

Appendix from B. P. Noonan and P. T. Chippindale, “Vicariant Origin of Malagasy Reptiles Supports Late Cretaceous Antarctic Land Bridge”

(Am. Nat., vol. 168, no. 6, p. 730)

Tables and Figures

Table A1

GenBank accession numbers of sequences used in this study: snakes

	cyt <i>b</i>	c-mos	NT-3	BDNF	RAG1
<i>Corallus</i>	U69763	AY987964	AY988044	AY988027	AY988061
<i>Epicrates</i>	U69777	AY099966	AY988045	AY988028	AY988062
<i>Eunectes</i>	U69810	AY099964	AY988046	AY988029	AY988063
<i>Boa</i>	U69740	AF471115	AY988047	AY988030	AY988064
<i>Candoia</i>	AY099984	AY099961	AY988048	AY988031	AY988065
<i>Acrantophis</i>	U69735	AY099963	AY988049	AY988032	AY988066
<i>Sanzinia</i>	U69866	AY099982	AY988050	AY988033	AY988067
<i>Exiliboa</i>	AY099989	AY099973	AY988051	AY988034	AY988068
<i>Morelia</i>	U69851	AF544723	AY988052	AY988035	AY988069
<i>Acrochordus</i>	AF217841	AF471124	AY988053	AY988036	AY988070
<i>Cylindrophis</i>	AF471032	AF471133	AY988054	AY988037	AY988071
<i>Anilius</i>	U69738	AY099965	AY988055	AY988038	AY988072
<i>Tropidophis</i>	U69868	AY099962	AY988056	AY988039	AY988073
<i>Eryx</i>	U69824	AY099975	AY988057	AY988040	AY988074
<i>Calabaria</i>	AY099985	AY099978	AY988058	AY988041	AY988075
<i>Charina</i>	AY099986	AY099971	AY988059	AY988042	AY988076
<i>Ramphotyphlops</i>	AY099990	AY099980	AY988060	AY988043	AY988077

Table A2

GenBank accession numbers of sequences used in this study: lizards

	RAG1	c-mos	NT-3	BDNF
<i>Leiolepis</i>	AY988011	AY987982	AY987994	AY987965
<i>Polychrus</i>	AY988012	AY987983	AY987995	AY987966
<i>Tropidurus</i>	AY988013	AY987984	AY987996	AY987967
<i>Crotaphytus</i>	AY988014	AY987985	AY987997	AY987968
<i>Basiliscus</i>	AY988015	AY987986	AY987998	AY987969
<i>Leiocephalus</i>	AY988016	AF315388	AY987999	AY987970
<i>Oplurus</i>	AY988017	AF315391	AY988000	AY987971
<i>Chalarodon</i>	AY988018	AY987987	AY988001	AY987972
<i>Diplolaemus</i>	AY988019	AY987988	AY988002	AY987973
<i>Liolaemus</i>	AY988020	AY367887	AY988003	AY987974
<i>Phrynosoma</i>	AY988021	AY987989	AY988004	AY987975
<i>Sceloporus</i>	AY988022	AF039478	AY988005	AY987976
<i>Chamaeleo</i>	AY988023	AY987990	AY988006	AY987977
<i>Physignathus</i>	AY988024	AY987991	AY988007	AY987978
<i>Uromastix</i>	AY988025	AY987992	AY988008	AY987979
<i>Brachylophus</i>	AY988026	AY987993	AY988009	AY987980
<i>Cordylus</i>	AY662643	AY217848	AY988010	AY987981

Table A3

GenBank accession numbers of sequences used in this study: turtles

	RAG1	POMC	NT-3	BDNF	12S	16S
<i>Erymnochelys</i>	AY988099	AY988092	AY988085	AY988078	U40641	AF113640
<i>Podocnemis</i>	AY988100	AY988097	AY988086	AY988079	U40649	AF113642
<i>Peltocephalus</i>	AY988101	AY988093	AY988087	AY988080	U40643	AF113643
<i>Pelomedusa</i>	AY988102	AY988094	AY988088	AY988081	U40642	AF113639
<i>Pelusios</i>	AY988103	AY988095	AY988089	AY988082	U40644	AF113641
<i>Hydromedusa</i>	AY988104	AY988098	AY988090	AY988083	U62017	AF113638
<i>Staurotypus</i>	AY988105	AY988096	AY988091	AY988084	U81326	AB090046

Table A4
Tissue sources used in this study

Specimen	Voucher
<i>Erymnochelys madagascariensis</i>	MVZ 238759
<i>Podocnemis expansa</i>	DZ 5385
<i>Peltocephalus dumeriliana</i>	NAIB
<i>Pelomedusa subrufa</i>	MVZ 238878
<i>Pelusios gabonensis</i>	ROM 19952
<i>Hydromedusa tectifera</i>	DZ 4460
<i>Staurotypus triporcatus</i>	UTA 52026
<i>Corallus caninus</i>	ZA A36702
<i>Epicrates cenchria</i>	UTA 50177
<i>Eunectes notaeus</i>	ZA 746701
<i>Boa constrictor</i>	^a
<i>Candoia carinata</i>	YPM 12872
<i>Acrantophis dumerili</i>	ZA 956705
<i>Sanzinia madagascariensis</i>	FW 986704
<i>Exiliboa placata</i>	UTA 37871
<i>Morelia spilota</i>	YPM 12876
<i>Acrochordus javanicus</i>	YPM 13598
<i>Cylindrophis ruffis</i>	MVZ 170854
<i>Anilius scytale</i>	YPM 10767
<i>Tropidophis haetianus</i>	BYU 48469
<i>Eryx conicus</i>	TP 28678
<i>Calabaria reinhardtii</i>	UTA 39598
<i>Charina bottae</i>	BYU 48468
<i>Ramphotyphlops sp.</i>	YPM 13663
<i>Leiolepis belliana</i>	MVZ 137446
<i>Polychrus marmoratus</i>	BPN 1050
<i>Tropidurus hispidus</i>	BPN
<i>Crotaphytus collaris</i>	UTA
<i>Basiliscus plumifrons</i>	UTA 44864
<i>Leiocephalus carinatus</i>	UTA
<i>Oplurus cuvieri</i>	MVZ 238791
<i>Chalarodon madagascariensis</i>	YPM 12866
<i>Diplolaemus darwini</i>	MVZ 232235
<i>Liolaemus pictus</i>	BYU 48406
<i>Phrynosoma cornutum</i>	UTA ^a
<i>Sceloporus horridus</i>	MC ^a
<i>Chamaeleo jacksoni</i>	UTA ^a
<i>Physignathus cocincinus</i>	MVZ 226496
<i>Uromastyx acanthinurus</i>	MVZ 162567
<i>Brachylophus fasciatus</i>	SD 188093
<i>Cordylus namaquensis</i>	CAS 223963

Note: Abbreviations: MVZ, Museum of Vertebrate Zoology; YPM, Yale Peabody Museum; SD, Zoological Society of San Diego; BYU, M. L. Bean Museum; ROM, Royal Ontario Museum; AMB, A. M. Bauer; TP, T. Papenfuss; UTA, University of Texas at Arlington; BPN, B. P. Noonan; ZA, Zoo Atlanta; FW, Fort Worth Zoo; DZ, Detroit Zoo.

^a Number not yet available.

Table A5
Citations for calibration points used in divergence time estimation

	Age (mya)	Citation	Notes
Lizards: ^a			
Chamaeleonid divergence	>47	Raxworthy et al. 2002	This calibration is based on an assumed molecular clock and has little effect on resulting estimations when excluded.
Iguanidae	<180 >25	Norell and de Queiroz 1991; Evans et al. 2002	Norell and de Queiroz (1991) present the earliest definitive pleurodont iguanian (<i>Armandisaurus</i>) with affinities to extant taxa from the early Miocene. The upper limit placed on the age of the extant iguanids is based on the observations of Evans et al. (2002) and the assumption that the origin of this group does not predate the earliest known iguanian in the Jurassic.
Acrodont-pleurodont iguanian split	<230 >165	Evans et al. 2002	The lower limit of this node is based on the early-middle (see Evans et al., p. 299) Jurassic <i>Bharatagama</i> from India. Acrodont dentition arose twice in the history of the Squamata, and this taxon places a lower limit on the age of the basal split among acrodont and pleurodont iguanians. The upper limit of this node follows Evans et al.’s (2002) assertion that the iguanian-scleroglossan dichotomy extends back “into the early Jurassic or even Late Triassic” and would necessarily predate the basal Iguanian split.
Snakes: ^b			
<i>Epicrates-Eunectes</i> split	>24	Rage 1984	Based on Miocene fossils of <i>Eunectes</i> (Rage 1984, p. 18) and <i>Pseudoepicrates</i> (Rage 1984, p. 20).
<i>Exiliboa-Charina</i> split	>55	Rage 1984	Based on Eocene fossils of <i>Dunnophis</i> (Rage 1984, p. 28), which incidentally provided early support for this novel phylogenetic grouping (Rage 1984, p. 29). See also Albino (1996, p. 188) for likely Paleocene record.
Acrochordoidea	>65	Rage 1984	Based on Paleocene <i>Nigerophis</i> (Rage 1984, p. 39).
Erycinae	>65	Rage 1984	Because this group is here demonstrated to be paraphyletic, fossil erycines are used to place a minimum age on the erycines exclusive of <i>Calabaria</i> (see tree below) because both the morphology and distribution of fossil forms is similar to that of extant non- <i>Calabaria</i> erycines, and there are no records from Africa (the range of <i>Calabaria</i>). Based on Paleocene <i>Helagras</i> and numerous Eocene taxa (Rage 1984, pp. 23–27). See also Albino (1996, p. 188).
Boinae	>55	Rage 1984; Albino 1993, 1996	Based on Eocene Boine <i>Cheilophis</i> (Rage 1984, p. 17) and Albino (1993; 1996, p. 188).
Booidea	>75	Rage 1984; Albino 1996, 2000	Based on Cretaceous <i>Dinylisia</i> (Rage 1984, p. 13) and other material presented by Albino (1996, p. 187; 2000, p. 247).
<i>Anilius-Tropidophis</i> split	>75	Rage 1984	Based on Cretaceous <i>Coniophis</i> (Rage 1984, pp. 12, 66–67). Placement here (rather than at the base of <i>Cylindrophis</i>) is based on Rage’s (1984, pp. 66–67) discussion of the relationships of <i>Coniophis</i> to modern anilioids, which are here found to be paraphyletic (see also Wilcox et al. 2002).

Table A5 (Continued)

	Age (mya)	Citation	Notes
South American Boine– <i>Candoia</i> + <i>Eryx</i> split	>55	Albino 1993, 1996	Based on appearance of boine boid and possible erycine material in the early Eocene of Patagonia. Placement at this node is based on the traditional interpretation (e.g., accepted at the time of publication of Albino’s studies) of the Boinae.
Turtles: ^c			
Cryptodiran-pleurodiran split	>210	Gaffney 1990	Based on Late Triassic <i>Proterochersis</i> and early Jurassic <i>Kayentachelys</i> .
Podocnemid-pelomedusid split	>100	Gaffney 1990	Based on mid-Cretaceous <i>Brasilemys</i> and <i>Araripemys</i> and E. S. Gaffney (personal communication).
<i>Erymnochelys</i> + <i>Podocnemis</i> clade	>65	Gaffney and Forster 2003	Based on early Paleocene cf. <i>Erymnochelys</i> . Gaffney and Forster (2003) also note the presence of a number of fossil specimens from mainland Oligocene-Miocene Africa that appear similar to the extant <i>Erymnochelys</i> . The authors note that the affinities of this material are deduced on the basis of characteristics that, within the extant pleurodira, are restricted to <i>Erymnochelys</i> but are widespread in fossil forms. Also, all of these records are from the late Cenozoic and, if these supposed relationships are correct, would simply suggest oceanic dispersal from Madagascar to the mainland some time in the Cenozoic. This certainly seems plausible because members of the predominantly African <i>Pelusios</i> appear to have crossed the Mozambique Channel and are currently found on Madagascar.
Chelid-pelomedusoid split	<150 >100	Gaffney 1990; de la Fuente et al. 2001; de Lapparent de Broin and de la Fuente 2001; de la Fuente 2003	Lower limit based on Late Cretaceous chelid taxa (above references and E. S. Gaffney [personal communication]). Upper limit assumes that the late Jurassic <i>Platycheilus</i> actually precedes the origin of the modern pleurodira.
<i>Pelomedusa</i> - <i>Pelusios</i> split	>25	Broadley 1981	Based on <i>Pelusios rusingae</i> of the Miocene (Broadley 1981, p. 680).

Note: See Noonan and Chippindale (2006) for a discussion of the phylogenetic hypothesis presented here.

^a Prior age of the root node was specified as 206 ± 25 mya. This is based on fossil material summarized by Evans et al. (2002) and their assertion that the iguanian-scleroglossan dichotomy dates to the Late Triassic/Early Jurassic.

^b Prior age of the root node was specified as 110 ± 30 mya. This is based on the supposition that the diversification of extant snake lineages is younger than the oldest fossil snake (Rage 1994). The use of this calibration was discussed by Noonan and Chippindale (2006).

^c Prior age of the root node was specified as 210 ± 30 mya. This is based on the age of the oldest pleurodire and the Triassic divergence between pleurodira and cryptodiria.

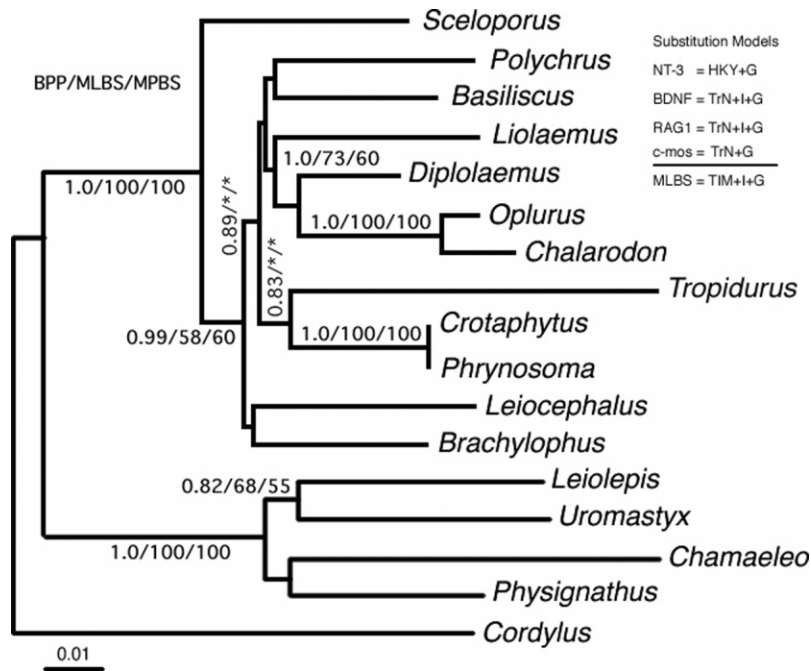


Figure A1: Notes on lizard phylogeny. As in previous studies, relationships among the iguanids were poorly resolved (Schulte et al. 2003; Townsend et al. 2004). Representatives from what were recovered by Schulte et al. (2003) as distinct lineages within the Iguanidae were included, and a close relationship of the South American *Diplolaemus* to the Malagasy taxa was verified. Diversification of extant iguanids appears to have occurred quite rapidly and hinders the resolution of intergeneric relationships (see also Schulte et al. 2003, their fig. 5; Townsend et al. 2004, their fig. 1). Poorly supported internodes are extremely short and have little effect on the estimation of the age of the Malagasy lineage (random permutations of relationships below the *Diplolaemus* + [*Oplurus*, *Chalarodon*] had little effect on age estimates). *BPP* = Bayesian posterior probability, *MLBS* = maximum likelihood bootstrap value, *MPBS* = maximum parsimony bootstrap value, *asterisk* = bootstrap value <50.

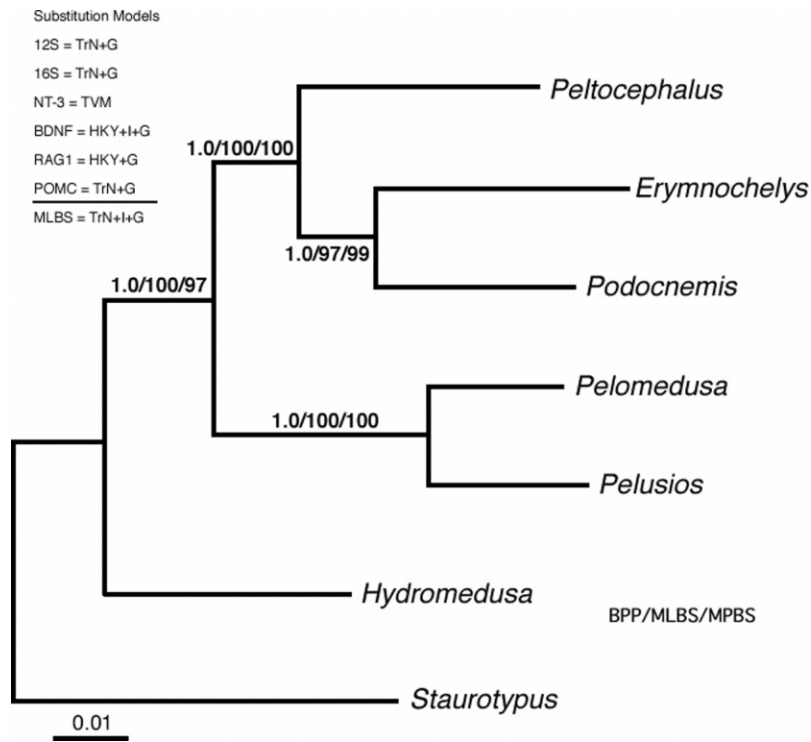


Figure A2: Notes on turtle phylogeny. Phylogenetic hypothesis of pelomedusoid relationships (outgroup is the kinosternid turtle *Staurotypus*) based on combined analysis of four nuclear and two mitochondrial loci. Podocnemidae consists of *Podocnemis*, *Peltocephalus*, and *Erymnochelys*. *BPP* = Bayesian posterior probability, *MLBS* = maximum likelihood bootstrap value, *MPBS* = maximum parsimony bootstrap value. Models of sequence evolution are indicated for each gene (used in partitioned Bayesian analysis), and *MLBS* model specified was used for the maximum likelihood analysis, which does not permit partitioning.