

**Supplementary Table S1.** GenBank/ENA accession numbers for *Micrurus* samples used herein. Outgroup alignments were obtained from ZAHER et al. (2019). Accession numbers for sequences generated for this study are in red. Voucher abbreviations for new sequences: AF, ANTOINE FOUQUET field number; ICN, Instituto de Ciencias Naturales, Universidad Nacional de Colombia, Bogotá; INSZ, Instituto Nacional de Salud de Colombia, Bogotá. Vouchers with asterisk (\*) indicate that sequences do not belong to the same individual.

Species	Voucher	mtDNA			ND4	nDNA Cmos
		12S	16S	cyt <i>b</i>		
<i>M. altirostris</i>	IB55595				AF228432	
<i>M. altirostris</i>	MCP5035				AF228431	
<i>M. baliocoryphus</i>	MZUSP10808				AF228433	
<i>M. brasiliensis</i>	CEPB2301				AF228427	
<i>M. brasiliensis</i>	IB55385				AF228428	
<i>M. carvalhoi</i>	CEPB2687				AF228438	
<i>M. carvalhoi</i>	IB55598				AF228435	
<i>M. cf. ibiboboca</i>	CEPB2312				AF228437	
<i>M. cf. ibiboboca</i>	IVB1757				AF228436	
<i>M. circinalis</i>	UWIZM2016_22	MK534134	MK534145	MK534164	MK534174	MK534154
<i>M. corallinus</i>	CEPB051				AF228424	
<i>M. diastema</i>	RH52446/M50*	Z46454	Z46484	KU754325	KU754434	
<i>M. dissoleucus</i>	UTAM673				JF308717	
<i>M. diutius</i>	CAS231787	MK534136	MK534149	MK534168	MK534178	MK534158
<i>M. diutius</i>	ROM22835				JF308707	
<i>M. diutius</i>	UWIZM2012_4	MK534135	MK534147	MK534166	MK534176	MK534156
<i>M. diutius</i>	UWIZM2016_24	MK534135	MK534148	MK534167	MK534177	MK534157
<i>M. elegans</i>	M22			KU754339	KU754449	
<i>M. filiformis</i>	ICN11380	MW665121	MT862136		MW662060	MW662077
<i>M. filiformis</i>	Piranha	MW665122	MT862137	MW662068	MW662061	MW662083
<i>M. frontalis</i>	CEPB1587				AF228425	
<i>M. frontalis</i>	CEPB2365				AF228426	
<i>M. fulvius</i>	Mitochondrial genome	GU045453	GU045453	GU045453	GU045453	
<i>M. helleri</i> – Amazonia	CEPB2289				AF228439	
<i>M. helleri</i> – Foothills	AF4455	MW665123	MW672259	MW662069	MW662067	MW662081
<i>M. helleri</i> – Foothills	ICN13076	MW665124	MW672255	MW662070	MW662062	MW662078
<i>M. helleri</i> – Foothills	ICN13077	MW665125	MW672256	MW662071	MW662063	MW662079
<i>M. helleri</i> – Foothills	INSZ012			MW662072	MW662066	
<i>M. helleri</i> – Foothills	INSZ158	MW665126	MW672257	MW662074		MW662080
<i>M. helleri</i> – Foothills	INSZ157	MW665127	MW672258	MW662073	MW662064	MW662082
<i>M. helleri</i> – Foothills	INSZMlem2	MW665128	MW672260	MW662075	MW662065	MW662076
<i>M. obscurus</i>	CEPB1807				AF228443	
<i>M. obscurus</i>	KU222205				JF308708	
<i>M. ortoni</i>	LSUMZH1529				JF308704	
<i>M. ortoni</i>	QCAZ2584				AF228442	
<i>M. pyrrhocryptus</i>	LSUMZH6130				JF308705	
<i>M. pyrrhocryptus</i>	MZUSP10809				AF228434	
<i>M. surinamensis</i>	LJV7110			EF137415	EF137407	EF137422
<i>M. surinamensis</i>	Vidal/KU214908*	AF544770	AF544799		JF308709	AF544708
<i>M. tener</i>	FTB2189/M449*	KR814629	KR814656		KU754431	KR814671

**Supplementary Table S2.** Questionable *Micrurus* sequences excluded from final analyses.

Species	Voucher	GenBank		Remarks
		ND4	cyt <i>b</i>	
<i>M. altirostris</i>	MHNLC4848	AF228429		Generates conflicting topology for the <i>M. frontalis</i> clade
<i>M. altirostris</i>	MHNLC4208	AF228430		Generates conflicting topology for the <i>M. frontalis</i> clade
<i>M. carvalhoi</i>	IB55598	AF228435		Generates long tree branch, influences BEAST topology
<i>M. decoratus</i>	IVB2453	AF228441		Clusters in different positions among analyses, reduces clade support for associated branches
<i>M. laticollaris</i>	M33	KU754446	KU754347	Clusters in different positions among analyses, reduces clade support for associated branches
<i>M. surinamensis</i>	CEPB1812	AF228444		Clusters outside <i>M. surinamensis</i>

**Supplementary Table S3.** ND4 sequences of *Micrurus lemniscatus* sensu lato with conflicting identifications in GenBank. <sup>1</sup> See identification by PIRES (2011); <sup>2</sup> see comments on identification in PIRES et al. (2014).

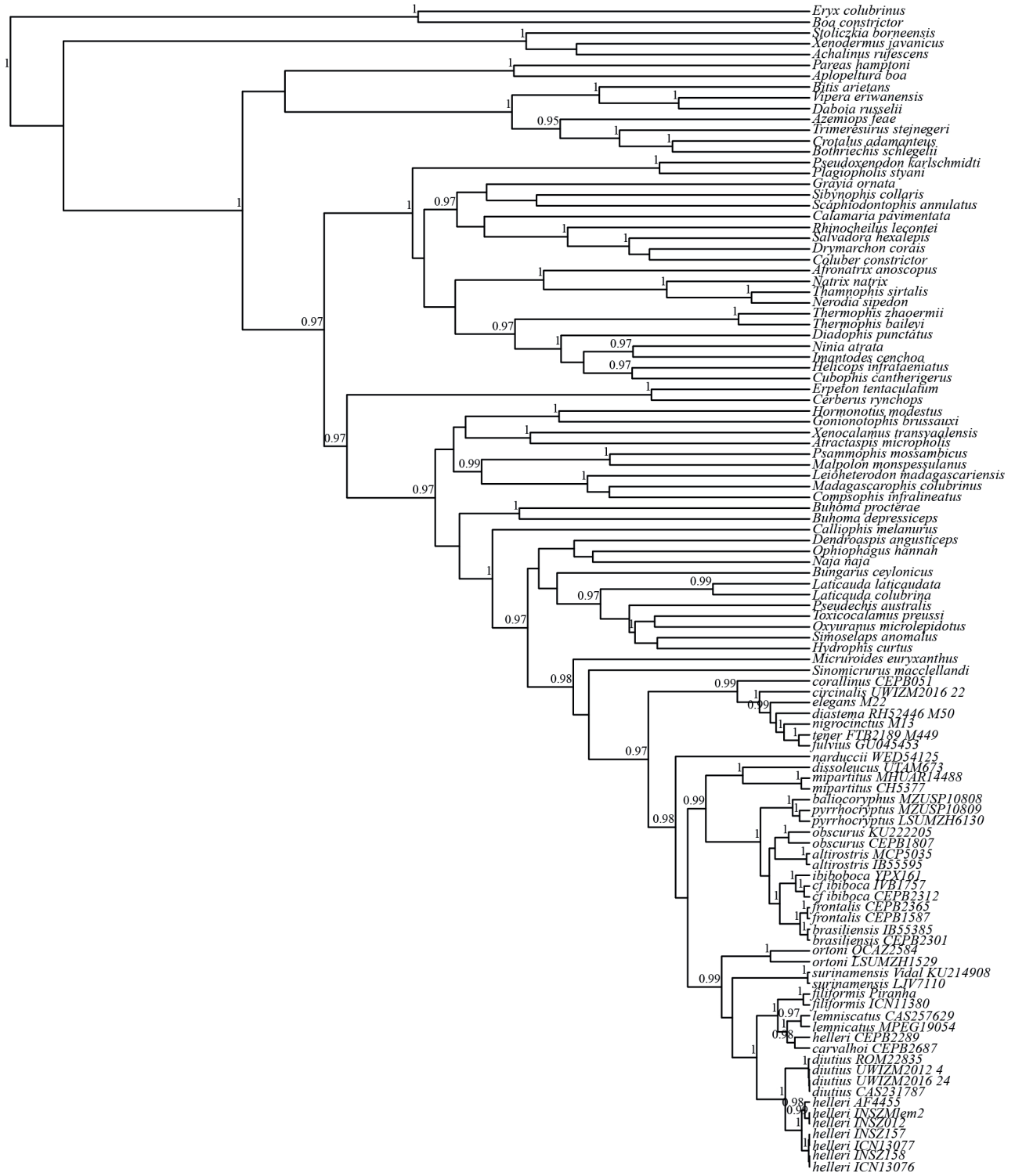
Accession number	GenBank identification	Voucher	RENJIFO et al. (2012)	JOWERS et al. (2019)	This study
AF228435	<i>M. l. lemniscatus</i>	IB55598	<i>M. l. carvalhoi</i>	<i>M. carvalhoi</i>	<i>M. carvalhoi</i>
AF228438	<i>M. lemniscatus</i> clone 1	CEPB2687	<i>M. l. carvalhoi</i>	<i>M. carvalhoi</i>	<i>M. carvalhoi</i>
AF228439	<i>M. lemniscatus</i> clone 2	CEPB2289	<i>M. l. helleri</i>	<i>M. helleri</i>	<i>M. sp.</i>
JF308706	<i>M. l. diutius</i>	MPEG19054	<i>M. l. diutius</i>	<i>M. lemniscatus</i>	<i>M. lemniscatus</i> <sup>1</sup>
JF308707	<i>M. l. lemniscatus</i>	ROM22835	<i>M. l. lemniscatus</i>	<i>M. diutius</i>	<i>M. diutius</i>
AF228436	<i>M. l. carvalhoi</i> clone 1	IVB1757	<i>M. cf. lemniscatus</i>	<i>M. cf. lemniscatus</i>	<i>M. cf. ibiboboca</i> <sup>2</sup>
AF228437	<i>M. l. carvalhoi</i> clone 2	CEPB2312	<i>M. cf. lemniscatus</i>	<i>M. cf. lemniscatus</i>	<i>M. cf. ibiboboca</i> <sup>2</sup>

**Supplementary Table S4.** Uncorrected p distances between *Micrurus* species for the ND4 gene. Distances are given as percentages. Taxa of and values for the *M. lemniscatus* complex are highlighted by asterisks.

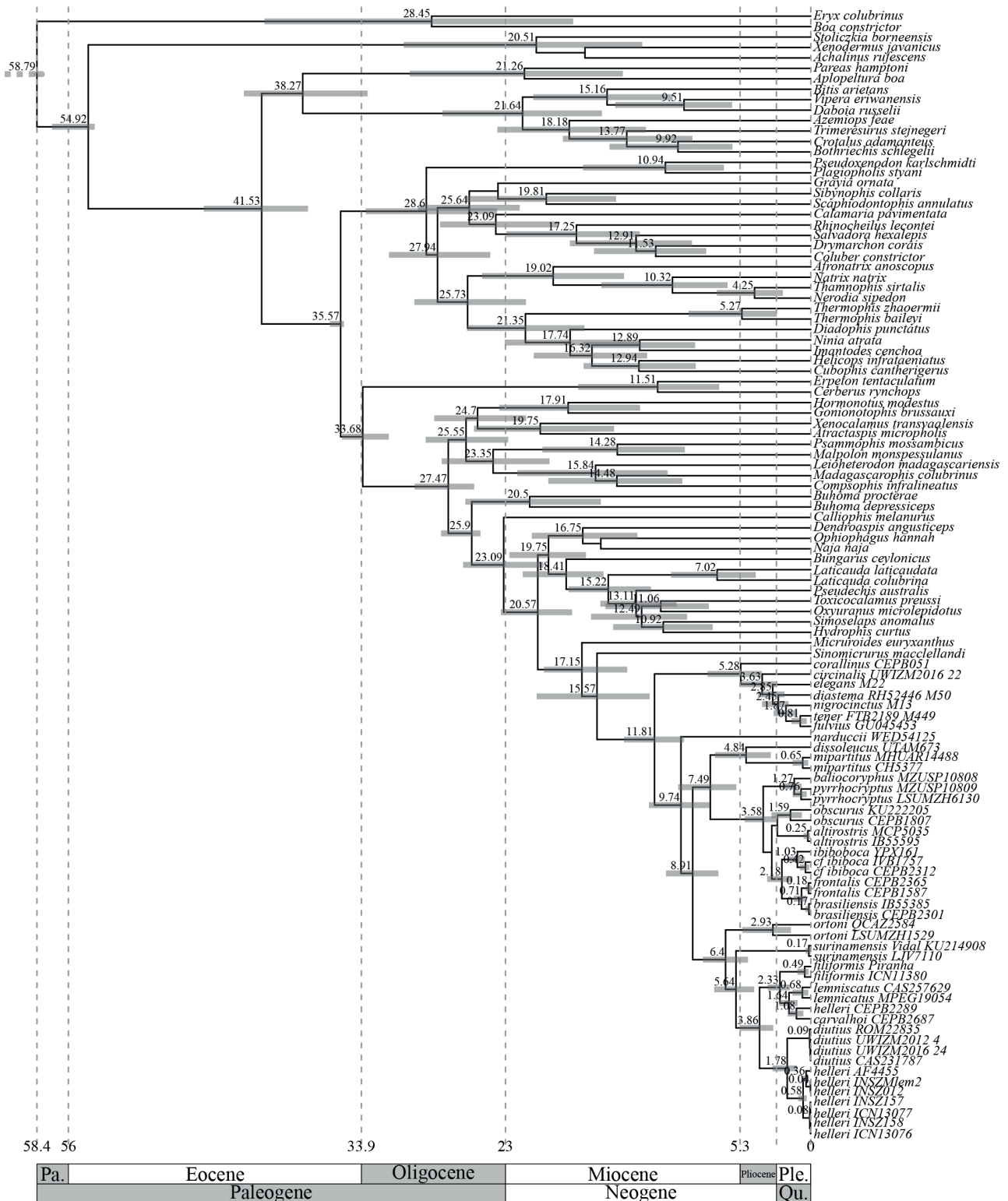
Species	1	2	3	4*	5	6	7	8	9*	10	11*	12	13	14*	15*	16	17	18*	19	20	21	22	23	24	25
1 <i>altirostris</i>																									
2 <i>baliocoryphus</i>	6.33																								
3 <i>brasiliensis</i>	5.75	7.00																							
4 <i>carvalhoi</i> *	10.00	10.50	10.00																						
5 <i>circinalis</i>	17.00	16.83	16.83	16.33																					
6 <i>corallinus</i>	16.00	15.50	16.17	14.83	9.17																				
7 <i>diastema</i>	17.83	17.50	18.33	17.17	7.50	12.00																			
8 <i>dissoleucus</i>	14.75	14.17	15.00	16.50	19.50	17.83	19.67																		
9 <i>diutius</i> *	12.33	13.17	11.83	7.17*	15.67	14.33	17.50	16.33																	
10 <i>elegans</i>	16.33	16.83	17.00	16.17	6.67	10.00	6.83	18.67	15.17																
11 <i>filiformis</i> *	12.50	13.50	12.42	6.33*	16.33	15.83	17.00	16.17	5.67*	16.33															
12 <i>frontalis</i>	6.42	7.92	1.58	10.75	17.17	15.75	18.92	15.42	12.75	17.58	13.42														
13 <i>fulvius</i>	18.17	17.50	18.00	17.00	8.00	11.17	5.83	20.00	17.00	6.83	17.00	18.25													
14 <i>helleri</i> sensu stricto*	13.14	14.30	11.83	8.27*	15.67	14.40	17.74	16.81	2.41*	15.39	6.49*	12.75	17.22												
15 “ <i>helleri</i> ” – Amazonia*	12.00	12.33	11.67	5.17*	17.00	16.00	17.67	16.67	8.00*	16.67	6.33*	12.25	17.50	8.87*											
16 <i>ibiboboca</i>	6.25	7.33	5.00	11.50	17.67	17.00	18.67	16.17	13.33	17.83	14.17	5.92	18.83	13.32	12.50										
17 cf. <i>ibiboboca</i>	6.00	6.58	4.92	11.42	17.83	17.17	18.50	16.50	13.17	17.83	14.00	5.83	18.50	13.67	11.92	2.83									
18 <i>lemniscatus</i> *	12.68	13.84	13.18	6.00*	16.85	16.01	17.85	17.18	6.34*	16.85	3.67*	13.93	17.68	6.92*	4.00*	14.18	14.01								
19 <i>mipartitus</i>	13.75	13.75	13.83	14.83	19.17	18.42	19.83	13.67	15.17	18.00	16.33	14.25	19.33	15.76	15.17	14.42	14.58	16.51							
20 <i>narducci</i>	14.58	15.33	14.33	15.50	19.33	19.67	19.67	18.33	14.17	18.83	15.17	15.08	19.50	14.38	15.67	15.17	14.92	16.18	17.50						
21 <i>nigrocinctus</i>	17.58	16.50	16.83	16.83	8.67	11.33	7.00	18.67	15.83	6.83	16.67	17.08	6.00	15.64	16.00	17.50	17.67	16.51	18.83	19.67					
22 <i>obscurus</i>	5.83	6.83	5.50	10.58	18.08	15.83	18.92	15.08	13.00	17.58	13.75	5.38	18.08	13.54	12.42	6.67	6.25	13.93	14.42	15.25	17.17				
23 <i>ortoni</i>	14.25	15.83	12.63	11.33	17.67	18.58	19.50	19.25	9.50	18.33	10.42	13.75	18.92	10.05	11.75	14.00	13.83	11.59	18.08	16.25	18.50	15.08			
24 <i>pyrrhocryptus</i>	7.67	2.00	8.17	10.75	17.67	16.33	17.83	14.42	13.25	17.33	13.42	8.92	18.00	14.15	12.50	8.17	7.46	13.76	14.75	15.42	17.00	7.88	16.54		
25 <i>surinamensis</i>	12.58	12.75	12.08	8.75	16.92	15.42	18.42	15.92	6.75	17.08	7.92	12.50	17.92	6.85	9.08	13.25	12.92	8.42	14.92	14.75	17.25	12.42	10.42	12.33	
26 <i>tener</i>	17.83	17.17	17.33	17.00	7.67	10.17	5.83	19.17	17.00	6.17	17.00	17.58	2.67	16.99	17.67	18.33	18.00	17.85	19.00	19.17	5.67	17.92	18.58	17.67	17.75



**Supplementary Figure S1.** Complete Maximum Likelihood tree based on 3,618 base pairs of the concatenated alignment of five genes (12S, 16S, cyt *b*, ND4, Cmos). Values above nodes correspond to ultrafast bootstrap values  $\geq 95$ .



**Supplementary Figure S2.** Complete Bayesian tree based on 3,618 base pairs of the concatenated alignment of five genes (12S, 16S, cyt *b*, ND4, Cmos). Values above nodes correspond to Bayesian posterior probabilities  $\geq 0.95$ .



**Supplementary Figure S3.** Complete Bayesian time tree with mean dates above nodes in million years before present. Grey bars indicate 95% Highest Posterior Density (HPD) intervals.



Supplementary Figure S4. Complete Maximum Likelihood tree including the specimen *Micrurus carvalhoi* IB55598 (in red). Values above nodes correspond to ultrafast bootstrap values  $\geq 95$ .

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