Around the world in 10 million years: biogeography of the nearly cosmopolitan true toads (Anura: Bufonidae)

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ABSTRACT

Aim The species-rich family of true toads (Anura: Bufonidae) has been the focus of several earlier studies investigating the biogeography of geographically widespread taxa. Herein, we employ newly developed Bayesian divergence estimate methods to investigate the biogeographical history of this group. Resulting age estimates are used to test several key temporal hypotheses including that the origin of the bufonid clade pre-dates Gondwanan vicariance (~105 million years ago, Ma). Area cladograms are also invoked to investigate the geographical origin of the family.

Location Worldwide, except the Australia–New Guinea plate, Madagascar and the Antarctic.

Methods A phylogenetic hypothesis of the relationships among true toads was derived from analysis of 2521 bp of DNA data including fragments from three mitochondrial (12S, tRNAval, 16S) and two nuclear (RAG-1, CXCR-4) genes. Analysis of multiple, unlinked loci with a Bayesian method for estimating divergence times allowed us to address the timing and biogeographical history of Bufonidae. Resulting divergence estimates permitted the investigation of alternative vicariance/dispersal scenarios that have been proposed for true toads.

Results Our area cladogram resulting from phylogenetic analysis of DNA data supports a South American origin for Bufonidae. Divergence estimates indicate that the family originated earlier than had been suggested previously (78–99 Ma). The age of the enigmatic Caribbean clade was dated to the late Palaeocene–early Eocene. A return of bufonids to the New World in the Eocene was followed by rapid diversification and secondary expansion into South America by the early Oligocene (Rupelian).

Main conclusions The South American origin of Bufonidae in the Upper Cretaceous was followed by relatively rapid expansion and radiation around the globe, ending with a return to the Americas via a Eurasian/North American land bridge in the Eocene. Though the exact route of this dispersal (Beringia or North Atlantic) remains unclear, an argument is made for the less frequently invoked North Atlantic connection. The origin of the enigmatic Caribbean lineage was found to be consistent with colonization following the bolide impact at the K/T boundary. These findings provide the first, firm foundation for understanding true toad divergence times and their truly remarkable and global radiation.

Keywords Anura, Bayes method, biogeography, Bufonidae, CXCR-4, divergence times, DNA, mtDNA, phylogeny, RAG-1, South America.

INTRODUCTION

One fundamental goal of modern systematics investigations is to use the resulting phylogenies to help understand global biogeographical patterns. Once a well-supported phylogenetic framework is accomplished, it can be employed to estimate divergence times to arrive at an overall picture of the spatial and temporal biogeographical framework of a taxonomic group.
Members of the species-rich true toad family Bufonidae, comprising c. 481 species (http://amphibiaweb.org), are native to most regions of the world except the Australia–New Guinea plate, Madagascar and the Antarctic. Their broad geographical distribution has prompted a great many studies focused on resolving the evolutionary relationships of bufonid frogs (e.g. Blair, 1972; Maxson, 1984; Graybeal, 1997; Pauly et al., 2004; Frost et al., 2006; Pramuk, 2006), however, the limited fossil record of this group has provided few calibration points and therefore prevented most workers from estimating divergence times to investigate their age and correlated biogeography. To explain the modern day distribution of true toads, several distinct biogeographical hypotheses proposing various combinations of vicariance and intercontinental dispersal events have been invoked. For example, earlier hypothetical origins for Bufonidae (reviewed in Pauly et al., 2004) range from an African (Tihen, 1962) to a South American origin (Blair, 1972; Maxson, 1984) with hypothesized dispersal and/or vicariance events explaining their modern day, nearly cosmopolitan distribution. Most recently, Pramuk (2006) hypothesized that her phylogeny for Bufonidae, derived from molecular and morphological data, is consistent with an origin that pre-dates Gondwanan vicariance (>105 million years ago, Ma). Similarly, earlier studies offered a Gondwanan vicariance scenario to explain the biogeographical patterns present in this family (e.g. Savage, 1973; Maxson, 1984). Here, we employ phylogenetic reconstruction methods and Bayesian analyses of divergence ages to compare general hypotheses of the spatial and temporal origin of Bufonidae.

The data set of Pramuk (2006), containing 3.5 kb of nuclear and mitochondrial data sequenced for 109 individuals, is currently the most complete for investigating relationships within Bufonidae, a previously analysed data matrix of c. 2821 bp of 12S–16S mtDNA and RAG-1 nuclear data (Pramuk, 2006) for 89 terminals was expanded by the addition of 750 bp of the nuclear exon CXCR-4. To provide additional distant Neobatrachian and Archaeobatrachian outgroups, and hence calibration points outside of Bufonidae for divergence time analysis, we included this nuclear marker to make our matrix compatible with that of Biju & Bossuyt (2003), which included homologous sequence data for 2521 bp of 12S and 16S rRNA, RAG-1 and CXCR-4. In total, new sequences were collected for 89 specimens representing 74 species, including data for 70 bufonids and four outgroup taxa.

To resolve a phylogeny of Bufonidae, genes with disparate rates of evolutionary change were sequenced to target a wide range of signal and to incorporate independently evolving molecular markers (Pennington, 1996). For example, regions of the 12S–16S mitochondrial genome were sequenced to give signal at intermediate and recent levels of divergence. The 12S–16S fragment was obtained with several sets of overlapping primers used previously for Bufo (Goebel et al., 1999; Pramuk, 2006) or modified from published primers. Portions of the nuclear RAG-1 and CXCR-4 exons were sequenced in order to provide signal at deeper levels of divergence and were selected based on their established phylogenetic utility for other groups of vertebrates (e.g. Biju & Bossuyt, 2003). All primers used in this study, and their original references, are listed in Table 1.

DNA extraction, polymerase chain reaction amplification and DNA sequencing

Previously published data for the 12S–16S fragment (Pauly et al., 2004) were used for the outgroups Ceratophrys cornuta and Hyla cinerea. Additionally, previously published sequences (Biju & Bossuyt, 2003) for CXCR-4 and portions of 12S and 16S rRNA data were included for 31 additional outgroup taxa. For a complete list of voucher specimens and their respective GenBank accession numbers, refer to Appendix S1 in Supplementary Material.

Prior to extraction, tissues were stored at −80 °C or fixed in 95–100% ethanol. The DNA was extracted from small amounts (c. 50 ng) of muscle or liver tissue with the Qiagen DNeasy Tissue Kit® and visualized on 1% high melt agarose gels in Tris–acetate–EDTA (TAE) buffer. We performed a polymerase chain reaction (PCR) in 13-μl reactions containing TaKaRa Hotstart Taq polymerase, 10× reaction buffer [100 mM Tris HCl (pH 8.3), 500 mM KCl, 15 mM MgCl₂]. Amplification followed published PCR conditions and was performed on a MJ Research thermal cycler. Cycle sequencing reactions were completed with Big Dye Sequencing kits (ABI Inc.). The PCR products were purified with Millipore MANU030 PCR plates. Double-stranded, purified products were used in 1/32 deoxy-termination sequencing reactions (10 μl total volume). Sequencing reactions were cleaned with Sephadex columns and sequencing was performed directly using an ABI 3100 automated sequencer.

The program Sequencher 3.1.1 (Gene Codes Corp.) was used to edit sequences. CLUSTALX (Thompson et al., 1997) was employed to perform preliminary alignment using default parameters (gap opening = 15; gap extension = 6.666; delay
Phylogenetic analyses

Maximum parsimony (MP), maximum likelihood (ML) and Bayesian analyses were performed on separate molecular partitions, and were also performed on the combined data sets. Initially, data from each of the three DNA fragments (12S–16S, CXCR-4, RAG-1) were analysed separately. Strong support for individual nodes is defined as nodes with bpp (Bayesian posterior probabilities) ≥ 0.95 (Alfaro et al., 2003) or npb (non-parametric bootstrap) ≥ 70 (Hillis & Bull, 1993). No strongly supported conflicting relationships were recovered, so all data were combined for subsequent phylogenetic analyses. Maximum parsimony analyses were performed with PAUP* (version 4.0b10; Swofford, 2002) using a heuristic search with 100 random addition sequence replicates and tree bisection–reconnection (TBR) branch swapping. Nodal support for MP results was assessed through nonparametric bootstrap analysis with 2000 bootstrap pseudoreplicates and 10 random taxon-addition replicates.

The most appropriate model of gene evolution for the ML (and Bayesian) analysis was estimated for each gene region and combined data sets using the Akaike information criterion (AIC) as implemented in Modeltest 3.06 PPC (Posada & Crandall, 1998). The ML analyses were performed on separate and combined data sets. For ML searches of all combined DNA data, Modeltest selected the best model as GTR + I + G (base frequencies: A, 0.3378; C, 0.2383; G, 0.1701; T, 0.2538; rate matrix: A–C, 1.6291; A–G, 4.7567; A–T, 2.0694; C–G, 1.0174; C–T, 9.5953; G–T, 1.0000; shape parameter for gamma distribution, 0.5244; proportion of invariant sites, 0.2216). The ML searches were run using 100 random addition replicates and TBR branch swapping. Confidence in the resulting topology was assessed with npb (Felsenstein, 1985) with 1000 bootstrap replicates, and heuristic searches of one random addition with TBR branch swapping per replicate.

The data sets were analysed in combined, mixed-model analyses using MrBayes 3.04b (Ronquist & Huelsenbeck, 2003). The analysis of combined data utilized eight model partitions for the 12S–16S, RAG-1 and CXCR-4 data sets (see Table 2 for a summary of each locus). To check for congruence on an identical topology, a minimum of two replicate searches were performed for each separate and combined data set. Analyses were initiated with random starting trees and each analysis was run for 20 × 10⁶ generations, with four Markov chains employed and with the chain sampled every 1000th generation. The application Tracer (version 1.2; Rambaut & Drummond, 2003) was used to view output of the sump file generated by MrBayes. Trees generated prior to reaching stationarity were discarded as burn-in. Most analyses reached stationarity relatively quickly (all reached 160,000 generations).

Divergence time estimates

We performed divergence time estimates using a relaxed Bayesian molecular clock with uncorrelated rates (beast 1.3; Drummond & Rambaut, 2003). This method was chosen over alternatives as recent work has shown that the autocorrelation of rates (e.g. multdivegene, Thorne et al., 1998; Thorne & Kishino, 2002) may not be a realistic way to model rate evolution (Drummond et al., 2006). An additional benefit of beast is the ability to

### Table 1 Amplification and sequencing primers used for the continuous 12S–16S region of the mitochondrial genome, and portions of the nuclear genes CXCR-4 and RAG-1.

<table>
<thead>
<tr>
<th>Primer name</th>
<th>Position</th>
<th>Primer sequence (5’ → 3’)</th>
<th>Goebel no.</th>
</tr>
</thead>
<tbody>
<tr>
<td>12SZL</td>
<td>2206–2225</td>
<td>AACGTTTGTGTCCTAAGCCCTT</td>
<td>35</td>
</tr>
<tr>
<td>12H2(R) mod.</td>
<td>2484–2503</td>
<td>GGTATGTAACCCAGCTTTT</td>
<td>N/A</td>
</tr>
<tr>
<td>12L6 mod.</td>
<td>2487–2508</td>
<td>ACTGGGATTAGATACCCTCAGCA</td>
<td>N/A</td>
</tr>
<tr>
<td>12SKH</td>
<td>2975–2996</td>
<td>TCCGRTYACCTCCCTGGTTACCAGA</td>
<td>70</td>
</tr>
<tr>
<td>12Sc(L)</td>
<td>2834–2853</td>
<td>AGGGCGGATTTAGAHGATAA</td>
<td>70</td>
</tr>
<tr>
<td>16H14(R) mod.</td>
<td>3753–3774</td>
<td>TCTTTHTACTAGTTTAACCAT</td>
<td>85</td>
</tr>
<tr>
<td>16L10</td>
<td>3622–3641</td>
<td>AGTGGGCCCTAAGACGCCCA</td>
<td>82</td>
</tr>
<tr>
<td>16H10</td>
<td>4054–4076</td>
<td>TGATTCGACCTCCCTGGCCAGGT</td>
<td>92</td>
</tr>
<tr>
<td>16L9</td>
<td>3956–3976</td>
<td>CGCCGTTTACCAAAACAT</td>
<td>88</td>
</tr>
<tr>
<td>16H13</td>
<td>4551–4572</td>
<td>CGGGCTCTGAATCTAGATCGTA</td>
<td>96</td>
</tr>
<tr>
<td>CXCR-4 C</td>
<td>–</td>
<td>GTC ATG GGC TAY CAR AAG AA</td>
<td>–</td>
</tr>
<tr>
<td>CXCR-4 F</td>
<td>–</td>
<td>TGA ATT TGG CCC RAG GAARGC</td>
<td>–</td>
</tr>
<tr>
<td>RAG-1 MartFl</td>
<td>–</td>
<td>AGCTCGACYGCACTAYCAVARATGTA</td>
<td>–</td>
</tr>
<tr>
<td>RAG-1 AmpR1</td>
<td>–</td>
<td>AACTCGAGTGCATTACCCTCAATRCA</td>
<td>–</td>
</tr>
</tbody>
</table>

Parameters = 30%; transition:transversion = 50%, with adjustments by eye. Alignment of the protein coding sequences was straightforward and they were translated into amino acids to verify alignment. Although they were relatively uncommon within nuclear genes, heterozygous bases were coded with IUPAC symbols. Published secondary structure models of the 16S and 12S genes for Eleutherodactylus canceatus and Xenopus laevis (De Rijk et al., 1994; Van de Peer et al., 1994) were used to infer the secondary structure of the non-protein coding genes. Alignments of ribosomal DNA were adjusted to conform to known secondary structure, and insertions and deletions preferentially were placed into loop regions rather than stems. Regions of the mtDNA that remained unalignable were deleted from analyses using default parameters in the program Gblocks version 0.91b (Casteasenas, 2000) on the Gblocks server (http://molevol.ibmh.csic.es/Gblocks.html).
simultaneously estimate phylogeny and divergence times. Fourteen fossil calibrations and three divergence estimates from the literature (presented in Table 3) were used to place priors on the age of nodes within our tree (including the root node). Prior information on clade ages derived from fossil material was implemented as the lower limit of the 95% credibility interval of a normal distribution on the age of the node uniting the descendant clade representative of that fossil and its sister clade. Upper constraints were placed on two of the deeper nodes of our tree (as above) based on generally accepted divergence time of the synapsid–diapsid split (necessarily more recent than the 338 Ma inferred timing of the amniote–amphibian, Ruta et al., 2003), and assuming that the diversification of the extant Anura is more recent than the oldest fossil anuran (*Prosalirus bitis* at 195 Ma; Jenkins & Shubin, 1998; Rocek, 2003). The prior on the age of the root node was based on the generally accepted teleost–tetrapod divergence time of 420 Ma (Ahlberg & Milner, 1994).

Table 3 Fourteen calibration points in addition to the root node calibration (employed simultaneously) and their corresponding nodes on our Bayesian tree (Fig. 1).

<table>
<thead>
<tr>
<th>Calibration (node)</th>
<th>Min. time estimate</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Teleost vs. Tetrapoda (root to tip mean)</td>
<td>420 Ma</td>
<td>San Mauro et al. (2005)</td>
</tr>
<tr>
<td><em>Homo, Gallus</em> (amniotes) vs. amphibians (A)</td>
<td>338 Ma</td>
<td>Ruta et al. (2003)</td>
</tr>
<tr>
<td>Divergence of diapsids from synapsids (<em>Gallus</em> vs. <em>Homo</em>) (B)</td>
<td>310 Ma</td>
<td>Benton (1997)</td>
</tr>
<tr>
<td>Oldest anuran (<em>C) Prosalisius bitis</em></td>
<td>195 Ma</td>
<td>Jenkins &amp; Shubin (1998)</td>
</tr>
<tr>
<td>Oldest discoglossid (F) <em>EoDiscoglossus</em></td>
<td>164 Ma</td>
<td>Evans et al. (1990)</td>
</tr>
<tr>
<td>Oldest leptodactylid (I) <em>Baurubatracus pricei</em></td>
<td>86 Ma</td>
<td>Báez &amp; Peri (1989)</td>
</tr>
<tr>
<td>Oldest ‘<em>Bufo</em>’ (K)</td>
<td>55 Ma (L. Palaeocene)</td>
<td>Báez &amp; Nicoli (2004)</td>
</tr>
<tr>
<td>Oldest bufonid (J)</td>
<td>57 Ma (L. Palaeocene)</td>
<td>Báez &amp; Gasparini (1979)</td>
</tr>
<tr>
<td>Oldest pelobatid (D) <em>Eopelobates</em></td>
<td>49 Ma (L. Eocene)</td>
<td>Antunes &amp; Russell (1981)</td>
</tr>
<tr>
<td>Oldest ranid (G)</td>
<td>37 Ma (L. Eocene)</td>
<td>Rage (1984)</td>
</tr>
<tr>
<td><em>Bufo</em>: Central–N. American split (L): <em>B. praevis</em></td>
<td>20 Ma (E. Miocene)</td>
<td>Tihen (1951)</td>
</tr>
<tr>
<td>Microhylidae (H) <em>Gastrophyryne cf. carolinensis</em></td>
<td>20 Ma (Hemingfordian, Miocene)</td>
<td>Sanchíz (1998)</td>
</tr>
<tr>
<td><em>Bufo marinus</em> (M)</td>
<td>Mid Miocene (11 Ma)</td>
<td>Sanchíz (1998)</td>
</tr>
</tbody>
</table>

The mitochondrial rRNA data proved useful in analysis of phylogenetic relationships, we did not include sequence data for these loci for the most distant outgroups (*Dario, Homo* and *Gallus*) because they were problematic for aligning across divergent taxa and we were thus obligated to exclude these data from the divergence time analyses. For the *beast* analyses we assumed a GTR + I + G model of nucleotide substitution (see above) and an uncorrelated lognormal model of rate variation. The prior for the rate at the root node was set to the median value of the sum of all root-to-tip branch lengths divided by time. The monophyly of some clades strongly supported by phylogenetic analysis was constrained for reasons of computational efficiency and a Yule prior was placed on the branching rates. The results of three independent, 10,000,000-generation analyses were compared and combined in Tracer 1.2 (Rambaut & Drummond, 2003). In order to ascertain the true ‘joint prior’ of the temporal constraints used in the *beast* analysis, and thus test the strength of signal in our data, we conducted one analysis with only a single ambiguous character in our data matrix.

## RESULTS

### Phylogeny and spatial origin

Our Bayesian phylogeny is relatively robust, with most nodes resulting in bpp > 0.95 and npb > 70 (Fig. 1) and is broadly congruent with trees derived from ML and MP methods, as well as
with trees from a prior analysis of mitochondrial, nuclear and morphological data (see Fig. 4 of Pramuk, 2006). However, our topology contrasts with the results of Frost et al. (see Fig. 70 of Frost et al., 2006) in several regards (see Discussion). Generally, conflicts between the topology of Pramuk (2006) and that presented herein (Fig. 1) are in poorly supported nodes. As the phylogenetic relationships of Bufonidae included in this analysis are discussed in depth elsewhere (Pramuk, 2006), and

**Figure 1** Bayesian consensus tree resulting from analysis of 3571 bp of combined mitochondrial (12S, tRNA\(^\text{val}\), 16S rRNA) and nuclear (CXCR-4 and RAG-1) data. Support values are reported as follows: MP bootstraps above nodes; Bayesian posterior probabilities and ML bootstraps, respectively, below nodes. Lettered nodes (A–M) correspond to fossil calibrations listed in Table 3.
because the topologies resulting from these studies are broadly congruent, we do not discuss in detail here the differences between these studies. The vast majority of nodes in our hypothesis (Fig. 1) that are relevant to the understanding of bufonid phylogeny are well supported, providing a reliable phylogenetic framework to assess divergence times. The slight discrepancies resulting from this study and the earlier analysis are likely to result from the slightly different composition of the data sets employed for both (i.e. in this study: addition of the nuclear marker CXCR-4, omission of the nuclear marker POMC and morphological data). The POMC data were excluded from this study because they were not very informative and were not readily available, unlike the CXCR-4 and RAG-1 fragments, for the added Archaeobatrachian and Neobatrachian outgroups.

The topology resulting from this analysis places the older South American clades of Bufonidae as the sister to all remaining true toads (Fig. 1). This topology is consistent with a South American origin for Bufonidae.

### Divergence time estimates and temporal origin

Estimates of divergence times obtained from our analyses suggest that Bufonidae is primarily a post-Gondwanan group [78.3–98.8; 88.2 Ma (95% credibility interval and median, respectively) Fig. 2, node 1], and that clades within it are largely the result of Palaeogene diversification, which agrees with previous estimates of the age of bufonids (e.g. San Mauro et al., 2005). Comparison of posterior estimates of the joint prior indicate that the sequence data are informing the posterior age estimates and that the resulting divergence time estimates are not largely the result of the temporal constraints employed (Fig. 2).

### DISCUSSION

#### Temporal origin

Our divergence time estimate for the ancestral node of Bufonidae (78.3–98.8 Ma; node 1; Fig. 2) places the origin of the family in the Upper Cretaceous. Well-constrained geological data (e.g. Pitman et al., 1993; Maisey, 2000) pinpoint the final separation of South America and Africa in the latest Albian of the Early Cretaceous (c. 105 Ma). On the basis of present-day distribution and morphological characters (e.g. Savage, 1973), divergence estimates from immunological distance data (Maxson, 1984), and area cladograms derived from molecular data (Pramuk, 2006), prior investigators have suggested a Gondwanan origin for the true toads. However, an ancient origin for the family has been met with scepticism (Pauly et al., 2004), primarily because of a lack of bufonid fossils that are old enough (none > 60 Ma) to support a pre-Gondwanan origin for the group. Our data fail to support an origin of Bufonidae on Gondwana, as our estimates place the origin of the family after the break-up of South America and Africa (Fig. 3a). Notably, the oldest fossil attributable to the genus formerly known as ‘Bufo’ dates from the Late Palaeocene of Itaborai, Brazil (c. 55 Ma; Báez & Nicoli, 2004), with the oldest bufonid being only slightly older (c. 57 Ma; Báez & Gasparini, 1979). The specimen attributed to ‘Bufo’ reportedly is of a species aligned with the Rhinella marmor group (Báez & Nicoli, 2004). Because this fossil was described on ‘an incomplete basal portion of the left ilium’ (Báez & Nicoli, 2004), it may be reasonable to assume it can only be assigned with confidence to the South American Rhinella clade. However, this fossil is considerably older than our posterior estimate for Rhinella (node 13, Fig. 2; 31–44 Ma). Complicating matters, the Bufonidae are notoriously...
morphologically conserved (Pramuk, 2006). Thus, this may be yet another instance of the conservative variation in morphology confounding the taxonomic assignment of material—a situation we would expect to be particularly problematic in assigning fragmentary fossil remains. It is worth noting that a similar problem has plagued cichlid fish biogeography for decades, as their apparent Gondwanan distribution was confounded by the fact that the oldest fossil material of this group was from the Eocene (c. 38–54 Ma; Chakrabarty, 2004). Recent investigations (e.g. Chakrabarty, 2004; but see Vences et al., 2001) have provided strong support for a Gondwanan origin of the Cichlidae and have highlighted the paucity of the fossil record from this time and the perils of inferring true absence.

Also confounding the hypothesis of a Gondwanan distribution is the absence of extant or fossil bufonids from Madagascar and Australia–New Guinea. Biological continuity of these land masses with South America via Antarctica into the Late Cretaceous (Madagascar) and Palaeogene (Australia) is well supported by both geological and biological data (e.g. Sampson et al., 1998; Hay et al., 1999; Noonan & Chippindale, 2006). However, this apparently enigmatic absence is not unique to bufonids. Other groups with a wide or ‘Gondwanan distribution’, such as boine snakes, iguanine lizards, pelomedusoid turtles, abelisaurid theropod dinosaurs, cichlid fish and gondwanatherian mammals, are also notably absent from Australia (Sampson et al., 1998; Vences et al., 2001; Noonan & Chippindale, 2006). That so many groups of Gondwanan age are absent from this continent argues for a barrier to dispersal on Antarctica (Janis, 1993). The absence from Madagascar is less common in Gondwanan groups, though these are taxa (e.g. reptiles, birds and mammals) that are likely to have a greater tolerance than anurans to climactic fluctuations and salinity that may have been encountered along this terrestrial connection. The absence of bufonids from Madagascar may also be explained simply as an effect of time. All of the aforementioned Gondwanan groups present on this island are either extinct or persist at very low levels of diversity (one to three species).

**Spatial origin**

One of the most striking aspects of this (Fig. 1) and other recent analyses of bufonid phylogeny (Pauly et al., 2004; Frost et al., 2006; Pramuk, 2006) is the paraphyly of the South American bufonids (now comprising the ‘older’ Atelopus, Melanophryniscus, Rhaebo, Nannophryne and the relatively ‘recent’ Rhinella). Given this surprising pattern of relationships and the inferred origin of the group in South America (see above), the origin of the South American Rhinella and their sister group (the North and Central American clade comprising Anaxyrus and Cranopsis), suggests a secondary invasion of the New World.

The post-Gondwanan age and phylogenetic placement of Old World bufonids suggests an out-of-South America dispersal in the early Palaeogene. The low tolerance of bufonids to salinity makes overwater dispersal of bufonids from South America to Africa or Eurasia unlikely, but not impossible, as long-distance saltwater dispersal has been invoked to explain the distribution
of other Neobatrachian frogs (see de Queiroz, 2005, for a review). The only plausible overland route for this group would be a northward expansion into Central America, North America, and then Eurasia via Beringia. This is similar to the hypothesis proposed by Blair (1972) (see also Fig. 1 of Pauly et al., 2004). Despite our relatively poor sampling of Asian bufonids, our recovered phylogenetic pattern, combined with presumed terrestrial connections (Beringia, Thulean and De Geer land bridges), leads us to favour the Beringian connection over those of the North Atlantic for this migration.

Our posterior estimates of divergence times support the New World clade comprising Rhinella, Cranopsis and Anaxyrus diverged from its Old World relatives in the Eocene (43.3 Ma, 36.5–50 Ma; median and credibility interval, respectively). There are three putative land bridges that joined Eurasia with North America at different times throughout the Cenozoic, including the Beringia, Thulean and De Geer land bridges (Fig. 3b). Here we investigate these three possible routes given our data and known geological evidence. While some authors have favoured an Asiatic origin for Nearctic–Palaearctic dispersal (e.g. Blair, 1972), frequently without consideration of documented alternative routes (Macey et al., 2006), the close relationships of the ‘recent’ New World clade with the exclusively Eurasian + African clades suggests the possibility a trans-Atlantic route. In addition, although Bufonidae could have migrated via Beringia during the Eocene, the high latitude of this route (69–75°N; Tiffney, 1985) probably prohibited its use by ectothermic taxa for most of this time (Davis, 2002; Fig. 3b). This pattern of European/North American/Palaearctic faunal similarity with an apparent disruption in the Eocene has been documented in numerous plant (Tiffney, 1985; Davis et al., 2002) and animal (e.g. Dawson et al., 1976; Estes & Hutchison, 1980; Dawson, 2001) groups.

We suggest, based on our divergence time estimates, that secondary dispersal of Bufonidae to the New World most likely occurred during the latest Palaeocene thermal maximum (LPTM), which occurred in the early Cenozoic (65–40 Ma) and reached its peak 55 Ma (lasting for c. 100–140 kyr (e.g. Peters & Sloan, 2000; Thomas, 2004) via the Thulean (Iceland–Faeroes) land bridge (situated below 62°N), which was significantly lower in latitude than the Beringia or the De Geer land connections (c. 74°N) and therefore more amenable to dispersal by ectothermic animals. An analysis of the δ13C record at the latest Palaeocene thermal maximum (Peters & Sloan, 2000) suggests that of the three land bridges, only the Thulean and Beringian routes are likely to have maintained year-round temperatures above freezing, though fossil evidence suggests the De Geer route was suitable for ectotherms (turtles; Dawson et al., 1976; Estes & Hutchison, 1980). It has been suggested that both the Thulean and De Geer routes became interrupted in the early Eocene (Peters & Sloan, 2000; Sanmartín et al., 2001), a timing that closely fits our findings.

Vertebrate palaeontological data indicate that the faunas of North America and Europe during the early Eocene were broadly overlapping. This similarity peaked in the early Eocene when approximately 60% of known European genera were shared with North America (Tiffney, 1985; Sanmartín et al., 2001). A detailed study of Neartic patterns of relationship by Sanmartín et al. (2001) revealed that though Beringian dispersal appears to have occurred more frequently than trans-Atlantic dispersal, the difference is insignificant. Furthermore, the findings of Sanmartín et al. (2001) indicate that the height of Beringian dispersal occurred in pre-Cretaceous and Quaternary times whereas trans-Atlantic dispersal peaked in the Palaeogene, again consistent with our Eocene estimate of the timing divergence between Eurasian and New World bufonids. Due to the very broad temporal scale of the inferred terrestrial connection between the eastern Palaearctic and the western Nearctic (via Beringia; see Fig. 10 of Sanmartín et al., 2001) that entirely overlaps the timing of a trans-Atlantic connection, divergence times alone cannot support one hypothesis in favour of the other. Such differentiation will rely on the temporal overlap of divergence times with the comparatively narrow window of a trans-Atlantic terrestrial connection and phylogenetic patterns, suggesting a close European/North American relationship.

North America + Central America–South America split

The sister group relationship and reciprocal monophyly of the South American Rhinella and the North (Anaxyrus) + Central (Cranopsis) American clades recovered here is consistent with the results of prior analyses of bufonids (e.g. Pramuk, 2006); here, the estimated split of these clades is 41 Ma and 34–47 Ma (median and credibility interval, respectively). The differentiation between the South and North + Central American groups appears to have followed shortly after the arrival of bufonids in the Americas with diversification within each clade beginning almost immediately. This pattern suggests that the initial invasion of the Americas was rapid and occurred at a time when there was little hindrance to southward dispersal from North America. Southward dispersal of ectothermic groups of organisms (e.g. bufonids) may have been facilitated by cooler global temperatures following the Eocene (Irving, 2005) and intermittent terrestrial connections (see Figs 3 & 5 of Sanmartín et al., 2001). Southward dispersal of North American taxa at this time has been suggested for other groups as well (e.g. the plant Styrax; Fritsch, 1999). Isolation of North America from South America (and potentially a Middle American isolate) from the Neogene until c. 3 Ma (see Fig. 5 of Sanmartín et al., 2001) suggests a mechanism for the diversification of these three geographical lineages.

Caribbean lineage

Our Bayesian estimates for the West Indian clade allow us to test dispersalist versus vicariant hypotheses for Peltophylyne, a subject that has been explored extensively (e.g. Pramuk, 2002; Frost et al., 2006). Our estimate for the age of this clade is 51 Ma (44–60 Ma), thus precluding the possibility of this taxon representing a Cretaceous
Phylogeny

Some aspects of our phylogeny differ markedly from those of the studies of Frost et al. (2006) and Pauly et al. (2004). These authors recovered Bufo margaritifer (Rhinella fide Frost et al., 2006) and Rhamphophryne festae as sister to bufonids from Asia including Bufo (=Ingerophrynus fide Frost et al., 2006) galeatus and Bufo divergens. In our analyses, Rhinella margaritifer and Rhamphophryne are sister groups and are nested within the large clade of South American Bufo (=Chaunus, fide Frost et al., 2006). These two taxa in the analysis of Frost et al. (2006) were represented by a relatively small subset of data (an average of 1342 bp of 12S and 16S data) resulting from an unpublished thesis (Gluesenkamp, 2001). We suspect that the phylogenetic placement recovered by Frost et al. (2006) is an artefact of poor taxon and character sampling within the Rhinella and Rhamphophryne clades. Frost et al. (2006) state ‘[if] Rhinella Fitzinger, 1828, [is] found to be nested within Chaunus Wagler, 1828, the name Rhinella will take precedence for the inclusive group’. In accordance with these authors we reassign Chaunus to Rhinella.

Another striking difference in this study compared with results of prior analyses is the well-supported placement of the North American clade (Anaxyrus) as sister to Central American taxa (Cranopsis). In contrast, the other analyses supported a [North America (South + Central America)] relationship (Pauly et al., 2004; Frost et al., 2006).

General conclusions

Despite numerous investigations into the evolutionary history of Bufonidae, ours is the first to employ newly developed Bayesian methods to estimate divergence times for this widespread family. Our study illustrates the utility of increasing outgroup sampling of groups with a relatively detailed fossil record to provide calibration points outside of a fossil-poor clade of interest. Our findings reveal a surprisingly recent age for the origin of the nearly cosmopolitan Bufonidae (78–98 Ma). The relatively rapid spread of this group across the globe in the Cenozoic, accompanied by regional diversification is truly remarkable – particularly so given that the earliest occurrence of any lineage outside South America is no earlier than 52 Ma (node 9, Fig. 2; 38–52 Ma). Subsequent to their dispersal out of South America, the entire radiation of the major lineages (genera) of extant bufonid frogs took place in the Eocene. Tracking the terrestrial route for this global dispersal is likely to remain unresolved due to the temporal overlap of alternative routes. Although a Beringian route has, of late, served as the preferred route for biogeographers examining patterns of biotic exchange between the Nearctic and Palearctic, the existence of a North Atlantic connection, and its suitability for temperate/tropical taxa, is argued here and must be considered in studies of Laurasian biogeography. What is clear is that the climatic fluctuations of the Eocene, recorded in so many other biotic and geological elements, played a significant role in shaping the current distribution of this group of amphibians.

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**BIOSKETCHES**

Jennifer Pramuk and Brice Noonan performed this research at Brigham Young University (BYU) where they had appointments as postdoctoral research associates in the laboratory of Jack W. Sites, Jr. Brice Noonan is now a post-doctoral associate at Duke University and Jennifer Pramuk is the Curator of Herpetology at the Bronx Zoo/Wildlife Conservation Society.

Jack W. Sites, Jr is a Professor of Integrative Biology at Brigham Young University. A portion of this research included mentorship of Tasia Robertson, who gained field and laboratory experiences while working on this project and graduated with a degree in biology from BYU in spring of 2006.

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SUPPLEMENTARY MATERIAL

The following supplementary material is available for this article:

Appendix S1 Outgroup and ingroup taxa included in this analysis.

This material is available as part of the online article from:


(This link will take you to the article abstract).

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