

Appendix from J. J. Wiens et al., “Evolutionary and Ecological Causes of the Latitudinal Diversity Gradient in Hylid Frogs: Treefrog Trees Unearth the Roots of High Tropical Diversity” (Am. Nat., vol. 168, no. 5, p. 579)

Expanded Material and Methods

Phylogenetic Analysis

We analyzed hylid relationships by combining four data sets. The first was that of Faivovich et al. (2005), which contains eight genes (mitochondrial 12S [ribosomal small subunit; 1,088 base pairs {bp}], 16S [ribosomal large subunit; 1,646 bp], and cytochrome *b* [385 bp] and nuclear RAG-1 [recombinase activating protein 1; 428 bp], rhodopsin [316 bp], seventh-in-absentia [397 bp], tyrosinase [530 bp], and 28S [887 bp]) for up to 276 taxa (228 hylids, 48 outgroups). The second data set was that of Wiens et al. (2005), with four genes (mitochondrial 12S [1,088 bp] and ND1 [NADH dehydrogenase subunit 1; 1,218 bp] and nuclear *c-myc* [proto-oncogene cellular myelocytomatosis; 832 bp] and POMC [proopiomelanocortin A; 550 bp]) and 144 morphological characters, for some or all of 198 taxa (169 hylids, 29 outgroups). The third set was that of Smith et al. (2005), which includes the same four genes used by Wiens et al. (2005) but with additional sequences and taxa. The fourth set consisted of several additional taxa based on new sequence data generated from the 12S gene (GenBank numbers 380346–380389), using standard methods and primers described by Smith et al. (2005) and Wiens et al. (2005). Data were also used from Darst and Cannatella (2004), Moriarty and Cannatella (2004), and Faivovich et al. (2004). These data were generally already incorporated by Faivovich et al. (2005) and Wiens et al. (2005). GenBank numbers (for both new and previously published data) are provided in table A2.

No alignments were available for the data sets from Faivovich et al. (2005). New alignments were performed for each data set with CLUSTAL X.1.81 (Thompson et al. 1994), using methods described by Wiens et al. (2005). For ribosomal genes (12S, 16S, and 28S), regions of the alignment that differed under different gap-opening penalties (12.5, 15, and 17.5) were considered to be ambiguously aligned and were excluded. Apart from gap opening, default parameters were used (gap opening = 15; gap extension = 6.666; delay divergent sequences = 30%; transition : transversion = 50%), with some adjustments made manually.

All four data sets were then combined into a single matrix. The completeness of taxa in the combined data matrix varied considerably. Simulations (Wiens 2003; Phillipe et al. 2004) and analyses of empirical data sets (Driskell et al. 2004; Phillipe et al. 2004; Wiens et al. 2005) suggest that highly incomplete taxa can be accurately placed in phylogenetic analyses, especially when the overall number of characters is large (e.g., thousands of characters, as in this study). Furthermore, simulations (Wiens 1998b) suggest that the inclusion of characters scored for only some of the taxa can improve phylogenetic accuracy (relative to excluding these characters), as do some analyses of empirical data (Wiens et al. 2005). However, these simulations also suggest that extensive missing data can reduce the ability of added characters to improve phylogenetic accuracy.

With these considerations in mind, we combined data sets so as to maximize the number of included hylid taxa and characters but to otherwise minimize the amount of missing data. When multiple genes from different studies were available for different individuals of the same species, we combined the data so that each taxon was represented by a single individual (rather than multiple individuals with extensive missing data). For the nonhylid outgroup taxa, we used only the taxa included by Wiens et al. (2005), but in several cases we combined these data with data from congeneric species (e.g., *Atelopus*, *Bufo*, *Ceratophrys*, *Cochranella*, *Colostethus*, *Eleutherodactylus*, *Flectonotus*, *Hemiphractus*, *Hyalinobatrachium*, *Leptodactylus*, *Melanophryniscus*, *Rana*, *Telmatobius*) or other related species for distant outgroup taxa (the microhylid microhylids *Kaloula* and *Gastrophryne*; the myobatrachine myobatrachids *Pseudophryne* and *Uperoleia*; the limnodynastine myobatrachids *Limnodynastes* and *Notaden*).

We generally would perform separate analyses of individual genes to look for clades that are strongly supported and incongruent (Wiens 1998a). However, given the large number of presumably unlinked loci included in this study (up to seven nuclear genes per taxon), we assume that the overall combined data will reflect species history and that discordant gene histories from individual genes will be overwhelmed.

In general, we favor model-based methods over parsimony. Unfortunately, Bayesian analyses of the entire combined data set (325 taxa, 8,420 characters) proved to be extremely slow (preliminary analyses suggested that a simple search would take >1 year to complete). Therefore, we first conducted parsimony analyses of the entire data set and then analyzed a subset of the data using Bayesian analysis. In general, we used the parsimony analysis to assign all species to major clades and then used the Bayesian analysis to confirm the relationships among these clades and to estimate branch lengths for comparative analyses. The smaller number of taxa also facilitated analyses of divergence dates (see below).

For the analysis of 325 taxa, the most parsimonious trees were sought using the parsimony ratchet (Nixon 1999). Ten parsimony ratchet searches were conducted, using the PAUPRat program of Sikes and Lewis (2001). The resulting trees from all searches were then filtered to include only the shortest trees, and the parsimony phylogeny was based on the strict consensus of these pooled shortest trees. Support for individual branches was evaluated using nonparametric bootstrapping (Felsenstein 1985a), with 200 bootstrap pseudoreplicates and 10 random-taxon-addition sequence replicates per bootstrap pseudoreplicate. Bootstrap values $\geq 70\%$ were considered strongly supported, following Hillis and Bull (1993; but see their extensive caveats). All parsimony searches utilized PAUP* 4.0b10 (Swofford 2002).

The Bayesian analysis included 140 taxa. These taxa were sampled such that (1) all major clades of hylids were included (e.g., higher taxa recognized by Faivovich et al. [2005]); (2) taxa were sampled within each major clade to ensure that the oldest lineages within each clade were included (to better estimate the age of the most recent common ancestor [MRCA] of the clade), as inferred based on the parsimony analyses; and (3) species were included that had been sampled for as many data sets as possible. To further streamline the analyses, data from the nuclear 28S gene and from morphology were excluded. The nuclear 28S gene contains very few informative characters and suggests several relationships that are highly inconsistent with the other data sets. Morphological data were available for a relatively small subset of taxa. Bayesian analyses of 12S, ND1, *c-myc*, and POMC by Wiens et al. (2005) supported use of separate partitions within each of the four genes and identified the best-fitting substitution model for each gene. The best-fitting model for each of the genes analyzed by Faivovich et al. (2005) was identified using hierarchical likelihood ratio tests implemented in MrModeltest, version 2.0 (Nylander 2004). Bayesian analyses of the new genes from Faivovich et al. (2005) were also conducted to determine whether partitions within these genes were supported (as described in Wiens et al. 2005; see also Brandley et al. 2005). The first, second, and third codon positions were treated as separate partitions for each protein-coding gene. Hypothesized stems and loops were treated as separate partitions for the 16S gene, and stems and loops were identified based on comparison to the model for *Rana catesbiana* from the European ribosomal RNA database as a starting point (<http://oberon.fvms.ugent.be:8080/rRNA/>). Previous work on the mitochondrial 12S gene suggests that placements of stems and loops are highly conserved across anurans (Wiens et al. 2005). The harmonic mean of the log likelihoods of the post-burn-in trees for the Bayesian analyses with and without partitions within each gene were compared using the Bayes factor (following Nylander et al. 2004). These comparisons showed that partitioning within each gene significantly improved the likelihood of each data set (J. J. Wiens, results not shown).

Bayesian analyses were performed using MrBayes, version 3.0b4 (Huelsenbeck and Ronquist 2001). Two replicate searches were performed on the combined, partitioned data set. Each analysis used four chains and default priors (Dirichlet for substitution rates and state frequencies, uniform for the gamma shape parameter and proportion of invariable sites, all topologies equally likely a priori, and branch lengths unconstrained : exponential). Analyses used 5.0×10^6 generations each, sampling every 1,000 generations. Plots of log likelihoods over time were examined for stationarity, and trees generated before achieving stationarity were discarded as burn-in. We also compared the harmonic mean of the log likelihoods and the topologies and clade posterior probabilities (Pp) for each analysis as an additional test for stationarity. The replicate analyses converged on identical topologies and similar mean log likelihoods and clade Pp. The phylogeny and branch lengths were estimated from the majority-rule consensus of the pooled post-burn-in trees from the two analyses. We considered clades with $Pp \geq 0.95$ to be strongly supported (following Wilcox et al. 2002; Alfaro et al. 2003; Erixon et al. 2003; Huelsenbeck and Rannala 2004).

Reconstructing Biogeographic Changes

Major dispersal events between biogeographic regions were estimated using parsimony and likelihood methods on the trees for 325 and 140 taxa, respectively. We first estimated biogeographic changes using parsimony reconstruction on the parsimony trees for 325 taxa, following the general approach of Ronquist (1994). The range of Hylidae and outgroups was divided into nine major biogeographic regions. These were recognized as separate character states, and additional "polymorphic" character states were recognized for taxa that spanned more than one region (e.g., a species that occurs in both South and Middle America). The regions were as follows: tropical northern South America (NSA), north of 30°S and including Trinidad and Tobago; temperate southern South America (SSA), south of 30°S; Middle America (MA), from Mexico to Panama; North America (NA), including the United States and Canada; the West Indies (WI); Australasia (AU), including Australia, New Guinea, and New Zealand; Europe (EU), including North Africa and the Middle East; Asia (AS); and sub-Saharan Africa (AF).

A step matrix was used to provide partial ordering of states based on shared polymorphism. Thus, polymorphic species were coded with a character state for each combination of regions, and transitions between polymorphic states were counted as half a step (e.g., NSA + MA to NSA is 0.5 step, NSA + MA to NA is 1.5 steps). We also used step matrices to partially order states to reflect obvious relative differences in geographic proximity of areas (see Stephens and Wiens 2003). We made the following assumptions: NSA to NA ordered to prefer passing through MA; MA to EU and AS passes through NA; all regions pass to AU through SSA; one step between WI and NA, MA, and NSA; changes between WI and other regions must pass through NA (EU and AS) or NSA; one step between NA and EU, NA and AS, and AS and EU; and one step between AF and all other regions (only one distant outgroup taxon). Parsimony reconstructions were performed using MacClade, version 4.0 (Maddison and Maddison 2000).

Biogeographic changes were also mapped onto the Bayesian tree for 140 taxa using maximum likelihood (Schluter et al. 1997; Pagel 1999b), implemented with Mesquite, version 1.5 (Maddison and Maddison 2004). Character states were the same as those utilized in the parsimony analyses, but complex ordering was difficult using maximum likelihood and was not utilized (we assumed equal probability for all changes between states); this had little impact on the results. Polymorphisms were treated as a separate character state. Three sets of branch lengths were used: those estimated from the Bayesian analysis of the combined molecular data and the ultrametric branch lengths based on the penalized likelihood analyses, using root ages of 100 and 160 million years (see below). To examine and summarize the results across the tree, the best estimate of the character state at each node was determined using the likelihood ratio test. If the log likelihoods of two states differed by 2.0 or more, then the state with the lower likelihood was rejected, and the alternate state was considered to be the best estimate for that branch (following Pagel 1999b). If the difference in log likelihoods was smaller (i.e., <2.0), the reconstruction for that branch was considered ambiguous.

Ancestral area analysis (as described above) tends to assume that ancestral species were present in only one region, whereas dispersal-vicariance analysis (Ronquist 1997) and the method of Ree et al. (2005) allow ancestral species to be more widely distributed. To address the robustness of our results (and given that the method of Ree et al. [2005] currently is impractical for large numbers of taxa), we performed dispersal-vicariance analysis using DIVA, version 1.1 (Ronquist 1996). We initially found that the data sets of both 325 and 140 taxa were too large to be analyzed using DIVA 1.1. We therefore pruned the 140-taxon tree to 86 taxa by identifying those clades in which all species had identical geographic distributions (in terms of the nine regions defined above) and reducing them to a single representative species. The reduced tree proved to be manageable for DIVA but still includes all the same potential biogeographic changes from the larger tree. Results of the DIVA analyses were very similar to those based on ancestral area analysis in that tropical South America was unambiguously inferred as the ancestral area for Hylidae in general and for most major clades within it, including Phyllomedusinae, Hylinae, Cophomantini, *Dendropsophus* clade, *Scinax* clade, and *Phrynohyas* clade (Lophiohylini).

We acknowledge that all three approaches are not without problems (e.g., Ree et al. 2005). For example, reconstruction of ancestral areas could potentially be affected by differences in rates of speciation or extinction in different regions (although we found little evidence for such differences in this study).

Estimating Ages of Clades

Estimates of the absolute ages of clades were used to determine the relationship between regional species richness and the time when a given region was colonized, absolute diversification rates of clades, and the age of major hyliid lineages relative to the Cenozoic expansion of the temperate regions. We used penalized likelihood (Sanderson 2002) as implemented in r8s (version 1.6 for Unix; Sanderson 2003) to estimate these ages, using a combination of molecular branch length information and estimates of absolute clade age based on fossils and other geological criteria. Molecular branch lengths were obtained from the Bayesian analysis of 140 taxa and 7,390 characters. Although some taxa were missing data for one or more genes, all taxa shared the 12S gene, and most had data for multiple nuclear genes. We used the following dates from the fossil record to constrain the minimum estimated ages of select nodes that were reconstructed in the phylogenetic analyses.

MRCA of Ranoidea: at least 36 million years old (myo). Carroll (1988) and Holman (1998) mention ranid fossils in the middle Eocene (~36–45 million years ago [mya]).

MRCA of Bufonidae: at least 55 myo. Duellman and Trueb (1986) mention *Bufo* in the Paleocene (55–65 mya).

Caudiverbera-Myobatrachidae clade: at least 45 myo. Carroll (1988) mentions fossils of *Caudiverbera* in the lower Eocene (minimum 45 mya).

MRCA of Hyliidae and sister group: at least 55 myo. According to Duellman and Trueb (1986), fossils of hylids date back to the Paleocene (55–65 mya). Because it is uncertain whether these fossils can be assigned to a clade within extant hylids, we used these fossils to date the age of the common ancestor of Hyliidae and its putative sister group (the clade including the hemiphractids and some leptodactylids).

MRCA of Pelodyadinae-Phyllomedusinae clade: at least 28 myo. Sanmartin and Ronquist (2004) summarize evidence suggesting that the last terrestrial connection between Australia and South America split 28 mya or earlier. Thus, the split between the Australasian pelodyadines and South American phyllomedusines must be at least 28 myo.

MRCA of *Acris*-*Pseudacris* clade: at least 15 myo. Holman (2003) suggested that the extinct fossil taxon *Acris barbouri* is likely to be the sister group to extant *Acris* species and is at least 15–19 myo (Miocene Hemingfordian North American land-mammal age [NALMA]). Thus, the split between *Acris* and *Pseudacris* is at least 15 myo. Various *Pseudacris* fossils are known from the middle Miocene Barstovian of North America (~12–15 mya; Holman 2003), but given that these fossils cannot be assigned confidently to clades within *Pseudacris*, we did not use this information (and given that the *Acris* fossils already show that the MRCA of the *Acris*-*Pseudacris* clade is at least 15 myo).

MRCA of Asian and European *Hyla*: at least 16 myo. Sanchiz (1998b) noted fossil *Hyla* similar to extant *Hyla arborea* and *Hyla meridionalis* in the lower Miocene of Austria (~16 mya). We assume that these *Hyla* are closely related to the *Hyla* extant in Europe. However, we cannot assume that these fossils are younger than the MRCA of the extant European species. We assume instead that the MRCA of the clade of European and Asian *Hyla* is at least 16 myo, based on these European fossils.

MRCA of *Hyla squirella*-*Hyla cinerea* clade: at least 15 myo. *Hyla goini* is a fossil species from Miocene Hemingfordian NALMA (15–19 mya) thought to be closely related to, if not actually conspecific with, extant *H. squirella* (Holman 2003). Thus, we assume that the split between *H. squirella* and its sister species (*H. cinerea*) is at least 15 myo.

MRCA of *Hyla gratiosa*-*Hyla versicolor* clade: at least 16 myo. *Hyla miocenica* is thought to be closely related to *Hyla chrysocelis* and *H. versicolor* and occurs in the early Miocene Barstovian (14–16 mya; Holman 2003). *Hyla miofloridana* (Miocene, Hemingfordian NALMA; 15–19 mya) is similar to *H. gratiosa* (Holman 2003). Among the species included in the r8s analysis, *Hyla avivoca*, *H. gratiosa*, and *H. versicolor* form a clade. Thus, we are confident that the MRCA of this clade is at least 15 myo. We differ from Smith et al. (2005) in that we exclude *Hyla swanstoni* (which suggests that North American *Hyla* are at least 33 myo) given that Sanchiz (1998a) questioned the assignment of this taxon to *Hyla* (Faivovich et al. 2005).

In order to estimate dates for the entire tree, r8s requires that a date be specified for at least one node of the tree (i.e., not just a minimum age constraint). We used two possible ages for the root of the tree. We considered the root of the tree to be equivalent to the MRCA of Neobatrachia, and we used two dates to bracket the age of Neobatrachia, 160 and 100 mya. The sister group of the Neobatrachia probably includes Pipoidea and/or Pelobatoidea, based on morphological (Ford and Cannatella 1993) and molecular evidence (Hoegg et al. 2004). Both groups appear in the fossil record in the Late Jurassic (minimum ~160 mya; Zug et al. 2001).

Neobatrachian fossils are absent in the fossil record before the Late Cretaceous (65–99 mya). Nevertheless, ranoids are widespread in Africa and Asia, strongly suggesting that neobatrachians originated well before the separation of Africa and South America, ~100 mya (Duellman and Trueb 1986).

The r8s program was implemented using the TN algorithm (truncated Newton method with bound constraints). Smoothing parameters were chosen by cross-validated assessment, using values from 10^0 to $10^{5.5}$ in exponential increments of 0.5. Analyses using 100 mya as the root age estimated 10.00 as the optimal smoothing value, whereas analyses using 160 mya selected 31.62. These smoothing values were used for these root ages to infer the ages of clades.

In order to assess confidence in the estimated ages of clades, we re-estimated these ages using a sample of 300 trees from the Bayesian phylogenetic analysis, sampling one tree every 20,000 generations from among the 6 million post-burn-in trees pooled from the two replicate searches. We then repeated the penalized likelihood analysis on each tree using the two root ages (using the best-fitting smoothing parameter for each root age from the original analysis but not retesting for each replicate) and summarized the range and standard deviation for the estimated age of each clade using the "profile" command in r8s. These values are provided in table A1. Finally, we note that for most of the analyses that use these estimates of absolute clade age (e.g., the estimates of time of colonization and diversification rate), it is the relative ages of the clades that are actually important, not the specific ages of individual clades.

Regional Species Richness versus Time of Colonization

The tropical conservatism hypothesis implicitly assumes a general relationship between how long a group has been in a region and how many extant species are present there. We performed linear regression (with Statview, ver. 4.1 for Macintosh; Abacus, Berkeley, CA) of the estimated minimum age of the first colonization of hylids in a region (independent variable, in millions of years) versus the natural log of the number of hylid species in that region (dependent variable), generally following Stephens and Wiens (2003). Models of diversification predict an exponential relationship between species richness and time (Magallón and Sanderson 2001), and we therefore used natural log-transformed values for species richness for each region. The age of the oldest split between two endemic lineages within a region represents a conservative estimate of the minimum age of hylids in that region, and this split was dated based on the penalized likelihood analysis (see above). For Middle America, we assume that the earliest split in the region is between the Middle American taxa and the North American *Acris-Pseudacris* clade (Faivovich et al. 2005; Smith et al. 2005; Wiens et al. 2005), rather than using the first split between endemic Middle American species. Regression analyses were performed using both potential root ages for Neobatrachia. We used the following seven regions: South America, Middle America, North America, West Indies, Australia, Europe, and Asia. We did not treat temperate South America as a separate unit because it has too few endemic species to estimate the age of the first split in the region ($n = 2$, and they are not closely related).

We took advantage of three recent Web-based summaries to estimate the number of species in each region. We first used the Global Amphibian Assessment Web site (<http://www.globalamphibians.org/>) to obtain initial summaries of number of species in each region (obtained December 13, 2004). We then updated species lists for each region using Amphibian Species of the World, version 3.0 (checked September 5, 2005) and the AmphibiaWeb database (<http://amphibiaweb.org/>; checked September 14, 2005), which are updated intermittently as new species are described.

Estimates of hylid species richness were generally very similar between these three references. Discrepancies generally involved recently described species that were not yet included in one or more lists. Other disagreements were generally resolved in favor of the Amphibian Species of the World list, which generally provides commentary and bibliographic information to support controversial taxonomic decisions. Recent phylogenetic studies show that hemiphractine hylids are not closely related to other hylid species (Darst and Cannatella 2004; Faivovich et al. 2005; Wiens et al. 2005). Hemiphractids therefore were subtracted from the number of hylids in each area. Estimates of species richness and dates of first colonization for each region are provided in table 1.

In theory, the relationship between the species richness of a region and the timing of the first colonization may be obfuscated by multiple invasions into the region, given that only the oldest colonization event is considered. A previous study suggests that this need not be problematic, perhaps because the number of species descended from each colonization event in each region is also strongly related to the relative timing of these colonization

events (Stephens and Wiens 2003). The results of our current study show a strong relationship between the timing of the initial colonization of each region and the present diversity of the region, which also suggests that this issue is not problematic here. Our biogeographic results suggest that most regions have been colonized only once (e.g., Europe, Australia) or twice (e.g., Asia, North America, West Indies) and/or the hylid fauna of each region is dominated (in terms of species numbers) by the descendants of the earliest colonization event (e.g., Middle America, South America, West Indies).

Latitudinal Variation in Rates of Diversification

The tropical conservatism hypothesis implicitly assumes that there is no relationship between the rate of diversification of a clade and its geographic location (e.g., temperate, tropical) or at least that differences in diversification rate between regions are not the major cause of the latitudinal gradient. We divided Hylidae into 11 clades and then performed linear regression of the diversification rate of each clade (dependent variable) and the latitudinal midpoint of the geographic range of that clade (independent variable). Given that there are many ways that a large phylogeny can be divided into clades, we generally used the largest clades that were strongly supported ($P_p \geq 0.95$ from Bayesian analysis) but treating the two independent clades of temperate North American hylids (*Acris-Pseudacris* and Holarctic *Hyla*) as separate units and treating the Australian pelodyadines and South American phyllomedusines separately. In summary, these 11 clades are subfamily Pelodyadinae; subfamily Phyllomedusinae; tribe Cophomantini (*Bokermannohyla*, *Aplastodiscus*, *Hyloscirtus*, *Hypsiboas*, and *Myersiohyla*); *Dendropsophus* clade (*Dendropsophus*, *Xenohyla*, *Scarthyla*, *Lysapsus*, and *Pseudis*); *Scinax* clade (*Scinax* and *Sphaenorhynchus*); tribe Lophiohylini (or *Phrynohyas* clade [Wiens et al. 2005], including *Aparasphenodon*, *Argenteohyla*, *Corythomantis*, *Itapotihyla*, *Nyctimantis*, *Osteopilus*, *Osteocephalus*, *Phrynohyas*, *Phyllodytes*, *Tepuihyla*, and *Trachycephalus*); *Acris-Pseudacris* clade (*Acris* and *Pseudacris*); *Plectrohyla* clade (*Exerodonta* and *Plectrohyla*); *Ptychohyla* clade (*Bromelohyla*, *Charadrahyla*, *Duellmanohyla*, *Ecnomihyla*, *Megastomahyla*, and *Ptychohyla*); *Smilisca* clade (including *Anotheca*, *Isthmohyla*, *Smilisca*, *Tlalocohyla*, and *Tripurion*); and Holarctic *Hyla* (including the genus *Hyla* sensu stricto).

We initially estimated the absolute diversification rate of each clade using the maximum likelihood estimator and utilizing the crown group age (where the crown group is the least inclusive monophyletic group that includes all the extant members of a clade):

$$\hat{r} = \frac{\log(n) - \log(2)}{t}, \quad (\text{A1})$$

where n is the number of species in the clade and t is the estimated age of the crown group (from Magallón and Sanderson 2001). This estimator assumes that extinction rates are negligible, which may be problematic. However, extinction rates would be very difficult to estimate for hylid frogs, and our primary use of this estimator is simply to make comparisons among extant clades. This metric is very similar to those used extensively by Coyne and Orr (2004) and Cardillo et al. (2005). Nevertheless, to address the robustness of our results using this model, we also performed a set of analyses using the method-of-moments estimators for stem and crown groups (eqq. [6] and [7] of Magallón and Sanderson 2001), which allow one to include a nonzero extinction rate (ϵ). Given that the extinction rate is unknown, we used an arbitrarily high rate ($\epsilon = 0.90$, following arguments in Magallón and Sanderson 2001). Nonphylogenetic analyses assuming high extinction rates and using stem group estimates gave results similar to those of analyses using equation (A1), and only the latter results are analyzed phylogenetically and presented.

Our phylogenetic analyses did not include all species of hylids. Nevertheless, recent phylogenetic revisions of hylids (Faivovich et al. 2005; Wiens et al. 2005) have assigned >95% of all described hylid species to these 11 clades, given minimal assumptions about the fit between taxonomy and phylogeny (e.g., given that the species of phyllomedusines included in our phylogenetic analyses form a monophyletic group, we assume that hylid species assigned to Phyllomedusinae by previous taxonomists belong to this clade as well). In general, the phylogenetic analyses in this study corroborate the assignment of many additional species to these clades. The age of each clade (t) was estimated from the penalized likelihood analysis, where the crown group age corresponds to the divergence date for the first split within the clade.

We estimated the latitudinal midpoint of each clade as the midpoint of the southernmost range extent of the southernmost species and the northernmost range extent of the northernmost species within that clade. We either

used georeferenced museum localities or estimated the latitude and longitude of range edges using maps from the Global Amphibian Assessment (IUCN et al. 2004) and ArcView GIS 3.3 (Environmental Systems Research Institute, Redlands, CA). Alternatively, we could have calculated the average of the latitudinal midpoints of each of the species within each clade, but there are >800 species, and georeferenced locality data are lacking for most. All analyses were based on the absolute value of each latitudinal midpoint (i.e., we did not distinguish between Northern and Southern Hemispheres).

We performed linear regression analyses using raw data on diversification rate and latitudinal midpoint for these 11 clades. We also performed an analysis using independent contrasts (Felsenstein 1985b) of diversification rate and latitudinal midpoint to account for the shared histories of these clades. Independent contrasts were calculated using COMPARE, version 4.6 (Martins 2004), and regressions were forced through the origin following Garland et al. (1992). Equal branch lengths (all branches set to 1), branch lengths based on the combined and partitioned molecular data, and branch lengths based on the penalized likelihood analysis were used. All regression analyses were performed using Statview. Summaries of estimated clade ages, species numbers, diversification rates, and latitudinal midpoints are provided in table 2.

We note that two of the clades that were well supported in the Bayesian analyses (*Dendropsophus* clade and *Scinax* clade) were not supported as monophyletic in the parsimony analyses. Specifically, the genus *Sphaenorhynchus* is placed (with very weak support) in the *Dendropsophus* clade in the parsimony analysis rather than in the *Scinax* clade. Overall, we favor the results of the Bayesian analysis regarding the position of these genera, given the better fit of the model to the data (i.e., the simple substitution model implicitly assumed in the parsimony analyses is strongly rejected) and the relatively strong support for their placement in the Bayesian analyses but weak support in the parsimony analyses. Nevertheless, in order to address the robustness of our results to this potential uncertainty, we also performed a regression analysis of diversification rates versus latitudinal position (nonphylogenetic) in which the four clades involved were treated as separate units (*Dendropsophus* + *Xenohyla*, *Scarthyla* + *Lysapsus* + *Pseudis*, *Scinax*, and *Sphaenorhynchus*). Results were similar to those of analyses using the *Dendropsophus* clade and *Scinax* clade as units and are not reported.

Several additional concerns may be raised regarding these analyses. First, it is possible (in theory) that we failed to sample the basal species within a given clade and that this failure might bias our estimates of diversification rates (e.g., if the basal clade is missed, the clade may actually be older than our estimates, and the diversification rate may be overestimated). However, it is important to note that almost every one of the clades that we use consists of two or more genera, that the monophyly of each genus has been addressed with phylogenetic analyses (figs. A1–A4), and that we included all of the relevant subclades (genera) within each clade. Thus, it seems unlikely that our failure to sample every species in every clade has led to our failing to sample the basal split within the clades that were used. Note also that the one clade that we used that contains only one genus (*Hyla*) was sampled very densely, and nearly two-thirds of the species (20 of 32) and all major geographic regions inhabited by *Hyla* were sampled. Furthermore, small errors in estimates of species numbers seem very unlikely to strongly influence estimated diversification rates for clades that are relatively old and species rich (as many hyliid clades are). Furthermore, we also performed analyses of diversification rates using stem group estimators and clade ages, which do not require that the basal species be sampled. These analyses gave results very similar to those of analyses using crown group ages and estimators.

Second, the ranges of clades can shift over time. However, we focus here on whether clades are primarily temperate or tropical, and there is little evidence to suggest that such transitions occur rapidly or frequently for entire hyliid clades.

Finally, some might argue that the failure to find a significant relationship merely indicates the low statistical power of the approach. However, we recently applied the same approach to caudate amphibians (using similar numbers of clades) and found r^2 as high as 0.800 (J. J. Wiens, unpublished data). Previous authors have also found significant relationships between latitude and diversification rates using similar methods (e.g., Cardillo et al. 2005).

Ecological Niche Modeling

We performed ecological niche modeling to test the prediction that cold winter temperatures limit dispersal of tropical lineages into temperate regions. We first used biogeographic analyses to identify clades that occur adjacent to temperate regions and to address qualitatively whether clades have converged on similar poleward range limits. Based on the availability of adequate locality data, our analyses focused primarily on the northern

range limits of six representative species from four primarily tropical clades in eastern Mexico. These species are *Scinax staufferi* (*Scinax* clade), *Agalychnis callidryas* and *Agalychnis moreletii* (Phyllomedusinae), *Dendropsophus ebraccatus* and *Dendropsophus microcephalus* (*Dendropsophus* clade), and *Phrynohyas venulosa* (Lophiohylini). We obtained both presence and absence localities for a given species and then determined how well different climatic variables (either alone or in combination) were able to predict the presence or absence of the species at its northern range limits.

Raw data for modeling consisted of georeferenced localities based on specimens in U.S. and Mexican museum collections (from the Comisión Nacional para el Conocimiento y Uso de la Biodiversidad database, provided by C. Alvarez). Localities less than ~1.5 km from each other were deleted to avoid redundancy. Duellman (2001) reviewed locality information for all hylid species in Middle America. To be conservative, we used only localities identical to or nearby those plotted by Duellman (2001). For a given species, presence localities consisted of all of the localities for that species in Mexico (we did not include localities farther south because we were interested in exploring the causes of the northernmost range limits of these species). The absence localities for a given species consisted of localities for *Smilisca baudinii* that are north of the range of that species. *Smilisca baudinii* is a nearly ubiquitous species in low and intermediate elevations in Mexico (Duellman 2001). It occurs syntopically with the other hylid species of interest at many localities and also extends a short distance into North America (south Texas). We used localities for *Smilisca* (rather than randomly selected localities) because they reflect localities where hylids have been collected but where the particular species of interest nevertheless appear to be absent. Because all six species occur primarily in the lowlands, only similar low-elevation localities along the Gulf Coast were included. Furthermore, only localities up to ~350 km north of the northern range extent of a given species were included. Limiting the extent of the northern localities should help to identify the causes of the range limits of a specific species. Although the choice of 350 km was arbitrary, this value is large enough to span a large number of localities (and to avoid potential local climatic idiosyncrasies at smaller spatial scales) but small enough to avoid spanning the two regions where most northern range limits for these six taxa coincide on the Gulf Coast (in central Veracruz and central Tamaulipas; see below).

For climatic data, we used the WORLDCLIM data (Hijmans et al. 2004, 2005), which consist of 19 Geographic Information System (GIS) “layers” based on monthly temperature and rainfall data, at 2.5-s resolution (table 3). Many of these variables are very similar to each other. In order to identify potentially redundant variables to be excluded, we performed two-tailed Spearman rank correlation analyses between all pairwise combinations of the 19 variables (SPSS 14.1 for Windows; SPSS, Chicago). The raw data were the values for all 19 variables at 444 Mexican localities for all six focal species (a locality in which multiple species occurred sympatrically was counted as only one). Pairs of variables with a correlation coefficient ≥ 0.75 were considered potentially redundant. Within a group of strongly correlated variables, we selected those variables that seemed most likely to limit geographic distributions (e.g., extreme rather than average temperatures). We included five temperature and four precipitation variables (table 3).

To determine which environmental variables were correlated with the northern range limits of species, we used general additive models (GAMs), following the guidelines of Wintle et al. (2005). GAMs may be preferable to general linear models and logistic regression because they can fit nonlinear response curves that are common in ecological data (Guisan et al. 2002). We first determined the shape of the response curves for each variable and then used backward stepwise variable selection on these curves to determine the final set of variables in each model for each species.

To fit models relating the presence and absence of species to climatic variables, we first conducted analyses on response shapes by fitting univariate GAMs with up to 4 degrees of freedom (df). Different degrees of freedom provide different functional forms of the response variables, where 1 df is a linear form and additional degrees of freedom fit more complex nonlinear forms. Four degrees was chosen somewhat arbitrarily but with consideration of the number of variables and sample sizes (Sokal and Rohlf 1994). This analysis allowed us to determine whether more complicated response curves for each variable for each species were justified by the data.

We then used a backward stepwise variable selection algorithm in R, version 2.1.1 (R Development Core Team 2005), which tests a series of nested models using Akaike’s Information Criterion (AIC; Akaike 1973; Venables and Ripley 2003; Wintle et al. 2005). We used backward variable selection as opposed to other automated methods (i.e., forward selection) because it tends to perform better when the dependent variables are somewhat correlated, as is the case with climate variables (Harrell 2001). As an alternate way of interpreting the

results (in addition to the AIC), we also ran logistic regression with the final backward model created with the AIC to obtain r^2 values (Cox and Snell approximation; SPSS 14.1).

Next, to identify which environmental variables had the most explanatory power in the final model, we determined the deviance of each variable that was included in the final model. The deviance for a variable is calculated as follows. First, the AIC score is determined for the full backward model. Then, the AIC is recalculated after the variable of interest is removed. The difference between the AIC for the full model and the AIC for the model without a given variable is the deviance; higher deviances indicate greater explanatory power. This is repeated for all variables for each species.

To further evaluate how well individual climatic variables predicted the actual range limits, we calculated the predicted values of presence and absence points based on univariate GAMs fit for each climate parameter in our final models. Following recommendations by Liu et al. (2005), we chose a model threshold for each univariate distribution model based on the mean of the predicted value for the presence points (i.e., all values above the mean were considered suitable, and those below the mean were considered unsuitable). For each univariate model for each species, we determined how many absence points were incorrectly predicted by a given univariate model (generally following Peterson et al. 1999). This analysis was intended to determine whether a given climatic variable can significantly predict the absence of a given species at its northern range limits.

In addition to the six species listed above, we also performed more limited niche modeling on six additional species (the hylid species *Ecnomiohyola miotympanum*, *Smilisca baudinii*, *Smilisca fodiens*, *Tlalocohyla smithii*, and *Tlalocohyla picta* and the phyllomedusine *Pachymedusa dacnicolor*). We obtained locality and climatic data as described above. We then used the BIOCLIMav extension (Beta 1.1; A. Moussalli, Cooperative Research Centre for Tropical Rainforest Ecology and Management, Brisbane) in ArcView GIS 3.3 to visualize the predicted climatic niche envelope of each species for each variable and qualitatively compared how well each of the nine climatic variables matched or overpredicted the northern range limit of each species.

Testing for Phylogenetic Conservatism in a Climatic Niche Variable

The tropical conservatism hypothesis predicts that dispersal of lineages between tropical and temperate climatic regimes should be relatively rare. We tested for phylogenetic dependence in the limiting climatic variable identified from the ecological niche modeling (following Smith et al. 2005). We first obtained georeferenced locality data for all 124 hylid species included in the preceding phylogenetic analyses (i.e., the data set of 140 taxa but with the 16 outgroup species excluded). Locality data were obtained from museum databases and from the literature. In many cases, the available localities were not georeferenced, and coordinates were obtained using standard internet resources (Global Gazetteer, ver. 2.1; <http://www.fallingrain.com/world/>). We obtained climatic data for each locality for 19 climatic variables using the WORLDCLIM data set at 2.5-s resolution (Hijmans et al. 2004, 2005), using the BIOCLIM extension for ArcView GIS 3.3 as described above. For each species, we estimated a mean value for the climatic variable by averaging the values for a given variable across localities. Climatic data were based on an average sample size of 12.5 localities per species (range 1–125). Although sample sizes were small for some species, many species are known from few localities and/or small geographic ranges. Furthermore, the basic units used in the statistical analyses were species, not individual localities.

Based on the results of the ecological niche modeling, temperature seasonality (Bio4) appears to limit dispersal of tropical clades into temperate regions. We tested for significant phylogenetic association in this variable using the measure of phylogenetic correlation (λ) introduced by Pagel (1999a). The value of λ generally varies between 0 and 1, with 0 indicating no phylogenetic signal and 1 indicating strong phylogenetic signal (similarity between species is directly proportional to the amount of shared branch lengths; Freckleton et al. 2002). We estimated the log likelihood of the data when λ is at its estimated maximum likelihood value and when λ is set to 0, assuming the null hypothesis that the data are not phylogenetically conserved. We then used the likelihood ratio test statistic ($-2 \log_e [H_0/H_1]$) to assess the difference between these models, where H_0 represents the null model ($\lambda = 0$) and H_1 the alternative model (λ estimated). Analyses were performed with the program Continuous (ver. 1.0d13; M. Pagel). Branch lengths were from the combined-data Bayesian analysis, pruned to include only the 124 hylid species. Analyses were also performed using the chronogram from the penalized likelihood analyses. In addition to analyses using the mean estimate of Bio4 across localities for a given species, the analyses were repeated using the maximum value of Bio4 within each species and then using the minimum value. These two analyses gave results very similar to those of analyses using mean values within species, and these results are not reported.

This analysis does not represent a test of phylogenetic niche conservatism per se. We consider one of the most important (and relevant) effects of niche conservatism to be limited biogeographic dispersal of a lineage, which is associated with that lineage being specialized to a given climatic niche (Wiens and Graham 2005). The analysis above merely quantifies the extent to which the limiting climatic variable is conserved across the phylogeny of hylids, or, more precisely, the extent to which they are consistent with a model in which the trait evolves across the phylogeny according to a Brownian motion model.

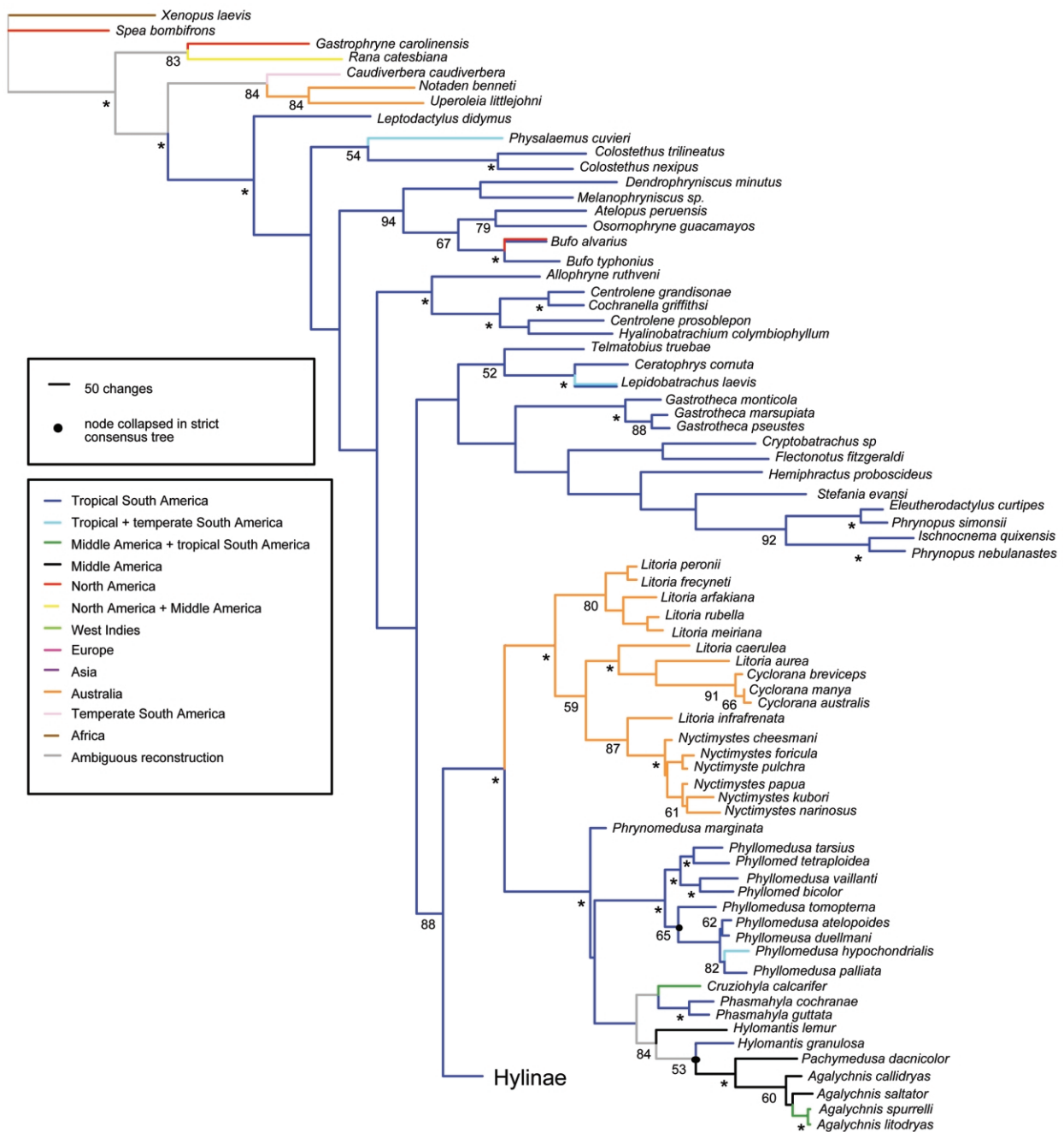


Figure A1: Partial phylogeny of hyliid frogs and outgroups, showing the basal portion of one of the 365 shortest trees from parsimony analysis of the combined data matrix with 325 taxa and 8,420 characters, with branch lengths proportional to the reconstructed number of changes at each branch. The remainder of the tree is shown in figures A2–A4. Ancestral areas are also reconstructed on the tree, using parsimony with a step matrix for weighting polymorphisms and general proximity of areas. Numbers adjacent to nodes indicate parsimony bootstrap values (values <50% not shown); asterisks indicate strongly supported clades with bootstrap values ≥ 0.95 . Black dots indicate those nodes that are collapsed in a strict consensus of all 365 shortest trees.

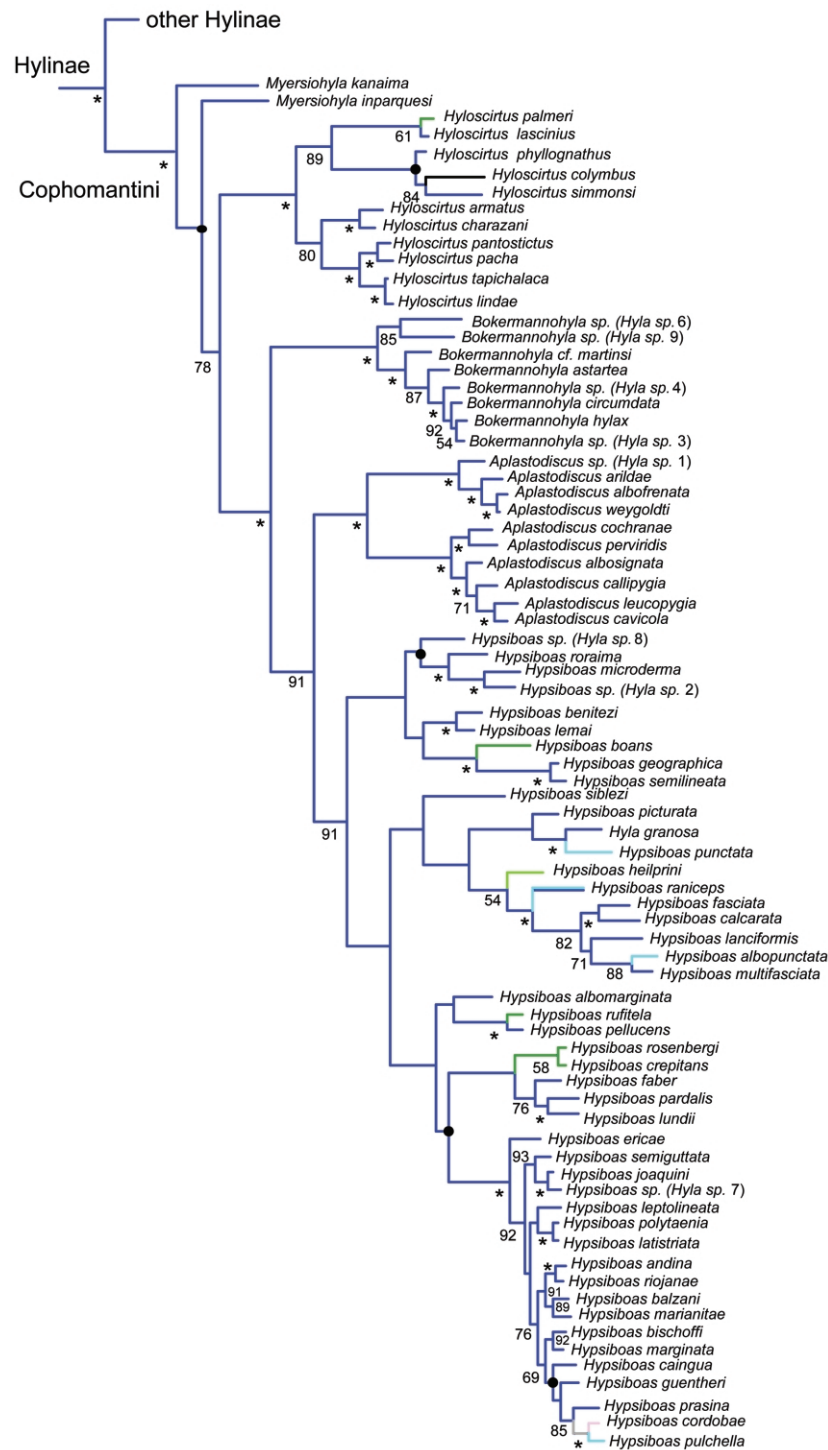


Figure A2: Phylogeny of hyloid frogs, showing relationships within the tribe Cophomantini of the subfamily Hyliinae. Numbers adjacent to nodes indicate parsimony bootstrap values (values <50% not shown); asterisks indicate strongly supported clades with bootstrap values ≥ 0.95 . Black dots indicate those nodes that are collapsed in a strict consensus of all 365 shortest trees.

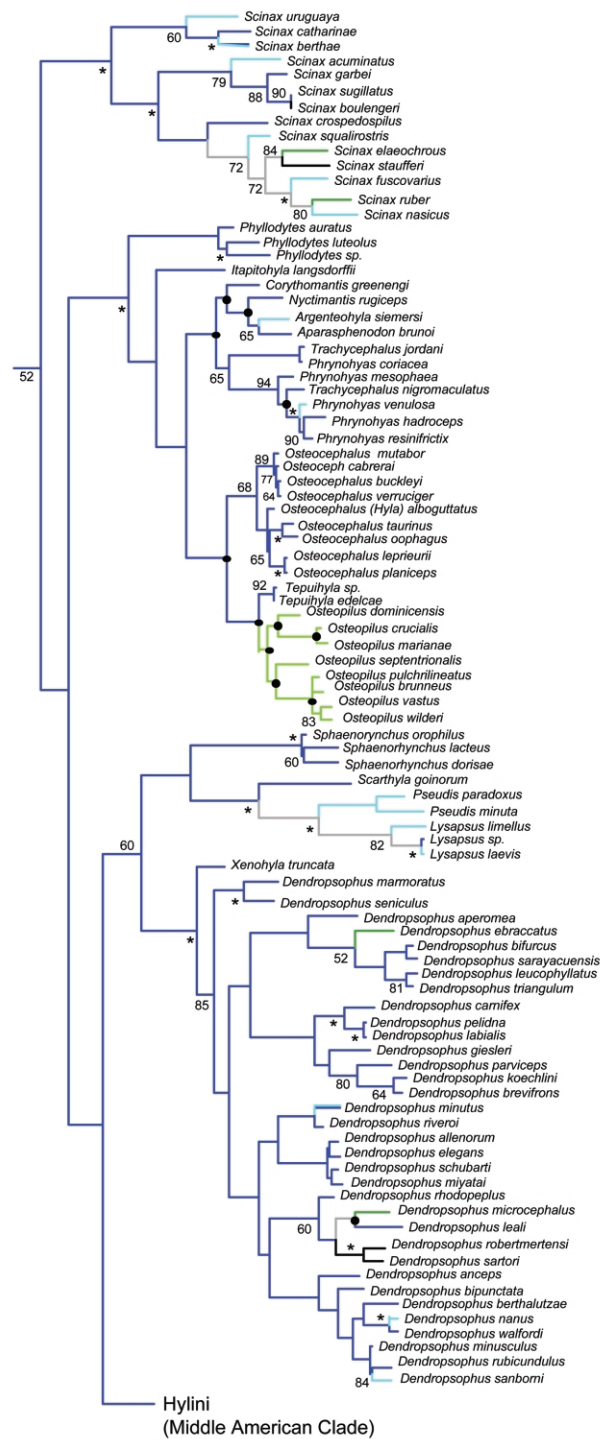


Figure A3: Phylogeny of hylid frogs, showing relationships within the subfamily Hyliinae, exclusive of the tribes Cophomantini and Hylini. Numbers adjacent to nodes indicate parsimony bootstrap values (values <50% not shown); asterisks indicate strongly supported clades with bootstrap values ≥0.95. Black dots indicate those nodes that are collapsed in a strict consensus of all 365 shortest trees.

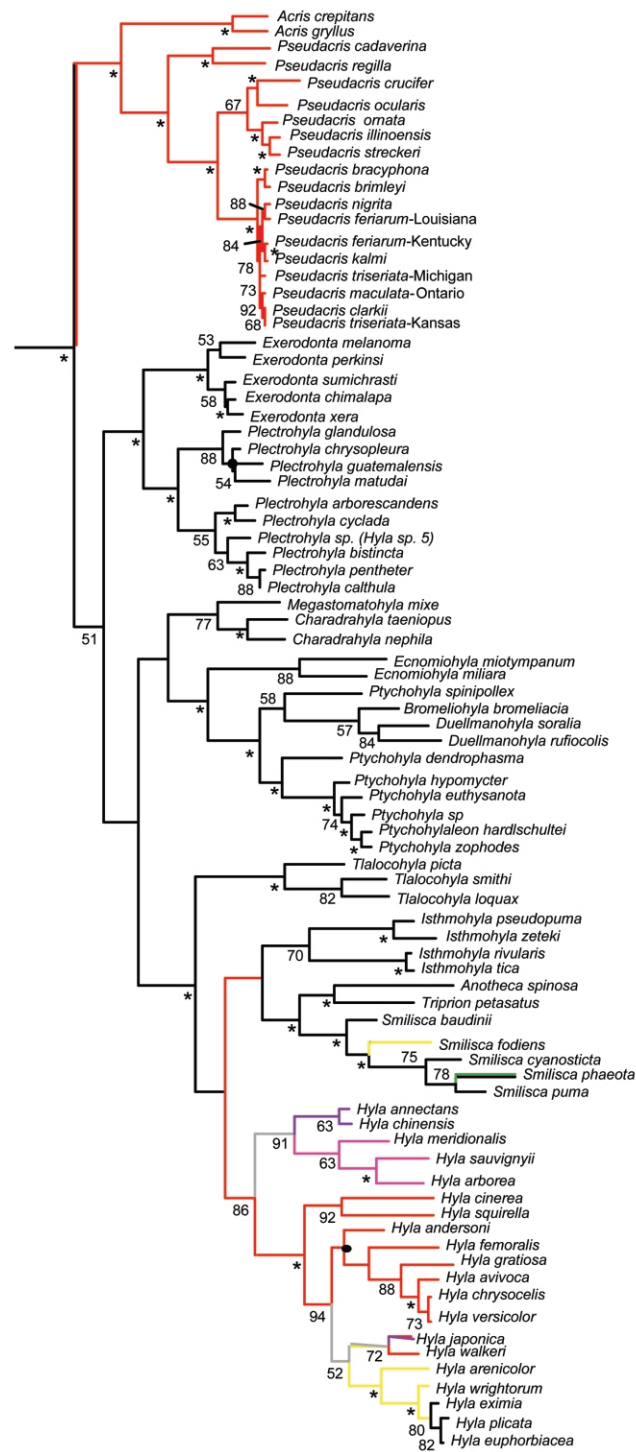


Figure A4: Phylogeny of hyloid frogs, showing relationships within the tribe Hylini (the Middle American clade) within the subfamily Hylinae. Numbers adjacent to nodes indicate parsimony bootstrap values (values <50% not shown); asterisks indicate strongly supported clades with bootstrap values ≥ 0.95 . Black dots indicate those nodes that are collapsed in a strict consensus of all 365 shortest trees.

Table A1

Mean, standard deviation, and range of values for estimated ages of clades, using two different root ages for Neobatrachia

Clade	Using 100-mya root age			Using 160-mya root age		
	Mean	SD	Range	Mean	SD	Range
Pelodyadinae	41.88	2.39	30.64–52.38	57.60	3.93	40.29–83.22
Phyllomedusinae	33.96	2.38	27.95–50.10	47.30	3.61	39.30–71.47
Cophomantini	50.97	2.68	36.64–57.45	69.68	4.66	38.93–83.29
<i>Dendropsophus</i> clade	49.13	3.29	24.56–54.74	66.35	5.14	31.45–78.70
<i>Scinax</i> clade	53.62	3.44	28.42–61.54	72.78	5.30	36.95–83.31
Lophiohylini	35.44	2.90	20.09–42.28	45.94	3.94	23.06–56.39
<i>Acris-Pseudacris</i> clade	34.93	2.19	23.58–40.47	45.17	3.42	24.94–53.93
<i>Plectrohyla</i> clade	31.20	2.73	16.47–37.32	39.19	3.78	13.73–47.03
<i>Ptychohyla</i> clade	39.49	3.31	18.93–45.09	51.16	4.90	20.51–61.88
<i>Smilisca</i> clade	32.73	2.66	16.82–37.71	42.15	4.18	16.06–51.65
Holarctic <i>Hyla</i>	31.22	2.03	20.26–35.43	39.34	3.18	22.54–47.18

Note: Data are based on 300 trees sampled from the post-burn-in trees from the combined Bayesian analysis.

Table A2
GenBank numbers for sequences used in phylogenetic analyses

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
Allophrynidae:												
<i>Allophryne ruthveni</i>	AY819328 ^s	AY819458 ^s	AY819077 ^s	AY819162 ^s	AY819242 ^s	AY843564 ^h	AY843786 ^h	AY844538 ^h	AY844361 ^h	...	AY844766 ^h	...
Bufonidae:												
<i>Atelopus peruensis</i>	AY819329 ^s	AY819459 ^s	AY819078 ^s	AY819163 ^s	AY819243 ^s	AY325996 ^d (<i>A. varius</i>)
<i>Bufo alvarius</i>	AY819330 ^s	AY819460 ^s	AY819079 ^s	AY819164 ^s	AY819244 ^s
<i>Bufo typhonius</i>	AY819331 ^s	AY819461 ^s	AY819080 ^s	AY819165 ^s	AY819245 ^s	AY843573 ^h (<i>Bufo arenarum</i>)	AY843795 ^h (<i>B. arenarum</i>)	AY844547 ^h (<i>B. arenarum</i>)	AY844370 ^h (<i>B. arenarum</i>)	...	AY844775 ^h (<i>B. arenarum</i>)	AY844205 ^h (<i>B. arenarum</i>)
<i>Dendrophryniscus minutus</i>	AY819332 ^s	AY819462 ^s	AY819081 ^s	AY819166 ^s	AY819246 ^s	AY843582 ^h	AY843804 ^h	AY844555 ^h
<i>Melanophryniscus</i> sp.	AY819333 ^s	AY819463 ^s	AY819082 ^s	AY819167 ^s	AY819247 ^s	AY843699 ^h (<i>Melano-phryniscus klappen-bachi</i>)	AY843944 ^h (<i>M. klappen-bachi</i>)	...	AY844478 ^h (<i>M. klappen-bachi</i>)	...	AY844899 ^h (<i>M. klappen-bachi</i>)	AY844306 ^h (<i>M. klappen-bachi</i>)
<i>Osornophryne guacomayos</i>	AY819334 ^s	AY819464 ^s	AY819083 ^s	AY819168 ^s	AY819248 ^s	AY326036 ^d
Centrolenidae:												
<i>Centrolenella grandisonae</i>	AY819335 ^s	AY819465 ^s	AY819084 ^s	AY819169 ^s	AY819249 ^s
<i>Cochranella griffithsi</i>	AY819337 ^s	AY819467 ^s	AY819086 ^s	AY819171 ^s	AY819251 ^s	AY843576 ^h (<i>Cochranella bejaranoi</i>)	AY843798 ^h (<i>C. bejaranoi</i>)	AY844549 ^h (<i>C. bejaranoi</i>)	AY844372 ^h (<i>C. bejaranoi</i>)	AY844029 ^h (<i>C. bejaranoi</i>)	AY844777 ^h (<i>C. bejaranoi</i>)	AY844208 ^h (<i>C. bejaranoi</i>)
<i>Centrolene prosoblepon</i>	AY819336 ^s	AY819466 ^s	AY819085 ^s	AY819170 ^s	AY819250 ^s	AY843574 ^h	AY843796 ^h	AY844548 ^h	AY844371 ^h	...	AY844776 ^h	AY844206 ^h
<i>Hyalinobatrachium colymbiophyllum</i>	AY819338 ^s	AY819468 ^s	AY819087 ^s	AY819172 ^s	AY819252 ^s	AY843595 ^h (<i>Hyalino-batrachium euryg-nathum</i>)	AY843814 ^h (<i>H. euryg-nathum</i>)	AY844567 ^h (<i>H. euryg-nathum</i>)	AY844383 ^h (<i>H. euryg-nathum</i>)	...	AY844793 ^h (<i>H. euryg-nathum</i>)	AY844217 ^h (<i>H. euryg-nathum</i>)
Dendrobatidae:												
<i>Colostethus nexipus</i>	AY819340 ^s	AY819470 ^s	AY819089 ^s	AY819174 ^s	AY819254 ^s	AY843577 ^h (<i>Colostethus talamancae</i>)	AY843799 ^h (<i>C. talamancae</i>)	AY844550 ^h (<i>C. talamancae</i>)	AY844373 ^h (<i>C. talamancae</i>)	...	AY844778 ^h (<i>C. talamancae</i>)	...
<i>Colostethus trilineatus</i>	AY819339 ^s	AY819469 ^s	AY819088 ^s	AY819173 ^s	AY819253 ^s
Leptodactylidae:												
Ceratophryinae:												
<i>Ceratophrys cornuta</i>	AY819342 ^s	AY819472 ^s	AY819091 ^s	AY819176 ^s	AY819255 ^s	AY843575 ^h (<i>Ceratophrys cranwelli</i>)	AY843797 ^h (<i>C. cranwelli</i>)	AY844207 ^h (<i>C. cranwelli</i>)
<i>Lepidobatrachus laevis</i>	AY819345 ^s	AY819475 ^s	AY819094 ^s	AY819179 ^s	AY819258 ^s
Leptodactylinae:												
<i>Leptodactylus didymus</i>	AY819346 ^s	AY819476 ^s	AY819095 ^s	AY819180 ^s	AY819259 ^s	AY843688 ^h (<i>Lepto-dactylus ocellatus</i>)	AY843934 ^h (<i>L. ocellatus</i>)	AY844681 ^h (<i>L. ocellatus</i>)	AY84470 ^h (<i>L. ocellatus</i>)	...	AY844784 ^h (<i>L. ocellatus</i>)	AY844302 ^h (<i>L. ocellatus</i>)

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Physalaemus cuvieri</i>	AY819347 ^g	AY819477 ^g	AY819096 ^g	AY819181 ^g	...	AY843729 ^h	AY843975 ^h	AY844717 ^h	AY844499 ^h	...	AY844922 ^h	AY844330 ^h
Telmatobiinae:												
<i>Caudiverbera</i>												
<i>caudiverbera</i>	AY819341 ^g	AY819471 ^g	AY819090 ^g	AY819175 ^g
<i>Eleutherodactylus curtipipes</i>	AY819343 ^g	AY819473 ^g	AY819092 ^g	AY819177 ^g	AY819256 ^g	AY326009 ^d (<i>Eleuthero-</i> <i>dactylus</i> <i>thymelensis</i>)
<i>Ischnocnema quixensis</i>	AY819344 ^g	AY819474 ^g	AY819093 ^g	AY819178 ^g	AY819257 ^g
<i>Phrynopis nebulanastes</i>	AY819405 ^g	...	AY819154 ^g	AY819320 ^g
<i>Phrynopis simonsii</i>	AY819406 ^g	...	AY819155 ^g	AY819321 ^g	AY819314 ^g
<i>Telmatobius truebae</i>	AY819348 ^g	AY819478 ^g	AY819097 ^g	AY819182 ^g	AY819260 ^g	AY843769 ^h (<i>Telmatobius</i> sp.)	AY844014 ^h (<i>Telmatobius</i> sp.)	AY844757 ^h (<i>Telmatobius</i> sp.)	AY844529 ^h (<i>Telmatobius</i> sp.)	...	AY844952 ^h (<i>Telmatobius</i> sp.)	AY84435 ^h (<i>Telmatobius</i> sp.)
Microhylidae:												
<i>Gastrophryne carolinensis</i>	AY819349 ^g	AY819479 ^g	AY819098 ^g	AY819183	AY819261 ^g	AY326064 ^d (<i>Kaloula</i> <i>conjuncta</i>)
Myobatrachidae:												
<i>Notaden benneti</i>	AY819350 ^g	AY819480 ^g	AY819099 ^g	AY819184 ^g	...	AY326071 ^d (<i>Limno-</i> <i>dynastes</i> <i>salmini</i>)
<i>Uperoleia littlejohni</i>	AY819351 ^g	AY819481 ^g	AY819100 ^g	AY819185 ^g	AY819262 ^g	AY843742 ^h (<i>Pseudo-</i> <i>phryne</i> <i>bibroni</i>)	AY843988 ^h (<i>P. bibroni</i>)	AY844729 ^h (<i>P. bibroni</i>)	AY844931 ^h (<i>P. bibroni</i>)	AY844338 ^h (<i>P. bibroni</i>)
Pelobatidae:												
<i>Spea bombifrons</i>	AY819327 ^g	AY819457 ^g	AY819076	AY819161 ^g	AY819241 ^g
Pipidae:												
<i>Xenopus laevis</i>	M27605 ^a	AY819456 ^g	AY819075	AY819160 ^g	AY819240 ^g
Ranidae:												
<i>Rana catesbiana</i>	AY819354 ^g	AY819484 ^g	AY819103 ^g	AY819188 ^g	...	AY326063 ^d (<i>Rana</i> <i>temporaria</i>)
Hemiphractidae:												
<i>Cryptobatrachus</i> sp.	AY326050 ^d	AY819485 ^g (<i>Crypto-</i> <i>batrachus</i> <i>boulengeri</i>)	AY326050 ^d
<i>Flectonotus fitzgeraldi</i>	AY819355 ^g	AY819486 ^g	AY819104 ^g	AY819189 ^g	AY819265 ^g	AY843589 ^h (<i>Flectonotus</i> sp.)	AY843809 ^h (<i>Flectonotus</i> sp.)	AY844562 ^h (<i>Flectonotus</i> sp.)	AY844379 ^h (<i>Flectonotus</i> sp.)	AY844038 ^h (<i>Flectonotus</i> sp.)	AY844788 ^h (<i>Flectonotus</i> sp.)	AY844215 ^h (<i>Flectonotus</i> sp.)
<i>Gastrotheca marsupiat</i>	AY819356 ^g	AY819487 ^g	AY819105 ^g	AY819190 ^g	...	AY843590 ^h	AY843810 ^h	AY844563 ^h	AY844380 ^h	AY844039 ^h	AY844789 ^h	...
<i>Gastrotheca monticola</i>	AY819357 ^g	AY819488 ^g	AY819106 ^g	AY819191 ^g
<i>Gastrotheca pseustes</i>	AY326051 ^d	AY326051 ^d

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Hemiphractus proboscideus</i>	AY819358 ^g	AY819489 ^g	AY819107 ^g	AY819192 ^g	AY819266 ^g	AY843594 ^h (<i>Hemi- phractus helioi</i>)	AY843813 ^h (<i>H. helioi</i>)	AY844566 ^h (<i>H. helioi</i>)	AY844382 ^h (<i>H. helioi</i>)	...	AY844792 ^h (<i>H. helioi</i>)	...
<i>Stefania evansi</i>	AY819359 ^g	AY819490 ^g	AY819108 ^g	AY819193 ^g	AY819267 ^g	AY843767 ^h	...	AY844755 ^h	...	AY844189 ^h	AY844950 ^h	AY844353 ^h
Hylidae:												
Hylinae:												
<i>Acris crepitans</i>	AY819360 ^g	AY819491 ^g	AY819109 ^g	AY819194 ^g	AY819268 ^g	AY843559 ^h	AY843782 ^h	AY844533 ^h	AY844358 ^h	AY844019 ^h	AY844762 ^h	AY844194 ^h
<i>Acris gryllus</i>	AY819418 ^g	AY843560 ^h	AY843783 ^h	AY844534 ^h	AY844359 ^h	AY844020 ^h	AY844763 ^h	...
<i>Anotheca spinosa</i>	AY819361 ^g	AY819492 ^g	AY819110 ^g	AY819195 ^g	AY819269 ^g	AY843566 ^h	AY843788 ^h	AY844540 ^h	AY844363 ^h	AY844022 ^h	AY844768 ^h	AY844198 ^h
<i>Aparasphenodon bruno</i>	AY843567 ^h	AY843567 ^h	AY843789 ^h	AY844541 ^h	AY844364 ^h	AY844023 ^h	AY844769 ^h	AY844199 ^h
<i>Aplastodiscus cochranae</i>	AY843568 ^h	AY843568 ^h	AY843790 ^h	AY844542 ^h	AY844365 ^h	AY844024 ^h	AY844770 ^h	AY844200 ^h
<i>Aplastodiscus perviridis</i>	AY843569 ^h	AY843569 ^h	AY843791 ^h	AY844543 ^h	AY844366 ^h	AY844025 ^h	AY844771 ^h	AY844201 ^h
<i>Argenteohyla siemersi</i>	AY843570 ^h	AY843570 ^h	AY843792 ^h	AY844544 ^h	AY844367 ^h	AY844026 ^h	AY844772 ^h	AY844202 ^h
<i>Corythomantis greeningi</i>	AY843578 ^h	AY843578 ^h	AY843800 ^h	AY844551 ^h	AY844374 ^h	AY844030 ^h	AY844779 ^h	AY844209 ^h
<i>Duellmanohyla ruficollis</i>	AY54931 ^f	AY843583 ^h	AY549368 ^h	AY844556 ^h	AY844377 ^h	AY844033 ^h	AY844782 ^h	AY844212 ^h
<i>Duellmanohyla soralia</i>	AY819362 ^g	AY819493 ^g	AY819111 ^g	AY819196 ^g	AY819270 ^g	AY843584 ^h	AY843806 ^h	AY844557 ^h	AY844378 ^h	AY844034 ^h	AY844783 ^h	...
<i>Hyla (Aplastodiscus) albofrenata</i>	DQ380346 ^f	AY819539 ^g
<i>Hyla (Osteocephalus) alboguttata</i>	DQ380347 ^f
<i>Hyla (Hypsiboas) albomarginata</i>	AY549316 ^f	AY549316 ^f	AY549369 ^h	AY844568 ^h	AY844384 ^h	...	AY844794 ^h	AY844218 ^h
<i>Hyla (Hypsiboas) albopunctata</i>	AY549317 ^f	AY819538 ^g	AY549317 ^h	AY549370 ^h	AY844569 ^h	...	AY844041 ^h	AY844795 ^h	...
<i>Hyla (Aplastodiscus) albosignata</i>	AY843596 ^h	AY843596 ^h	AY843817 ^h	AY844570 ^h	AY844385 ^h	AY844042 ^h	AY844796 ^h	AY844219 ^h
<i>Hyla (Dendropsophus) allenorum</i>	DQ380348 ^f
<i>Hyla (Dendropsophus) anceps</i>	AY843597 ^h	AY843597 ^h	AY843818 ^h	AY844571 ^h	AY844386 ^h	AY844043 ^h	AY844797 ^h	AY844220 ^h
<i>Hyla (Hyla) andersoni</i>	AY291115 ^e	DQ055812 ⁱ	DQ055785 ⁱ	DQ055756 ⁱ	DQ055730 ⁱ	AY843598 ^h	AY843819 ^h	AY844572 ^h	...	AY844044 ^h	AY844798 ^h	...
<i>Hyla (Hypsiboas) andina</i>	AY819420 ^g	AY549319 ^h	AY549372 ^h	AY844573 ^h	AY844387 ^h	...	AY844799 ^h	...
<i>Hyla (Hyla) annectans</i>	AY819421 ^g	DQ055813 ⁱ	DQ055786 ⁱ	DQ055757 ⁱ	DQ055731 ⁱ	AY843600 ^h	AY843821 ^h	AY844574 ^h	AY844388 ^h	AY844045 ^h	AY844800 ^h	...
<i>Hyla (Dendropsophus) aperomea</i>	AY819450 ^g	AY819549 ^g
<i>Hyla (Hyla) arborea</i>	DQ055835 ^f	DQ055814 ^f	DQ055787 ^f	DQ055758 ^f	DQ055732 ^f	AY843601 ^h	AY843822 ^h	AY844575 ^h	AY844389 ^h	AY844046 ^h	...	AY844221 ^h
<i>Hyla (Plectrohyla) arborescandens</i>	AY843602 ^h	AY843602 ^h	AY843823 ^h	AY844576 ^h	AY844390 ^h	AY844047 ^h	AY844801 ^h	AY844222 ^h
<i>Hyla (Hyla) arenicolor</i>	AY819363 ^g	AY819494 ^g	AY819112 ^g	AY819197 ^g	AY819271 ^g	AY843603 ^h	AY843824 ^h	AY844577 ^h	AY844391 ^h	AY844048 ^h	AY844802 ^h	...
<i>Hyla (Aplastodiscus) arildae</i>	AY843604 ^h	AY843604 ^h	AY843825 ^h	AY844578 ^h	AY844392 ^h	AY844049 ^h	AY844803 ^h	AY844223 ^h
<i>Hyla (Hyloscirtus) armata</i>	AY819423 ^g	AY549321 ^h	AY549374 ^h	AY844579 ^h	AY844393 ^h	AY844050 ^h	AY844804 ^h	AY844224 ^h
<i>Hyla (Bokermannohyla) astartea</i>	AY549322 ^f	AY819495 ^g	AY819113 ^g	AY819198 ^g	AY819272 ^g	AY549322 ^f	AY549375 ^h	AY844580 ^h	AY844225 ^h

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Hyla (Hyla) avivoca</i>	DQ055836 ⁱ	DQ055815 ⁱ	...	DQ055759 ⁱ	DQ055733 ⁱ	AY843605 ^h	AY843828 ^h	AY844581 ^h	AY844394 ^h	AY844051 ^h	AY844805 ^h	...
<i>Hyla (Hypsiboas) balzani</i>	AY549323 ⁱ	AY549313 ^h	AY549376 ^h	AY844582 ^h	AY844395 ^h	...	AY844806 ^h	AY844226 ^h
<i>Hyla (Hypsiboas) benitezi</i>	DQ380349 ⁱ	AY843606 ^h	AY843830 ^h	AY844583 ^h	AY844396 ^h
<i>Hyla (Dendropsophus) berthaltutzeae</i>	AY843607 ^h	AY843607 ^h	AY843831 ^h	AY844584 ^h	AY844397 ^h	AY844052 ^h	AY844807 ^h	AY844228 ^h
<i>Hyla (Dendropsophus) bifurca</i>	DQ380350 ⁱ
<i>Hyla (Dendropsophus) bipunctata</i>	AY843608 ^h	AY843608 ^h	AY843832 ^h	AY844585 ^h	...	AY844053 ^h	AY844808 ^h	AY844229 ^h
<i>Hyla (Hypsiboas) bischoffi</i>	AY549324 ⁱ	AY549324 ⁱ	AY549377 ^h	AY844586 ^h	AY844398 ^h
<i>Hyla (Plectrohyla) bistincta</i>	AY843609 ^h	AY843609 ^h	AY843834 ^h	AY844587 ^h	AY844399 ^h	AY844054 ^h	...	AY844230 ^h
<i>Hyla (Hypsiboas) boans</i>	AY819364 ^g	AY819496 ^g	AY819114 ^g	AY819199 ^g	AY819273 ^g	AY843610 ^h	AY843835 ^h	AY844588 ^h	...	AY844055 ^h	AY844809 ^h	AY844231 ^h
<i>Hyla (Dendropsophus) brevifrons</i>	DQ380351 ⁱ	AY843611 ^h	AY843836 ^h	AY844589 ^h	AY844400 ^h	...	AY844810 ^h	AY844232 ^h
<i>Hyla (Bromelohyla) bromeliacia</i>	AY819426 ^g	DQ055816 ⁱ	DQ055788 ⁱ	DQ055760 ⁱ	DQ055734 ⁱ	AY843612 ^h	AY843837 ^h	AY844590 ^h	AY844401 ^h	AY844056 ^h	AY844811 ^h	AY844233 ^h
<i>Hyla (Hypsiboas) caingua</i>	AY549326 ⁱ	AY549330 ^h	AY549379 ^h	AY844591 ^h	...	AY844057 ^h	AY844812 ^h	AY844234 ^h
<i>Hyla (Hypsiboas) calcarata</i>	DQ380352 ⁱ	AY843613 ^h	AY843839 ^h	AY844235 ^h
<i>Hyla (Hypsiboas) callipygia</i>	AY843614 ^h	AY843614 ^h	AY843840 ^h	AY844592 ^h	AY844402 ^h	AY844058 ^h	AY844813 ^h	AY844236 ^h
<i>Hyla (Plectrohyla) calthula</i>	AY843615 ^h	AY843615 ^h	AY843841 ^h	AY844593 ^h	AY844403 ^h	AY844059 ^h	...	AY844237 ^h
<i>Hyla (Dendropsophus) carnifex</i>	AY819424 ^g	AY843616 ^h	AY843842 ^h	...	AY844404 ^h	AY844060 ^h	...	AY844238 ^h
<i>Hyla (Aplastodiscus) cavicola</i>	AY843617 ^h	AY843617 ^h	AY843843 ^h	AY844594 ^h	AY844405 ^h	...	AY844814 ^h	...
<i>Hyla (Hyloscirtus) charazani</i>	AY843618 ^h	AY843618 ^h	AY843844 ^h	AY844595 ^h	AY844406 ^h	AY844061 ^h	...	AY844239 ^h
<i>Hyla (Exerodonta) chimalapa</i>	AY843619 ^h	AY843619 ^h	AY843845 ^h	AY844596 ^h	AY844407 ^h	AY844062 ^h	AY844815 ^h	AY844240 ^h
<i>Hyla (Hyla) chinensis</i>	AF31512 ^c	DQ055817 ⁱ	DQ055789 ⁱ	DQ055761 ⁱ
<i>Hyla (Hyla) chrysocelis</i>	AY291116 ^c	AY291116 ^c
<i>Hyla (Hyla) cinerea</i>	AY819366 ^g	AY819498 ^g	AY819116 ^g	AY819201 ^g	AY819275 ^g	AY549327 ^h	AY549380 ^h	AY844597 ^h	AY844408 ^h	AY844063 ^h	AY844816 ^h	AY844241 ^h
<i>Hyla (Bokermannohyla) circumdata</i>	AY549328 ⁱ	AY549328 ⁱ	AY549381 ^h	AY844598 ^h	AY844409 ^h	AY844064 ^h	AY844817 ^h	AY844242 ^h
<i>Hyla (Hyloscirtus) colymba</i>	DQ380353 ⁱ	AY819553 ^g	AY819157 ^g	AY819323 ^g	AY819316 ^g	AY843620 ^h	AY843848 ^h	AY844599 ^h	AY844410 ^h	AY844065 ^h	AY844818 ^h	AY844243 ^h
<i>Hyla (Hypsiboas) cordobae</i>	AY549331 ⁱ	AY549331 ⁱ	AY549383 ^h	AY844600 ^h	AY844411 ^h	AY844066 ^h	AY844819 ^h	AY844244 ^h
<i>Hyla (Hypsiboas) crepitans</i>	DQ380354 ⁱ	AY843621 ^h	AY843850 ^h	AY844601 ^h	AY844412 ^h	AY844067 ^h
<i>Hyla (Plectrohyla) cyclada</i>	AY843622 ^h	AY843622 ^h	AY843851 ^h	AY844602 ^h	AY844413 ^h	AY844068 ^h	AY844820 ^h	AY844245 ^h
<i>Hyla (Ptychohyla) dendrophasma</i>	AY819425 ^g	AY819540 ^g	DQ055790 ⁱ	DQ055762 ⁱ	DQ055735 ⁱ	AY843623 ^h	AY843852 ^h	AY844603 ^h	AY844414 ^h	AY844069 ^h	AY844821 ^h	AY844246 ^h

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Hyla (Dendropsophus) ebraccata</i>	AY819367 ^g	AY819499 ^g	AY819117 ^g	AY819202 ^g	AY819276 ^g	AY843624 ^h	AY843853 ^h	AY844604 ^h	AY844415 ^h	AY844070 ^h	AY844822 ^h	AY844247 ^h
<i>Hyla (Dendropsophus) elegans</i>	DQ380355 ⁱ
<i>Hyla (Hypsiboas) ericae</i>	AY549332 ^f	AY549332 ^f	AY549385 ^h	AY844605 ^h	AY844416 ^h	AY844071 ^h
<i>Hyla (Hyla) euphorbiacea</i>	DQ055837 ⁱ	DQ055818 ⁱ	DQ055791 ⁱ	DQ055763 ⁱ	DQ055736 ⁱ	AY843625 ^h	AY843855 ^h	AY844606 ^h	...	AY844072 ^h	AY844823 ^h	AY844248 ^h
<i>Hyla (Hyla) eximia</i>	AY843626 ^h	AY843626 ^h	AY843856 ^h	AY844073 ^h	AY844824 ^h	AY844249 ^h
<i>Hyla (Hypsiboas) faber</i>	DQ380356 ⁱ	AY549334 ^f	AY549387 ^h	AY844607 ^h	AY844825 ^h	...
<i>Hyla (Hypsiboas) fasciata</i>	AY819427 ^g	AY549335 ^h	AY549335 ^h	AY549388 ^h	AY844608 ^h
<i>Hyla (Hyla) femoralis</i>	DQ055838 ⁱ	DQ055819 ⁱ	DQ055792 ⁱ	DQ055764 ⁱ	DQ055737 ⁱ	Y843627 ^h	AY843859 ^h	AY844609 ^h	...	AY844074 ^h	AY844826 ^h	AY844250 ^h
<i>Hyla (Hypsiboas) geographica</i>	AY819428 ^g	AY819541 ^g	AY843628 ^h
<i>Hyla (Dendropsophus) giesleri</i>	AY843629 ^h	AY843629 ^h	AY843860 ^h	...	AY844417 ^h	AY844075 ^h	AY844827 ^h	AY844251 ^h
<i>Hyla (Hypsiboas) granosa</i>	AY549336 ^f	AY819542 ^g	AY549336 ^f	AY843861 ^h	AY844610 ^h	AY844828 ^h	...
<i>Hyla (Hyla) gratiosa</i>	DQ055839 ⁱ	DQ055820 ⁱ	DQ055793 ⁱ	DQ055765 ⁱ	DQ055738 ⁱ	AY843630 ^h	AY843862 ^h	AY844611 ^h	AY844418 ^h	AY844076 ^h	AY844829 ^h	AY844252 ^h
<i>Hyla (Hypsiboas) guentheri</i>	AY549421 ^f	AY549421 ^f	AY549390 ^h	AY844612 ^h	AY844830 ^h	AY844253 ^h
<i>Hyla (Hypsiboas) heilprini</i>	DQ380357 ⁱ	AY843632 ^h	AY843864 ^h	AY844613 ^h	AY844831 ^h	...
<i>Hyla (Bokermannohyla) hylax</i>	DQ380358 ⁱ	AY549338 ^h	AY549391 ^h	AY844614 ^h	AY844419 ^h	AY844077 ^h	AY844832 ^h	AY844254 ^h
<i>Hyla (Myersiohyla) imparquesi</i>	AY843672 ^h	AY843672 ^h	...	AY844663 ^h	...	AY844114 ^h	AY844876 ^h	AY844291 ^h
<i>Hyla (Hyla) japonica</i>	DQ055840 ⁱ	DQ055821 ⁱ	DQ055794 ⁱ	DQ055766 ⁱ	DQ055739 ⁱ	AY843633 ^h	AY843866 ^h	AY844615 ^h	AY844420 ^h	AY844407 ^h	AY844833 ^h	AY844255 ^h
<i>Hyla (Hypsiboas) joaquina</i>	AY549340 ^f	AY549339 ^h	AY549392 ^h	AY844616 ^h	AY844421 ^h	...	AY844834 ^h	AY844256 ^h
<i>Hyla (Myersiohyla) kanaima</i>	AY843634 ^h	AY843634 ^h	AY843868 ^h	AY844617 ^h	AY844422 ^h	AY844079 ^h	AY844835 ^h	...
<i>Hyla (Dendropsophus) koechlini</i>	AY819369 ^g	AY819501 ^g	AY819119 ^g	AY819204 ^g	AY819278 ^g
<i>Hyla (Dendropsophus) labialis</i>	AY843635 ^h	AY843635 ^h	AY843869 ^h	AY844618 ^h	...	AY844080 ^h	AY844836 ^h	AY844257 ^h
<i>Hyla (Hypsiboas) lanciformis</i>	AY819429 ^g	AY819543 ^g	AY843636 ^h	AY843870 ^h	AY844619 ^h	...	AY844081 ^h	AY844837 ^h	AY844258 ^h
<i>Hyla (Hyloscirtus) lascinia</i>	DQ380359 ⁱ
<i>Hyla (Hypsiboas) latistriata</i>	AY549360 ^h	AY549360 ^h	AY549413 ^h	AY844668 ^h	AY844293 ^h
<i>Hyla (Dendropsophus) leali</i>	AY819451 ^g	AY819550 ^g
<i>Hyla (Hypsiboas) lemai</i>	AY843637 ^h	AY843637 ^h	AY843871 ^h	AY844620 ^h	AY844423 ^h	AY844082 ^h	AY844838 ^h	AY844259 ^h
<i>Hyla (Hypsiboas) leptolineata</i>	AY549341 ^f	AY549341 ^f	AY549394 ^h	AY844621 ^h	AY844424 ^h	AY844083 ^h	AY844839 ^h	AY844260 ^h
<i>Hyla (Dendropsophus) leucophyllata</i>	DQ380360 ⁱ
<i>Hyla (Aplastodiscus) leucopygia</i>	AY819430 ^g	AY819544 ^g	AY843638 ^h	AY843873 ^h	AY844622 ^h	AY844425 ^h	AY844084 ^h	AY844840 ^h	AY844261 ^h

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Hyla (Hyloscirtus) lindae</i>	DQ380361 ^l
<i>Hyla (Tlalocohyla) loquax</i>	AY819431 ^s	DQ055822 ⁱ	DQ055795 ⁱ	DQ055767 ⁱ	DQ055740 ^j
<i>Hyla (Hypsiboas) lundii</i>	AY843639 ^h	AY843639 ^h	AY843874 ^h	AY844623 ^h	...	AY844085 ^h	AY844841 ^h	AY844262 ^h
<i>Hyla (Hypsiboas) marginata</i>	AY549342 ^f	AY549342 ^f	AY549395 ^h	AY844624 ^h	AY844426 ^h	...	AY844842 ^h	AY844263 ^h
<i>Hyla (Hypsiboas) marianitae</i>	AY549344 ^f	AY549344 ^f	AY549397 ^h	AY844625 ^h	AY844427 ^h	...	AY844843 ^h	...
<i>Hyla (Dendropsophus) marmorata</i>	AY819432 ^s	AY843640 ^h	AY843877 ^h	...	AY844428 ^h
<i>Hyla (Bokermannohyla) martinsi</i>	AY843641 ^h	AY843641 ^h	AY843878 ^h	AY844626 ^h	...	AY844086 ^h	AY844844 ^h	AY844264 ^h
<i>Hyla (Exerodonta) melanomma</i>	AY819433 ^s	DQ055823 ⁱ	DQ055796 ⁱ	DQ055768 ⁱ	DQ055741 ⁱ	AY843642 ^h	AY843879 ^h	AY844627 ^h	AY844429 ^h	AY844087 ^h	AY844845 ^h	AY844265 ^h
<i>Hyla (Hyla) meridionalis</i>	AY819370 ^s	AY819502 ^s	AY819120 ^s	AY819205 ^s	AY819279 ^s
<i>Hyla (Dendropsophus) microcephala</i>	AY819371 ^s	AY819503 ^s	AY819121 ^s	AY819206 ^s	AY819280 ^s	AY843643 ^h	AY843880 ^h	AY844628 ^h	AY844430 ^h	...	AY844846 ^h	AY844266 ^h
<i>Hyla (Hypsiboas) microderma</i>	AY843644 ^h	AY843644 ^h	AY843881 ^h	AY844267 ^h
<i>Hyla (Ecnomiohyla) miliaria</i>	DQ055841 ⁱ	DQ055824 ⁱ	DQ055797 ⁱ	DQ055769 ⁱ	DQ055742 ⁱ	AY843777 ^h	AY843882 ^h	AY844629 ^h	AY844431 ^h	AY844088 ^h	AY844847 ^h	AY844268 ^h
<i>Hyla (Dendropsophus) minuscula</i>	DQ380362 ^j
<i>Hyla (Dendropsophus) minuta</i>	AY549345 ^h	AY549345 ^h	AY549398 ^h	...	AY844432 ^h	AY844089 ^h
<i>Hyla (Ecnomiohyla) miotympanum</i>	AY819372 ^s	AY819504 ^s	AY819122 ^s	AY819207 ^s	AY819281 ^s	AY843645 ^h	AY843884 ^h	AY844630 ^h	AY844433 ^h	AY844090 ^h	AY844848 ^h	...
<i>Hyla (Megastomatohyla) mixe</i>	AY843656 ^h	AY843656 ^h	AY843885 ^h	AY844631 ^h	AY844434 ^h	AY844091 ^h	AY844849 ^h	AY844269 ^h
<i>Hyla (Dendropsophus) miyatai</i>	AY843647 ^h	AY843647 ^h	AY843886 ^h	AY844632 ^h	AY844435 ^h	AY844092 ^h	AY844850 ^h	...
<i>Hyla (Hypsiboas) multifasciata</i>	DQ380363 ^j	AY843648 ^h	AY843887 ^h	AY844633 ^h	AY844436 ^h	AY844093 ^h	AY844851 ^h	AY844270 ^h
<i>Hyla (Dendropsophus) nana</i>	AY819373 ^s	AY819505 ^s	AY819123 ^s	AY819208 ^s	AY819282 ^s	AY549346 ^h	AY843888 ^h	AY844634 ^h	AY844437 ^h	...	AY844852 ^h	AY844271 ^h
<i>Hyla (Charadrahyla) nephila</i>	AY843649 ^h	AY843649 ^h	AY843889 ^h	AY844635 ^h	AY844438 ^h	AY844094 ^h	AY844853 ^h	AY844272 ^h
<i>Hyla (Hyloscirtus) pacha</i>	DQ380364 ^j	AY326057 ^d
<i>Hyla (Hyloscirtus) palmeri</i>	DQ380365 ^j	AY819554 ^s	AY819158 ^s	AY819324 ^s	AY819317 ^s	AY843650 ^h	AY843890 ^h	AY844636 ^h	AY844439 ^h	AY844095 ^h	AY844854 ^h	AY844273 ^h
<i>Hyla (Hyloscirtus) pantosticta</i>	AY326052 ^d	AY326052 ^d
<i>Hyla (Hypsiboas) pardalis</i>	DQ380366 ^j	AY843651 ^h	AY843891 ^h	AY844637 ^h	...	AY844096 ^h	AY844855 ^h	...
<i>Hyla (Dendropsophus) parviceps</i>	DQ380367 ^j	AY843652 ^h	AY843892 ^h	AY844638 ^h	AY844440 ^h	AY844097 ^h	AY844856 ^h	AY844274 ^h
<i>Hyla (Dendropsophus) pelidna</i>	AY819434 ^s

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Hyla</i> (<i>Hypsiboas</i>) <i>pellucens</i>	DQ380368 ^j	AY326058 ^d
<i>Hyla</i> (<i>Plectrohyla</i>) <i>pentheter</i>	AY819449 ^g	DQ055825 ⁱ	DQ055798 ⁱ	DQ055770 ⁱ	DQ055743 ⁱ
<i>Hyla</i> (<i>Exerodonta</i>) <i>perkinsi</i>	AY843653 ^h	AY843653 ^h	AY843893 ^h	AY844639 ^h	AY844441 ^h	AY844098 ^h	AY844857 ^h	AY844275 ^h
<i>Hyla</i> (<i>Hylascirtus</i>) <i>phyllognatha</i>	DQ380369 ^j
<i>Hyla</i> (<i>Tlalocohyla</i>) <i>picta</i>	AY843654 ^h	AY843654 ^h	AY843894 ^h	AY844640 ^h	AY844442 ^h	AY844099 ^h	AY844858 ^h	AY844276 ^h
<i>Hyla</i> (<i>Hypsiboas</i>) <i>picturata</i>	DQ380370 ^j	AY326055 ^d
<i>Hyla</i> (<i>Hyla</i>) <i>plicata</i>	DQ055842 ⁱ	DQ055826 ⁱ	...	DQ055771 ⁱ	DQ055744 ⁱ
<i>Hyla</i> (<i>Hypsiboas</i>) <i>polytaenia</i>	AY819374 ^g	AY819506 ^g	AY819124 ^g	AY819209 ^g	AY819283 ^g	AY843655 ^h	AY843895 ^h	AY844641 ^h	AY844443 ^h	...	AY844859 ^h	...
<i>Hyla</i> (<i>Hypsiboas</i>) <i>prasina</i>	AY549347 ^f	AY549347 ^f	AY549400 ^h	AY844642 ^h	...	AY844100 ^h	AY844860 ^h	...
<i>Hyla</i> (<i>Isthmohyla</i>) <i>pseudopuma</i>	AY819435 ^g	DQ055827 ⁱ	DQ055799 ⁱ	DQ055772 ⁱ	DQ055745 ⁱ	AY843656 ^h	AY843897 ^h	AY844643 ^h	AY844444 ^h	AY844075 ^h	AY844861 ^h	AY844277 ^h
<i>Hyla</i> (<i>Hypsiboas</i>) <i>pulchella</i>	AY549352 ^f	AY549352 ^f	AY549405 ^h	AY844644 ^h	AY844445 ^h	AY844102 ^h	AY844862 ^h	AY844278 ^h
<i>Hyla</i> (<i>Osteopilus</i>) <i>pulchrilineata</i>	AY819436 ^g
<i>Hyla</i> (<i>Hypsiboas</i>) <i>punctata</i>	AY549353 ^f	AY549353 ^f	AY549406 ^h	AY844645 ^h
<i>Hyla</i> (<i>Hypsiboas</i>) <i>raniceps</i>	AY819375 ^g	AY819507 ^g	AY819125 ^g	AY819210 ^g	AY819284 ^g	AY843657 ^h	AY843900 ^h	AY844646 ^h	...	AY844103 ^h	AY844863 ^h	...
<i>Hyla</i> (<i>Hypsiboas</i>) <i>riojana</i>	AY549356 ^f	AY549355 ^h	AY549408 ^h	AY844648 ^h	AY844447 ^h	...	AY844865 ^h	AY844279 ^h
<i>Hyla</i> (<i>Dendropsophus</i>) <i>riveroi</i>	DQ380372 ^j
<i>Hyla</i> (<i>Isthmohyla</i>) <i>rivularis</i>	AY819437 ^g	DQ055828 ⁱ	DQ055800 ⁱ	DQ055773 ⁱ	DQ055746 ⁱ	AY843659 ^h	AY843902 ^h	AY844649 ^h	...	AY844117 ^h
<i>Hyla</i> (<i>Dendropsophus</i>) <i>rhodopepla</i>	DQ380371 ^j	AY843658 ^h	...	AY844647 ^h	AY844446 ^h	...	AY844864 ^h	...
<i>Hyla</i> (<i>Dendropsophus</i>) <i>robertmertensi</i>	AY819452 ^g	AY819551 ^g
<i>Hyla</i> (<i>Hypsiboas</i>) <i>roraima</i>	AY843660 ^h	AY843660 ^h	AY843903 ^h	AY844650 ^h	AY844448 ^h	AY844104 ^h	AY844866 ^h	AY844280 ^h
<i>Hyla</i> (<i>Hypsiboas</i>) <i>rosenbergi</i>	AY819438 ^g	AY819545 ^g
<i>Hyla</i> (<i>Dendropsophus</i>) <i>rubicundula</i>	AY843661 ^h	AY843661 ^h	AY843904 ^h	AY844651 ^h	AY844449 ^h	AY844281 ^h
<i>Hyla</i> (<i>Hypsiboas</i>) <i>rufitela</i>	AY819439 ^g	AY843662 ^h	AY843905 ^h	AY844652 ^h	...	AY844105 ^h	AY844867 ^h	AY844282 ^h
<i>Hyla</i> (<i>Dendropsophus</i>) <i>sanborni</i>	AY843663 ^h	AY843663 ^h	AY843906 ^h	AY844653 ^h	AY844450 ^h	AY844106 ^h	AY844868 ^h	AY844283 ^h
<i>Hyla</i> (<i>Dendropsophus</i>) <i>sarayacuensis</i>	DQ380373 ^j	AY843664 ^h	AY844451 ^h	...	AY844869 ^h	...
<i>Hyla</i> (<i>Dendropsophus</i>) <i>sartori</i>	AY819453 ^g	AY819552 ^g	AY819156 ^g	AY819322 ^g	AY819315 ^g
<i>Hyla</i> (<i>Hyla</i>) <i>savignyi</i>	DQ055843 ⁱ	DQ055829 ⁱ	DQ055801 ⁱ	DQ055774 ⁱ	DQ055747 ⁱ	AY843665 ^h	AY843907 ^h	AY844654 ^h	...	AY844107 ^h	...	AY844284 ^h
<i>Hyla</i> (<i>Dendropsophus</i>) <i>schubarti</i>	DQ380374 ^j

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Hyla</i> (<i>Hypsiboas</i>) <i>semiguttata</i>	AY549358 ^f	AY549358 ^f	AY549410 ^h	AY844655 ^h	AY844452 ^h	...	AY844870 ^h	AY844285 ^h
<i>Hyla</i> (<i>Hypsiboas</i>) <i>semilineata</i>	AY843778 ^h	AY843778 ^h	AY843909 ^h	AY844656 ^h	AY844453 ^h	AY844108 ^h	AY844871 ^h	AY844286 ^h
<i>Hyla</i> (<i>Dendropsophus</i>) <i>senicula</i>	AY843666 ^h	AY843666 ^h	AY843910 ^h	AY844657 ^h	AY844454 ^h	AY844109 ^h	AY844872 ^h	AY844287 ^h
<i>Hyla</i> (<i>Hypsiboas</i>) <i>sibileszi</i>	DQ380375 ⁱ	AY819546 ^g	AY843667 ^h	AY843911 ^h	AY844658 ^h	AY844455 ^h	AY844110 ^h	AY844873 ^h	AY844288 ^h
<i>Hyla</i> (<i>Hyloscirtus</i>) <i>simmonsii</i>	DQ380376 ⁱ	AY819555 ^g	AY819159 ^g	AY819325 ^g	AY819318 ^g
<i>Hyla</i> (<i>Talocohyla</i>) <i>smithii</i>	AY819377 ^g	AY819509 ^g	AY819127 ^g	AY819212 ^g	AY819286 ^g	AY843668 ^h	AY843912 ^h	AY844659 ^h	...	AY844111 ^h	AY844874 ^h	...
<i>Hyla</i> (<i>Hyla</i>) <i>squirella</i>	AY819378 ^g	AY819510 ^g	AY819128 ^g	AY819213 ^g	AY819287 ^g	AY843678 ^h	AY843923 ^h	AY844670 ^h	AY844462 ^h	AY844120 ^h	AY844883 ^h	AY844296 ^h
<i>Hyla</i> (<i>Exerodonta</i>) <i>sumichrasti</i>	AY819454 ^g	...	DQ055802 ⁱ	DQ055776 ⁱ
<i>Hyla</i> (<i>Charadrahyla</i>) <i>taeniopus</i>	AY819455 ^g	AY819556 ^g	DQ055803 ^f	AY819326 ^g	AY819319 ^g	AY843679 ^h	AY843924 ^h	AY844671 ^h	AY844463 ^h	AY844119 ^h	AY844882 ^h	AY844295 ^h
<i>Hyla</i> (<i>Hyloscirtus</i>) <i>tapichalaca</i>	AY563625 ^f	AY563625 ^f	AY843925 ^h	AY844672 ^h	...	AY844121 ^h	...	AY844297 ^h
<i>Hyla</i> (<i>Isthmohyla</i>) <i>tica</i>	AY819440 ^g	DQ055830 ⁱ	DQ055804 ⁱ	DQ055777 ⁱ	DQ055748 ⁱ
<i>Hyla</i> (<i>Dendropsophus</i>) <i>triangulum</i>	DQ380377 ⁱ	AY843680 ^h	AY843926 ^h	AY844673 ^h	AY844464 ^h	AY844122 ^h	...	AY844298 ^h
<i>Hyla</i> (<i>Scinax</i>) <i>uruguayana</i>	AY843681 ^h	AY843681 ^h	AY843927 ^h	AY844674 ^h	...	AY844123 ^h	AY844884 ^h	AY844299 ^h
<i>Hyla</i> (<i>Hyla</i>) <i>versicolor</i>	AY819441 ^g	DQ055831 ⁱ	DQ055805 ⁱ	DQ055778 ⁱ	DQ055749 ⁱ	AY843682 ^h	AY843928 ^h	AY844675 ^h	AY844465 ^h	AY844124 ^h	AY844885 ^h	...
<i>Hyla</i> (<i>Dendropsophus</i>) <i>walfordi</i>	AY843647 ^h	AY843647 ^h	AY843929 ^h	AY844676 ^h	AY844886 ^h	...
<i>Hyla</i> (<i>Hyla</i>) <i>walkeri</i>	AY843684 ^h	AY843684 ^h	AY843930 ^h	AY844677 ^h	AY844466 ^h	AY844125 ^h
<i>Hyla</i> (<i>Aplastodiscus</i>) <i>weygoldti</i>	AY843685 ^h	AY843685 ^h	AY843931 ^h	AY844678 ^h	AY844467 ^h	...	AY844887 ^h	...
<i>Hyla</i> (<i>Hyla</i>) <i>wrightorum</i>	AY819368 ^g	AY819500 ^g	AY819118 ^g	AY819203 ^g	AY819277 ^g
<i>Hyla</i> (<i>Exerodonta</i>) <i>xera</i>	AY843686 ^h	AY843686 ^h	AY843932 ^h	AY844679 ^h	AY844468 ^h	AY844126 ^h	AY844888 ^h	AY844300 ^h
<i>Hyla</i> (<i>Isthmohyla</i>) <i>zeteki</i>	AY819442 ^g	...	DQ055806 ⁱ	DQ055779 ⁱ	DQ055750 ⁱ
<i>Hyla</i> (<i>Aplastodiscus</i>) sp. 1 (aff. <i>ehrdardtii</i>)	AY843639 ^h	AY843639 ^h	AY843913 ^h	AY844660 ^h	AY844456 ^h	...	AY844875 ^h	...
<i>Hyla</i> (<i>Hypsiboas</i>) sp. 2	AY843670 ^h	AY843670 ^h	AY843914 ^h	AY844661 ^h	AY844457 ^h	AY844112 ^h	...	AY844289 ^h
<i>Hyla</i> (<i>Bokermannohyla</i>) sp. 3	AY843673 ^h	AY843673 ^h	AY843916 ^h	AY844664 ^h	...	AY844115 ^h
<i>Hyla</i> (<i>Bokermannohyla</i>) sp. 4	AY843674 ^h	AY843674 ^h	AY843917 ^h	AY844665 ^h	AY844458 ^h	AY844116 ^h	AY844877 ^h	...
<i>Hyla</i> (<i>Plectrohyla</i>) sp. 5 (aff. <i>thorectes</i>)	AY843675 ^h	AY843675 ^h	AY843918 ^h	AY844666 ^h	AY844459 ^h	AY844118 ^h	AY844878 ^h	...
<i>Hyla</i> (<i>Bokermannohyla</i>) sp. 6 (aff. <i>pseudopseudis</i>)	AY843676 ^h	AY843676 ^h	AY843919 ^h	AY844667 ^h	AY844460 ^h	AY844101 ^h	AY844879 ^h	AY844292 ^h
<i>Hyla</i> (<i>Hypsiboas</i>) sp. 7 (aff. <i>semiguttata</i>)	AY549359 ^h	AY549359 ^h	AY549412 ^h	AY844880 ^h	...
<i>Hyla</i> (<i>Hypsiboas</i>) sp. 8	AY843671 ^h	AY843671 ^h	AY843915 ^h	AY844662 ^h	...	AY844113 ^h	...	AY844290 ^h

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Hyla</i> (<i>Bokermannohyla</i>) sp. 9 (aff. <i>alvarengai</i>)	AY843677 ^h	AY843677 ^h	AY843922 ^h	AY844669 ^h	AY844461 ^h	...	AY844881 ^h	AY844294 ^h
<i>Lysapsus laevis</i>	AY843696 ^h	AY843696 ^h	AY843941 ^h	AY844689 ^h	AY844476 ^h	AY844133 ^h	AY844896 ^h	AY844305
<i>Lysapsus limellum</i>	AY843697 ^h	AY843697 ^h	AY843942 ^h	AY844690 ^h	AY844477 ^h	...	AY844897 ^h	...
<i>Lysapsus</i> sp.	AY819352 ^s	AY819482 ^s	AY819101 ^s	AY819186 ^s	AY819263 ^s
<i>Nyctimantis rugiceps</i>	AY843780 ^h	AY843780 ^h	AY843945 ^h
<i>Osteocephalus buckleyi</i>	DQ380378 ^j
<i>Osteocephalus cabrerai</i>	AY843705 ^h	AY843705 ^h	AY843950 ^h	AY844696 ^h	AY844481 ^h	AY844136 ^h	AY844902 ^h	AY844310 ^h
<i>Osteocephalus</i> (<i>Itapitohyla</i>) <i>langsdoeffii</i>	AY819379 ^s	AY819511 ^s	AY819129 ^s	AY819214 ^s	AY819288 ^s	AY843706 ^h	AY843951 ^h	AY844697 ^h	AY844482 ^h	AY844137 ^h	AY844903 ^h	AY844311 ^h
<i>Osteocephalus lepieurii</i>	AY549361 ^f	AY549361 ^f	AY843952 ^h	AY844698 ^h	AY844483 ^h	AY844138 ^h	AY844904 ^h	AY844312 ^h
<i>Osteocephalus mutabor</i>	DQ380379 ^j
<i>Osteocephalus oophagus</i>	AY843708 ^h	AY843708 ^h	AY843953 ^h	AY844699 ^h	AY844484 ^h	AY844139 ^h
<i>Osteocephalus planiceps</i>	DQ380380 ^j
<i>Osteocephalus taurinus</i>	AY819380 ^s	AY819512 ^s	AY819130 ^s	AY819215 ^s	AY819289 ^s	AY843709 ^h	AY843954 ^h	AY844700 ^h	AY844485 ^h	AY844140 ^h	AY844905 ^h	AY844313 ^h
<i>Osteocephalus verruciger</i>	DQ380381 ^j
<i>Osteopilus brunneus</i>	DQ380382 ^j
<i>Osteopilus crucialis</i>	AY819419 ^s	AY843710 ^h	AY843955 ^h	AY844314 ^h
<i>Osteopilus dominicensis</i>	AY819443 ^s	AY843711 ^h	AY843956 ^h	AY844701 ^h	AY844486 ^h	AY844141 ^h	...	AY844315 ^h
<i>Osteopilus marianae</i>	DQ380383 ^j
<i>Osteopilus pulchrilineatus</i>	AY819436 ^s
<i>Osteopilus septentrionalis</i>	AY819381 ^s	AY819513 ^s	AY819131 ^s	AY819216 ^s	AY819290 ^s	AY843712 ^h	AY843957 ^h	...	AY844487 ^h	AY844142 ^h	AY844906 ^h	AY844316 ^h
<i>Osteopilus vastus</i>	DQ380384 ^j	AY843713 ^h	AY843958 ^h	AY844143 ^h	AY844907 ^h	AY844317 ^h
<i>Osteopilus wilderi</i>	DQ380385 ^j
<i>Phrynohyas coriacea</i>	DQ380386 ^j
<i>Phrynohyas hadroceps</i>	AY843717 ^h	AY843717 ^h	AY843962 ^h	AY844704 ^h	AY844490 ^h	AY844146 ^h	...	AY844319 ^h
<i>Phrynohyas mesophaea</i>	AY843718 ^h	AY843718 ^h	AY843963 ^h	AY844705 ^h	AY844491 ^h	AY844147 ^h	AY844910 ^h	AY844320 ^h
<i>Phrynohyas resinifricrix</i>	AY843719 ^h	AY843719 ^h	AY843964 ^h	AY844706 ^h	AY844492 ^h	AY844148 ^h	AY844911 ^h	AY844321 ^h
<i>Phrynohyas venulosa</i>	AY819382 ^s	AY819514 ^s	AY819132 ^s	AY819217 ^s	AY819291 ^s	AY549362 ^h	AY549415 ^h	AY844707 ^h	AY844493 ^h	AY844149 ^h	AY844912 ^h	AY844322 ^h
<i>Phyllodytes auratus</i>	AY819383 ^s	AY819515 ^s	AY819133 ^s	AY819218 ^s	AY819292 ^s
<i>Phyllodytes luteolus</i>	AY843721 ^h	AY843721 ^h	AY843965 ^h	AY844708 ^h	AY844494 ^h	AY844150 ^h	AY844913 ^h	AY844324 ^h
<i>Phyllodytes</i> sp.	AY843722 ^h	AY843722 ^h	AY843966 ^h	AY844709 ^h	...	AY844151 ^h	AY844914 ^h	AY844325 ^h
<i>Plectrohyla chrysopleura</i>	AY819384 ^s	AY819516 ^s	AY819134 ^s	AY819219 ^s	AY819293 ^s
<i>Plectrohyla glandulosa</i>	AY843730 ^h	AY843730 ^h	AY843967 ^h	AY844718 ^h	AY844500 ^h	AY844159 ^h	AY844923 ^h	AY844331 ^h
<i>Plectrohyla guatemalensis</i>	AY819444 ^s	DQ055833 ⁱ	DQ055807 ⁱ	DQ055780 ⁱ	DQ055751 ⁱ	AY843731 ^h	AY843976 ^h	AY844719 ^h	AY844501 ^h	AY844160 ^h	AY844924 ^h	AY844332 ^h
<i>Plectrohyla matudi</i>	AY843732 ^h	AY843732 ^h	AY843977 ^h	AY844720 ^h	AY844502 ^h	AY844161 ^h	AY844925 ^h	AY844333 ^h
<i>Pseudacris brachyphona</i>	AY326049 ^d	AY326049 ^d
<i>Pseudacris brimleyi</i>	AY291094 ^e	AY291094 ^e
<i>Pseudacris cadaverina</i>	AY819365	AY819497 ^s	AY819115 ^s	AY819200 ^s	AY819274 ^s	AY843734 ^h	AY843978 ^h	AY844722 ^h	...	AY844162 ^h	...	AY844334 ^h
<i>Pseudacris clarkii</i>	AY291093 ^e	AY291093 ^e
<i>Pseudacris crucifer</i>	AY819385 ^s	AY819517 ^s	AY819135 ^s	AY819220 ^s	AY819294 ^s	AY843735 ^h	AY843980 ^h	AY844723 ^h	...	AY844163 ^h	AY844927 ^h	...
<i>Pseudacris feriarum</i>	AY291084 ^e	AY291084 ^e

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Pseudacris feriarum</i>	AY291085 ^e	AY291085 ^e
<i>Pseudacris illinoensis</i>	AY291110 ^e	AY291110 ^e
<i>Pseudacris kalmi</i>	AY291087 ^e	AY291087 ^e
<i>Pseudacris maculata</i>	AY291082 ^e	AY291082 ^e
<i>Pseudacris nigrita</i>	AY819386 ^g	AY819518 ^g	AY819136 ^g	AY819221 ^g	AY819295 ^g	AY291077 ^e
<i>Pseudacris ocularis</i>	AY291098 ^e	AY843736 ^h	AY843981 ^h	AY844724 ^h	...	AY844164 ^h
<i>Pseudacris ornata</i>	AY291106 ^e	AY291106 ^e
<i>Pseudacris regilla</i>	AY819376 ^g	AY819508 ^g	AY819126 ^g	AY819211 ^g	AY819285 ^g	AY843737 ^h	AY843982 ^h	AY844725 ^h	AY844504 ^h	AY844165 ^h
<i>Pseudacris streckeri</i>	AY291108 ^e	AY291108 ^e
<i>Pseudacris triseriata</i>	AY291091 ^e	AY291091 ^e	AY843983 ^h	AY844726 ^h	...	AY844166 ^h	AY844928 ^h	AY844335 ^h
<i>Pseudacris triseriata</i>	AY291092 ^e	AY291092 ^e
<i>Pseudis minuta</i>	AY843739 ^h	AY843739 ^h	AY843984 ^h	...	AY844505 ^h	...	AY844929 ^h	AY844336 ^h
<i>Pseudis paradoxus</i>	AY819353 ^g	AY819483 ^g	AY819102 ^g	AY819187 ^g	AY819264 ^g	AY843730 ^h	AY843985 ^h	AY844727 ^h	AY844506 ^h	AY844167 ^h	...	AY844337 ^h
<i>Pternohyla fodiens</i>	AY819387 ^g	AY819519 ^g	AY819137 ^g	AY819222 ^g	AY819296 ^g	AY843743 ^h	AY843986 ^h	AY844730 ^h	AY844508 ^h	AY844169 ^h	AY844932 ^h	AY844339 ^h
<i>Ptychohyla euthysanota</i>	AY843744 ^h	AY843744 ^h	AY843989 ^h	AY844731 ^h	AY844509 ^h	AY844170 ^h	AY844933 ^h	AY844340 ^h
<i>Ptychohyla hypomycter</i>	AY819445 ^g	DQ055832 ⁱ	DQ055809 ⁱ	DQ055782 ⁱ	DQ055753 ⁱ	AY843745 ^h	AY843990 ^h	AY844732 ^h
<i>Ptychohyla leonhardschultzei</i>	AY843746 ^h	AY843746 ^h	AY843991 ^h	AY844733 ^h	AY844510 ^h	AY844171 ^h	AY844934 ^h	AY844341 ^h
<i>Ptychohyla salvadorensis</i>	...	AY819547 ^g	DQ055810 ⁱ	DQ055783 ⁱ	DQ055754 ⁱ
<i>Ptychohyla spinipollex</i>	AY819388 ^g	AY819520 ^g	AY819138 ^g	AY819223 ^g	AY819297 ^g	AY843748 ^h	AY843992 ^h	AY844735 ^h	AY844512 ^h	AY844173 ^h	AY844936 ^h	AY844343 ^h
<i>Ptychohyla zophodes</i>	AY843749 ^h	AY843749 ^h	AY843994 ^h	AY844736 ^h	AY844513 ^h	AY844174 ^h	AY844937 ^h	AY844344 ^h
<i>Ptychohyla</i> sp.	AY843747 ^h	AY843747 ^h	AY843993 ^h	AY844734 ^h	AY844511 ^h	AY844172 ^h	AY844935 ^h	AY844342 ^h
<i>Scarthyla goinorum</i>	AY819389 ^g	AY819521 ^g	AY819139 ^g	AY819224 ^g	AY819298 ^g	AY843752 ^h	AY843997 ^h	AY844738 ^h	AY844514 ^h	...	AY844938 ^h	...
<i>Scinax acuminatus</i>	AY843753 ^h	AY843753 ^h	AY843998 ^h	AY844739 ^h	AY844515 ^h	AY844176 ^h	AY844939 ^h	...
<i>Scinax berthae</i>	AY843754 ^h	AY843754 ^h	AY843999 ^h	AY844740 ^h	AY844940 ^h	AY844345 ^h
<i>Scinax boulengeri</i>	AY843755 ^h	AY843755 ^h	AY844000 ^h	AY844741 ^h	AY844516 ^h	AY844177 ^h
<i>Scinax catharinae</i>	AY819390 ^g	AY819522 ^g	AY819140 ^g	AY819225 ^g	AY819299 ^g	AY843756 ^h	AY844001 ^h	AY844742 ^h	AY844517 ^h	...	AY844941 ^h	AY844346 ^h
<i>Scinax crosopedospilus</i>	AY819391 ^g	AY819523 ^g	AY819141 ^g	AY819226 ^g	AY819300 ^g
<i>Scinax elaeochrous</i>	AY819446 ^g	AY847757 ^h	AY844002 ^h	AY844743 ^h	AY844518 ^h	AY844178 ^h	AY844942 ^h	...
<i>Scinax fuscovarius</i>	AY847758 ^h	AY847758 ^h	AY844003 ^h	AY844744 ^h	AY844519 ^h	AY844179 ^h	AY844943 ^h	AY844347 ^h
<i>Scinax garbei</i>	AY326033 ^f	AY326033 ^f
<i>Scinax nasicus</i>	AY847759 ^h	AY847759 ^h	AY844004 ^h	AY844745 ^h	AY844520 ^h	AY844180 ^h	...	AY844348 ^h
<i>Scinax ruber</i>	AY819447 ^g	AY549365 ^f	AY549418 ^h	AY844746 ^h	AY844521 ^h	AY844181 ^h	AY844944 ^h	...
<i>Scinax squalirostris</i>	AY847760 ^h	AY847760 ^h	...	AY844747 ^h	AY844522 ^h	AY844182 ^h	AY844945 ^h	AY844349 ^h
<i>Scinax staufferi</i>	To be added	To be added	To be added	To be added	To be added	AY843761 ^h	AY844006 ^h	AY844748 ^h	AY844523 ^h	AY844183 ^h
<i>Scinax sugillatus</i>	AY819392 ^g	AY819524 ^g	AY819142 ^g	AY819227 ^g	AY819301 ^g
<i>Smilisca baudinii</i>	AY549366 ^f	AY549366 ^f	AY844007 ^h	AY844749 ^h	AY844946 ^h	...
<i>Smilisca cyanosticta</i>	AY819393 ^g	AY819525 ^g	AY819143 ^g	AY819228 ^g	AY819302 ^g	AY843763 ^h	AY844008 ^h	AY844750 ^h	AY844524 ^h	AY844184 ^h	AY844947 ^h	AY844350 ^h
<i>Smilisca phaeota</i>	AY819448 ^g	AY819548 ^g	DQ055811 ⁱ	DQ055784 ^f	DQ055755 ^f	AY843764 ^h	AY844009 ^h	AY844751 ^h	...	AY844185 ^h	AY844948 ^h	AY844351 ^h
<i>Smilisca puma</i>	AY843765 ^h	AY843765 ^h	AY844010 ^h	AY844752 ^h	AY844525 ^h	AY844186 ^h	AY844949 ^h	...
<i>Sphaenorhynchus dorisae</i>	DQ380387	AY843766 ^h	AY844011 ^h	AY844753 ^h	AY844526 ^h	AY844187 ^h
<i>Sphaenorhynchus lacteus</i>	AY819394 ^g	AY819526 ^g	AY819144 ^g	AY819229 ^g	AY819303 ^g	AY549367 ^h	AY844012 ^h	AY844754 ^h	AY844527 ^h	AY844188 ^h	...	AY844352 ^h

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Sphaenorhynchus orophilus</i>	DQ380388
<i>Tepuihyla edelcae</i>	AY843770 ^b	AY843770 ^b	AY844530 ^h
<i>Tepuihyla</i> sp.	DQ380389
<i>Trachycephalus jordani</i>	AY819395 ^e	AY819527 ^e	AY819145 ^e	AY819230 ^e	AY819304 ^e	AY843771 ^h	AY844015 ^h	AY844758 ^h	AY844531 ^h	AY844190 ^h	AY844953 ^h	AY844356 ^h
<i>Trachycephalus nigromaculatus</i>	AY843772 ^h	AY843772 ^h	AY844016 ^h	AY844759 ^h	...	AY844191 ^h
<i>Triplicornis petasatus</i>	AY819396 ^e	AY819528 ^e	AY819146 ^e	AY819231 ^e	AY819305 ^e	AY843774 ^h	AY844017 ^h	AY844761 ^h	AY844532 ^h	AY844193 ^h	AY844955 ^h	AY844357 ^h
<i>Xenohyla truncata</i>	AY843775 ^h	AY843775 ^h	AY844018 ^h
Pelodyadinae:												
<i>Cyclorana australis</i>	AY843580 ^h	AY843580 ^h	AY843802 ^h	AY844553 ^h	AY844376 ^h
<i>Cyclorana brevipes</i>	AY819411 ^e	AY819537 ^e
<i>Cyclorana manya</i>	AY819397 ^e	AY819529 ^e	AY819147 ^e	AY819232 ^e	AY819306 ^e
<i>Litoria arfakiana</i>	AY326039 ^d	AY326039 ^d
<i>Litoria</i> cf. <i>aurea</i>	AY819398 ^e	AY819530 ^e	AY819148 ^e	AY819233 ^e	AY819307 ^e	AY843691 ^h	AY843937 ^h	AY844684 ^h	...	AY844130 ^h	AY844892 ^h	...
<i>Litoria caerulea</i>	AY819399 ^e	AY819531 ^e	AY819149 ^e	AY819234 ^e	AY819308 ^e	AY843692 ^h	AY843938 ^h	AY844685 ^h	...	AY844131 ^h	AY844893 ^h	...
<i>Litoria freycineti</i>	AY843693 ^h	AY843693 ^h	AY843939 ^h	AY844686 ^h	AY844473 ^h	...	AY844894 ^h	...
<i>Litoria infrafronata</i>	AY843694 ^h	AY843694 ^h	AY843940 ^h	AY844687 ^h	AY844474 ^h	AY844304 ^h
<i>Litoria meiriana</i>	AY843695 ^h	AY843695 ^h	...	AY844688 ^h	AY844475 ^h	AY844132 ^h	AY844895 ^h	...
<i>Litoria peronii</i>	AY819408 ^e
<i>Litoria rubella</i>	AY819407 ^e	AY819536 ^e
<i>Nyctimystes cheesmani</i>	AY819409 ^e
<i>Nyctimystes foricula</i>	AY819400 ^e	...	AY819150 ^e	AY819235 ^e	AY819309 ^e
<i>Nyctimystes kubori</i>	AY326037 ^d	AY326037 ^d	AY843947 ^h	AY844693 ^h	AY844479 ^h
<i>Nyctimystes narinusus</i>	AY843703 ^h	AY843703 ^h	AY843948 ^h	AY844694 ^h	...	AY844135 ^h	...	AY844308 ^h
<i>Nyctimystes papua</i>	AY819410 ^e
<i>Nyctimystes pulcher</i>	AY843701 ^h	AY843701 ^h	AY843946 ^h	AY844692 ^h	...	AY844134 ^h
Phyllomedusinae:												
<i>Agalychnis (Cruziohyla) calcarifer</i>	AY843562 ^h	AY843562 ^h	AY843785 ^h	AY844536 ^h	AY844196 ^h
<i>Agalychnis callidryas</i>	AY819412 ^e	AY843563 ^h	...	AY844537 ^h	AY844765 ^h	...
<i>Agalychnis litodryas</i>	AY326043 ^d	AY326043 ^d
<i>Agalychnis saltator</i>	AY326044 ^d	AY326044 ^d
<i>Agalychnis spurrelli</i>	AY819401 ^e	AY819532 ^e	AY819151 ^e	AY819236 ^e	AY819310 ^e
<i>Hylomantis granulosa</i>	AY843687 ^h	AY843687 ^h	AY843933 ^h	AY844680 ^h	AY844469 ^h	AY844127 ^h	AY844889 ^h	AY844301 ^h
<i>Pachymedusa dacnicolor</i>	AY819402 ^e	AY819533 ^e	AY819152 ^e	AY819237 ^e	AY819311 ^e	AY843714 ^h	AY843959 ^h	AY844702 ^h	AY844488 ^h	AY844144 ^h	AY844908 ^h	AY844318 ^h
<i>Phasmahyla cochraniae</i>	AY843715 ^h	AY843715 ^h	AY843960 ^h
<i>Phasmahyla guttata</i>	AY843716 ^h	AY843716 ^h	AY843961 ^h	AY844703 ^h	AY844489 ^h	AY844145 ^h	AY844909 ^h	...
<i>Phrynomedusa marginata</i>	AY819417 ^e
<i>Phyllomedusa atelopoides</i>	AY819413 ^e
<i>Phyllomedusa bicolor</i>	AY843723 ^h	AY843723 ^h	AY843968 ^h	AY844710 ^h	AY844495 ^h	AY844152 ^h	AY844915 ^h	...
<i>Phyllomedusa duellmani</i>	AY819414 ^e

Table A2 (Continued)

Species ^{a,b}	Gene											
	12S	ND1	POMC	Cmyc-ex2	Cmyc-ex3	16S	Cytochrome <i>b</i>	Rhodopsin	RAG-1	Tyrosinase	SIA	28S
<i>Phyllomedusa hypochondrialis</i>	AY819415 ^g	AY843724 ^h	AY843969 ^h	AY844711 ^h	AY844496 ^h	AY844153 ^h	AY844916 ^h	...
<i>Phyllomedusa lemur</i>	AY819403 ^g	AY819534 ^g	...	AY819238 ^g	AY819312 ^g	AY843687 ^h	AY843970 ^h	AY844712 ^h	...	AY844154 ^h	AY844917 ^h	...
<i>Phyllomedusa palliata</i>	AY326046 ⁱ	AY326046 ⁱ
<i>Phyllomedusa tarsius</i>	AY819416 ^g	AY843726 ^h	AY843971 ^h	AY844713 ^h	...	AY844155 ^h	AY844918 ^h	AY844326 ^h
<i>Phyllomedusa tetraploidea</i>	AY843727 ^h	AY843727 ^h	AY843972 ^h	AY844714 ^h	...	AY844156 ^h	AY844919 ^h	AY844327 ^h
<i>Phyllomedusa tomodopterna</i>	AY819404 ^g	AY819535 ^g	AY819153 ^g	AY819239 ^g	AY819313 ^g	AY843728 ^h	AY843973 ^h	AY844715 ^h	AY844497 ^h	AY844157 ^h	AY844920 ^h	AY844328 ^h
<i>Phyllomedusa vaillanti</i>	AY549363 ^j	AY549363 ^j	AY549416 ^h	AY844716 ^h	AY844498 ^h	AY844158 ^h	AY844921 ^h	AY844329 ^h

^a Taxa used in analyses of 140 species are underlined.
^b Generic names given are those used in GenBank, whereas generic names in parentheses are those used in current taxonomy and this article.
^c J.-P. Jiang and K.-Y. Zhou, unpublished, October 2000.
^d Darst and Cannatella 2004.
^e Moriarty and Cannatella 2004.
^f Faivovich et al. 2004.
^g Wiens et al. 2005.
^h Faivovich et al. 2005.
ⁱ Smith et al. 2005.
^j This study.