

Supplementary Material

***BEAST species tree**

Relaxed Clock dating:

Mitochondrial loci included ND2 and 16S, and nuclear loci included regions of BDNF, BRCA1, BRCA2, CMOS, EXPH5, KIF24, MC1R, MXRA5, and RAG1 protein coding genes. We used the molecular clock parameter settings previously used by Barley et al. [1] to generate substitution rate prior distributions. These included uncorrelated relaxed molecular clocks for mitochondrial genes, with 95 % normal distribution rate priors. Each rate prior included mean \pm standard deviation (SD) parameters. Specifically, we used a mean rate of 0.00895 % divergence per million years (\pm 0.333 SD) for ND2, and a mean rate of 0.008 % divergence per million years (\pm 0.333 SD) for 16S. These rate distributions encompass rates of mitochondrial divergence previously reported for skinks [2–4]). Additionally, as in [1], we used uniform rate distributions for nuclear loci, with means ranging from 0–50 % divergence per million years (\pm 0.5 SD) to allow for a wide range of actual rates for nuclear loci.

Ancestral State Reconstruction

Mesquite ancestral state reconstruction analyses were conducted to infer ancestral presence or absence of extreme matrotrophy in mabuyine skinks. We inferred ancestral states under 1) parsimony or 2) likelihood under the asymmetrical 2-parameter Markov k-state model.

Missing Data

DNA alignment missing data was low (28.5 %) and every individual was sequenced at 16S. Additionally, all species except *Brasiliscincus heathi* were sequenced at BDNF, EXPH5, MC1R, and RAG1, and all species except *Notomabuya frenata* were sequenced at CMOS.

Table S1. GenBank accession codes for sequences used in this study. The first column indicates species; column two indicates an individual's catalogue number (first individual if a chimera); column three indicates the second individual for chimeras (NA if not a chimera); the remaining columns indicate GenBank accession numbers for the 11 loci sequenced. Bolded GenBank numbers correspond to catalogue numbers in column three and unbolded GenBank numbers correspond to catalogue numbers in column two.

Species	CL number: individual 1	CL number: individual 2	16S	ND2	BDNF	BRCA1	BRCA2	CMOS	EXPH5	KIF24	MC1R	MXRA5	RAG1
<i>Chioninia delalandii</i>	BMNH 2000.18 (M45)	UMa (R52)	AY151482	KX231461	KX231427	KX231490	KX231532	AF335081	KX231409	KX231519	KX231391	KX231505	KX231373
<i>Chioninia vaillanti</i>	BMNH 2000.10 (M50)	UMa (49Mva6F)	AY151483	KX231462	KX231428	KX231491	—	AF335088	KX231410	—	KX231392	—	KX231374
<i>Dasia olivacea</i>	BRK 392	NA	KX231445	KX231463	KX231429	KX231492	KX231533	KX231476	KX231411	—	KX231393	KX231506	KX231375
<i>Dasia vittata</i>	BRK 391	NA	KX231446	KX231464	KX231430	—	—	KX231477	KX231412	KX231520	KX231394	KX231507	KX231376
<i>Eumecia anchietae</i>	PEM R16786	NA	KX231447	—	KX231431	KX231493	KX231534	—	KX231413	KX231521	KX231395	—	KX231377
<i>Eumecia anchietae</i>	PEM R16779	NA	KX231448	—	KX231432	KX231494	KX231535	KX231478	KX231414	KX231522	KX231396	—	KX231378
<i>Eutropis longicaudata</i>	ZMKU R00704	NA	KX231449	KX231465	KX231433	KX231495	KX231536	KX231479	KX231415	KX231523	KX231397	KX231508	KX231379

<i>Eutropis macularia</i>	CAS 247949	NA	KX231450	KX231466	KX231434	KX231496	KX231537	KX231480	KX231416	—	KX231398	KX231509	KX231380
<i>Eutropis multifasciata</i>	FMNH 269170	NA	KX231451	KX231467	KX231435	KX231497	KX231538	KX231481	KX231417	KX231524	KX231399	KX231510	KX231381
<i>Eutropis rudis</i>	FMNH 239732	NA	KX231452	KX231468	KX231436	KX231498	KX231539	KX231482	KX231418	KX231525	KX231400	KX231511	KX231382
<i>Notomabuya frenata</i>	UAM 60	NA	KX231453	KX231469	KX231437	KX231499	—	—	KX231419	KX231526	KX231401	KX231512	KX231383
<i>Trachylepis boulengeri</i>	PEM R5533	NA	KX231454	KX231470	KX231438	KX231500	KX231540	KX231483	KX231420	KX231527	KX231402	KX231513	KX231384
<i>Trachylepis depressa</i>	PEM R17745	PEM R15573	KX231455	—	KX231439	KX231501	KX231541	KX231484	KX231421	KX231528	KX231403	KX231514	KX231385
<i>Lubuya ivensii</i>	HF166	NA	KX231456	KX231471	KX231440	KX231502	—	KX231485	KX231422	KX231529	KX231404	KX231515	KX231386
<i>Lubuya ivensii</i>	HF217	NA	KX231457	KX231472	KX231441	—	—	KX231486	KX231423	—	KX231405	—	KX231387
<i>Lubuya ivensii</i>	PEM R20005	NA	KX231458	KX231473	KX231442	—	—	KX231487	KX231424	—	KX231406	KX231516	KX231388
<i>Caledoniscincus austrocaledonicus</i>	AMS R163262	NA	KX231459	KX231474	KX231443	KX231503	KX231542	KX231488	KX231425	KX231530	KX231407	KX231517	KX231389
<i>Cryptoblepharus novocaledonicus</i>	AMS R163245	NA	KX231460	KX231475	KX231444	KX231504	KX231543	KX231489	KX231426	KX231531	KX231408	KX231518	KX231390

<i>Brasiliscincus heathi</i>	MRT3671	NA	DQ238922.1					DQ238922.1					
<i>Brasiliscincus heathi</i>	907011	NA	DQ238909.1					DQ238909.1					

Table S2. Most recent common ancestor ages (t ; median and 95 % highest posterior density (95 % HPD)) in millions of years (Ma) for higher-level mabuyine clades (figure 1). Neotropical Mabuyinae does not include New World *Trachylepis* species.

Clade	Median t (Ma)	95 % HPD range of t (Ma)
<i>Dasia</i> + <i>Eutropis</i>	37.82	25.15–54.62
<i>Lubuya</i> + <i>Eumecia</i>	9.46	5.37–14.93
Neotropical Mabuyinae	14.49	4.86–27.06
<i>Trachylepis</i> + <i>Chioninia</i>	27.28	17.8–39.61
Neotropical Mabuyinae + <i>Trachylepis</i> + <i>Chioninia</i>	31.85	21.4–46.45
Neotropical Mabuyinae + <i>Trachylepis</i> + <i>Chioninia</i> + <i>Labuya</i> + <i>Eumecia</i>	34.16	22.7–49.16
Neotropical Mabuyinae + <i>Trachylepis</i> + <i>Chioninia</i> + <i>Labuya</i> + <i>Eumecia</i> + <i>Dasia</i> + <i>Eutropis</i> (i.e., Mabuyinae)	39.94	26.08–56.73

Table S3. Literature sources for parity mode (viviparous or oviparous) and dominant nutritional pattern (lecithotrophy or matrotrophy).

Species	Parity	Primary nutritional pattern(s)	Sources
<i>Eutropis longicaudata</i>	Oviparous	Lecithotrophy (inferred from oviparity)	[5]
<i>Eutropis macularia</i>	Oviparous	Lecithotrophic (inferred from oviparity)	[6]
<i>Eutropis multifasciata</i>	Viviparous	Unknown, but at least some lecithotrophy is likely because yolk is present in comparable amounts to oviparous species	[7]
<i>Eutropis rudis</i>	Oviparous	Lecithotrophic (inferred from oviparity)	[8,9]
<i>Dasia olivacea</i>	Oviparous	Lecithotrophic (inferred from oviparity)	[10,11]
<i>Dasia vittata</i>	Oviparous	Lecithotrophic (inferred from oviparity)	[12,13]
<i>Lubuya ivensii</i>	Viviparous	Matrotrophy (inferred from small size of recently ovulated eggs, which have very little yolk)	[14]
<i>Eumecia anchietae</i>	Viviparous	Matrotrophy (inferred from small size of recently ovulated eggs, which have very little yolk)	[15]
<i>Notomabuya frenata</i>	Viviparous	Matrotrophy (inferred from having tiny recently ovulated eggs)	[16,17]
<i>Brasiliscincus heathi</i>	Viviparous	Matrotrophy (inferred from having tiny recently ovulated eggs)	[18]
<i>Trachylepis boulengeri</i>	Oviparous	Lecithotrophic (inferred from oviparity)	[19,20]
<i>Trachylepis depressa</i>	Oviparous	Lecithotrophic (inferred from oviparity)	[21]
<i>Chioninia vaillantii</i>	Viviparous	Substantial lecithotrophy likely (inferred from the presence of opaque eggs with some yolk visible (personal observation)); contribution of matrotrophy is unknown.	[22]
<i>Chioninia delalandii</i>	Viviparous	Contributions of matrotrophy or lecithotrophy are unknown.	[23]

Figure S1. Parsimony ancestral state reconstruction of the presence or absence of extreme matrotrophy in mabuyine skinks. Black circles = present, white circles = absent, gray circles = unknown state.

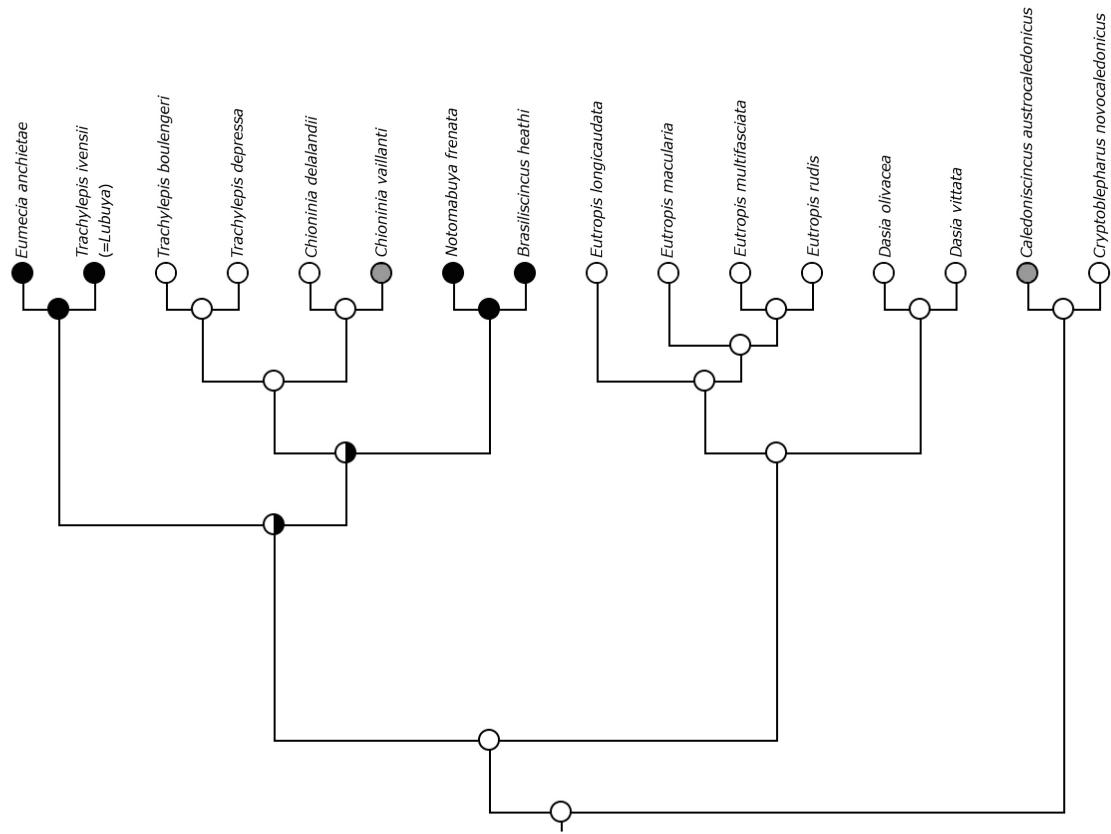
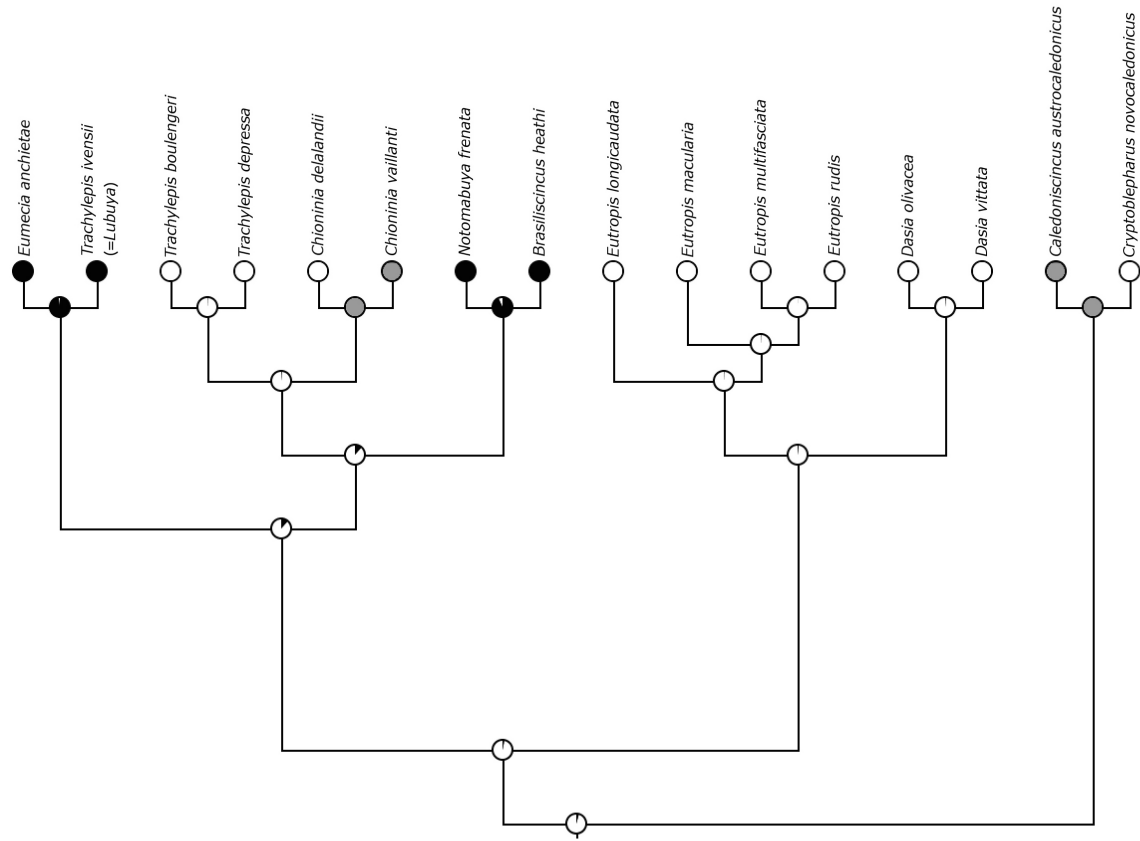


Figure S2. Likelihood ancestral state reconstruction of the presence or absence of extreme matrotrophy in mabuyine skinks. Black circles = present, white circles = absent, gray circles = unknown state.



Supplementary Material References

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