

Supplemental Information for

A framework for resolving cryptic species: a case study from the lizards of the Australian Wet Tropics

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Table S1. Sampling details for the putative lineages included in this study. Although we sample 1 – 2 individuals per lineage in the current study, previous mtDNA and multi-locus nDNA sequencing was done across more individuals in each lineage. Those data showed that mtDNA-nDNA concordance and that the lineages are geographically circumscribed.

putative lineage	mtDNA sampling	nDNA sampling	present study sampling
<i>C. rhomboidalis</i> N	8	7	1
<i>C. rhomboidalis</i> S	8	7	1
<i>C. rubrigularis</i> N	21	19	2
<i>C. rubrigularis</i> S	24	23	2
<i>C. wundalthini</i>	4	0	2
<i>L. coggeri</i> C	47	7	2
<i>L. coggeri</i> EU	2	0	2
<i>L. coggeri</i> N	79	28	2
<i>L. coggeri</i> S	110	34	2
<i>L. robertsi</i> BFHR	16	12	2
<i>L. robertsi</i> BK	14	7	1
<i>L. robertsi</i> CU	11	5	2
<i>L. robertsi</i> TU	12	10	1
average	27.4	12.2	1.7

Table S2. Details on samples included in the study, including their nominal species, putative lineage, and revised species designations. Also included is information on sample locality and data on sequencing quality: trimmed sequencing yield; number of loci retained; number of sites retained (coverage: >20×, quality: >20, quality depth: > 5); and average coverage at sites retained.

sample	nominal species	putative lineage	revised species	locality	latitude	longitude	sequencing yield (Mb)	# of loci	# of sites (Mb)	avg. cov.	SRA
ABTC80487	<i>C. rhomboidalis</i>	<i>C. rhomboidalis</i> N	<i>C. rhomboidalis</i>	Cockatoo Creek, Mt Elliot	-19.4469	146.9611	940.7	2657	2.6	155.3	SAMN05207387
ABTC14188	<i>C. rhomboidalis</i>	<i>C. rhomboidalis</i> S	<i>C. rhomboidalis</i>	Eungella	-20.9166	148.5	373.9	2600	2.3	92.9	SAMN05207388
ABTC11016	<i>C. rubrigularis</i>	<i>C. rubrigularis</i> N	<i>C. crypta sp. nov.</i>	Mt Lewis	-16.5833	145.2833	2037.4	2707	2.8	181.7	SAMN05207324
ABTC11021	<i>C. rubrigularis</i>	<i>C. rubrigularis</i> N	<i>C. crypta sp. nov.</i>	Kuranda, near Barron Falls	-16.8167	145.6333	1258.7	2687	2.6	168.8	SAMN05207344
ABTC77086	<i>C. rubrigularis</i>	<i>C. rubrigularis</i> S	<i>C. rubrigularis</i>	Longlands Gap	-17.4472	145.4758	865.6	2642	2.6	62.4	SAMN05207386
SS46	<i>C. rubrigularis</i>	<i>C. rubrigularis</i> S	<i>C. rubrigularis</i>	Sutties Gap Rd, Awt	-17.6936	145.6947	635.5	3311	2.5	142.2	SAMN03787434
CvBB1	<i>C. storri</i>	<i>C. storri</i>	<i>C. storri</i>	Bakers Blue, near Mt Molloy	-16.53	145.33	1267.9	3311	3.1	162.1	SAMN08865937
conx5328	<i>C. wundalthini</i>	<i>C. wundalthini</i>	<i>C. wundalthini</i>	Cape Melville	-14.2311	144.4622	779.5	2665	2.7	130.9	SAMN05207374
conx5330	<i>C. wundalthini</i>	<i>C. wundalthini</i>	<i>C. wundalthini</i>	Cape Melville	-14.2311	144.4622	504.6	2649	2.5	101.6	SAMN05207382
ABTC24236	<i>L. amacula</i>	<i>L. amacula</i>	<i>L. amacula</i>	Kroombit Tops 8k W	-24.3711	150.9278	1054.4	2669	2.3	155.3	SAMN08865938
ABTC3944	<i>L. amacula</i>	<i>L. amacula</i>	<i>L. amacula</i>	McAfees Lookout	-27.4333	152.9	436.9	2654	2.2	104	SAMN08865939
SEW8451	<i>L. coggeri</i>	<i>L. coggeri</i> C	<i>L. coggeri</i>	Mt Lewis	-16.9759	145.7031	921.5	3303	2.4	72.6	SAMN03787429
SS136	<i>L. coggeri</i>	<i>L. coggeri</i> C	<i>L. coggeri</i>	Mt Lewis	-16.977	145.704	2547.4	2252	0.8	43.9	SAMN01828491
conx5113	<i>L. coggeri</i>	<i>L. coggeri</i> EU	<i>L. elliotensis sp. nov.</i>	Mt Elliott	-19.5031	146.9911	1110.7	2665	2.3	147.6	SAMN08865940
conx5124	<i>L. coggeri</i>	<i>L. coggeri</i> EU	<i>L. elliotensis sp. nov.</i>	Mt Elliott	-19.5031	146.9911	763.9	2663	2.3	139.5	SAMN08865941
SS67	<i>L. coggeri</i>	<i>L. coggeri</i> N	<i>L. coggeri</i>	Mt Lewis NP	-16.5776	145.3085	2732	2182	0.8	47	SAMN01828495
SS74	<i>L. coggeri</i>	<i>L. coggeri</i> N	<i>L. coggeri</i>	Mt Lewis NP	-16.5839	145.3017	2088.6	1733	0.5	37.7	SAMN01828497
SEW3573	<i>L. coggeri</i>	<i>L. coggeri</i> S	<i>L. similis sp. nov.</i>	Herberton Range, AWT	-17.603	145.6324	485.4	3271	2.7	95.4	SAMN08865942
SS60	<i>L. coggeri</i>	<i>L. coggeri</i> S	<i>L. similis sp. nov.</i>	S. Johnstone River, QLD	-17.7	145.693	552.6	3280	2.3	132.4	SAMN03787435
LRBF2	<i>L. robertsi</i>	<i>L. robertsi</i> BFAU	<i>L. bellendenkerensis sp. nov.</i>	Mt Bartle Frere, 1120m	-17.38	145.816	672.5	2468	2.6	119.7	SAMN08865943
SEW4466	<i>L. robertsi</i>	<i>L. robertsi</i> BFAU	<i>L. bellendenkerensis sp. nov.</i>	Mount Hypipamee NP	-17.4601	145.4736	1334.6	2471	2.7	146	SAMN08865944
SEW6378	<i>L. robertsi</i>	<i>L. robertsi</i> BK	<i>L. bellendenkerensis sp. nov.</i>	Mt Bellenden Ker	-17.2656	145.8522	991.9	2466	2.5	156.9	SAMN08865945
N72303	<i>L. robertsi</i>	<i>L. robertsi</i> CU	<i>L. robertsi</i>	Mt Lewis	-16.5833	145.2833	291.1	2464	2.4	61.2	SAMN08865946
N72305	<i>L. robertsi</i>	<i>L. robertsi</i> CU	<i>L. robertsi</i>	Mt Lewis	-16.5833	145.2833	162.1	2463	2.2	27.9	SAMN08865947
SEW4175	<i>L. robertsi</i>	<i>L. robertsi</i> TU	<i>L. robertsi</i>	Thornton Peak	-16.1683	145.3665	548.7	2466	2.4	121.3	SAMN08865948

Table S3. NCBI GenBank ascension numbers for the mitochondrial data included in this study. These same individuals were used to determine mtDNA characters for species diagnosis (see Appendix).

sample IDs	GenBank IDs	nominal species	lineage
	AJ290527.1	<i>Carlia rhomboidalis</i>	<i>Carlia rhomboidalis</i> N
	DQ350058.1 - DQ350064.1	<i>Carlia rhomboidalis</i>	<i>Carlia rhomboidalis</i> N
	AJ290528.1	<i>Carlia rhomboidalis</i>	<i>Carlia rhomboidalis</i> S
	DQ350065.1 - DQ350071.1	<i>Carlia rhomboidalis</i>	<i>Carlia rhomboidalis</i> S
	AJ290532.1 - AJ290533.1	<i>Carlia rubrigularis</i>	<i>Carlia rubrigularis</i> N
	DQ350016.1 - DQ350034.1	<i>Carlia rubrigularis</i>	<i>Carlia rubrigularis</i> N
	AJ290531.1	<i>Carlia rubrigularis</i>	<i>Carlia rubrigularis</i> S
	DQ350035.1 - DQ350057.1	<i>Carlia rubrigularis</i>	<i>Carlia rubrigularis</i> S
	AJ290538.1	<i>Carlia storri</i>	<i>Carlia storri</i>
	AJ290539.1	<i>Carlia storri</i>	<i>Carlia storri</i>
	FJ379458.1	<i>Carlia storri</i>	<i>Carlia storri</i>
conx5328	MH184611	<i>Carlia wundalthini</i>	<i>Carlia wundalthini</i>
conx5329	MH184610	<i>Carlia wundalthini</i>	<i>Carlia wundalthini</i>
conx5330	MH184612	<i>Carlia wundalthini</i>	<i>Carlia wundalthini</i>
conx5331	MH184613	<i>Carlia wundalthini</i>	<i>Carlia wundalthini</i>
conx264	MH184614	<i>Lampropholis amicula</i>	<i>Lampropholis amicula</i>
QRFA243	MH184616	<i>Lampropholis amicula</i>	<i>Lampropholis amicula</i>
AMICI	MH184615	<i>Lampropholis amicula</i>	<i>Lampropholis amicula</i>
	HM029784.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> C
	HM029798.1 - HM029802.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> C
	HM029804.1 - HM029806.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> C
	HM029810.1 - HM029814.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> C
	HM029817.1 - HM029837.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> C
	HM029890.1 - HM029892.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> C
	HM029963.1 - HM029971.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> C
conx1520	MH184617	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> EU
conx1521	MH184618	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> EU
	HM029783.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029785.1 - HM029797.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029803.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029807.1 - HM029809.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029815.1 - HM029816.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029838.1 - HM029883.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029883.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029901.1 - HM029910.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029938.1 - HM029962.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029982.1 - HM029988.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029998.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> N
	HM029884.1 - HM029889.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> S
	HM029893.1 - HM029937.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> S
	HM029972.1 - HM029981.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> S

HM029989.1 - HM029997.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> S
HM030004.1 - HM030022.1	<i>Lampropholis coggeri</i>	<i>Lampropholis coggeri</i> S
HM030326.1	<i>Lampropholis robertsi</i>	<i>Lampropholis robertsi</i> BFHR
HM030334.1 - HM030335.1	<i>Lampropholis robertsi</i>	<i>Lampropholis robertsi</i> BFHR
HM030339.1 - HM030351.1	<i>Lampropholis robertsi</i>	<i>Lampropholis robertsi</i> BFHR
HM030315.1 - HM030325.1	<i>Lampropholis robertsi</i>	<i>Lampropholis robertsi</i> BK
HM030336.1 - HM030338.1	<i>Lampropholis robertsi</i>	<i>Lampropholis robertsi</i> BK
HM030327.1 - HM030331.1	<i>Lampropholis robertsi</i>	<i>Lampropholis robertsi</i> CU
HM030352.1 - HM030357.1	<i>Lampropholis robertsi</i>	<i>Lampropholis robertsi</i> CU
HM030332.1 - HM030333.1	<i>Lampropholis robertsi</i>	<i>Lampropholis robertsi</i> TU
HM030358.1 - HM030367.1	<i>Lampropholis robertsi</i>	<i>Lampropholis robertsi</i> TU

Table S4. Number of adult specimens measured for morphological and scale counts. *C. rhomboidalis* and *C. wundalthini* were not measured because they are distinct for both color and morphology. See Appendix 1 for full list of specimens examined; all specimens are maintained at the Queensland Museum.

putative lineages	individuals
<i>C. rhomboidalis</i>	0
<i>C. rubrigularis</i> N	29
<i>C. rubrigularis</i> S	31
<i>C. wundalthini</i>	0
<i>L. robertsi</i> TU/CU	24
<i>L. robertsi</i> BK/BFAU	19
<i>L. coggeri</i> N/C	31
<i>L. coggeri</i> S	29
<i>L. coggeri</i> EU	16

Table S5. Genetic diversity and divergence estimates for pairwise lineage-comparisons for both mitochondrial and exome data, at silent sites only. Shown are raw divergence (d_{xy}), within-lineage genetic diversity for each lineage (π), and net divergence (d_a). Each pairwise comparison is coded as either being between (1) recognized: two lineages that were already recognized as distinct species, (2) elevated: two lineages that were elevated to species in the current study, or (3) population: lineages for which there is insufficient evidence to elevate them to species. Many of the lineages that we propose to elevate are more genetically divergent than recognized species.

lineage 1	lineage 2	type	mtDNA d_e	mtDNA π_e	mtDNA π_i	mtDNA d_i	nDNA d_e	nDNA π_e	nDNA π_i	nDNA d_i
<i>C. rhomboidalis</i> N	<i>C. rhomboidalis</i> S	population	0.1302	0.0142	0.0503	0.098	0.005	0.0034	0.0027	0.0018
<i>C. rhomboidalis</i> N	<i>C. rubrigularis</i> S	recognized	0.242	0.0142	0.0458	0.212	0.0113	0.0034	0.0075	0.006
<i>C. rhomboidalis</i> N	<i>C. rubrigularis</i> N	recognized	0.327	0.0142	0.0278	0.306	0.0159	0.0034	0.0069	0.0107
<i>C. rhomboidalis</i> N	<i>C. wundalthingi</i>	recognized	0.3859	0.0142	0	0.3788	0.0164	0.0034	0.002	0.0136
<i>C. rubrigularis</i> N	<i>C. rubrigularis</i> S	elevated	0.3328	0.0278	0.0458	0.2961	0.0131	0.0069	0.0075	0.0061
<i>C. rubrigularis</i> S	<i>C. wundalthingi</i>	recognized	0.3864	0.0458	0	0.3635	0.0137	0.0075	0.002	0.0091
<i>C. rubrigularis</i> N	<i>C. wundalthingi</i>	recognized	0.1914	0.0278	0	0.1775	0.0097	0.0069	0.002	0.0052
<i>L. robertsi</i> CU	<i>L. robertsi</i> TU	population	0.2059	0.0174	0.0103	0.1921	0.011	0.0052	0.0023	0.0072
<i>L. robertsi</i> BFAU	<i>L. robertsi</i> TU	elevated	0.2898	0.046	0.0103	0.2616	0.0186	0.0042	0.0023	0.0154
<i>L. robertsi</i> BK	<i>L. robertsi</i> TU	elevated	0.2535	0.0007	0.0103	0.2481	0.0195	0.003	0.0023	0.0168
<i>L. robertsi</i> BFAU	<i>L. robertsi</i> BK	population	0.2561	0.046	0.0007	0.2328	0.0141	0.0042	0.003	0.0105
<i>L. coggeri</i> C	<i>L. coggeri</i> N	population	0.0791	0.0044	0.0654	0.0443	0.0105	0.0064	0.0029	0.0051
<i>L. coggeri</i> C	<i>L. coggeri</i> EU	elevated	0.233	0.0044	0.0044	0.2285	0.0126	0.0064	0.0054	0.0072
<i>L. coggeri</i> C	<i>L. coggeri</i> S	elevated	0.3105	0.0044	0.0649	0.2759	0.0148	0.0064	0.0076	0.0079
<i>L. coggeri</i> EU	<i>L. coggeri</i> S	elevated	0.2751	0.0044	0.0649	0.2405	0.0191	0.0054	0.0076	0.0125

Table S6. D-statistic estimates for all trios tested for introgression between species 1 and 3, including standard deviation as measured across 200 bootstraps and significance assessed by a one-tailed z-score, corrected for multiple testing. Comparisons for which the d-statistic was positive between species 1 and 3 were not tested; a positive value suggests introgression between species 2 and 3 instead and these are evaluated in other trios. Comparisons with a 'NA' d-statistic are sister-species; sister species cannot be tested in the d-statistic framework.

species 1	species 2	species 3	outgroup	d-stat	st. dev.	z-score	p-val	sig.
<i>C. rhomboidalis</i> N		<i>C. rhomboidalis</i> S	<i>C. storri</i>	NA				
<i>C. rhomboidalis</i> N	<i>C. rhomboidalis</i> S	<i>C. rubrigularis</i> S	<i>C. storri</i>	-0.083	0.094	-0.8837	0.1884	FALSE
<i>C. rhomboidalis</i> N	<i>C. rhomboidalis</i> S	<i>C. wundalthini</i>	<i>C. storri</i>	-0.1759	0.0784	-2.2454	0.0124	FALSE
<i>C. rhomboidalis</i> S	<i>C. rhomboidalis</i> N	<i>C. rubrigularis</i> S	<i>C. storri</i>	0.083				
<i>C. rhomboidalis</i> S	<i>C. rhomboidalis</i> N	<i>C. wundalthini</i>	<i>C. storri</i>	0.1759				
<i>C. rubrigularis</i> N	<i>C. wundalthini</i>	<i>C. rhomboidalis</i> N	<i>C. storri</i>	-0.2751	0.0676	-4.067	2.38E-05	TRUE
<i>C. rubrigularis</i> N	<i>C. wundalthini</i>	<i>C. rhomboidalis</i> S	<i>C. storri</i>	-0.2881	0.0601	-4.7936	8.19E-07	TRUE
<i>C. rubrigularis</i> N	<i>C. wundalthini</i>	<i>C. rubrigularis</i> S	<i>C. storri</i>	-0.3762	0.0537	-7.0051	1.23E-12	TRUE
<i>C. rubrigularis</i> S	<i>C. rhomboidalis</i> N	<i>C. wundalthini</i>	<i>C. storri</i>	-0.0573	0.0558	-1.0274	0.1521	FALSE
<i>C. wundalthini</i>		<i>C. rubrigularis</i> N	<i>C. storri</i>	NA				
<i>L. coggeri</i> C	<i>L. coggeri</i> N	<i>L. coggeri</i> EU	<i>L. amacula</i>	-0.082	0.0931	-0.8802	0.1894	FALSE
<i>L. coggeri</i> C	<i>L. coggeri</i> N	<i>L. coggeri</i> S	<i>L. amacula</i>	-0.3988	0.0907	-4.3973	5.48E-06	TRUE
<i>L. coggeri</i> EU	<i>L. coggeri</i> N	<i>L. coggeri</i> S	<i>L. amacula</i>	-0.2383	0.0564	-4.2259	1.19E-05	TRUE
<i>L. coggeri</i> N		<i>L. coggeri</i> C	<i>L. amacula</i>	NA				
<i>L. coggeri</i> N	<i>L. coggeri</i> C	<i>L. coggeri</i> EU	<i>L. amacula</i>	0.082				
<i>L. coggeri</i> N	<i>L. coggeri</i> C	<i>L. coggeri</i> S	<i>L. amacula</i>	0.3988				
<i>L. robertsi</i> BFAU		<i>L. robertsi</i> BK	<i>L. amacula</i>	NA				
<i>L. robertsi</i> BFAU	<i>L. robertsi</i> BK	<i>L. robertsi</i> CU	<i>L. amacula</i>	-0.0075	0.0494	-0.1525	0.4394	FALSE
<i>L. robertsi</i> BFAU	<i>L. robertsi</i> BK	<i>L. robertsi</i> TU	<i>L. amacula</i>	-0.0089	0.0447	-0.1984	0.4213	FALSE
<i>L. robertsi</i> BK	<i>L. robertsi</i> BFAU	<i>L. robertsi</i> CU	<i>L. amacula</i>	0.0075				
<i>L. robertsi</i> BK	<i>L. robertsi</i> BFAU	<i>L. robertsi</i> TU	<i>L. amacula</i>	0.0089				
<i>L. robertsi</i> CU		<i>L. robertsi</i> TU	<i>L. amacula</i>	NA				

Table S7. Trait loadings on each principal component (PC) from the Principal Component Analysis (PCA) of the morphological traits in the '*Carlia rubrigularis*' species group. PC1 reflects body size; PCs 2–5 reflect shape variation. Trait abbreviations are defined in the text.

Trait	Principal Component Loadings (% of variance)				
	PC1 (66.6%)	PC2 (16.4%)	PC3 (10.7%)	PC4 (3.7%)	PC5 (2.6%)
SVL	0.929	0.193	-0.054	0.158	-0.268
AG	0.640	0.751	0.034	-0.050	0.149
L2	0.814	-0.296	-0.449	0.150	0.159
HL	0.905	-0.231	-0.045	-0.353	-0.047
HW	0.760	-0.277	0.572	0.108	0.087

Table S8. Trait loadings on each principal component (PC) from the Principal Component Analysis (PCA) of the morphological traits in the '*Lampropholis robertsi*' species group. PC1 reflects body size; PCs 2–5 reflect shape variation. Trait abbreviations are defined in the text.

Trait	Principal Component Loadings (% of variance)				
	PC1 (83.7%)	PC2 (10.3%)	PC3 (3.4%)	PC4 (1.8%)	PC5 (0.9%)
SVL	0.950	0.247	0.022	-0.128	-0.144
AG	0.845	0.516	0.040	0.102	0.089
L2	0.892	-0.320	0.316	0.040	0.010
HL	0.951	-0.183	-0.141	-0.175	0.106
HW	0.931	-0.226	-0.218	0.178	-0.052

Table S9. Trait loadings on each principal component (PC) from the Principal Component Analysis (PCA) of the morphological traits in the '*Lampropholis coggeri*' species group. PC1 reflects body size; PCs 2–5 reflect shape variation. Trait abbreviations are defined in the text.

Trait	Principal Component Loadings (% of variance)				
	PC1 (73.9%)	PC2 (13.7%)	PC3 (6.0%)	PC4 (4.4%)	PC5 (1.9%)
SVL	0.934	0.237	0.047	-0.087	-0.249
AG	0.775	0.595	0.129	0.079	0.152
L2	0.797	-0.463	0.378	0.081	0.027
HL	0.901	-0.181	-0.175	-0.339	0.105
HW	0.882	-0.171	-0.326	0.295	-0.001

Table S10. Characteristic roots and vectors for CV1 and CV2 for MANOVA testing for shape differences between lineages in the '*Lampropholis coggeri*' species group.

Characteristic Roots & Vectors for MANOVA				
	PC2	PC3	PC4	PC5
CV1 (69%)	0.489	-0.213	0.295	-0.049
CV2 (31%)	-0.042	0.542	-0.043	-0.324

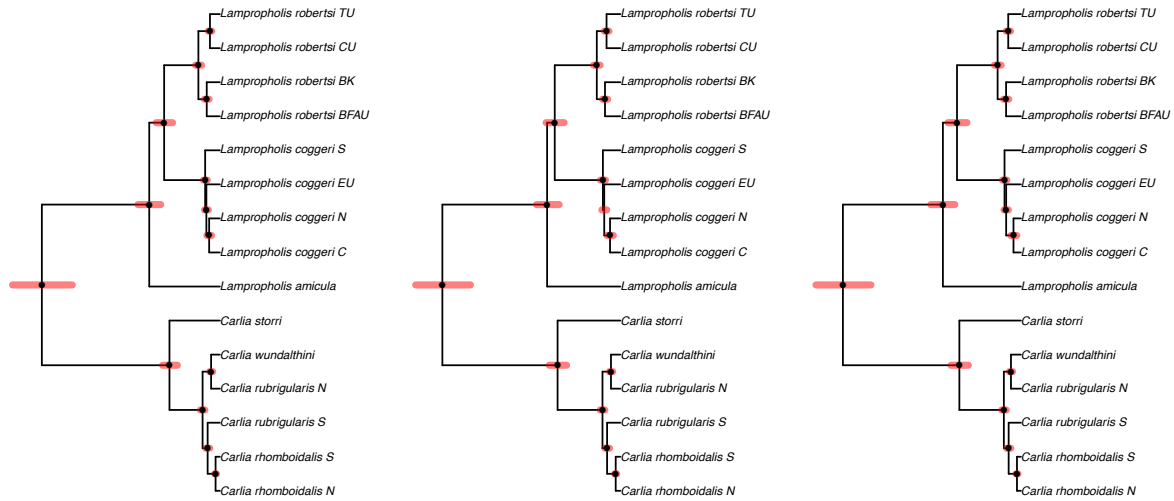


Figure S1: Species tree of all lineages; each panel depicts a tree inferred using STARBEAST2 with a random set of 200 exons. Nodes with $\geq 95\%$ local posterior probability are indicated with black circles. Red bars at nodes indicate the 95% highest posterior density in branching times. The topology and branching times are quantitatively and qualitatively similar across trees.

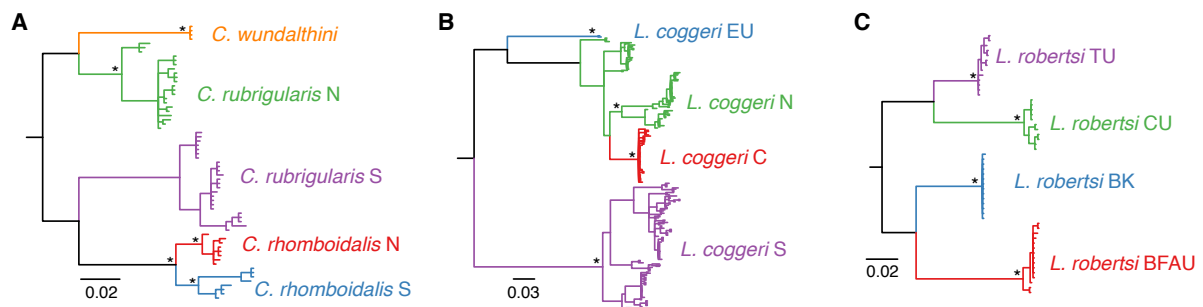


Figure S2: Mitochondrial gene trees inferred using MRBAYES for (A) the ‘*Carlia rubrigularis*’ species group, which consists of five lineages: *C. wundalthini*, *C. rubrigularis* N, *C. rubrigularis* S, *C. rhomboidalis* N, and *C. rhomboidalis* S, (B) the ‘*Lampropholis coggeri*’ group, which consists of four lineages: *L. coggeri* N, *L. coggeri* C, *L. coggeri* S, and *L. coggeri* EU, and (C) the ‘*Lampropholis robertsi*’ group, which consists of four lineages: *L. robertsi* CU, *L. robertsi* BFAU, *L. robertsi* TU, and *L. robertsi* BK. Gene trees were rooted with *C. storri* and *L. amacula*; not shown. Asterisks mark major nodes with $\geq 95\%$ posterior support. Colors follow Fig. 1. The mitochondrial gene tree topologies are similar to the species tree topology inferred using exon data (Fig. 1; Fig. S1).