

Zootaxa 4004 (1): 001–075 www.mapress.com/zootaxa/

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http://dx.doi.org/10.11646/zootaxa.4004.1.1 http://zoobank.org/urn:lsid:zoobank.org:pub:BCAD1EAC-7DE9-4981-9E7B-11D041DE56AF

ZOOTAXA



Phylogenetic systematics of egg-brooding frogs (Anura: Hemiphractidae) and the evolution of direct development

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Magnolia Press Auckland, New Zealand SANTIAGO CASTROVIEJO-FISHER, JOSÉ M. PADIAL, IGNACIO DE LA RIVA, JOSÉ P. POMBAL, JR., HELIO R. DA SILVA, FERNANDO J. M. ROJAS-RUNJAIC, ESTEBAN MEDINA-MÉNDEZ & DARREL R. FROST

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(*Zootaxa* 4004)

75 pp.; 30 cm.

20 Aug. 2015

ISBN 978-1-77557-771-3 (paperback)

ISBN 978-1-77557-772-0 (Online edition)

FIRST PUBLISHED IN 2015 BY Magnolia Press P.O. Box 41-383 Auckland 1346 New Zealand e-mail: zootaxa@mapress.com http://www.mapress.com/zootaxa/

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ISSN 1175-5326(Print edition)ISSN 1175-5334(Online edition)

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Abstract

Egg-brooding frogs (Hemiphractidae) are a group of 105 currently recognized Neotropical species, with a remarkable diversity of developmental modes, from direct development to free-living and exotrophic tadpoles. Females carry their eggs on the back and embryos have unique bell-shaped gills. We inferred the evolutionary relationships of these frogs and used the resulting phylogeny to review their taxonomy and test hypotheses on the evolution of developmental modes and bellshaped gills. Our inferences relied on a total evidence parsimony analysis of DNA sequences of up to 20 mitochondrial and nuclear genes (analyzed under tree-alignment), and 51 phenotypic characters sampled for 83% of currently valid hemiphractid species. Our analyses rendered a well-resolved phylogeny, with both Hemiphractidae (sister of Athesphatanura) and its six recognized genera being monophyletic. We also inferred novel intergeneric relationships [((Cryptobatrachus, Flectonotus), (Stefania, (Fritziana, (Hemiphractus, Gastrotheca))))], the non-monophyly of all species groups previously proposed within Gastrotheca and Stefania, and the existence of several putative new species within Fritziana and Hemiphractus. Contrary to previous hypotheses, our results support the most recent common ancestor of hemiphractids as a direct-developer. Free-living aquatic tadpoles apparently evolved from direct-developing ancestors three to eight times. Embryos of the sister taxa Cryptobatrachus and Flectonotus share a pair of single gills derived from branchial arch I, while embryos of the clade including the other four genera have two pairs of gills derived from branchial arches I and II respectively. Furthermore, in Gastrotheca the fusion of the two pairs of gills is a putative synapomorphy. We propose a revised taxonomy concordant with our optimal topologies.

Key words: Cryptobatrachus, Flectonotus, Fritziana, Gastrotheca, gills, Hemiphractus, Neotropics, parsimony, Stefania, taxonomy, total evidence, tree-alignment

Introduction

Anuran systematics has experienced considerable progress in the last decade due to the ever-increasing amounts of molecular data and taxon sampling (e.g., Darst & Cannatella 2004; Faivovich *et al.* 2005; Frost *et al.* 2006; Grant *et al.* 2006; Roelants *et al.* 2007; Guayasamin *et al.* 2008; Hedges *et al.* 2008; Pyron & Wiens 2011). This growth of evidence allowed for more severe testing of hypotheses previously constructed on the basis of relatively small datasets. In many cases, the results of independent studies based on somewhat different sets of characters and taxa, and using different optimization criteria, converged on the same or relatively similar solutions, suggesting that evidence for inferred relationships was unambiguous and immune to different assumption sets. Such is the case of Nobleobatrachia, a clade including roughly 50% of all known species of anurans and the vast majority of Neotropical frogs (Frost *et al.* 2006; Roelants *et al.* 2007; Pyron & Wiens 2011) suggest that stronger tests based on more evidence and rigorous analyses are necessary to recover well-resolved relationships or, at least, to elucidate the causes of incongruence (e.g., Padial *et al.* 2014). As explained below, one of the most notable and yet unresolved cases in anuran systematics concerns the position and inter-relationships of egg-brooding frogs.

The name "egg-brooding frogs" informally refers to all species of non-aquatic Neotropical frogs in which females carry their eggs on their backs¹, either inside a pouch, hence the common name marsupial frogs, or exposed on the dorsum (Fig. 1). Egg brooding frogs are placed in the family Hemiphractidae Peters, 1862, currently containing 105 recognized species belonging to six genera (Frost 2014): *Cryptobatrachus, Flectonotus, Fritziana, Gastrotheca, Hemiphractus*, and *Stefania*. Most species of egg-brooding frogs inhabit Neotropical lowland or montane rainforest, with a few species known from humid high-elevation Andean grasslands or the rocky summits of the tepuis of the Guiana Shield. Thus, there are species of egg-brooding frogs in all major humid terrestrial biomes of the Neotropics including Central America (Costa Rica and Panama), Chocó and Darién (Colombia, Ecuador, and Panama), the Andes (from Venezuela and northern Colombia to northern Argentina), the Caribbean coastal mountains (Colombia, Venezuela, and the islands of Trinidad and Tobago), the Amazonian lowlands (Bolivia, Brazil, Colombia, Ecuador, and Peru), the Guiana Shield (Brazil, Guyana, and Venezuela), and the Atlantic Forest (Brazil).

Besides the remarkable adaptations that egg-brooding frogs have evolved to carry eggs on their backs, many species in this group undergo development without a free-living larval phase. This trait has been observed in species of *Cryptobatrachus*, *Hemiphractus*, and *Stefania*. Contrarily, development in frogs of the genera *Flectonotus* and *Fritziana* involves a free-living tadpole. In the genus *Gastrotheca* some species are direct-developers while others have aquatic larvae. Such unusual variation in developmental modes led some researchers to point at *Gastrotheca* as the only group of anurans in which free-living tadpoles had re-evolved from ancestors with direct-development (Duellman & Hillis 1987; Duellman *et al.* 1988; Wiens *et al.* 2007).

Regardless of their developmental mode, all species of egg-brooding frogs for which the character has been studied have embryos with unique bell-shaped gills (Noble 1927; del Pino & Escobar 1981). Also, many species of egg-brooding frogs present ornamented skulls (*i.e.*, exostosis of some of its dorsal surfaces), which form spectacular shapes in species of the genus *Hemiphractus* (e.g., Trueb 1974; Mendelson *et al.* 2000). Species of the genus *Hemiphractus* also have tooth-like structures ("fangs") on their mandibles associated with a carnivorous diet (Trueb 1974; Sheil *et al.* 2001)—most frogs are insectivorous—and *Gastrotheca guentheri* is the only anuran known to have mandibular teeth (Boulenger 1882).

Due to the uniqueness of some of their characteristics and the exceptional possibilities they provide to study the evolution of the biphasic life cycle of amphibians, egg-brooding frogs have received considerable attention. Multiple aspects of their biology have been studied in detail, such as their development (e.g., del Pino & Escobar 1981; del Pino *et al.* 2007), tadpole and adult morphology (Wassersug & Duellman 1984; Tyler & Duellman 1995), and systematics (e.g., Duellman & Hillis 1987; Duellman *et al.* 1988; Mendelson *et al.* 2000; Duellman *et al.* 2011a). However, and as explained below, despite many recent efforts to elucidate the phylogenetic relationships of egg-brooding frogs, recent studies show conflicting results, to the point that even the monophyly of the family is still contested.

^{1.} The term marsupial frogs has been used interchangeably with egg-brooding frogs (e.g., Duellman *et al.* 1988; Mendelson *et al.* 2000). We use the former term for species which females have a dorsal pouch (*i.e.*, species of the genera *Flectonotus* and *Gastrotheca*), in accordance with its more restricted original definition (Duellman & Maness 1980).



FIGURE 1. Representatives of the supraspecific taxa of Hemiphractidae recognized in this study. (a) A female of *Cryptobatrachus remotus* from Venezuela carrying on its back its recently hatched froglets, embryos undergo direct development (photo by FJMR-R); (b) A gravid female of *Flectonotus pygmaeus* from Venezuela carrying its eggs on a pouch on its back formed by two longitudinal flaps of skin that are adherent middorsally, endotrophic tadpoles hatch from the eggs and complete their development in water (photo by Mauricio Rivera-Correa); (c) An adult of *Fritziana goeldi* from Brazil (photo by JPP); (d) An adult female of the terrestrial *Hemiphractus scutatus* from Colombia (photo by SC-F); (e) An adult male of *Hemiphractus proboscideus* from Peru (photo by Giussepe Gagliardi-Urrutia); (f) A female of *Stefania ginesi* from Venezuela carrying its eggs on its back, embryos undergo direct development and hatch as froglets (photo by FJMR-R); (g) A female of *Gastrotheca albolineata* from Brazil carrying its eggs inside an enclosed pouch with a posterior opening, embryos undergo direct development and emerge from the pouch as froglets (photo by JPP); (f) An adult male of *Gastrotheca marsupiata* from Peru (photo by JMP); (i) A female of *Gastrotheca megacephala* from Brazil (photo by JPP); (j) An adult male of *Gastrotheca walkeri* from Venezuela (photo by FJMR-R).



FIGURE 1. (Continued)

The phylogenetic relationships of egg-brooding frogs. After a long history of taxonomic changes (see Frost 2014), the monophyly of egg-brooding frogs, as the subfamily Hemiphractinae within Hylidae, came to be accepted although rarely tested (e.g., Noble 1927, 1931; Duellman & Hoogmoed 1984; Silva 1998; Mendelson et al. 2000; Burton 2004). Molecular analyses have been nonetheless inconclusive about the monophyly and phylogenetic position of this taxon. The first analysis of hemiphractid relationships based on mtDNA sequences analyzed under parsimony, maximum likelihood (ML), and Bayesian approaches (BA), refuted their monophyly and did not find them closely related to Hylidae (Darst & Cannatella 2004). Faivovich et al. (2005), using a different method (parsimony under tree-alignment), also retrieved egg-brooding frogs as non-monophyletic and distantly related to Hylidae. Shortly after, Wiens et al. (2005) published a complementary study of hylid phylogenetics, with only partially overlapping taxon and character sampling with respect to previous studies. Their analyses, based on different permutations of data partitions, number of taxa, and optimization criteria were inconclusive. Under BA, egg-brooding frogs were recovered as monophyletic in most cases except for the analyses of mitochondrial genes alone and the 12S alone. Under parsimony, egg-brooding frogs were non-monophyletic in all cases except on the basis of phenotypic data alone or when a dataset with fewer taxa was analyzed². Also, both parsimony and BA of phenotypic data recovered egg-brooding frogs as a clade within hylids, while all other datasets retrieved them as distantly related to hylids regardless of the optimization criterion. Frost et al. (2006), as part of their analysis of the relationships of extant amphibians and using the same method and taxon sampling of egg-brooding frogs but a somewhat different character sampling than Faivovich et al. (2005), also retrieved eggbrooding frogs as non-monophyletic and distributed in three clades to which they assigned the rank of family: Amphignathodontidae for Fritziana (as Flectonotus in their study) and Gastrotheca; Cryptobatrachidae for Cryptobatrachus and Stefania; and Hemiphractidae for Hemiphractus. Two subsequent studies found conflicting results regarding the monophyly of hemiphractids (Wiens et al. 2006, 2007). Wiens et al. (2006: Supp. data) recovered egg-brooding frogs as non-monophyletic under parsimony analysis of DNA sequences, while Wiens et

^{2.} Because Wiens *et al.* (2005) did not show their parsimony topologies, non-monophyly is inferred from the absence of support values in the relevant clades according to the legends of their Figs 2, 3, 4, 5, and 8.

al. (2007) found egg-brooding frogs monophyletic under BA of DNA sequences. One key difference between the two studies by Wiens et al. (2006, 2007) is that Wiens *et al.* (2007) excluded *Cryptobatrachus* from their results.

In an attempt to explain the disagreement of previous studies, Guayasamin et al. (2008) pointed out that inferences based on parsimony or mitochondrial genes alone recovered egg-brooding frogs as non-monophyletic (Darst & Cannatella 2004; Faivovich et al. 2005; Wiens et al. 2006: Supp. data; Frost et al. 2006; Guayasamin et al. 2008) or monophyletic with weak support (Wiens et al. 2005), while inferences based on datasets including nuclear genes under a Bayesian approach yielded a highly supported clade of egg-brooding frogs (Wiens et al. 2005, 2007; Guayasamin et al. 2008). According to this pattern, differences among studies could be explained by the effect that different assumptions of methods (parsimony versus probabilistic inferences) had on molecular datasets with different rates of character evolution. However, the compared studies also differed in the number of taxa and characters sampled, the exhaustiveness of tree searches, method of alignment, model parameters, as well as modes of presenting data (e.g., strict consensus trees versus single optimal trees or majority rule consensuses). Thus, many alternative factors provided appealing explanations but none of these were tested. Furthermore, a key and yet overlooked aspect in this discussion was that all the studies that recovered a monophyletic Hemiphractidae lacked at least the taxon Cryptobatrachus. Nevertheless, Guayasamin et al. (2008) returned all egg-brooding frogs to Hemiphractidae and this taxonomy has prevailed since then. Most subsequent studies dealing directly or indirectly with the relationships of egg-brooding frogs that recovered a monophyletic Hemiphractidae also lacked at least Cryptobatrachus (e.g., Heinicke et al. 2009; Duellman et al. 2011a; Fisher-Reid & Wiens 2011; Pyron & Wiens 2011; Wiens 2011; Wiens & Morrill 2011; Gomez-Mestre et al. 2012; Blackburn & Duellman 2013). As such, no complete test of the monophyly of the group was ever performed. A recent analysis of Brachycephaloidea that included 13 outgroup species of the six genera of hemiphractids (Padial et al. 2014) found hemiphractids as monophyletic using the same methods as Faivovich et al. (2005) or Frost et al. (2006) but not under ML or parsimony when the alignment of DNA sequences was based on similarity. Therefore, it remains unclear whether disagreements among studies were due to artifacts or assumptions of methods, differences in taxon and character sampling, the mere shortcomings of heuristic searches, or any other of the many methodological differences among studies.

Besides the monophyly of egg-brooding frogs, other problems persist at both higher and lower levels. The position of egg-brooding frogs remains uncertain even in analyses that recovered a monophyletic Hemiphractidae, with some studies supporting a sister relationship with Brachycephaloidea (Wiens *et al.* 2007; Heinicke *et al.* 2009; Padial *et al.* 2014) while other studies (Pyron & Wiens 2011; Fouquet *et al.* 2013) found them as the sister group of Athesphatanura. Also, the taxon sampling of previous studies of egg-brooding frogs was not exhaustive with regard to available evidence, hampering a strong test of their monophyly and the intergeneric relationships of the whole group. Thus, what is still missing is a thorough analysis of the phylogenetic relationships of egg-brooding frogs that includes all evidence used by previous studies plus additional characters and taxa.

The evolution of developmental modes. Egg-brooding frogs exhibit a remarkable pattern of developmental modes. Available phylogenies with a dense taxon sampling of egg-brooding frogs (Wiens *et al.* 2007; Blackburn & Duellman 2013) suggest that, within *Gastrotheca*, there are closely related species with drastically different developmental modes. For example, the direct developer *G nicefori* is nested within a clade of six species that have a free-living and feeding tadpole. However, there are also contrasting differences at deep nodes, with all species of *Flectonotus* and *Fritziana* having free-living tadpoles while species of the closely related *Hemiphractus* are direct-developers (Wiens *et al.* 2007; Blackburn & Duellman 2013).

Although previous studies investigated the evolution of developmental modes in egg-brooding frogs (Duellman & Hillis 1987; Duellman *et al.* 1988; Mendelson *et al.* 2000; Wiens *et al.* 2007; Gomez-Mestre *et al.* 2012), both the ambiguity of phylogenetic relationships and the absence of key taxa have precluded a strong test of the evolution of direct development. Wiens *et al.* (2007) suggested that the presence of a free-living tadpole in some species of *Gastrotheca* evolved a single time from a direct-developing ancestor but they found this optimization to be very sensitive to different assumptions. Gomez-Mestre *et al.* (2012) inferred that the most recent common ancestor (MRCA) of egg-brooding frogs had a free-living tadpole and that direct-development evolved multiple times from it, rejecting the hypothesis of the re-evolution of a tadpole stage from a direct-developing ancestor. Relevant is that both Wiens *et al.* (2007) and Gomez-Mestre *et al.* (2012) excluded *Cryptobatrachus*, and *Cryptobatrachus* and *Fritziana*, respectively. In summary, what is lacking is a robust test where all relevant taxa and characters under scrutiny are included as evidence to infer the evolutionary history of the group.

Goals of this study. The main goal of this study is to test previous hypotheses of phylogenetic relationships of egg-brooding frogs. To do so, and given the complexity and diversity of previous results based on disparate and non-overlapping datasets, we have gathered DNA sequences of all species available in GenBank and generated new sequences for key taxa. Furthermore, we combined this molecular data with phenotypic characters used in previous studies. In addition, we test the hypothesis that in some species of egg-brooding frogs a free-living tadpole re-evolved from an ancestor with direct development (Wiens *et al.* 2007) and discuss the evolution of other remarkable characters such as bell-shaped external gills.

Material and methods

Optimality criterion and nucleotide homology. We chose the criterion of parsimony (unweighted) so that our phylogenetic inferences minimize *ad hoc* assumptions and maximize falsifiability and explanatory power of evidence (Wiley 1975; Farris 1983; Farris *et al.* 2001; Kluge 2001a, b, 2009; Kluge & Grant 2006; Grant & Kluge 2009). We applied parsimony to tree-alignment (Sankoff 1975; Sankoff & Rousseau 1975; Sankoff *et al.* 1976; Wheeler 1996) to infer the minimum number of transformation events needed to explain observed differences (including indels) in DNA sequences (Grant & Kluge 2004; 2009; Kluge & Grant 2006; Wheeler *et al.* 2006; Grant & Kluge 2009; Ruge 2009; Padial *et al.* 2014).

Taxon sampling. Our primary goals, testing the monophyly of Hemiphractidae and the phylogenetic relationships of as many species of egg-brooding frogs as possible, required careful design of taxon sampling. It was necessary to include a broad representation of outgroup taxa, whose character variation may bring to test the monophyly and sister relationship of egg-brooding frogs as inferred by previous studies, and as many species of egg-brooding frogs as possible.

To test the monophyly of egg-brooding frogs within Nobleobatrachia, we included representatives of all currently used families within this clade following the taxonomy outlined in Frost (2014). We selected specific outgroup terminals trying to maximize character coverage (*i.e.*, homologous sequences available from Genbank and phenotypic characters sampled by Mendelson *et al.* 2000) and phylogenetic structure according to the trees of the two most densely sampled anuran phylogenies (Frost *et al.* 2006; Pyron & Wiens 2011) (see Appendix 1 for a detailed explanation of outgroup selection). The identification of outgroup terminals was updated according to Blotto *et al.* (2013), Fouquet *et al.* (2013), Padial *et al.* (2014), and Faivovich *et al.* (2014). Among outgroups, we included a particularly dense taxon sampling for Brachycephaloidea (50 terminals with representatives of all genera with sequences available in GenBank) and Athesphatanura (71 terminals representing all 14 families currently recognized). Additionally, we added six non-Nobleobatrachian anurans of which *Heleophryne purcelli* was used as the root. All in all, our dataset included 127 outgroup terminals (Appendix 1).

Our final dataset includes 96 terminals of egg-brooding frogs representing 83% of currently recognized species and all past and present recognized genera and infrageneric groups, as well as species from all major ecoregions in which these anurans occur. Information on the specimens used in this study is listed in Appendices 1 and 2.

Fifteen ingroup terminals could be identified only to the genus level. *Cryptobatrachus* sp. KU 204000 is a cleared-and-stained specimen studied by Mendelson *et al.* (2000) and is only coded for phenotypic data. *Fritziana* sp. MNRJ 44592, *Fr.* aff. *fissilis* sp. 1 CFBH 5726, *Fr.* aff. *fissilis* sp. 2 MNRJ 44622, and *Fr.* aff. *fissilis* sp. 3 (labeled *Fritziana* cf. *fissilis* by Duellman *et al.* 2011a) likely represent four new species of *Fritziana* according to Duellman *et al.* (2011a) and our own results. *Gastrotheca* sp. A QCAZ 22635, *G* sp. B QCAZ 21105, *G* sp. C QCAZ 47299, *G* sp. D QCAZ 42725, and *G.* sp. E QCAZ 21213 were considered to be representatives of five new species by Blackburn & Duellman (2013). Analyses of DNA sequences of three genes from 27 samples of *Gastrotheca* from Bolivia (results not shown, De la Riva, Padial, and Castroviejo-Fisher, unpublished results) revealed three non-sister lineages for which there are available names but correspondences between species names and populations remain unclear. For example, specimens of the species that we herein labelled G. sp. 2 have been previously identified as *G. cf. marsupiata* (Faivovich *et al.* 2005), *G. piperata* (Duellman & Köhler 2005), and *G. lauzuricae* (Blackburn & Duellman 2013). This is not surprising as examination of voucher specimens (including type material) of *G. lauzuricae*, *G. piperata*, and *G. splendens*, as well as the current synonyms *Hylodes coeruleomaculatus* and *Nototrema bolivianum*, indicate that diagnostic morphological characters that are purported to provide evidence of divergence among some species are polymorphic and shared among species (De la Riva,

Padial, and Castroviejo-Fisher, unpublished results). On the other hand, some characters that might support the validity of some species were neglected. Furthermore, given that these three lineages occur in sympatry, assigning specimens to available species remains challenging. Because the necessarily deep analysis of the alpha taxonomy and nomenclature of Bolivian *Gastrotheca* was beyond the scope of this study, we refer to these three species from Bolivia as *G* sp. 1 IDIR 4073 (MNCN/ADN 576), *G* sp. 2 for specimens *G* cf. *marsupiata* MNK 5286 of Faivovich *et al.* (2005) [which was re-determined as *G piperata* by Duellman & Köhler (2005)] and *G lauzuricae* CBG 1020 (MNCN/ADN 9529) of Blackburn & Duellman (2013), and *G* sp. 3 for specimens ZFMK 66954 (MNCN/ADN 25033) and MNCN 43052. Finally, *Stefania* aff. *evansi* ROM 44254 and *S*. sp. IRSNB 15853 are considered new species following Kok *et al.* (2012).

We also updated the identification of three terminals. *Cryptobatrachus* sp. JDL 14865 of Darst & Cannatella (2004) is *C. fuhrmanni* (J.D. Lynch in litt. to W.E. Duellman, the latter in litt. to SC-F). The relevant tissue is most likely from the specimen now catalogued as KU 204892 and not KU 204292 as suggested by Schmid *et al.* (2013 "2012"); according to a search on HerpNET2 on 4 January 2014, the voucher KU 204292 is a specimen of *Anaxyrus terrestris* from Jasper, South Carolina. *Flectonotus* sp. CFBH 5726³ of Faivovich *et al.* (2005) is a species of *Fritziana* following Duellman *et al.* (2011a) and Teixeira *et al.* (2012); our comparisons of DNA sequences with other species of *Fritziana* in GenBank and our own sequences suggest it is a new species. *Gastrotheca fissipes* JLG 90 of Faivovich *et al.* (2005) is the subsequently named *G. megacephala* following Izecksohn *et al.* (2009), Teixeira *et al.* (2012) and Blackburn & Duellman (2013).

Seven species are represented by more than one terminal because preliminary comparisons of DNA sequences and subsequent phylogenetic analyses showed large divergences and, in some cases, non-sister relationships. These redundant terminals were *Cryptobatrachus fuhrmanni* JDL 14865 and MHUA A 5160, *Gastrotheca excubitor* MUSM 26280 and KU 173171, *G griswoldi* MHNSM 20588 and KU 181701, *G nicefori* KU 181071 and MHUA A 5716, *G riobambae* KU 178468 and UIMNH 94580, *Hemiphractus scutatus* JMP 2150 and RWM 10453, and *H. fasciatus* MVUP 1927, CHP 6397, EVACC 207, EVACC 065, EVACC 061, and CHP 6670.

For 21 terminals (*Cryptobatrachus remotus*, *Flectonotus fitzgeraldi*, *Fl. pygmaeus*, *Fritziana fissilis*, *Gastrotheca cornuta*, *G. dunni*, *G. ernestoi*, *G. marsupiata*, *G. megacephala*, *G. microdiscus*, *G. nebulanastes*, *G. pseustes*, *G.* sp. 2, *G.* sp. 3, *G. testudinea*, *Hemiphractus bubalus*, *H. fasciatus* sp. 1, *H. fasciatus* sp. 2, *H. helioi*, *Stefania evansi*, and *S. scalae*) sequences from different individuals of the same species were merged to construct a single complete composite sequence for the combined analyses. In this way we reduced the number of terminals, amount of missing data, number of possible optimal trees, and the potential effect of wildcards. We only applied this approach after checking for compliance to the following criteria: specimens were found as sister terminals in our own exploratory phylogenetic analyses as well as in the literature (Duellman *et al.* 2011a; Blackburn & Duellman 2013; Crawford *et al.* 2013) and, when sisters, the uncorrected proportional genetic distances (p-distances) between shared mitochondrial DNA fragments were <1%.

Similarly, molecular data from different specimens of the same species were sometimes available (e.g., there are in GenBank DNA sequences of ND1 for seven specimens of *Stefania evansi*). We used the same criteria mentioned above to exclude redundant specimens sampled for overlapping data.

Molecular data. We downloaded all DNA sequences of egg-brooding frogs deposited in GenBank prior to May 31, 2013. After discarding markers that were available only for one species (e.g., the sequence of VegT mRNA was only available for *Gastrotheca riobambae*) we were left with complete or partial sequences of the following 20 mitochondrial and nuclear genes: tRNAPhe, 12S rRNA, tRNAVal, two non-overlapping fragments of the 16S rRNA, tRNALeu, NADH dehydrogenase subunit 1 (ND1), cytochrome oxidase I (COI), cytochrome b (cytb), 28S rRNA, proto-oncogene cellular myelocytomatosis exons 2 (C-MYC 2) and 3 (C-MYC 3), chemokine receptor 4 (CXCR4), histone (H3a), proopiomelanocortin A (POMC), two non-overlapping fragments of the recombination activating gene 1 (RAG1), rhodopsin exon 1 (Rho), seven in absentia homolog 1 (SIAH), solute carrier family 8 member 3 (SLC8A3), and tyrosinase (Tyr). We also produced 168 new sequences representing 15 genes from 23 specimens of 19 species of egg-brooding frogs (Appendix 2). Amplification, sequencing, and editing protocols follow those of Guayasamin *et al.* (2008). Primers not listed in Guayasamin et al. (2008) are presented in Appendix 3.

^{3.} The voucher code of this specimen was reported by Faivovich *et al.* (2005) as CFBH 5720 but the correct code is CFBH 5726 (C.F.B. Haddad in litt. to J.M. Padial).

Phenotypic data. The backbone of the phenotypic data used in this study is the 51 phenotypic characters for 28 egg-brooding frog species and five hylid outgroups analyzed by Mendelson *et al.* (2000). We refer the reader to Mendelson *et al.* (2000) for detailed descriptions of the phenotypic characters. Prior to integrating the phenotypic dataset into our study, we updated the identification of some terminals of Mendelson *et al.* (2000). *Gastrotheca fissipes* KU 193298 is *G megacephala* following Izecksohn *et al.* (2009), Teixeira *et al.* (2012), and Blackburn & Duellman (2013). *Gastrotheca excubitor* KU 173218 is a paratype of *G. nebulanastes* following Duellman *et al.* (2011b). *Hemiphractus johnsoni* KU 153436 is a paratype of *H. helioi* according to Sheil & Mendelson (2001). *Stefania evansi* KU 167671–74, 181122–24 are *S. scale* according to Señaris *et al.* (1997 "1996").

As noted above, we found that sequences of different specimens of Cryptobatrachus fuhrmanni, Gastrotheca excubitor, G griswoldi, G riobambae, Hemiphractus fasciatus, and H. scutatus can be highly divergent and in some cases non-sister terminals (see Results), suggesting the existence of more than one species under those names. Therefore, matching phenotypic data and DNA sequences under a single terminal involved some uncertainty. We assigned the phenotypic characters of C. fuhrmanni KU 169378 to the terminal C. fuhrmanni JDL 14865 because both specimens come from the northern part of the Cordillera Oriental of Colombia, while specimen C. fuhrmanni MHUA A 5160 comes from the Cordillera Central of Colombia. We assigned the phenotypic characters of G excubitor (KU 146840-41 and KU 164088-89) to the terminal G excubitor KU 173171 on the basis of the geographic proximity and the fact that the specimens were identified by W. E. Duellman, one of the authors of the original description of G excubitor Duellman and Fritts, 1972. We assigned the phenotypic characters of G griswoldi (KU 138232 and KU 146844-5) to the terminal G griswoldi KU 181701 because all these specimens come from near the type locality in Junín, Peru, while G griswoldi MHNSM 20588 is from Huánuco, Peru. Phenotypic data for *G riobambae* (KU 99126, KU 99128–29, KU 138575–76, and KU 148543– 44) were assigned to the terminal G riobambae KU 178468 because all specimens were collected within the known distribution of the species (Frenkel et al. 2010), while G riobambae UIMNH 94580 comes from San Rafael, Azuay, Ecuador, which is in the lowlands of the Pacific coast of Ecuador near the Gulf of Guayaquil and outside the known distribution of G riobambae. The phenotypic observations of H. fasciatus are based on specimens KU 93509-10 from Darién, Panama, were assigned to H. fasciatus sp. 1 because specimens of this terminal also come from Darién, Panama, while specimens of terminals H. fasciatus sp. 2 and sp. 3 come from Chepo and Coclé, Panama, respectively. Lastly, the phenotypic observations of H. scutatus KU 129752 were assigned to H. scutatus JMP 2150 because this specimen is closest to the type locality, Rio Solimões, Amazonas, Brazil (see Hoogmoed & Gruber 1983; Glaw & Franzen 2006).

We updated Mendelson's *et al.* (2000) phenotypic dataset with the observations of del Pino & Escobar (1981) on gills and of Sheil *et al.* (2001) for *Hemiphractus*. Also, characters 41, 46, and 47 of Mendelson *et al.* (2000) were modified as described below.

Character 41. Pouch type. Mendelson *et al.* (2000) coded our states 1 and 2 as the same character state (*i.e.*, 41—1 dorsolateral folds of skin); however, the descriptions of del Pino (1980), Duellman & Gray (1983), Duellman *et al.* (2011a), and our own observations allow clear distinction between the folds present in females of *Flectonotus* and *Fritziana*. Accordingly, we code Character 41 as follows:

0—Pouch absent.

1-Lateral skin folds not adherent middorsally.

2—Pouch formed by two longitudinal flaps of skin that are adherent middorsally over the eggs, forming an enclosed pouch.

3—Enclosed pouch with a posterior opening.

Character 46. State of development of young at hatching. We recognize the same character states as in Mendelson *et al.* (2000) but we included new information from Duellman *et al.* (2011a) and Schmid *et al.* (2013 "2012").

Character 47. Deposition of eggs. Mendelson *et al.* (2000) recognized three character states (0—eggs in water; 1—eggs on dorsum; 2—eggs on leaves). In the context of our study, we preferred to include more character states to better represent the diversity known within anurans:

0—Aquatic eggs deposited in water.

1—Terrestrial eggs (*i.e.*, not in water) deposited in a nest.

- 2—Terrestrial eggs, arboreal.
- 3—Terrestrial eggs deposited on substrate (e.g., rocks, burrows, ground).
- 4—Terrestrial eggs on dorsum.
- 5—Aquatic eggs deposited in a nest.

Because we were particularly interested in the evolution of direct development in Nobleobatrachia, we augmented (whenever possible) our observations of character 46 to all ingroup and outgroup taxa. We obtained additional information on life history modes of egg-brooding frogs from Wiens *et al.* (2007), Blackburn & Duellman (2013), and citations therein, and for outgroup taxa from references cited in Appendix 4.

Phylogenetic analyses. To be able to incorporate into the tree-alignment analysis all homologous (as defined by primers and sequencing) DNA sequences with different lengths due to missing data, each marker has to be independently prealigned and divided into putatively homologous sections (Wheeler *et al.* 2006). To do so we used MAFFT v7 (Katoh & Standley 2013) under the "auto" strategy and default parameters to generate the prealignments. The resulting multiple sequence alignments were visualized in SE-AL v2.0a11 (http://tree.bio.ed.ac.uk/software/ seal/) and modified so that: (i) clear artifacts created by the alignment program were corrected (*i.e.*, the end and/or the beginning of shorter fragments within a gene were sometimes placed at the corresponding end or beginning of the whole alignment by the program and we placed them at the beginning or end of the corresponding sequence); and (ii) outgroup sequences were not longer than the longest egg-brooding frog sequence for that marker (*i.e.*, sequences of outgroups were trimmed when necessary). The prealignments of each marker were used to divide them into shorter contiguous fragments without missing data also using SE-AL v2.0a11. This strategy generated putatively homologous fragments where length variation among DNA sequences is only due to insertions and/or deletions of nucleotides, a requisite for tree-alignment analysis in POY (Wheeler *et al.* 2006). Fragment partitions were located in conserved regions (no gaps and few or none nucleotide substitutions) according to the multiple sequence alignments.

We employed parsimony analyses as implemented in POY 5.1.1 (Varón et al. 2010; Wheeler et al. 2014) with equal weights for all transformations (including insertion/deletion events) and all characters coded as non-additive (except those indicated otherwise by Mendelson et al. 2000). The DNA sequence fragments described above were analyzed under direct optimization (Wheeler 1996). Searches were conducted using the automated "search" function, which attempts as many builds (*i.e.*, Wagner trees), swaps [*i.e.*, tree bisection–reconnection (TBR) branch swapping], ratchets (Nixon 1999), and tree-fusings (Goloboff 1999) as possible within the specified time. We stored the shortest and unique trees of each search, allowing the parallel processors to exchange trees and add the pool of selected best and unique trees to the subsequent interactions of the command (Varón et al. 2010). Five consecutive 48-hour searches followed by a final search of 240 hours (totalling 480 hours) were implemented in parallel at the American Museum of Natural History Cluster Enyo, using 32 processors. The resulting shortest trees were submitted to a final round of swapping using iterative pass optimization (Sankoff et al. 1976; Wheeler 2003a) in POY. As we have observed that POY 5.1.1 does not always report all the equally parsimonious trees, the optimal alignment resulting from iterative pass optimization was converted to a data matrix (Wheeler 2003b) and driven searches were conducted in TNT (Goloboff et al. 2008a; equal costs for all transformations, non-additive characters but those indicated by Mendelson et al. 2000, gaps treated as fifth state) until a stable strict consensus was reached at least five times. In this way, we assessed whether additional equally parsimonious trees were supported by evidence derived from the tree-alignment matrix.

We calculated Goodman-Bremer (GB) values (Goodman *et al.* 1982; Bremer 1988; see Grant & Kluge 2008a) for each supported clade in TNT using the optimal tree-alignment matrix and the parameters specified in the bremer.run macro (available at http://www.zmuc.dk/public/phylogeny/tnt/), which begins by searching for trees N steps longer than the optimum (10 random addition sequence Wagner builds and TBR swapping saving two trees per replicate) for suboptimal trees using inverse constraints for each node of the most parsimonious tree. Swapping of each constrained search was limited to 20 minutes and constrained searches were repeated three times. We calculated jackknife (JK) frequencies from 1000 pseudoreplicates searched with 100 RAS + TBR and a maximum of 10 trees saved per replicate, gaps treated as fifth state, and removal probability of 0.36 (~ e⁻¹), which purportedly renders jackknife and bootstrap values comparable (Farris *et al.* 1996). We caution that, as in analyses of similarity-alignment matrices, the resulting clade frequencies are conditional on this particular alignment and not the data themselves. Given that the tree-alignment matrix is derived from the optimal tree, the resulting clade frequencies are expected to be higher than would be obtained from matrices aligned according to different guide trees (e.g., a

UPGMA or neighbor-joining tree, as in MAFFT and CLUSTAL, respectively). Padial *et al.* (2014) corroborated this expectation for JK but found higher GB values in a similarity-aligned matrix than by resampling the tree-alignment matrix for the same sequence data.

Results

Tree searches of the complete dataset in POY yielded 23 most parsimonious trees (79567 steps). A final round of swapping using iterative pass optimization on these trees further reduced the cost (79313 steps). The implied alignment contains 18349 molecular transformation series that combined with the 51 phenotypic characters yielded a static dataset of 18400 transformation series (all alignments are available from https://drive.bitcasa.com/send/DIDPyZKS1pzh7NkMHbC3Ki_DCyD1zHDk4gd_VXMpatjY). Tree searches of this static dataset in TNT found 63 most parsimonious trees (Fig. 2).

Egg-brooding frogs were recovered as a natural group (GB = 1; JK = 99) nested within Nobleobatrachia (GB = 159; JK = 100) and sister of all other frog families within Nobleobatrachia except those of Brachycephaloidea (GB = 63; JK = 99). We recovered *Ceuthomantis smaragdinus* as the sister taxon of all other nobleobatrachians, therefore rendering a non-monophyletic Brachycephaloidea and Craugastoridae. The families Alsodidae, Aromobatidae, Batrachylidae, Bufonidae, Centrolenidae, Ceratophryidae, Dendrobatidae, Hylidae, Hylodidae, Leptodactylidae, and Odontophrynidae were recovered as monophyletic while Cycloramphidae and Rhinodermatidae were recovered as non-monophyletic because our optimal trees placed *Thoropa miliaris* as the sister of *Rhinoderma darwinii*. The families Allophrynidae and Telmatobiidae were represented by just one terminal each. Given the diversity of Nobleobatrachia, it is obvious that our taxon sampling was not designed to evaluate all the internal relationships of its different families or the relationships among them. Consequently, our results outside of egg-brooding frogs should not be interpreted as tests of previous hypotheses of relationships based on denser taxon sampling (e.g., Padial *et al.* 2014, for Brachycephaloidea).

Within egg-brooding frogs all genera were recovered as monophyletic. Nevertheless, we obtained some unexpected relationships. The first split separates a clade (GB = 4; JK = 98) containing *Cryptobatrachus* + *Flectonotus*, which is a novel sister relationship. The relationships within *Cryptobatrachus* are not resolved in the strict consensus.

Stefania (GB = 51; JK = 99) was inferred as the sister taxon of a clade containing *Gastrotheca*, *Fritziana*, and *Hemiphractus* (GB = 8; JK = 99), which is another novel sister relationship (GB = 8; JK = 98). Within *Stefania* neither the *S. evansi* nor the *S. goini* species groups are monophyletic. A clade formed by *S. ginesi* and *S. satelles* forms the sister group of the remaining species. Within the latter clade, *S. schuberti* is sister of the other species, which are arranged in three main clades. One clade includes *S. ayangannae*, *S. coxi*, *S. riveroi*, and *S. sp.* [a putative new species according to Kok *et al.* (2012)]. The second contains *S. riae*, *S. roraimae*, and *S. woodleyi*. The third clade includes *S. evansi*, *S. scalae*, and *S. aff. evansi* [another putative new species according to Kok *et al.* (2012)].

Fritziana (GB = 77; JK = 100) is recovered as the sister of *Gastrotheca* and *Hemiphractus* (GB = 29; JK = 99), which is another novel sister relationship. The relationships among members of *Fritziana* are pectinate, with *F*. *goeldii* as the sister of the remaining species. *Fritziana fissilis* was recovered paraphyletic with respect to *F. ohausi*, and there are large genetic divergences among the seven terminals (genetic p-distances of 532 bp of the marker 16S rRNA = 5.7-12.1%).

Hemiphractus (GB = 17; JK = 100) was inferred to be the sister group of *Gastrotheca* (GB = 17; JK = 100), also a novel sister relationship. We obtained *H. helioi* as sister of the other species. *Hemiphractus bubalus*, *H. johnsoni*, and *H. proboscideus* are sister of a clade that contains *H. scutatus*, represented by two terminals with large genetic distances (genetic p-distances between 491 bp of the marker 16S rRNA = 8.2%), and *H. fasciatus*, represented by three terminals with relatively large nucleotide disparity (genetic p-distances between 533 bp of the marker 16S rRNA = 2.5–5.7%).



FIGURE 2. Phylogenetic relationships of egg-brooding frogs and outgroups inferred from parsimony analysis of phenotypic characters and DNA sequences under direct optimization. This topology reflects one of the 63 most parsimonious trees (tree costs = 79313 steps) with the evolution of direct development shown by the color of branches. Numbers above and below branches, or separated by a slash, represent Goodman-Bremer values and jackknife proportions respectively and black dots on nodes indicate collapsed clades in the strict consensus. A skeletal topology, with the magnified section marked in black, is shown on the left side. White stars indicate taxa represented in the phenotypic dataset of Mendelson *et al.* (2000) and black stars indicate taxa only represented by phenotypic data from Mendelson *et al.* (2000). (a) Relationships among outgroups; we cropped the root (*Heleophryne purcelli*) for ease of representation. (b) Relationships among egg-brooding frogs showing the taxonomy proposed in this work; terminals without a voucher code indicate that sequences from different individuals of the same species were joined to construct a single composite sequence.



FIGURE 2. (Continued)

Within *Gastrotheca* we recovered a clade (GB = 23; JK = 100) that contains *G walkeri*, of the *G williamsoni* group of Schmid *et al.* (2013 "2012"), as the sister taxon of a clade that includes species of the *G longipes* group (GB = 10; JK = 87) *sensu* Schmid *et al.* (2013 "2012"), referred to as the Northwest South American clade by Blackburn & Duellman (2013). This clade is the sister group of a clade that includes the rest of species in the genus. Within this latter clade, we recovered a clade (GB = 11; JK = 97) with five species from the Atlantic Forest of Brazil, followed in succession by a second clade (GB = 11; JK = 96) of species from the Atlantic Forest, by *G ovifera*, and by *G zeugocystis*, which is the sister species of all the remaining sampled species, which in turn are part of the following three main clades.

The first clade partially corresponds to the *Gastrotheca plumbea* group of Schmid *et al.* (2013 "2012"), also called the Northern Andes clade by Blackburn & Duellman (2013), but includes *G galeata* (GB = 5; JK = 75) and excludes *G argenteovirens*, *G aureomaculata*, *G dunni*, *G nicefori*, *G riobambae*, *G ruizi*, and *G trachyceps*. The second clade contains part of the *G plumbea* group of Schmid *et al.* (2013 "2012") (*G argenteovirens*, *G aureomaculata*, *G dunni*, *G nicefori*, *G ruizi*, and *G trachyceps*) and two sister samples of nominal *G nicefori* with marked genetic divergences (genetic p-distances between 417 bp of the marker 12S rRNA = 3.8% and between 492 bp of the marker 16S rRNA = 1.2%). *Gastrotheca riobambae* is paraphyletic, with terminal KU 178468 not being closely related to *G riobambae* UIMNH 94580, which belongs to the third clade. The third clade, partially matches the content of the *G marsupiata* group of Schmid *et al.* (2013 "2012"), called the Central Andes clade by Blackburn & Duellman (2013), but with the exclusion of *Gastrotheca zeugocystis* (GB = 5; JK = 95). Within this clade, the terminal *G. riobambae* UIMNH 94580 mentioned above is the sister of *G pseustes*, with genetic p-distances between 399 bp of the marker 16S rRNA = 0.5%, and was collected at a locality where *G pseustes* has been found (Ron & Frenkel, 2010). Also within this clade, the samples identified in GenBank as *Gastrotheca griswoldi* (MHNSM 20588 and KU 181701) are not sister terminals in all most parsimonious trees and *G. excubitor* (KU 173171 and MUSM 26280) is paraphyletic.

Discussion

Our analyses of combined molecular and phenotypic characters recovered the monophyly of egg-brooding frogs and corroborated the monophyly of all genera. No other study has included as many species and characters as ours, nor has any other study combined all previous phenotypic and molecular data used so far to infer the relationships of this group. As such, our analyses provide a more robust test of the monophyly of egg-brooding frogs and their internal relationships. Below, we discuss alternative explanations for the differences found among previous studies concerning the monophyly and phylogenetic position of Hemiphractidae. We also discuss how our novel hypothesis of relationships bears on the evolution of several phenotypic traits in egg-brooding frogs, with emphasis on direct-development. At the end, we provide a section with a revised taxonomy.

The monophyly of egg-brooding frogs. Different studies inferred hemiphractids as non-monophyletic on the basis of DNA sequences or DNA sequences combined with phenotypic data analyzed under different optimality criteria [Darst & Cannatella 2004 (parsimony, ML, BA); Faivovich et al. 2005 (parsimony); Wiens et al. 2005 (parsimony, but not BA); Frost et al. 2006 (parsimony); Wiens et al. 2006: Supp. data (at least parsimony⁴)]. This was interpreted as the result of long-branch attraction (LBA) and/or predominance of fast evolving mitochondrial genes (presumably assuming "saturation" and high levels of homoplasy) biasing parsimony analysis (Wiens 2007; Wiens et al. 2007; Guayasamin et al. 2008). Missing from the argument was that the datasets analyzed under probabilistic methods and used to support the monophyly of egg-brooding frogs lacked key taxa. For example, Wiens et al. (2007) removed Cryptobatrachus from their analyses because of its unstable position and Guayasamin et al. (2008) did not include Cryptobatrachus. Padial et al. (2014) challenged the hypothesis that LBA and "saturation" of mitochondrial genes was biasing parsimony analysis because they found a monophyletic Hemiphractidae using parsimony under tree-alignment with a dataset that included taxa missing in previous analyses (e.g., Cryptobatrachus and Fritziana). It could be argued that increasing taxon sampling provided the conditions to break long branches in the parsimony analyses of Padial et al. (2014); however, they only included 13 species of hemiphractids that were represented by DNA sequences dominated by mtDNA genes obtained from previously published studies. Relevant is that Padial et al. (2014) found that neither ML nor parsimony analyses

^{4.} Wiens et al. (2006) neither showed nor discussed hemiphractid relationships inferred from their BA.

recovered the monophyly of hemiphractids when DNA sequences were aligned using conventional methods based on structural similarity. One could be inclined to conclude that the method of alignment (*i.e.*, similarity versus treealignment) was the key factor explaining the contradictory results of Padial *et al.* (2014). However, neither Faivovich *et al.* (2005) nor Frost *et al.* (2006) recovered a monophyletic Hemiphractidae, in spite of using the same method of tree-alignment as and comparable tree searches to Padial *et al.* (2014).

We conclude that we face a complex case, in which one cannot tell apart, by mere comparison of the results of previous studies, the potential effects that non-mutually exclusive factors—such as differences in taxon and character sampling, optimality criteria, exhaustiveness of tree searches, treatment of indels, data partition schemes, model selection, and alignment parameters—could have on the incongruence observed among different studies regarding the monophyly of hemiphractids. However, rather than trying to single out the causes of incongruence among studies, we have focused on the analysis of available evidence. The strength of our study is that we revisited all previous phylogenetic hypotheses by building a dataset in a cumulative and constructive approach (*i.e.*, adding data to what others have generated). Thus, our tree summarizes the state of understanding of hemiphractid evolutionary relationships.

The phylogenetic position of Hemiphractidae. During most of their taxonomic history, species of eggbrooding frogs were thought to be part of Hylidae (e.g., Duméril & Bibron 1841; Boulenger 1904; Peracca 1914; Miranda-Ribeiro 1920; Noble 1927, 1931) or related to them (e.g., Peters 1862), while species now included in Hemiphractus and even some species of Cryptobatrachus were instead placed in Cystignathidae (e.g., Gravenhorst 1825; Duméril & Bibron 1841; Günther 1859 "1858"; Cope 1866; Ruthven 1916) (see Frost 2014, for a detailed account of nomenclatural changes). Lutz (1968) considered most egg-brooding frogs to form a clade, her hylid subfamily Opisthodelphinae, leaving Hemiphractus scutatus outside of this group because of its reduced digital discs. Although she provided the first explicit phylogenetic hypothesis of their relationships, her non-quantitative hypothesis has largely been ignored (but see Mendelson et al. 2000). For several decades most studies (e.g., Trueb 1970, 1974; Duellman 1970; Mendelson et al. 2000) followed Noble's (1927, 1931) conclusion that hemiphractids were hylids⁵. This notion was increasingly questioned in the late 1990s and early 2000s. Silva (1998) and Burton (2004), using phenotypic data, retrieved egg-brooding frogs as monophyletic and the sister of Phyllomedusinae in a clade with a basal polytomy including Allophrynidae + Centrolenidae, Hylinae + Pseudinae, and Pelodryadinae, rendering Hylidae as non-monophyletic. Haas (2003), in his analysis of anuran relationships primarily based on larval morphology, also recovered egg-brooding frogs as neither the sister of nor included within Hylidae. Molecular phylogenies also started to challenge the hypothesis that egg-brooding frogs were hylids, although taxon sampling was still limited to one or two species of hemiphractids (Ruvinsky & Maxson 1996; Austin 2002; Darst & Cannatella 2004). It was the study of Faivovich et al. (2005) that decisively challenged this long-standing hypothesis and formalized their results transferring egg-brooding frogs to "Leptodactylidae". Wiens et al. (2005) recovered hemiphractids as a clade within hylids when analyzing phenotypic data only, while their more explanatory analyses combining molecular and phenotypic data retrieved the groups as distantly related. Frost et al. (2006), as part of their broader analysis of extant amphibians, also retrieved egg-brooding frogs as nonmonophyletic and distributed in three clades, none of them closely related to hylids.

Nonetheless, although the previous view of hemiphractids as hylids started to be abandoned, the phylogenetic position of hemiphractids (and their monophyly, see above) remained unclear. Wiens *et al.* (2005) were the first to suggest a sister relationship between reciprocally monophyletic Hemiphractidae and Brachycephaloidea. Later, Heinicke *et al.* (2009) analyzed two datasets of DNA sequences from up to 17 genes from representatives of 13 genera of Brachycephaloidea, three genera of hemiphractids (*Hemiphractus, Stefania,* and *Flectonotus*) and representatives of all other families of Nobleobatrachia of Frost *et al.* (2006) and recovered Brachycephaloidea and Hemiphractidae as sister taxa, a clade which they named Orthobatrachia. The monophyly of Orthobatrachia has indeed been questioned by several subsequent studies with larger taxon and character sampling (Pyron & Wiens 2011; Fouquet *et al.* 2013: Fig. 2; Zhang *et al.* 2013; but see Padial *et al.* 2014). Schmid *et al.* (2013 "2012") did not endorse the results of those studies that refuted the monophyly of Orthobatrachia and constrained their topology to support their claims about the evolution of direct development. Our analyses nonetheless recovered Hemiphractidae as the sister group of Athesphatanura, supporting the results of Pyron & Wiens (2011) and Fouquet

5. Noble (1927, 1931) did not mention either of the then recently-named taxa *Flectonotus* (Miranda-Ribeiro, 1926) and *Fritziana* (as *Fritzia* by Miranda-Ribeiro, 1920) even though these genera had been noted in their original descriptions to share with the other marsupial frogs the transport of eggs in a specialized pouch in the dorsum of females.

et al. (2013: Fig. 2). As explained below, these findings have important implications for understanding the evolution of reproductive modes in hemiphractids and other groups (Athesphatanura and Brachycephaloidea). However, due to our limited sampling of taxa outside Hemiphractidae, the sister relationships of the group remain to be tested in the context of a larger analysis of Nobleobatrachia.

Phylogenetic relationships within Hemiphractidae. The monophyly of the six currently recognized genera was corroborated by our results. However, the relationships among hemiphractid genera recovered by our analyses (Fig. 3a) differ from those of previous studies (e.g., Wiens *et al.* 2007; Duellman *et al.* 2011a; Fisher-Reid & Wiens 2011; Pyron & Wiens 2011; Gomez-Mestre *et al.* 2012; Blackburn & Duellman 2013) that consistently recovered the relationships depicted in Figure 3b. As discussed in the previous section, the aforementioned studies differ from ours in analytical approach and sampling. Also, several clades among our optimal topologies received low support (specially GB values but not exclusively). For example, Hemiphractidae, Cryptobatrachinae, and Hemiphractinae are supported by GB = 1, 4, and 8 respectively. Also the genus *Cryptobatrachus* is supported by GB = 2 and JK = 70. Both optimal and expected support measures (Wheeler 2010) are often interpreted, prospectively, as indicative of clade stability—*i.e.*, relationships with high support are expected to be recovered in future studies based on additional samples (e.g., Siddall 2002; Hovenkamp 2004, 2009; Guayasamin *et al.* 2009; Vences *et al.* 2013).

Misfortune during our parsimony searches presented us with an illustrative example that contradicts this expectation. By mistake, we performed the same parsimony analyses presented herein but on a dataset that lacked the marker SLC8A3. This marker contains up to 1132 bp of relatively low variability (e.g., no indels and 321 parsimony informative characters according to a similarity alignment) and it was sampled only for 47 taxa (13 of them hemiphractids). The results of the analyses of the two datasets differed markedly (Fig. 3a, c), both in topology and clade support, and the only relationships among hemiphractid genera that did not change were the less supported (i.e., Cryptobatrachinae and Hemiphractinae). These results are not surprising as clade support values are not a measure of the power of additional evidence to overturn a hypothesis of relationships (Brower 2006; Grant & Kluge 2007, 2008b; Goloboff *et al.* 2008b; Wheeler 2010).



FIGURE 3. Summary of different hypothesis of phylogenetic relationships among hemiphractid genera indicating support; numbers above and below branches represent Goodman-Bremer values and jackknife proportions respectively. (a) Topology obtained from the parsimony total evidence analysis performed in this work (see Material and methods for details). (b) Topology obtained from maximum likelihood and Bayesian analyses of DNA sequences of 16S, ND1, POMC, and RAG1 by Blackburn & Duellman (2013). (c) Topology obtained from the parsimony analysis performed in this work but excluding the marker SLC8A3 from our dataset. See main text for discussion.

Branch length between several sister terminals is minimal and deserve discussion. Differentiation between the pairs of sister species *Cryptobatrachus fuhrmanni* and *C*. sp., and *Hemiphractus bubalus* and *H. johnsoni* is due to the fact that both *C*. sp. and *H. johnsoni* were only sampled for phenotypic characters. Given that most phenotypic characters included in our study are variable at the genus level (Mendelson *et al.* 2000), it is no surprise that only very few differences are observed between sister species. Within the *Gastrotheca marsupiata* species group (*sensu*)

this work) there are several cases of remarkably short branches between sister terminals putatively belonging to different species. This could indicate taxonomic issues (e.g., synonyms), misidentification of samples (from specimens to tubes), contamination of samples, or actual low molecular divergence. Potential taxonomic issues and possible misidentifications are discussed in the Systematics section.

Evolution of direct development. Our results support the MRCA of hemiphractids as a direct-developer (Fig. 2). Free-living aquatic tadpoles evolved within hemiphractids from direct development at least two different times and a maximum of eight. These surprising results constitute the first empirical evidence of the evolution of a freeliving tadpole from a direct-developer ancestor in anurans. The results of Mendelson et al. (2000) were ambiguous due to a basal polytomy, and the results of Wiens et al. (2007: 1892 and Fig. 1) and Gomez-Mestre et al. (2012: Fig. S2)—both using ML character reconstruction with a model with different rates of change between character states—recovered the MRCA of egg-brooding frogs as having a tadpole, with direct development evolving several times from it. However, Wiens et al. (2007) and Gomez-Mestre et al. (2012) favored a sub-optimal character reconstruction arguing that their own optimal solution was misleading. This sub-optimal solution implied that, within Gastrotheca, the free-living tadpole of various species evolved from a common ancestor with direct development. Our results also suggest that the diversification of Athesphatanura, the largest radiation in Nobleobatrachia both in terms of diversity of species and phenotypes, may have been coupled with a shift in the MRCA from direct-development to free-living tadpoles. Contrarily, the ancestors of both Nobleobatrachia and Athesphatanura + Hemiphractidae were inferred by Gomez-Mestre et al. (2012) as having a free-living tadpole. Limitations in taxon sampling hamper, nonetheless, an adequate test of this hypothesis. Regardless, our results highlight, once more, the importance of taxon sampling in the reconstruction of character evolution.

What constitutes "direct development" is important here inasmuch as this term has been differently defined through the literature (Altig & Johnston 1989; Hanken 2003, and references therein) since it was first coined by F.M. Balfour in the nineteenth century for ontogeny from which the larval stage has been lost (according to Hall 2000). In anurans, the term has been applied to frogs that go through a free-living (i.e., outside the egg capsule) but truncated endotrophic larval stage, to frogs that have no discernible larval morphology and appear to develop directly from gastrula to froglet. For example, all species of *Breviceps* for which the character is known have an embryo that hatches as an endotrophic tadpole, with apparently no mouthparts, that develops into a froglet while in a subterranean jelly nest (Channing 2001; Channing & Howel 2006; Harper et al. 2010)-a condition that several sources report as direct development (De Villiers 1929; McDiarmid & Altig 1999; Müller et al. 2007; Harper et al. 2010⁶). Given the disparity of available definitions, for purposes of this discussion we consider direct developers those species in which the embryo hatches from the egg as a fully formed, albeit miniature adult (*i.e.*, stage 46 of Gosner 1960). However, the ontogenetic trajectory of larval development within the egg capsule of nominal directdevelopers should not be conflated with the notion that both larva-specific features and metamorphosis were lost during development. Detailed studies reveal that in amphibians direct development does not necessarily involve the complete loss of larval features (Wassersug & Duellman 1984; McDiarmid & Altig 1999; Blackburn 2004; Müller 2006; Kerney et al. 2007, 2012; Ziermann & Diogo 2013) but, rather, the loss of the ability to live outside of the egg capsule.

If we consider that a free-living larval stage evolving from a direct developing ancestor has only been inferred in hemiphractids (this study), *Desmognathus* salamanders (Chippindale *et al.* 2004), and Seychelles caecilians (San Mauro *et al.* 2014), it is remarkable that in hemiphractids this apparent re-acquisition of free-living larvae has occurred two to eight times independently. Even more outstanding is that there is no evidence of a reversal in the older, more species-rich, and closely related group, Brachycephaloidea. As suggested by Kerney *et al.* (2012), the degree of developmental repatterning and loss of larval structures might constrain the re-appearance of a free-living larval stage. While in Brachycephaloidea larval characters are more reduced or even skipped (Elinson 2013; Ziermann & Diogo 2013, and references therein), in *Gastrotheca*, species with direct development pass through basically the same early developmental stages as those with free-living tadpoles (Wassersug & Duellman 1984) and retain at least some rudiments of oral features typical of species with a free-living tadpole (this is also the case for species of *Stefania*). However, these larval characters present in the direct developing embryos of *Gastrotheca* and *Stefania* need to be studied in detail and included in a cladistic analysis in order to understand their origin.

^{6.} This different use of terminology might be the reason why Gomez-Mestre *et al.* (2012) also treated *Breviceps* as a possible case of a free-living tadpole evolving from a direct developing ancestor.

A scenario that also needs further investigation is the amount of yolk available to the embryo. The reversion from direct development in *Gastrotheca* can be seen as an endotrophic tadpole that remains on the mother's pouch for only some time, and only when the yolk is almost depleted is the embryo released as a free-living and feeding tadpole. This is part of the continuum that has been recognized between direct development and free-living and feeding tadpoles (McDiarmid & Altig, 1999). Within *Gastrotheca*, the evolution of a tadpole from a direct-developing ancestor has happened at least once, at the base of the Andean radiation. However, the branching pattern and distribution of the character in the most exclusive clade containing *G galeata* KU 181700 and *G ochoai* KU 173499 implies several equally parsimonious solutions. The basal branches of the *Gastrotheca* Andean radiation are very short and result in several polytomies in the strict consensus (Fig. 2b).

Although the re-evolution of free-living larvae from direct-developing ancestors within Gastrotheca has already been discussed (e.g., Duellman & Hillis 1987; Duellman et al. 1988; Wiens et al. 2007), our analysis indicates that this has happened not only in Gastrotheca but also in Flectonotus and Fritziana. Contrary to what happens in species of Gastrotheca with a free-living larva, the sister group of Flectonotus has direct development (species of the genus Cryptobatrachus) with embryos not showing tadpole oral features (Wassersug & Duellman 1984). Tadpoles of *Flectonotus* are endotrophic and hatch at stages 38-41 of Gosner (1960) while those of Fritziana are facultative exotrophic and hatch at stages 30-41 (Duellman & Maness 1980; del Pino & Escobar 1981; Duellman & Gray 1983; Weygoldt & Carvalho-e-Silva 1991; Duellman et al. 2011). Although tadpoles of both Flectonotus and Fritziana lack labial teeth and papillae, those of Flectonotus have jaw sheaths weakly cornified and ventral velum small and present only laterally with the resulting gap equal to about half the width of the buccal floor, while those of *Fritziana* have small and keratinized jaw sheaths and complete ventral velum in the floor of the mouth (Duellman & Gray 1983; Wassersug & Duellman 1984). Tadpoles of Gastrotheca are known to hatch at different stages (\geq 31 of Gosner 1960), have labial teeth, papillae, keratinized jaw sheaths, complete ventral velum in the floor of the mouth, and filter rows of one filter plate overlapping the facing filter plate, so that uninterrupted gill filter rows bridge the gill slits (Wassersug & Duellman 1984). Thus, it is obvious from our cursory review of the literature that the free-living tadpole stage in *Flectonotus*, *Fritziana* and *Gastrotheca* has been gained not only independently but also at different developmental stages and with different morphological and trophic features.

The available information on the distribution of life-history strategies allows us to make some predictions about their occurrence in other groups, in a manner similar to Smith and Wheeler's (2006) approach to venomous fishes. We predict that in all species of *Fritziana* the embryo hatches as an aquatic tadpole. On the other hand, we expect that in females of all species of *Stefania*, Atlantic Forest *Gastrotheca*, and the species herein represented by the sample *G excubitor* MUSM 26280, a froglet emerges from the egg capsule. With the data at hand, we cannot make an educated guess about the hatching stage of embryos in the species herein represented by the sample *G griswoldi* MHNSM 20588.

Evolution of external gills. The monophyly of Hemiphractidae is supported by the phenotypic synapomorphies of female transport of eggs in a specialized depression or sac in the dorsum and bell-shaped gills in embryos (Noble 1927; Mendelson et al. 2000; this work). The evolution of both characters might be related to challenges faced by terrestrial eggs, such as desiccation, predation, and gas exchange. While transport of eggs by an adult might decrease predation and water loss, the presence of expanded, non-ephemeral, and vascularized external gills in embryos have been related to enhancing gas exchange (Warkentin 2002; Nokhbatolfoghahai & Downie 2008). External gills are present in the embryos of many anurans, both with aquatic and terrestrial eggs (Duellman & Trueb 1986; Nokhbatolfoghahai & Downie 2008). One might expect large, vascularized, and nonephemeral external gills in embryos of species with direct development because these eggs are usually larger than those of species with a tadpole stage (implying a proportionally smaller surface area for gas exchange) and the eggs hatch when their rate of oxygen consumption is at or near a peak (Mitchell & Seymour 2000). Interestingly, this prediction is only met by hemiphractid embryos, while other direct-developing anurans show no external gills or they are rudimentary and ephemeral. The tail has been proposed as an alternative respiratory surface (e.g., Peters 1876; Townsend & Stewart 1985; Thibaudeau & Altig 1999; Nokhbatolfoghahai et al. 2010). Observations on species of Brachycephaloidea (the other major radiation of direct-developing Neotropical frogs with terrestrial eggs) show a highly vascularized and expanded tail applied close to the perivitelline membrane, suggesting a role in respiratory exchange [e.g., Craugastor augusti (Valett & Jameson 1961 but see Townsend & Stewart 1985: 433), Pristimantis urichi (Nokhbatolfoghahai et al. 2010), Ischnocnema guentheri (Lynn & Lutz 1946), and several

species of *Eleutherodactylus* (e.g., Sampson 1904; Noble 1925; Lynn 1942; Townsend & Stewart 1985)]. Nonetheless, external gills have been reported for a number of *Eleutherodactylus* such as *E. portoricensis* (Gitlin 1944; Townsend & Stewart 1985), *E. martinicensi* (Chibon 1960), *E. johnstonei* (Adamson *et al.* 1960), *E. planirostris* (Hughes 1959), and *E. inoptatus* Noble (1925, 1927), but in all cases the external gills are small and ephemeral, which is the norm in anurans.

Also relevant is that Gitlin (1944) reported that the external gills of *Eleutherodactylus portoricensis* are derived from the third branchial arch while in hemiphractids they derive from the first or the first and second arches (del Pino & Escobar 1981; Mendelson *et al.* 2000). Within hemiphractids, the sister taxa *Cryptobatrachus* and *Flectonotus* have a single pair of gills derived from branchial arch I, while in *Gastrotheca*, *Fritziana*, *Hemiphractus*, and *Stefania* two pairs of gills are derived from branchial arches I and II respectively (see character 43). Unfortunately, the branchial arch origin of external gills, when present in anuran embryos, is seldom reported in the literature and we could not infer the ancestral state for hemiphractids. In any case, we hypothesize that the external gills of hemiphractids are homologous to those of other Nobleobatrachia so that their unique bell shape and non-transient nature are modifications within the same transformation series.

Within the clade containing *Gastrotheca*, *Fritziana*, *Hemiphractus*, and *Stefania* further variation exists regarding the fusion of the gill stalks (character 44) and of the two pairs of bell-shaped gills (character 45). On one hand, the fusion of the gill stalks is reconstructed as a derived character within *Gastrotheca* with at least five origins (*G christiani*, *G galeata*, *G guentheri*, *G testudinea*, and the MRCA of *G griswoldi* KU 181701 and *G pseustes*). On the other hand, the fusion of the two pairs of bell-shaped gills has been observed in the 21 species of *Gastrotheca* where the character has been studied and in *H. fasciatus*. However, the character is unknown for *G fissipes*, *G megacephala*, *G prasina*, *G pulchra*, and *G recava*.

Systematics

On the basis of our results, we provide a revised taxonomy of the family Hemiphractidae. We recognized two subfamilies, six genera, and four species groups of *Gastrotheca*. Unambiguous transformations (*i.e.*, shared by all optimal trees) for the supraspecific taxa included in this section are listed in Appendix 5. Because the majority of the phenotypic characters that we analyzed have only been scored for a handful of hylid species (characters of Mendelson *et al.* 2000), their status as synapomorphies needs to be tested in a dataset with a larger representation of non-hylids nobleobatrachians. In addition to a diagnosis for all supraspecific taxa considered, we provide a characterization summarizing the main known phenotypic characteristics of each genus. A graphical summary of our taxonomy is presented in Fig. 2b.

Family: Hemiphractidae Peters, 1862

Immediately more inclusive taxon. Unclear. We recovered a sister relationship with Athesphatanura (see also Pyron & Wiens 2011; Fouquet *et al.* 2013) and the more inclusive taxon would be a clade nearly equivalent to Cladophrynia (Frost *et al.* 2006) but with the inclusion of *Hemiphractus*. Other works (e.g., Heinicke *et al.* 2009; Padial *et al.* 2014) recovered a sister relationship with Brachycephaloidea and the most inclusive taxon would be Orthobatrachia.

Sister taxon. Unclear. Athesphatanura (Pyron & Wiens 2011; Fouquet *et al.* 2013; this work) or Brachycephaloidea (Heinicke *et al.* 2009; Padial *et al.* 2014).

Content. Cryptobatrachinae Frost, Grant, Faivovich, Bain, Haas, Haddad, de Sá, Channing, Wilkinson, Donnellan, Raxworthy, Campbell, Blotto, Moler, Drewes, Nussbaum, Lynch, Green, and Wheeler, 2006, and Hemiphractinae Peters, 1862

Type genus. Hemiphractus Wagler, 1828.

Diagnosis. (1) bell-shaped gills in embryos (character 42, $0 \rightarrow 1$); (2) female transport of eggs in a specialized depression or sac in the dorsum (character 47, $0 \rightarrow 4$). All unambiguous transformations are listed in Appendix 5.

A broad *m. abductor brevis plantae halluces* has been suggested as a synapomorphy (Burton 2004; Faivovich *et al.* 2005) but this character has not been included in our analysis. Direct developing has also been suggested as a

synapomorphy (Mendelson *et al.* 2000) and in our analysis the MRCA of Hemiphractidae is reconstructed as a direct developer; however, the ancestral state of the MRCA of Athesphatanura + Hemiphractidae is ambiguous and no transformation could be inferred with certainty.

Distribution. Neotropical lowlands and montane rainforests, with a few species known from humid highelevation Andean grasslands and the rocky summits of the tepuis of the Guiana Shield (Argentina, Bolivia, Brazil, Colombia, Costa Rica, Ecuador, Guyana, Panama, Peru, both islands of Trinidad and Tobago, and Venezuela).

Comments. According to the results of Heinicke *et al.* (2009), Hemiphractidae is the sister taxon of Brachycephaloidea and they named this clade Orthobatrachia. However, all studies with denser taxon sampling of Athesphatanura and Brachycephaloidea, and similar character sampling (Pyron & Wiens 2011; Gomez-Mestre *et al.* 2012; Fouquet *et al.* 2013; this work) reject Orthobatrachia. Padial *et al.* (2014) recovered Orthobatrachia with a dense taxon sampling of Brachycephaloidea but their samples of Athesphatanura were limited to eight species of Hylidae and two species of Leptodactylidae. The phylogenetic position of Hemiphractidae remains unsolved.

Subfamily: Cryptobatrachinae Frost, Grant, Faivovich, Bain, Haas, Haddad, de Sá, Channing, Wilkinson, Donnellan, Raxworthy, Campbell, Blotto, Moler, Drewes, Nussbaum, Lynch, Green, and Wheeler, 2006

Immediately more inclusive taxon. Hemiphractidae Peters, 1862.

Sister taxon. Hemiphractinae Peters, 1862.

Content. Cryptobatrachus Ruthven, 1916, and Flectonotus Miranda-Ribeiro, 1926.

Type genus. Cryptobatrachus Ruthven, 1916.

Diagnosis. (1) Absence of supraorbital flange (character 36, 1–>0), with the same characters state coded for *Fritziana ohausi, Gastrotheca griswoldi*, and *G. marsupiata*; (2) one pair of bell-shaped gills exclusively derived from branchial arch I (although this character is diagnostic from its sister taxon, it was not retrieved as a synapomorphy because the ancestral state is unknown). All unambiguous transformations are listed in Appendix 5.

Distribution. Northern Andes of Colombia and Venezuela (Cordilleras Oriental, Central and Occidental, Sierra de Perijá, and Cordillera de Mérida), Sierra Nevada de Santa Marta in Colombia, Cordillera de la Costa in Venezuela, and both islands of Trinidad and Tobago.

Comments. The sister relationship between *Cryptobatrachus* and *Flectonotus* was unexpected. Several studies assumed a sister relationship of *Cryptobatrachus* with *Stefania* (e.g., Duellman & Hoogmoed 1984; Lynch 2008; Wiens *et al.* 2007; Schmid *et al.* 2013 "2012") based on overall external similarity. Frost *et al.* (2006) recovered a sister relationship between *Cryptobatrachus* and *Stefania*, a clade to which they assigned the family rank.

Genus: Cryptobatrachus Ruthven, 1916

Immediately more inclusive taxon. Cryptobatrachinae Frost, Grant, Faivovich, Bain, Haas, Haddad, de Sá, Channing, Wilkinson, Donnellan, Raxworthy, Campbell, Blotto, Moler, Drewes, Nussbaum, Lynch, Green, and Wheeler, 2006.

Sister taxon. Flectonotus Miranda-Ribeiro, 1926.

Content (6 species): *Cryptobatrachus boulengeri* Ruthven, 1916, *C. conditus* Lynch, 2008, *C. fuhrmanni* (Peracca, 1914), *C. pedroruizi* Lynch, 2008, *C. remotus* Infante-Rivero, Rojas-Runjaic, and Barrio-Amorós, 2009, and *C. ruthveni* Lynch, 2008.

Type species. Cryptobatrachus boulengeri Ruthven, 1916, by original designation.

Diagnosis. (1) ventral crest of alae of parasphenoid present (character 3, 0–>1), with the same characters state coded for *Gastrotheca dendronastes*, *G galeata*, *G guentheri*, *G microdiscus*, *G plumbea*, *G riobambae*, and *Hemiphractus*; (2) cultriform process posterior to orbitonasal foramina (character 5, 1–>0), with the same characters state coded for *Stefania scalae*; (3) anteromedial process of neopalatine present (character 11, 0–>1); (4) medial contact of vomers (character 17, 0–>1), with the same character state coded for *Fritziana ohausi*, *G dendronastes*, *G guentheri*, *G plumbea*, *G walkeri*, *H. bubalus*, and *H. johnsoni*; (5) subarticular adhesive pads on distal subarticular tubercles of outer fingers (although this character was not included in our analysis). Because the relationships among *Cryptobatrachus* are ambiguous (a polytomy in our strict consensus tree), the transformations

reported herein are only shared among some of the optimal trees (Appendix 5). Nonetheless, at least the character states listed above in points 3 and 5 seem to be shared among all species of the genus (Lynch 2008), therefore representing unambiguous transformations regardless of the branching order within the genus.

Characterization. (1) one pair of bell-shaped gills derived from branchial arch I covering 25–50% of body of the embryo; (2) females carrying exposed eggs on their backs; (3) direct development; (4) embryos without oral larval features; (5) males without vocal sacs or apertures and apparently not vocalizing; (6) superficial mandibular musculature Type A of Tyler & Duellman (1995) (*i.e.*, the *m. submentalis* is of moderate size, the *m. intermandibularis* is differentiated by the presence of an apical element, the fibers of which are in contact medially, the customary sheet-like element of the *m. intermandibularis* bears a median raphe, the *m. interhyoideus* extends slightly posterior to the mandibles); (7) sphenethmoid weakly ossified anteriorly; (8) subarticular adhesive pads on distal subarticular tubercles of outer fingers; (9) ventral out-growth of the palatine growing medially until it articulates with the distal edge of the dentigerous process (del Pino & Escobar 1981; Duellman & Hoogmoed 1984; Wassersug & Duellman 1984; Tyler & Duellman 1995; Mendelson *et al.* 2000; Lynch 2008).

Distribution. Mountain rainforests of the northern Andes of Colombia and Venezuela (Cordilleras Oriental, Central and Occidental, and Sierra de Perijá) and Sierra Nevada de Santa Marta in Colombia.

Comments. The monophyly of the genus has been corroborated on the basis of phenotypic characters (Duellman & Hoogmoed 1984; Mendelson *et al.* 2000; Lynch 2008). Most molecular studies did not include DNA sequences of more than one terminal (Darst & Cannatella 2004; Faivovich *et al.* 2005; Wiens *et al.* 2005, 2006; Frost *et al.* 2006; Schmid *et al.* 2013 "2012"; Zhang *et al.* 2013). Padial *et al.* (2014) is the only exception and found that *C. boulengeri* and *C. fuhrmanni* did not form a monophyletic group. Lynch's (2008) most extensive study evaluated phenotypic characters and recognized six species, proposing the following phylogenetic relationships on the basis of morphological characters: *Stefania (C. nicefori, (C. fuhrmanni, (C. boulengeri, C. conditus, C. pedroruizi, C. ruthveni)*)).

Although the genus *Cryptobatrachus* is monophyletic (Fig. 2b), its intrageneric relationships are ambiguous in our strict consensus tree (*i.e.*, a polytomy). Thus, the relationships postulated by Lynch (2008) cannot be rejected nor corroborated. According to the large genetic distances observed in the sequences of putative *C. fuhrmanni* studied here, it seems that there could be at least two species under this name. Most likely, the new species would correspond to populations from the Cordillera Oriental of Colombia, for which the name *C. fuhrmanni orientalis* Rivero, 1968 "1966" might be available. However, we refrain from taking any taxonomic action until detailed comparisons are performed. We follow Infante-Rivero *et al.* (2009 "2008") and consider *C. nicefori* Cochran and Goin, 1970 (a species only known from the holotype) as a hyline unassigned to genus ("*Hyla*" *nicefori*), although possibly in *Hyloscirtus*.

Genus: Flectonotus Miranda-Ribeiro, 1926

Immediately more inclusive taxon. Cryptobatrachinae Frost, Grant, Faivovich, Bain, Haas, Haddad, de Sá, Channing, Wilkinson, Donnellan, Raxworthy, Campbell, Blotto, Moler, Drewes, Nussbaum, Lynch, Green, and Wheeler, 2006.

Sister taxon. Cryptobatrachus Ruthven, 1916.

Content (2 species): Flectonotus fitzgeraldi (Parker, 1934) and F. pygmaeus (Boettger, 1893).

Type species. Nototrema pygmaeum Boettger, 1893.

Diagnosis. (1) pouch formed by two longitudinal flaps of skin that are adherent middorsally over the eggs forming an enclosed pouch (character 41, 0–>2); (2) endotrophic tadpoles hatching at stage \geq 30 of Gosner (1960) (character 46, 3–>2). All unambiguous transformations are listed in Appendix 5.

Characterization. (1) one pair of bell-shaped gills derived from branchial arch I covering $\leq 25\%$ of the body of embryo; (2) females carrying eggs on their backs inside a pouch formed by two longitudinal flaps of skin that are adherent middorsally over the eggs, forming an enclosed pouch; (3) in females that are not reproductively active, flaps either meeting along the midline of the dorsum, thereby closing the dorsal pouch, or leaving a gap of 1–2 mm; (4) embryos hatching as non-feeding tadpoles at advance stage (38–41 of Gosner, 1960); (5) tadpoles with jaw sheaths weakly cornified, lacking labial teeth and papillae, and ventral velum small and present only laterally with the resulting gap equal to about half the width of the buccal floor; (6) nasal bones small, slender, widely separated medially by the sphenethmoid; (7) males producing advertisement calls and having gaping holes as vocal sac

apertures; (8) superficial mandibular musculature Type A of Tyler and Duellman (1995) (*i.e.*, the *m. submentalis* is of moderate size, the *m. intermandibularis* is a single, undifferentiated sheet bearing a median raphe, the *m. interhyoideus* extends slightly posterior to the mandibles) (del Pino & Escobar 1981; Duellman & Gray 1983; Wassersug & Duellman 1984; Tyler & Duellman 1995; Mendelson *et al.* 2000; Duellman *et al.* 2011).

Distribution. Restricted to the montane rainforests of the northern Cordillera Oriental of Colombia, Cordillera de Mérida and Cordillera de la Costa in Venezuela, and both islands of Trinidad and Tobago.

Comments. Detailed reviews are provided by Duellman & Gray (1983) and Duellman *et al.* (2011). Weygoldt & Carvalho-e-Silva (1991) accepted the tree of Duellman & Gray (1983), within which *Flectonotus* was recovered as paraphyletic with respect to *Fritziana* (see also Duellman *et al.* 2011: Fig. 1). Mendelson *et al.* (2000) recovered *Flectonotus pygmaeus* as the sister of the clade formed by *Fritziana goeldii* + *Fritziana ohausi.* In that study *Flectonotus* + *Fritziana* was supported by the synapomorphies: 1) quadratojugal not articulating with the maxilla; 2) brooding pouch formed by dorsolateral folds of skin; 3) overlap between *m. intermandibularis* and *m. submentalis*; and 4) absence of supplementary elements of *m. intermandibularis.* Nevertheless, Mendelson *et al.* (2000) could not test the monophyly of *Flectonotus* with respect to *Fritziana* because they only included *Flectonotus pygmaeus* in their analysis. Duellman *et al.* (2011), using DNA sequences of representatives of all species of both groups, found both genera to be monophyletic and not sister taxa, therefore justifying the resurrection of *Fritziana* from the synony of *Flectonotus.* Our results corroborate the hypothesis of Duellman *et al.* (2011).

Subfamily: Hemiphractinae Peters, 1862

Immediately more inclusive taxon. Hemiphractidae Peters, 1862.

Sister taxon. Cryptobatrachinae Frost, Grant, Faivovich, Bain, Haas, Haddad, de Sá, Channing, Wilkinson, Donnellan, Raxworthy, Campbell, Blotto, Moler, Drewes, Nussbaum, Lynch, Green, and Wheeler, 2006.

Content. Fritziana Mello-Leitão, 1937, Gastrotheca Fitzinger, 1843, Hemiphractus Wagler, 1828, and Stefania Rivero, 1968

Type genus. Hemiphractus Wagler, 1828.

Diagnosis. (1) Posteromedial process of vomer smooth (character 12, 0–>1), with a reversal in *Fritziana* ohausi, the MRCA of *Gastrotheca plumbea* and *G. testudinea*, and a transformation into a different character state in *Hemiphractus*; (2) postorbital process short (character 20, 0–>1), with the same character state coded for *Cryptobatrachus fuhrmanni*, a reversal in *F. goeldii* and *G. griswoldi*, and a transformation into a different character state state in *G. guentheri*, *G. megacephala*, and *Hemiphractus*; (3) zygomatic ramus long, articulating only with postorbital process of maxilla (character 39, 0–>2), with transformations into different character states in *F. goeldii*, *F. ohausi*, *G. galeata*, *G. griswoldi*, *G. walkeri*, *H. bubalus*, *H. johnsoni*, *H. proboscideus*, *H. scutatus*, and *Stefania scalae*; (4) two pairs of bell-shaped gills derived from branchial arches I and II (although this character is diagnostic from its sister taxon, it was not retrieved as a synapomorphy because the ancestral state is unknown). All unambiguous transformations are in Appendix 5.

Distribution. Neotropical lowlands and montane rainforests with a few species known from humid highelevation Andean grasslands and the rocky summits of the tepuis of the Guiana Shield (Argentina, Bolivia, Brazil, Colombia, Costa Rica, Ecuador, Guyana, Panama, Peru, and Venezuela).

Genus: Fritziana Mello-Leitão, 1937

Immediately more inclusive taxon. Hemiphractinae Peters, 1862.

Sister taxon. An unnamed clade containing Gastrotheca Fitzinger, 1843 and Hemiphractus Wagler, 1828.

Content (4 species): *Fritziana fissilis* (Miranda-Ribeiro, 1920), *F. goeldii* (Boulenger, 1895), *F. ohausi* (Wandolleck, 1907), and *F. ulei* Miranda-Ribeiro, 1926.

Type species. Hyla goeldii Boulenger, 1895.

Diagnosis. (1) neopalatines not extending medially to ossified sphenethmoid (character 9, 1–>0), with the same characters state coded for *Gastrotheca griswoldi*, *G. testudinea*, and *G. walkeri*; (2) quadratojugal not

articulating with maxilla (character 23, 0–>1), with the same characters state coded for *Flectonotus pygmaeus*; (3) distal ends of alary processes diverging laterally (character 26, 0–>1), with the same characters state coded for *G* marsupiata, *G* megacephala, and *G* walkeri; (4) facultative endotrophic tadpoles hatching at stage \geq 30 of Gosner (1960) (character 46, 3–>2); (5) lateral skin folds not adherent middorsally over eggs (although this character is diagnostic from all other hemiphractids, it was not retrieved as a synapomorphy because the ancestral state is unknown). All unambiguous transformations are listed in Appendix 5.

Characterization. (1) two pairs of bell-shaped gills derived from branchial arches I and II covering $\leq 25\%$ of the embryo; (2) females of *Fritziana goeldii* and *F. ohausi* carrying eggs on their backs with lateral skin folds only bordering the eggs laterally, in some females of *F. fissilis* the lateral folds either cover the eggs middorsally but are not adherent, whereas in others the middorsal area is not covered; (3) longitudinal folds becoming apparent on the female's back only during mating; (4) embryos hatching as facultative non-feeding tadpoles at an advanced stage (\geq 30 of Gosner 1960); (5) tadpoles with small and keratinized jaw sheaths, lacking labial teeth and papillae, and complete ventral velum in the floor of the mouth; (6) large nasals nearly in contact anterior to the sphenethmoid; (7) males producing advertisement calls and having gapping holes as vocal sac apertures; (8) superficial mandibular musculature Type A of Tyler & Duellman (1995) (del Pino & Escobar 1981; Duellman & Gray 1983; Wassersug & Duellman 1984; Weygoldt & Carvalho-e-Silva 1991; Tyler & Duellman 1995; Mendelson *et al.* 2000; Duellman *et al.* 2011).

Distribution. Endemic to the Atlantic Forest of eastern Brazil.

Comments. Pertinent literature is shared with *Flectonotus*. Thus, the remarks made above for *Flectonotus* apply to this genus. Duellman *et al.* (2011) inferred *F. ohausi* to be sister of the clade *F. fissilis* + *F. goeldii*. Schmid *et al.* (2013 "2012") obtained a different topology (*F. goeldii*, (*F. cf. fissilis*, (*F. fissilis* + *F. ohausi*))), in which *F. cf. fissilis* might represent a new species.

It is obvious from our molecular results that the current species diversity within *Fritziana* is vastly underestimated and that as many as four more species might be recognized. These putative new species are currently hidden under the name *Fritziana fissilis*. Careful examination of the external morphology of the preserved specimens sequenced in our study revealed that they match the description of *F. fissilis*. Furthermore, we did not find diagnostic characters among the specimens. We identified the specimen MNRJ 62845 as *Fritziana fissilis sensu stricto* because it was collected near the type locality in Município Nova Friburgo, Rio de Janeiro, Brazil but this identification should be considered tentative and revisited as more evidence becomes available. The species *Fritziana ulei* (Miranda-Ribeiro, 1926) was recently considered valid by Folly *et al.* (2014) and might be included in our analysis inasmuch as this species in only known from three specimens limiting our understanding of the variation of current diagnostic features.

Genus: Gastrotheca Fitzinger, 1843

Immediately more inclusive taxon. An unnamed clade containing *Gastrotheca* Fitzinger, 1843 and *Hemiphractus* Wagler, 1828.

Sister taxon. Hemiphractus Wagler, 1828.

Content (68 species): *Gastrotheca abdita* Duellman, 1987, *G aguaruna* Duellman, Barley, and Venegas, 2014, *G albolineata* (Lutz and Lutz, 1939), *G andaquiensis* Ruiz-Carranza and Hernández-Camacho, 1976, *G angustifrons* (Boulenger, 1898), *G antomia* Ruiz-Carranza, Ardila-Robayo, Lynch, and Restrepo-Toro, 1997, *G antoniiochoai* (De la Riva and Chaparro, 2005), *G aratia* Duellman, Barley, and Venegas, 2014, *G argenteovirens* (Boettger, 1892), *G atympana* Duellman, Lehr, Rodríguez, and von May, 2004, *G aureomaculata* Cochran and Goin, 1970, *G bufona* Cochran and Goin, 1970, *G carinaceps* Duellman, Trueb, and Lehr, 2006, *G christiani* Laurent, 1967, *G chrysosticta* Laurent, 1976, *G cornuta* (Boulenger, 1898), *G dendronastes* Duellman, 1983, *G dunni* B. Lutz, 1977, *G dysprosita* Duellman, 2013, *G ernestoi* Miranda-Ribeiro, 1920, *G espeletia* Duellman and Hillis, 1987, *G excubitor* Duellman and Fritts, 1972, *G fissipes* (Boulenger, 1888), *G flamma* Juncá and Nunes, 2008, *G fulvorufa* (Andersson, 1911), *G galeata* Trueb and Duellman, 1978, *G gracilis* Laurent, 1969, *G griswoldi* Shreve, 1941, *G guentheri* (Boulenger, 1882), *G helenae* Dunn, 1944, *G lateonota* Duellman and Trueb, 1988, *G lauzuricae* De la Riva, 1992, *G litonedis* Duellman and Hillis, 1987, *G marsupiata* (Duméril and Bibron, 1841), *G megacephala* Izecksohn, Carvalho-e-Silva, and Peixoto, 2009, *G microdiscus* (Andersson, 1910), *G monticola* Barbour and Noble, 1920, *G nebulanastes*

Duellman, Catenazzi, and Blackburn, 2011, *G nicefori* Gaige, 1933, *G ochoai* Duellman and Fritts, 1972, *G orophylax* Duellman and Pyles, 1980, *G ossilaginis* Duellman and Venegas, 2005, *G ovifera* (Lichtenstein and Weinland, 1854), *G pacchamama* Duellman, 1987, *G pachachacae* Catenazzi and von May, 2011, *G peruana* (Boulenger, 1900), *G phalarosa* Duellman and Venegas, 2005, *G phelloderma* Lehr and Catenazzi, 2011, *G piperata* Duellman and Köhler, 2005, *G plumbea* (Boulenger, 1882), *G prasina* Teixeira, Vechio, Recoder, Carnaval, Strangas, Damasceno, Sena, and Rodrigues, 2012, *G pseustes* Duellman and Hillis, 1987, *G psychrophila* Duellman, 1974, *G pulchra* Caramaschi and Rodrigues, 2007, *G rebeccae* Duellman and Trueb, 1988, *G recava* Teixeira, Vechio, Recoder, Carnaval, Strangas, Damasceno, Sena, and Burrowes, 1986, *G splendens* (Schmidt, 1857), *G stictopleura* Duellman, Lehr, and Aguilar, 2001, *G testudinea* (Jiménez de la Espada, 1870), *G trachyceps* Duellman, 1987, *G walkeri* Duellman, 1980, *G weinlandii* (Steindachner, 1892), *G williamsoni* Gaige, 1922, and *G zeugocystis* Duellman, Lehr, Rodríguez, and von May, 2004.

Type species. Hyla marsupiata Duméril and Bibron, 1841.

Diagnosis. (1) Enclosed pouch with a posterior opening (character 41, 0->3); (2) presence of two fused pairs of bell-shaped gills derived from branchial arches I and II (character 45, 1->0), with the same character state coded for *Hemiphractus fasciatus*. All unambiguous transformations are listed in Appendix 5.

Characterization. (1) Two fused pairs of bell-shaped gills derived from branchial arches I and II (the gill stalks can be fused or not) covering most of the embryo; (2) females carrying eggs on their backs inside an enclosed pouch with a posterior opening; (3) in females that have reproduced but are not reproductively active the posterior opening is present; (4) in most species embryos go through direct development but in some species embryos hatch as feeding tadpoles at an advanced stage (\geq 31 of Gosner, 1960); (5) embryos of species with direct development having oral larval features, although their quantity dramatically varies among species; (6) tadpoles having labial teeth, papillae, keratinized jaw sheaths, and complete ventral velum in the floor of the mouth, filter rows of one filter plate overlapping the facing filter plate, so that uninterrupted gill filter rows bridge the gill slits; (7) males of most species producing advertisement calls and having vocal sac apertures either absent or present as gaping holes, slits, or small orifices; (8) superficial mandibular musculature Type A or B of Tyler & Duellman (1995) (del Pino & Escobar 1981; Wassersug & Duellman 1984; Tyler & Duellman 1995; Mendelson *et al.* 2000).

Distribution. Lowland and mountain rainforests, and humid high grasslands of the Andes, with an ample distribution from Costa Rica through Panama and the tropical Andes to Ecuador in the Pacific and northern Argentina in the east, Cordillera de la Costa of Venezuela, and the Brazilian Atlantic Forest.

Comments. The literature dealing with this large genus of egg-brooding frogs is extensive and includes studies on the taxonomy (e.g., Duellman & Fritts 1972; Duellman 1974; Duellman & Hillis 1987; Duellman et al. 1988; Duellman & Venegas 2005; Teixeira et al. 2012), developmental biology (del Pino & Escobar 1981; del Pino et al. 2007 and references therein), and adult and tadpole morphology (e.g., Wassersug & Duellman 1984; Tyler & Duellman 1995; Haas 2003; Burton 2004). Dubois (1987 "1986") recognized three subgenera (Gastrotheca, Duellmania, and Opisthodelphys), an arrangement that has been largely ignored because the taxa proved to be nonmonophyletic (Mendelson et al. 2000; Wiens et al. 2007), and were based on notions that did not regard monophyly as of classificatory importance. Duellman et al. (1988), on the basis of immunological distances, recognized four species groups (the G marsupiata, G nicefori, G ovifera, and G plumbea groups). Except for the G marsupiata group, the monophyly of these groups has not been corroborated. Mendelson et al. (2000) included 17 species of Gastrotheca and rejected the monophyly of all previously suggested species groups. They also recovered Hemiphractus nested within Gastrotheca. However, Mendelson et al. (2000) continued to recognize both genera pending a more complete phylogenetic study. Subsequent studies (e.g., Faivovich et al. 2005, Wiens et al. 2005, 2007) have not recovered Hemiphractus nested within Gastrotheca. Wiens et al. (2007) found that none of the species groups of Duellman et al. (1988) were monophyletic, rearranged the content of the G marsupiata and G plumbea groups (the later including G nicefori, which had formerly been placed in a monotypic group), and left all of the species of the former G ovifera group plus G fissipes, G walkeri, and G galeata unassigned to a group. Teixeira et al. (2012) found, on the basis on DNA sequences, that the Atlantic forest species of Gastrotheca do not form a monophyletic group. Subsequently, Blackburn & Duellman (2013) presented additional corroborating evidence of the non-monophyly of the Atlantic Forest species of Gastrotheca. Schmid et al. (2013 "2012") proposed five species groups (although the content of these groups was not explicitly stated), with Govifera and G galeata unassigned to a group and with the following relationships (G fissipes group ((G

williamsoni group, G. longipes group) (G. galeata (G. ovifera (G. plumbea group, G. marsupiata group))))). However, their study presents some problems. First, the tree was inferred from a partially constrained topology (Schmid *et al.* 2013 "2012": 86) such that Hemiphractidae was monophyletic, *Eleutherodactylus* + *Diasporus* was the closest relative of Hemiphractidae, and the remaining outgroups were set to follow the results of Heinicke *et al.* (2009). Second, the species contents of the *G. longipes*, *G. marsupiata*, and *G. plumbea* groups were not explicitly stated and cannot be deduced from the publication. Third, there is evidence in the form of DNA sequences suggesting that the *G. fissipes* group, at least as formulated by Schmid *et al.* (2013 "2012"), is not monophyletic (Teixeira *et al.* 2012; Blackburn & Duellman 2013). Fourth, the monophyly of the *G. williamsoni* group was not evaluated because only *G. walkeri* was included in the phylogeny.

According to Haas (2003), the following larval characters sampled for *Gastrotheca riobambae* are potential synapomorphies of *Gastrotheca*: (1) *m. subarcualis rectus* I portion with origin from ceratobranchial III absent (Haas 35.0); (2) functional larval *m. levator mandibulae lateralis* present (Haas 56.0); (3) *ramus mandibularis* (cranial nerve V3) posterior runing through the *m. levator mandibulae externus* group (Haas 65.1); (4) posterior palatoquadrate clearly concave with bulging and pronounced margin (Haas 68.1); (5) processus pseudopterygoideus long (Haas 77.2); and (6) dorsal connection from processus muscularis to commissura quadrato-orbitalis (Haas 78.2). However, some or all of these characters may be located as less inclusive levels of universality within the genus or might be shared with members of *Flectonotus* and/or *Fritziana*. None of the different subgeneric taxonomies (*i.e.*, subgenera, species groups, clades) historically proposed for *Gastrotheca* (*i.e.*, Dubois 1987 "1986"; Duellman *et al.* 1988; Wiens *et al.* 2007; Schmid *et al.* 2013 "2012"; Blackburn & Duellman, 2013) are monophyletic according to our results. Subsequently, we recognyzed four monophyletic species groups: *G. fissipes* species group, *G. longipes* species group, *G. marsupiata* species group, and *G microdiscus* species group (see respective accounts for details).

It is obvious from our phylogenetic results and comparison of genetic distances that some of the identifications of DNA sequences available in the literature deserve careful examination of the voucher specimens to reassess the taxonomic identity of those samples [compare *G excubitor* KU 173171 (Wiens *et al.* 2007) versus MUSM 26280 (Duellman *et al.* 2011b); *G griswoldi* MHNSM 20588 (Lehr *et al.* 2005) versus KU 181701 (Wiens *et al.* 2007); *G nicefori* KU 181071 (Wiens *et al.* 2007) versus MHUA A 5716 (this work); and *G riobambae* KU 178468 (Wiens *et al.* 2007) versus UIMNH 94580 (Ruvinsky & Maxson 1996)]. In the case of *G nicefori*, our sample MHUA A 5716 comes from near the type locality [Pensilvania, Departamento Caldas, Colombia, according to the original description by Gaige (1933)], while KU 181071 comes from Venezuela (Táchira: 11 km S Delicias, 1750 m a.s.l.). The available name *Gastrotheca yacambuensis* Yústiz, 1976, could correspond to the Venezuelan populations (see also Barrio-Amorós, 1999 "1998") but we refrain from taking any taxonomic actions until more samples become available. The specimen *G riobambae* UIMNH 94580 most likely is a misidentified specimen of *G pseustes*, inasmuch as it was collected from a locality far from the known distribution of *G riobambae* (Frenkel *et al.* 2010), where specimens of *G pseustes*, and the genetic distances between the two samples = 0.5% (see Results). However, direct examination of the voucher UIMNH 94580 is needed to confirm its identification.

Gastrotheca fissipes species group

Immediately more inclusive taxon. An unnamed clade containing the *Gastrotheca fissipes* species group and *G. marsupiata* species group.

Sister taxon. An unnamed clade containing the *Gastrotheca marsupiata* species group and the *G. microdiscus* species group.

Content (6 species): Gastrotheca fissipes, G. flamma, G. megacephala, G. prasina, G. pulchra, and G. recava.

Diagnosis. Unambiguous transformations are restricted to nucleotides (Appendix 5), inasmuch as our dataset mainly contains phenotypic characters for a single species (*G megacephala*); however, several characters (*i.e.*, 16, 20, 22, 26, 27, 34, 35, 37, 38, 40) include transformations that are potential synapomorphies of this clade.

Distribution. Atlantic forest, from the State of Espírito Santo in the south to the State of Pernambuco in the north.

Comments. Although *Gastrotheca flamma* is not included in our phylogeny, it is tentatively assigned to this clade on overall similarity with *G. pulchra*.

Gastrotheca longipes species group

Immediately more inclusive taxon. Gastrotheca Fitzinger, 1843.

Sister taxon. An unnamed clade containing all other species of Gastrotheca.

Content (12 species): *Gastrotheca andaquiensis*, *G. angustifrons*, *G. antomia*, *G. bufona*, *G. cornuta*, *G. dendronastes*, *G. guentheri*, *G. helenae*, *G. longipes*, *G. walkeri*, *G. weinlandii*, and *G. williamsoni*.

Diagnosis. (1) vomers with medial contact (character 17, $0 \rightarrow 1$), with the same character state coded for *Cryptobatrachus*, *Fritziana ohausi*, *Gastrotheca plumbea*, *Hemiphractus helioi*, *H. johnsoni*, and a reversal in *G cornuta*; (2) pouch type 2 (del Pino 1980), with the same characters state coded for *G ovifera* (although this character was not included in our analysis). All unambiguous transformations are listed in Appendix 5.

Distribution. Lowlands and highlands of Central America (Costa Rica and Panama) and South America (Colombia, Ecuador, Peru, and Venezuela).

Comments. Although *Gastrotheca andaquiensis*, *G. angustifrons*, *G. antomia*, *G. bufona*, and *G. williamsoni* are not included in our phylogeny, they are tentatively assigned to this clade based on overall similarity with the other species (Duellman *et al.* 1988; Ruiz-Carranza *et al.* 1997).

Gastrotheca marsupiata species group

Immediately more inclusive taxon. An unnamed clade containing the *Gastrotheca marsupiata* species group and the *Gastrotheca microdiscus* species group.

Sister taxon. Gastrotheca microdiscus species group.

Content (46 species): Gastrotheca abdita, G. aguaruna, G. antoniiochoai, G. aratia, G. argenteovirens, G. atympana, G. aureomaculata, G. carinaceps, G. christiani, G. chrysosticta, G. dunni, G. dysprosita, G. espeletia, G. excubitor, G. galeata, G. gracilis, G. griswoldi, G. lateonota, G. lauzuricae, G. litonedis, G. lojana, G. marsupiata, G. monticola, G. nebulanastes, G. nicefori, G. ochoai, G. orophylax, G. ovifera, G. ossilaginis, G. pacchamama, G. pachachacae, G. peruana, G. phalarosa, G. phelloderma, G. piperata, G. plumbea, G. pseustes, G. psychrophila, G. rebeccae, G. riobambae, G. ruizi, G. splendens, G. stictopleura, G. testudinea, G. trachyceps, and G. zeugocystis.

Diagnosis. (1) postchoanal process forming less than half posteromedial border of choana (character 16, 12–>0), with the same character state coded for *Cryptobatrachus* sp. *Gastrotheca cornuta*, *G guentheri*, *G walkeri*, *Hemiphractus fasciatus*, and *H. helioi*, and a transformation into different character states in *G galeata*, *G excubitor*, and *G marsupiata*; (2) occipital artery in a closed canal and opens into orbit (character 38, 12–>3), with a transformation into a different character state in *G excubitor*, *G griswoldi*, *G marsupiata*, *G pseustes*, and *G testudinea*. All unambiguous transformations are listed in Appendix 5.

Distribution. Highlands of Argentina, Bolivia, Colombia, Ecuador, Panama, Peru and Venezuela.

Comments. Gastrotheca aguaruna, G aratia and G lojana are assigned to this clade following the phylogenetic tree of Duellman *et al.* (2014). Although G abdita, G carinaceps, G dysprosita, G espeletia G ossilaginis, G pachachacae, G phalarosa, and G phelloderma are not included in our analysis, they are tentatively assigned to this clade based on overall morphological similarity to other species of this clade and biogeographic affinities (all are high Andean species). As explained in Materials and methods (see also Duellman & De la Riva 1999) the taxonomy of Bolivian species G lauzuricae, G piperata, and G splendens needs to be thoroughly revised.

Gastrotheca microdiscus species group

Immediately more inclusive taxon. An unnamed clade containing the *Gastrotheca marsupiata* species group and the *Gastrotheca microdiscus* species group.

Sister taxon. Gastrotheca marsupiata species group.

Content (4 species): Gastrotheca albolineata, G. ernestoi, G. fulvorufa, G. microdiscus.

Diagnosis. Unambiguous transformations are restricted to nucleotides (Appendix 5).

Distribution. Atlantic forest biome, from the State of Espírito Santo in the north to the State of Santa Catarina in the south.

Genus: Stefania Rivero, 1968

Immediately more inclusive taxon. Hemiphractinae Peters, 1862.

Sister taxon. An unnamed clade containing *Gastrotheca* Fitzinger, 1843, *Fritziana* Mello-Leitão, 1937, and *Hemiphractus* Wagler, 1828.

Content (19 species): *Stefania ackawaio* MacCulloch and Lathrop, 2002, *S. ayangannae* MacCulloch and Lathrop, 2002, *S. breweri* Barrio-Amorós and Fuentes-Ramos, 2003, *S. coxi* MacCulloch and Lathrop, 2002, *S. evansi* (Boulenger, 1904), *S. ginesi* Rivero, 1968, *S. goini* Rivero, 1968, *S. marahuaquensis* (Rivero, 1961), *S. neblinae* Carvalho, MacCulloch, Bonora, and Vogt, 2010, *S. oculosa* Señaris, Ayarzagüena, and Gorzula, 1997, *S. riae* Duellman and Hoogmoed, 1984, *S. riveroi* Señaris, Ayarzagüena, and Gorzula, 1997, *S. roraimae* Duellman and Hoogmoed, 1984, *S. satelles* Señaris, Ayarzagüena, and Gorzula, 1997, *S. scalae* Rivero, 1970, *S. schuberti* Señaris, Ayarzagüena, and Gorzula, 1997, *S. tamacuarina* Myers and Donnelly, 1997, and *S. woodleyi* Rivero, 1968.

Type species. *Hyla evansi* Boulenger, 1904.

Diagnosis. Unambiguous transformations are restricted to nucleotides (Appendix 5), inasmuch as the majority of phenotypic characters were coded only for *Stefania scalae*.

Characterization. (1) two pairs of bell-shaped gills derived from branchial arches I and II covering most of the embryo; (2) females carrying exposed eggs on their backs; (3) direct development; (4) embryos with reduced oral larval features; (5) males without vocal sacs or apertures, but at least some species vocalizing; (6) superficial mandibular musculature Types A and B of Tyler and Duellman (1995); (7) sphenethmoid well ossified anteriorly; (8) zygomatic ramus of the squamosal close to or in contact with the maxilla (del Pino & Escobar 1981; Señaris *et al.* "1997" [1996]; Duellman & Hoogmoed 1984; Wassersug & Duellman 1984; Tyler & Duellman 1995; Mendelson *et al.* 2000; Sinsch & Juraske 2006).

Distribution. Restricted to the rainforests and shrub areas of the uplands and highlands of the Guiana Shield in Brazil, Guyana, and Venezuela.

Comments. Rivero (1970) defined two species groups. Species of the *Stefania evansi* group have a head "as broad as long or longer than broad" while the head in species of the *S. goini* group is "much broader than long". Not surprisingly, giving the A and not-A definitions of these groups, Duellman & Hoogmoed (1984) recovered a monophyletic *S. goini* group, which was nested within a paraphyletic *S. evansi* group. Subsequent studies continued to recognize the two nominal groups and assigned species accordingly (e.g., Señaris *et al.* 1997 "1996"; MacCulloch & Lathrop 2002; Barrio-Amorós & Fuentes-Ramos 2003). Wiens *et al.* (2007) included DNA sequences of five species, three of the *S. goini* group (*S. coxi, S. ginesi,* and *S. schuberti*) and two of the *S. evansi* group (*S. evansi* and *S. scalae*) and, counter to the results of Duellman & Hoogmoed (1984), retrieved a monophyletic *S. evansi* group nested within a paraphyletic *S. goini* group. Kok *et al.* (2012) analyzed DNA sequences of the mitochondrial genes 16S and ND1 of 45 specimens of *Stefania* representing 11 nominal species and some putative new species. Their topology (a MrBayes majority-rule consensus tree) indicated that neither the *S. goini* groups are monophyletic. According to our results, the *Stefania evansi* and *S. goini* species groups are non-monophyletic. As reported by Kok *et al.* (2012), the samples *Stefania* aff. *evansi* and *Stefania* sp. correspond to undescribed species.

Genus: Hemiphractus Wagler, 1828

Immediately more inclusive taxon. An unnamed clade containing *Gastrotheca* Fitzinger, 1843 and *Hemiphractus* Wagler, 1828.

Sister taxon. Fritziana Mello-Leitão, 1937.

Content (6 species): *Hemiphractus bubalus* (Jiménez de la Espada, 1870), *H. fasciatus* Peters, 1862, *H. helioi* Sheil and Mendelson, 2001, *H. johnsoni* (Noble, 1917), *H. proboscideus* (Jiménez de la Espada, 1870), and *H. scutatus* (Spix, 1824).

Type species. Rana scutata Spix, 1824.

Diagnosis. (1) Alae narrow laterally (character 2, 0–>1), with the same character state coded for *Gastrotheca* galeata, *G. griswoldi*, and a reversal in *Hemiphractus scutatus*; (2) ventral crests of alae present (character 3, 0–

>1), with the same character state coded for Cryptobatrachus, G. dendronastes, G. galeata, G. guentheri, G. microdiscus, G plumbea, and G riobambae; (3) ventral ridge of neopalatine present, with rounded or sharp serrations (character 10, $1 \rightarrow 2$), with the same character state coded for G argenteovirens, G galeata, and G ovifera; (4) posteromedial process of vomer serrated (character 12, 1–>2); (5) prechoanal process forming less than half anteromedial border of choana (character 15, $2 \rightarrow 1$), with the same character state coded for C. fuhrmanni, G. guentheri, G. marsupiata, and G. pseustes, a reversal in H. proboscideus, and a transformation into a different character state in *H. bubalus*; (6) bifurcation of pre- and postchoanal processes posterior to level of dentigerous process (character 18, 0->2), with the same character state coded for G marsupiata; (7) postorbital process long (character 20, 1->2), with the same character state coded for G guentheri and G megacephala; (8) broad overlap of articulation of maxilla and premaxilla from anterior view (character 21, 0->1); (9) pterygoid process of maxilla present (character 22, 0->1), with the same character state coded for G guentheri and G megacephala; (10) pars temporalis present (character 24, 0->1); (11) lingual process of premaxilla present (character 25, 0->1); (12) occipital crest present (character 29, $0 \rightarrow 1$), with the same character state coded for G dendronastes, G galeata, and G ovifera; (13) squamosal crest present (character 30, $0 \rightarrow 1$), with the same character state coded for G argenteovirens, G. cornuta, G. dendronastes, G. galeata, G. guentheri, and G. ovifera; (14) nasal crest present (character 31, 0->1), with the same character state coded for G galeata and G guentheri and a reversal in H. scutatus; (15) postorbital flange plate-like, dorsal to crista parotica (character 37, $0 \rightarrow 2$), with the same character state coded for G galeata and G megacephala; (16) mm. intermandibularis and submentalis separated (character 48, 1->0), with the same character state coded for G cornuta and G guentheri; (17) aponeurosis of m. *intermandibularis* large (character 50, 2->0), with the same character state coded for C. sp., G guentheri, and G testudinea. All unambiguous transformations are listed in Appendix 5.

Characterization. (1) two pairs of bell-shaped gills (fused in *Hemiphractus fasciatus*) derived from branchial arches I and II covering most of the embryo; (2) females carrying exposed eggs on their backs; (3) direct development; (4) embryos without oral larval features; (5) males without vocal sacs or apertures and apparently not vocalizing; (6) superficial mandibular musculature Type C of Tyler & Duellman (1995) (*i.e.*, the *m. submentalis* is small, the *m. intermandibularis* is a single, undifferentiated sheet bearing a large, median aponeurosis, the *m. interhyoideus* does not extend posteriorly beyond the mandibles); (7) cultriform process of parasphenoid becoming distinctly narrow anteriorly; (8) presence of a zygomatic ridge; (9) presence of a supraorbital ridge and odontoids on the dentary and angulosplenial; (10) presence of prominent, triangular, paraoccipital processes; (11) presence of a fleshy proboscis (Trueb 1974; del Pino & Escobar 1981; Wassersug & Duellman 1984; Tyler & Duellman 1995; Mendelson *et al.* 2000; Sheil *et al.* 2001).

Distribution. Lowland and montane rainforests of Panama, Pacific slopes of Colombia and northwestern Ecuador, and upper Amazon Basin and Amazonian slopes of the Andes in Bolivia, Brazil, Colombia, Ecuador, and Peru.

Comments. Detailed taxonomic reviews can be found in Trueb (1974) and Sheil *et al.* (2001). The monophyly of the genus has been recovered on the basis of morphology and DNA sequences (Mendelson *et al.* 2000; Sheil *et al.* 2001; Wiens *et al.* 2007). However, Mendelson *et al.* (2000) found *Hemiphractus* to be nested within *Gastrotheca* but, as noted above, this arrangement has not been corroborated by DNA sequences (e.g., Faivovich *et al.* 2005; Wiens *et al.* 2005, 2007; Padial *et al.* 2014). Sheil *et al.* (2001) recovered two main clades, each with three species: ((*H. helioi* (*H. fasciatus*, *H. scutatus*)) (*H. johnsoni* (*H. proboscideus*, *H. bubalus*))). Wiens *et al.* (2007) included sequences of four species and obtained a partially different topology with *H. scutatus* sister of the other three species: (((*H. proboscideus*, *H. bubalus*)) *H. helioi*) *H. scutatus*).

Our topology is almost identical to that obtained by Sheil *et al.* (2001) on the basis of phenotypic characters except that in our topology *Hemiphractus helioi* is sister of all other species in the genus instead of sister of *H. fasciatus* + *H. scutatus*. Our results indicate that the samples identified as *H. fasciatus* and *H. scutatus* could correspond, in each case, to more than one species. In the case of *H. fasciatus*, we found three divergent mitochondrial lineages, a result already advanced by Crawford *et al.* (2013). The available name *H. panamensis* (Stejneger, 1917), currently placed under the synonymy of *H. fasciatus* by Trueb (1974), could correspond to one of those lineages. For *H. scutatus*, we found two divergent lineages. *Hemiphractus scutatus* currently contains the synonyms *H. boulengeri* Miranda-Ribeiro, 1926 and *H. divaricatus* Cope, 1868, considered as synonyms by Myers & Carvalho (1945) and Trueb (1974), respectively.

Acknowledgements

We are thankful to April Wen and Neida Vasquez for help to gather DNA sequences from GenBank. We thank Beatriz Álvarez and Isabel Rey (MNCN), Frank Glaw (ZSM), Philippe J. R. Kok (IRSNB), and Vivian P. Páez (MHUA), who generously allowed us to study samples under their care, Alan Channing, Ana C. Carnaval, Christopher A. Phillips, David C. Blackburn, Iván Gómez-Mestre, Juan C. Chaparro, Julián Faivovich, Mauro Teixeira Junior, Ryan R. Kerney, Tod W. Reeder, and William E. Duellman, who answered miscellaneous questions regarding specimens and literature, Giussepe Gagliardi-Urrutia and Mauricio Rivera-Correa, who kindly let us use their photographs, Andrew J. Crawford, Jörn Köhler, and Julián Faivovich, who provided insightful comments that helped improving a previous version of the manuscript, and Julian Faivovich, Mark E. Siddall, Pedro L. V. Peloso, Taran Grant, and Ward Wheeler, who helped with phylogenetic analyses and computational issues. All errors are our own. Research permits include MMAyA-VM-DGBAP Nº 0908/10 (DGB and Colección Boliviana de Fauna to IDIR in Bolivia), SISBIO #12600-2 (Instituto Brasileiro de Meio Ambiente e dos Recursos Renováveis, IBAMA, to JMP Jr. in Brazil), "permiso de estudio con fines de investigación científica en Diversidad Biológica #27 of 22 June 2012" and "contrato de acceso a recursos genéticos para investigación científica sin interés comercial #092" (Autoridad Nacional de Licencias Ambientales and Ministerio de Ambiente y Desarrollo Sostenible to SC-F in Colombia), # 030605BR006 and # 191205SP011 (Guyana Environmental Protection Agency to Philippe J. R. Kok in Guyana), 416-2009-AG-DGFFS-DGEFFS (Dirección General Forestal y de Fauna Silvestre to JMP in Peru), license #001866 of 8 December 2003 (Ministry of Agriculture, Land and Marine Resources to Frank Glaw in Trinidad and Tobago), #01-03-03-1146 (2005-2006), #4100 (2007-2008), Permiso Inparques PAA-215-2008, and access to genetic resources permit #0076 of 22 February 2011 (Ministerio del Poder Popular para el Ambiente and Inparques to MHNLS in Venezuela). This work was supported by Conselho Nacional de Desenvolvimento Científico e Tecnológico, project 442981/2014-7 (PI: SC-F), Ministerio de Economía y Competitividad, Spanish Government, Projects CGL2013-47547-P (PI: Carles Vilà) and CGL2014-56160-P (PI: IDIR), the Science Research Mentoring Program at the American Museum of Natural History, Fundação Carlos Chagas de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ), and Fundação de Amparo à Pesquisa do Estado de São Paulo Proc. 2012/10000-5 (PI: Taran Grant).

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Author contributions

SC-F and DRF designed the study, SC-F, JMP, IDIR, JPPJr, FJMR-R, HRdS, and EM-M generated the data, SC-F and JMP analyzed the data, SC-F, JMP, and DRF wrote the manuscript, IDIR, JPPJr, FJMR-R, HRdS, and EM-M read and improved the manuscript.

Authors' note

While this paper was in press, we examined the gills of the embryos of *Gastrotheca megacephala* (UESC 13685) and *G pulchra* (UESC 8120) of the *Gastrotheca fissipes* species group. The embryos of both species were in state 46 of Gosner (1960) and have gill stalks not fused (character 44 -1) and bell-shaped gills fused distally (character 45-1). Our observation further supports the presence of two fused pairs of bell-shaped gills derived from branchial arches I and II (character 45, 1–>0) as a synapomorphy for *Gastrotheca*.

APPENDIX 1. Terminals, voucher codes (only included for ingroup taxa), and GenBank accession numbers of DNA sequences used in this study. Acronyms follow Frost (2014) except for CBG (Centro de Biodiversidad y Genética, Cochabamba), CHP (Círculo Herpetológico de Panama), CORBIDI (Centro de Ornitología y Biodiversidad), CTMZ (tissue collection at MZUSP), DCC (David C. Cannatella field series), EVACC (El Valle Amphibian Conservation Center), JDL (John D. Lynch field series), JLG (João Luis Gasparini field series), JMP (José M. Padial field series), LM (Linda Maxson field series), MNCN/ADN (tissue collection at MNCN), MJH (Martin J. Henzl field series), MTR (Miguel T. Rodrigues field series), MVUP (Museo de Vertebrados de la Universidad de Panamá), VUB (unknown, from Kok *et al.* 2012), Vz (unknown, from Wiens *et al.* 2007).

Taxon*	tRNA Phe	128	tRNA Val	168 (1)	168 (2)	tRNA Leu	ND1	COI	cytb	288	C-MYC 2
Acris crepitans	_	EF566970	EF566970	EF566970	AY819491	AY819491	AY819491	_	AY843782	AY844194	AY819194
Adelophryne patamona	_	EU186679	EU186679	EU186679	GQ345247	GQ345247	GQ345247	_	GQ345201	GQ345136	GQ345149
Adenomera andreae	_	HQ290944	HQ290944	HQ290944	HQ290944	HQ290944	HQ290944	KC520689	JQ321766	_	
Adenomera hylaedactyla	_	KC603939	KC603939	KC603939	_	_	_	KC603995	KC603967	_	
Agalychnis annae	_	GQ366221	GQ366221	GQ366221	GQ366291	GQ366291	GQ366291	_	GQ365913	_	EF174320
Agalychnis callidryas	—	DQ283423	DQ283423	DQ283423	FJ489334	FJ489334	FJ489334	FJ766570	—	—	EF174321
Allobates femoralis	_	AY364543	AY364543	AY364543	HQ290951	HQ290951	HQ290951	DQ502811	HQ290531	DQ283465	—
Allophryne ruthveni	_	AY843564	AY843564	AY843564	AY819458	AY819458	AY819458	_	AY843786	_	AY819162
Alsodes neuquensis		AY843565	AY843565	AY843565	JX204017	JX204017	JX204017	JX203891	AY843787	AY844197	—
Amazophrynella minuta	_	AY843582	AY843582	AY843582	AY819462	AY819462	AY819462	DQ502828	AY843804	_	AY819166
Amietophrynus brauni	_	FJ882822	FJ882822	FJ882822	FJ882822	FJ882822	_	_	_	DQ283726	—
Atelognathus patagonicus	_	AY843571	AY843571	AY843571	_	_	_	JX203909	AY843793	AY844203	
Barycholos pulcher	_	EU186727	_	EU186709	_	_	_	_	_	_	
Barycholos ternetzi	_	—	_	DQ283094	_	_	_	_	_	DQ283496	
Batrachyla leptopus	_	AY843572	AY843572	AY843572	_	_	_	_	AY843794	AY844204	
Batrachyla taeniata	_	AY578817	—	DQ864550	—	—	—	—	KC603962	—	—
Brachycephalus alipioi	_	HQ435676	—	HQ435690	—	—	—	_	HQ435703	—	—
Brachycephalus ephippium	—	DQ283091	DQ283091	DQ283091	GQ345243	GQ345243	GQ345243	—	HQ435706	DQ283494	GQ345145
Bryophryne cophites	_	EF493537	EF493537	EF493537	—	—	—	—	—	—	—
Bufo japonicus	AB303363	AB303363	AB303363	AB303363	AB303363	AB303363	AB303363	AB303363	AB303363	_	
Calyptocephalella gayi		DQ283439	DQ283439	DQ283439	AY819471	AY819471	AY819471	JX298374	JX298415	DQ283748	AY819175
Ceratophrys (C. cornuta, C.	—	DQ347035 C.	DQ347035 C.	FJ882777 C.	AY523774 C.	AY523774 C.	AY523774 C.	_	L10983 C.	—	_
cranwelli, C. ornata) Cauthomantis smaraadirus		cranwelli GO345132	cranwelli GO345132	cranwelli GO345132	cranwelli GO345132	cranwelli	cranwelli GO345251		ornata GO345206	GO345140	GO345154
Ceunomanus smaragainus	_	JQ343132	0Q343132	0Q343132	0Q343132	_	0Q343231	_	0Q343200	0Q343140	00345154

Taxon*	tRNA Phe	128	tRNA Val	16S (1)	168 (2)	tRNA Leu	ND1	COI	cytb	285	C-MYC 2
Chacophrys pierottii	_	DQ283328	DQ283328	DQ283328	_	_	_	_	_	_	_
Colostethus pratti	—	HQ290969	HQ290969	HQ290969	HQ290969	HQ290969	HQ290969	DQ502865	HQ290547	DQ503011	—
Craugastor augusti	_	AY326011	AY326011	AY326011	_	_	_	_	_	_	_
Craugastor podiciferus	_	EF493360	EF493360	EF493360	EF493360	_	_	_	GQ345197	_	AY211319
Craugastor punctariolus	—	DQ283168	DQ283168	DQ283168	—	—	_	FJ766667	—	DQ283558	—
Craugastor ranoides	—	DQ283105	—	DQ283106	—	—	_	—	DQ350246	DQ283505	AY211287
Craugastor rhodopis	_	DQ283317	DQ283317	DQ283317	—	_	_	_	_	DQ283648	AY211315
Crossodactylodes sp	_	KC603957	KC603957	KC603958	_	_	_	KC603985	KC603963	_	_
Crossodactylus schmidti	_	AY843579	AY843579	AY843579	_		HQ290948	DQ502738	AY843801	AY844210	_
Cryptobatrachus boulengeri LM	_	_	_	_	AY819485	AY819485	AY819485	_	_	_	_
Cryptobatrachus fuhrmanni JDL 14865	_	AY326050	AY326050	AY326050	JX564861	JX564861	JX564861	JX564861	JX564861	—	—
Cryptobatrachus fuhrmanni MHUA A 5160		KR559912	KR270398	KR270398 + KR270414	—	_	_		_	—	
Cryptobatrachus remotus MHNLS 18853 + MHNLS 17664		KR559914	KR559914	KR270400 + KR270416	KR138379	KR138379	KR138379				
Cycloramphus acangatan	—	HQ634162	—	FJ685683	—	—	—	—	FJ685663	—	—
Cycloramphus boraceiensis	—	DQ283097	DQ283097	AY162397	—	—	—	DQ502856	DQ502588	DQ283498	_
Dendrobates auratus	—	DQ347026	DQ347026	AY364565	—	—	HQ290980	FJ766698	AY843803	AY844211	—
Dendropsophus nanus	—	AY549346	AY549346	AY549346	GQ366298	GQ366298	GQ366298	—	AY549399	AY844271	AY819208
Diasporus aff diastema	—	—	—	FJ784484	—	—	—	FJ766810	—	—	—
Diasporus diastema	—	EU186682	EU186682	EU186682	EU186682	—	—	—	GQ345200	GQ345135	GQ345148
Duttaphrynus melanostictus	—	AB331714	AB331714	FJ882791	FJ882791	NC 005794	NC 005794	NC 005794	—	DQ283658	—
Edalorhina perezi	—	AY843585	AY843585	AY843585	—	—	—	—	AY843807	DQ283474	—
Eleutherodactylus cooki	—	EF493539	EF493539	EF493539	EF493539	—	_	—	HQ831648	—	—
Eleutherodactylus coqui	—	GQ345176	GQ345176	GQ345176	—	—	_	—	EF637038	—	—
Eleutherodactylus marnockii	—	DQ283102	—	DQ283101	—	—	_	—	—	DQ283502	—
Eleutherodactylus nitidus	—	EU186730	—	DQ283316	—	—	—	—	—	DQ283647	—
Eleutherodactylus planirostris	—	DQ283107	DQ283107	DQ283107	GQ345246	GQ345246	GQ345246	—	HQ831615	DQ283629	_
Eleutherodactylus thorectes	—	EF493384	EF493384	EF493384	EF493384	—	_	_	HQ831649	—	—
Eleutherodactylus tonyi	—	EF493790	—	EF493602	—	—	—	—	HQ831643	—	—

Taxon*	tRNA Phe	128	tRNA Val	16S (1)	16S (2)	tRNA Leu	ND1	COI	cytb	285	C-MYC 2
Engystomops petersi	—	FJ668190	FJ668190	FJ668190	_	_	_	_	_	_	
Engystomops pustulosus	_	DQ337242	DQ337242	DQ337248	_	—	—	FJ766700	_	_	_
Espadarana prosoblepon	_	AY843574	AY843574	AY843574	_	—	AY286065	FJ766592	AY843796	AY844206	AY819170
Eupsophus roseus	_	AY843587	AY843587	AY843587	JX204054	JX204054	JX204054	DQ502852	AY843808	_	_
Fejervarya limnocharis	NC 005055	NC 005055	NC 005055	NC 005055	NC 005055	NC 005055	NC 005055	NC 005055	NC 005055	_	_
Flectonotus fitzgeraldi ZSM 1610 2006 + KU 192399	_	AY819355	KR270401	KR270401+ KR270417	AY819486	AY819486	AY819486	_	_	_	AY819189
Flectonotus pygmaeus MHNLS 17478 + KU 184958		DQ679232	KR270402	KR270402+ KR270418	DQ679341	DQ679341	DQ679341	_	_	_	—
Fritziana fissilis MNRJ 62845	—	KR559916	KR270403	KR270403 + KR270419	—						—
<i>Fritziana</i> aff. <i>fissilis</i> sp. 2 MNRJ 44622	—	KR559917	KR270404	KR270404 + KR270421	—	_	_	_	_	_	—
<i>Fritziana</i> aff. <i>fissilis</i> sp. 3 MZSUP 133700	—	—	_	JN157634	KC844943	KC844943	KC844943	_	_	_	—
<i>Fritziana</i> aff. <i>fissilis</i> sp. 1 CFBH 5726 + MZUSP 13546		AY843589	AY843589	AY843589	KC844944	KC844944	KC844944	_	AY843809	AY844215	—
Fritziana goeldi MNRJ 34921	—	KR559918	KR270405	KR270405 + KR270423	_	_	_		_	_	—
Fritziana ohausi MZUSP 139225	—	—	—	JN157635	KC844945	KC844945	KC844945	—	—	—	—
Fritziana sp. MNRJ 44592	—	—	KR270406	KR270406+ KR270424	—	_	_	_	_	_	—
<i>Gastrotheca albolineata</i> MNRJ 54401	—	KR559919	KR270407	KR270407+ KR270425	KC844949	KC844949	KC844949	—	_	_	—
Gastrotheca antoniiochoai MUSM 27944				JN157622	KC844950	KC844950	KC844950				_
<i>Gastrotheca argenteovirens</i> KU 181168		DQ679233	_	DQ679383	DQ679342	DQ679342	DQ679342	_	_	_	_
Gastrotheca atympana MHNSM 18692	—	DQ679234	_	DQ679384	DQ679343	DQ679343	DQ679343	_	_	_	_
<i>Gastrotheca aureomaculata</i> KU 181194	_	DQ679235	_	DQ679385	DQ679344	DQ679344	DQ679344	_	_	_	_
Gastrotheca christiani FML 2881	DQ679236	DQ679236	—	DQ679386	DQ679345	DQ679345	DQ679345	—	—	—	—
Gastrotheca chrysosticta LM 58	DQ679237	DQ679237	—	DQ679387	DQ679346	DQ679346	DQ679346	—	—	—	—
Gastrotheca sp. 1 IDLR 4073 (MNCN/ADN 566)	—	—	—	KR270428	—	—	—	—	KR138416	—	—
										continued	l on the next page

Taxon*	tRNA Phe	128	tRNA Val	16S (1)	16S (2)	tRNA Leu	ND1	COI	cytb	285	C-MYC 2
Gastrotheca cornuta USNM		AY843591	AY843591	AY843591	DQ679347	DQ679347	DQ679347	FJ766706	AY843811	_	
572472 + AMNH 107251											
Gastrotheca dendronastes KU	_	DQ679239	—	DQ679389	DQ679348	DQ679348	DQ679348	—	—	_	—
181203		DO(70240		KD270426	DO(70240	DO(70240	DO(70240				
Gastrotneca aunti ICN 10059 +	_	DQ679240	_	KR2/0426	DQ6/9349	DQ679349	DQ679349		_	_	_
Gastrotheca ernestoi MNR I	KR 559920	KR559920	KR270408	KR270408+	KC844952	KC844952	KC844952				
57129 + MNRJ 64000	100337720	10037720	1112/0100	KR270427	10011002	ReoTiyoz	Reothysz				
Gastrotheca excubitor KU 173171	DQ679241	DQ679241	_	DQ679391	DQ679350	DQ679350	DQ679350	_	_	_	_
Gastrotheca excubitor MUSM				IN157623							
26280				011107020							
Gastrotheca fissipes ZUFRJ 7901	_	_	_	_	JX262925	JX262925	JX262925	_	_		JX262895
Gastrotheca fulvorufa CTMZ	_	_	_	KC844929	KC844954	KC844954	KC844954		_		
07467											
Gastrotheca galeata KU 181700	DQ679242	DQ679242	_	DQ679392	DQ679351	DQ679351	DQ679351	_	—	_	_
Gastrotheca gracilis DCC 006	_	DQ679243	_	_	_	_	_	_		_	_
Gastrotheca griswoldi KU 181701	_	DQ679244	_	_	DQ679352	DQ679352	DQ679352	_	_	_	_
Gastrotheca griswoldi MHNSM	_	AM039716	_	AM039648	_	_	_	_	_	_	_
20588											
Gastrotheca guentheri KU	_	DQ679245	_	DQ679393	DQ679353	DQ679353	DQ679353	_	_	_	_
173112											
Gastrotheca helenae KU 181070	DQ679246	DQ679246	_	DQ679394	DQ679354	DQ679354	DQ679354	—		—	—
Gastrotheca lateonota QCAZ	_	_	—	KC844923	KC844948	KC844948	KC844948	_	—	_	_
45113											
Gastrotheca sp. 2 MNK 5286 +	_	AY843590	AY843590	AY843590	KC844955	KC844955	KC844955	—	AY843810	_	_
CBG 1020											
Gastrotheca litonedis KU 202690	_	DO679247	_	DO679395	DO679355	DO679355	DO679355				_
	DO(70249	DQ(7)211		DQ(793)(DQ(7)355	DQ(7)355	DQ(7)355				
258905	DQ679248	DQ6/9248	_	DQ6/9396	DQ6/9356	DQ6/9356	DQ6/9356	_	_	_	_
Gastrotheca marsupiata KU	AY819356	AY819356	_	DQ679397	AY819487	AY819487	AY819487		_	_	AY819190
214813 + KU 214814											
Gastrotheca sp. 3 ZFMK 66954 +		_	_	KR270429	_	—	_	—	KR138417	_	_
MNCN 43052											
Gastrotheca megacephala JLG 90	—	AY843592	AY843592	AY843592	KC844953	KC844953	KC844953	—	—	—	—
+ CFBH T377											

Taxon*	tRNA Phe	128	tRNA Val	16S (1)	16S (2)	tRNA Leu	ND1	COI	cytb	285	C-MYC 2
Gastrotheca microdiscus CFBH T	—	—	_	KC844932	KC844958	KC844958	KC844958	—	—	—	_
1250 + CFBH T 3068 Gastrotheca monticola KU 212036	AY819357	AY819357	_	DQ679398	AY819488	AY819488	AY819488	—	_	—	AY819191
<i>Gastrotheca nebulanastes</i> MUSM 27943 + MCZ 265218	_	—	_	JN157625	KC844959	KC844959	KC844959	—			—
Gastrotheca nicefori KU 181071	_	DQ679249	_	DQ679399	DQ679357	DQ679357	DQ679357	_	_	—	_
<i>Gastrotheca nicefori</i> MHUA A 5716	_	KR559921	KR270409	KR270409	KR138380	KR138380	KR138380	_	—	_	—
Gastrotheca ochoai KU 173499	—	DQ679250	—	DQ679400	DQ679358	DQ679358	DQ679358	—	—	—	—
<i>Gastrotheca orophylax</i> KU 178568	DQ679251	DQ679251	—	DQ679401	DQ679359	DQ679359	DQ679359	—	—	—	—
Gastrotheca ovifera KU 185758	—	DQ679252	—		DQ679360	DQ679360	DQ679360	—		—	—
<i>Gastrotheca pachachacae</i> MUSM 28492	—	_	_	JN157620	_	_	_	_	—	_	_
Gastrotheca peruana KU 181740	DQ679253	DQ679253	—	DQ679402	DQ679361	DQ679361	DQ679361	—		—	
Gastrotheca plumbea KU 178499	DQ679254	DQ679254	_	DQ679403	DQ679362	DQ679362	DQ679362	_	_	_	_
<i>Gastrotheca prasina</i> MZUSP 147060	—	JX262891	_	_	JX262922	JX262922	JX262922	_	—	—	JX262899
<i>Gastrotheca pseustes</i> QCAZ 42862 + TNHC 62492	_	AY326051	AY326051	AY326051	KC844962	KC844962	KC844962	—	—	—	—
Gastrotheca psychrophila KU 142634	DQ679255	DQ679255	_	DQ679404	DQ679363	DQ679363	DQ679363	—			_
Gastrotheca pulchra MTR 16228	—	JX262894	—	_	—	—	—	—		—	JX262898
<i>Gastrotheca rebeccae</i> CORBIDI 08006	_	_	—	KC844937	KC844963	KC844963	KC844963	—	—	—	—
<i>Gastrotheca recava</i> MZUSP 147044	_	JX262890	_	_	JX262921	JX262921	JX262921	—	—	—	JX262903
<i>Gastrotheca riobambae</i> KU 178468	_	DQ679256	_	DQ679405	DQ679364	DQ679364	DQ679364	—	—	—	—
<i>Gastrotheca riobambae</i> UIMNH 94580	—	U39974	_	U39976	_	—	—	_	—	_	_
Gastrotheca ruizi KU 200002	_	DQ679257	—	DQ679406	DQ679365	DQ679365	DQ679365	—		—	
Gastrotheca sp. A QCAZ 22635	_	_	_	KC844935	KC844961	KC844961	KC844961	_	_	_	—
Gastrotheca sp. B QCAZ 21105	_	—	_	KC844939	KC844965	KC844965	KC844965	—	—	—	_
Gastrotheca sp. C QCAZ 47299	_	—	_	KC844934	KC844960	KC844960	KC844960	_	—	—	—

Taxon*	tRNA Phe	128	tRNA Val	168 (1)	168 (2)	tRNA Leu	ND1	COI	cytb	288	C-MYC 2
Gastrotheca sp. D QCAZ 42725	_	—	—	KC844938	KC844964	KC844964	KC844964	—	_	—	—
Gastrotheca sp. E QCAZ 21213	_	_	_	KC844922	KC844947	KC844947	KC844947	—	_	_	_
Gastrotheca stictopleura MTD 45230	DQ679258	DQ679258	_	DQ679407	DQ679366	DQ679366	DQ679366	_	_	_	_
Gastrotheca testudinea QCAZ 16444 + CBG 774		—	—	KR270430	KC844966	KC844966	KC844966	—	KR559927		—
Gastrotheca trachyceps KU 181189	DQ679259	DQ679259	_	DQ679408	DQ679367	DQ679367	DQ679367	—	_	—	_
Gastrotheca walkeri Vz 89–96	_	DQ679260		DQ679409	DQ679368	DQ679368	DQ679368	_	_	_	
Gastrotheca weinlandii KU 143105	DQ679261	DQ679261	—	DQ679410	DQ679369	DQ679369	DQ679369	_	_	_	_
<i>Gastrotheca zeugocystis</i> MHNSM 18675		DQ679262	_	DQ679411	_		—		—	_	—
Haddadus binotatus	_	EF493361	EF493361	EF493361	EF493361	_	_	_	GQ345198	DQ283493	GQ345147
Heleophryne purcelli	—	AY843593	AY843593	AY843593	_	—	AY948755	_	AY843812	AY844216	_
Hemiphractus bubalus KU 143107 + KU 178588	—	DQ679263	—	DQ679412	DQ679370	DQ679370	DQ679370	_	_	GQ345134	_
<i>Hemiphractus fasciatus</i> MVUP 1927		_	—	FJ784476	_			FJ766707	_		_
Hemiphractus fasciatus sp1 CHP 6397 + EVACC 207 + EVACC 065	_	_	_	KC014933	KC844967	KC844967	KC844967	KC014710	_	_	_
<i>Hemiphractus fasciatus</i> sp2 EVACC 061 + CHP 6670	_	—	—	KC129342	KC844968	KC844968	KC844968	KC014706	—	—	—
Hemiphractus helioi MHNCP 9063 + MJH 3689		AY843594	AY843594	AY843594	_		—		AY843813	_	—
Hemiphractus proboscideus KU 217513	AY819358	AY819358	—	DQ679413	AY819489	AY819489	AY819489	_	—	—	AY819192
Hemiphractus scutatus JMP 2150 (MNCN/ADN 46913)	—	KR559923	KR270411	KR270411+ KR270432	—	_	—	KR559926	—	—	—
Hemiphractus scutatus USNM 317196	_	DQ679264		DQ679414	DQ679371	DQ679371	DQ679371		—		_
Holoaden bradei	—	EF493378		EF493366	EF493366	—	—	_	_	_	_
Holoaden luederwaldti	_	EU186728	_	EU186710	_	_	_	_	_	_	_
Hydrolaetare caparu	—	KC603953	KC603953	KC603954	—	—	_	KC603988	KC603975	_	_
Hyla arenicolor	—	EF566960	EF566960	EF566960	AY819494	AY819494	AY819494	—	AY843824	—	AY819197

Taxon*	tRNA Phe	128	tRNA Val	168 (1)	168 (2)	tRNA Leu	ND1	COI	cytb	288	C-MYC 2
Hyla chinensis	_	AY458593	AY458593	AY458593	AY458593	AY458593	AY458593	AY458593	AY458593	_	DQ055761
Hyla cinerea	—	AY680271	AY680271	AY680271	AY819498	AY819498	AY819498	FJ226785	AY843846	AY844241	AY819201
Hylodes phyllodes	—	DQ283096	DQ283096	DQ502171	—	—	—	DQ502873	DQ502606	DQ503009	—
Hylorina sylvatica	—	JX204222	JX204222	JX204222	_	_	—	—	—	—	_
Hyloxalus chlorocraspedus	—	DQ502080	DQ502080	DQ502080	—	—	—	DQ502800	DQ502511	DQ502975	—
Hypodactylus brunneus	—	EF493357	EF493357	EF493357	GQ345248	GQ345248	GQ345248	—	GQ345203	GQ345138	GQ345151
Hypodactylus dolops	—	EF493394	EF493394	EF493394	EF493394	—	—	—	—	—	—
Hypsiboas boans	—	AY843610	AY843610	AY843610	AY819496	AY819496	AY819496		AY843835	AY844231	AY819199
Hypsiboas lanciformis	—	AY843636	AY843636	AY843636	AY819543	AY819543	AY819543		AY843870	AY844258	—
Insuetophrynus acarpicus	—	JX204223	JX204223	JX204223	—	—	—	JX203938	AY691185	—	—
Ischnocnema guentheri	—	EF493533	EF493533	EF493533	EF493533	—	—	—	GQ345196	—	—
Ischnocnema juipoca	—	DQ283093	DQ283093	DQ283093	—	_	—	—	—	DQ283495	_
Lepidobatrachus laevis	—	DQ283152	DQ283152	DQ283152	AY819475	AY819475	AY819475	—	—	DQ283543	AY819179
Leptodactylus melanonotus	_	AY943224 + FJ882762	FJ882762	AY943224 + FJ882762	—	—	AY948760	_	_	_	AY337266
Leptodactylus latrans	—	AY843688	AY843688	AY843688	—	—	—	—	AY843934	AY844302	—
Limnodynastes salmini	—	AY326071	AY326071	AY326071	—	—	—	—	—	—	—
Limnomedusa macroglossa	—	AY843689	AY843689	AY843689	—	—	—	—	AY843935	—	—
Lithodytes lineatus	—	AY326012	AY326012	AY326012	HQ290949	HQ290949	HQ290949	KC604003	JQ321833	AY844303	—
Litoria caerulea	—	AY326038	AY326038	AY326038	AY819531	AY819531	AY819531	AY883980	AY843938	—	AY819234
Litoria infrafrenata	—	AY843694	AY843694	AY843694	GQ366302	GQ366302	GQ366302	FJ952337	AY843940	AY844304	—
Lynchius nebulanastes	—	EU186704	EU186704	EU186704	—	—	—	—	—	—	AY819320
Lynchius parkeri	—	EU186705	EU186705	EU186705	—	—	—	—	—	—	—
Macrogenioglottus alipioi	—	KC593360	KC593360	KC593360	KC593353	KC593353	KC593353	—	FJ685665	—	—
Mannophryne trinitatis	—	EU342504	EU342504	DQ502131	—	_	—	DQ502838	DQ502562	—	_
Megaelosia goeldii	—	DQ283072	DQ283072	DQ283072	—	_	—	DQ502839	DQ502563	—	_
Melanophryniscus klappenbachi	—	AY843699	AY843699	AY843699	—	_	—	DQ502739	AY843944	AY844306	_
Myersiohyla kanaima	—	AY843634	AY843634	AY843634	GQ366307	GQ366307	GQ366307	—	AY843868	—	—
Noblella lochites	—	EU186699	EU186699	EU186699	—	—	—	—	—	—	—
Noblella sp. MTD 45180	—	AM039714	—	AM039646	—	_	—	—	—	—	_

Taxon*	tRNA Phe	128	tRNA Val	16S (1)	16S (2)	tRNA Leu	ND1	COI	cytb	285	C-MYC 2
Nymphargus bejaranoi	_	AY843576	AY843576	AY843576	_	_	_	_	AY843798	AY844208	EU663314
Odontophrynus achalensis	_	DQ283248	DQ283248	DQ283248	_	_	—	_	—	DQ283611	_
Oreobates cruralis	_	EU186666	EU186666	EU186666	EU186666	_	_	_	—	_	
Oreobates saxatilis	_	JF809931	_	JF809962	_	_	—	_	_	_	_
Paratelmatobius cardosoi	_	EU224404	EU224404	EU224404	_	_	—	_	—	_	_
Phrynopus auriculatus	_	EF493708	EF493708	EF493708	_	_	—	_	—	_	_
Phrynopus bracki	_	EF493709	EF493709	EF493709	EF493709	_	_	_	GQ345202	GQ345137	GQ345150
Phyllodytes luteolus	_	AY843721	AY843721	AY843721	GQ366314	GQ366314	GQ366314	_	AY843966	AY844324	_
Physalaemus cuvieri	_	AY843729	AY843729	AY843729	JX204060	JX204060	JX204060	_	AY843975	AY844330	AY819181
Physalaemus gracilis	AY943229	AY943229	_	AY943242	AY943242	_	—	_	—	DQ283728	_
Phyzelaphryne miriamae	_	EU186689	EU186689	EU186689	EU186689	_	—	_	—	_	_
Pleurodema brachyops	_	AY843733	AY843733	AY843733	_	_	—	_	AY843979	_	_
Pleurodema diplolister	_	JQ937187	JQ937187	JQ937187	_	_	—	KC603986	KC603981	_	_
Pristimantis cruentus	_	EF493697	EF493697	EF493697 +	FJ882747	FJ882747	FJ882747	FJ766786	_	_	_
		EE402512	EE402512	FJ784557	13/010472	13/010472	43/010472				13/010177
Pristimantis curtipes	_	EF493513	EF493513	EF493513	AY8194/3	AY8194/3	AY8194/3		_	_	AY8191//
Pristimantis gaigeae	—			FJ/84490	— FE402255	_	_	FJ/66/92	_	—	AY211290
Pristimantis ridens	_	EF493355	EF493355	EF493355	EF493355	_	_	FJ/66808	_	_	AY211306
Pristimantis simonsii	—	EU186665	EU186665	EU186665	EU186665	_	_	—	-	—	AY819321
Proceratophrys avelinoi	_	DQ283038	DQ283038	DQ283038	—	—	—	_	FJ685671	—	_
Pseudis minutus	_	—	AY843739	—	GQ366339	GQ366339	GQ366339	—	AY843985	AY844336	
Pseudopaludicola falcipes	_	AY843741	AY843741	AY843741	_	_	—	KC520684	KC593350	—	_
Psychrophrynella guillei	_	AY843720	AY843720	AY843720	_	_	—	—	_	AY844323	
Psychrophrynella wettsteini	_	EU186696	EU186696	EU186696	GQ345250	GQ345250	GQ345250	—	_	GQ345139	GQ345153
Rheobates palmatus	—	EU342508	EU342508	EU342508	HQ290967	HQ290967	HQ290967	DQ502925	HQ290545	—	
Rhinella arenarum	_	AY843573	AY843573	AY843573	JX204061	JX204061	JX204061	_	AY843795	AY844205	_
Rhinoderma darwinii	_	AY364357	_	AY364378	_	_	AY523783	DQ502858	DQ502589	DQ283654	_
Rupirana cardosoi	—	KC603955	KC603955	KC603956	—	—	—	KC603987	KC603964	—	—
Scinax staufferi	—	AY843761	AY843761	AY843761	GQ366340	GQ366340	GQ366340	—	AY844006	—	—
Scythrophrys sawayae	—	EU224417	EU224417	EU224417	—	_	—	—	—	DQ283500	—

Taxon*	tRNA Phe	12S	tRNA Val	16S (1)	16S (2)	tRNA Leu	ND1	COI	cytb	28S	C-MYC 2
Smilisca baudinii	_	AY843762	AY843762	AY843762	DQ388762	DQ388762	DQ388762		AY844007		DQ388738
Sooglossus thomasseti	—	DQ283452	DQ283452	DQ283452	—	—	—	—	AY341742	DQ283755	—
Stefania aff. evansi ROM 44254	_	—	—	JQ742195	_	—	JQ742366	_	_	—	
Stefania ayangannae ROM 42906	—	—	—	JQ742212	—	—	JQ742380	—	—	—	
Stefania coxi ROM 39478	—	DQ679265	_	DQ679415	DQ679372	DQ679372	JQ742350 + DQ679372	—	_	_	—
<i>Stefania evansi</i> AMNH A 164211 + ROM 39450 + ROM 39451 + IRSNB 14586	_	AY819359	AY843767	AY843767	AY819490	AY819490	AY819490	_	_	AY844353	AY819193
Stefania ginesi LM 1056	DQ679266	DQ679266	—	DQ679417	DQ679373	DQ679373	DQ679373	—	—	—	—
Stefania riae VUB 3754	—	—	—	JQ742172	—	—	JQ742343	—	—	—	
Stefania riveroi IRSNB 15703	—	—	—	JQ742177	—	—	JQ742348	—	—	—	—
Stefania roraimae ROM 42843	—	—	—	JQ742214	—	—	JQ742276	—	—	—	—
Stefania satelles IRSNB 15839	—	—	—	JQ742175	—	—	JQ742346	—	—	—	—
<i>Stefania scalae</i> KU 181122 + MHNLS 17152	—	DQ679267	DQ679267	KR270413 + KR270434	DQ679374	DQ679374	JQ742362 + DQ679374	—	—	_	—
Stefania schuberti MNHN 2002 692		AY843768	AY843768	AY843768		_	_		AY844013	AY844354	_
Stefania sp. IRSNB 15853	_	—	—	JQ742181	_	—	JQ742352	_	—	—	—
Stefania woodleyi IRSNB 13799	_	—	—	JQ742185	_	—	JQ742356	_	—	—	—
Strabomantis biporcatus	—	EU186691	EU186691	EU186691	GQ345249	GQ345249	GQ345249	_	GQ345204	—	GQ345152
Strabomantis bufoniformis	_	DQ283165	DQ283165	DQ283165	_		—	FJ766635	—	DQ283555	—
Telmatobius truebae	AY819348	AY819348	—	DQ679378	AY819478	AY819478	AY819478	—	—	—	AY819182
Thoropa miliaris	—	DQ283331	DQ283331	DQ283331	—	—	—	DQ502874	FJ685662	—	
Trachycephalus typhonius	—	AY549362	AY549362	AY549362	GQ366341	GQ366341	GQ366341		EU034077	AY844322	AY819217
Uperoleia laevigata	—	DQ283221	DQ283221	DQ283221	—	—	—	—	—	—	
Yunganastes ashkapara	—	FJ438807	—	EU192233 + FJ438796	—	_	_	—	_	—	
Yunganastes fraudator	_	JF809938	—	FJ539065	_	—	—	_	_	—	
Zachaenus parvulus	_	KC593362	KC593362	KC593362		_	_	_	_	_	_

APPENDIX 1. (Continued)

Taxon*	C-MYC 3	CXCR4	H3a	РОМС	RAG1 (1)	RAG1 (2)	Rho	SIAH	SLC8A1	SLC8A3	Tyr
Acris crepitans	AY819268	EF107468	DQ284107	AY819109	EF107304 +		AY844533	AY844762	EF107244	EF107403	AY844019
Adelophryne patamona	GQ345167	GQ345185	GQ345215	GQ345262	GQ345280 +	EU186751	GQ345302	GQ345312	GQ345233	GQ345331	EU186772
Adenomera andreae	_	_	_	KC604061	GQ345296 KC604015 + KC604037	_	KC604094	_	HQ290704	_	KC520698
Adenomera hylaedactyla	—	_	DQ284093	KC604063	KC604037 KC604017 +	—	KC604095	_	_	—	JN691529
Agalychnis annae	_	GQ365977	_	EF158394	EF174311	_	_	GQ366159			GQ366198
Agalychnis callidryas	_	AB612054	DQ284401	EF158395	AY323765	EF493362	AY844537	AY844765	AB612055	_	DQ283018
Allobates femoralis	_	_	DQ502325	HQ290831	DQ503327	_	DQ503215	DQ503077	HQ290711	_	HQ290891
Allophryne ruthveni	AY819242	_	_	AY819077	EU663432	_	AY844538	AY844766	_	_	—
Alsodes neuquensis	_	_	DQ284118	_	AY844362	_	AY844539	AY844767	_	_	—
Amazophrynella minuta	AY819246	DQ306496	DQ284096	AY819081	DQ158346 +	_	AY844555	_	_	_	EF364362
Amietophrynus brauni	_	DQ306514	_	DQ158279	EF107331	_	DQ284021	DQ282873	EF107272	EF107435	DQ283011
Atelognathus patagonicus	_	_	_	_	AY844368	—	AY844545	AY844773	_	_	AY844027
Barycholos pulcher	_	_	_	_	_	EU186744	_	_	_	_	EU186765
Barycholos ternetzi	_	_	DQ284144	_	_	—	DQ283810	_	_	_	DQ282921
Batrachyla leptopus	_	_	DQ284119	_	AY844369	_	AY844546	AY844774	_	_	AY844028
Batrachyla taeniata	_	_	_	KC604075	KC604007	_	_	_	_	_	—
Brachycephalus alipioi	—	—	—	—	—	HQ435718	—	—	—	—	HQ435732
Brachycephalus ephippium	GQ345162	GQ345180	GQ345212	GQ345256	GQ345275 +	EU186761	DQ283808	DQ282673	GQ345228	GQ345326	DQ282919
Bryophryne cophites	_	_	_	_	-	EF493423	_	_	_	_	EF493508
Bufo japonicus	_	AB612061	_	JN653306	AB612057	_	_	_	AB612062	_	AB612059
Calyptocephalella gayi	_	EF107495	DQ284415	AY819090	AY583337	_	DQ284036	DQ282893	EF107275	EF107440	JX298244
Ceratophrys (C. cornuta, C. cranwelli, C. ornata)	_	AY364188 C. cranwelli	_	AY819091 C. cornuta	AY364218 C. cranwelli	_	AY364399 C. cranwelli		AY523718 C. cranwelli	AY948886 C. cranwelli	DQ347168 C. cranwelli
Ceuthomantis smaragdinus	GQ345169	GQ345190	GQ345220	GQ345267	GQ345285	—	GQ345305	GQ345317	GQ345238	GQ345336	—
Chacophrys pierottii	_	_	_	_	_	_	_	_	_	_	_
Colostethus pratti	_	_	DQ502362	HQ290847	DQ503361	_	DQ503247	DQ503112	HQ290727	_	HQ290907
Craugastor augusti	AY211289	—	DQ284291	_	_	_	DQ283935	DQ282786	_	—	DQ282963

Taxon*	C-MYC 3	CXCR4	H3a	РОМС	RAG1 (1)	RAG1 (2)	Rho	SIAH	SLC8A1	SLC8A3	Tyr
Craugastor podiciferus	GQ345164— AY211319	GQ345182		GQ345258	GQ345277 + GO345292	EF493450			GQ345230	GQ345328	EF493481
Craugastor punctariolus	_	_	DQ284206	_	_	_	DQ283862	—	_	_	_
Craugastor ranoides	AY211287	—	DQ284154	—	—	—	DQ283820	—	—	—	DQ282928
Craugastor rhodopis	AY211315	—	DQ284317	—	—	—	DQ283960	DQ282808	—	—	DQ282968
Crossodactylodes sp	—	—	—	KC604048	KC604011 + KC604033	—	KC604105	—	—	—	KC604077
Crossodactylus schmidti	—	—	DQ284050	HQ290828	DQ503298	—	_	AY844780	HQ290708	—	AY844031
Cryptobatrachus boulengeri LM	—	—	—	—	—	—	—	—	—	—	—
Cryptobatrachus fuhrmanni JDL 14865	—	—	—	—	—	—	—	—	—	—	—
Cryptobatrachus fuhrmanni MHUA A 5160	—	—	—	KR270358	KR138418	—	—	—	—	—	—
Cryptobatrachus remotus MHNLS 18853 + MHNLS 17664	_	KR138404	—	KR270360	KR138419	KR138394	_	_	KR138381	KR270375	KR270387
Cycloramphus acangatan		_	_	_	HQ634170 + FJ685703	_	_	—	_	—	_
Cycloramphus boraceiensis	—	—	DQ284147	—	DQ503357	—	DQ283813	DQ282675	—	—	DQ282924
Dendrobates auratus	—	AY364184	DQ284072	HQ290857	EU325909	—	AY364395	AY844781	AY948823	AY948879	DQ347160
Dendropsophus nanus	AY819282	GQ365985	DQ284051	AY819123	AY844437	—	AY844634	AY844852	_	—	—
Diasporus aff diastema	—	—	—	—	—	—	—	—	—	—	—
Diasporus diastema	—	GQ345184	GQ345214	GQ345261	GQ345279 + GQ345295	EU186752	—	GQ34531	GQ345232	GQ345330	EU186773
Duttaphrynus melanostictus	—	DQ306508	DQ284324	DQ158317	EU712821	_	AF249097	DQ282815	AY948805	AY948851	_
Edalorhina perezi	—	_	DQ284095	_	_	_	AY844558	AY844784	_	_	_
Eleutherodactylus cooki	GQ345166	—	GQ345213	HQ831999	HQ831830 + GO345294	EF493413	—	GQ345310	—	—	EF493455
Eleutherodactylus coqui		EF107500	—	—	EF107341	—	—	—	EF107282	EF107445	—
Eleutherodactylus marnockii	—	EF107463	DQ284151	—	EF107300	EF493399	DQ283817	DQ282677	EF107238	EF107388	EF493476
Eleutherodactylus nitidus	—	_	DQ284316	—	_	—	DQ283959	DQ282807	_	—	—
Eleutherodactylus planirostris	—	_	DQ284294	HQ831975	HQ831774	EF493396	DQ283937	DQ282788	—	—	DQ282964
Eleutherodactylus thorectes	—	_	—	HQ832000	HQ831831	EF493416	—	—	_	_	EF493473
Eleutherodactylus tonyi	_	_	_	HQ831994	HQ831824	_	_	_	_	_	_
Engystomops petersi	_	_	_	_	GQ375543	_	FJ668238	_	_	_	_
Engystomops pustulosus	_	EF107462	_	_	EF107299	_	_	_	EF107237	EF107387	_

Taxon*	C-MYC 3	CXCR4	H3a	РОМС	RAG1 (1)	RAG1 (2)	Rho	SIAH	SLC8A1	SLC8A3	Tyr
Espadarana prosoblepon	AY819250	AY364193	_	AY819085	EU663453	_	AY364404	AY844776	AY948834	AY948896	_
Eupsophus roseus	_	—	DQ284120	KC604074	KC604032	—	AY844560	AY844786	_	—	AY844036
Fejervarya limnocharis	_	AB277307	DQ284356	AB526646	—	AB277335	DQ458271	AY844787	AB277321	AB526674	EU980027
Flectonotus fitzgeraldi ZSM 1610 2006 + KU 192399	AY819265	GQ345177	—	KR270361	DQ679274	KR138395	—	—	GQ345224	GQ345322	KR270388
<i>Flectonotus pygmaeus</i> MHNLS 17478 + KU 184958	—	—	—	DQ679310	DQ679275	—	—	—	—	—	—
Fritziana fissilis MNRJ 62845	—	KR138406	—	—	—	—	—	—	KR138384	—	KR270389
<i>Fritziana</i> aff. <i>fissilis</i> sp. 2 MNRJ 44622	—	KR138407	—	KR270362	KR138422	KR138396	—	—	KR138385	KR270377	KR270390
Fritziana aff. fissilis sp. 3 MZSUP 133700	_	—	—	JN157627	KC844990	—	_	_	_	—	_
<i>Fritziana</i> aff. <i>fissilis</i> sp. 1 CFBH 5726 + MZUSP 13546	—	—	—	JN157628	AY844379	—	AY844562	AY844788	—	—	AY844038
Fritziana goeldi MNRJ 34921	—	KR138408	—	KR270363	—	—	—	—	KR138386	KR270378	KR270391
Fritziana ohausi MZUSP 139225	—	—	—	JN157629	KC844991	—	—	—	—	—	—
Fritziana sp. MNRJ 44592	—	KR138409	—	KR270364	—	—	—	—	—	KR270379	—
<i>Gastrotheca albolineata</i> MNRJ 54401	—	KR138410	—	KR270365	KR138423	KR138397	—	—	KR138387	KR270380	KR270392
<i>Gastrotheca antoniiochoai</i> MUSM 27944	—	_	—	KC844972	KC844993	—	—	—	—	—	_
Gastrotheca argenteovirens KU 181168	—	—	—	DQ679311	—	—	—	—	—	—	—
Gastrotheca atympana MHNSM 18692	—	—	—	DQ679312	DQ679276	—	—	—	—	—	—
<i>Gastrotheca aureomaculata</i> KU 181194	—	_	—	—	DQ679277	—	—	_	—	—	—
Gastrotheca christiani FML 2881	—	—	—	DQ679313	DQ679278	—	—	—	—	—	_
Gastrotheca chrysosticta LM 58	—	—	—	—	DQ679279	—	_	_	_	—	_
Gastrotheca sp. 1 IDLR 4073 (MNCN/ADN 566)	—	_	—	_	_	—	KR270372	_	_	_	_
<i>Gastrotheca cornuta</i> USNM 572472 + AMNH 107251	_	_	_	DQ679314	DQ679280	_	_	_	—	_	AY844040
Gastrotheca dendronastes KU 181203	—	—	—	DQ679315	DQ679281	—	—	—	—	—	—
Gastrotheca dunni ICN 10059 + MHUA A 4800	—	—	—	DQ679316	DQ679282	—	—	—	—	—	—
<i>Gastrotheca ernestoi</i> MNRJ 57129 + MNR I 64000		KR138411		KR270366	KR138424	KR138398			KR138388	KR270381	KR270393
Gastrotheca excubitor KU 173171	_	—	—	DQ679317	DQ679283	—	—	—	_	—	—

Taxon*	C-MYC 3	CXCR4	H3a	РОМС	RAG1 (1)	RAG1 (2)	Rho	SIAH	SLC8A1	SLC8A3	Tyr
<i>Gastrotheca excubitor</i> MUSM 26280		_	_	—	—	_	—	_	_	—	_
Gastrotheca fissipes ZUFRJ 7901	—	—	—	—	—	—	JX262904	JX262911	—	—	—
<i>Gastrotheca fulvorufa</i> CTMZ 07467	—	—	—	KC844977	KC844997	_	—	_	_	—	—
Gastrotheca galeata KU 181700	_	_	_	DQ679318	DQ679284	—	_	_	_	—	_
Gastrotheca gracilis DCC 006	—	—	—	DQ679319	—	—	—	—	—	—	
Gastrotheca griswoldi KU 181701	_	—	_	DQ679320	—	—	—	_	—	_	
<i>Gastrotheca griswoldi</i> MHNSM 20588	—	—	—	—	—	—	—	—	—	—	—
Gastrotheca guentheri KU 173112	—	—	—	DQ679321	DQ679285	—	—	—	—	—	—
Gastrotheca helenae KU 181070	—	—	_	DQ679322	DQ679286	_	_	_	—	_	_
Gastrotheca lateonota QCAZ	—	—	—	KC844970	—	—	—	—	—	—	—
<i>Gastrotheca</i> sp. 2 MNK 5286 + CBG 1020	—	—	DQ284069	—	AY844380	—	AY844563	AY844789	—	—	AY844039
Gastrotheca litonedis KU 202690	_	_	_	DQ679323	DQ679287	—	_	—	_	_	—
<i>Gastrotheca longipes</i> USNM 258905	—	—	—	DQ679324	DQ679288	—		—	—	—	—
<i>Gastrotheca marsupiata</i> KU 214813 + KU 214814	—	—	—	AY819105	DQ679289	—	—	—	_	—	—
Gastrotheca sp. 3 ZFMK 66954 + MNCN 43052	—	—	—	—	—	—	KR270373	—	—	—	—
<i>Gastrotheca megacephala</i> JLG 90 + CFBH T377	—	—	—	KC844976	AY844381 + KC844996	—	AY844564	AY844790	—	—	—
Gastrotheca microdiscus CFBH T	_	_	—	KC844979	KC844999	—	—	—	_	_	_
Gastrotheca monticola KU	_	—	_	AY819106	DQ679290	_	_	_	_	_	—
<i>Gastrotheca nebulanastes</i> MUSM	_	—	_	KC844982	KC845001	_	_	_	_	_	—
Gastrotheca nicefori KU 181071	_	—	_	DQ679325	DQ679291	_	—	—	—	—	_
<i>Gastrotheca nicefori</i> MHUA A 5716	_	—	_	KR270367	_	_	—	_	_	_	_
Gastrotheca ochoai KU 173499	—	—	—	DQ679326	DQ679292	—	—	—	—	—	—
Gastrotheca orophylax KU	_	—	—	DQ679327	DQ679293	—	—	_	_	_	_
Gastrotheca ovifera KU 185758	_	—	—	—	—	_	_	—	—	—	—

Taxon*	C-MYC 3	CXCR4	H3a	POMC	RAG1 (1)	RAG1 (2)	Rho	SIAH	SLC8A1	SLC8A3	Tyr
Gastrotheca pachachacae MUSM 28492	_	_	_	KC844983	KC845002	_	_	_	_	_	
Gastrotheca peruana KU 181740	—	—	—	—	—	_	—	—	—	—	—
Gastrotheca plumbea KU 178499	_	_	—	DQ679328	DQ679294	—	_	_	_	_	—
<i>Gastrotheca prasina</i> MZUSP 147060	—	—	—	—	_	—	JX262908	JX262915	—	_	—
<i>Gastrotheca pseustes</i> QCAZ 42862 + TNHC 62492	—	—	_	KC844986	—	_	_	—	_	—	—
<i>Gastrotheca psychrophila</i> KU 142634	—	—	_	DQ679329	DQ679295	_	—	_	—	—	_
Gastrotheca pulchra MTR 16228	—	—	—	—	—	—	JX262907	JX262914	—	—	—
Gastrotheca rebeccae CORBIDI	—	—	—	KC844987	—	—	—	—	—	—	—
Gastrotheca recava MZUSP 147044	_	—	_	_	_	_	JX262910	JX262919	_	_	_
Gastrotheca riobambae KU 178468	—	—	—	—	DQ679296	—	—	—	—	—	—
<i>Gastrotheca riobambae</i> UIMNH 94580	—	—	—	—	—	—	—	—	—	—	—
Gastrotheca ruizi KU 200002	—	—	—	—	DQ679297	_	—	—	—	—	—
Gastrotheca sp. A QCAZ 22635	_	—	—	KC844985	_	—	_	_	_	—	—
Gastrotheca sp. B QCAZ 21105	_	_	_	KC844989	_	_	_	_	_	_	—
Gastrotheca sp. C QCAZ 47299	_	_	—	KC844984	_	—	_	_	_	_	—
Gastrotheca sp. D QCAZ 42725	_	_	_	KC844988	_	_	_	_	_	_	_
Gastrotheca sp. E QCAZ 21213	_	_	—	—	—	—	_	_	_	_	—
Gastrotheca stictopleura MTD 45230	—	—	—	DQ679330	DQ679298	—	—	—	—	—	—
Gastrotheca testudinea QCAZ	_	_	—	_	_	_	_	_	_	—	_
Gastrotheca trachyceps KU 181189	_	_	_	DQ679331	DQ679299	_	_	_	_	_	_
Gastrotheca walkeri Vz 89–96	—	_	—	DQ679332	DQ679300	—	—	—	—	_	—
<i>Gastrotheca weinlandii</i> KU 143105	_	—	_	DQ679333	DQ679301	_	—	_	_	_	_
Gastrotheca zeugocystis MHNSM 18675	—	—	—	DQ679334	DQ679302	—	—	—	—	—	—
Haddadus binotatus	GQ345165	GQ345183	DQ284142	GQ345259	GQ345278 + GQ345293	EF493397	DQ283807	GQ345309	GQ345231	GQ345329	DQ282918
Heleophryne purcelli	—	AY364191	DQ284113	—	AY364221	—	AY364402	AY844791	AY948833	AY948892	—
Hemiphractus bubalus KU 143107 + KU 178588	—	GQ345179	—	DQ679335	DQ679303	—	—	—	GQ345226	GQ345324	—

Taxon*	C-MYC 3	CXCR4	H3a	РОМС	RAG1 (1)	RAG1 (2)	Rho	SIAH	SLC8A1	SLC8A3	Tyr
Hemiphractus fasciatus MVUP 1927	_	_	_	_	_	_	_	_	_	_	_
Hemiphractus fasciatus sp1 CHP 6397 + EVACC 207 + EVACC	_	_	_	_	_	_	_	_	_	_	_
065 <i>Hemiphractus fasciatus</i> sp2 EVACC 061 + CHP 6670	_	_	_	_	_	_	_	_	_	_	_
Hemiphractus helioi MHNCP 9063 + MJH 3689	—	KR138412	DQ284084	KR270368	KR138425	KR138399	AY844566	AY844792	KR138389	KR270382	KR270394
Hemiphractus proboscideus KU 217513	AY819266	—	—	AY819107	DQ679304	—	—	—	—	—	—
Hemiphractus scutatus JMP 2150 (MNCN/ADN 46913)	_	KR138413	_	KR270369	KR138426	KR138400	_	_	KR138390	KR270383	KR270395
Hemiphractus scutatus USNM 317196	_	_	_	DQ679336	DQ679305	_	_	_	_	_	_
Holoaden bradei	—	_	_	_	_	EF493449		_	_	_	EU186779
Holoaden luederwaldti	—	—	—	—	—	EU186747	_	—	—	—	EU186768
Hydrolaetare caparu	_	—	_	KC604050	KC604031 + KC604035	_	KC604107	—	—	—	KC604081
Hyla arenicolor	AY819271	AY364190	_	AY819112	AY364220 + AY844391	_	AY844577	AY844802	EF107241	EF107393	AY844048
Hyla chinensis	_	_	HM998949	DQ055789	_	_	_	_	HM998954	_	—
Hyla cinerea	AY819275	DQ306493	DQ284057	AY819116	AY323766	_	AY844597	AY844816	_	_	AY844063
Hylodes phyllodes	—	—	DQ284146	—	DQ503367	—	DQ503253	DQ282674	—	—	DQ282923
Hylorina sylvatica	—	—	—	—	—	—	—	—	—	—	—
Hyloxalus chlorocraspedus	—	—	—	—	DQ503325	—	DQ503212	DQ503074	—	—	DQ503153
Hypodactylus brunneus	—	GQ345187	GQ345218	GQ345264	GQ345282 + GO345298	EF493422	—	GQ345315	GQ345235	GQ345333	EF493484
Hypodactylus dolops	_	—	—	—	_	EF493414	GQ345304	—	—	—	EF493483
Hypsiboas boans	AY819273	—	DQ284086	AY819114	—	—	AY844588	AY844809	—	—	AY844055
Hypsiboas lanciformis	—	_	_	_	_	_	AY844619	AY844837	_	_	AY844081
Insuetophrynus acarpicus	_	_	_	_	JX204088	_	JX204152	JX204285	_	_	—
Ischnocnema guentheri	GQ345163	GQ345181	_	GQ345257	GQ345276 + GO345291	EF493407	_	GQ345308	GQ345229	GQ345327	EF493510
Ischnocnema juipoca	_	_	DQ284143		_	_	DQ283809	_	_	_	DQ282920
Lepidobatrachus laevis	AY819258	EF107461	DQ284191	AY819094	EF107298	—	DQ283851	DQ282707	EF107236	EF107386	_

Taxon*	C-MYC 3	CXCR4	H3a	РОМС	RAG1 (1)	RAG1 (2)	Rho	SIAH	SLC8A1	SLC8A3	Tyr
Leptodactylus melanonotus	AY337266	AY364194	_	_	AY364224	_	AY364405	_	AY948838	AY948900	DQ347193
Leptodactylus latrans	_	DQ306492	DQ284104	DQ158259	DQ158343 + AV844470	_	AY844681	AY844890	_	_	_
Limnodynastes salmini	—	AY364189	_	—	AY364219	_	AY364400	_	AY523719	AY948889	
Limnomedusa macroglossa	—	—	DQ284127	—	AY844471	—	AY844682	AY844891	—	_	AY844128
Lithodytes lineatus	—	—	DQ284112	KC604060	KC604025 +	—	AY844683	—	HQ290709		AY844129
Litoria caerulea	AY819308	AY948783	_	AY819149	AY844472 AY323767	EF493446	AY844685	AY844893	AY948821	AY948877	AY844131
Litoria infrafrenata	—	GQ365990	—	—	AY844474	—	AY844687	—	—	_	_
Lynchius nebulanastes	—	—	—	AY819154	_	—	—	—	—	—	—
Lynchius parkeri	—	—	—	—	_	—	—	—	—	—	—
Macrogenioglottus alipioi	—	—	—	—	KC593355	—	KC593357	KC593363	—	—	KC593367
Mannophryne trinitatis	—	—	DQ284108	JX036003	DQ503345	—	DQ503236	DQ503097	GQ345227	GQ345325	—
Megaelosia goeldii	—	—	DQ284109	—	DQ503346	—	DQ283797	—	—	—	DQ282911
Melanophryniscus klappenbachi	—	—	DQ284060	—	DQ503299	—	DQ283765	AY844899	—	—	
Myersiohyla kanaima	—	GQ365994	—	—	AY844422	—	AY844617	AY844835	—	—	AY844079
Noblella lochites	—	—	—	—	—	EU186756	—	—	—	—	EU186777
Noblella sp. MTD 45180	—	—	—	—	—	—	—	—	—	—	
Nymphargus bejaranoi	—	—	DQ284066	EU663239	EU663522	—	—	AY844777	—	—	AY844029
Odontophrynus achalensis	—	—	DQ284273	—	—	—	DQ283918	DQ282773	—	—	
Oreobates cruralis	—	—	—	—	—	EU186743	—	—	—	—	EU186764
Oreobates saxatilis	—	—	DQ284091	—	—	JF809910	DQ283788	DQ282661	—	—	JF809888
Paratelmatobius cardosoi	—	—	—	—	—	—	—	—	—	—	
Phrynopus bracki	GQ345168	GQ345186	GQ345217	GQ345263	GQ345281 +	EF493421	GQ345303	GQ345314	GQ345234	GQ345332	EF493507
Phyllodytes luteolus	_	_	_	GQ366043	AY844494	_	AY844708	AY844913	_	_	AY844150
Physalaemus cuvieri	_	—	—	AY819096	AY844499	_	AY844717	AY844922	—	_	_
Physalaemus gracilis	_	—	—	_	_	_	DQ284022	DQ282875	—	_	_
Phrynopus auriculatus	_	—	—	_	_	_	_	—	—	_	_

Taxon*	C-MYC 3	CXCR4	H3a	РОМС	RAG1 (1)	RAG1 (2)	Rho	SIAH	SLC8A1	SLC8A3	Tyr
Phyzelaphryne miriamae	_	_	_	_	_	EU186753	_	_	_	_	EU186774
Pleurodema brachyops	_	_	DQ284111	_	AY844503	_	AY844721	AY844926	—	—	—
Pleurodema diplolister	_	_	_	KC604052	HQ634173	_	JQ937153	JQ937222	—	_	KC604080
Pristimantis cruentus	_	AY948792	GQ345216	_	AY948935	_	—	GQ345313	AY948836	AY948898	_
Pristimantis curtipes	AY819256	_	_	AY819092	DQ679272	EF493435	_	_	_	_	EF493497
Pristimantis gaigeae	AY211290	_	_	_	_	_	—	—	—	_	_
Pristimantis ridens	AY211306	_	_	_	_	_	—	—	—	_	_
Pristimantis simonsii	AY819314	_	_	AY819155	_	_	—	—	—	_	_
Proceratophrys avelinoi	_	_	DQ284065	_	FJ685711	_	DQ283769	—	—	—	DQ282903
Pseudis minutus	_	GQ366028	_	GQ366070	AY844505	_	—	AY844929	_	_	_
Pseudopaludicola falcipes	_	_	DQ284117	KC604051	HQ634171 + AV844507	_	AY844728	AY844930	KC593352	_	KC520700
Psychrophrynella guillei	_	_	DQ284371	_	_	_	—	—	_	_	DQ282995
Psychrophrynella wettsteini	_	GQ345189	GQ345219	GQ345266	GQ345284 +	EU186755	—	GQ345316	GQ345237	GQ345335	EU186776
Rheobates palmatus	_	_	_	HQ290845		_	DQ503271	_	HQ290725	_	DQ503172
Rhinella arenarum	_	DQ306529	DQ284103	DQ158271	DQ158354 +	_	AY844547	AY844775	_	_	_
Rhinoderma darwinii	_	AY364192	DQ284320	_	AY364222	_	AY364403	DQ282813	AY523733	AY948895	_
Rupirana cardosoi	—	—	—	KC604049	KC604012 +	—	KC604106	—	—	—	KC604078
Scinax staufferi	_	GQ366029	_	GQ366071	AY844523	_	AY844748	_	_	_	AY844183
Scythrophrys sawayae	—	—	DQ284149	—	—	—	DQ283815	—	—	—	DQ282926
Smilisca baudinii				DQ388720	DQ830932	_	AY844749	AY844946			
Sooglossus thomasseti	_	AY364187	DQ284425	_	AY323778	_	DQ284042	—	AY948828	AY948884	DQ347167
Stefania aff. evansi ROM 44254	_	_	_	_	_	_	—	_	—	_	_
Stefania ayangannae ROM 42906	_	_	_	_	—	_	—	—	—	—	_
Stefania coxi ROM 39478	_	_	_	DQ679337	DQ679306	_	—	—	_	—	_
<i>Stefania evansi</i> AMNH A 164211 + ROM 39450 + ROM 39451 + IRSNB 14586	AY819267	KR138414	_	KR270370	KR138427+ DQ679307	KR138401	AY844755	AY844950	KR138391	KR270384	AY844189

Taxon*	C-MYC 3	CXCR4	H3a	РОМС	RAG1 (1)	RAG1 (2)	Rho	SIAH	SLC8A1	SLC8A3	Tyr
Stefania ginesi LM 1056	_	GQ345178	GQ345211	DQ679338	DQ679308	_	_	_	GQ345225	GQ345323	_
Stefania riae VUB 3754	—	—	—	—	—	_	—	—	—	—	—
Stefania riveroi IRSNB 15703	—	—	—	_	_	_	—	_	_	_	—
Stefania roraimae ROM 42843	_	—	_	_	_	_	_	_	_	_	_
Stefania satelles IRSNB 15839	_	—	_	_	_	_	_	_	_	_	_
<i>Stefania scalae</i> KU 181122 +	_	KR138415	_	KR270371	KR138428 +	KR138402	_	_	KR138392	KR270385	KR270397
Stefania schuberti MNHN 2002 692	—	—	—	—	AY844528	—	AY844756	AY844951	—	—	—
Stefania sp. IRSNB 15853	—	_	_	—	_	_	—	_	_	_	
Stefania woodleyi IRSNB 13799	—	—	—	—	—	_	—	—	—	—	—
Strabomantis biporcatus	—	GQ345188	—	GQ345265	GQ345283	EU186754	—	—	GQ345236	GQ345334	EU186775
Strabomantis bufoniformis	—	—	DQ284203	—	—	_	—	DQ282718	—	—	DQ282942
Telmatobius truebae	AY819260	—	—	AY819097	DQ679271	—	—	—	—	—	—
Thoropa miliaris	—	—	DQ502369	—	FJ685702	—	—	—	—	—	JX298241
Trachycephalus typhonius	AY819291	GQ366030		AY819132	EU034147	_	AY364396	AY844912	AY948824	AY948880	DQ347161
Uperoleia laevigata	_	EF107474	DQ284251	_	EF107310	_	DQ283898	DQ282758	EF107251	EF107410	_
Yunganastes ashkapara	_	—	_	_	_	JF809919	_	_	_	_	JF809898
Yunganastes fraudator	_	—	_	_	_	JF809916	_	_	_	_	JF809895
Zachaenus parvulus	_	—	—	_	_	_	_	_	_	_	_

*We selected outgroups with the objective to perform a strong test of the monophyly and relationships of Hemiphractidae. We included representatives of all currently used families of Nobleobatrachia with a denser taxon sampling within Terrarana and Hylidae because they have been historically associated with hemiphractids. Other criteria used to select terminals included:

Species diversity within a give taxon (e.g., we included more species of *Pristimantis*, with more 400 spp., than of *Adelophryne*, 9 spp.). This helps braking long branches, which often complicate tree-searches.

An attempt to maximize character coverage (*i.e.*, homologous sequences available from Genbank and phenotypic characters sampled by Mendelson *et al.* 2000). Species with more available characters were selected over those with less available characters.

An attempt to maximize phylogenetic structure according to the trees of the two most densely sampled anuran phylogenies (Frost *et al.* 2006; Pyron & Wiens 2011). For example, during exploratory analyses with fewer terminals of Leptodactylidae, members of this family were "all over the tree". We augmented the number of terminals until we recovered a monophyletic Leptodactylidae, which is a highly corroborated clade.

Constraints associated with phenotypic characters. Only a few outgroup terminals were sampled for the large majority of phenotypic characters (*Agalychnis annae*, *Hypsiboas boans*, *H. lanciformis*, and *Smilisca baudinii* from Mendelson *et al.* 2000). This meant that we could not take the luxury to exclude any of them (hence the two species of *Hypsiboas*). Also, the paucity of phenotypic character sampling created some unexpected results. The monophyly of Hylidae was not recovered because *A. annae* and *S. baudinii* broke it. Because they were the only outgroup taxa with phenotypic characters, we thought that those characters were affecting the non-monophyly of Hylidae. Thus we included some closely related terminals (other species of *Agalychnis* and *Hyla*, the sister taxon of *Smilisca*) that had as many as possible homologous sequences in GenBank. The inclusion of these taxa resulted in a monophyletic Hylidae.

APPENDIX 2. Specimens, voucher codes, localities, and GenBank accession numbers of DNA sequences generated in this study. Acronyms follow Frost (2014) except for CBG (Centro de Biodiversidad y Genética, Cochabamba), JMP (José M. Padial field series), IDIR (Ignacio De la Riva field series), and MNCN/ADN (tissue collection at MNCN). Not all samples were sequenced for all markers because PCRs or sequencing reactions did not work for all samples and all markers despite several attempts and/or sequence variation for the same marker among samples of the same species was low (*i.e.*, genetic p-distances < 1%) and those samples were recovered as sister taxa in exploratory analyses.

Genus	Species	Voucher	Locality	tRNA	128	tRNA	168	tRNA
				-Phe		-Val		Leu
Cryptobatrachus	fuhrmanni	MHUA A 5160	Colombia: Departamento Antiaoquia: Municipio Gómez	_	KR559912	KR270398	KR270398 +	
			Plata: La Clara (1085 m)				KR270414	
Cryptobatrachus	remotus	MHNLS 17664 (MNCN/ADN	Venezuela: Estado Zulia: Municipio Jesús Enrique Losada:	KR559913	KR559913	KR270399	KR270399+	—
		59450)	sierra de Perijá, cuenca alta del río Socuy, fundo El Progreso (10°43'13.30"N, 72°29'16.60"W; ± 845)				KR270415	
Cryptobatrachus	remotus	MHNLS 18853 (MNCN/ADN	Venezuela: Estado Zulia: Municipio Rosario de Perijá: sierra	KR559914	KR559914	KR270400	KR270400 +	KR138379
		59452)	de Perijá, cerro Las Antenas, caño detrás de la casa de las				KR270416 +	
			antenas (10°20'37"N, 72°33'41"W; ± 1467 m)				KR138379	
Flectonotus	fitzgeraldi	ZSM 1610 2006 (MNCN/ADN	Trinidad and Tobago: Tobago: Gilpin Trace entrance		_	KR270401	KR270401+	
		51094)	(11°17'01"N, 60°36'25"W; 495 m)				KR270417	
Flectonotus	pygmaeus	MHNLS 17478 (MNCN/ADN	Venezuela: Estado Aragua: Río Cata (100 m)		KR559915	KR270402	KR270402+	—
		51083)					KR270418	
Fritziana	fissilis	MNRJ 62845	Brazil: Estado Rio de Janeiro: Município Nova Friburgo:	KR559916	KR559916	KR270403	KR270403 +	—
			Baixo Caledônia				KR270419	
Fritziana	fissilis	MNRJ 74620	Brazil: Estado Rio de Janeiro: Parnaso	—	—	—	KR270420	_
Fritziana	aff. <i>fissilis</i>	MNRJ 44622	Brazil: Estado Rio de Janeiro: P.E. Três Picos, Cachoeiras de	KR559917	KR559917	KR270404	KR270404 +	_
	sp. 2		Macacu				KR270421	
Fritziana	aff. <i>fissilis</i>	MNRJ 56922	Brazil: Estado Rio de Janeiro: Vale da Pedra Branca,	_	_	_	KR270422	
	sp. 2		Cachoeiras de Macacu					
Fritziana	goeldi	MNRJ 34921	Brazil: Estado Espírito Santo: Estação Biológica Santa Lúcia,	KR559918	KR559918	KR270405	KR270405 +	
			Santa Teresa				KR270423	
Fritziana	sp.	MNRJ 44592	Brazil: Estado Rio de Janeiro: Município Teresópolis: Serra	—	—	KR270406	KR270406+	
			dos órgãos				KR270424	
Gastrotheca	albolineata	MNRJ 54401	Brazil: Estado Rio de Janeiro: Vale da Pedra Branca,	—	KR559919	KR270407	KR270407+	
			Cachoeiras de Macacu				KR270425	
Gastrotheca	dunni	MHUA A 4800	Colombia: Departamento Antiaoquia: Municipio Belmira: Páramo Belmira (4000 m)	—	—	—	KR270426	

Genus	Species	Voucher	Locality	tRNA	128	tRNA	168	tRNA
				-Phe		-Val		Leu
Gastrotheca	ernestoi	MNRJ 57129	Brazil: Estado Rio de Janeiro: Município Nova Friburgo	KR559920	KR559920	KR270408	KR270408+	_
							KR270427	
Gastrotheca	nicefori	MHUA A 5716	Colombia: Departamento Antiaoquia: Municipio La Estrella:	_	KR559921	KR270409	KR270409+	KR138380
			La Blanquita (2345 m)				KR138380	
Gastrotheca	sp. 1	IDIR 4073	Bolivia: Departamento Cochabamba: Aguirre (17°19'22"S,	—			KR270428	—
		(MNCN/ADN 566)	65°43'01"W; 4192 m)					
Gastrotheca	sp. 3	ZFMK 66954 (MNCN/ADN	Bolivia: Departamento Cochabamba: Incachaca (17º15'S,		_		KR270429	—
		25033)	65°49'W; 2300 m)					
Gastrotheca	sp. 3	MNCN 43052 (MNCN/ADN	Bolivia: Departamento Cochabamba: Provincia Chapare:				_	—
		2474)	Camino Tubos Penstock (17º12'21.6"S, 65º50'14.2"W; 2123					
			m)					
Gastrotheca	testudinea	CBG 774	Bolivia: Departamento La Paz: Pilón Lajas, Boquerón (1000		—	_	KR270430	
			m)					
Hemiphractus	helioi	MHNCP 9063	Peru: Departamento Loreto: Requena (4°59'13.24"S,	KR559922	KR559922	KR270410	KR270410+	_
			73°59'4.03"W, 114 m)				KR270431	
Hemiphractus	scutatus	JMP 2150 (tissue sample,	Colombia: Departamento Amazonas: Leticia: Km 11 carretera	KR559923	KR559923	KR270411	KR270411+	_
		specimen not collected,	(4°6'28.31"S, 69°57'2.37"W; 100 m)				KR270432	
		MNCN/ADN 46913)						
Stefania	evansi	IRSNB 14586 (MNCN/ADN	Guyana: Potaro-Siparuni district: Muri Muri trail, Kaieteur		KR559924	KR270412	KR270412 +	
		51121)	National Park (5°10'N, 59°30'W; 430 m)				KR270433	
Stefania	scalae	MHNLS 17152 (MNCN/ADN	Venezuela: Estado Bolívar: km 127 on the El Dorado-Santa		KR559925	KR270413	KR270413 +	
		50654)	Helena de Uairén road (860 m)				KR270434	

Genus	Species	Voucher	ND1	COI	cytb	CXCR4	POMC	Rag1 (1)	Rag1(2)	Rho	SLC8A1	SLC8A3	Tyr
Cryptobatrachus	fuhrmanni	MHUA A 5160	_	_	_	_	KR270358	KR138418	_	_	_	_	_
Cryptobatrachus	remotus	MHNLS 17664 (MNCN/ADN 59450)	—	—	—	KR138403	KR270359	KR138419	KR138393	—	KR138381	KR270374	KR270386
Cryptobatrachus	remotus	MHNLS 18853 (MNCN/ADN 59452)	KR13837 9	_	_	KR138404	KR270360	KR138420	KR138394	_	KR138382	KR270375	KR270387
Flectonotus	fitzgeraldi	ZSM 1610 2006 (MNCN/ADN 51094)	—		—	KR138405	KR270361	KR138421	KR138395		KR138383	KR270376	KR270388
Flectonotus	pygmaeus	MHNLS 17478 (MNCN/ADN 51083)	—	—	—		—	—	—	—	—	—	—
Fritziana	fissilis	MNRJ 62845	—		—	KR138406	—	—	—	—	KR138384	—	KR270389
Fritziana	fissilis	MNRJ 74620	_	_	_	_	_	_	_	_	_	_	_
Fritziana	aff. <i>fissilis</i> sp. 2	MNRJ 44622	—	_	—	KR138407	KR270362	KR138422	KR138396	—	KR138385	KR270377	KR270390
Fritziana	aff. <i>fissilis</i> sp. 2	MNRJ 56922	—	—	—	—	—	—	—	—	—	—	—
Fritziana	goeldi	MNRJ 34921	_	_	—	KR138408	KR270363	_	_	_	KR138386	KR270378	KR270391
Fritziana	sp.	MNRJ 44592	_	_		KR138409	KR270364	_	_	_	_	KR270379	_
Gastrotheca	albolineata	MNRJ 54401	_	_		KR138410	KR270365	KR138423	KR138397	_	KR138387	KR270380	KR270392
Gastrotheca	dunni	MHUA A 4800	_	_		_	_	_	_	_	_	_	_
Gastrotheca	ernestoi	MNRJ 57129	_	_		KR138411	KR270366	KR138424	KR138398	_	KR138388	KR270381	KR270393
Gastrotheca	nicefori	MHUA A 5716	KR13838 0		_		KR270367			_	_		_
Gastrotheca	sp. 1	IDIR 4073 (MNCN/ADN 566)	—	—	KR138416	—	—	—	_	KR270372	—	_	—
Gastrotheca	sp. 3	ZFMK 66954 (MNCN/ADN 25033)	—	—	—	—	—	—	—	—	—	—	—
Gastrotheca	sp. 3	MNCN 43052 (MNCN/ADN 2474)	—	_	KR138417		_		—	KR270373	—	—	
Gastrotheca	testudinea	CBG 774	—		KR559927	—	—	—	—	—		—	—
Hemiphractus	helioi	MHNCP 9063	_	_	_	KR138412	KR270368	KR138425	KR138399	_	KR138389	KR270382	KR270394
Hemiphractus	scutatus	JMP 2150 (tissue sample, specimen not collected, MNCN/ADN 46913)	—	KR559 926	_	KR138413	KR270369	KR138426	KR138400		KR138390	KR270383	KR270395
Stefania	evansi	IRSNB 14586 (MNCN/ADN 51121)	—	—	—	KR138414	KR270370	KR138427	KR138401	_	KR138391	KR270384	KR270396
Stefania	scalae	MHNLS 17152 (MNCN/ADN 50654)	—			KR138415	KR270371	KR138428	KR138402		KR138392	KR270385	KR270397

Marker	Primer name	Source	Primer sequence (5'-3')
CXCR4	CXC-F1	This work	TCCAGAACCATGACTGATAAGTA
	CXC-R1	This work	CAAGGCTTCTGTGATGGAGATCC
SLC8A1	NCX-F1	This work	CATCTCAAGAAAAAGAGATAAC
	NCX-R1	This work	ACTTGATAGTTAGCCAGCTCAA
	NCX-F2	This work	AGGAGGCAAGAAGAGATATGGC
	NCX-R2	This work	ATAGTAACTGTGGYYGTTGAGG
SLC8A3	SLC-F1	This work	TAACRTCRCAAGAACGRGAAAT
	SLC-R1	This work	CCATCTAGAAAATGAGAATTCA
	SLC-F2	This work	GGTGGCRGACCGACGTCTTCTC
	SLC-R2	This work	AAGATGTCATCAATAATCC
POMC	POMC-1	Blackburn & Duellman (2013)	GAATGTATYAAAGMMTGCAAGATGGWCCT
	POMC-7	Blackburn & Duellman (2013)	TGGCATTTTTGAAAAGAGTCAT
RAG1 Amp-	Amp-RAG-1 F	Wiens et al. (2007), Blackburn & Duellman (2013)	AGCTGCAGYCARTACCAYAARATGTA
Hemi	Hemi-RAG1-R	Wiens et al. (2007), Blackburn & Duellman (2013)	CTCTGCAGCATTTCCAATGTCAC
RAG1	R182	Heinicke et al. (2009)	GCCATAACTGCTGGAGCATYAT
R182/R270	R270:	Heinicke et al. (2009)	AGYAGATGTTGCCTGGGTCTTC

APPENDIX 3. Primers used in this study. We sequenced genes SLC8A1 and SLC8A3 in two partially overlapping fragments by combining pairs F1-R1 and F2-R2 respectively. RAG1 Amp-Hemi and RAG1 R182/R270 correspond to two non-overlapping fragments of the gene RAG1. F = Forward, R = Reverse. Primers not included in the table are listed in Guayasamin *et al.* (2008).

APPENDIX 4. References used to code life reproductive modes of outgroup taxa.

Taxa	Reference
Acris crepitans	Johnson (1991)
Adenomera andreae	Crump (1974), Haddad & Prado (2005)
Adenomera hylaedactyla	Hödl (1990), Haddad & Prado (2005)
Agalychnis annae	Savage (2002)
Agalychnis callidryas	Warketin (1999), Savage (2002)
Allobates femoralis	Weygold (1980)
Allophryne ruthveni	Kok & Kalamandeen (2008)
Alsodes neuquensis	Lavilla (1988)
Amazophrynella minuta	Duellman & Lynch (1969)
Amietophrynus brauni	Spraguea & Zimkus (2011)
Atelognathus patagonicus	Martinazzo et al. (2011)
Barycholos pulcher	Heyer (1969)
Barycholos ternetzi	Caramaschi & Pombal Jr. (2001)
Batrachyla leptopus	Formas <i>et al.</i> (1976)
Brachycephalus alipioi	Pombal Jr. & Gasparini (2006)
Brachycephalus ephippium	Pombal Jr. (1999)
Bryophryne cophites	Lynch (1975)
Bufo japonicus	Iwai & Kagaya (2005)
Calyptocephalella gayi	Diaz & Valencia (1985), Castañeda et al. (2006)
Ceratophrys cornuta	Duellman & Lizana (1994)
Ceratophrys cranwelli	Vera Candioti (2005)
Ceratophrys ornata	Natale <i>et al.</i> (2010)
Chacophrys pierottii	Quinzio <i>et al</i> . (2006)
Colostethus pratti	Lynch (2006)
Craugastor augusti	Jameson (1950)
Craugastor podiciferus	Schlaepfer & Figueroa-Sandy (1998)
Craugastor punctariolus	Fenolio et al. (2010), Konstant (2007)
Craugastor ranoides	Sunyer <i>et al.</i> (2009)
Craugastor rhodopis	Campbell (1998)
Crossodactylus schmidti	Faivovich (1998)
Cycloramphus acangatan	Dixo & Verdade (2006)
Cycloramphus boraceiensis	Haddad & Prado (2005)
Dendropsophus nanus	Lavilla (1990)
Diasporus diastema	Dunn (1937), Ovaska & R, (2001)
Duttaphrynus melanostictus	Mogali et al. (2011)
Edalorhina perezi	Schlüter (1990)
Eleutherodactylus cooki	Joglar et al. (1996), Burggren et al. (2003)
Eleutherodactylus coqui	Townsend & Stewart (1985)
Eleutherodactylus marnockii	Jameson (1955)
Eleutherodactylus planirostris	Goin (1947), Olson et al. (2012)
Eleutherodactylus thorectes	Martínez et al. (2011)
Eleutherodactylus tonyi	Stuart <i>et al.</i> (2008)

APPENDIX 4. (Continued)

Taxa	Reference
Engystomops petersi	Crump (1974)
Engystomops pustulosus	Montealegre-Delgado et al. (2013)
Espadarana prosoblepon	Hoffman (2010)
Eupsophus roseus	Formas & Pugin (1978)
Fejervarya limnocharis	Wu & Kam (2009)
Haddadus binotatus	Canedo & Rickli (2006), Hartmann et al. (2010)
Holoaden luederwaldti	Martins (2010)
Hyla arenicolor	Zweifel (1961)
Hyla chinensis	Hsu et al. (2006)
Hyla cinerea	Roth & Jackson (1987)
Hylodes phyllodes	Weber & Caramaschi (2013)
Hylorina sylvatica	Cárdenas-Rojas et al. (2007)
Hyloxalus chlorocraspedus	Caldwell (2005)
Hypodactylus brunneus	Lynch (1975)
Hypsiboas boans	Duellman (1970), Lynch (2006)
Hypsiboas lanciformis	Lynch & Suárez (2011)
Insuetophrynus acarpicus	Formas <i>et al.</i> (1980)
Ischocnema guentheri	Lynn & Lutz (1946), Giaretta & Facure (2008)
Lepidobatrachus laevis	Ruibal & Thomas (1988)
Leptodactylus latrans	Rodrigues (2008), Kwet et al. (2010)
Leptodactylus melanonotus	Hoffmann (2006)
Limnodynastes salmini	Davies & Watson (1994)
Limnomedusa macroglossa	Kaefer et al. (2009)
Lithodytes lineatus	Lamar & Wild (1995)
Litoria caerulea	Cabrera-Guzmán et al. (2013)
Litoria infrafrenata	Banks et al. (1983)
Macrogenioglottus alipioi	Lisboa et al. (2011)
Mannophryne trinitatis	Kenny (1969), Downie et al. (2001)
Megaelosia goeldii	Nuin (2003)
Melanophryniscus klappenbachi	Kurth et al. (2013), Haad et al. (2011)
Myersiohyla kanaima	MacCulloch & Amy Lathrop (2005)
Noblella lochites	Lynch (1976)
Nymphargus bejaranoi	Köhler (2000), Aguayo (2009)
Odontophrynus achalensis	Haas (2003), González et al. (2014)
Oreobates cruralis	Padial et al. (2012)
Oreobates saxatilis	Duellman (1990)
Paratelmatobius cardosoi	Pombal Jr. & Haddad (1999)
Phrynopus bracki	Hedges (1990)
Phyllodytes luteolus	Giaretta (1996)
Physalaemus cuvieri	Bokermann (1962), Rossa-Feres et al. (2006)
Physalaemus gracilis	Langone (1989)
Pleurodema brachyops	Molina (2004 "2002")

APPENDIX 4. (Continued)

Taxa	Reference
Pleurodema diplolister	Cardoso & Arzabe (1993)
Pristimantis cruentus	Myers (1969)
Pristimantis curtipes	Lynch (1981)
Pristimantis gaigeae	Hill et al. (2010)
Pristimantis ridens	Sunyer <i>et al.</i> (2009)
Proceratophrys avelinoi	De Sá & Langone (2002)
Pseudis minutus	Melchiors et al. (2004)
Pseudopaludicola falcipes	Laufer & Barreneche (2008)
Psychrophrynella wettsteini	Ergueta (1993), De la Riva (2007)
Rheobates palmatus	Dunn (1944), Anganoy-Criollo (2013)
Rhinella arenarum	Bionda <i>et al.</i> (2012)
Rhinoderma darwini	Jorquera et al. (1982)
Rupirana cardosoi	Acuña & Lugli (2009)
Scinax staufferi	Savage (2002)
Smilisca baudinii	Torres-Orozco et al. (2002)
Sooglossus thomasseti	Gerlach (2007)
Strabomantis biporcatus	Heatwole (1962)
Strabomantis bufoniformis	Castro-Herrera et al. (2012)
Telmatobius truebae	Aguilar et al. (2007)
Thoropa miliaris	Barth (1956), Giaretta & Gomes (2004)
Trachycephalus typhonius	Savage (2002)
Uperoleia laevigata	Tyler (1994)
Yunganastes fraudator	De la Riva & Lynch (1997)
Zachaenus parvulus	Lutz (1947), Haddad & Prado (2005)

APPENDIX 5. Unambiguous transformations inferred in this study for the supraspecific taxa reported in the Systematics section. Because the relationships among *Cryptobatrachus* are ambiguous (a polytomy in our strict consensus tree) the transformations reported herein are only shared among some of the optimal trees.

Hemiphractidae	Char. 4263: 1> 3	Char. 9355: 3> 1
Char. 41: 0> 1	Char. 4349: 3> 0	Char. 9581: 3> 1
Char. 46: 0> 4	Char. 5992: 0> 2	Char. 9906: 2> 1
Char. 83: 0> 2	Char. 6021: 1> 3	Char. 10063: 1> 3
Char. 519: 1> 4	Char. 6180: 3> 1	Char. 10136: 3> 1
Char. 810: 0> 3	Char. 6229: 3> 1	Char. 10253: 0> 2
Char. 819: 4> 0	Char. 8093: 1> 3	Char. 10371: 3> 1
Char. 1249: 3> 1	Char. 8499: 3> 2	Char. 10424: 1> 0
Char. 1395: 4> 2	Char. 8845: 3> 0	Char. 10855: 3> 1
Char. 2257: 1> 0	Char. 8848: 3> 1	Char. 10957: 2> 1
Char. 2343: 4> 1	Char. 8984: 0> 2	Char. 11102: 1> 0
Char. 2344: 0> 1	Char. 9151: 02> 3	Char. 11909: 1> 3
Char. 2378: 3> 1	Char. 9210: 1> 3	Char. 11936: 1> 4
Char. 3145: 4> 1	Char. 9238: 2> 0	Char. 11970: 4> 0
Char. 3183: 4> 0	Char. 9260: 0> 1	Char. 12012: 0> 1
Char. 3228: 3> 4	Char. 9287: 0> 1	Char. 12076: 1> 0
Char. 3406: 0> 4	Char. 9291: 0> 2	Char. 12243: 0> 3
Char. 3862: 0> 1	Char. 9349: 1> 3	Char. 12248: 0> 3

Char. 12323: 3> 4
Char. 12355: 0> 1
Char. 12521: 0> 3
Char. 12616: 3> 01
Char. 12707: 0> 1
Char. 12713: 3> 1
Char. 12729: 0> 1
Char. 12781: 0> 4
Char. 12849: 3> 4
Char. 12860: 1> 3
Char. 12900: 0> 1
Char. 12972: $3 -> 1$
Char. $13260: 2 -> 3$
Char. $13232 \cdot 3 -> 1$
Char. $13454: 0 \rightarrow 3$
Char $13698 \cdot 1 = > 0$
Char. $13706: 2 \rightarrow 0$
Char. $1/353: 3 \rightarrow 0$
Char 14333. $3 - > 0$
Char 14599. $3 - 2$
Char $140/4$. 2> 0
Char. 14766: $0 \rightarrow 2$
Char. $14/81: 2> 0$
Char. 14796: 1> 3
Char. 14809: $0 -> 3$
Char. 14928: 1> 3
Char. 15022: 1> 3
Char. 15449: 1> 3
Char. 16662: 2> 1
Char. 16998: 0> 2
Char. 17421: 3> 0
Char. 17474: 2> 0
Char. 17541: 1> 3
Char. 18098: 1> 3
Char. 18161: 1> 3
Char. 18249: 2> 0
Cryptobatrachinae
Char. 35: 1> 0
Char. 556: 3> 0
Char. 707: 4> 1
Char. 723: 0> 2
Char. 815: 3> 0
Char. 828: 0> 2
Char. 841: 1> 4
Char. 851: 0> 4
Char. 965: 1> 3
Char. 1011: 2> 0
Char. 1088: 1> 0
Char. 1759: 1> 3
Char. 1867: 1> 3
Char. 2027: 4> 0
Char. 2040: 4> 3
Char. 2078: 3> 1
Char. 2079: $0 \rightarrow 2$
Char. $2115: 3 -> 1$
Char 2181: 0> 4
Char. 2247. 4> 1
Char 2272: $0 > 1$
1 nar / 3 / / 1 - 2 1

Char. 2569: 3> 0
Char. 2675: 0> 13
Char $2702: 0 > 3$
Chai. 2792. 0> 3
Char. 2999: 0> 2
Char. $3101: 3 -> 0$
Char. 3254: 1> 4
Char. 3310: 0> 3
Char 3354 · 1> 3
Char $2421:1 > 0$
Char. $344 /: 0> 1$
Char. 3457: 3> 1
Char. 3639: 0> 3
Char. 3645: 3> 1
Char. 3673: 3> 4
Char 3756 4> 1
Char $4068: 0 -> 2$
Char. $4000: 0 \rightarrow 2$
Cliai. 4099. 0 4
Char. $4177: 0> 1$
Char. 4926: 1> 4
Char. 5082: 4> 2
Char. 5137: 1> 4
Char. 5226: 3> 4
Char $5330: 3 - > 4$
Char. $5350: 5 \neq 1$
Char $5351.0 - 4$
Char. 5352: 3> 4
Char. 5355: $3> 2$
Char. 5377: 3> 1
Char. 5671: 2> 4
Char. 5812: 0> 2
Char. 6068: 4> 3
Char $6072:1 \rightarrow 0$
Char. $6089: 2 > 1$
Char (110: $4 > 0$
Char. 0119: 4> 0
Char. 6161: $0> 4$
Char. 6182: 0> 1
Char. 6213: 1> 0
Char. 6217: 3> 0
Char. 6239: 2> 0
Char $9520: 1 -> 3$
Char. $9520: 1 \rightarrow 3$
Char $0707 \cdot 2 > 1$
Char. $9/9/: 3> 1$
Char. 10054: $0 \rightarrow 2$
Char. 10149: 3> 1
Char. 11469: 2> 0
Char. 11957: 3> 0
Char. 12026: 1> 4
Char. 12048: 3> 0
Char 12059: $3 \rightarrow 0$
Char 12000.1 ~ 02
Char. 12500 . $1 - 203$
Char. $124/4$: $13> 0$
Char. 12513: 0> 3
Char. 12518: 0> 4
Char. 12523: 3> 0
Char. 12532: 4> 12
Char. 12546: 0> 3
Char. 12608: 3> 1
Char 12678 1> 3
Char. 12678: $1 \rightarrow 3$

Char. 12795: 0> 1
Char. 12813: 3> 1
Char. 12833: 4> 2
Char. 12884: 3> 0
Char. 12886: 0> 3
Char. 12899: 3> 1
Char. 12917: 4> 2
Char. 12927: 1> 4
Char. 12929: 0> 3
Char. 13005: 3> 2
Char. 13186: 1> 3
Char. 13905: 1> 3
Char. 13994: 3> 1
Char. 14085: 0> 2
Char. 14186: 1> 3
Char. 14285: 0> 2
Char. 15112: 2> 0
Char. 15572: 3> 1
Char. 15743: 3> 1
Char. 16796: 2> 0
Char. 17235: 0> 2
Char. 17313: 0> 3
Char. 17468: 0> 3
Char. 17737: 1> 4
Char. 17927: 1> 3
Countab ata a alura

Cryptobatrachus Some trees: Char. 2: 0 --> 1 Char. 4: 1 --> 0 Char. 10: 0 --> 1 Char. 16: 0 --> 1 Char. 549: 3 --> 0 Char. 609: 2 --> 4 Char. 704: 4 --> 3 Char. 839: 0 --> 2 Char. 966: 3 --> 1 Char. 1028: 3 --> 1 Char. 1038: 0 --> 1 Char. 1258: 0 --> 3 Char. 1547: 2 --> 0 Char. 2026: 1 --> 4 Char. 2058: 1 --> 3 Char. 2165: 1 --> 0 Char. 2277: 3 --> 0 Char. 2378: 1 --> 0 Char. 2605: 0 --> 3 Char. 2698: 4 --> 0 Char. 2702: 4 --> 1 Char. 2739: 1 --> 0 Char. 2774: 3 --> 1 Char. 2883: 1 --> 0 Char. 2924: 1 --> 3 Char. 2949: 3 --> 1 Char. 2962: 0 --> 2 Char. 2996: 1 --> 0 Char. 2998: 3 --> 0 Char. 3057: 0 --> 2 Char. 3304: 4 --> 3

Char. 3323: 1> 3
Char. 3369: 1> 0
Char. 3436: 3> 4
Char. 3439: 0> 2
Char. 3537: 1> 3
Char. 3548: 1> 3
Char. 3551: 1> 3
Char. 3686: 3> 4
Char. 3696: 1> 0
Char. 3786: 13> 0
Char. 3891: 3> 0
Char. 3894: 1> 3
Char. 3897: 0> 2
Char. 4096: 4> 1
Char. 4167: 03> 1
Char. 4191: 13> 0
Char. 4288: 0> 3
Char. 4397: 0> 3
Char. 4505: 13> 4
Char. 4661: 2> 0
Char. 4684: 3> 1
Char. 4808: 4> 1
Char. 5094: 4> 1
Char. 5356: 4> 1
Char. 5551: 2> 3
Char. 5583: 1> 0
Char. 5635: 1> 3
Char. 5639: 1> 3
Char. 5666: 4> 2
Char. 5673: 1> 0
Char. 5682: 3> 1
Char. 5718: 0> 1
Char. 5811: 1> 3
Char. 5833: $3 - > 0$
Char. 5861: $2 \rightarrow 0$
Char. 5944: 2> 0
Char. 5952: $1> 3$
Char. 5998: $3> 2$
Char. $6029: 02> 1$
Char. $6031: 0> 2$
Char. $6154: 4 \rightarrow 3$
Char. $6155: 4 \rightarrow 3$
Char. $6165: 4 \rightarrow 3$
Char $6728: 1 -> 4$
Char $6229: 1 \rightarrow 4$
Char. $6236: 0 -> 2$
Char. 11914: 3> 0
Char. 11949: 1> 3
Char. 12041: 01> 3
Char. 12151: 1> 0
Char. 12203: 1> 3
Char. 12216: 1> 0
Char. 12235: 0> 3
Char. 12249: 2> 0
Char. 12258: 1> 3
Char. 12279: 1> 0

Char $2540: 3 -> 1$	
Char $2587: 2 \rightarrow 0$	
Chai: $2567.2 \rightarrow 0$	
Char. $266/: 1> 0$	
Char. 2694: $0 \rightarrow 4$	
Char. 2700: 0> 4	
Char. 2712: 3> 4	
Char. 2837: 1> 0	
Char. $2872: 3 - > 0$	
Char $2885: 1 -> 3$	
Char. 2005: $1 \rightarrow 5$	
Chai: $2910. 4 - 2075. 1 > 2$	
Char. 29/5: 1> 3	
Char. 3053: 1> 3	
Char. $3056: 0> 3$	
Char. 3283: 4> 2	
Char. 3332: 3> 1	
Char. 3337: 3> 0	
Char. 3346: 3> 1	
Char. 3352: 0> 1	
Char $3355: 0 -> 2$	
Char. 3350: $3 \rightarrow 2$	
Char. $3333.3 - 1$	
Char. $336/: 3> 1$	
Char. $3374: 0> 3$	
Char. 3398: 4> 0	
Char. 3464: 3> 1	
Char. 3514: 0> 1	
Char. 3567: 0> 2	
Char. 3622: 0> 1	
Char $3858: 1 -> 0$	
Char $3862: 1 -> 3$	
Char 2012: $2 > 1$	
Cliar. $3913.3 - 1$	
Char. $3935: 3> 0$	
Char. 3992: 0> 4	
Char. 3996: 2> 4	
Char. 4019: 0> 3	
Char. 4060: 0> 4	
Char. 4062: 2> 4	
Char. 4064: 2> 4	
Char. 4067: 0> 1	
Char $4072 \cdot 1 -> 4$	
Char. $4074: 0 \rightarrow 4$	
Char. $4077: 2 > 4$	
Cliai. $4087.2 - 24$	
Char. 4088: $2> 4$	
Cnar. 4089: 0> 4	
Char. 4093: 1> 4	
Char. 4098: 1> 4	
Char. 4100: 1> 4	
Char. 4102: 0> 4	
Char. 4105: 2> 4	
Char. $4139: 1 - > 0$	
Char $4297.0 = > 1$	
Char $4401 \cdot 3 = > 2$	
Char $4400: 1 > 2$	
Char. 4409: 1> 3	
Cnar. 4439: 1> 3	
Char. 4519: 2> 0	
Char. 4577: 1> 3	
Char. 4628: 3> 1	
Char $4662 \cdot 2 \to 0$	

Char. 4663: 2> 0
Char. 4667: 3> 1
Char. 4718: 2> 0
Char. 4743: 3> 1
Char. 4768: 0> 2
Char. 4773: 2> 0
Char. 4776: 3> 4
Char. 4779: 0> 4
Char. 4787: 1> 4
Char. $4822: 0 -> 3$
Char. $4894: 3 - > 4$
Char $4898: 3> 4$
Char 4949: $3 -> 4$
Char 4997: 1> 4
Char 5011: 1> 0
Char. 5362: 1> 4
Char. 5380: $2 \rightarrow 4$
Char. 5305: $1 \rightarrow 4$
Char. 5395. 1> 4 Char. 5407: $2 > 4$
Char. $5407.5 - 24$
Char. 5418: $0 - 2 = 4$
Char. 5420. $2 \rightarrow 4$
Char. 5451. 2> 1 Char. 5457: $0 > 4$
Char. $5457: 0> 4$
Char. 5460: $3 - 2 = 1$
Char. 5466: $3 - 2$
Char. $54/9: 0> 3$
Char. 5601: $4 - > 0$
Char. $5628: 3> 0$
Char. $5692: 0 -> 2$
Char. $5693: 3 -> 1$
Char. $5/00: 3 -> 1$
Char. $5/15: 3 -> 1$
Char. 5735: 0> 2
Char. 5758: 3> 0
Char. 5764: 3> 1
Char. 5771: 1> 3
Char. 5781: 3> 1
Char. 5787: 3> 1
Char. 5820: 1> 0
Char. 5872: 0> 2
Char. 5880: 1> 3
Char. 5890: 3> 1
Char. 5959: 0> 2
Char. 6007: 3> 1
Char. 6038: 0> 3
Char. 6098: 1> 4
Char. 6101: 0> 4
Char. 6130: 1> 0
Char. 6140: 0> 3
Char. 6169: 0> 4
Char. 11926: 0> 4
Char. 11954: 1> 4
Char. 11978: 3> 4
Char. 12000: 4> 3
Char. 12056: 0> 3
Char. 12068: 1> 3
Char. 12114: 0> 3

Char. 12115: 1> 3
Char. 12133: 3> 1
Char. 12143: 0> 2
Char. 12160: 0> 2
Char 12222: $0 \rightarrow 3$
Char 12222: $0 \rightarrow 0$
Char $12253: 1 \rightarrow 0$
Char. 12275: $0 \rightarrow 3$
Char. 12275: $0 \rightarrow 5$
Char 12225: $4 > 2$
Char. 12333. 4> 2
Char. 12340: $1 - > 0$
Char. 12353: $2 \rightarrow 1$
Char. 12354: $2 \rightarrow 1$
Char. $12409: 2> 1$
Char. $12431: 0> 1$
Char. 124/3: 1> 3
Char. $12510: 3> 1$
Char. $12530: 3> 0$
Char. 13076: 1> 3
Char. 13142: 0> 2
Char. 13149: 0> 3
Char. 13182: 1> 3
Char. 13201: 1> 3
Char. 13202: 1> 3
Char. 13206: 3> 1
Char. 13296: 3> 1
Char. 13326: 1> 3
Char. 13329: 1> 0
Char. 13392: 0> 1
Char. 13409: 2> 0
Char. 13426: 2> 0
Char. 13434: 3> 0
Char. 13462: 3> 1
Char. 13468: 0> 3
Char. 13497: 2> 0
Char. 13737: 0> 3
Char. $13744: 2 \rightarrow 0$
Char. 13759: 3> 1
Char. $13784: 1 -> 0$
Char $13803: 3 -> 0$
Char. 13811: $3 \rightarrow 1$
Char 13829: $3 -> 1$
Char 13860: $1 -> 3$
Char 13869: $2 \rightarrow 0$
Char 13899: $3 -> 1$
Char 13911: $0 \rightarrow 2$
Char 13973: $0 \rightarrow 2$
Char 14000: $2 = > 0$
Char $14073: 1 \rightarrow 0$
Char $14082:0 = 51$
Char $14082.0 - 71$
Char. 14009. $2 = 2$
Char. 14077. $0 - 2$
Char. 14242. $2 = -73$ Char. 14202: $2 = -73$
Char. 14302. $2 \rightarrow 3$
Char 14411: $2 > 0$
Char. 14411: $2 \rightarrow 0$
Char. 14430: 0> 2

Char. 14540: 0> 2
Char. 14555: 1> 0
Char. 14556: 3> 1
Char. 17655: 0> 2
Char. 17688: 3> 0
Char. 17736: 3> 4
Char. 17741: 3> 1
Char. 17745: 3> 1
Char. 17757: 0> 2
Char. 17801: 3> 0
Char. 17804: 3> 1

Hemiphractinae Char 11: 0 --> 1

Char. 11: $0 \rightarrow 1$
Char. 19: 0> 1
Char. 38: 0> 2
Char. 203: 0> 1
Char. 235: 0> 3
Char. 359: 0> 1
Char. 409: 3> 1
Char. 459: 3> 0
Char. 571: 0> 3
Char. 681: 3> 1
Char. 781: 2> 0
Char. 1990: 3> 0
Char. 2210: 3> 0
Char. 2408: 3> 1
Char. 2450: 0> 3
Char. 2551: 0> 3
Char. 3130: 1> 0
Char. 3184: 0> 1
Char. 3384: 3> 1
Char. 3439: 0> 3
Char. 4625: 3> 1
Char. 5496: 1> 3
Char. 5498: 0> 2
Char. $6047: 2 - > 0$
Char. $6132: 3 -> 1$
Char. $6167: 3 -> 0$
Char. 6169: 0> 1
Char. 6185: 4> 2
Char. 6224: 0> 2
Char. $8591: 2 \rightarrow 0$
Char. $9551: 2 \rightarrow 1$
Char. $9815: 4 -> 3$
Char. 9882: $2 \rightarrow 1$
Char. $10075: 2 \rightarrow 0$
Char. $10116: 2 \rightarrow 0$
Char. $10211: 2 \rightarrow 0$
Char $10305: 0 -> 3$
Char $10472: 3 -> 1$
Char $10569: 3 -> 1$
Char. 11896: $0 \rightarrow 2$
Char. 11919: $4 \rightarrow 0$
Char. 11920: $4 \rightarrow 0$
Char. $12131: 0 \rightarrow 2$
Char. 12319: $4 \rightarrow 0$

Char. 12606: 0> 1
Char. 12647: 1> 0
Char. 12923: 3> 0
Char. 12970: 0> 2
Char. 12978: 3> 1
Char. 13169: 1> 0
Char. 13787: 0> 3
Char. 14236: 1> 3
Char. 14239: 3> 1
Char. 14245: 1> 3
Char. 14423: 3> 0
Char. 14708: 3> 0
Char. 14959: 1> 3
Char. 15143: 0> 3
Char. 15682: 0> 2
Char. 16956: 1> 3
Char. 17688: 3> 1
Char. 17777: 1> 3
Char. 17820: 0> 2
Char. 18034: 2> 0
Char. 18303: 3> 1
Fritziana
$\frac{\Gamma}{2} \frac{\Gamma}{2} \frac{\Gamma}$
Char. 22: $0 > 1$
Char. 22: $0 \rightarrow 1$
Char. 25. $0 \rightarrow 1$
Char. J> 0
Char $15:3 -> 2$
Char. 45: $3 \rightarrow 2$ Char. 47: $1 \rightarrow 2$
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1 Char. 238: 3> 1
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1 Char. 238: 3> 1 Char. 279: 3> 1
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1 Char. 238: 3> 1 Char. 279: 3> 1 Char. 332: 0> 2
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1 Char. 238: 3> 1 Char. 279: 3> 1 Char. 332: 0> 2 Char. 351: 0> 1
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1 Char. 238: 3> 1 Char. 279: 3> 1 Char. 332: 0> 2 Char. 351: 0> 1 Char. 414: 0> 3
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1 Char. 238: 3> 1 Char. 279: 3> 1 Char. 332: 0> 2 Char. 351: 0> 1 Char. 414: 0> 3 Char. 553: 4> 1
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1 Char. 238: 3> 1 Char. 279: 3> 1 Char. 332: 0> 2 Char. 351: 0> 1 Char. 414: 0> 3 Char. 553: 4> 1 Char. 571: 3> 4
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1 Char. 238: 3> 1 Char. 279: 3> 1 Char. 332: 0> 2 Char. 351: 0> 1 Char. 414: 0> 3 Char. 553: 4> 1 Char. 571: 3> 4 Char. 600: 0> 3
Char. 45: $3 \rightarrow 2$ Char. 47: $1 \rightarrow 2$ Char. 95: $3 \rightarrow 0$ Char. 108: $3 \rightarrow 1$ Char. 238: $3 \rightarrow 1$ Char. 279: $3 \rightarrow 1$ Char. 32: $0 \rightarrow 2$ Char. 351: $0 \rightarrow 1$ Char. 414: $0 \rightarrow 3$ Char. 553: $4 \rightarrow 1$ Char. 571: $3 \rightarrow 4$ Char. 600: $0 \rightarrow 3$ Char. 626: $4 \rightarrow 3$
Char. 45: $3 \rightarrow 2$ Char. 47: $1 \rightarrow 2$ Char. 95: $3 \rightarrow 0$ Char. 108: $3 \rightarrow 1$ Char. 238: $3 \rightarrow 1$ Char. 279: $3 \rightarrow 1$ Char. 32: $0 \rightarrow 2$ Char. 351: $0 \rightarrow 1$ Char. 414: $0 \rightarrow 3$ Char. 553: $4 \rightarrow 1$ Char. 571: $3 \rightarrow 4$ Char. 600: $0 \rightarrow 3$ Char. 626: $4 \rightarrow 3$ Char. 723: $0 \rightarrow 1$
Char. 45: $3 \rightarrow 2$ Char. 47: $1 \rightarrow 2$ Char. 95: $3 \rightarrow 0$ Char. 108: $3 \rightarrow 1$ Char. 238: $3 \rightarrow 1$ Char. 279: $3 \rightarrow 1$ Char. 32: $0 \rightarrow 2$ Char. 351: $0 \rightarrow 1$ Char. 414: $0 \rightarrow 3$ Char. 553: $4 \rightarrow 1$ Char. 571: $3 \rightarrow 4$ Char. 600: $0 \rightarrow 3$ Char. 626: $4 \rightarrow 3$ Char. 723: $0 \rightarrow 2$
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $32: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1 Char. 238: 3> 1 Char. 279: 3> 1 Char. 332: 0> 2 Char. 351: 0> 1 Char. 414: 0> 3 Char. 553: 4> 1 Char. 571: 3> 4 Char. 600: 0> 3 Char. 626: 4> 3 Char. 723: 0> 1 Char. 758: 0> 2 Char. 810: 3> 1 Char. 815: 3> 0
Char. 45: 3> 2 Char. 47: 1> 2 Char. 95: 3> 0 Char. 108: 3> 1 Char. 238: 3> 1 Char. 279: 3> 1 Char. 332: 0> 2 Char. 351: 0> 1 Char. 414: 0> 3 Char. 553: 4> 1 Char. 571: 3> 4 Char. 600: 0> 3 Char. 626: 4> 3 Char. 723: 0> 1 Char. 758: 0> 2 Char. 810: 3> 1 Char. 815: 3> 0 Char. 819: 0> 1
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $32: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$ Char. $815: 3> 0$ Char. $819: 0> 1$ Char. $864: 0> 2$
Char. 45: $3 \rightarrow 2$ Char. 47: $1 \rightarrow 2$ Char. 95: $3 \rightarrow 0$ Char. 108: $3 \rightarrow 1$ Char. 238: $3 \rightarrow 1$ Char. 279: $3 \rightarrow 1$ Char. 279: $3 \rightarrow 1$ Char. 332: $0 \rightarrow 2$ Char. 351: $0 \rightarrow 1$ Char. 414: $0 \rightarrow 3$ Char. 553: $4 \rightarrow 1$ Char. 571: $3 \rightarrow 4$ Char. 600: $0 \rightarrow 3$ Char. 626: $4 \rightarrow 3$ Char. 723: $0 \rightarrow 1$ Char. 758: $0 \rightarrow 2$ Char. 810: $3 \rightarrow 1$ Char. 815: $3 \rightarrow 0$ Char. 819: $0 \rightarrow 1$ Char. 864: $0 \rightarrow 2$ Char. 872: $3 \rightarrow 1$
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $32: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$ Char. $819: 3> 1$ Char. $819: 0> 1$ Char. $864: 0> 2$ Char. $872: 3> 1$ Char. $940: 0> 1$
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $32: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$ Char. $815: 3> 0$ Char. $819: 0> 1$ Char. $872: 3> 1$ Char. $872: 3> 1$ Char. $940: 0> 1$ Char. $1033: 0> 1$
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $32: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $52: 4> 3$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$ Char. $815: 3> 0$ Char. $819: 0> 1$ Char. $864: 0> 2$ Char. $872: 3> 1$ Char. $940: 0> 1$ Char. $1033: 0> 1$ Char. $1068: 1> 3$
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $279: 3> 1$ Char. $32: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$ Char. $815: 3> 0$ Char. $819: 0> 1$ Char. $864: 0> 2$ Char. $872: 3> 1$ Char. $1033: 0> 1$ Char. $1068: 1> 3$ Char. $1088: 1> 2$
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $279: 3> 1$ Char. $32: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$ Char. $815: 3> 0$ Char. $819: 0> 1$ Char. $864: 0> 2$ Char. $872: 3> 1$ Char. $1033: 0> 1$ Char. $1068: 1> 3$ Char. $1088: 1> 2$ Char. $1112: 0> 3$
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $32: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$ Char. $815: 3> 0$ Char. $819: 0> 1$ Char. $864: 0> 2$ Char. $1033: 0> 1$ Char. $1068: 1> 3$ Char. $1088: 1> 2$ Char. $1112: 0> 3$ Char. $1193: 0> 3$
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $332: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$ Char. $815: 3> 0$ Char. $819: 0> 1$ Char. $864: 0> 2$ Char. $1033: 0> 1$ Char. $1068: 1> 3$ Char. $1088: 1> 2$ Char. $1112: 0> 3$ Char. $1193: 0> 3$ Char. $1209: 3> 1$
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $32: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$ Char. $815: 3> 0$ Char. $819: 0> 1$ Char. $872: 3> 1$ Char. $1033: 0> 1$ Char. $1033: 0> 1$ Char. $1068: 1> 3$ Char. $1193: 0> 3$ Char. $1193: 0> 3$ Char. $1209: 3> 1$ Char. $1258: 0> 1$
Char. $45: 3> 2$ Char. $47: 1> 2$ Char. $95: 3> 0$ Char. $108: 3> 1$ Char. $238: 3> 1$ Char. $279: 3> 1$ Char. $32: 0> 2$ Char. $351: 0> 1$ Char. $414: 0> 3$ Char. $553: 4> 1$ Char. $571: 3> 4$ Char. $600: 0> 3$ Char. $523: 4> 1$ Char. $626: 4> 3$ Char. $723: 0> 1$ Char. $758: 0> 2$ Char. $810: 3> 1$ Char. $815: 3> 0$ Char. $819: 0> 1$ Char. $872: 3> 1$ Char. $1033: 0> 1$ Char. $1033: 0> 1$ Char. $1088: 1> 2$ Char. $1112: 0> 3$ Char. $1123: 0> 3$ Char. $1123: 0> 3$ Char. $1209: 3> 1$ Char. $1258: 0> 1$ Char. $1508: 0> 1$

Char.	1893:	0	> 3
Char.	1949:	1	>4
Char.	1970:	1	> 0
Char.	2011:	0	> 1
Char	2395	1	>4
Char.	2395.	1	
Char.	2402.	4	
Char.	2496:	3	>1
Char.	2543:	3	>0
Char.	2623:	0	> 1
Char.	2629:	3	 >2
Char.	2774:	3	> 1
Char.	2792:	0	>4
Char.	2872:	3	> 0
Char.	2927:	3	> 1
Char	2933	3	> 1
Char.	2042	0	>1
Char.	2067	2	> 0
Char.	2907.	2	> 0
Char.	3041:	0	>1
Char.	3218:	4	> [
Char.	3250:	0	>3
Char.	3412:	0	 > 3
Char.	3438:	4	> 0
Char.	3457:	3	> 1
Char.	3476:	4	> 2
Char	3501	3	> 0
Char.	3719	0	> 1
Char.	2754	2	> 1
Char.	2027	5	
Char.	383/:	0	> 3
Char.	3889:	0	> 3
Char.	3902:	3	>0
Char.	3935:	3	 >1
Char.	4022:	4	 > 1
Char.	4071:	3	> 1
Char.	4106:	0	>2
Char.	4164:	0	> 2
Char.	4172	0	> 1
Char.	4177	0	> 3
Char.	4212	1	~ 2
Chan.	4212.	1	~ 2
Cliar.	4243.	1	/ _
Char.	4250:	2	>4
Char.	4258:	0	>1
Char.	4275:	1	>3
Char.	4288:	0	> 3
Char.	4297:	0	> 3
Char.	4396:	3	> 1
Char.	4490:	4	> 1
Char	4603.	2	> 0
Char.	4698	0	> 2
Char.	1000	2	> 1
Char.	1010	2 2	/ I _ 1
Char.	4949:	3	> 1
Char.	5081:	4	>0
Char.	5247:	4	> 1
Char.	5248:	4	 > 1
Char.	5301:	4	> 3
Char.	5398:	4	 > 2
Char.	5409:	3	>4
Char.	5479:	0	> 3

Char. 5495: 0> 2
Char. 5576: 4> 1
Char. 5715: 3> 1
Char. 5767: 3> 1
Char. 5808: 1> 3
Char 5812: $0 \rightarrow 2$
Char 5832: $2 \rightarrow 2$
Char $052: 2 \rightarrow 0$
Char $0542: 7 > 1$
Char. $9342: 3> 1$
Char. 9566: $3 - > 1$
Char. 9754: 1> 3
Char. 9812: 1> 4
Char. 9833: 1> 3
Char. 9837: 0> 1
Char. 9841: 0> 2
Char. 9877: 3> 0
Char. 9885: 1> 0
Char. 9892: 0> 3
Char. 9929: 2> 3
Char. 9938: 02> 1
Char $10036: 3 -> 2$
Char 10060: $3 \rightarrow 2$
Char $10000: 3 \rightarrow 1$
Char $10007: 2 > 0$
Char $10106.2 \rightarrow 0$
Char 10100. $2 \rightarrow 0$
Char. 10114: $3 - > 1$
Char. 10115: 2> 0
Char. $10127: 2> 3$
Char. 10671: 0> 1
Char. 10786: 2> 1
Char. 11186: 2> 0
Char. 11246: 1> 3
Char. 11440: 3> 1
Char. 11457: 0> 1
Char. 11498: 0> 1
Char. 11517: 3> 1
Char. 11541: 0> 3
Char. 11546: 1> 3
Char. 11601: 2> 0
Char. 11637: 1> 3
Char. 11851: 0> 1
Char. 11857: 3> 1
Char. 13005: 3> 2
Char. 13132: 1> 3
Char. 13192: 1> 0
Char. 13236: 1> 0
Char. 13326: 1> 3
Char. 13364: 2> 0
Char 13481 \cdot 0> 1
Char. 13489: $2 \rightarrow 0$
Char $13551 \cdot 0 -> 2$
Char $13577 \cdot 3 => 1$
Char $16520 \cdot 1 = > 0$
Char $16550 \cdot 1 - 0$
Chai. 10559. 1 20
1 hor 1661/1.1 ~ .
Char. 16634: $3 \rightarrow 1$
Char. 16634: $3 \rightarrow 1$ Char. 16662: $1 \rightarrow 2$

Char. 16742: 3> 1
Char. 17151: 0> 2
Char. 17160: 0> 2
Char. 17437: 2> 0
Char. 17655: 0> 2
Char. 17680: 4> 3
Char. 17707: 3> 1
Char. 17723: 0> 2
Char. 17765: $3 \rightarrow 1$
Char. 17768: $3 \rightarrow 1$
Char 17861: $1 -> 3$
Char 17866: $3 \rightarrow 1$
Char 17882: $2 \rightarrow 3$
Char 17801: $0 \rightarrow 2$
Char 17001: $2 > 1$
Char. $17901.3 - 71$ Char. $17051.2 > 0$
Char 17951. $2 - > 0$
Char. 1/966: $0> 2$
Char. $1/967: 2> 0$
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Char. 18164: 1> 0
Char. 18231: 2> 0
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Char. 18268: 3> 0
Char. 18269: 2> 0
Char. 18284: 0> 1
Gastrotheca
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<i>Gastrotheca</i> Char. 40: 01> 3 Char. 44: 1> 0
<i>Gastrotheca</i> Char. 40: 01> 3 Char. 44: 1> 0 Char. 144: 0> 2
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Char. 3431: 1> 0
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Char. 3542: 0> 3
Char. 3548: 1> 0
Char. 3551: 1> 0
Char. 3647: 4> 1
Char. 3673: 3> 0
Char. 3754: 3> 0
Char. 3894: 1> 3
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Char. 4164: 0> 1
Char. 4189: 2> 0
Char. 4264: 1> 4
Char. 4998: 4> 0
Char. 5000: $4 \rightarrow 0$
Char. 5078: 4> 3
Char. 5179: $4 \rightarrow 0$
Char. 5180: $4 \rightarrow 0$
Char. $5217: 4 -> 3$
Char. $6072: 1 -> 0$
Char. $6095: 0 -> 4$
Char. $6126: 4 \rightarrow 3$
Char. $6120. 4 \rightarrow 3$
Char. $6127: 4 \rightarrow 9$
Char. $6219: 1 \rightarrow 0$
Char. $6229: 1 \rightarrow 0$
Char $10287 \cdot 1 => 3$
Char $10207: 1 \longrightarrow 3$
Char $10316: 0 \rightarrow 1$
Char $10374: 1 \rightarrow 0$
Char $10607: 1 \rightarrow 2$
Char $11982: 3 -> 4$
Char $12002: 4 \rightarrow 0$
Char $12002. + -> 0$
Char $12076: 0 \rightarrow 1$
Char $12133: 3 \rightarrow 0$
Char $12133: 3 \rightarrow 0$
Char $12231: 1 \rightarrow 0$
Char $12207: 1 \rightarrow 0$
Char. $12361: 3 \rightarrow 0$
Char $12301: 3 \longrightarrow 0$
Char $12475: 0 \rightarrow 2$
Char $12480: 1 \rightarrow 2$
Char $12513: 0 \rightarrow 3$
Char $12548: 1 \rightarrow 0$
Char. 12540 . $1 \rightarrow 0$
Char $12007: 0 \rightarrow 1$
Char 13068: $0 \rightarrow 1$
Char $13108 \cdot 3 = > 1$
Char $13790.5 - 7$
Char $13212.0 - 2$
Char $13247.5 - 7$
Char $13335 \cdot 0 = > 2$
Char 13300. $3 = > 1$
Char $13301 \cdot 1 = > 0$
Char $13441 \cdot 3 = > 1$
Chu. 13771. 3> 1

Char. 13487: 3> 1 Char. 13681: 0> 2 Char. 13706: 0> 2 Char. 13784: 1> 3 Char. 13787: 3> 0 Char. 13906: 3> 1 Char. 14016: 3> 1 Char. 14047: 0> 3 Char. 14152: 3> 1
Char. 14359: 3> 1 Char. 14396: 3> 1 Char. 14493: 3> 2 Char. 14527: 3> 1 Char. 14610: 3> 1 Char. 14611: 1> 0 Char. 14616: 0> 3 Char. 14690: 0> 1 Char. 14723: 3> 1
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Char. 18284: 0> 3 Char. 18291: 3> 2 Char. 18371: 2> 0 <i>G. fissipes</i> species group Char. 241: 4> 1 Char. 243: 0> 3 Char. 355: 0> 1 Char. 372: 1> 0
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Char. 16063: 0> 1 Char. 16120: 3> 1 Char. 16120: 3> 2 Char. 16250: 0> 2 Char. 16362: 3> 1 Char. 16439: 3> 1 G longipes species group Char. 15: 1> 0 Char. 16: 0> 1

Char. 16: 0 --> 1 Char. 276: 1 --> 3 Char. 306: 0 --> 3
Char. 405: 0> 2
Char. 624: 4> 3
Char. 625: 4> 0
Char. 757: 3> 0
Char. 973: $0 - 2$
Char $1039: 3 - > 0$
Char 1208: $0 \rightarrow 0$
Char. 1447: $4 \rightarrow 1$
Char $1512:0 > 2$
Char 1611: $0 > 2$
Char. $1(79, 1) > 0$
Char. $16/8$: 1> 0
Char. $1/2/: 0> 2$
Char. 1819: 4> 0
Char. 1920: 3> 0
Char. 4681: 3> 1
Char. 4985: 4> 0
Char. 5011: 1> 0
Char. 5315: 1> 0
Char. 6100: 3> 0
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Char. 11926: 0> 1
Char. 11970: 0> 1
Char. 12005: 1> 3
Char. 12041: $0 \rightarrow 3$
Char 12077: $1 -> 3$
Char $12127: 1 -> 0$
Char $12127: 1 \rightarrow 0$
Char 12258: $1 \rightarrow 3$
Char 12204: $1 > 0$
Char 12210: $1 > 2$
Char. 12210. 1 > 3
Char. 12323: $1 - 23$
Char. 12353: $2 - > 0$
Char. 12384: $1 - > 3$
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G. marsupiata species group
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Char. 80: 2> 0

Char. 1168: 1> 3
Char. 11923: 4> 3
Char $11927: 4> 3$
Char 11072: $4 \rightarrow 3$
Char 12022: $2 > 1$
Char. 12022: 2> 1
Char. $12175: 3 -> 1$
Char. 12231: 3> 1
Char. 12330: 1> 3
Char. 12390: 3> 0
Char. 12539: 3> 1
Char. 12609: 0> 1
Char $17777: 3> 1$
C mianadisaus ananias anonn
Cl 1052 2 > 0
Char. $1053: 3 - > 0$
Char. 1296: 1> 3
Char. 1308: 2> 0
Char. 1387: 3> 1
Char. 1611: 0> 2
Char. 1725: 2> 0
Char. 1743: 2> 0
Char 1833: $4 - > 3$
Char 1912: $0 \rightarrow 3$
Char 2202: $4 > 2$
Chai. 2293. 4> 3
Char. $2357: 3> 4$
Char. 2425: $3 \rightarrow 1$
Char. 2641: 1> 4
Char. 2678: 0> 2
Char. 2932: 0> 3
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Char. 3481: 3> 4
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Char. $3544: 0> 3$
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Char. $3544: 0 \rightarrow 3$ Char. $3613: 0 \rightarrow 3$ Char. $3736: 3 \rightarrow 1$ Char. $3736: 3 \rightarrow 1$ Char. $3815: 3 \rightarrow 0$ Char. $3959: 3 \rightarrow 1$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4164: 1 \rightarrow 4$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4315: 4 \rightarrow 2$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $5583: 1 \rightarrow 2$ Char. $5583: 1 \rightarrow 0$ Char. $5628: 1 \rightarrow 3$ Char. $6038: 0 \rightarrow 3$ Char. $6103: 13 \rightarrow 4$ Char. $6105: 13 \rightarrow 0$
Char. $3544: 0 \rightarrow 3$ Char. $3613: 0 \rightarrow 3$ Char. $3736: 3 \rightarrow 1$ Char. $3736: 3 \rightarrow 1$ Char. $3815: 3 \rightarrow 0$ Char. $3959: 3 \rightarrow 1$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4164: 1 \rightarrow 4$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 2$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $5583: 1 \rightarrow 2$ Char. $5628: 1 \rightarrow 3$ Char. $5628: 1 \rightarrow 3$ Char. $6038: 0 \rightarrow 3$ Char. $6103: 13 \rightarrow 4$ Char. $6105: 13 \rightarrow 0$ Char. $6181: 3 \rightarrow 4$
Char. $3544: 0 \rightarrow 3$ Char. $3613: 0 \rightarrow 3$ Char. $3736: 3 \rightarrow 1$ Char. $3736: 3 \rightarrow 1$ Char. $3815: 3 \rightarrow 0$ Char. $3959: 3 \rightarrow 1$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4164: 1 \rightarrow 4$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4315: 4 \rightarrow 2$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $5583: 1 \rightarrow 2$ Char. $5628: 1 \rightarrow 3$ Char. $5628: 1 \rightarrow 3$ Char. $6038: 0 \rightarrow 3$ Char. $6103: 13 \rightarrow 4$ Char. $6105: 13 \rightarrow 2$ Char. $6181: 3 \rightarrow 4$ Char. $11919: 0 \rightarrow 4$
Char. $3544: 0 \rightarrow 3$ Char. $3613: 0 \rightarrow 3$ Char. $3736: 3 \rightarrow 1$ Char. $3736: 3 \rightarrow 1$ Char. $3815: 3 \rightarrow 0$ Char. $3959: 3 \rightarrow 1$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4164: 1 \rightarrow 4$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 2$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $5583: 1 \rightarrow 2$ Char. $5628: 1 \rightarrow 3$ Char. $5628: 1 \rightarrow 3$ Char. $6038: 0 \rightarrow 3$ Char. $6103: 13 \rightarrow 4$ Char. $6105: 13 \rightarrow 2$ Char. $6181: 3 \rightarrow 4$ Char. $11919: 0 \rightarrow 4$ Char. $11920: 0 \rightarrow 4$
Char. $3544: 0 \rightarrow 3$ Char. $3613: 0 \rightarrow 3$ Char. $3736: 3 \rightarrow 1$ Char. $3736: 3 \rightarrow 1$ Char. $3815: 3 \rightarrow 0$ Char. $3959: 3 \rightarrow 1$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4164: 1 \rightarrow 4$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 2$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $5583: 1 \rightarrow 0$ Char. $5628: 1 \rightarrow 3$ Char. $6038: 0 \rightarrow 3$ Char. $6103: 13 \rightarrow 4$ Char. $6105: 13 \rightarrow 0$ Char. $11919: 0 \rightarrow 4$ Char. $11920: 0 \rightarrow 4$ Char. $11940: 13 \rightarrow 4$
Char. $3544: 0 \rightarrow 3$ Char. $3613: 0 \rightarrow 3$ Char. $3736: 3 \rightarrow 1$ Char. $3736: 3 \rightarrow 1$ Char. $3815: 3 \rightarrow 0$ Char. $3959: 3 \rightarrow 1$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4164: 1 \rightarrow 4$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 2$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $5583: 1 \rightarrow 0$ Char. $5583: 1 \rightarrow 0$ Char. $5628: 1 \rightarrow 3$ Char. $6038: 0 \rightarrow 3$ Char. $6103: 13 \rightarrow 4$ Char. $6105: 13 \rightarrow 0$ Char. $11919: 0 \rightarrow 4$ Char. $11920: 0 \rightarrow 4$ Char. $11940: 13 \rightarrow 4$ Char. $11940: 13 \rightarrow 4$
Char. $3544: 0 \rightarrow 3$ Char. $3613: 0 \rightarrow 3$ Char. $3736: 3 \rightarrow 1$ Char. $3736: 3 \rightarrow 1$ Char. $3815: 3 \rightarrow 0$ Char. $3959: 3 \rightarrow 1$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4164: 1 \rightarrow 4$ Char. $4241: 4 \rightarrow 1$ Char. $5806: 1 \rightarrow 1$ Char. $5836: 1 \rightarrow 1$ Char. $6038: 0 \rightarrow 3$ Char. $6103: 13 \rightarrow 4$ Char. $6103: 13 \rightarrow 4$ Char. $11919: 0 \rightarrow 4$ Char. $11920: 0 \rightarrow 4$ Char. $11940: 13 \rightarrow 4$ Char. $11952: 3 \rightarrow 4$ Char. $12012: 1 \rightarrow 3$
Char. $3544: 0 \rightarrow 3$ Char. $3613: 0 \rightarrow 3$ Char. $3736: 3 \rightarrow 1$ Char. $3736: 3 \rightarrow 1$ Char. $3815: 3 \rightarrow 0$ Char. $3959: 3 \rightarrow 1$ Char. $3959: 3 \rightarrow 1$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4164: 1 \rightarrow 4$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 1$ Char. $4241: 4 \rightarrow 2$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $4684: 3 \rightarrow 1$ Char. $5583: 1 \rightarrow 0$ Char. $5628: 1 \rightarrow 3$ Char. $6038: 0 \rightarrow 3$ Char. $6103: 13 \rightarrow 4$ Char. $6105: 13 \rightarrow 0$ Char. $6105: 13 \rightarrow 0$ Char. $11919: 0 \rightarrow 4$ Char. $11920: 0 \rightarrow 4$ Char. $11940: 13 \rightarrow 4$ Char. $11940: 13 \rightarrow 4$ Char. $11952: 3 \rightarrow 4$ Char. $12012: 1 \rightarrow 3$ Char. $12246: 2 \rightarrow 1$
Char. $3544: 0 \rightarrow 3$ Char. $3613: 0 \rightarrow 3$ Char. $3736: 3 \rightarrow 1$ Char. $3736: 3 \rightarrow 1$ Char. $3815: 3 \rightarrow 0$ Char. $3959: 3 \rightarrow 1$ Char. $3959: 3 \rightarrow 1$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4061: 1 \rightarrow 0$ Char. $4164: 1 \rightarrow 4$ Char. $4241: 4 \rightarrow 1$ Char. $5806: 1 \rightarrow 1$ Char. $6038: 0 \rightarrow 3$ Char. $6103: 13 \rightarrow 4$ Char. $6103: 13 \rightarrow 4$ Char. $6103: 13 \rightarrow 4$ Char. $11919: 0 \rightarrow 4$ Char. $11920: 0 \rightarrow 4$ Char. $11940: 13 \rightarrow 4$ Char. $11940: 13 \rightarrow 4$ Char. $11940: 13 \rightarrow 4$ Char. $11952: 3 \rightarrow 4$ Char. $11920: 1 \rightarrow 3$ Char. $12246: 3 \rightarrow 1$ Char. $12126: 1 \rightarrow 3$

Char. 13311: 0 --> 2 Char. 13364: 2 --> 0 Char. 14255: 0 --> 2 Char. 14308: 3 --> 1 Char. 14455: 1 --> 3 Char. 14484: 1 --> 0 Char. 14496: 1 --> 3 Char. 17693: 0 --> 3 Char. 17831: 3 --> 2

Hemiphractus

4
Char. 1: 0> 1
Char. 2: 0> 1
Char. 9: 1> 2
Char. 11: 1> 2
Char. 14: 2> 1
Char. 17: 1> 2
Char 19: 1> 2
Char 20: $0 \rightarrow 1$
Char 21: $0 \rightarrow 1$
Char 23: $0 \rightarrow 1$
Char. 23: $0 \rightarrow 1$
Char. 24. 0> 1 Char. 28: $0 > 1$
Char 20: $0 > 1$
Char. 29: $0 \rightarrow 1$
Char. $30: 0> 1$
Char. 36: 01> 2
Char. $4'/: 1> 0$
Char. 49: $2 -> 0$
Char. 121: 3> 1
Char. 126: $2 \rightarrow 0$
Char. 215: 1> 3
Char. 238: 3> 0
Char. 249: 2> 0
Char. 329: 2> 0
Char. 343: 0> 3
Char. 374: 3> 0
Char. 393: 3> 1
Char. 480: 3> 1
Char. 524: 2> 4
Char. 531: 4> 0
Char. 556: 3> 0
Char. 686: 0> 1
Char. 784: $0 \rightarrow 2$
Char. 786: $3 -> 1$
Char $803: 3 -> 4$
Char $851:0 -> 4$
Char 886: $0 \rightarrow 4$
Char $1052: 4 \rightarrow 3$
Char. $1052.4 -> 3$
Char 1115: $2 > 0$
Char 1270: $2 \rightarrow 0$
Char $12/0: 2 - > 0$
Char $1254:4 > 1$
Char. 1354: 4> 1
Char. 1385: 3> 1
Char. 1397: 2> 1
Char. 1520: 3> 0
Char. 1542: 1> 3

Char. 376: 3 --> 1

Char. 609: 2 --> 3

Char. 905: 4 --> 1

Char. 925: 3 --> 4

Char. 1627: 2> 0	Char. 4787: 1> 3	Char. 11670: 0> 1
Char. 1684: 3> 1	Char. 4798: 4> 3	Char. 11720: 0> 1
Char. 1694: 1> 3	Char. 4800: 0> 3	Char. 11726: 0> 2
Char. 1760: 1> 2	Char. 4926: 1> 4	Char. 11799: 2> 0
Char. 1761: 2> 0	Char. 4949: 3> 4	Char. 11801: 3> 0
Char. 1901: 3> 4	Char. 4972: 0> 4	Char. 13168: 0> 2
Char. 1912: 0> 2	Char. 5089: 0> 4	Char. 13169: 0> 1
Char. 1999: 1> 0	Char. 5092: 0> 4	Char. 13181: 2> 0
Char. 2037: 0> 1	Char. 5172: 0> 4	Char. 13214: 3> 1
Char. 2078: 3> 1	Char. 5176: 2> 4	Char. 13256: 0> 1
Char. 2122: 2> 0	Char. 5193: 0> 4	Char. 13277: 0> 2
Char. 2229: 3> 0	Char. 5212: 0> 4	Char. 13345: 0> 2
Char. 2468: 1> 4	Char. 5226: 3> 4	Char. 13400: 3> 2
Char. 2496: 3> 0	Char. 5242: 0> 4	Char. 13406: 0> 1
Char. 2500: 3> 0	Char. 5330: 3> 4	Char. 13435: 0> 2
Char. 2527: 0> 1	Char. 5355: 3> 1	Char. 13468: 0> 1
Char. 2587: 2> 0	Char. 5451: 2> 0	Char. 13483: 1> 0
Char. 2604: 0> 3	Char. 5466: 3> 1	Char. 13517: 1> 2
Char. 2612: 3> 0	Char. 5482: 0> 1	Char. 13616: 1> 3
Char. 2626: 1> 3	Char. 5545: 2> 4	Char. 13747: 3> 1
Char. 2687: 0> 4	Char. 5583: 1> 0	Char. 13911: 0> 3
Char. 2762: 1> 0	Char. 5628: 1> 0	Char. 14062: 0> 1
Char. 2824: 2> 0	Char. 5651: 0> 4	Char. 14074: 1> 3
Char. 2931: 0> 3	Char. 5671: 2> 4	Char. 14097: 0> 1
Char. 2954: 3> 0	Char. 5685: 3> 0	Char. 14248: 2> 0
Char. 2968: 0> 2	Char. 5692: 0> 3	Char. 14293: 2> 3
Char. 3034: 0> 2	Char. 5718: 0> 1	Char. 14354: 2> 0
Char. 3056: 0> 3	Char. 5802: 0> 1	Char. 14358: 0> 3
Char. 3092: 4> 1	Char. 9560: 1> 3	Char. 14411: 2> 3
Char. 3202: 0> 1	Char. 9615: 2> 0	Char. 14511: 3> 1
Char. 3354: 1> 0	Char. 9632: 2> 0	Char. 15143: 3> 0
Char. 3359: 3> 0	Char. 9742: 0> 2	Char. 15342: 2> 0
Char. 3369: 1> 0	Char. 9752: 1> 3	Char. 15350: 1> 3
Char. 3377: 1> 0	Char. 9767: 1> 2	Char. 15538: 3> 1
Char. 3378: 3> 1	Char. 9770: 0> 2	Char. 15617: 1> 3
Char. 3384: 1> 3	Char. 9815: 3> 4	Char. 15633: 02> 3
Char. 3461: 4> 0	Char. 9838: 2> 1	Char. 15636: 1> 2
Char. 3466: 4> 2	Char. 9851: 0> 3	Char. 15679: 3> 2
Char. 3501: 3> 1	Char. 9887: $2 \rightarrow 0$	Char. 15682: 2> 0
Char. 3576: 1> 0	Char. 9927: 1> 3	Char. 15732: 2> 1
Char. 3624: 2> 1	Char. 10075: 0> 2	Char. 15733: 1> 3
Char. 3663: 0> 2	Char. 10128: 3> 0	Char. 15744: 0> 2
Char. 3713: 4> 2	Char. 10155: 3> 2	Char. 16615: 1> 3
Char. 3730: 0> 3	Char. 10695: 3> 1	Char. 16700: 3> 1
Char. 3815: 3> 1	Char. 10810: 1> 3	Char. 16874: 2> 0
Char. 3875: 0> 1	Char. 10858: 3> 2	Char. 16919: 1> 3
Char. 3903: 3> 1	Char. 10999: 1> 3	Char. 17028: 0> 3
Char. 3976: 0> 3	Char. 11005: 0> 2	Char. 17079: 0> 2
Char. 4065: 3> 0	Char. 11062: 1> 3	Char. 17193: 0> 2
Char. $4080: 0 -> 1$	Char. 11066: 0> 1	Char. 17235: 0> 2
Char. 4263: 3> 4	Char. 11210: 1> 3	Char. 17376: 1> 3
Char. 4270: 0> 1	Char. 11370: 1> 3	Char. 17457: 1> 3
Char. 4288: 0> 1	Char. 11424: 3> 0	Char. 17489: 3> 2
Char. 4334: 0> 3	Char. 11505: 1> 2	Char. 17531: 0> 2
Char. 4396: 3> 4	Char. 11559: 1> 3	Char. 17578: 1> 3
Char. 4667: 3> 0	Char. 11594: 3> 1	Char. 17741: 3> 1
Char. 4736: 3> 0	Char. 11640: 0> 2	Char. 17907: 2> 1

Char. 17935: 1> 3
Char. 17997: 3> 1
Char $18152 \cdot 1 -> 3$
Char $18204: 0 -> 2$
Char $18281: 0 \rightarrow 2$
Char $18294: 3 \rightarrow 1$
Char $18312: 0 \rightarrow 2$
Char. 18342: $2 \rightarrow 2$
Char 18377: $0 \rightarrow 2$
Char. 10577. 0> 2
Stefania
Char. 78: 3> 1
Char. 213: 3> 1
Char. 310: 0> 1
Char. 414: 0> 2
Char. 427: 3> 1
Char. 595: 0> 2
Char. 628: 4> 1
Char. 629: 4> 1
Char. 757: 3> 2
Char. 765: 1> 3
Char. 777: 3> 1
Char. 886: 0> 4
Char. 954: 3> 1
Char. 1057: 4> 1
Char. 1161: 0> 2
Char. 1207: 0> 2
Char. 1258: 0> 3
Char. 1320: 1> 3
Char. 1378: 0> 2
Char. 1454: 4> 0
Char. 1494: 4> 0
Char. 1552: 3> 1
Char. 1892: 4> 3
Char. 1929: 0> 3
Char. 4464: 4> 3
Char. 4558: 3> 4
Char. 4570: 4> 0
Char. 4626: 1> 3
Char. 4636: 2> 0
Char. 4703: 1> 3
Char. 4721: 2> 0
Char. 4738: 0> 3

Char. 4858: 1> 3
Char. 5125: 4> 1
Char. 5126: 4> 1
Char. 5129: 4> 1
Char. 5130: 4> 1
Char. 5154: 4> 2
Char. 5156: 4> 2
Char. 5172: 0> 2
Char. 5303: 4> 0
Char. 5426: 2> 0
Char. 5457: 0> 1
Char. 5466: 3> 1
Char. 5678: 0> 2
Char. 5829: 1> 0
Char. 6038: 0> 3
Char. 6061: 3> 0
Char. 6095: 0> 2
Char. 6112: 0> 3
Char. 6129: 4> 1
Char. 6140: 0> 3
Char. 6148: 3> 1
Char. 6160: 3> 0
Char. 6179: 4> 0
Char. 6222: 1> 0
Char. 9675: 3> 1
Char. 9814: 4> 2
Char. 9875: 0> 3
Char. 9892: 0> 2
Char. 10109: 3> 1
Char. 10731: 3> 2
Char. 10758: 3> 0
Char. 10828: 3> 1
Char. 10852: 3> 0
Char. 10988: 0> 2
Char. 11080: 1> 3
Char. 11496: 3> 1
Char. 11532: 3> 1
Char. 11616: 1> 3
Char. 12045: 3> 1
Char. 12049: 3> 0
Char. 12114: 0> 3
Char. 12130: 3> 1
Char. 12139: 1> 2
Char. 12214: 0> 2

Char. 12294: 1 --> 0 Char. 12298: 0 --> 2 Char. 12370: 1 --> 0 Char. 12378: 0 --> 3 Char. 12416: 1 --> 0 Char. 12450: 0 --> 2 Char. 12639: 0 --> 2 Char. 12666: 2 --> 0 Char. 12767: 2 --> 3 Char. 13198: 3 --> 0 Char. 13211: 1 --> 3 Char. 13293: 3 --> 1 Char. 13376: 1 --> 2 Char. 13382: 0 --> 2 Char. 13392: 0 --> 2 Char. 13400: 3 --> 1 Char. 13401: 0 --> 1 Char. 13402: 1 --> 3 Char. 13439: 3 --> 0 Char. 13441: 3 --> 1 Char. 13453: 3 --> 1 Char. 13681: 0 --> 2 Char. 13808: 2 --> 0 Char. 13856: 1 --> 3 Char. 13893: 3 --> 0 Char. 14147: 2 --> 0 Char. 14152: 3 --> 1 Char. 14176: 1 --> 3 Char. 14411: 2 --> 3 Char. 14473: 3 --> 2 Char. 14563: 1 --> 3 Char. 14650: 3 --> 0 Char. 14820: 2 --> 0 Char. 15011: 1 --> 3 Char. 15065: 1 --> 3 Char. 16576: 3 --> 0 Char. 16865: 2 --> 0 Char. 17355: 3 --> 0 Char. 17516: 3 --> 2 Char. 17581: 0 --> 2 Char. 17844: 0 --> 1