SESmpd), and functional diversity as SESmpd from the functional dendrogram (see main text). Localities are as follow: Bosque Protector Cashca Totoras (BPCT; P1), Pilaló (P2), Paramo of Antisana (P3), Paramo of Guamaní (P4), Quebrada Zapadores (P5), Río Azuela (P6) and Río Faisanes (P7).



Supplementary Material Chapter 4

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Table S1. Collection localities and GenBank sequence accession numbers of the specimens used in the phylogenetic analysis. New sequences generated in this study are shown in bold. Sequences with marked with (*) are 16S, the rest of the sequences correspond to the 12S + tRNAval + 16S genetic region.

Specimen	Locality	GenBank code
I. alvarius USMN 320001	USA: Arizona	DQ158425
I. valliceps USNM 534129	Mexico: Vera Cruz	DQ158493
A. exsul MVZ 137717	USA: California, Buckhorn Spring	DQ158450
A. microscaphus USNM 320147	USA: Nuevo Mexico	DQ158476
A. fowleri USNM 314864	USA: Mississippi, Oktibbeha, Starkville	DQ158451
R. granulosa AMNH A139020	Guyana: Southern Rupununi Savanna, Aishalton (on Kubabawau Creek), 150 m	DQ283332
R. granulosa USNM 302450	Brazil: Roraima	DQ158457
R. granulosa (a)	Brazil: Porto Trombetas	GU178789
R. granulosa (b)	Brazil: Porto Trombetas	GU178788
R. crucifer ZUEC-DCC3392	Brazil: Rio de Janeiro: Mage, Campo de Escouteiras, Santo Aleixo	AY680260
R. crucifer USNM 303015	Brazil: Sao Paulo	DQ158447
R. marina (a)	Costa Rica: Heredia, Chilamate	DQ415563*
R. marina USNM 534124	Honduras: Colon, Quebrada Machin	DQ415569*
R. marina UTA A-50638	Honduras: El Paraiso, Las Manos	DQ415568*
R. marina UTA A-50870	Guatemala: Izabal, Montañas del Mico	DQ415567*
R. marina KU 289772	El Salvador: Ahuachapan, El Imposible	DQ415565*
R. marina KU 289750	El Salvador: Ahuachapan, El Imposible	DQ158473*
R. marina UTA A-50876	Guatemala: Huehuetenango, near Nenton	DQ415566*
R. marina UTA A-54870	Mexico: Guerrero, near Atoyac	DQ415561*
R. marina UTA A-54871	Mexico: Veracruz, south of Cardel	DQ415559*
R. marina UTA A-54868	Mexico: Sinaloa, near Cosala	DQ415562*
R. marina UTA A-54869	Mexico: Guerrero, near Atoyac	DQ415560*
R. marina UNAM-JRM 4834	Mexico: Veracruz, near El Viejón	DQ415553*
R. marina UNAM-JRM 4848	Mexico: Veracruz, north of Palma Sola	DQ415549*
R. marina UTA A-54878	Mexico: Veracruz, near El Viejón	DQ415558*
R. marina UNAM-JRM 4835	Mexico: Veracruz, near El Viejón	DQ415554*
R. marina UTA A-54879	Mexico: Veracruz, near El Viejón	DQ415556*
R. marina UTA A-54873	Mexico: Veracruz, near El Viejón	DQ415552*
R. marina UNAM-JRM 4844	Mexico: Veracruz, north of Palma Sola	DQ415550*
R. marina UTA A-54881	Mexico: Veracruz, near El Viejón	DQ415555*
R. marina UTA A-54875	Mexico: Veracruz, north of Palma Sola	DQ415547*
R. marina UNAM-JRM 4846	Mexico: Veracruz, north of Palma Sola	DQ415548*
R. marina UTA A-54877	Mexico: Veracruz, near El Viejón	DQ415557*
R. marina UTA A-54882	Mexico: Veracruz, near El Viejón	DQ415551*
R. marina KU 217482	Ecuador: Loja, Vilcabamba	DQ158474
***R. marina* QCAZ 47445**	Ecuador: Loja, San Bernabé	
***R. marina* QCAZ 47444**	Ecuador: Loja, San Bernabé	
***R. marina* QCAZ 46001**	Ecuador: Imbabura, Zona de amortiguamiento de la Reserva Cotacachi-Cayapas, near Aguas river Verdes	
***R. marina* QCAZ 37033**	Ecuador: Pichincha, Manuel Cornejo Astorga, Tandapi	
***R. marina* QCAZ 50702**	Ecuador: Manabí, San Andrés de Rocafuerte	
***R. marina* QCAZ 17965**	Ecuador: Pichincha, Guayllabamba, Guayllabamba river	

R. marina **QCAZ 12039**	Ecuador: Santo Domingo de los Tsáchilas, Saracay Hotel	
R. marina **QCAZ 40424**	Ecuador: Rosa Zarate, Laguna del Cube	
R. marina **QCAZ 39353**	Ecuador: Pichincha, Tababela airport	
R. marina KU 202274	Ecuador: Pichincha	AY680259
R. marina **QCAZ 45989**	Ecuador: Imbabura, Zona de amortiguamiento de la Reserva Cotacachi-Cayapas, near Aguas Verdes river	
R. marina **QCAZ 40806**	Ecuador: Azuay, near bridge over León river, Oña-Cuenca old road	
R. marina **QCAZ 28528**	Ecuador: Pichincha, secondary road, near Tinalandia, riverside of Toachi river, near pipeline.	
R. marina **QCAZ 37088**	Ecuador: Santo Domingo de los Tsáchilas, Chihuilpe, Chihuilpe river	
R. marina **QCAZ 35433**	Ecuador: Pichincha, Pedro Vicente Maldonado	
R. marina **QCAZ 49447**	Ecuador: Manabí, Reserva Lalo Loor	
R. marina **QCAZ 23486**	Ecuador: Guayas, trail to Cerro Más Vale	
R. marina **QCAZ 41327**	Ecuador: Guayas, Bosque Protector Cerro Blanco	
R. marina **QCAZ 23324**	Ecuador: Guayas, Santa Elena, road Palmas – Balsas	
R. marina **QCAZ 13893**	Ecuador: Cañar, 300 m from Manta Real on the road to Aurora	
R. ***marina*** **QCAZ 24579**	Ecuador: Manabí, Puerto Rico, Alándaluz	
R. ***marina*** **QCAZ 50701**	Ecuador: Manabí, San Andrés de Rocafuerte	
R. marina **QCAZ 50698**	Ecuador: Manabí, Puerto Cayo	
R. marina **QCAZ 23305**	Ecuador: Guayas, road El Palmar – Balsas, 20 km from El Palmar	
R. arenarum (a)	Uruguay: Rocha	GU178785
R. arenarum AR 305	Argentina	DQ158429
R. arenarum MACN 38639	Argentina: San Luis, ruta 20 entre Bardas Blancas y km 330	AY843573
R. achavali ZVCB 3801	Uruguay	GU178787
R. icterica AF 312	Brazil: Sao Paulo, Carapicuiba	DQ158462
R. icterica (a)	Brazil: Sao Paulo	GU178786
R. rubescens AF 388	Brazil: Minas Gerais, Santa Barbara	DQ158486
R. poeppigii USNM 268824	Peru: Madre Dios	DQ158481
R. poeppigii **QCAZ 39177**	Ecuador: Pastaza, Tarangaro community, Campo Villano, Bloque 10-Agip Oil	
R. marina MJH 3678	Peru: Puerto Inca	DQ283062
R. poeppigii **QCAZ 40785**	Ecuador: Zamora Chinchipe, Piuntza	
R. poeppigii MNCN/ADN6044	Bolivia: La Paz	GU178779
R. marina (b)	Brazil: Canaa dos Carajás	GU178782
R. schneideri BB 1224	Argentina: Santiago del Estero, Dto. Guasayaan, Do'a Luisa	DQ283065
R. schneideri KU 289057	Paraguay: San Luis de la Sierra	DQ415572*
R. marina (c)	Brazil: Santarém	GU178781
R. marina KU 205236	Peru: Cuzco	AY325994
R. marina **QCAZ 44399**	Ecuador: Orellana, Napo river, Chiru Isla, Banco norte	
R. marina **QCAZ 44274**	Ecuador: Orellana, Napo river, Edén, Banco sur	
R. marina **QCAZ 44305**	Ecuador: Orellana, Napo river, Chiru Iisla, Banco sur	
R. marina **QCAZ 44084**	Ecuador: Sucumbíos, Napo river, 2.5 km south from Pañacocha, Banco norte	

***R. marina* QCAZ 43782**	Ecuador: Orellana, 9 km south from Coca, 50 m from Napo River, Banco sur	
R. marina (d)	Brazil: Viseu	GU178783
R. jimi	Brazil: Natal	GU178784
***R. marina* QCAZ 44524**	Ecuador: Orellana, Napo river, San Vicente, Banco norte	
***R. marina* QCAZ 43876**	Ecuador: Orellana, Napo river, La Primavera (El Descanso), Banco norte	
R. schneideri VUB 1965	Suriname	FJ882831
***R. marina* QCAZ 44041**	Ecuador: Sucumbíos, Napo river, La Selva Lodge entrance, Banco norte	
***R. marina* QCAZ 44307**	Ecuador: Orellana, Napo river, Chiru Isla, Banco sur	
***R. marina* QCAZ 43781**	Ecuador: Orellana, 9 km south from El Coca, 50 m from Napo river, Banco sur	
R. marina (e)	Brazil: Porto Trombetas	GU178780
***R. marina* QCAZ 44306**	Ecuador: Orellana, Napo river, Chiru Iisla, Banco sur	
***R. marina* QCAZ 37177**	Ecuador: Pastaza, Pomona, Bosque Tropical Fundación Hola Vida	
***R. marina* QCAZ 44276**	Ecuador: Orellana, Napo river, Edén, Banco sur	
***R. marina* QCAZ 44812**	Ecuador: Orellana, Napo river, Nuevo Rocafuerte, Banco sur	
***R. marina* QCAZ 43877**	Ecuador: Orellana, Napo river, La Primavera (El Descanso), Banco norte	
***R. marina* QCAZ 44040**	Ecuador: Sucumbíos, Napo river, La Selva Lodge entrance, Banco norte	
***R. marina* QCAZ 44275**	Ecuador: Orellana, Napo river, Edén, Banco sur	
***R. marina* QCAZ 44083**	Ecuador: Sucumbíos, Napo river, 2.5 km south from Pañacocha, Banco norte	
***R. marina* QCAZ 15867**	Ecuador: Napo, Salado river	
***R. marina* QCAZ 48904**	Ecuador: Napo, Benavides Residence, Wildsumaco Wildlife Sanctuary, Wildsumaco Lodge	
***R. marina* QCAZ 15413**	Ecuador: Pastaza, Centro Experimental Fátima, 9 km north from Puyo	
***R. marina* QCAZ 28402**	Ecuador: Sucumbíos, Playas de Cuyabeno	
***R. marina* QCAZ 43751**	Ecuador: Orellana, 5 km south from El Coca, near Napo river, Banco Sur	
***R. marina* QCAZ 44015**	Ecuador: Orellana, Napo river, Áñangu, Banco sur	
***R. marina* QCAZ 28022**	Ecuador: Sucumbíos, Zábalo	
***R. marina* QCAZ 32484**	Ecuador: Morona Santiago, 900 m south east from Bobonaza	
***R. marina* QCAZ 44085**	Ecuador: Sucumbíos, Napo river, 2.5 km south from Pañacocha, Banco norte	
***R. marina* QCAZ 44663**	Ecuador: Orellana, Napo river, Santa Teresita 4 km north east from Nuevo Rocafuerte, Banco norte	
***R. marina* QCAZ 44622**	Ecuador: Orellana, Napo river, Huiririma, Banco sur	
***R. marina* QCAZ 48905**	Ecuador: Napo, Benavides Residence, Wildsumaco Wildlife Sanctuary, Wildsumaco Lodge	
***R. marina* QCAZ 44811**	Ecuador: Orellana, Napo river, Nuevo Rocafuerte, Banco sur	
***R. marina* QCAZ 43724**	Ecuador: Orellana, El Coca, Banco norte	
***R. marina* QCAZ 44664**	Ecuador: Orellana, Napo river, Santa Teresita 4 km north west from Nuevo Rocafuerte, Banco norte	

***R. marina* QCAZ 44833**	Ecuador: Orellana, Napo river, Nuevo Rocafuerte, Banco sur
***R. marina* QCAZ 39418**	Ecuador: Pastaza, Bataburo Lodge, south from Cononaco
***R. marina* QCAZ 43869**	Ecuador: Orellana, Napo river, La Primavera, Banco sur
***R. marina* QCAZ 44014**	Ecuador: Parque Nacional Yasuní, Napo river, Comunidad Añangu, Banco sur
***R. marina* QCAZ 41846**	Ecuador: Morona Santiago: Gral. Leonidas Plaza Gutiérrez (Limón), 6,6 km north of Parque central of General Leonidas Plaza (Río Napinaza)
***R. marina* QCAZ 17046**	Ecuador: Morona Santiago, Limón Indanza
***R. marina* QCAZ 41865**	Ecuador: Morona Santiago, General Leonidas Plaza Gutiérrez (Limón), Napinaza river
***R. marina* QCAZ 32485**	Ecuador: Morona Santiago, 900 m south east from Bobonaza
***R. marina* QCAZ 26268**	Ecuador: Pastaza, 5Km from Puyo on the road to Tena
***R. marina* QCAZ 25628**	Ecuador: Pastaza, Pomona, Fundación Hola Vida

Table S2. Descriptive statistics for morphometric measurements and proportions (in percentage) of 106 toads (*Rhinella marina species group*) used in the linear morphometric analyses. Mean ± SD is given with range below. Abbreviations are: SVL = Snout-vent length; TL = Tibia length; FL = Foot length; FEL = Femur length; HL = Head length; HW = Head width; IOD = Interorbiltal distance; IND = Internarial distance; END = Eye-nostril distance; ED = Eye diameter; TD = Tympanum diameter; THL = Thumb length; TF = Third finger length. All measurements are given in mm. Toads from Central America correspond to *R. horribilis,* toads from western Ecuador correspond to *R. bellus* sp. nov., and toads from eastern Ecuador correspond to *R. marina*.

Variables	**Central America (*n=20*)**	**Western Ecuador (*n*=60)**	**Eastern Ecuador (*n*=26)**
SVL	117.34 ± 18.37	94.08 ± 15.83	99.94 ± 11.38
	81.40–148.20	65.62–140.94	79.74–133.84
TL	44.91 ± 7.30	38.96 ± 6.21	41.46 ± 4.85
	30.40–58.70	27.7–58.24	33.17–56.91
FL	44.73 ± 6.81	39.36 ± 6.67	42.75 ± 4.70
	31.80–55.20	27.15–62.79	33.56–53.87
FEL	45.02 ± 8.63	39.42 ± 6.88	43.28 ± 5.37
	25.60–62.60	25.94–59.20	34.28–61.35
HL	36.23 ± 5.63	30.74 ± 4.44	32.65 ±3.74
	26.70–48.90	22.69–42.87	23.70–41.73
HW	44.22 ± 7.33	37.51 ± 6.02	41.17 ± 4.67
	30.50–55.50	25.87–52.41	32.55–54.80
IOD	16.64 ± 2.81	13.89 ± 2.35	15.90 ± 1.94
	11.40–21.50	6.24–20.01	11.93–21.19
IND	7.80 ± 1.46	6.40 ± 1.13	7.30 ± 0.84
	4.60–10.10	3.38–9.32	5.82–9.36
END	7.07 ± 1.15	6.36 ± 0.98	6.49 ± 0.88
	5.10–9.20	4.71–8.73	4.99–8.80
ED	11.87 ± 1.91	10.99 ± 1.45	11.90 ± 1.08
	9.40–15.70	8.41–15.75	9.46–14.82
TD	4.94 ± 0.81	4.36 ± 0.73	4.46 ± 0.56
	3.40–6.50	3.15–6.63	3.33–5.75
THL	13.31 ± 1.81	11.90 ± 2.07	12.75 ± 1.84
	10.20–16.70	7.59–17.75	9.38–18.10
TF	12.50 ± 1.68	13.01 ± 2.07	14.84 ± 1.95
	9.10–14.90	8.43–18.11	12.45–20.31
TD/HL	13.75 ± 1.86	14.26 ± 1.78	13.73 ± 1.54
	9.41–16.62	11.46–20.11	10.95–17.93
TL/SVL	38.26 ± 1.63	41.51 ± 1.69	41.52 ± 1.84
	34.28–40.93	38.24–44.61	36.05–45.03

HL/SVL	30.96 ± 2.27 29.08–38.69	32.83 ± 1.75 27.57–36.29	32.70 ± 1.64 28.24–35.16
HW/SVL	37.66 ± 1.71	39.94 ± 1.69	41.22 ± 1.34
	34.08–40.29	35.82–43.77	39.05–43.63
TF/FL	28.05 ± 1.52	33.23 ± 3.24	34.75 ± 2.74
	25.37–30.50	25.93–39.65	30.15–39.36

Figure S1. Configuration of landmarks for the analysis of variation in the shape of the skull. The shape of the skull of each specimen was described by a set of 13 landmarks and 11 pairs of partial warps, including the uniform component (see main text).

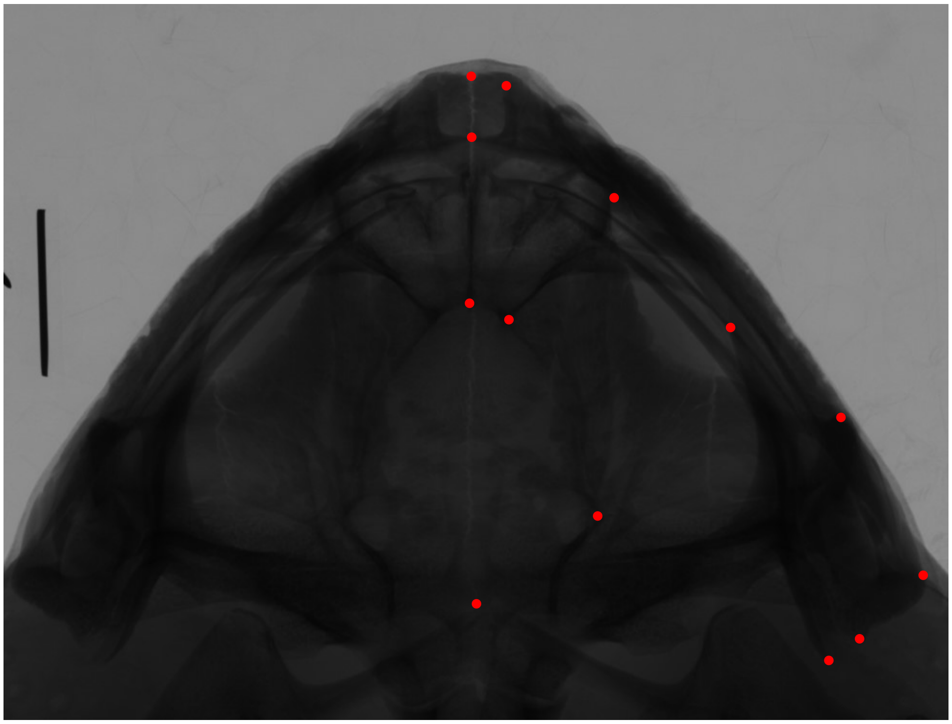

Figure S2. Axes I and II from principal components analysis (PCA) based on 13 continuously varying lineal morphological characters (see methods in the main text). Individuals are classified by sex. For eigenvectors and eigenvalues see Table 4.

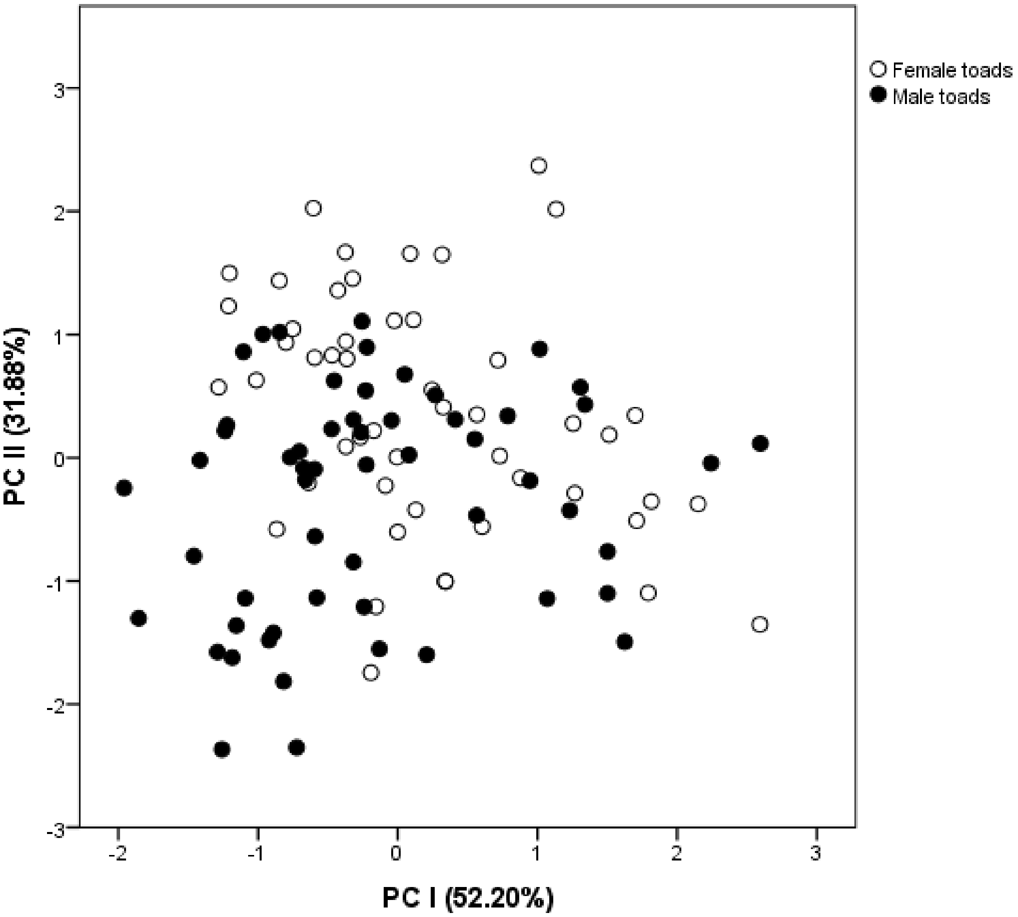

Table S3. Results of a MANOVA using scores from the first two rotated principal components (PC's; see methods) to evaluate differences among of populations (i.e. eastern Ecuador, western Ecuador, Central America) only on males or females. We also performed post-hoc multiple comparison tests with the Bonferroni corrected approach.

Multivariate Tests

Sex			Value	*F*	Hypothesis df	Error df	*p*
Females	Intercept	Pillai's Trace	0.328	11.247[b]	2	46	0
	Clades/populations	**Pillai's Trace**	**0.63**	**10.815**	**4**	**94**	**0**
Males	Intercept	Pillai's Trace	0.107	3.115[b]	2	52	0.053
	Clades/populations	**Pillai's Trace**	**0.591**	**11.106**	**4**	**106**	**0**

Tests of Between-Subjects Effects

Sex			Type III Sum of Squares	df	Mean Square	*F*	*p*
Females	Intercept	PC I	2.885	1	2.885	4.299	.044
		PC II	8.235	1	8.235	17.327	.000
	Clades/populations	**PC I**	**11.622**	**2**	**5.811**	**8.660**	**.001**
		PC II	**23.420**	**2**	**11.710**	**24.638**	**.000**
	Error	PC I	31.540	47	.671		
		PC II	22.338	47	.475		
Males	Intercept	PC I	1.529	1	1.529	2.030	.160
		PC II	2.089	1	2.089	3.378	.072
	Clades/populations	**PC I**	**18.214**	**2**	**9.107**	**12.089**	**.000**
		PC II	**12.991**	**2**	**6.496**	**10.506**	**.000**
	Error	PC I	39.928	53	.753		
		PC II	32.769	53	.618		

Pairwise multiple comparisons (Bonferroni)

Sex				Mean Difference	Std. Error	*p*
Females	PC I	Central America	Eastern Ecuador	1.111228*	.3681067	.012
			Western Ecuador	1.095721*	.2734228	.001
		Eastern Ecuador	Central America	-1.111228*	.3681067	.012
			Western Ecuador	-.015507	.3271430	1.000
		Western Ecuador	**Central America**	**-1.095721***	**.2734228**	**.001**
			Eastern Ecuador	**.015507**	**.3271430**	**1.000**
	PC II	Central America	Eastern Ecuador	-2.114130*	.3097909	.000
			Western Ecuador	-1.130148*	.2301069	.000
		Eastern Ecuador	Central America	2.114130*	.3097909	.000
			Western Ecuador	.983982*	.2753167	.002

		Western Ecuador	**Central America**	**1.130148***	**.2301069**	**.000**
			Eastern Ecuador	**-.983982***	**.2753167**	**.002**
Males	PC I	Central America	Eastern Ecuador	1.528288*	.3866219	.001
			Western Ecuador	1.782661*	.3632149	.000
		Eastern Ecuador	Central America	-1.528288*	.3866219	.001
			Western Ecuador	.254372	.2572069	.982
		Western Ecuador	**Central America**	**-1.782661***	**.3632149**	**.000**
			Eastern Ecuador	**-.254372**	**.2572069**	**.982**
	PC II	Central America	Eastern Ecuador	-.621395	.3502513	.245
			Western Ecuador	.445964	.3290463	.543
		Eastern Ecuador	Central America	.621395	.3502513	.245
			Western Ecuador	1.067359*	.2330108	.000
		Western Ecuador	**Central America**	**-.445964**	**.3290463**	**.543**
			Eastern Ecuador	**-1.067359***	**.2330108**	**.000**

Table S4. Standardized canonical discriminant function coefficients, eigenvalues, and percentage of explained variance for canonical variables (CV I, CV II) of Canonical Variates Analysis of 3 toad populations and 106 specimens. This analysis was based on 13 continuously varying lineal morphological characters (see methods). Abbreviations are: SVL = Snout-vent length; TL = Tibia length; FL = Foot length; FEL = Femur length; HL = Head length; HW = Head width; IOD = Interorbiltal distance; IND = Internarial distance; END = Eye-nostril distance; ED = Eye diameter; TD = Tympanum diameter; THL = Thumb length; TF = Third finger length.

Variables	CV I	CV II
Log SVL	2.775	.231
Log TL	-.418	-2.118
Log FL	.113	-.008
Log FEL	-.188	.446
Log HL	1.082	-.579
Log HW	-1.679	2.344
Log IOD	-.283	.869
Log IND	.096	.605
Log END	.026	-.771
Log ED	-.880	-.223
Log TD	.198	-.143
Log THL	.908	-.251
Log TF	-1.731	.130
Eigenvalue	**2.89**	**0.53**
% of variance explained	**84.60**	**15.40**
Cumulative %	**84.60**	**100**

Table S5. Coefficients of first two first principal components (relative warp [RW] axes) from a Principal component analysis (PCA) based on shape variables of 84 specimens (see methods in the main text).

Shape variables	RW I	RW II
x1	0.102701	0.055277
y1	0.028933	-0.163857
x2	0.154713	0.128417
y2	0.126801	-0.10357
x3	0.283869	0.146947
y3	0.306024	0.052625
x4	-0.078018	-0.195742
y4	-0.200776	-0.154039
x5	-0.230008	-0.023626
y5	-0.415298	0.515033
x6	-0.223542	-0.39701
y6	-0.299833	0.036318
x7	-0.097952	-0.2691
y7	-0.166039	-0.189727
x8	0.072561	0.04327
y8	-0.117451	0.031577
x9	0.111692	0.035844
y9	0.051619	-0.013727
x10	0.08523	0.128461
y10	0.255215	-0.144399
x11	-0.199331	-0.169883
y11	-0.127334	0.162967
x12	0.05085	0.092802
y12	0.321476	-0.150776
x13	-0.032766	0.424342
y13	0.236662	0.121575
% of variance explained	**66.95**	**7.65**
Cumulative %	**66.95**	**74.60**

Figure S3. Axes (relative warps) I and II from principal components analysis (PCA) based on shape variables of 84 specimens (see methods in the main text). Specimens are classified by geographic region. For eigenvectors and eigenvalues see Table S5. Individuals from western Ecuador correspond to *Rhinella bellus* sp. nov., individuals from eastern Ecuador correspond to *R. marina*, and individuals from Central America correspond to *R. horribilis*.