

1 APPENDIX S1

2 EXPANDED MATERIALS AND METHODS

3 *Body Size Ranges in Treefrog Assemblages*

4 To assess the similarity of body size ranges found across treefrog assemblages, we
5 compiled body size data and species lists from regional assemblages throughout the world and
6 local sites within regions. We use the term “treefrog” in a general sense, indicating the treefrog
7 ecomorph rather than a specific clade of frogs (i.e., arboreal frogs with enlarged toe pads; Pough
8 et al. 2002). It should be noted that we excluded some potential “treefrogs” and focus only on the
9 most species-rich treefrog clade within each region. Although we expect that there will be
10 evolution of body-size extremes in many regions, we do not necessarily expect this pattern in
11 every clade in every region. More specifically, we did not deal with frogs of the family
12 Centrolenidae (mostly small bodied) and Hemiphractidae (mostly large bodied; sensu Wiens et al.
13 2005), which occur primarily in montane regions of South America but are less species-rich than
14 South American hylids and have specialized life histories (IUCN et al. 2006). These two clades
15 are not closely related to hylid treefrogs or each other (Wiens et al. 2006b). We note that both
16 centrolenids and hemiphractids have each evolved a broad range of body sizes, but not
17 necessarily at every location, and their body size evolution may be constrained by interactions
18 with each other and with sympatric hylids. Furthermore, around the world there are various
19 lineages that are at least semi-arboreal that show seemingly continuous variation from no toepads
20 to toepads, including *Eleutherodactylus* and some frogs of the families Microhylidae and Ranidae
21 (Duellman and Trueb 1986). Because it would be difficult to identify all species within these
22 groups that would be considered “treefrogs,” we only included the major treefrog clades within
23 each region.

24 Regions were delineated with respect to geographic areas of independent treefrog
25 evolutionary history, determined by examining species composition and using the phylogenies of
26 Bossuyt et al. (2006) for ranoid frogs, Wiens et al. (2006b) for hylid treefrogs, and Roelants et al.

27 (2007) and Wiens (2007) for overall frog phylogeny. Each region was considered to be largely
28 independent because nearly its entire treefrog fauna arose from either (1) a single treefrog
29 colonization within the region (regions 3, 5, 6, and 8 below), or (2) an independent origin of the
30 treefrog ecomorph (regions 1, 2, 4, and 7 below). For the four regions that slightly deviated from
31 our criteria for independence, we present the body size range of only the descendents of the
32 primary colonization (regions 3 and 6) or independent evolution of the treefrog ecomorph
33 (regions 1 and 2), such that the ranges presented are independent. These regions are (1) Africa
34 (sub-Saharan only), (2) Madagascar, (3) Holarctic (North Africa, Europe, temperate northern
35 Asia, and North America), (4) Southeast Asia and India, (5) Australasia (Australia and New
36 Guinea), (6) Middle America (Mexico to Panama), (7) South America (the Amazon Basin and
37 Brazilian Atlantic forest), and (8) the Caribbean (without Trinidad and Tobago). Literature data
38 on local sites indicated that most local sites within these regions had body size ranges similar to
39 those for the entire region. However, a formal comparison of local sites surveyed to date within
40 all regions was problematic for two reasons. First, difficulties existed in comparing different sites
41 across different regions due to differences in sampling intensities at different sites. Second, at the
42 local scale, the occurrence of widespread taxa that occurred in many local assemblages posed
43 problems for comparisons within a region, since such local assemblages were not independent in
44 their taxonomic composition. Thus, we present two examples of well-sampled local sites within
45 each region to document that local assemblages may also exhibit the size ranges typical of the
46 regional fauna. Because high-elevation treefrogs can have substantial variation in body size at
47 different altitudes (e.g. Amezcuita 1999), we chose only low-elevation communities. Note that
48 although species lists may not necessarily indicate syntopic species that are currently interacting
49 per se, such lists were the finest resolution we could obtain, particularly for tropical areas.

50 We used snout-to-vent length (SVL) as a metric of body size (see next section). Because
51 most sources of local species composition did not list the SVL data for local populations, we used
52 maximum reported SVL for all species to maintain consistency. This also helped avoid sampling

53 artifacts, in which a species is known or expected to be present but has not been sampled enough
54 to get an accurate estimate of the maximum SVL within that local site. Although the mean SVL
55 may be preferable to maximum SVL, data for the mean of most species were not available.
56 Similarly, we use maximum SVL to maximize the amount of body size data, but results were
57 similar using only male maximum SVL. Maximum SVL data were gathered primarily from field
58 guides or surveys that covered broad regions, as follows: Africa (Schlötz 1999; Channing 2001),
59 Madagascar (Glaw and Vences 1994), Holarctic (Conant and Collins 1998; Fei et al. 1999;
60 Arnold 2003; Stebbins 2003; Goris and Maeda 2004; Lannoo 2005), Southeast Asia and India
61 (Berry 1975; Manthey and Grossman 1997; Daniel 2002), Australasia (Menzies 1977; Barker et
62 al. 1995), Middle America (Duellman 2001), South America (many sources; see Table S1), and
63 the Caribbean (Trueb and Tyler 1974; Schwartz and Henderson 1991). We recognize that this
64 literature does not include all species from some regions (e.g., India, Australasia). However, the
65 sources do cover a sufficiently large number of species to document the occurrence of the body
66 size range characteristic of treefrog assemblages (see RESULTS).

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68 *Morphometrics*

69 To ascertain whether body size is the major axis of morphological differentiation among
70 Caribbean treefrog species (compared to a trait like gape width, for example), we examined
71 morphometric variation in the group. Museum specimens were measured at the U.S. National
72 Museum of Natural History (see Appendix B). With one exception, between four and ten
73 individuals of each sex of each species were measured, depending on specimen availability. We
74 attempted to measure only sexually mature individuals (estimated by nuptial pad presence in
75 males and size in females; Duellman and Trueb 1986, p. 56). If more than 10 individuals were
76 available for a given sex-species combination, the largest 10 individuals were sampled to ensure
77 sampling of sexually mature individuals at the large end of the body size distribution for each
78 species (given that we use maximum SVL in subsequent analyses).

79 Morphometric data consisted of 12 linear measurements typically used to quantify body
80 shape and size in treefrogs (e.g., Duellman 2001). These included: (1) snout-to-vent length (SVL;
81 tip of snout to anterior margin of cloaca), (2) tibia length (tip of knee to tip of heel), (3) foot
82 length (proximal edge of inner metatarsal tubercle to tip of fourth toe), (4) head length (posterior
83 corner of jaw to tip of snout), (5) head width (distance between posterior corners of jaw), (6)
84 interorbital distance (width of bone between two orbits), (7) internarial distance, (8) eye-to-nostril
85 distance (posterior tip of nostril to anterior corner of eye), (9) eye diameter (distance between
86 anterior and posterior corners of eye), (10) hand length (proximal edge of outer palmar tubercle to
87 tip of third finger), (11) thumb length (insertion point of thumb into hand to tip of thumb), and
88 (12) radioulnar length (elbow to distal edge of outer palmar tubercle). All measurements were ln-
89 transformed before analysis.

90 Because these measurements were highly correlated with one another, we partitioned
91 them into orthogonal axes of variation by performing principal components analysis (PCA;
92 Manly 1994) on the correlation matrix. We examined the proportion of variation explained by
93 each component and examined the loadings for each variable to interpret each component in
94 terms of the original variables. The PCA was conducted in JMP IN (Version 4.0.4, SAS Institute,
95 Inc., Cary, NC, 2001).

96 Sexual size dimorphism (SSD) is widespread among *Osteopilus* species, with females
97 larger than males (results not shown). Thus, sexual selection could be responsible for some of the
98 variation in size. However, we expect that sexual selection has played a small role at most in the
99 overall diversification of body sizes within *Osteopilus*, because female-biased SSD in frogs has
100 been typically ascribed to fecundity selection (i.e., unidirectional toward larger female size; Shine
101 1979; Woolbright 1983). In contrast, we see evidence for either diversification into all sizes or
102 into predominantly smaller sizes within *Osteopilus* (see *Results*). Additionally, all subsequent
103 analyses were also conducted using only males, but the results were qualitatively identical when
104 the maximum size of either sex was used.

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Community Analyses

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A simple test to investigate whether the body sizes of treefrog species on Jamaica and Hispaniola may be structured non-randomly is to compare two models of community assembly. Our approach is similar to those of Fox and Brown (1993) and Gillespie (2004), but instead of simulating community assembly under a null model (as in the former) or calculating probabilities based on random assembly only (as in the latter), we compare the direct probability of a given community structure under two different models of assembly. First, in a random assembly model, the probability of occurrence of a certain body size in a local community (here, Jamaica and Hispaniola) is directly proportional to the frequency of that body size within the source pool [here, the mainland (South American) treefrog species pool]. In an alternative model, underrepresented body sizes in the source pool have a greater chance of arriving in a community, perhaps due to competition among species of similar body sizes (e.g., although very large species of treefrogs are relatively rare, they may have greater odds than a medium-sized species of invading a community in which a medium-sized species already exists). This latter model will be called the “biased assembly” model for convenience. [Note that one could also view this as a test of random versus biased body size evolution, in which the Caribbean species are assumed to form a star phylogeny (cf. Schluter 1990). However, for brevity we will use the “assembly” terminology throughout.]

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One criticism of this approach would be that previous phylogenetic analyses indicated that most of the Caribbean species form a clade (Faivovich et al. 2005; Wiens et al. 2006b), and thus an assembly model of multiple invasions from South America is not realistic (see Losos 1990 for a similar example). Although we concur with this criticism, we emphasize that this test is only documenting the low probability of seeing the even body size spacing in Caribbean communities, given the frequencies of possible body sizes hylids could be; it is not meant to realistically model the actual assembly or evolution of Caribbean communities. We use this test

131 as part of many tests (see below) that each lend support to the idea that Caribbean communities
132 are highly structured with respect to body size.

133 The model of random community assembly was based on the hypergeometric probability
134 model, a simple model of sampling from a population without replacement (Sokal and Rohlf
135 1995). Here, the “population” is the pool of South American and Caribbean treefrogs, and the
136 “samples” are the treefrog communities on Jamaica and Hispaniola (see below). The
137 hypergeometric model is appropriate for sampling from a population that is divided up into
138 discrete categories, in this case body size classes. With two categories (e.g., 0 and 1), the
139 probability of obtaining d_0 species of body size type 0 in a sample of size n (Sokal and Rohlf
140 1995) is

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$$142 \quad P(x = d_0 | n, D_0, D_1) = \frac{\binom{D_0}{d_0} \binom{D_1}{n - d_0}}{\binom{D_0 + D_1}{n}}$$

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144 where D_0 and D_1 are the total number of species of type 0 and 1, respectively, within the sampled
145 population (e.g., source pool).

146 This can easily be extended to additional discrete categories. In this analysis, we use four
147 categories, one each for small, medium, large, and very large body size (based on Duellman
148 2001; see Table S3 for corresponding variable definitions). Thus, the probability of the body size
149 distribution within a community (d_0 small, d_1 medium, d_2 large, and $n - d_0 - d_1 - d_2$ very large),
150 given random sampling, the sampling distribution of body sizes (i.e., the source pool of tropical
151 South American and Caribbean treefrogs), and sample size (n = total species within the
152 community) is

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$$P(\mathbf{x} = \mathbf{d} \mid n, \mathbf{D}) = \frac{\binom{D_0}{d_0} \binom{D_1}{d_1} \binom{D_2}{d_2} \binom{D_3}{n - d_0 - d_1 - d_2}}{\binom{D_0 + D_1 + D_2 + D_3}{n}}$$

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156 where $\mathbf{d} = (d_0, d_1, d_2)$ and $\mathbf{D} = (D_0, D_1, D_2, D_3)$.

157 For the source pool, we used maximum reported SVL of the Caribbean species as well as
 158 South American hylids, since Caribbean treefrogs (both *Osteopilus* and *Hypsiboas*) are deeply
 159 nested within South American clades (Faivovich et al. 2005; Wiens et al. 2005, 2006b),
 160 suggesting that Caribbean treefrogs initially dispersed from northern South America.
 161 Additionally, using only Caribbean species, for example, may make our analyses susceptible to
 162 the “Narcissus effect” of community assembly analyses (Colwell and Winkler 1984). This effect
 163 results in an underestimation of the effect of competition, due to sampling from a post-
 164 competition source pool in which body sizes that have been excluded from the observed
 165 communities or never evolved due to competition aren’t included. Maximum SVL was obtained
 166 from literature sources for all nine Caribbean species as well as for 445 of the 453 South
 167 American species of the family Hylidae listed in Frost (2007). SVL data and references are
 168 presented in Table S1. (Note that we also conducted analyses using only maximum male SVL,
 169 but this gave qualitatively similar results). Here, we calculated the probability of seeing one
 170 small, one medium, one large, and one very large species in Jamaica, and one medium, one large,
 171 and two very large species in Hispaniola given 47 small, 86 medium, 52 large, and 15 very large
 172 species in mainland South America and the Caribbean [Table S3; note that the total number of
 173 species in our “species pool” was only 200, because we experienced computational difficulties
 174 using the full species pool of 454 (e.g., the normalization constant Q for the biased model was as
 175 high as 10^{763} during parameter estimation). Instead, we used 200 species, with the proportion of
 176 species in each body size category determined from all 454 species. Although this reduction of

177 the species pool may influence our results, it probably does so only slightly and should not
 178 qualitatively alter them, as further drastic reductions in the size of the assumed species pool (to
 179 100 and 50 species) gave quantitatively similar results as using 200 species (results not shown)].
 180 Hypergeometric probabilities of body size distributions for Jamaica and Hispaniola were
 181 calculated by hand.

182 The hypergeometric distribution is appropriate for obtaining the probability of the body
 183 size distribution within a community if no sampling bias exists (i.e., “random” assembly).
 184 However, if community assembly is influenced by processes that prevent certain types from
 185 entering, such as competition preventing similarly sized species from coexisting within a
 186 community, then a sampling bias would exist. To incorporate this bias, it is appropriate to use the
 187 non-central hypergeometric distribution (McCullagh and Nelder 1989). This distribution
 188 incorporates additional parameters to estimate the bias in sampling from the different categories.
 189 The sampling biases for sizes small, medium, large, and very large frogs are ω_0 , ω_1 , ω_2 , and ω_3 ,
 190 respectively. Thus, the probability of a particular community body size distribution conditioned
 191 on the sampling biases [$\boldsymbol{\omega} = (\omega_0, \omega_1, \omega_2, \omega_3)$], sampling distribution (\mathbf{D}), and number of species
 192 within the community (n) is

$$194 \quad P(\mathbf{x} = \mathbf{d} \mid n, \mathbf{D}, \boldsymbol{\omega}) = \omega_0^{d_0} \omega_1^{d_1} \omega_2^{d_2} \omega_3^{n-d_0-d_1-d_2} \frac{\binom{D_0}{d_0} \binom{D_1}{d_1} \binom{D_2}{d_2} \binom{D_3}{n-d_0-d_1-d_2}}{\binom{D_0+D_1+D_2+D_3}{n}} Q^{-1}$$

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 196 where Q is a normalization constant. This equation can be reparameterized in terms of ratios
 197 (following Munch and Conover 2003; see also McCullagh and Nelder 1989) comparing the bias
 198 parameters of classes 0-2 to class 3, as in $\psi_0 = \omega_0/\omega_3$. Additionally, the terms that do not depend

199 on d_0 , d_1 , and d_2 can be taken out of the equation because those constant terms will also be in the
 200 normalization constant and thus will cancel out. Doing this, we arrive at

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$$P(\mathbf{x} = \mathbf{d} | n, \mathbf{D}, \boldsymbol{\psi}) = Q^{-1} \left(\frac{\psi_0^{d_0} \psi_1^{d_1} \psi_2^{d_2}}{d_0! d_1! d_2! (n - d_0 - d_1 - d_2)! (D_0 - d_0)! (D_1 - d_1)! (D_2 - d_2)! (D_3 - n + d_0 + d_1 + d_2)!} \right)$$

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207 where the normalization constant, Q , is equal to

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$$Q = \sum_{i=0}^4 \sum_{j=0}^{4-i} \sum_{k=0}^{4-i-j} \left(\frac{\psi_0^i \psi_1^j \psi_2^k}{i! j! k! (n - i - j - k)! (D_0 - i)! (D_1 - j)! (D_2 - k)! (D_3 - n + i + j + k)!} \right)$$

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211 Note that the probabilities derived above are for a single community only. If we assume that the
 212 communities of Hispaniola and Jamaica were assembled independently (see Results), their
 213 probabilities can be multiplied for a combined likelihood of the body size distributions occurring
 214 on both islands. Unique bias parameters for each island (total of six free parameters) or a single
 215 parameter for each size category across the two islands (three free parameters) can be estimated.
 216 Here, we use the latter strategy because we expect that the same processes are driving the similar
 217 body size distributions on the two islands. Maximum-likelihood estimates (MLEs) and
 218 confidence intervals of the bias parameters were calculated in MatLab (ver. 6.5, The MathWorks
 219 Inc., Natick, MA). MatLab code is available from the authors upon request.

220 The two models were compared via a likelihood ratio (LR) test, which can be used to
 221 compare nested models (Edwards 1972). Here, the random assembly model is a special case of
 222 (i.e., nested within) the biased assembly model when all $\psi_i = 1$. The LR -test statistic is

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$$LR = 2 \ln \left(\frac{\ell_{Hisp}(\hat{\psi}_0, \hat{\psi}_1, \hat{\psi}_2) * \ell_{Jam}(\hat{\psi}_0, \hat{\psi}_1, \hat{\psi}_2)}{\ell_{Hisp}(\text{all } \psi_i = 1) * \ell_{Jam}(\text{all } \psi_i = 1)} \right)$$

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226 where $\hat{\psi}_i$ = maximum likelihood estimate of bias parameter i . Given the random assembly
227 model, this LR is expected to be asymptotically distributed as $\chi^2_{p,\alpha}$, where p = the number of free
228 parameters differing between the two models and α = the desired level of statistical significance.
229 In this case, $p = 3$ and we set $\alpha = 0.05$.

230 A limitation to this approach exists in that the body size categories are somewhat
231 arbitrary. Although we used those of Duellman (2001), which best captured the even spacing of
232 body sizes among Caribbean species, we could have used the categories of Savage (2002) or any
233 other arbitrary distinction. Indeed, despite the similar body size ratios among species on Jamaica
234 and Hispaniola (results not shown), the body sizes of Hispaniolan species are shifted higher than
235 Jamaican species, resulting in zero “small” but two “very large” species on Hispaniola (Table
236 S3). One could alter the model for use of continuous body size distributions, with probabilities of
237 biased assembly related to amount of distributional overlap. However, this also is problematic,
238 because one must specify a function relating the amount of overlap in intraspecific body size
239 distributions and the probability of biased assembly, which we see as equally arbitrary as discrete
240 categories (see also Dayan and Simberloff 2005).

241

242 *Phylogenetic Analyses*

243 *Taxon sampling*

244 A previous analysis (Wiens et al. 2006b) showed that eight of the nine species of
245 Caribbean treefrogs form a monophyletic group (*Osteopilus*) within the hylid clade Lophiohylini
246 (sensu Faivovich et al. 2005), but provided only weak support for relationships within *Osteopilus*
247 and among genera within Lophiohylini. To better estimate relationships within *Osteopilus*, we
248 obtained new molecular data for Lophiohylini. We sampled all nine treefrog species from the
249 Greater Antilles, including all *Osteopilus* and *Hypsiboas heilprini*. In addition, we included 14

250 other species of Lophiohylini, with at least one representative of each currently recognized genus
251 (Table S4). Finally, for outgroups to Lophiohylini, we sampled multiple species of each of the
252 other major clades of Hyalinae (Table S4; Faivovich et al. 2005; Wiens et al. 2006b).

253 Because we needed phylogenies with branch lengths to estimate the rate of body size
254 evolution in non-*Osteopilus* neotropical treefrogs, we also conducted Bayesian analyses (see
255 below) to estimate phylogenies of Cophomantini, the *Dendropsophus* clade (sensu Wiens et al.
256 2006b), Phyllomedusinae, and the *Scinax* clade (sensu Wiens et al. 2006b). We used data from
257 the 325-taxon data set for hylid frogs and outgroups assembled by Wiens et al. (2006b), which
258 had been analyzed using only parsimony. We analyzed these four clades separately to reduce the
259 number of taxa and thus make the analyses more tractable for Bayesian methods.

260

261 *Molecular data*

262 For our analysis within Lophiohylini, molecular data were sequenced from five
263 mitochondrial and four nuclear gene regions. The mitochondrial data included the ribosomal
264 small subunit [12S; 1016 base pairs (bp); also including adjacent tRNA-Phe and tRNA^{Val}],
265 cytochrome oxidase I (COI; 584 bp), cytochrome *b* (385 bp), NADH dehydrogenase subunit 1
266 (ND1; 1242 bp; including adjacent tRNA genes), and NADH dehydrogenase subunit 2 (ND2; 580
267 bp). The nuclear genes included proopiomelanocortin A (POMC; 601 bp), proto-oncogene
268 cellular myelocytomatosis exon 2 (*c-myc*; 417 bp), recombinase activating protein 1 (RAG-1;
269 1399 bp), and tensin 3 (TNS3; 512 bp). Additional molecular data were obtained from Faivovich
270 et al. (2005) for 13 taxa for which we lacked tissue samples (some non-*Osteopilus* Lophiohylini)
271 for three genes (12S, cytochrome *b*, RAG-1). In addition, their data for four additional genes
272 were added, both for those 13 species and for the 10 species included in both our sampling and
273 theirs. These additional genes included both mitochondrial [ribosomal large subunit (16S; 1646
274 bp)] and nuclear [tyrosinase (530 bp), sevenin-absentia (SIA; 307 bp), rhodopsin (316 bp)]
275 markers. All sequences for the Cophomantini, *Dendropsophus* clade, *Scinax* clade, and

276 Phyllomedusinae were obtained from Darst and Cannatella (2004), Faivovich et al. (2004, 2005),
277 and Wiens et al. (2005, 2006b). Because our taxon and gene sampling for these clades was
278 identical to that within the 325-taxon dataset of Wiens et al. (2006b), Genbank numbers for these
279 analyses can be found within the online appendix of Wiens et al. (2006b).

280 DNA was extracted from ethanol preserved tissues using standard methods and was
281 amplified using the polymerase chain reaction (PCR); specific protocols are available from the
282 authors upon request. Primer sequences are listed in Table S5. PCR products were purified and
283 sequenced directly using an ABI 3100 automated sequencer. Sequences were edited using SeqEd
284 1.0.3 (Applied Biosystems, Foster City, CA). GenBank numbers are given in Table S4, and
285 voucher specimen numbers can be found within each sequence's GenBank entry.

286 Sequence data from the current study and previous studies were combined into a single
287 matrix. Preliminary analyses of genes sequenced both for this study and by Faivovich et al.
288 (2005) (i.e., 12S, cytochrome *b*, RAG-1) supported the monophyly of different individuals within
289 species of *Osteopilus* species for which multiple individuals were sampled across studies (*O.*
290 *crucialis*, *O. dominicensis*, *O. septentrionalis*, and *O. vastus*). Therefore, we combined data
291 across studies for individual taxa so as to minimize the amount of missing data for any given
292 taxon. Nevertheless, our combination of data from different studies still resulted in missing data
293 for some taxa. Our analyses should be largely insensitive to this issue for a number of reasons.
294 First, within the group of interest (*Osteopilus*), little missing data existed for the nine genes for
295 which we generated DNA sequences. Secondly, both simulation (reviewed by Wiens 2006) and
296 empirical (Driskell et al. 2004, Wiens et al. 2005) studies indicate that even highly incomplete
297 taxa can be accurately placed within a phylogeny if the overall number of characters is large (i.e.,
298 thousands of characters, as is the case here), and in many cases the addition of taxa with
299 incomplete data can increase phylogenetic accuracy relative to excluding those taxa entirely
300 (Wiens 1998b, 2005).

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302 *DNA sequence alignment and phylogenetic analysis*

303 Alignment of protein-coding genes was straightforward. Sequence data were converted
304 into amino acid residues (for alignment only) and aligned by eye using Se-AL 1.d1 (Rambaut
305 1995). Ribosomal DNA and tRNA sequences were aligned first by Clustal X version 1.8.1
306 (Thompson et al. 1994). Adjustments were made by eye in PAUP* (ver. 4.0b10, Swofford 2002)
307 to conform to proposed secondary structure (see below). Clustal X alignments were conducted
308 using default settings (gap opening = 15; gap extension = 6.666; delay divergent sequences =
309 30%; transition:transversion = 50%), and regions that differed under different gap-opening
310 penalties (12.5, 15, and 17.5) were excluded from analyses. Secondary structure for ribosomal
311 DNA was inferred by comparing our sequences to the proposed structure for the hylid *Pseudacris*
312 *regilla* (12S; Graybeal 1997) and the ranid *Rana catesbeiana* (16S; Nagae 1988), as listed on the
313 European ribosomal RNA database (<http://www.psb.ugent.be/rRNA/>). Minor adjustments were
314 made to conform to nucleotide complementarity within stems, as well as to avoid placing
315 insertions and deletions within stems. Wiens et al. (2005) found that the secondary structure
316 model of 12S for *P. regilla* was very similar to those proposed for all non-hylid frog taxa. Thus,
317 we expect that these models should be accurate for our analyses within hylids.

318 Our primary estimate of phylogeny was based on a partitioned Bayesian analysis of all
319 the genes combined. However, both parsimony and Bayesian analyses of the separate and
320 combined genes were conducted. In order to test among genes for strongly supported
321 incongruence that might be indicative of incongruent gene histories (Wiens 1998a), we analyzed
322 the data from each gene separately, the mitochondrial data alone, and then the nuclear data alone.
323 Strong statistical support was considered to be a bootstrap value of $\geq 70\%$ (Hillis and Bull 1993)
324 or Bayesian posterior probability (Pp) of ≥ 0.95 (Wilcox et al. 2002; Alfaro et al. 2003;
325 Huelsenbeck and Rannala 2004). We found no strongly supported incongruence among genes or
326 sets of genes (see *Results*). As a result, we combined data from all 13 genes into one combined
327 analysis, because we consider the best estimate of phylogeny to come from a combined analysis

328 of all data (de Queiroz and Gatesy 2007). The combined data matrix, as well as our best estimate
329 of the topology of Lophiohyliini (see *Results*), has been archived within TreeBASE
330 (www.treebase.org) under study accession number S2202.

331 Parsimony analyses were conducted in PAUP*. We used a heuristic search with random-
332 taxon-addition and tree bisection-reconnection (TBR) branch swapping. To foster a thorough
333 search of tree space, we conducted 1,000 replicate searches and retained a single tree per
334 replicate. Statistical support for individual branches was assessed by non-parametric bootstrap
335 (Felsenstein 1985a). We performed 500 pseudoreplicate searches, using 10 random-taxon-
336 addition sequence replicates per pseudoreplicate, TBR branch swapping, and saving a single tree
337 per replicate.

338 Bayesian analyses were performed in MrBayes 3.1 (Huelsenbeck and Ronquist 2001).
339 All analyses consisted of two replicate Monte-Carlo Markov chains, each run for 6 million
340 generations total, with trees sampled every 1,000 generations. Visual observation of the log-
341 likelihood and parameter traces indicated that all analyses converged on the posterior distribution
342 before 200,000 generations in both replicates. Comparison of the log-likelihoods, parameter
343 means, and topology for each replicate and of the branch lengths and posterior probabilities for
344 each branch suggested that in all searches, both replicates reached the same posterior distribution.
345 Thus, after conservatively eliminating the trees produced from the first million generations of
346 each replicate as burn-in, the sampled trees from both replicates in each analysis were pooled to
347 estimate the phylogeny. Default priors were used, except that the gamma distribution shape
348 parameter prior was set to exponential (as suggested by Zwickl and Holder 2004) with a mean
349 (0.75) derived from maximum-likelihood or Bayesian posterior estimates from previous studies
350 of the same genes in other frogs (e.g., Symula et al. 2003; Fromhage et al. 2004; Crawford and
351 Smith 2005; van der Meijden et al. 2006). Our prior mean (0.75) is intermediate to those
352 estimates and is close to the estimated value for a combined analysis of nuclear and mitochondrial
353 data (van der Meijden et al. 2006).

354 Models for Bayesian analyses were chosen using a two-step process. First, models for
355 each gene were chosen with MrModeltest 2.2 (Nylander 2004), a modification of Modeltest
356 (Posada and Crandall 1998). The Akaike Information Criterion (AIC) was used to select the best
357 fitting model for each gene (Pol 2004; Posada and Buckley 2004). Stem and loop regions of the
358 12S and 16S genes were assigned their own model, as we expected stems and loops to evolve
359 under substantially different substitution models. Additionally, a separate model was assigned to
360 the tRNA preceding ND1. Models for protein-coding genes were assigned for the entire gene;
361 when within-gene partitions were specified (see below for partitioning strategy), each codon
362 partition was assigned the model of its gene but with its own codon-specific rate parameters (i.e.,
363 we did not test among classes of models due to the small size of some codon-specific partitions).

364 Secondly, we decided upon an optimal gene-partitioning strategy by conducting
365 successive analyses, with a different partitioning strategy for each analysis, and comparing the
366 model fit of each partitioning strategy by using the Bayes factor (Nylander et al. 2004). The four
367 partitioning strategies included, in increasing order of complexity: (1) one partition each for all
368 structural (ribosomal and tRNA) mitochondrial genes, all protein-coding mitochondrial genes,
369 and all nuclear genes, (2) a different partition for each gene, (3) separate partitions within
370 mitochondrial genes (stems and loops for 12S and 16S; codon positions for protein-coding genes)
371 but only a single partition for each nuclear gene, and (4) a separate partition for each codon
372 position within all protein-coding genes, as well as stems and loops for 12S and 16S. After each
373 analysis, model parameter traces were inspected to identify potential cases of overpartitioning
374 (diffuse, undersampled posterior distributions; Nylander et al. 2004) and/or non-identifiability of
375 parameters (Rannala 2002; Castoe et al. 2004). Finally, the harmonic mean of the ln-likelihoods
376 of the trees from the pooled posterior sample (i.e., post-burn-in trees) was calculated to compare
377 partitioning strategies using the Bayes factor (Nylander et al. 2004). As in previous papers (e.g.,
378 Nylander et al. 2004), we considered a Bayes factor of > 10 to be very strong evidence in favor of
379 a higher-partitioned model.

405 *Osteopilus* community evolution may represent the early stages of older treefrog assemblages,
406 which are represented by South American communities (see *Discussion*).

407 Comparing rates of evolution requires trees with comparable branch lengths (i.e., in the
408 same units) for all the relevant clades. Because somewhat different molecular data sets were
409 available for different clades (e.g., Lophiohylini vs. other clades), we obtained comparable branch
410 lengths across all clades by estimating a chronogram separately for each clade and then
411 combining branch lengths across the tree by using time as a common currency (see Wiens et al.
412 2006a). We converted the molecular branch lengths from the Bayesian analysis of the combined
413 data into units of time using a penalized likelihood method (PL; Sanderson 2002) in the program
414 *r8s* (version 1.6 for Unix; Sanderson 2003). PL “smooths” out the rate heterogeneity in
415 molecular branch lengths, producing an ultrametric tree. When combined with dates for one or
416 more nodes, the procedure can produce branch lengths in units of time.

417 For this analysis, we used the “allcompat” command when summarizing trees from the
418 posterior distribution for each Bayesian phylogenetic analysis. This command produces a fully-
419 bifurcating tree, but one which includes some clades with $P_p < 0.50$. We did this to eliminate
420 polytomies, which are potentially problematic for PL analyses. Although some nodes were
421 therefore resolved but poorly supported, we do not expect this to be a problem for two reasons.
422 First, most trees (4 of 5) had few nodes with $P_p < 0.50$. Second, the group with the most poorly
423 resolved clades, the *Dendropsophus* clade, had very low variability in SVL among species, such
424 that alternative resolutions of weakly resolved nodes should not greatly affect the inferred rate of
425 body size evolution.

426 We used branch lengths from the Bayesian analysis of the combined data. To determine
427 the optimal level of rate smoothing, we used the Truncated-Newton (TN) algorithm in *r8s*, with
428 cross-validation assessment of potential smoothing parameters ranging from 10^{-1} to $10^{4.5}$,
429 evaluated at each exponential increment of 0.5.

430 For each of our clades we used the age of each clade estimated by Wiens et al. (2006b) to
431 calibrate the ultrametric trees produced by *r8s*. The chronogram of Wiens et al. (2006b) was
432 based on 9 fossil calibration points, including all relevant hylid fossils. Wiens et al. (2006b)
433 presented two sets of dates (age of Neobatrachia of 100 or 160 million years), and we used both
434 to estimate two sets of divergence times for each clade.

435 To calculate rates of body-size evolution, we used the likelihood method of O’Meara et
436 al. (2006) in the program *Brownie*. The parameter calculated by this method (σ^2) is the variance
437 of character change that accumulates at each step of a Brownian motion random-walk model of
438 trait evolution (Felsenstein 1985b). Because this parameter influences the rate at which the
439 overall character variance in a clade accumulates, it can be thought of as the rate of
440 morphological evolution (Martins 1994; Collar et al. 2005). Rates were calculated for (1)
441 *Osteopilus*, (2) Lophiohylini exclusive of *Osteopilus*, (3) Cophomantini, (4) the genus
442 *Dendropsophus*, (5) the *Scinax* clade, (6) Phyllomedusinae, and (7) all major South American
443 clades combined exclusive of *Osteopilus* (i.e., groups 2-6 above). The phylogeny for the last
444 group was constructed with a “supertree” approach (Sanderson et al. 1998). Individually-
445 estimated Bayesian phylogenies and chronograms (see above) for groups 2-6 were manually
446 added to a dated “backbone” chronogram from Wiens et al. (2006b). Estimating a phylogeny,
447 branch lengths, and chronogram for all taxa simultaneously would have been difficult given the
448 large number of taxa, large number of diverse genes, and complex models of character evolution
449 (i.e., Bayesian analysis of the entire tree was not possible due to the prohibitive computational
450 time; see Wiens et al. 2006b for an explanation).

451 To test for a significantly higher rate of body-size evolution in *Osteopilus*, we conducted
452 a censored test (O’Meara et al. 2006) between *Osteopilus* and other South American hylids, from
453 which *Osteopilus* is derived and in which relative conservatism in body size within clades seems
454 to occur. Censored tests prune the clade of interest (here, *Osteopilus*) from the tree, estimate rates
455 for the pruned subtree and for the larger tree without the subtree, and then compare the

456 likelihoods of the one-rate (for the entire tree) and two-rate (as above) models. To compare the
457 likelihoods, we used a likelihood ratio (*LR*) test. O'Meara et al. (2006) noted that the *LR* can be
458 biased when comparing groups of different sample size (numbers of species), as we have here.
459 However, they stated that the bias would tend to underestimate the rate for the smaller group. In
460 our case, underestimating the rate in *Osteopilus* would make our results more conservative.

461 For body size we used the maximum reported SVL for each species, irrespective of sex
462 (to maximize the amount of data available). However, we do not expect this to systematically
463 bias our results, as sexual dimorphism occurs to some extent in all major hyliid clades and the
464 absence of sex-specific size data was dependent on literature sources, rather than clade-specific.
465 An analysis using maximum male size gave qualitatively identical results (not shown).
466 Maximum SVL was ln-transformed before analysis to model rate of proportional change, rather
467 than absolute change (i.e., additive changes in a ln-transformed variable are equivalent to
468 multiplicative changes in the original variable) (O'Meara et al. 2006). We obtained SVL data
469 from the literature for 171 of the 175 species that were included in our phylogeny. Our
470 phylogenetic sampling from all clades except *Osteopilus* was not complete; thus, a concern exists
471 that our results are not representative of body size evolution in the undersampled clades.
472 However, we expect our results to be conservative for two reasons. First, we sampled some of
473 the largest and smallest known species from each clade. When coupled with incomplete taxon
474 sampling, we expect that our inclusion of the full range of body sizes within these clades will
475 inflate the rate for the non-*Osteopilus* clades, thus reducing the potential significance of a high
476 rate of body size evolution in *Osteopilus*. Secondly, common distributional statistics (mean,
477 median, and variance) from our samples approximate those for all members of each clade, for
478 which body sizes were obtained for the community assembly analyses (see above). Thus, we
479 suggest that our incomplete taxon sampling did not influence our results in any predictable
480 manner, except perhaps to make them more conservative.

481 A significantly higher rate of body-size evolution in *Osteopilus* would imply a higher
482 probability of seeing the observed body-size extremes than if body size evolved in *Osteopilus*
483 under the lower rate for all South American and Caribbean hylids. However, we note that this, by
484 itself, is not a direct test of how unlikely it is that we see such extremes. Thus, we calculated a
485 simple odds ratio of the probability of seeing such extremes given the rate of body-size evolution
486 from the two-rate model (a separate rate is estimated for *Osteopilus*) versus the one-rate model
487 (one rate for all South American and Caribbean hylids). To do this, we calculated the probability
488 of obtaining body sizes equal to or more extreme than the smallest and largest species on Jamaica
489 and Hispaniola (four total) by sampling from a normal distribution with mean equal to the mean
490 of all *Osteopilus* and variance obtained in one of two ways. In both cases, the variance was
491 calculated as the product of the root-to-tip distance on the ultrametric *Osteopilus* phylogeny and
492 the rate of evolution. In the first case, we used the rate estimated for *Osteopilus* in the above two-
493 rate model of evolution. In the second, we used the rate estimated from the one-rate model. We
494 then calculated an odds ratio (simply the ratio of the two probabilities) to compare the probability
495 of seeing the observed body size extremes within the Caribbean based on the two rates.

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1110 FIGURE LEGEND

1111 Figures S1 and S2. Phylogeny of South American Hylidae, estimated by (1) separate Bayesian
1112 analyses of each major South American clade, (2) converting branch lengths into units of time
1113 using the program r8s, and (3) connecting these clades together by placing on an ultrametric
1114 phylogeny (with branch lengths in units of time) of the Hylidae, as estimated by Wiens et al.
1115 (2006b). See methods for further details. Branch lengths are in units of time, with the upper and
1116 lower scale bars reflecting divergence times estimated using the younger and older (respectively)
1117 sets of calibration dates. Nodal values indicate Bayesian posterior probabilities (Pp). Nodal
1118 asterisks indicate Pp = 1.0. Note that (1) deep nodes do not show nodal support values because
1119 we did not estimate relationships among the major clades in this study, and (2) two major hylid
1120 clades, the Pelodyadinae (Australian treefrogs) and the Middle American clade, are not included
1121 on this phylogeny, as they were not appropriate for our rate of body size evolution analyses.

1122 Table S1. Maximum snout-to-vent length (SVL) data used to determine the species pool of the
 1123 community analyses. SVL_{max} in millimeters (mm).

Species	SVL _{max}	Reference
<i>"Hyla" alboguttata</i>	46	Duellman 1978
<i>"Hyla" warreni</i>	36.2	Duellman and Hoogmoed 1992
<i>Agalychnis litodryas</i>	70.2	Duellman 2001
<i>Agalychnis spurrelli</i>	92.8	Cochran and Goin 1970
<i>Aparasphenodon bokermanni</i>	71.1	Pombal 1993
<i>Aparasphenodon brunoi</i>	75	Cochran 1955
<i>Aparasphenodon venezolanus</i>	58	Rivero 1961
<i>Aplastodiscus albofrenatus</i>	40	Lutz 1973
<i>Aplastodiscus albosignatus</i>	52	Lutz 1973
<i>Aplastodiscus arildae</i>	41.6	Heyer et al. 1990
<i>Aplastodiscus callipygius</i>	50.7	Cruz and Peixoto "1984" [1985]
<i>Aplastodiscus cavicola</i>	37.3	Cruz and Peixoto "1984" [1985]
<i>Aplastodiscus cochranae</i>	50.3	Garcia et al. 2001
<i>Aplastodiscus ehrhardti</i>	39.1	Cruz and Peixoto "1985" [1987]
<i>Aplastodiscus eugenioi</i>	39	Carvalho-e-Silva and Carvalho-e-Silva 2005
<i>Aplastodiscus flumineus</i>	50.4	Cruz and Peixoto "1984" [1985]
<i>Aplastodiscus ibirapitanga</i>	43.4	Cruz Pimenta and Silvano 2003
<i>Aplastodiscus leucopygius</i>	45.1	Cruz and Peixoto "1984" [1985]
<i>Aplastodiscus musicus</i>	50	Cochran 1955
<i>Aplastodiscus perviridis</i>	46.1	Garcia et al. 2001
<i>Aplastodiscus sibilatus</i>	33.6	Cruz et al. 2003
<i>Aplastodiscus weygoldti</i>	41.7	Cruz and Peixoto "1985" [1987]
<i>Argenteohyla siemersi</i>	70	Cei 1980
<i>Bokermannohyla ahenea</i>	56.7	Napoli and Caramaschi 2004
<i>Bokermannohyla alvarengai</i>	80	Lutz 1973
<i>Bokermannohyla astartea</i>	44.1	Heyer et al. 1990
<i>Bokermannohyla caramaschii</i>	70	Napoli 2005
<i>Bokermannohyla carvalhoi</i>	67	Peixoto 1981
<i>Bokermannohyla circumdata</i>	71	Lutz 1973
<i>Bokermannohyla claresignata</i>	61	Lutz 1973
<i>Bokermannohyla clepsydra</i>	39	Cochran 1955
<i>Bokermannohyla diamantina</i>	51.7	Napoli and Juncá 2006
<i>Bokermannohyla feioi</i>	40.3	Napoli and Caramaschi 2004
<i>Bokermannohyla gouveai</i>	69	Pombal and Haddad 1993
<i>Bokermannohyla hylax</i>	63.4	Heyer et al. 1990
<i>Bokermannohyla ibitiguara</i>	44.1	Cardoso 1983

<i>Bokermannohyla ibitipoca</i>	42.7	Caramaschi and Feio 1990
<i>Bokermannohyla izecksohni</i>	50.8	Jim and Caramaschi 1979
<i>Bokermannohyla langei</i>	66	Lutz 1973
<i>Bokermannohyla lucianae</i>	49.2	Napoli and Silva-Pimenta 2003
<i>Bokermannohyla luctuosa</i>	60.6	Pombal and Haddad 1993
<i>Bokermannohyla martinsi</i>	64	Lutz 1973
<i>Bokermannohyla nanuzae</i>	42	Bokermann and Sazima 1973b
<i>Bokermannohyla pseudopseudis</i>	44	Lutz 1973
<i>Bokermannohyla ravida</i>	47.6	Caramaschi et al. 2001
<i>Bokermannohyla saxicola</i>	45	Lutz 1973
<i>Bokermannohyla sazimai</i>	36.4	Caramaschi and Feio 1990
<i>Bokermannohyla vulcaniae</i>	53.3	de Vasconcelos and Giaretta 2003
<i>Corythomantis greeningi</i>	86.5	Jared et al. 1999
<i>Cruziohyla calcarifer</i>	78.5	Duellman 2001
<i>Cruziohyla craspedopus</i>	73	Hoogmoed and Cadle 1990
<i>Dendropsophus acreanus</i>	35	Lutz 1973
<i>Dendropsophus allenorum</i>	26.2	Duellman 2005
<i>Dendropsophus amicornum</i>	22.6	Mijares-Urrutia 1998
<i>Dendropsophus anataliasiasi</i>	21.8	Napoli and Caramaschi 1999a
<i>Dendropsophus anceps</i>	42	Lutz 1973
<i>Dendropsophus aperomeus</i>	25	Duellman 1982
<i>Dendropsophus araguaya</i>	20.5	Napoli and Caramaschi 1998
<i>Dendropsophus baileyi</i>	23	Cochran 1952
<i>Dendropsophus battersbyi</i>	33	Rivero 1961
<i>Dendropsophus berthae</i>	24	Lutz 1973
<i>Dendropsophus bifurcus</i>	35	Duellman 1978
<i>Dendropsophus bipunctatus</i>	28	Lutz 1973
<i>Dendropsophus bogerti</i>	33.3	Cochran and Goin 1970
<i>Dendropsophus bokermanni</i>	28	Duellman 1978
<i>Dendropsophus branneri</i>	21	Lutz 1973
<i>Dendropsophus brevifrons</i>	25	Duellman 1978
<i>Dendropsophus cachimbo</i>	24.2	Napoli and Caramaschi 1999a
<i>Dendropsophus carnifex</i>	32.5	Duellman 1969
<i>Dendropsophus cerradensis</i>	19.3	Napoli and Caramaschi 1998
<i>Dendropsophus coffeus</i>	26	Köhler et al. 2005
<i>Dendropsophus columbianus</i>	35.4	Duellman and Trueb 1983
<i>Dendropsophus cruzi</i>	25	Pombal and Bastos 1998
<i>Dendropsophus decipiens</i>	21	Lutz 1973
<i>Dendropsophus delarivai</i>	26.6	Köhler and Lötters 2001b
<i>Dendropsophus dutrai</i>	38.1	Gomes and Peixoto 1996
<i>Dendropsophus ebraccatus</i>	36.8	Cochran and Goin 1970

<i>Dendropsophus elegans</i>	35.7	Bastos and Haddad 1996
<i>Dendropsophus elianae</i>	26	Napoli and Caramaschi 2000
<i>Dendropsophus gaucheri</i>	19.2	Lescure and Marty 2000 Guyane
<i>Dendropsophus giesleri</i>	31.5	Weygoldt and Peixoto 1987
<i>Dendropsophus grandisonae</i>	20.8	Goin 1966
<i>Dendropsophus gryllatus</i>	30.6	Duellman 1973
<i>Dendropsophus haddadi</i>	24	Bastos and Pombal 1996
<i>Dendropsophus haraldschultzi</i>	25	Rodríguez and Duellman 1994
<i>Dendropsophus jimi</i>	22.3	Napoli and Caramaschi 1999b
<i>Dendropsophus joannae</i>	20.6	Köhler and Lötters 2001a
<i>Dendropsophus koechlini</i>	29	Duellman 2005
<i>Dendropsophus labialis</i>	56	Amezquita 1999
<i>Dendropsophus leali</i>	28	Duellman 2005
<i>Dendropsophus leucophyllatus</i>	50	Lescure and Marty 2000
<i>Dendropsophus limai</i>	19	Bokermann 1962a
<i>Dendropsophus luteoocellatus</i>	31	Rivero 1961
<i>Dendropsophus marmoratus</i>	56	Rodríguez and Duellman 1994
<i>Dendropsophus mathiassoni</i>	21.4	Cochran and Goin 1970
<i>Dendropsophus melanargyreus</i>	50	Lescure and Marty 2000
<i>Dendropsophus meridensis</i>	42	Rivero 1961
<i>Dendropsophus meridianus</i>	23	Lutz 1973
<i>Dendropsophus microcephalus</i>	30.9	Duellman 2001
<i>Dendropsophus microps</i>	33	Lutz 1973
<i>Dendropsophus minusculus</i>	24	Duellman 1997
<i>Dendropsophus minutus</i>	25.9	Duellman 1997
<i>Dendropsophus miyatai</i>	20.4	Vigle and Goberdhan-Vigle 1990
<i>Dendropsophus nahdereri</i>	49	Lutz 1973
<i>Dendropsophus nanus</i>	23.8	Prado and Haddad 2005
<i>Dendropsophus novaisi</i>	32	Lutz 1973
<i>Dendropsophus oliveirai</i>	20	Carvalho-e-Silva et al. 2003
<i>Dendropsophus padreluna</i>	34.4	Kaplan and Ruiz 1997
<i>Dendropsophus parviceps</i>	27	Duellman 1978
<i>Dendropsophus pauiniensis</i>	24	Heyer 1977
<i>Dendropsophus pelidna</i>	38.5	Duellman 1989
<i>Dendropsophus phlebodes</i>	27.8	Duellman 2001
<i>Dendropsophus praestans</i>	31.5	Duellman and Trueb 1983
<i>Dendropsophus pseudomeridianus</i>	22.7	Cruz et al. 2000
<i>Dendropsophus rhea</i>	20.7	Napoli and Caramaschi 1999b
<i>Dendropsophus rhodopeplus</i>	29	Duellman 1978
<i>Dendropsophus riveroi</i>	23	Rodríguez and Duellman 1994
<i>Dendropsophus rossalleni</i>	23	Rodríguez and Duellman 1994

<i>Dendropsophus rubicundulus</i>	25.4	Napoli and Caramaschi 1999a
<i>Dendropsophus ruschii</i>	29	Weygoldt and Peixoto 1987
<i>Dendropsophus sanborni</i>	20	Lutz 1973
<i>Dendropsophus sarayacuensis</i>	37	Rodríguez and Duellman 1994
<i>Dendropsophus schubarti</i>	25.5	Duellman 2005
<i>Dendropsophus seniculus</i>	43	Lutz 1973
<i>Dendropsophus soaresi</i>	31.7	Caramaschi and Jim 1983
<i>Dendropsophus stingi</i>	26.2	Kaplan 1994
<i>Dendropsophus studerae</i>	29.6	Carvalho-e-Silva et al. 2003
<i>Dendropsophus subocularis</i>	26.1	Duellman and Crump 1974
<i>Dendropsophus timbeba</i>	22.5	Martins and Cardoso 1987
<i>Dendropsophus tintinnabulum</i>	20	Lutz 1973
<i>Dendropsophus triangulum</i>	42	Rodríguez and Duellman 1994
<i>Dendropsophus tritaeniatus</i>	22	Bokermann 1965
<i>Dendropsophus virolinensis</i>	32.2	Kaplan and Ruiz 1997
<i>Dendropsophus walfordi</i>	19.5	Bokermann 1962b
<i>Dendropsophus werneri</i>	23	Lutz 1973
<i>Dendropsophus xapuriensis</i>	18.4	Martins and Cardoso 1987
<i>Dendropsophus yaracuyanensis</i>	36.6	Mijares-Urrutia and Rivero 2000
<i>Ecnomiohyla phantasmagoria</i>	109.7	Cochran and Goin 1970
<i>Ecnomiohyla tuberculosa</i>	90	Rodríguez and Duellman 1994
<i>Hylomantis aspera</i>	41.7	Cruz 1988
<i>Hylomantis buckleyi</i>	54.7	Cannatella 1980
<i>Hylomantis danieli</i>	80.8	Ruiz-Carranza et al. 1988
<i>Hylomantis granulosa</i>	38.7	Cruz 1988
<i>Hylomantis hulli</i>	37.1	Duellman and Mendelson 1995
<i>Hylomantis medinai</i>	49	Funkhouser 1962
<i>Hylomantis psilopygion</i>	47.3	Cannatella 1980
<i>Hyloscirtus albopunctulatus</i>	41.5	Cochran and Goin 1970
<i>Hyloscirtus alytolylax</i>	43.9	Duellman 1972
<i>Hyloscirtus armatus</i>	74.5	Duellman et al. 1997
<i>Hyloscirtus bogotensis</i>	57.8	Ruiz-Carranza and Lynch 1982
<i>Hyloscirtus callipeza</i>	33	Duellman 1989
<i>Hyloscirtus caucanus</i>	63.3	Ardila-Robayo et al. 1993
<i>Hyloscirtus charazani</i>	55	Vellard 1970
<i>Hyloscirtus denticulatus</i>	52.2	Duellman 1972
<i>Hyloscirtus estevesi</i>	22	Rivero 1968
<i>Hyloscirtus jahni</i>	34.5	Rivero 1961
<i>Hyloscirtus larinopygion</i>	55.6	Duellman and Berger 1982
<i>Hyloscirtus lascinius</i>	47	Rivero 1969
<i>Hyloscirtus lindae</i>	68.1	Duellman and Altig 1978

<i>Hyloscirtus lynchi</i>	46.4	Ruiz-Carranza and Ardila-Robayo 1991
<i>Hyloscirtus pacha</i>	66.5	Duellman and Hillis 1990
<i>Hyloscirtus palmeri</i>	50	Duellman 2001
<i>Hyloscirtus pantostictus</i>	64.1	Duellman and Berger 1982
<i>Hyloscirtus phyllognathus</i>	39.3	Duellman 1972
<i>Hyloscirtus piceigularis</i>	41	Ruiz-Carranza and Lynch 1982
<i>Hyloscirtus platydactylus</i>	42.3	Duellman 1972
<i>Hyloscirtus psarolaimus</i>	63.4	Duellman and Hillis 1990
<i>Hyloscirtus ptychodactylus</i>	77.3	Duellman and Hillis 1990
<i>Hyloscirtus sarampiona</i>	68.8	Ruiz-Carranza and Lynch 1982
<i>Hyloscirtus simmonsii</i>	44.3	Duellman 1989
<i>Hyloscirtus staufferorum</i>	59.7	Duellman and Coloma 1993
<i>Hyloscirtus tapichalaca</i>	66.5	Kizirian et al. 2003
<i>Hyloscirtus torrenticola</i>	35.5	Duellman and Altig 1978
<i>Hypsiboas albomarginatus</i>	62	Lutz 1973
<i>Hypsiboas alboniger</i>	64.7	Duellman et al. 1997
<i>Hypsiboas albopunctatus</i>	75	Lutz 1973
<i>Hypsiboas alemani</i>	30.5	Rivero 1964
<i>Hypsiboas andinus</i>	62.7	Duellman et al. 1997
<i>Hypsiboas atlanticus</i>	40.2	Caramaschi and Velosa 1996
<i>Hypsiboas balzani</i>	52.3	Duellman et al. 1997
<i>Hypsiboas beckeri</i>	33.9	Caramaschi and Cruz 2004
<i>Hypsiboas benitezi</i>	37	Rivero 1961
<i>Hypsiboas bischoffi</i>	69	Lutz 1973
<i>Hypsiboas boans</i>	132	Duellman 2001
<i>Hypsiboas buriti</i>	31.9	Caramaschi and Cruz 1999
<i>Hypsiboas caingua</i>	33.1	Lavilla and Cei 2001
<i>Hypsiboas calcaratus</i>	61	Rodríguez and Duellman 1994
<i>Hypsiboas callipleura</i>	45	Boulenger 1902
<i>Hypsiboas cinerascens</i>	54	Rodríguez and Duellman 1994
<i>Hypsiboas cipoensis</i>	37.5	Cruz and Caramaschi 1998
<i>Hypsiboas cordobae</i>	50	Lutz 1973
<i>Hypsiboas crepitans</i>	75	Lutz 1973
<i>Hypsiboas cymbalum</i>	49	Lutz 1973
<i>Hypsiboas dentei</i>	54	Lescure and Marty 2000
<i>Hypsiboas ericae</i>	36.9	Caramaschi and Cruz 2000
<i>Hypsiboas exastis</i>	99	Caramaschi and Rodrigues 2003
<i>Hypsiboas faber</i>	104	Heyer et al. 1990
<i>Hypsiboas fasciatus</i>	51	Rodríguez and Duellman 1994
<i>Hypsiboas freicanecae</i>	42.2	Carnaval and Peixoto 2004
<i>Hypsiboas fuentei</i>	57	Goin and Goin 1968

<i>Hypsiboas geographicus</i>	85	Lescure and Marty 2000
<i>Hypsiboas goianus</i>	37.6	Cruz and Caramaschi 1998
<i>Hypsiboas guentheri</i>	47	Lutz 1973
<i>Hypsiboas heilprini</i>	54.3	Trueb and Tyler 1974
<i>Hypsiboas hobbsi</i>	42.5	Cochran and Goin 1970
<i>Hypsiboas hutchinsi</i>	56	Pyburn and Hall 1984
<i>Hypsiboas joaquina</i>	51.5	Lutz 1973
<i>Hypsiboas lanciformis</i>	94	Rodríguez and Duellman 1994
<i>Hypsiboas latistriatus</i>	51.6	Caramaschi and Cruz 2004
<i>Hypsiboas lemai</i>	35.4	Duellman 1997
<i>Hypsiboas leptolineatus</i>	32.2	Cruz and Caramaschi 1998
<i>Hypsiboas leucocheilus</i>	81.2	Caramaschi and Niemeyer 2003
<i>Hypsiboas lundii</i>	76	Bokermann and Sazima 1973b
<i>Hypsiboas marginatus</i>	51.1	Caramaschi and Cruz 2000
<i>Hypsiboas marianitae</i>	56.8	Duellman et al. 1997
<i>Hypsiboas melanopleura</i>	47.7	Duellman et al. 1997
<i>Hypsiboas microderma</i>	34	Rodríguez and Duellman 1994
<i>Hypsiboas multifasciatus</i>	75	Lescure and Marty 2000
<i>Hypsiboas nympa</i>	36	Faivovich et al. 2006
<i>Hypsiboas ornatissimus</i>	42	Lescure and Marty 2000
<i>Hypsiboas palaestes</i>	50.9	Duellman et al. 1997
<i>Hypsiboas pardalis</i>	75	Lutz 1973
<i>Hypsiboas pellucens</i>	61.6	Cochran and Goin 1970
<i>Hypsiboas phaeopleura</i>	36.9	Caramaschi and Cruz 2000
<i>Hypsiboas polytaenius</i>	41.5	Cruz and Caramaschi 1998
<i>Hypsiboas pombali</i>	65.7	Caramaschi et al. 2004b
<i>Hypsiboas prasinus</i>	55	Cochran 1955
<i>Hypsiboas pugnax</i>	80	Duellman 2001
<i>Hypsiboas pulchellus</i>	50	Lutz 1973
<i>Hypsiboas pulidoi</i>	23.2	Rivero 1968
<i>Hypsiboas punctatus</i>	41.7	Duellman 1974a
<i>Hypsiboas raniceps</i>	82	Caramaschi and Niemeyer 2003
<i>Hypsiboas rhythmicus</i>	34.2	Señaris and Ayarzagüena 2002
<i>Hypsiboas riojanus</i>	56	Cei 1980
<i>Hypsiboas roraima</i>	45.5	Duellman and Hoogmoed 1992
<i>Hypsiboas rosenbergi</i>	93.2	Duellman 2001
<i>Hypsiboas rubracylus</i>	50.4	Cochran and Goin 1970
<i>Hypsiboas secedens</i>	57	Lutz 1973
<i>Hypsiboas semiguttatus</i>	41.6	Caramaschi and Cruz 2000
<i>Hypsiboas sibleszi</i>	35.7	Duellman 1997
<i>Hypsiboas stenocephalus</i>	30.4	Caramaschi and Cruz 1999

<i>Hypsiboas varelae</i>	52.9	Lavilla and Cei 2001
<i>Hypsiboas wavrini</i>	113	Hoogmoed 1990
<i>Itapotihyla langsdorffii</i>	99	Lutz 1973
<i>Lysapsus caraya</i>	16.5	Gallardo 1964
<i>Lysapsus laevis</i>	21	Parker 1935
<i>Lysapsus limellum</i>	23	Prado and Haddad 2005
<i>Myersiohyla aromatica</i>	46.6	Ayarzagüena and Señaris 1993
<i>Myersiohyla inparquesi</i>	50.4	Ayarzagüena and Señaris 1993
<i>Myersiohyla kanaima</i>	49.1	Duellman and Hoogmoed 1992
<i>Myersiohyla loveridgei</i>	42	Rivero 1961
<i>Nyctimantis rugiceps</i>	67.5	Duellman and Trueb 1976
<i>Osteocephalus buckleyi</i>	64.1	Cochran and Goin 1970
<i>Osteocephalus cabrerai</i>	62.4	Duellman and Mendelson 1995
<i>Osteocephalus carri</i>	64.1	Cochran and Goin 1970
<i>Osteocephalus deridens</i>	50.6	Jungfer et al. 2000
<i>Osteocephalus elkejungingerae</i>	22	Henle 1981
<i>Osteocephalus exophthalmus</i>	32.7	Smith and Noonan 2001
<i>Osteocephalus fuscifacies</i>	53.2	Jungfer et al. 2000
<i>Osteocephalus heyeri</i>	47.7	Lynch 2002
<i>Osteocephalus leoniae</i>	40.1	Faivovich et al. 2006
<i>Osteocephalus leprieurii</i>	62	Rodríguez and Duellman 1994
<i>Osteocephalus mutabor</i>	75.7	Jungfer and Hodl 2002
<i>Osteocephalus oophagus</i>	62.7	Lescure and Marty 2000
<i>Osteocephalus pearsoni</i>	54.7	Trueb and Duellman 1971
<i>Osteocephalus planiceps</i>	89.2	Ron and Pramuk 1999
<i>Osteocephalus subtilis</i>	38.8	Martins and Cardoso 1987
<i>Osteocephalus taurinus</i>	103.9	Ron and Pramuk 1999
<i>Osteocephalus verruciger</i>	73	D. S. Moen unpublished
<i>Osteocephalus yasuni</i>	61.9	Ron and Pramuk 1999
<i>Osteopilus brunneus</i>	76	Schwartz and Henderson 1991
<i>Osteopilus crucialis</i>	122	Schwartz and Henderson 1991
<i>Osteopilus dominicensis</i>	98.7	Trueb and Tyler 1974
<i>Osteopilus marianae</i>	40	Schwartz and Henderson 1991
<i>Osteopilus pulchrilineatus</i>	42.8	Trueb and Tyler 1974
<i>Osteopilus septentrionalis</i>	140	Schwartz and Henderson 1991
<i>Osteopilus vastus</i>	141.9	Trueb and Tyler 1974
<i>Osteopilus wilderi</i>	28.7	Trueb and Tyler 1974
<i>Phasmahyla cochranae</i>	33.9	Heyer et al. 1990
<i>Phasmahyla exilis</i>	34.5	Cruz 1980
<i>Phasmahyla guttata</i>	35	Cochran 1955
<i>Phasmahyla jandaia</i>	32	Bokermann and Sazima 1978

<i>Phrynohyas coriacea</i>	67.6	Lescure and Marty 2000
<i>Phrynohyas hadroceps</i>	60	Lescure and Marty 2000
<i>Phrynohyas imitatrix</i>	70.1	Lutz 1973
<i>Phrynohyas lepida</i>	58.7	Pombal et al. 2003
<i>Phrynohyas mesophaea</i>	100	Lutz 1973
<i>Phrynohyas resinifictrix</i>	100	Lescure and Marty 2000
<i>Phrynohyas venulosa</i>	113.7	Duellman 2001
<i>Phrynomedusa appendiculata</i>	37.4	Heyer et al. 1990
<i>Phrynomedusa bokermanni</i>	46	Cruz 1991
<i>Phrynomedusa fimbriata</i>	45.6	Cruz 1985
<i>Phrynomedusa marginata</i>	31	Izecksohn and Cruz 1976
<i>Phrynomedusa vanzolinii</i>	36.5	Cruz 1991
<i>Phyllodytes acuminatus</i>	24.5	Bokermann 1966b
<i>Phyllodytes auratus</i>	35	Murphy 1997
<i>Phyllodytes brevirostris</i>	24	Peixoto and Cruz 1988
<i>Phyllodytes edelmi</i>	28.7	Peixoto et al. 2003
<i>Phyllodytes gyrinaethes</i>	27.9	Peixoto et al. 2003
<i>Phyllodytes kautskyi</i>	38	Peixoto and Cruz 1988
<i>Phyllodytes luteolus</i>	23	Bokermann 1966b
<i>Phyllodytes melanomystax</i>	26.6	Caramaschi et al. 1992
<i>Phyllodytes punctatus</i>	22.8	Caramaschi and Peixoto 2004
<i>Phyllodytes tuberculosus</i>	26	Bokermann 1966b
<i>Phyllodytes wuchereri</i>	27.1	Caramaschi et al. 2004a
<i>Phyllomedusa atelopoides</i>	45	Duellman 2005
<i>Phyllomedusa azurea</i>	44.4	Caramaschi 2006
<i>Phyllomedusa bahiana</i>	74.5	Pombal and Haddad 1992
<i>Phyllomedusa baltea</i>	63.5	Cannatella 1982
<i>Phyllomedusa bicolor</i>	135	Lescure et Marty 2000
<i>Phyllomedusa boliviana</i>	76.4	Vaira 2001
<i>Phyllomedusa burmeisteri</i>	79	Cochran 1955
<i>Phyllomedusa camba</i>	84	de la Riva 1999
<i>Phyllomedusa centralis</i>	42	Bokermann 1965
<i>Phyllomedusa coelestis</i>	64.8	Duellman and Mendelson 1995
<i>Phyllomedusa distincta</i>	66	Pombal and Haddad 1992
<i>Phyllomedusa duellmani</i>	54.2	Cannatella 1982
<i>Phyllomedusa ecuatoriana</i>	55.4	Cannatella 1982
<i>Phyllomedusa hypochondrials</i>	46	Prado and Haddad 2005
<i>Phyllomedusa iheringii</i>	75	Cei 1980
<i>Phyllomedusa itacolomi</i>	46.1	Caramaschi et al. 2006
<i>Phyllomedusa megacephala</i>	49.1	Caramaschi 2006
<i>Phyllomedusa neildi</i>	76	Barrio-Amorós 2006

<i>Phyllomedusa nordestina</i>	43.7	Caramaschi 2006
<i>Phyllomedusa oreades</i>	42.6	Brandão 2002
<i>Phyllomedusa palliata</i>	62.3	Duellman 2005
<i>Phyllomedusa perinesos</i>	65.2	Cannatella 1982
<i>Phyllomedusa rohdei</i>	36	Cochran 1955
<i>Phyllomedusa sauvagii</i>	70	Cei 1980
<i>Phyllomedusa tarsius</i>	111.8	Duellman 1974b
<i>Phyllomedusa tetraploidea</i>	69.4	Pombal and Haddad 1992
<i>Phyllomedusa tomopterna</i>	59	Rodríguez and Duellman 1994
<i>Phyllomedusa trinitatis</i>	95.5	Barrio-Amorós 2006
<i>Phyllomedusa vaillantii</i>	84	Rodríguez and Duellman 1994
<i>Phyllomedusa venusta</i>	97.7	Duellman 2001
<i>Pseudis bolbodactyla</i>	51.4	Caramaschi and Cruz 1998
<i>Pseudis cardosoi</i>	55.9	Kwet 2000
<i>Pseudis fusca</i>	51	Caramaschi and Cruz 1998
<i>Pseudis minuta</i>	50.5	Kwet 2000
<i>Pseudis paradoxa</i>	75	Lescure and Marty 2000
<i>Pseudis tocantins</i>	37.7	Caramaschi and Cruz 1998
<i>Scarthyla goinorum</i>	23	Duellman 2005
<i>Scarthyla vigilans</i>	20.8	Solano 1971
<i>Scinax acuminatus</i>	48	Prado and Haddad 2005
<i>Scinax agilis</i>	19.5	Faivovich 2005
<i>Scinax albicans</i>	44	Lutz 1973
<i>Scinax alcatraz</i>	32	Lutz 1973
<i>Scinax altae</i>	25	Dunn 1933
<i>Scinax alter</i>	32	Lutz 1973
<i>Scinax angrensis</i>	32	Lutz 1973
<i>Scinax arduous</i>	19.5	Peixoto 2002
<i>Scinax argyreornatus</i>	15.8	Faivovich 2005
<i>Scinax ariadne</i>	46.5	Lutz 1973
<i>Scinax aromothyella</i>	31.8	Faivovich 2005
<i>Scinax atratus</i>	20	Peixoto 1988a
<i>Scinax auratus</i>	23	Lutz 1973
<i>Scinax baumgardneri</i>	29	Rivero 1961
<i>Scinax berthae</i>	25	Faivovich 2005
<i>Scinax blairi</i>	32.5	Fouquette and Pyburn 1972
<i>Scinax boesemani</i>	33	Lescure et Marty 2000
<i>Scinax brienii</i>	40	Lutz 1973
<i>Scinax caldarum</i>	35	Lutz 1973
<i>Scinax camposseabrai</i>	35.9	Caramaschi and Cardoso 2006
<i>Scinax canastrensis</i>	38	Cardoso and Haddad 1982

<i>Scinax carnevallii</i>	32	Caramaschi and Kisteumacher 1989
<i>Scinax castroviejoi</i>	48.7	de la Riva 1993
<i>Scinax catharinae</i>	45	Lutz 1973
<i>Scinax centralis</i>	21.2	Pombal and Bastos 1996
<i>Scinax chiquitanus</i>	36.2	Duellman 2005
<i>Scinax constrictus</i>	35.6	Lima et al. 2004
<i>Scinax crospedospilus</i>	37.6	Heyer et al. 1990
<i>Scinax cruentommmus</i>	32	Duellman 1978
<i>Scinax curicica</i>	31.5	Pugliese et al. 2004
<i>Scinax cuspidatus</i>	29	Lutz 1973
<i>Scinax danae</i>	29.5	Duellman 1986
<i>Scinax duartei</i>	37	Lutz 1973
<i>Scinax elaeochrous</i>	40.3	Duellman 2001
<i>Scinax eurydice</i>	42	Lutz 1973
<i>Scinax exiguus</i>	24.5	Duellman 1986
<i>Scinax flavidus</i>	30.5	La Marca 2004
<i>Scinax flavoguttatus</i>	43.1	Lutz 1973
<i>Scinax funereus</i>	43	Duellman 1978
<i>Scinax fuscomarginatus</i>	24	Cochran 1955
<i>Scinax fuscovarius</i>	48	Lutz 1973
<i>Scinax garbei</i>	49.1	Duellman and Mendelson 1995
<i>Scinax granulatus</i>	40	Lutz 1973
<i>Scinax hayii</i>	53	Lutz 1973
<i>Scinax heyeri</i>	35.6	Peixoto and Weygoldt 1987
<i>Scinax hiemalis</i>	33	Haddad and Pombal 1987
<i>Scinax humilis</i>	34	Lutz 1973
<i>Scinax ictericus</i>	33.5	Duellman 2005
<i>Scinax jolyi</i>	43.7	Lescure and Marty 2000
<i>Scinax jureia</i>	33.6	Pombal and Gordo 1991
<i>Scinax karenanneae</i>	30.5	Pyburn 1993
<i>Scinax kennedyi</i>	37.3	Pyburn 1973
<i>Scinax lindsayi</i>	25.4	Pyburn 1992
<i>Scinax littoralis</i>	39.9	Pombal and Gordo 1991
<i>Scinax littoreus</i>	25.5	Peixoto 1988b
<i>Scinax longilineus</i>	48	Lutz 1973
<i>Scinax luizotavioi</i>	27.5	Caramaschi and Kisteumacher 1989
<i>Scinax machadoi</i>	26	Bokermann and Sazima 1973a
<i>Scinax manriquei</i>	32.5	Barrio-Amoros et al. 2004
<i>Scinax maracaya</i>	28	Cardoso and Sazima 1980
<i>Scinax melloi</i>	18.7	Peixoto 1988a
<i>Scinax nasicus</i>	39	Lutz 1973

<i>Scinax nebulosus</i>	40	Lutz 1973
<i>Scinax obtriangulatus</i>	39	Lutz 1973
<i>Scinax oreites</i>	39.3	Duellman and Wiens 1993
<i>Scinax pachyrcrus</i>	33	Lutz 1973
<i>Scinax parkeri</i>	23.9	Duellman 1986
<i>Scinax pedromedinae</i>	31.5	Duellman 2005
<i>Scinax peixotoi</i>	25.1	Brasileiro et al. 2007
<i>Scinax perereca</i>	42.2	Pombal et al. 1995
<i>Scinax perpusillus</i>	25	Lutz 1973
<i>Scinax pinima</i>	29	Bokermann and Sazima 1973a
<i>Scinax proboscideus</i>	46	Lescure and Marty 2000
<i>Scinax quinquefasciatus</i>	30	Fowler 1913
<i>Scinax ranki</i>	28.7	Andrade and Cardoso 1987
<i>Scinax rizibilis</i>	34	Lutz 1973
<i>Scinax rostratus</i>	45.7	Duellman 2001
<i>Scinax ruber</i>	45	Rivero 1961
<i>Scinax similis</i>	41	Lutz 1973
<i>Scinax squalirostris</i>	29	Lutz 1973
<i>Scinax strigilatus</i>	28	Cochran 1955
<i>Scinax sugillatus</i>	45.4	Duellman 1973
<i>Scinax trapicheiroi</i>	40	Lutz 1973
<i>Scinax trilineatus</i>	22.5	Hoogmoed and Gorzula 1979
<i>Scinax uruguayus</i>	25.8	Langone 1990
<i>Scinax v-signatus</i>	27	Lutz 1973
<i>Scinax wandae</i>	26.9	Pyburn and Fouquette 1971
<i>Scinax x-signatus</i>	42.5	Heyer et al. 1990
<i>Sphaenorhynchus bromelicola</i>	30	Bokermann 1966a
<i>Sphaenorhynchus carneus</i>	23	Rodríguez and Duellman 1994
<i>Sphaenorhynchus dorisae</i>	40	Rodríguez and Duellman 1994
<i>Sphaenorhynchus lacteus</i>	48	Duellman 1978
<i>Sphaenorhynchus orophilus</i>	32	Heyer et al. 1990
<i>Sphaenorhynchus palustris</i>	36	Bokermann 1966a
<i>Sphaenorhynchus pauloalvini</i>	24	Bokermann 1973
<i>Sphaenorhynchus planicola</i>	24	Cochran 1955
<i>Sphaenorhynchus platycephalus</i>	33	Harding 1991
<i>Sphaenorhynchus prasinus</i>	31	Bokermann 1973
<i>Sphaenorhynchus surdus</i>	28	Cochran 1952
<i>Tepuihyla aecii</i>	36.8	Mijares-Urrutia et al. 1999
<i>Tepuihyla celsae</i>	56.2	Mijares-Urrutia et al. 1999
<i>Tepuihyla edelcae</i>	45.7	Mijares-Urrutia et al. 1999
<i>Tepuihyla galani</i>	49.5	Mijares-Urrutia et al. 1999

<i>Tepuihyla luteolabris</i>	59.2	Ayarzagüena et al. 1992
<i>Tepuihyla rimarum</i>	44.6	Mijares-Urrutia et al. 1999
<i>Tepuihyla rodriguezi</i>	38.1	Duellman and Hoogmoed 1992
<i>Tepuihyla talbergae</i>	32.7	Duellman and Yoshpa 1996
<i>Trachycephalus atlas</i>	98	Bokermann 1966c
<i>Trachycephalus jordani</i>	75.4	Cochran and Goin 1970
<i>Trachycephalus nigromaculatus</i>	86	Cochran 1955
<i>Xenohyla eugenioi</i>	45.5	Caramaschi 1998
<i>Xenohyla truncata</i>	42	Lutz 1973

1124 Table S2. Proportion of diet overlap, as assessed by Schoener's (1970) index of proportional overlap (see METHODS).

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	<i>O. brunneus</i>	<i>O. dominicensis</i>	<i>O. marianae</i>	<i>O. pulchrilineatus</i>	<i>O. septentrionalis</i>	<i>O. vastus</i>	<i>O. wilderi</i>
<i>O. brunneus</i>	1	0.5773	0.65	0.2	0.55	0.4	0.2703
<i>O. dominicensis</i>	0.5773	1	0.5955	0.4	0.5379	0.6182	0.2526
<i>O. marianae</i>	0.65	0.5955	1	0.25	0.5	0.3833	0.1351
<i>O. pulchrilineatus</i>	0.2	0.4	0.25	1	0.0833	0.4	0.0541
<i>O. septentrionalis</i>	0.55	0.5379	0.5	0.0833	1	0.2167	0.2455
<i>O. vastus</i>	0.4	0.6182	0.3833	0.4	0.2167	1	0.2559
<i>O. wilderi</i>	0.2703	0.2526	0.1351	0.0541	0.2455	0.2559	1

1126 Table S3. Setup of community assembly analyses. Species were placed into categories based on the maximum recorded snout-to-vent
 1127 length (SVL). For each size category, D_i and d_i represent the number of species in the total species pool and Caribbean communities,
 1128 respectively. For each D_i , larger numbers indicate the total number of species that fit in that size category, whereas the smaller numbers in
 1129 parentheses indicate the reduced number used for analysis (see Materials and Methods). All size categories are based on Duellman
 1130 (2001). Jamaican and Hispaniolan species are listed in their respective categories, followed by their maximum SVL in parentheses. All
 1131 Caribbean species are of the genus *Osteopilus* unless otherwise noted.

Size categories

	Small ($X < 30\text{mm}$)	Medium ($30 \leq X < 50\text{mm}$)	Large ($50 \leq X < 80\text{mm}$)	Very Large ($X \geq 80\text{mm}$)
South American + Caribbean treefrogs	$D_0 = 107$ (47)	$D_1 = 195$ (86)	$D_2 = 117$ (52)	$D_3 = 35$ (15)
Jamaica	$d_0 = 1$ <i>O. wilderi</i> (29)	$d_1 = 1$ <i>O. marianae</i> (40)	$d_2 = 1$ <i>O. brunneus</i> (76)	$d_3 = 1$ <i>O. crucialis</i> (122)
Hispaniola	$d_0 = 0$	$d_1 = 1$ <i>O. pulchrilineatus</i> (43)	$d_2 = 1$ <i>Hypsiboas heilprini</i> (54)	$d_3 = 2$ <i>O. dominicensis</i> (99) <i>O. vastus</i> (142)

1132 Table S4. Genbank accession numbers for DNA sequences analyzed in the analysis of Lophiohylini. Genbank numbers for Cophomantini, the
 1133 *Dendropsophus* clade, Phyllomedusinae, and the *Scinax* clade can be found in Wiens et al. 2006. The first part of the table reflects data for
 1134 mitochondrial genes, while the second part reflects nuclear data.

Taxon	Mitochondrial gene					
	12S	16S	ND1	ND2	COI	cytochrome <i>b</i>
Outgroups						
<i>Acris crepitans</i>	AY819360 ^b	AY843559 ^c	AY819491 ^b	AY843782 ^c
<i>Aplastodiscus leucopygius</i>	AY819430 ^b	AY843638 ^c	AY819544 ^b	AY843873 ^c
<i>Dendropsophus ebraccatus</i>	AY819367 ^b	AY843624 ^c	AY819499 ^b	EU034096 ^g	...	EU034061 ^g
<i>Dendropsophus koechlini</i>	AY819369 ^b	...	AY819501 ^b
<i>Dendropsophus microcephalus</i>	AY819371 ^b	AY843643 ^c	AY819503 ^b	AY843880 ^c
<i>Dendropsophus nanus</i>	AY819373 ^b	AY549346 ^c	AY819505 ^b	AY843888 ^c
<i>Duellmanohyla soralia</i>	AY819362 ^b	AY843584 ^c	AY819493 ^b	AY843806 ^c
<i>Hyla cinerea</i>	AY819366 ^b	AY549327 ^c	AY819498 ^b	AY549380 ^c
<i>Hyloscirtus colymba</i>	DQ380353 ^e	AY843620 ^c	AY819553 ^b	EU034095 ^g	...	AY843848 ^c
<i>Hyloscirtus polytaeniis</i>	AY819374 ^b	AY843655 ^c	AY819506 ^b	AY843895 ^c
<i>Hypsiboas boans</i>	AY819364 ^b	AY843610 ^c	AY819496 ^b	AY843835 ^c
<i>Hypsiboas heilprini</i>	DQ380357 ^e	AY843632 ^c	EU034080 ^g	EU034062 ^g
<i>Hypsiboas raniceps</i>	AY819375 ^b	AY843657 ^c	AY819507 ^b	AY843900 ^c
<i>Plectrohyla guatemalensis</i>	AY819444 ^b	AY843731 ^c	DQ055833 ^d	AY843976 ^c
<i>Pseudacris regilla</i>	AY819376 ^b	AY843737 ^c	AY819508 ^b
<i>Pseudis paradoxus</i>	AY819353 ^b	AY843730 ^c	AY819483 ^b	AY843985 ^c
<i>Scinax catharinae</i>	AY819390 ^b	AY843756 ^c	AY819522 ^b	AY844001 ^c
<i>Scinax crospedospilus</i>	AY819391 ^b	...	AY819523 ^b
<i>Smilisca cyanosticta</i>	AY819393 ^b	AY843763 ^c	AY819525 ^b	AY844008 ^c
<i>Sphaenorhynchus lacteus</i>	AY819394 ^b	AY549367 ^c	AY819526 ^b	AY844012 ^c
Lophiohylini						
<i>Aparasphenodon brunoi</i>	AY843567 ^c	AY843567 ^c	AY843789 ^c

<i>Argenteohyla siemersi</i>	AY843570 ^c	AY843570 ^c	AY843792 ^c
<i>Corythomantis greeningi</i>	AY843578 ^c	AY843578 ^c	AY843800 ^c
<i>"Hyla" alboguttata</i>	DQ380347 ^e	...	EU034081 ^g	EU034097 ^g	...	EU034063 ^g
<i>Itapotihyla langsdorfii</i>	AY819379 ^b	AY843706 ^c	AY819511 ^b	AY843951 ^c
<i>Nyctimantis rugiceps</i>	EU034032 ^g	AY843780 ^c	...	EU034098 ^g	...	AY843945 ^c
<i>Osteocephalus buckleyi</i>	DQ380378 ^e	...	EU034082 ^g	EU034064 ^g
<i>Osteocephalus cabrerai</i>	AY843705 ^c	AY843705 ^c	AY843950 ^c
<i>Osteocephalus leprieurii</i>	AY549361 ^a	AY549361 ^a	AY843952 ^c
<i>Osteocephalus mutabor</i>	DQ380379 ^e
<i>Osteocephalus oophagus</i>	AY843708 ^c	AY843708 ^c	AY843953 ^c
<i>Osteocephalus planiceps</i>	DQ380380 ^e	EU034099 ^g	EU034049 ^g	...
<i>Osteocephalus taurinus</i>	AY819380 ^b	AY843709 ^c	AY819512 ^b	EU034100 ^g	EU034050 ^g	EU034065 ^g
<i>Osteocephalus verruciger</i>	DQ380381 ^e	EU034101 ^g	...	EU034066 ^g
<i>Osteopilus brunneus</i>	DQ380382 ^e	...	EU034083 ^g	EU034102 ^g	EU034051 ^g	EU034067 ^g
<i>Osteopilus crucialis</i>	AY819419 ^e	AY843710 ^c	EU034084 ^g	EU034103 ^g	EU034052 ^g	AY843955 ^c
<i>Osteopilus dominicensis</i>	AY819443 ^b	AY843711 ^c	EU034085 ^g	EU034104 ^g	EU034053 ^g	EU034068 ^g
<i>Osteopilus marianae</i>	DQ380383 ^e	...	EU034086 ^g	...	EU034054 ^g	EU034069 ^g
<i>Osteopilus pulchrilineatus</i>	AY819436 ^b	...	EU034087 ^g	EU034105 ^g	EU034055 ^g	EU034070 ^g
<i>Osteopilus septentrionalis</i>	AY819381 ^b	AY843712 ^c	AY819513 ^b	EU034106 ^g	EU034056 ^g	EU034071 ^g
<i>Osteopilus vastus</i>	DQ380384 ^e	AY843713 ^c	EU034091 ^g	...	EU034057 ^g	EU034075 ^g
<i>Osteopilus wilderi</i>	DQ380385 ^e	...	EU034092 ^g	EU034110 ^g	EU034058 ^g	...
<i>Phrynohyas coriacea</i>	DQ380386 ^e	...	EU034093 ^g	EU034111 ^g	...	EU034076 ^g
<i>Phrynohyas hadroceps</i>	AY843717 ^c	AY843717 ^c	AY843962 ^c
<i>Phrynohyas imitatrix</i>	EU034036 ^g	EU034112 ^g
<i>Phrynohyas mesophaea</i>	AY843718 ^c	AY843718 ^c	AY843963 ^c
<i>Phrynohyas resinifictrix</i>	AY843719 ^c	AY843719 ^c	AY843964 ^c
<i>Phrynohyas venulosa</i>	AY819382 ^b	AY549362 ^c	AY819514 ^b	EU034077 ^g
<i>Phyllodytes auratus</i>	AY819383 ^b	...	AY819515 ^b	EU034078 ^g
<i>Phyllodytes luteolus</i>	AY843721 ^c	AY843721 ^c	AY843965 ^c
<i>Phyllodytes sp.</i>	AY843722 ^c	AY843722 ^c	AY843966 ^c

<i>Tepuihyla edelcae</i>	AY843770 ^c	AY843770 ^c
<i>Tepuihyla sp.</i>	DQ380389 ^e	...	EU034094 ^g	...	EU034059 ^g	...
<i>Trachycephalus jordani</i>	AY819395 ^b	AY843771 ^c	AY819527 ^b	EU034113 ^g	EU034060 ^g	EU034079 ^g
<i>Trachycephalus nigromaculatus</i>	AY843772 ^c	AY843772 ^c	AY844016 ^c
<i>Osteopilus septentrionalis</i> individuals used in preliminary analyses						
USNM 315332	AY819381 ^b	...	AY819513 ^b	EU034106 ^g	EU034056 ^g	EU034071 ^g
USNM 317832	EU034033 ^g	...	EU034088 ^g	EU034107 ^g	...	EU034072 ^g
USNM 497935	EU034034 ^g	...	EU034089 ^g	EU034108 ^g	...	EU034073 ^g
USNM 317831	EU034035 ^g	...	EU034090 ^g	EU034109 ^g	...	EU034074 ^g

Taxon	Nuclear gene						
	POMC	<i>cmyc</i> exon 2	Rhodopsin	RAG-1	Tyrosinase	SIA	TNS3
Outgroups							
<i>Acris crepitans</i>	AY819109 ^b	AY819194 ^b	AY844533 ^c	AY844358 ^c	AY844019 ^c	AY844762 ^c	...
<i>Aplastodiscus leucopygius</i>	AY844622 ^c	AY844425 ^c	AY844084 ^c	AY844840 ^c	...
<i>Dendropsophus ebraccatus</i>	AY819117 ^b	AY819202 ^b	AY844604 ^c	AY844415 ^c	AY844070 ^c	AY844822 ^c	...
<i>Dendropsophus koechlini</i>	AY819119 ^b	AY819204 ^b
<i>Dendropsophus microcephalus</i>	AY819121 ^b	AY819206 ^b	AY844628 ^c	AY844430 ^c	...	AY844846 ^c	...
<i>Dendropsophus nanus</i>	AY819123 ^b	AY819208 ^b	AY844634 ^c	AY844437 ^c	...	AY844852 ^c	...
<i>Duellmanohyla soralia</i>	AY819111 ^b	AY819196 ^b	AY844557 ^c	AY844378 ^c	AY844034 ^c	AY844783 ^c	...
<i>Hyla cinerea</i>	AY819116 ^b	AY819201 ^b	AY844597 ^c	AY844408 ^c	AY844063 ^c	AY844816 ^c	DQ830949 ^f
<i>Hyloscirtus colymba</i>	AY819157 ^b	AY819323 ^b	AY844599 ^c	AY844410 ^c	AY844065 ^c	AY844818 ^c	...
<i>Hyloscirtus polytaeniis</i>	AY819124 ^b	AY819209 ^b	AY844641 ^c	AY844443 ^c	...	AY844859 ^c	...
<i>Hypsiboas boans</i>	AY819114 ^b	AY819199 ^b	AY844588 ^c	...	AY844055 ^c	AY844809 ^c	...
<i>Hypsiboas heilprini</i>	EU034114 ^g	EU034037 ^g	AY844613 ^c	AY844831 ^c	...
<i>Hypsiboas raniceps</i>	AY819125 ^b	AY819210 ^b	AY844646 ^c	...	AY844103 ^c	AY844863 ^c	...
<i>Plectrohyla guatemalensis</i>	DQ055807 ^d	DQ055780 ^d	AY844719 ^c	AY844501 ^c	AY844160 ^c	AY844924 ^c	...
<i>Pseudacris regilla</i>	AY819126 ^b	AY819211 ^b	AY844725 ^c	...	AY844165 ^c

<i>Pseudis paradoxus</i>	AY819102 ^b	AY819187 ^b	AY844727 ^c	AY844506 ^c	AY844167 ^c
<i>Scinax catharinae</i>	AY819140 ^b	AY819225 ^b	AY844742 ^c	AY844517 ^c	...	AY844941 ^c	...
<i>Scinax crospedospilus</i>	AY819141 ^b	AY819226 ^b
<i>Smilisca cyanosticta</i>	AY819143 ^b	AY819228 ^b	AY844750 ^c	AY844524 ^c	AY844184 ^c	AY844947 ^c	DQ830957 ^f
<i>Sphaenorhynchus lacteus</i>	AY819144 ^b	AY819229 ^b	AY844754 ^c	AY844527 ^c	AY844188 ^c
Lophiohylini							
<i>Aparasphenodon brunoii</i>	AY844541 ^c	AY844364 ^c	AY844023 ^c	AY844769 ^c	...
<i>Argenteohyla siemersi</i>	AY844544 ^c	AY844367 ^c	AY844026 ^c	AY844772 ^c	...
<i>Corythomantis greeningi</i>	AY844551 ^c	AY844374 ^c	AY844030 ^c	AY844779 ^c	...
<i>"Hyla" alboguttata</i>	EU034115 ^g	EU034132 ^g	EU034151 ^g
<i>Itapotihyla langsdorffii</i>	AY819129 ^b	AY819214 ^b	AY844697 ^c	AY844482 ^c	AY844137 ^c	AY844903 ^c	...
<i>Nyctimantis rugiceps</i>
<i>Osteocephalus buckleyi</i>	EU034116 ^g	EU034038 ^g	...	EU034133 ^g	EU034152 ^g
<i>Osteocephalus cabrerai</i>	AY844696 ^c	AY844481 ^c	AY844136 ^c	AY844902 ^c	...
<i>Osteocephalus leprieurii</i>	AY844698 ^c	AY844483 ^c	AY844138 ^c	AY844904 ^c	...
<i>Osteocephalus mutabor</i>	EU034117 ^g	EU034039 ^g
<i>Osteocephalus oophagus</i>	AY844699 ^c	AY844484 ^c	AY844139 ^c
<i>Osteocephalus planiceps</i>	EU034118 ^g	EU034040 ^g	...	EU034134 ^g	EU034153 ^g
<i>Osteocephalus taurinus</i>	AY819130 ^b	AY819215 ^b	AY844700 ^c	EU034135 ^g	AY844140 ^c	AY844905 ^c	EU034154 ^g
<i>Osteocephalus verruciger</i>	EU034119 ^g	EU034041 ^g	EU034155 ^g
<i>Osteopilus brunneus</i>	EU034120 ^g	EU034042 ^g	...	EU034136 ^g	EU034156 ^g
<i>Osteopilus crucialis</i>	EU034121 ^g	EU034157 ^g
<i>Osteopilus dominicensis</i>	EU034122 ^g	...	AY844701 ^c	EU034137 ^g	AY844141 ^c	...	EU034158 ^g
<i>Osteopilus marianae</i>	EU034123 ^g	EU034043 ^g	...	EU034138 ^g	EU034159 ^g
<i>Osteopilus pulchrilineatus</i>	EU034124 ^g	EU034044 ^g	...	EU034139 ^g	EU034160 ^g
<i>Osteopilus septentrionalis</i>	AY819131 ^b	AY819216 ^b	...	EU034140 ^g	AY844142 ^c	AY844906 ^c	EU034161 ^g
<i>Osteopilus vastus</i>	EU034128 ^g	EU034046 ^g	...	EU034144 ^g	AY844143 ^c	AY844907 ^c	EU034162 ^g
<i>Osteopilus wilderi</i>	EU034129 ^g	EU034047 ^g	...	EU034145 ^g	EU034163 ^g
<i>Phrynohyas coriacea</i>	EU034130 ^g	EU034048 ^g	...	EU034146 ^g	EU034164 ^g
<i>Phrynohyas hadroceps</i>	AY844704 ^c	AY844490 ^c	AY844146 ^c

<i>Phrynohyas imitatrix</i>
<i>Phrynohyas mesophaea</i>	AY844705 ^c	AY844491 ^c	AY844147 ^c	AY844910 ^c	...
<i>Phrynohyas resinifictrix</i>	AY844706 ^c	AY844492 ^c	AY844148 ^c	AY844911 ^c	...
<i>Phrynohyas venulosa</i>	AY819132 ^b	AY819217 ^b	AY844707 ^c	EU034147 ^g	AY844149 ^c	AY844912 ^c	EU034165 ^g
<i>Phyllodytes auratus</i>	AY819133 ^b	AY819218 ^b	...	EU034148 ^g	EU034166 ^g
<i>Phyllodytes luteolus</i>	AY844708 ^c	AY844494 ^c	AY844150 ^c	AY844913 ^c	...
<i>Phyllodytes sp.</i>	AY844709 ^c	...	AY844151 ^c	AY844914 ^c	...
<i>Tepuihyla edelcae</i>	AY844530 ^c
<i>Tepuihyla sp.</i>	EU034131 ^g	EU034149 ^g
<i>Trachycephalus jordani</i>	AY819145 ^b	AY819230 ^b	AY844758 ^c	EU034150 ^g	AY844190 ^c	AY844953 ^c	EU034167 ^g
<i>Trachycephalus nigromaculatus</i>	AY844759 ^c	...	AY844191 ^c

Osteopilus septentrionalis individuals used in preliminary analyses

USNM 315332	AY819131 ^b	AY819216 ^b	...	EU034140 ^g
USNM 317832	EU034125 ^g	EU034045 ^g	...	EU034141 ^g
USNM 497935	EU034126 ^g	EU034142 ^g
USNM 317831	EU034127 ^g	EU034143 ^g	EU034161 ^g

- 1136
1137 ^a = Faivovich et al. 2004
1138 ^b = Wiens et al. 2005
1139 ^c = Faivovich et al. 2005
1140 ^d = Smith et al. 2005
1141 ^e = Wiens et al. 2006
1142 ^f = Smith et al. 2007
1143 ^g = this study

1144 Table S5. Primers used to amplify and sequence DNA sequence data. Primers are listed in the order in which they occur on each gene.
 1145

Primer	Direction ^a	Sequence (5'-3')	Source
12S			
MVZ59	F	ATAGCACTGAAAAYGCTDAGATG	Graybeal 1997
t-Phe-frog	F	ATAGCRCTGAARAYGCTRAGATG	Modified “MVZ 59” (Graybeal 1997)
t-Phe3-frog	F	TTGGTCCTAACCTTGTAATC	this study
t-Val3-frog	R	CCATGTTACGACTTGCTCT	this study
t-Val-frog	R	TGTAAGCGARAGGCTTTKGTAAAGCT	Wiens et al. (2005)
MVZ50	R	TYTCGGTGTAAGYGARAKGCTT	Graybeal 1997
COI			
COX	F	TGATTCTTTGGGCATCCTGAAG	Schneider et al. 1998
COY	R	GGGGTAGTCAGAATAGCGTCG	Schneider et al. 1998
cytochrome <i>b</i>			
MVZ15	F	GAACTAATGGCCACAWWTACGNAA	Moritz et al. 1992
H15149	R	AAACTGCAGCCCCTCAGAAATGATATTTGTCCTCA	Kocher et al. 1989
ND1			
16S-frog	F	TTACCCTRGGGATAACAGCGCAA	Wiens et al. 2005
ND1 F1	F	AGCCATAATCATCTGAACC	Smith et al. 2005
ND1 F2	F	GCMATAATYATYTGAACCC	Smith et al. 2005
WL379	F	GCAATAATYATYTGAACMCC	this study
WL384	R	GAGATWGTTTGWGCAACTGCTCG	this study
ND1 R1	R	TCCTCCCTATCAAGGAGGTCC	Smith et al. 2005
tMet-frog	R	TTGGGGTATGGGCCAAAAGCT	Wiens et al. 2005
ND2			
L4437b	F	CAGCTAAAAAAGCTATCGGGCCCATACC	Macey et al 1997
ND2r102	R	CAGCCTAGGTGGGCGATTG	Sarah Smith, pers. com.

<i>cmc</i> exon 2			
cmc1U	F	GAGGACATCTGGAARAARTT	Crawford 2003
cmc-ex2d R	R	TCATTCAATGGGTAAGGGAAGACGACC	Wiens et al. 2005
POMC			
POMC-1	F	GAATGTATYAAAGMMTGCAAGATGGWCCT	Wiens et al. 2005
POMC-6	F	TCTGCMGAGTCACCRGTGTTTC	Smith et al. 2005
WL382	R	ATTCATTTTGTACTTCCG	this study
POMC-7	R	TGGCATTTTTGAAAAGAGTCAT	Smith et al. 2005
POMC-2	R	TAYTGRCCCTTYTTGTGGGCRIT	Wiens et al. 2005
RAG-1			
RS1F	F	TGCAGTCAGTAYCAYAARATGTAC	Paul Chippindale pers. com.
WL385	F	AGAAGAACGAAAGAAATGGCAGGC	this study
R1-GFF	F	GAGAAGTCTACAAAAAVGGCAAAG	Faivovich et al. 2005
WL386	R	GTTTCCTTGGACATGAGTTTTTC	this study
R1-GFR	R	GAAGCGCCTGAACAGTTTATTAC	Faivovich et al. 2005
TNS3			
WL423	F	CAGCATAGGTACTTTATCATCATCAG	Smith et al. 2007
WL421	R	CAGTGTTGGAGAAGATGGTATGTC	Smith et al. 2007

1146

1147 ^aF indicates “forward;” primers amplify the gene from the 5’ end of the published DNA sequence. R primers amplify DNA in the opposite

1148 direction on the complimentary strand (“reverse”).

1149 Table S6. Ratios of body sizes of Jamaican and Hispaniolan treefrogs. Ratios are calculated as the maximum snout-to-vent length (SVL) of row
 1150 species divided by maximum SVL of column species. The maximum reported SVL is in parentheses behind each species's name.

<u>Jamaica</u>	<i>O. wilderi</i>	<i>O. marianae</i>	<i>O. brunneus</i>	<i>O. crucialis</i>
<i>Osteopilus wilderi</i> (29 mm)	1.00			
<i>Osteopilus marianae</i> (40 mm)	1.38	1.00		
<i>Osteopilus brunneus</i> (76 mm)	2.62	1.90	1.00	
<i>Osteopilus crucialis</i> (122 mm)	4.21	3.05	1.61	1.00
<u>Hispaniola</u>	<i>O. pulchrilineatus</i>	<i>H. heilprini</i>	<i>O. dominicensis</i>	<i>O. vastus</i>
<i>Osteopilus pulchrilineatus</i> (43mm)	1.00			
<i>Hypsiboas heilprini</i> (54 mm)	1.26	1.00		
<i>Osteopilus dominicensis</i> (99 mm)	2.30	1.83	1.00	
<i>Osteopilus vastus</i> (142 mm)	3.30	2.63	1.43	1.00

1151

1152

APPENDIX S2

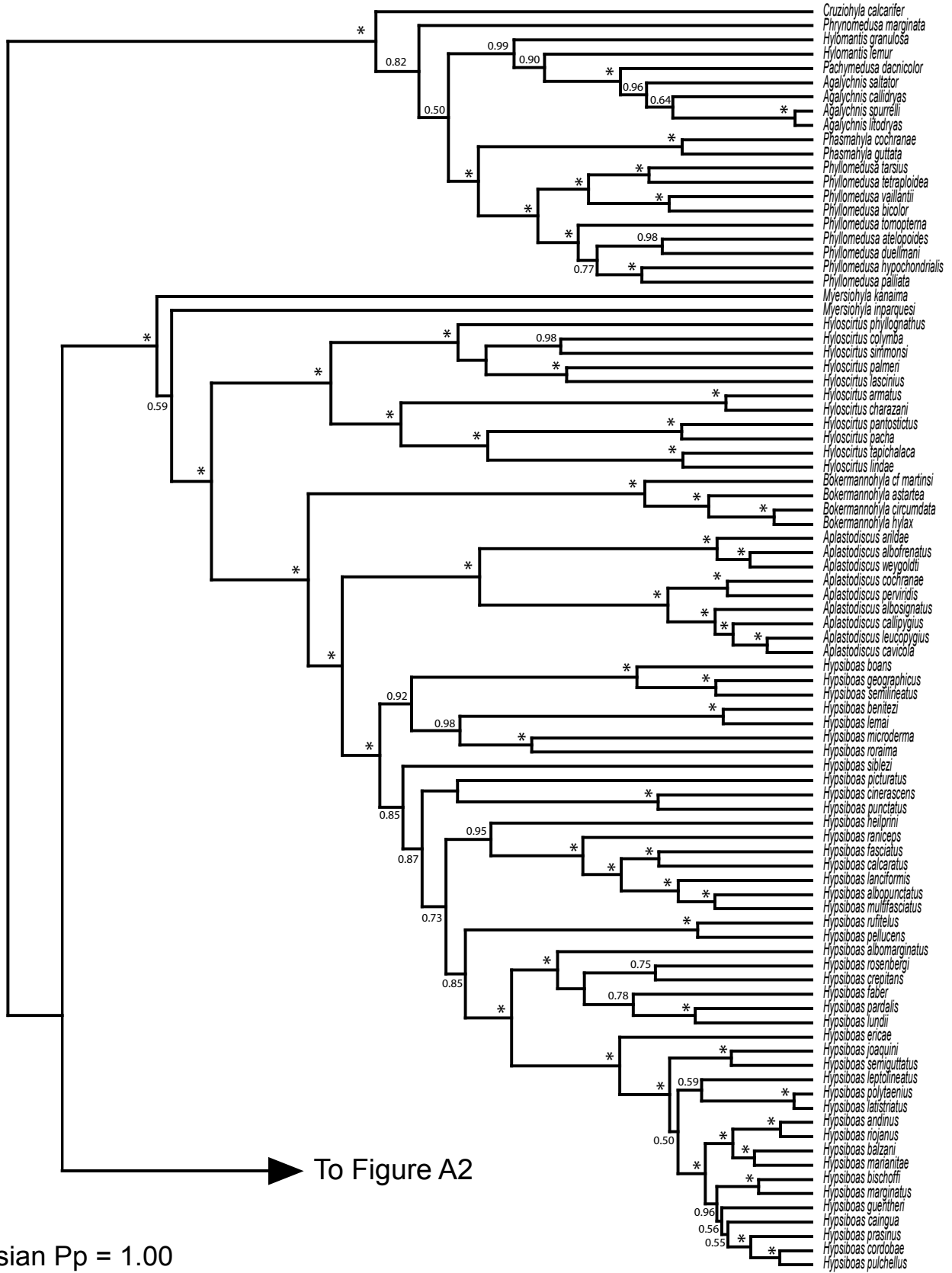
1153 Specimens measured for the morphometric analysis of *Osteopilus*. All specimens were from the
1154 Smithsonian Museum of Natural History (USNM); species names are followed by the USNM
1155 specimen number.

1156

1157 *O. brunneus*. – 251411–251412, 251415, 251419, 251477, 251490–251491, 251495, 251498,
1158 251543–251544, 251549–251551, 251582, 251584, 251596, 251612–251614. *O. crucialis*. –
1159 167627, 251619, 252456, 327244. *O. dominicensis*. – 224937, 259578, 259589–259591, 259593,
1160 259595, 259599, 259606–259610, 259613. *O. marianae*. – 139250, 251620–251629, 266469–
1161 266471, 327177. *O. pulchrilineatus*. – 65730, 74560, 74566, 140234, 140236, 329642–329656.
1162 *O. septentrionalis*. – 137858–137860, 137868, 137890, 137892, 137895, 137899, 137901–
1163 137903, 137886, 236538–236539, 311987, 315785, 315797, 335668, 335670, 497935. *O. vastus*.
1164 – 55301, 65753–65759, 66984, 66986, 74512, 74514–74516, 74519, 118837–118838. *O. wilderi*.
1165 – 251194–251195, 251218, 251220–251223, 251225–251226, 251258, 251265, 251279, 251282,
1166 251290, 251340, 251368–251370, 251373, 251993.

1167

Figure A1



70 60 50 40 30 20 10 0 Younger divergence dates

Figure A2

To Figure A1

