*Materials and Methods*

*Phylogenomics and Divergence Dating*

We assembled an exon-capture dataset comprising 143 frog samples across 113 species that span nearly all microhylid subfamilies (10 of 12 recognized). Exceptions are limited to Hoplophryninae and Melanobatrachinae frogs of East Africa and India. Sampling focused on the Asterophryinae which are found across Southeast Asia, with greatest diversity in Wallacea and Sahul. Our sampling of the Asterophryinae represents 71 species across 14 of 17 recognized genera (with exceptions Gastrophrynoides, Paedophryne, Siamophryne, Vietnamophryne). Table of sampling information in Microhylidae\_SampleInfo.csv. We generated new Anchored Hybrid Enrichment (AHE—Lemmon et al. 2012) data for 95 samples and combined these with outgroup samples from Hime et al.’s (2021) amphibian phylogenomic dataset. Data from different AHE projects were combined using custom scripts which relied on *metablastr* to identify orthologous loci (*blast\_best\_reciprocal\_hit*) (Benoit & Drost 2021), *mafft* to align them (*--add*, *--keeplength*) (Katoh et al. 2013), and *AMAS* to manipulate alignments (Borowiec 2016). We reconstructed individual genealogies for our exon-capture data (n = 450) under maximum-likelihood in IQTREE (Nguyen et al. 2015), allowing the program to assign the best fitting model of nucleotide substitution using ModelFinder (Kalyaanamoorthy et al. 2017) and then perform 1,000 ultrafast bootstraps (Minh et al. 2013). We then estimated a species tree using the quartet-based summary method ASTRAL III (Zhang et al. 2018) with IQTREE gene trees as input. To estimate divergence times among taxa on the ASTRAL species tree we applied a series of fossil calibrations first compiled by Feng et al. (2019) (Table S2) and used the Bayesian divergence time software MCMCtree (Rannala & Young 2007). We started by concatenating all exonic loci (n=390; Supp. *Sequence Identity*) and partitioning them into two partitions, first and second codons together, and third codons separately, following the strategy of dos Reis et al. (2018). Complex partitioning strategies such as filtering by evolutionary rate are possible but less influential than the absolute number of partitions (dos Reis et al. 2012). Additional data partitions ultimately incur substantial computational costs for modest increases in dating precision, and so we opted instead for a more conservative approach. We then used *baseml* to estimate approximate likelihoods (dos Reis & Yang 2011) and branch lengths before running *mcmctree* on the gradient and Hessian (in.BV file) for ten replicate analyses. We inspected mcmc files for stationarity and compared for convergence, then combined them using logCombiner, and used this combined mcmc file to summarize divergence times on our tree (*print = -1* in .ctl file). Sample, alignment, and gene trees are available alongside all other materials on Dryad (doi:) and GitHub (https://github.com/IanGBrennan/Microhylidae).

*Morphological Evolution*

To investigate the morphological evolution of boulder living *Cophixalus* we started by collecting linear measurements of the Australian clade (17 species more closely related to *C. australis* than to *C. crepitans*). We measured the snout-vent length (SVL), hind limb length (HLL), head width (HW), and width of the third toepad (THIRD). Specifics of how these measurements were taken are provided in the Supplementary Material. Measurements were then averaged to determine species mean values that were used for downstream analyses (only males? only females?).

What else:

* PCA of all traits (plotted)
* Clustering algorithm on PCA values
* Estimated range size and plotted against mean (max?) elevation to show increasing threat (IUCN) as a function of small ranges and high elevations
* Translated mean traits into log-shape ratios to remove effect of size
* *l1ou* on LSR to show convergent shifts towards bigger size in boulder living frogs
* *ratematrix* to show that rate correlations among traits are not distinct between boulder living and regular *Cophixalus* (limited by small sample size), though trait correlations do seem ‘tighter’ in boulder frogs
* Allometry tests of each trait against LSR ‘size’. Determined there is an allometric effect of size on SVL (shorter with increasing size) and toepad width (larger with increasing size), but no effect on head width or hindlimb length (isometry).
* Anything I’ve missed?

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