

Supplementary Material

Phylogenetic relationships in the Eugongylini (Squamata: Scincidae): generic limits and biogeography

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Table S1. Oligonucleotide primers used in this study. The letters L and H refer to the light and heavy strands. Values in ‘5’ position’ refer to the position of the 5’ position in the complete *Eumeces egregius* mtDNA sequence (Kumazawa and Nishida, 1999).

Gene	Primer Name	Sequence (5’–3’)	5’ Position	Source
ND2	L4221	AAGGATTACTTTGATAGAGT	3691	Macey et al. (1997)
	L4437	AAGCTTTTCGGGCCCATACC	3833	Macey et al. (1997)
	H4980	ATTTTTCGTAGTTGGGTTTGRTT	4396	Macey et al. (1997)
	ND2r102	CAGCCTAGGTGGGCGATTG	4432	Sadlier et al. (2004)
	H5540	TTTAGGGCTTTGAAGGC	4947	Macey et al. (1997)
	H5617	AAAATRTCTGRGTTGCATTCAG	5019	Macey et al. (1997)
c-mos (nuclear)	G303(F)	ATTATGCCATCMCCTMTTCC	NA	Saint et al. (1998)
	G74(R)	TGAGCATCCAAAGTCTCCAATC	NA	Saint et al. (1998)
Rag-1 (nuclear)	G396(F)	TCTGAATGGAAATTCAAGCTGTT	NA	Groth and Barrowclough (1999)
	G440(F)	CATGATAAAGGGAGAGTRGAAGA	NA	Smith (2001)
	G425(R)	AAAGCAAGGATAGCGACAAGAG	NA	Smith (2001)

References

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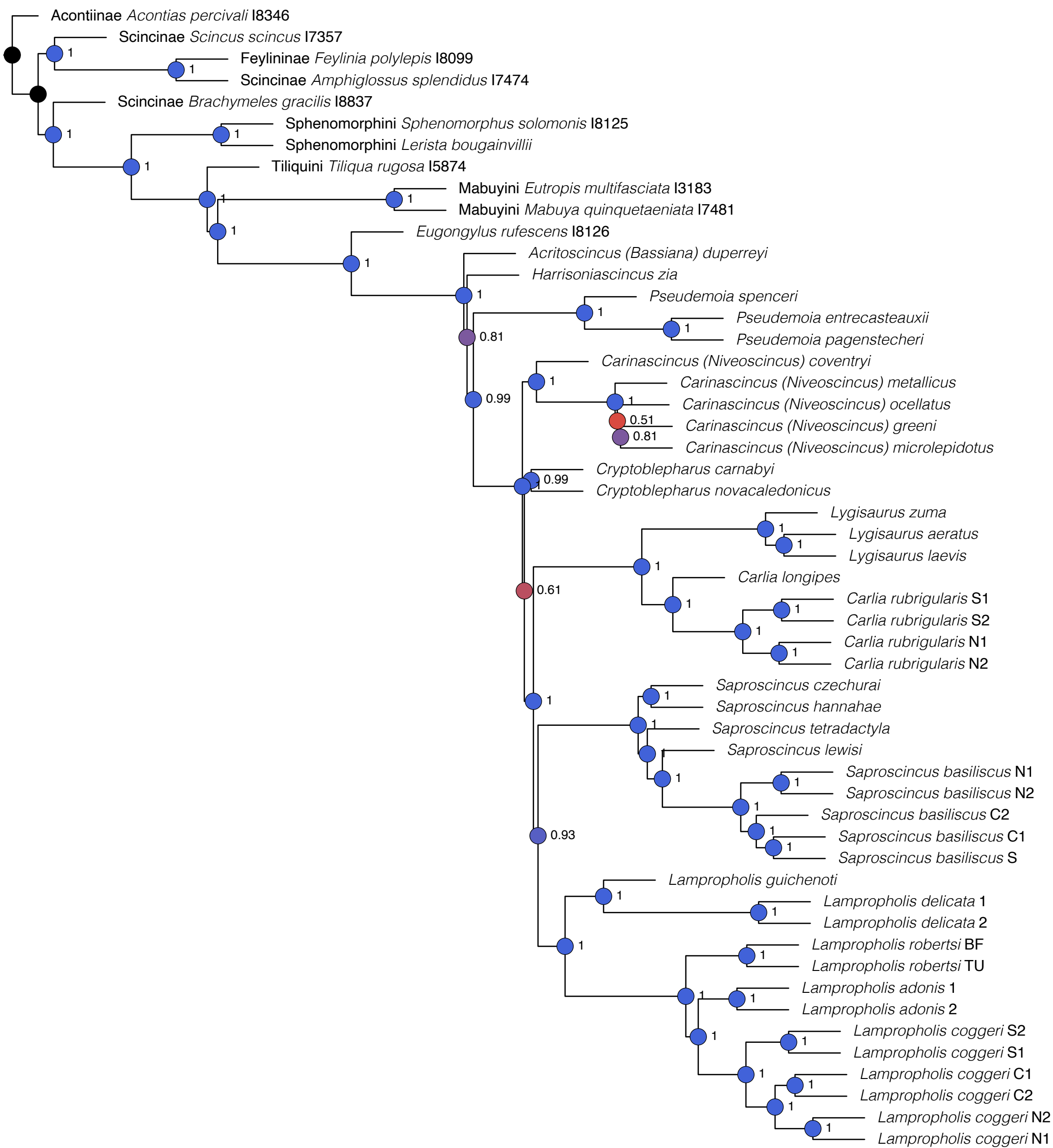
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Table S2. Summary of secondary calibrations used in estimating divergence times among the skink tribe Eugongylini. Node letters correspond to labelled circles at nodes in Figures 1 and 2. All calibrations were implemented as Cauchy distributions which are uniform distributions between the minimum and maximum values and include 2.5% of the distribution above and below the min/max values. Calibrations on nodes A–H were implemented on both the phylogenomic backbone dating tree and the fully sampled species tree. Nodes marked with * (I–K) indicate calibrations implemented only on the fully sampled MCMCTREE analysis.

Node	MCMCTREE Calibration	Minimum (mya)	Maximum (mya)
A	'>1.116<1.204'	111.6	120.4
B	'>0.938<1.017'	93.8	101.7
C	'>0.887<0.962'	88.7	96.2
D	'>0.773<0.838'	77.3	83.8
E	'>0.606<0.658'	60.6	65.8
F	'>0.39<0.52'	39	52
G	'>0.18<0.27'	18	22
H	'>0.12<0.22'	12	22
I*	'>0.08<0.16'	8	16
J*	'>0.05<0.17'	5	17
K*	'>0.04<0.10'	4	10

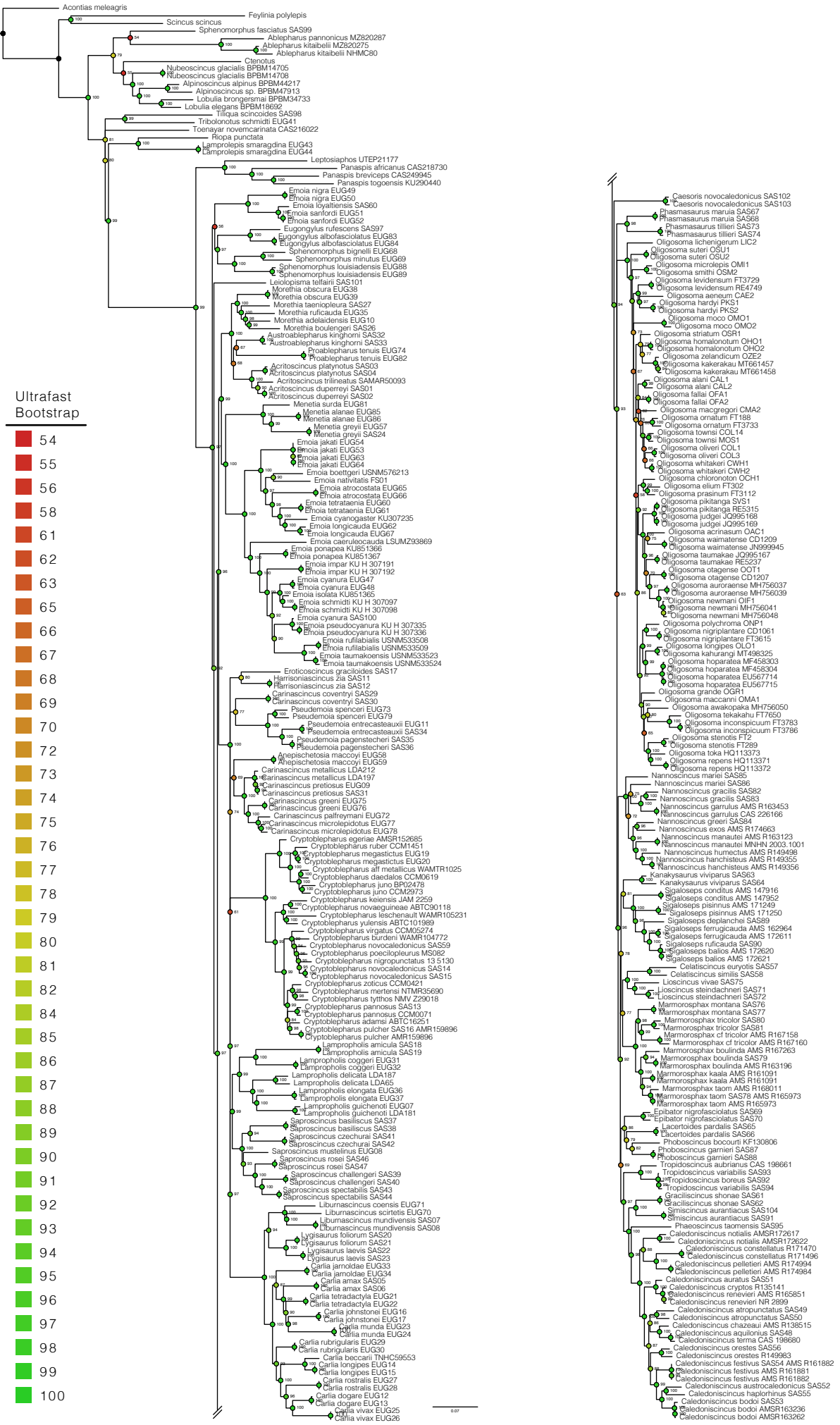
Supplementary Figure S1. Scincid species tree as estimated by ASTRAL using IQTREE genetree inputs estimated from Anchored Hybrid Enrichment data (Brandley *et al.* 2015; Burbrink *et al.* 2020). These data provide a relatively well resolved topology among many of the Australian eugongyline genera. However, lack of resolution among some major clades and genera highlights the rapid divergence and difficulty in estimating intergeneric relationships. We used this topology to provide a backbone constraint for our estimation of the eugongyline tree from Sanger sequenced data by first collapsing nodes with <0.90 support (local posterior probability), see inset Fig.2.

Supplementary Figure S2. Eugongylini species tree as estimated by IQTREE from our three gene mitonuclear Sanger dataset, partitioned by locus, with minimal backbone constraint informed by the topology of Supplementary Figure 1. Colored circles at nodes indicate ultrafast bootstrap (UFB) support values as estimated by IQTREE, with $UFB \geq 90$ indicating strong support, $UFB \geq 70 < 90$ indicating moderate support, and $UFB < 70$ indicating low or equivocal support.



Eugongylini

2.0



Ultrafast Bootstrap

