

Supplementary Materials and Methods for:
Populating a Continent:
Phylogenomics Reveal the Timing of Australian Frog Diversification

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Data are available from the Dryad Digital Repository:

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and from the GitHub repository:

https://github.com/IanGBrennan/Crown_Frogs

Developing Figure 1

Figure 1 aims to provide background on the richness and spatial distribution of the focal frog clades, alongside evolutionary context for the accumulation of vertebrate biodiversity on the Australian continent. Neither the top or bottom visualizations are intended to provide an explanation of the *processes* dictating Australian vertebrate diversity. Instead they are visualizations of the *patterns* of contemporary Australian vertebrate diversity.

We downloaded Australian annual rainfall data from NASA using the R package *nasapower*, and combined this with species occurrence records downloaded from the Atlas of Living Australia. Annual rainfall is an easily interpretable measure of water availability in an environment, and as such provides a reflection of habitat suitability for frogs. However, we acknowledge that composite environmental variables such as actual evapotranspiration (AET) may be a better predictor of contemporary frog richness patterns (Powney et al., 2010; Coops et al., 2018).

To plot the relationship between clade age and richness of Australian terrestrial vertebrates we collected data from all available non-nested (each clade is only represented once) clades from the literature. Data are compiled in the supplement *Comparative_Radiations.csv* and can be plotted using the script *Comparative_Radiations.R*. We also incorporated information where available about the biogeographic origin of each group to visualize the contrast between young clades from Asia and old Gondwanan groups. The included regression helps to visualize an interesting *pattern* in the data: species richness increases with clade age. However, we do not present this as an evolutionary explanation for varied richness among Australian terrestrial vertebrate groups.

Sequence Identity

To confirm sequence identity we downloaded a fasta file of *Xenopus* genes from Ensembl (UCB_Xtro_10.0) and used *metablast* to do a reciprocal blast against the Anchored

Hybrid Enrichment loci. Of the 450 loci, 390 matched to *Xenopus* exons, and the remainder to intronic and flanking sequences (see *RBH_AHE_Xenopus.csv* in Supplementary Material for list). Downstream divergence time analysis relied on partitioning loci by codon position and so only exonic targets were retained for this exercise. AHE exons are listed under the column *query_id* and *Xenopus* matches under *subject_id* with gene name indicated by *subject_id_name*.

Phylogenetics

Phylogeny reconstruction in the era of phylogenomics has simultaneously resolved many longstanding systematic questions and instigated new ones. The search for the most accurate species tree has reignited debates about concatenation versus coalescent methods and their pros and cons. Here we address two common issues resulting in phylogenetic error: incomplete lineage sorting (ILS) and rate variation among lineages and sites (heterotachy). Identifying and modelling heterotachy generally requires long alignments to accurately model rate variation, so most methods rely on concatenated sequence alignments. Because of the ancient age of our focal group and sparse sampling among major groups we risk biases due to heterotachy. To estimate a species tree from our concatenated alignment we used the General Heterogeneous evolution On a Single Topology (GHOST) method. GHOST is implemented in IQTREE and requires a user specified number of mixture (rate) classes and model. We separately fit unlinked GTR models with 2—5 mixture classes (e.g.: *-m GTR*H4*). AIC comparison identified the 4-class model as preferred ($H*2$ AICc = 13754122; $H*3$ AICc = 13604562; $H*4$ AICc = 13500200; $H*5$ AICc = 13523685).

Concatenation methods are however expected to perform poorly when the true branching pattern includes nested rapid divergence events. In this case high rates of ILS may bias phylogenetic signal, trapping concatenation in the anomaly zone. To counter this we estimated a species tree using ASTRAL with IQTREE genetrees as input.

Biogeography

To assess the biogeographic history of Australian frogs we combined our phylogenetic hypothesis with known fossil information and reconstructed ancestral ranges in *BioGeoBEARS* (Matzke 2014). We started by dividing the geographic distribution of our sampled taxa into eight discrete areas that (1) summarize the general biogeographic history of frogs, (2) are relevant to

our sampling and questions, and (3) make sense on a geological timescale with reference to plate tectonics over the last 220 million years. These areas correspond to Africa, Asia (excluding the Indian subcontinent), Australo-Papua, Europe, Madagascar, North America, South America, and Antarctica. For single tips that represent a genus or subfamily we coded their geographic range accordingly, however this never resulted in an overrepresentation of areas that might inflate dispersal estimates. Our primary objective was to identify the ancestral distributions of each Australian frog clade to provide an estimate of their origins.

While Antarctica seems a strange inclusion in our discrete bioregions owing to its current climate and lack of frogs, a recent discovery has identified the continent's first anuran (Mörs et al. 2020). This information is vital to our understanding of the connectivity of the Gondwanan supercontinent as well as the biogeographic history of Australian frogs. To incorporate this sample we added a tip to our tree with an appropriate estimated age following Mörs et al. (2020). Due to our limited sampling of extant Calyptocephalellidae however, the addition of this taxon dramatically imbalances range reconstruction. To correct for this and account for the ancient known history of calyptocephalellids in South America (Moura et al. 2021; Nicoli et al. 2022) we included two additional South American fossil taxa, one younger—*Calyptocephalella canqueli* (following Muzzopappa & Báez 2009) and one older—*Calyptocephalella satan* (following Nicoli et al. 2022). Note, here we consider *C. satan* as interchangeable with the similarly aged *Baurubatrachus pricei* (following Báez & Gómez 2018), being representative of a broader extinct South American calyptocephalellid diversity (Nicoli et al. 2022). While the taxonomy and phylogenetic relationships of extant (*Calyptocephalella gayi*, *Telmatobufo* spp.) and extinct (*C. canqueli*, *C. satan*, et al.) calyptocephalellids is unresolved, we believe this sampling strategy is an appropriate solution for the question at hand.

In addition to the origins of Australian frogs we were interested in identifying how pelodryadids arrived in Australia. Specifically we aimed to test if they arrived via dispersal through Antarctica or overwater dispersal from South America. To test these hypotheses we added an ancestor (*Pelodryadidae_Ancestor*) to our tree along the stem leading to the Pelodryadidae. *BioGeoBEARS* accommodates sampled ancestors as “hooks”, which are represented by a non-zero terminal edge length shorter than an arbitrary threshold (here: 0.000001 million years). This allowed us to force the ancestral pelodryadid to either have had a range in Antarctica (Hypothesis 1; H1; South America→Antarctica→Australia), or have

remained in South America prior to an overwater dispersal event (Hypothesis 2; H2; South America→Australia).

The biogeographic history of frogs has played out on a very long timescale (>200 million years) and across continents that have moved dramatically relative to one another. To capture the complex interplay of plate tectonics and biogeography we incorporated several elements that might make this scenario more realistic. We first divided the anuran tree into six equal slices of 30 million years (0—30, 30—60, ... 150—180) and one slice of 40 million years (180—220). At the upper bound of each time slice (30, 60 ... 180, 220) we then reconstructed continental positions in GPlates following Landis (2017) and extracted pairwise distances (in km) among areas from the closest points of two areas, using the measuring tool in GPlates. Additionally, we characterized regions as (a) in contact with one another, (b) separated by ocean, or (c) separated by another landmass. We used the area distances through time to construct distance matrices following Van Dam & Matzke (2016), and the area adjacency information to construct dispersal matrices.

Constructing these time-specific matrices allowed us to compare a set of scenarios that include the traditional DEC model (Dispersal Extinction Cladogenesis), DEC+j which allows jumps in range expansion (range discontinuity), DEC+x which estimates a parameter x corresponding to a correction for dispersal probability as a function of distance between areas ($\text{dispersal} * \text{relative_distance}^x$), DEC+j+x which allows jumps and corrects for distance among areas, DEC+x+w which estimates x (correcting for distance) in addition to a parameter w which can be interpreted as correcting for different levels of area adjacency ($\text{dispersal} * \text{dispersal_multiplier}^w$), and finally DEC+j+x+w which can be interpreted as allowing for jumps in range expansion (j) while correcting for geographic distance between areas (x) and types of adjacency/separation (w). Ultimately the most complex model (DEC+j+x+w) is an attempt to account for differences in the geographic distance between areas (x) as well as what separates them (w), through time, while allowing taxa to make rapid dispersal events (j). Estimating w unfortunately necessitates the manual input of dispersal multipliers which scale dispersal probability, however these are ultimately corrected by estimating their relationship via w . We established conservative manual dispersal multipliers for adjacent areas (1), areas split by another contiguous landmass (0.5), and areas split by ocean (0.25). Finally, we fit all six models

to both the H1 and H2 datasets. We compared models by calculating AIC values, delta AIC against the best fit, and AIC weights as the relative contribution to the pool of models.

Table S1. Taxon sampling for this project.

Geography	Superfamily/Clade	Family	Subfamily	Genus species	Registration
Outgroup	Pipoidea	Pipidae	—	<i>Xenopus tropicalis</i>	NCBI Genome
Outgroup	Pipoidea	Pipidae	—	<i>Pipidae Pipa pipa</i>	MVZ 247511
Outgroup	Pipoidea	Rhinophrynidae	—	<i>Rhinophrynus dorsalis</i>	MVZ 164756
Outgroup	Leiopelmatoidea	Ascaphidae	—	<i>Ascaphus montanus</i>	REF AscMon
Outgroup	Discoglossoidea	Bombinatoridae	—	<i>Bombina microdeladigitata</i>	CAS 242112
Outgroup	Discoglossoidea	Alytidae	—	<i>Alytes obstetricans</i>	MVZ 231914
Outgroup	Pelobatoidea	Scaphiopodidae	—	<i>Spea hammondi</i>	MVZ 145187
Outgroup	Pelobatoidea	Pelodytidae	—	<i>Pelodytes ibericus</i>	MVZ 186009
Outgroup	Pelobatoidea	Megophryidae	—	<i>Leptolalax bourreti</i>	AMCC 106489
Outgroup	Pelobatoidea	Pelobatidae	—	<i>Pelobates syriacus</i>	MVZ 234650
Outgroup	—	Heleophrynidae	—	<i>Heleophryne purcelli</i>	SANBI 1954
Outgroup	Ranoidea	Ptychadenidae	—	<i>Ptychadena mascareniensis</i>	ESP/CJR R1068
Outgroup	Ranoidea	Phrynobatrachidae	—	<i>Phrynobatrachus keniensis</i>	MVZ 226261
Outgroup	Ranoidea	Microhylidae	Phrynomatinae	<i>Phrynomantis annectens</i>	ESP/CJR R1330
Outgroup	Ranoidea	Microhylidae	Otophryinae	<i>Otophryne robusta</i>	PLVP PT459
Outgroup	Ranoidea	Microhylidae	Gastrophryinae	<i>Stereocyclops incrassatus</i>	PLVP PT273
Outgroup	Ranoidea	Microhylidae	Scaphiophryinae	<i>Scaphiophryne brevis</i>	PLVP PT312
Outgroup	Ranoidea	Microhylidae	Cophylinae	<i>Plethodontohyla notosticta</i>	AMCC 128714
Outgroup	Ranoidea	Microhylidae	Kalophryinae	<i>Kalophrynus interlineatus</i>	ABTC 105933
Outgroup	Ranoidea	Microhylidae	Dyscophinae	<i>Dyscophus guineti</i>	MVZ 238744
Outgroup	Ranoidea	Microhylidae	Microhylinae	<i>Kaloula picta</i>	ABTC 76311
Outgroup	Ranoidea	Microhylidae	Microhylinae	<i>Microhyla berdmorei</i>	ABTC 106005
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Liophryne rhododactyla</i>	ABTC 49542
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Callulops doriae</i>	ABTC 98415
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Hylophorbus rainerguntheri</i>	ABTC 98304
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Genyophryne thomsoni</i>	PLVP PT452
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Barygenys flavigularis</i>	PLVP PT439
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Copiula pipilans</i>	ABTC 114698
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Austrochaperina guttata</i>	ABTC 141506
Australian Clade	Ranoidea	Microhylidae	Asterophryinae	<i>Austrochaperina gracilipes</i>	ABTC 79186
Australian Clade	Ranoidea	Microhylidae	Asterophryinae	<i>Austrochaperina robusta</i>	conx5153
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Oreophryne brachypus</i>	ABTC 104804
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Aphantophryne pansa</i>	ABTC 49605
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Cophixalus parkeri</i>	ABTC 49557
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Cophixalus balbus</i>	ABTC 114884
Outgroup	Ranoidea	Microhylidae	Asterophryinae	<i>Cophixalus bewaniensis</i>	ABTC 112107
Australian Clade	Ranoidea	Microhylidae	Asterophryinae	<i>Cophixalus crepitans</i>	conx1112
Australian Clade	Ranoidea	Microhylidae	Asterophryinae	<i>Cophixalus infacetis</i>	conx5295
Australian Clade	Ranoidea	Microhylidae	Asterophryinae	<i>Cophixalus hosmeri</i>	conx5267
Outgroup	Myobatrachoidea	Calyptocephalellidae	—	<i>Calyptocephalella gayi</i>	PMH 1
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Rheobatrachus silus</i>	ABTC 7324
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Rheobatrachus vitellinus</i>	ABTC 105698
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Mixophyes balbus</i>	ABTC 25323
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Mixophyes hihiorlo</i>	ABTC 45861
Australian Clade	Myobatrachoidea	Limnodynastidae	—	<i>Platyplectrum fletcheri</i>	ABTC 24892

Australian Clade	Myobatrachoidea	Limnodynastidae	—	<i>Platyplectrum ornatus</i>	ABTC 15543
Australian Clade	Myobatrachoidea	Limnodynastidae	—	<i>Heleioporus australiacus</i>	ABTC 67742
Australian Clade	Myobatrachoidea	Limnodynastidae	—	<i>Neobatrachus albipes</i>	ABTC 15833
Australian Clade	Myobatrachoidea	Limnodynastidae	—	<i>Notaden nichollsi</i>	ABTC 15833
Australian Clade	Myobatrachoidea	Limnodynastidae	—	<i>Limnodynastes dumerilii</i>	ABTC 104299
Australian Clade	Myobatrachoidea	Limnodynastidae	—	<i>Philoria sphagnicola</i>	ABTC 25832
Australian Clade	Myobatrachoidea	Limnodynastidae	—	<i>Adelotus brevis</i>	ABTC 24210
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Taudactylus liemi</i>	ABTC 50947
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Paracrinia haswelli</i>	ABTC 26441
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Anistisia (Geocrinia) alba</i>	ABTC 106079
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Assa darlingtoni</i>	ABTC 136278
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Crinia (Bryobatrachus) nimbus</i>	ABTC 25297
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Crinia signifera</i>	ABTC 25676
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Spicospina flammocaerulea</i>	ABTC 144371
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Uperoleia laevigata</i>	MM 1227
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Pseudophryne major</i>	ABTC 16479
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Metacrinia nichollsi</i>	ABTC 17124
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Arenophryne rotunda</i>	ABTC 114066
Australian Clade	Myobatrachoidea	Myobatrachidae	—	<i>Myobatrachus gouldii</i>	WAM R156759
Outgroup	Hyloidea	Hemiphractidae	—	<i>Stefania evansi</i>	BPN1286
Outgroup	Hyloidea	Ceratophryidae	—	<i>Ceratophrys cornuta</i>	MVZ 247561
Outgroup	Hyloidea	Hylidae	Cophomantinae	<i>Hypsiboas crepitans</i>	YPM 10666
Outgroup	Hyloidea	Hylidae	Lophohylineae	<i>Osteopilus dominicensis</i>	MCZA148702
Outgroup	Hyloidea	Hylidae	Scinaxinae	<i>Scinax staufferi</i>	MVZ 257781
Outgroup	Hyloidea	Hylidae	Pseudinae	<i>Pseudis paradoxa</i>	LSUMNS 12511
Outgroup	Hyloidea	Hylidae	Dendropsophinae	<i>Dendropsophus microcephalus</i>	MVZ 264263
Outgroup	Hyloidea	Hylidae	Acrisinae	<i>Pseudacris nigrita</i>	REF PseNig
Outgroup	Hyloidea	Hylidae	Hylinae	<i>Smilisca fodiens</i>	YPM 014191
Outgroup	Hyloidea	Phyllomedusidae	—	<i>Cruziohyla calcarifer</i>	QCAZ 48552
Outgroup	Hyloidea	Phyllomedusidae	—	<i>Phyllomedusa vallantii</i>	QCAZ 48818
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria citropa</i>	ABTC 7146
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria (Nyctimystes) dayi</i>	ABTC 15997
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria genimaculata</i>	ABTC 42824
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria wilcoxii</i>	ABTC 16804
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria andiirmalin</i>	ABTC 142651
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria xanthomera</i>	ABTC 102385
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria gilleni</i>	ABTC 30786
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria raniformis</i>	ABTC 12854
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria thesaurensis</i>	ABTC 50489
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria dahlui</i>	ABTC 102434
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Cyclorana cultripes</i>	ABTC 16892
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria infrafrenata</i>	ABTC 86210
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria brevipalmata</i>	ABTC 127632
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Nyctimystes disrupta</i>	ABTC 48225
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria revelata</i>	ABTC 80814
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria burrowsi</i>	ABTC 17631
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria tyleri</i>	ABTC 3925
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria balatus</i>	ABTC 100638

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Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria dorsalis</i>	ABTC 79181
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria adalaidensis</i>	ABTC 28282
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria angiana</i>	ABTC 48210
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria fallax</i>	ABTC 102409
Australian Clade	Hyloidea	Pelodyadidae	—	<i>Litoria tornieri</i>	ABTC 11777

Table S2. Fossil calibrations implemented in MCMCtree analysis of frog divergence dates. Node number (#) corresponds to nodes in supplementary figure below.

#	Node Calibrated	Fossil	Minimum	Soft Max.	Source (see Feng et al. 2017)
1	Anura	† <i>Liaobatrachus zhaoi</i>	129.7	252	Chang et al. (2009)
2	Alytoidea	† <i>Iberobatrachus angelae</i>	125	252	Gomez et al. (2016)
3	Pipanura	† <i>Rhadinosteus parvus</i>	148.1	252	Cannatella (2015)
4	Pipoidea	† <i>Neusibatrachus wilferti</i>	127.2	52	Gomez et al. (2016)
5	Pipidae	† <i>Pachycentra taqueti</i>	83.6	48.1	Cannatella (2015)
6	Pelobatoidea	† <i>Elkobatrachus brocki</i>	46.1	148.1	Henrici and Haynes (2006)
7	Pelodytes + (Pelobatidae + Megophryidae)	† <i>Miopelodytes gilmorei</i>	38.9	148.1	Henrici and Haynes (2006)
8	Pelobatidae + Megophryidae	† <i>Macropelobates osborni</i>	28.1	148.1	Cohen et al. (2013)
9	Acosmanura	† <i>Eurycephalella alcinae</i>	113	252	Baez (2009)
10	Neobatrachia	† <i>Beelzebufo ampinga</i>	66	148.1	Rogers et al. (2013)
11	Myobatrachoidea	† <i>Calyptocephalella pichileufensis</i>	47.5	48.1	Gomez et al. (2011)
12	Ranoidea	† <i>Thamastosaurus gezei</i>	33.9	148.1	Rage and Rocek (2007)
13	Ptychadena + Phrynobatrachus	<i>Ptychadenidae fossil</i>	25	148.1	Blackburn et al. (2015)

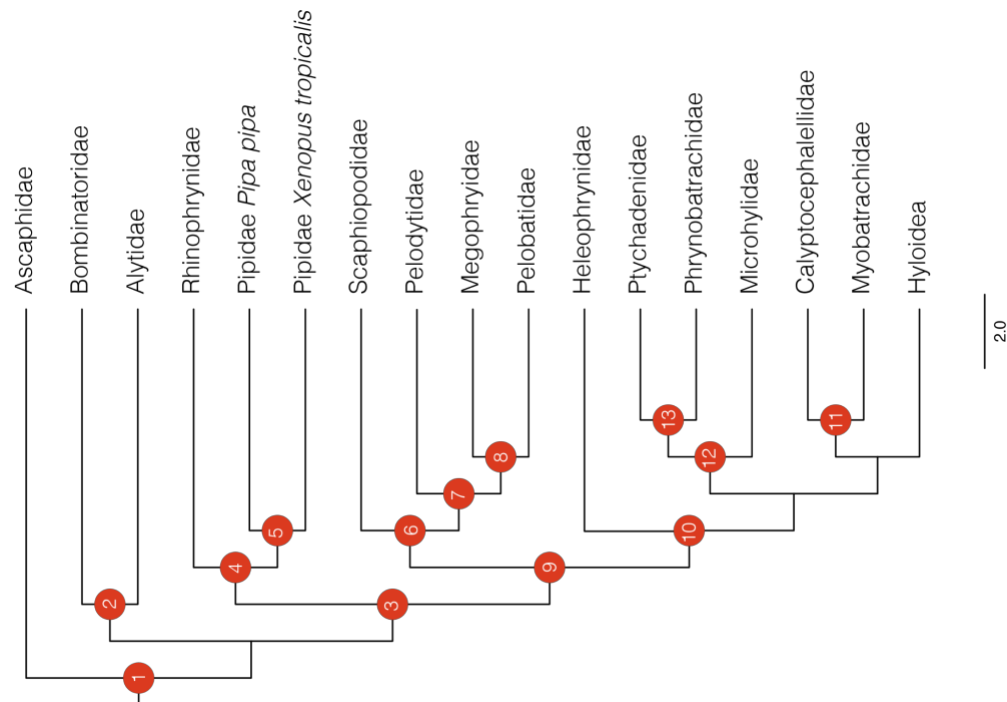


Table S3. Results of biogeographic ancestral range reconstruction in *BioGeoBEARS*. Hypothesis *H1* refers to the dispersal of pelodyadid frogs from South America through Antarctica to Australia, whereas

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H2 refers to the over water dispersal of pelodryadid frogs from South America directly to Australia. Models are sorted according to deltaAIC scores, indicating the preferred model at the top.

Model	Hypothesis	No. Param.	LnL	AIC	deltaAIC	AICw
DEC+j+x+w	H1	5	-91.47	192.94	0	59.7
DEC+j+x	H1	4	-93.49	194.98	2.04	21.5
DEC+j+x+w	H2	5	-93.08	196.16	3.22	11.9
DEC+j+x	H2	4	-94.66	197.32	4.38	6.69
DEC+x+w	H2	4	-102.71	213.42	20.48	0
DEC+j	H2	3	-104.91	215.82	22.88	0
DEC+x+w	H1	4	-105	218	25.06	0
DEC+x	H2	3	-106.47	218.94	26	0
DEC+x	H1	3	-107.85	221.7	28.76	0
DEC+j	H1	3	-109.33	224.66	31.72	0
DEC	H2	2	-114.67	233.34	40.4	0
DEC	H1	2	-121.56	247.12	54.18	0



Figure S1. Data completeness across all samples. Left histogram shows data completeness as percent of bases in total alignment (concatenated alignment length 523,036 bp) exclusive of gaps (-) and missing bases (N). Right histogram shows data completeness as the absolute number of loci included per sample, as a representation of the number of gene trees per sample.

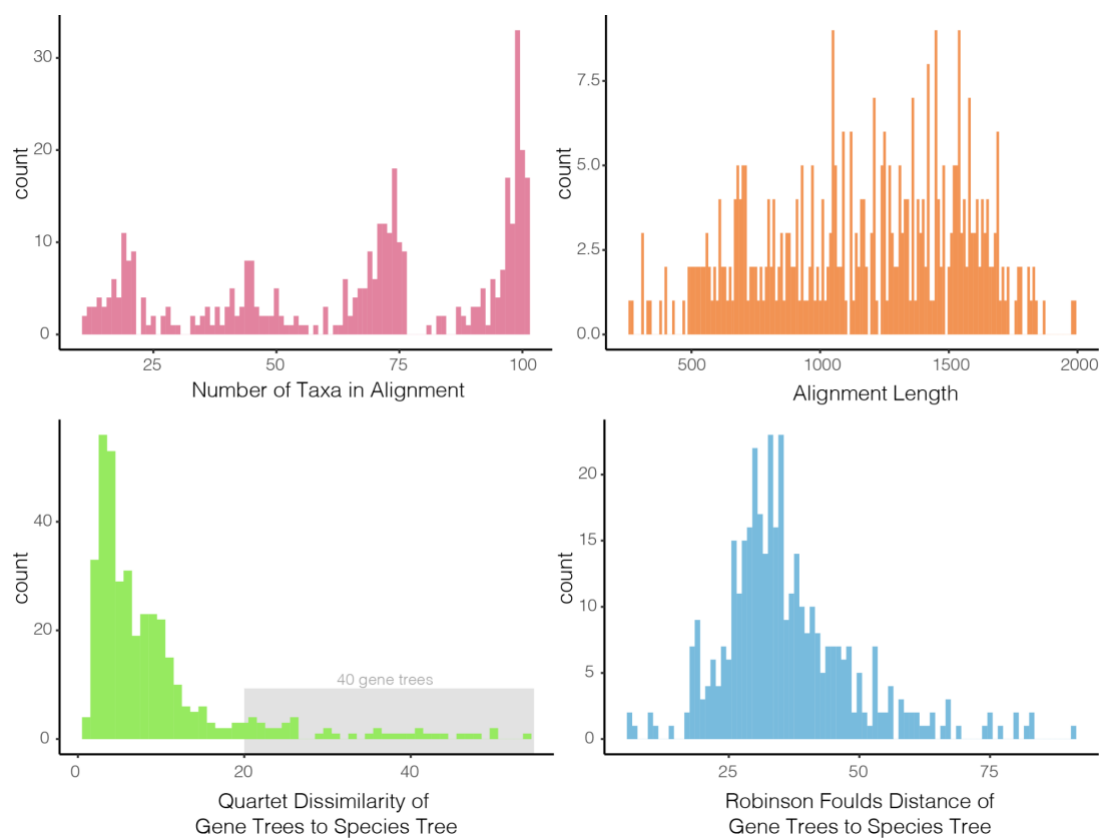


Figure S2. Basic summary statistics of the 450 locus alignments and gene trees. Top row shows histograms of the number of taxa in (max=101, min=11) and length of each alignment. Bottom row shows gene tree--species tree distances as quartet dissimilarity scores and Robinson Foulds distances, two different measures of topological similarity. Both quartet dissimilarity and RF scores are estimated by first subsetting the species tree to match gene tree sampling.

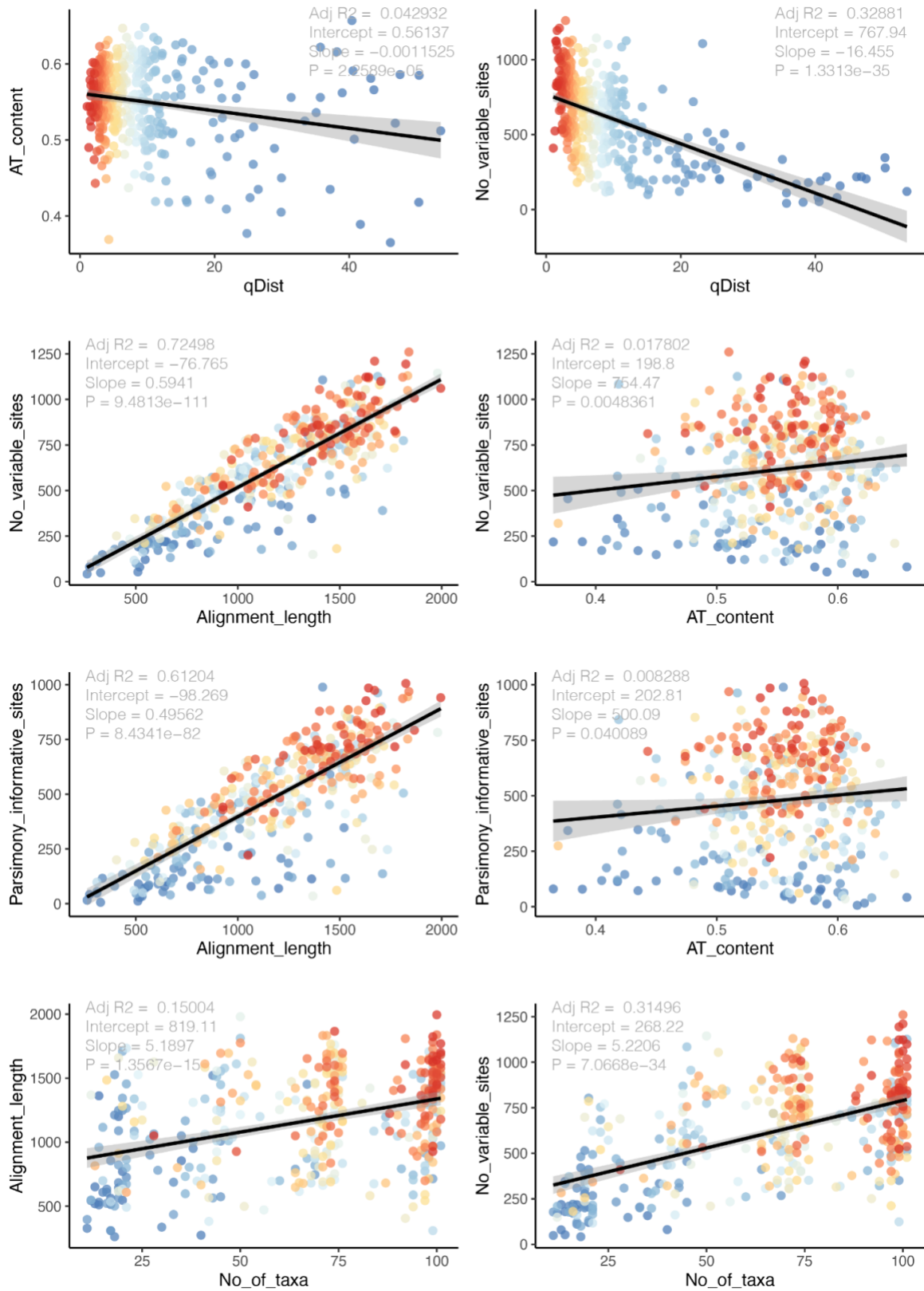


Figure S3. Detailed summary statistics of the 450 locus alignments and gene trees. Top row compares AT content and number of variable sites against quartet distance between each gene tree and the species tree (a measure of topological similarity). The second and third rows compare measures of locus informativeness (number of variable sites, number of parsimony informative sites) against alignment length and AT content. The bottom row shows alignment length and number of variable sites as a function of the number of taxa in the alignment. In all plots points (representing trees or alignments) are colored according to the quartet distance from the species tree.

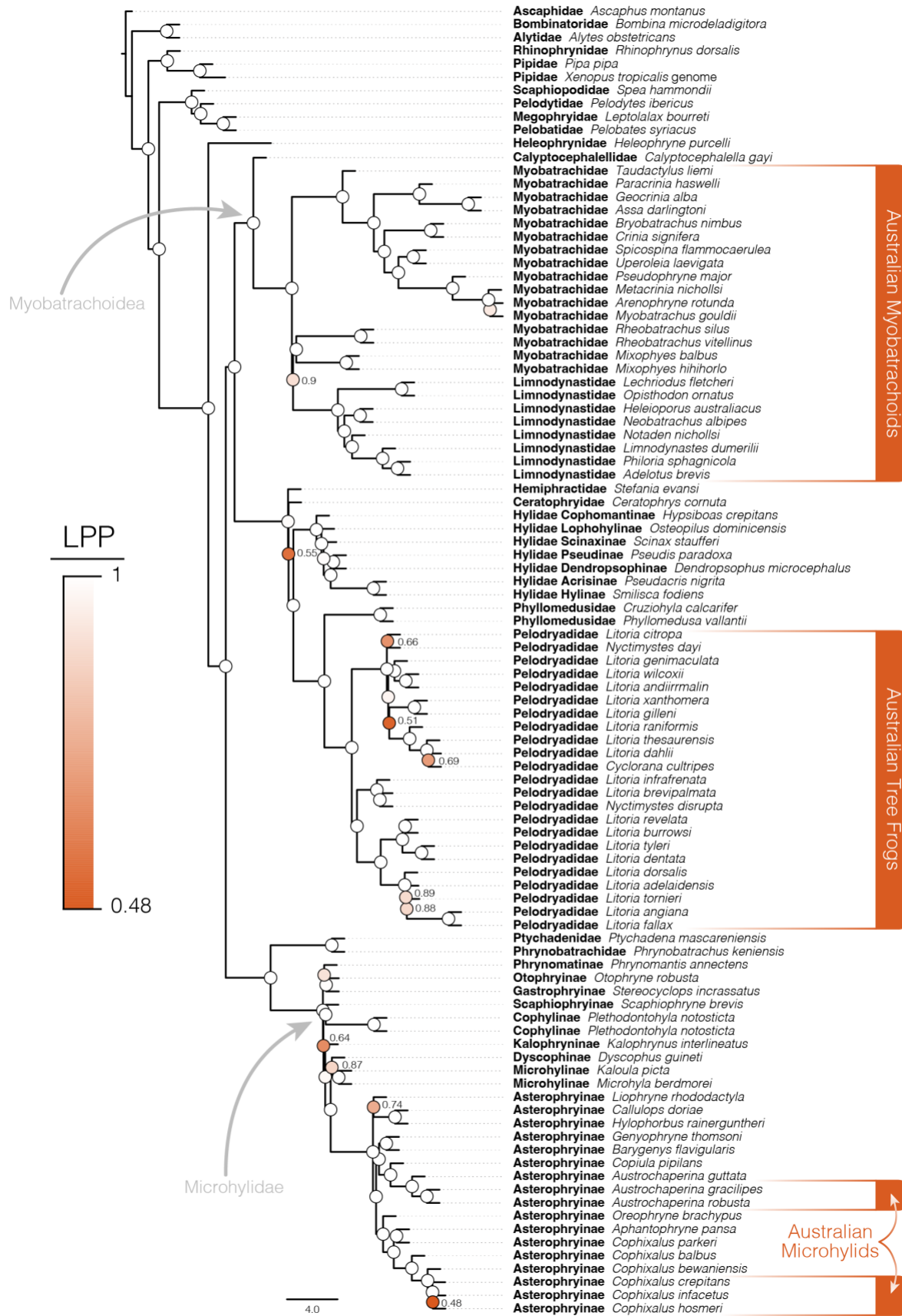


Figure S4. Species tree of Australian frogs and appropriate outgroup taxa estimated using ASTRAL with locus trees estimated by IQTREE as input. Phylogenetic resolution among major frog groups and within Australian frog clades is consistently high. Ultrafast bootstrap support values (Hoang et al. 2018) are shown at nodes and colored according to local posterior probabilities (LPP), values >0.9 are considered strongly supported and not indicated at nodes (white circles).



Figure S5. Species tree of Australian frogs and appropriate outgroup taxa estimated from the concatenated sequence alignment under the GHOST model implemented in IQTREE. Phylogenetic resolution among major frog groups and within Australian frog clades is consistently high. Only ultrafast bootstrap support values less than 100 are noted, here by grey branches and text (Hoang et al. 2018). This topology is highly consistent with the phylogeny estimated using ASTRAL (Fig.2, S4), however three differences are highlighted by orange branches and arrows indicating their location. Branch lengths are weighted averages over four heterotachy classes.

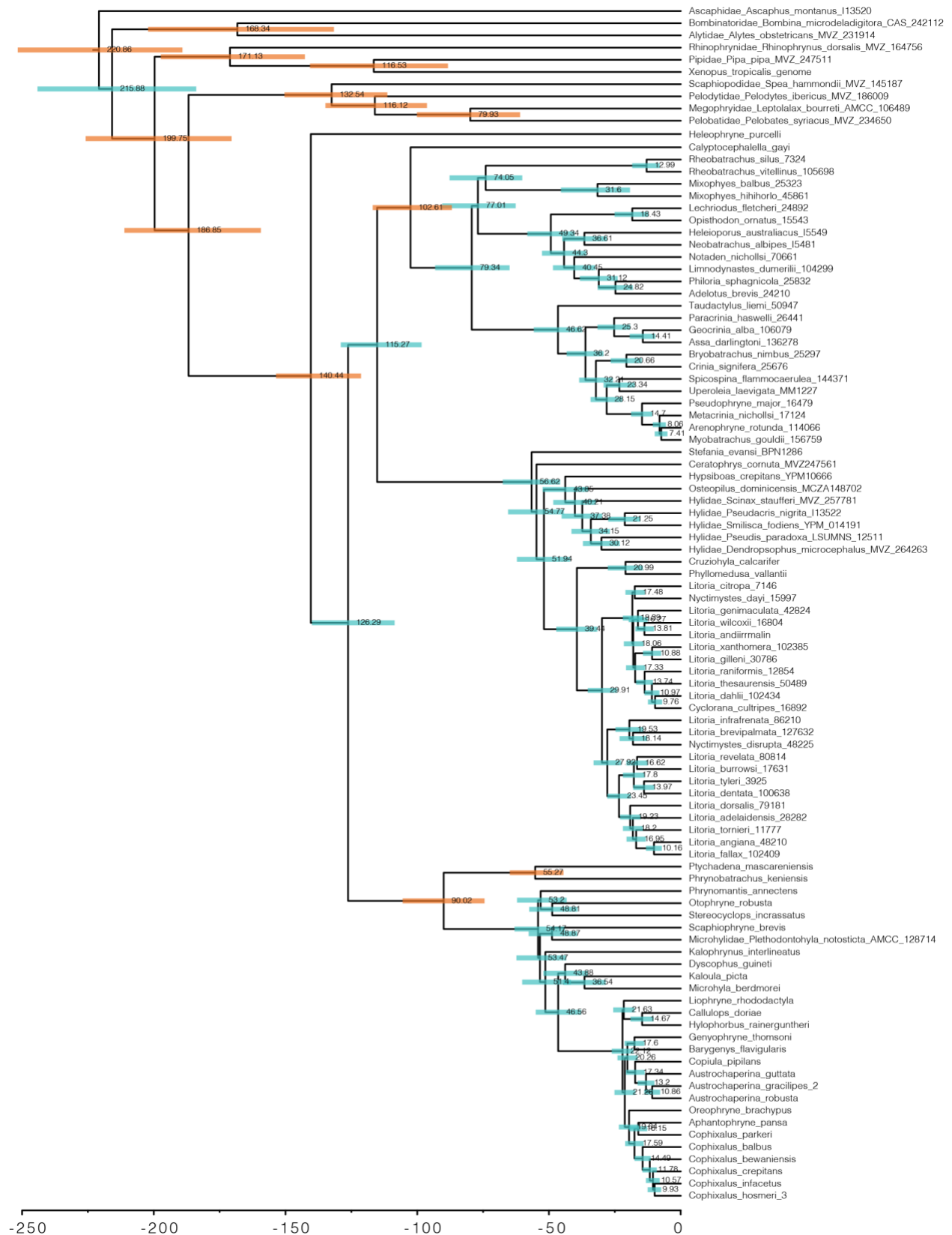


Figure S6. Species tree of Australian and outgroup frogs estimated with ASTRAL from IQTREE genetrees and time-calibrated with MCMCtree. Shaded bars at nodes indicate 95% confidence estimates on ages and numbers indicate mean age estimates. Orange shaded bars indicate nodes which were calibrated with from fossil evidence (see Table S2).

Time-Stratified DEC+J+X+W Frogs H1

ancstates: global optim, 3 areas max. d=0.0011; e=2e-04; x=-0.5129; w=1.5756; j=0.1366; LnL=-91.47

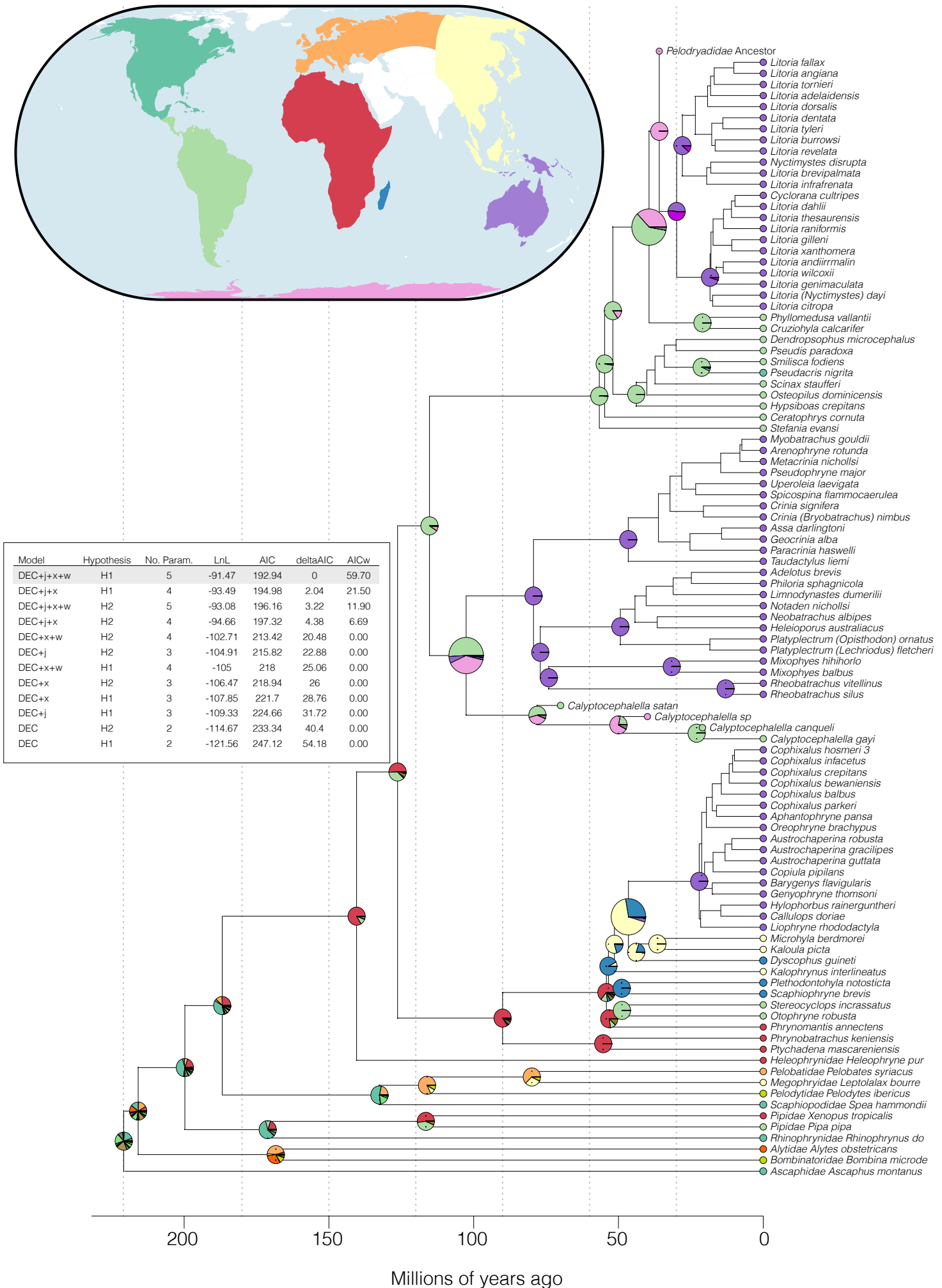


Figure S7. Biogeographic history of frogs with a focus on the range reconstruction of Australian clades. Inset table shows the 12 models fit to the data (6 models across two ‘datasets’), ordered by deltaAIC. Ancestral range estimates under the preferred model DEC+*j*+*x*+*w* *H1* are shown at right as pie charts on the phylogenomic tree with several fossil taxa added. Pie chart for the most recent common ancestor of each Australian clade is enlarged to enhance visualization. The eight bioregions are shown in the inset map and colors correspond to the tip state of taxa on the tree. Additional colors in the pie charts correspond to combinations of areas, but are not discussed further.

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