

# Supporting information 1

Body size prediction in scorpions: a phylogenetic comparative examination of linear measurements of individual body parts

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## Contents

Species List . . . . .	2
List of articles utilized for gathering morphological data . . . . .	7
ModelFinder results . . . . .	14
Calibration points . . . . .	15
R Function for defining lognormal priors . . . . .	18
Interaction models . . . . .	22
Phylogenetic multiple regressions . . . . .	25
References . . . . .	26

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## Species List

List of scorpion species included in the phylogenetic and statistical analyses. Accession codes for new sequences are in blue. For each species, the number of male and female individuals used to calculate species means is provided, with missing data (“-”) for species included solely for reconstructing the phylogenetic tree.

Species	Females	Males	Total	COI	16S	18S	28S
<i>Aegaeobuthus cyprius</i>	1	1	2	DQ310849	DQ310812	-	-
<i>Aegaeobuthus nigrocinctus</i>	0	2	2	ON255557	ON262578	-	-
<i>Alayotityus delacruzi</i>	4	4	8	-	DQ990826	-	-
<i>Alayotityus juraguaensis</i>	1	0	1	-	DQ990827	-	-
<i>Alayotityus nanus</i>	2	0	2	-	DQ990828	-	-
<i>Alayotityus sierramaestrae</i>	1	0	1	-	KY674447	-	-
<i>Ananteris ashaninka</i>	1	1	2	ON255558	-	ON259096	ON259166
<i>Ananteris balzanii</i>	2	5	7	KY674491	KY674448	-	KY674470
<i>Ananteris franckeii</i>	5	5	10	PQ341284	-	-	-
<i>Ananteris mauryi</i>	28	23	51	PQ341283	-	-	-
<i>Ananteris platnicki</i>	1	1	2	ON255559	ON262579	ON259097	ON259167
<i>Androctonus amoreuxi</i>	3	2	5	ON255560	ON262580	-	MW557083
<i>Androctonus australis</i>	3	2	5	ON255561	ON262581	ON259098	ON259168
<i>Androctonus bicolor</i>	2	3	5	KF548120	KJ538332	-	-
<i>Androctonus bourdoni</i>	0	1	1	ON255562	ON262582	-	-
<i>Androctonus crassicauda</i>	1	1	2	ON255563	ON262583	GQ335459	-
<i>Androctonus gonneti</i>	1	0	1	ON255564	ON262584	-	-
<i>Androctonus hoggarensis</i>	2	1	3	JN018150	-	JN018267	JN018364
<i>Androctonus liouvillei</i>	1	1	2	-	ON262585	-	ON259170
<i>Androctonus mauritanicus</i>	1	2	3	ON255565	ON262586	ON259099	ON259169
<i>Androctonus sergenti</i>	1	0	1	ON255566	ON262587	ON259100	ON259171
<i>Babycurus gigas</i>	1	2	3	ON255569	ON262590	ON259103	ON259174
<i>Barbaracurus sofomarensis</i>	1	2	3	ON255570	ON262591	ON259104	ON259175
<i>Barbaracurus zambonellii</i>	1	1	2	ON255571	ON262592	ON259105	ON259176
<i>Buthacus occidentalis</i>	0	1	1	JN018151	-	JN018268	JN018365
<i>Buthacus stockmanni</i>	1	1	2	ON255572	ON262593	ON259106	ON259177
<i>Buthaeolus harrisoni</i>	2	2	4	ON255573	ON262594	ON259107	ON259178
<i>Buthoscorpio sarasinorum</i>	1	0	1	ON255574	ON262595	ON259108	ON259179
<i>Buthus albengai</i>	1	0	1	JN885909	-	-	-
<i>Buthus atlantis</i>	1	1	2	ON255575	ON262596	ON259109	ON259180
<i>Buthus awashensis</i>	1	1	2	ON255576	ON262597	ON259110	ON259181
<i>Buthus draa</i>	1	1	2	ON255577	ON262598	-	-
<i>Buthus elmoutaouakili</i>	0	1	1	ON255578	ON262599	-	ON259182
<i>Buthus lienhardi</i>	1	1	2	ON255579	ON262600	-	-
<i>Buthus malhommei</i>	1	1	2	JN885935	-	-	-
<i>Buthus mardochei</i>	1	1	2	ON255580	ON262601	-	ON259183
<i>Buthus maroccanus</i>	2	0	2	ON255581	-	ON259111	ON259184
<i>Buthus occitanus</i>	1	2	3	ON255582	ON262602	-	-
<i>Buthus paris</i>	2	2	4	ON255583	ON262603	-	-
<i>Centruroides arctimanus</i>	1	1	2	MK479161	MK479008	MK479059	MK479110
<i>Centruroides baerji</i>	1	1	2	MK479162	MK479009	MK479060	ON259185
<i>Centruroides balsasensis</i>	1	1	2	MK479163	MK479010	MK479061	MK479112
<i>Centruroides baracoae</i>	6	6	12	ON255586	ON262606	ON259112	ON259187
<i>Centruroides barbudensis</i>	1	1	2	MK479165	MK479012	MK479063	MK479114

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Species	Females	Males	Total	COI	16S	18S	28S
<i>Centruroides borinquensis</i>	1	1	2	MK479167	MK479014	MK479065	MK479116
<i>Centruroides chamulaensis</i>	2	2	4	MK479168	MK479015	MK479066	MK479117
<i>Centruroides edwardsii</i>	3	4	7	MK479169	MK479016	MK479067	MK479118
<i>Centruroides elegans</i>	1	1	2	MK479170	MK479017	MK479068	MK479119
<i>Centruroides exilimanus</i>	2	2	4	MK479171	MK479018	MK479069	MK479120
<i>Centruroides farri</i>	1	0	1	MK479172	MK479019	MK479070	MK479121
<i>Centruroides flavopictus</i>	0	3	3	MK479173	MK479020	MK479071	MK479122
<i>Centruroides gracilis</i>	5	4	9	KY982180	KY981894	KY981989	ON259189
<i>Centruroides guanensis</i>	3	3	6	MK479211	MK479058	MK479109	MK479160
<i>Centruroides hoffmanni</i>	2	1	3	MZ429061	MK479025	MK479076	ON259190
<i>Centruroides infamatus</i>	2	1	3	KY982181	KY981895	KY981990	MK479128
<i>Centruroides limpidus</i>	0	3	3	MK479184	MK479031	MK479082	MK479133
<i>Centruroides luceorum</i>	3	0	3	MK479185	MK479032	MK479083	MK479134
<i>Centruroides lucidus</i>	3	4	7	ON255590	ON262610	-	ON259191
<i>Centruroides marcanoi</i>	0	4	4	MK479186	MK479033	MK479084	ON259192
<i>Centruroides meisei</i>	6	6	12	MK479187	MK479034	MK479085	MK479136
<i>Centruroides meridionalis</i>	0	2	2	MK479189	MK479035	MK479086	MK479137
<i>Centruroides nigrimanus</i>	1	2	3	MK479191	MK479038	MK479089	MK479140
<i>Centruroides nigrovariatus</i>	1	2	3	MK479192	MK479039	MK479090	MK479141
<i>Centruroides nozius</i>	2	2	4	MK479193	MK479040	MK479091	MK479142
<i>Centruroides ochraceus</i>	2	2	4	MK479194	MK479041	MK479092	MK479143
<i>Centruroides ornatus</i>	3	2	5	MK479195	MK479042	MK479093	MK479144
<i>Centruroides platnicki</i>	3	2	5	MK479196	MK479043	MK479094	MK479145
<i>Centruroides pococki</i>	1	1	2	MK479197	MK479044	MK479095	MK479146
<i>Centruroides rileyi</i>	3	4	7	KY982183	KY981897	KY981992	KY982087
<i>Centruroides robertoi</i>	1	1	2	ON255592	ON262612	-	ON259193
<i>Centruroides schmidtii</i>	7	8	15	KY982184	KY981898	KY981993	KY982089
<i>Centruroides serrano</i>	1	1	2	MK479200	MK479047	MK479098	MK479149
<i>Centruroides simplex</i>	1	1	2	MK479202	MK479048	MK479099	MK479154
<i>Centruroides sissomi</i>	1	0	1	MK479201	MK479049	MK479100	MK479150
<i>Centruroides taino</i>	4	4	8	MK479204	MK479051	MK479102	MK479152
<i>Centruroides tapachulaensis</i>	4	4	8	MK479205	MK479052	MK479103	MK479153
<i>Centruroides testaceus</i>	2	1	3	MK479207	MK479054	MK479105	MK479155
<i>Centruroides thorellii</i>	1	1	2	MK479208	MK479055	MK479106	MK479157
<i>Centruroides tuxtla</i>	1	1	2	MK479209	MK479056	MK479107	MK479158
<i>Centruroides vittatus</i>	0	1	1	KY982185	KY981899	KY981994	MK479159
<i>Chaneke hofereki</i>	1	2	3	ON255594	ON262613	ON259116	ON259195
<i>Charmus laneus</i>	2	0	2	ON255595	ON262614	ON259117	ON259196
<i>Compsobuthus arabicus</i>	1	1	2	-	AY226177	-	-
<i>Compsobuthus eritreensis</i>	1	1	2	ON255597	ON262616	ON259118	ON259198
<i>Compsobuthus somalilandus</i>	1	1	2	ON255600	-	-	-
<i>Femtobuthus shutuae</i>	1	1	2	ON255601	ON262620	ON259119	ON259201
<i>Gint amoudensis</i>	2	2	4	OM722200	OM809158	-	-
<i>Gint banfasae</i>	1	2	3	OM722193	OM809151	-	-
<i>Gint calviceps</i>	0	1	1	-	OM809149	-	-
<i>Gint dabakalo</i>	1	1	2	OM722190	OM809147	-	-
<i>Gint gaitako</i>	1	1	2	OM722188	OM809145	ON259120	ON259202
<i>Gint gubanensis</i>	0	1	1	OM722182	OM809139	-	-
<i>Gint maidensis</i>	1	1	2	OM722180	OM809137	-	-
<i>Grosphus madagascariensis</i>	1	1	2	ON255602	ON262621	ON259121	ON259203
<i>Heteroctenus abudi</i>	4	3	7	KY982186	ON262622	KY981995	ON259204
<i>Heteroctenus bonettii</i>	4	3	7	KY982189	KY981903	KY981998	KY982094
<i>Heteroctenus garridoi</i>	1	1	2	KY982191	KY981905	KY982000	KY982096
<i>Heteroctenus junceus</i>	4	4	8	KY982198	KY981912	KY982007	KY982097
<i>Heteroctenus princeps</i>	3	4	7	KY982200	KY981914	KY982009	ON259205
<i>Hottentotta flavidulus</i>	2	0	2	ON255606	ON262625	-	ON259207

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Species	Females	Males	Total	COI	16S	18S	28S
<i>Hottentotta franzwerneri</i>	0	1	1	JF820094	-	-	-
<i>Hottentotta gentili</i>	1	1	2	ON255607	ON262626	-	ON259208
<i>Hottentotta hottentotta</i>	1	0	1	ON255608	ON262627	ON259124	ON259209
<i>Hottentotta tamulus</i>	1	1	2	KT716032	-	-	-
<i>Ischnotelson peruassu</i>	1	1	2	KY982208	KY981922	KY982017	KY982112
<i>Isometrus maculatus</i>	11	5	16	KY982207	KY981921	KY982016	KY982111
<i>Isometrus thwaitesi</i>	1	0	1	ON255611	ON262630	ON259126	ON259212
<i>Jaguajir agamemnon</i>	1	0	1	KY982209	KY981923	KY982018	KY982113
<i>Jaguajir pintoii</i>	2	2	4	KY982220	KY981934	KY982029	KY982124
<i>Jaguajir rochae</i>	15	15	30	KY982224	KY981938	KY982033	KY982128
<i>Karasbergia methueni</i>	1	0	1	ON255613	ON262632	ON259128	ON259214
<i>Leiurus abdullahbayrami</i>	2	1	3	ON255614	ON262633	ON259129	ON259215
<i>Leiurus quinquestriatus</i>	3	2	5	JQ514258	JQ514241	-	-
<i>Lissothus occidentalis</i>	0	1	1	ON255615	ON262634	ON259130	ON259216
<i>Lychas mucronatus</i>	3	2	5	JN018153	AF370855	JN018270	JN018367
<i>Lychas obsti</i>	1	1	2	ON255616	ON262635	ON259131	ON259217
<i>Lychas scutillus</i>	1	1	2	ON255617	ON262636	-	ON259218
<i>Mesobuthus afghanus</i>	1	1	2	AJ550707	-	-	-
<i>Mesobuthus eupeus</i>	1	1	2	AJ550701	AY228141	-	-
<i>Mesobuthus haarlovi</i>	0	2	2	ON255618	ON262637	ON259132	ON259219
<i>Mesobuthus philippovitschi</i>	1	1	2	HM567348	-	-	-
<i>Mesobuthus phillipsi</i>	1	1	2	ON255619	ON262638	ON259133	ON259220
<i>Mesobuthus thersites</i>	1	1	2	AJ550700	-	-	-
<i>Microbuthus gardneri</i>	1	1	2	ON255620	ON262639	ON259134	ON259221
<i>Microbuthus kristensenorum</i>	2	0	2	ON255621	ON262640	ON259135	ON259222
<i>Microbuthus satyrus</i>	1	1	2	ON255622	ON262641	ON259136	ON259223
<i>Microtityus consuelo</i>	3	3	6	ON255623	ON262642	-	ON259224
<i>Microtityus fundorai</i>	1	1	2	-	DQ990830	-	-
<i>Microtityus solegladi</i>	2	2	4	ON255624	ON262643	ON259137	ON259225
<i>Neobuthus awashensis</i>	1	1	2	ON255625	ON262644	-	-
<i>Neobuthus eritreaensis</i>	1	1	2	ON255626	ON262645	ON259138	ON259226
<i>Neobuthus kutcheri</i>	2	2	4	OM722176	OM809133	-	-
<i>Odontobuthus brevidigitus</i>	1	1	2	ON255627	ON262646	ON259139	ON259227
<i>Odontobuthus tavighiaie</i>	1	1	2	KF701324	KJ659599	-	-
<i>Odontobuthus tirgari</i>	1	1	2	KF701322	KJ659602	-	-
<i>Olivierus caucasicus</i>	0	2	2	MG586931	MG586916	-	-
<i>Olivierus elenae</i>	1	0	1	AJ783604	MG586917	-	-
<i>Olivierus gorelovi</i>	1	1	2	AJ783515	-	-	-
<i>Olivierus intermedius</i>	1	1	2	MG586940	MG586926	-	-
<i>Olivierus kreuzbergi</i>	1	1	2	AJ550697	MG586929	-	-
<i>Olivierus martensii</i>	1	1	2	DQ340065	-	FJ948787.1	FJ948787
<i>Olivierus nenilini</i>	1	1	2	AJ783522	-	-	-
<i>Orthochirus afghanus</i>	1	0	1	ON255630	ON262649	-	-
<i>Orthochirus innesi</i>	3	1	4	ON255632	ON262651	ON259142	ON259230
<i>Parabuthus kajibu</i>	1	1	2	ON255634	ON262653	ON259144	ON259232
<i>Physoctonus debilis</i>	23	15	38	KY982238	KY981952	KY982048	KY982143
<i>Physoctonus striatus</i>	0	2	2	KY982241	KY981955	KY982051	KY982146
<i>Picobuthus wahibaensis</i>	1	1	2	ON255636	ON262655	ON259145	ON259234
<i>Reddyanus basilicus</i>	0	1	1	ON255638	ON262658	ON259148	ON259237
<i>Reddyanus ceylonensis</i>	1	1	2	ON255639	ON262659	-	ON259238
<i>Reddyanus petrzekai</i>	1	1	2	ON255641	ON262661	ON259150	ON259240
<i>Rhopalurus caribensis</i>	1	1	2	KY982243	KY981957	KY982053	KY982147
<i>Rhopalurus laticauda</i>	4	7	11	KY982247	KY981961	KY982057	KY982149
<i>Rhopalurus ochoai</i>	3	3	6	MF508635	MF402014	MF508621	MF508628
<i>Somalicharmus whitmanae</i>	0	1	1	ON255642	ON262662	ON259151	ON259241
<i>Thaicharmus mahunkai</i>	2	0	2	ON255644	ON262664	ON259153	ON259243

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Species	Females	Males	Total	COI	16S	18S	28S
<i>Tityus argentinus</i>	1	1	2	KY674493	KY674452	-	KY674474
<i>Tityus atriventer</i>	0	1	1	KY982264	KY981978	KY982074	-
<i>Tityus bahiensis</i>	1	1	2	KY982265	KY981979	KY982075	OK493233
<i>Tityus blaseri</i>	1	1	2	OK561901	OK493248	-	OK493221
<i>Tityus braziliae</i>	7	1	8	PQ341280	OK493239	-	OK493225
<i>Tityus cf. stigmurus SF247</i>	4	6	10	PQ341281	-	-	-
<i>Tityus cf. stigmurus SF464</i>	0	3	3	PQ341282	-	-	-
<i>Tityus clathratus</i>	1	5	6	KY982266	KY981980	KY982076	KY982171
<i>Tityus confluens</i>	2	2	4	KY674496	KY674456	-	KY674478
<i>Tityus crassimanus</i>	0	2	2	ON255647	ON262667	ON259156	ON259246
<i>Tityus curupi</i>	1	1	2	KY674440	KY674424	-	KY674429
<i>Tityus discrepans</i>	1	1	2	KY982267	KY981981	KY982077	KY982172
<i>Tityus elii</i>	1	2	3	-	ON262669	-	ON259248
<i>Tityus forcipula</i>	2	2	4	OK561898	OK493251	-	OK493230
<i>Tityus gaffini</i>	1	1	2	ON255649	ON262670	-	ON259249
<i>Tityus kuryi</i>	11	2	13	KY982268	KY981982	KY982078	KY982173
<i>Tityus mattogrossensis</i>	2	2	4	KY674498	KY674458	-	KY674480
<i>Tityus neglectus</i>	1	4	5	PQ341279	-	-	-
<i>Tityus neibae</i>	1	1	2	ON255650	ON262671	ON259158	ON259250
<i>Tityus nematochirus</i>	1	1	2	OL416036	-	-	OL416386
<i>Tityus obscurus</i>	0	1	1	OK561905	OK493243	-	OK493229
<i>Tityus panguana</i>	1	1	2	OK561908	OK493244	-	OK493231
<i>Tityus paraguayensis</i>	1	1	2	KY674499	-	-	-
<i>Tityus pictus microdon</i>	1	2	3	KY982271	KY981985	KY982081	KY982176
<i>Tityus potameis</i>	1	1	2	OK561899	OK493245	-	OK493232
<i>Tityus pusillus</i>	30	30	60	PQ341278	-	KP276456	KP276376
<i>Tityus serrulatus</i>	3	2	5	OK561900	OK493247	-	OK493220
<i>Tityus smithii</i>	2	2	4	ON255651	ON262672	ON259159	ON259251
<i>Tityus spelaeus</i>	17	0	17	-	OK493249	-	OK493224
<i>Tityus stigmurus</i>	10	4	14	OK561896	OK493240	-	OK493227
<i>Tityus uruguayensis</i>	1	1	2	KY674445	KY674428	-	KY674484
<i>Troglorhopalurus lacrau</i>	1	0	1	MF508640	MF508619	MF508626	MF508632
<i>Troglorhopalurus translucidus</i>	4	2	6	MF508641	MF508620	MF508627	MF508634
<i>Trypanothacus barnesi</i>	1	1	2	ON255652	ON262673	ON259160	ON259252
<i>Vachoniolus globimanus</i>	1	1	2	-	AY226179	-	-
<i>Xenobuthus xanthus</i>	2	1	3	ON255657	ON262679	ON259164	ON259258
<i>Zabius birabeni</i>	1	1	2	KY982272	KY981986	KY982082	KY674485
<i>Zabius fuscus</i>	1	1	2	KY982273	KY981987	KY982083	KY674486
<i>Aegaeobuthus gibbosus</i>	-	-	-	ON255556	ON262577	ON259095	ON259165
<i>Ananteris sp. R033MACr35702</i>	-	-	-	KY674492	KY674449	-	KY674471
<i>Androctonus sp.</i>	-	-	-	ON255567	ON262588	ON259101	ON259172
<i>Apistobuthus pterygocercus</i>	-	-	-	ON255568	ON262589	ON259102	ON259173
<i>Centruroides bani</i>	-	-	-	MK479164	ON262605	MK479062	ON259186
<i>Centruroides bicolor</i>	-	-	-	MK479166	MK479013	MK479064	MK479115
<i>Centruroides exilicauda</i>	-	-	-	KY982179	KY981893	KY981988	KY982084
<i>Centruroides fulvipes</i>	-	-	-	MK479174	MK479021	MK479072	ON259188
<i>Centruroides griseus</i>	-	-	-	MK479176	MK479023	MK479074	MK479125
<i>Centruroides hentzi</i>	-	-	-	MK479177	MK479024	MK479075	MK479126
<i>Centruroides insulanus</i>	-	-	-	MK479180	MK479027	MK479079	MK479129
<i>Centruroides insularis</i>	-	-	-	MK479181	MK479028	MK479078	MK479130
<i>Centruroides koesteri</i>	-	-	-	MK479182	MK479029	MK479080	MK479131
<i>Centruroides limbatus</i>	-	-	-	MK479183	MK479030	MK479081	MK479132
<i>Centruroides morenoi</i>	-	-	-	MK479188	MK479036	MK479087	MK479138
<i>Centruroides nigrescens</i>	-	-	-	MK479190	MK479037	MK479088	MK479139
<i>Centruroides pallidiceps</i>	-	-	-	AY995836	-	-	-
<i>Centruroides sasae</i>	-	-	-	MK479198	MK479045	MK479096	MK479147

Continues on the next page

Species	Females	Males	Total	COI	16S	18S	28S
<i>Centruroides sculpturatus</i>	-	-	-	MK479199	MK479046	MK479097	MK479148
<i>Centruroides suffusus</i>	-	-	-	MK479203	MK479050	MK479101	MK479151
<i>Centruroides tecomanus</i>	-	-	-	MK479206	MK479053	MK479104	MK479156
<i>Compsobuthus acutecaritus</i>	-	-	-	ON255596	ON262615	-	ON259197
<i>Compsobuthus acaindroni</i>	-	-	-	ON255598	ON262617	-	ON259199
<i>Compsobuthus matthiesseni</i>	-	-	-	ON255599	ON262618	-	ON259200
<i>Compsobuthus sp.</i>	-	-	-	-	ON262619	-	-
<i>Hottentotta conspersus</i>	-	-	-	ON255605	ON262624	ON259123	ON259206
<i>Hottentotta jabalpurensis</i>	-	-	-	MK696578	-	-	-
<i>Hottentotta jayakari</i>	-	-	-	-	AY226176	-	-
<i>Hottentotta minusalta</i>	-	-	-	ON255609	ON262628	-	ON259210
<i>Hottentotta pachyurus</i>	-	-	-	KT716023	-	-	-
<i>Hottentotta rugiscutis</i>	-	-	-	KT716025	-	-	-
<i>Hottentotta trilineatus</i>	-	-	-	ON255610	ON262629	ON259125	ON259211
<i>Hottentotta vinchu</i>	-	-	-	MH820411	-	-	-
<i>Ischnotelson guambiensis</i>	-	-	-	KY982205	KY981919	KY982014	KY982109
<i>Janalychas srilankensis</i>	-	-	-	ON255612	ON262631	ON259127	ON259213
<i>Janalychas tricaris</i>	-	-	-	KT716037	-	-	-
<i>Odontobuthus bidentatus</i>	-	-	-	KF701316	KJ659596	-	-
<i>Odontobuthus doriae</i>	-	-	-	KF701313	KJ659608	-	-
<i>Olivierus fuscus</i>	-	-	-	MG586937	MG586921	-	-
<i>Olivierus kaznakovi</i>	-	-	-	ON255628	ON262647	ON259140	ON259228
<i>Olivierus longichelus</i>	-	-	-	PP229938	-	-	-
<i>Olivierus parthorum</i>	-	-	-	AJ783516	-	-	-
<i>Orthochiroides vachoni</i>	-	-	-	ON255629	ON262648	ON259141	ON259229
<i>Orthochirus bicolor</i>	-	-	-	KT716038	-	-	-
<i>Orthochirus fomichevi</i>	-	-	-	MT232527	-	-	-
<i>Orthochirus glabrifrons</i>	-	-	-	ON255631	ON262650	-	-
<i>Orthochirus iranus</i>	-	-	-	-	MK170441	-	-
<i>Parabuthus brevimanus</i>	-	-	-	ON255633	ON262652	ON259143	ON259231
<i>Parabuthus laevifrons</i>	-	-	-	JN018154	-	JN018271	JN018368
<i>Parabuthus pallidus</i>	-	-	-	ON255635	ON262654	-	ON259233
<i>Parabuthus transvaalicus</i>	-	-	-	JQ514247	JQ514229	-	-
<i>Reddyanus loebli</i>	-	-	-	ON255640	ON262660	ON259149	ON259239
<i>Teruelius flavopiceus</i>	-	-	-	ON255643	ON262663	ON259152	ON259242
<i>Thaicharmus sp.</i>	-	-	-	ON255645	ON262665	ON259154	ON259244
<i>Tityopsis inexpectata</i>	-	-	-	ON255646	ON262666	ON259155	ON259245
<i>Tityus carvalhoi</i>	-	-	-	KY674495	KY674455	-	-
<i>Tityus cf. bastosi</i>	-	-	-	KY674494	KY674454	-	KY674476
<i>Tityus charreyroni</i>	-	-	-	OK561903	OK493237	-	OK493222
<i>Tityus ecuadoriensis</i>	-	-	-	ON255648	ON262668	ON259157	ON259247
<i>Tityus metuendus</i>	-	-	-	KY982269	KY981983	KY982079	KY982174
<i>Tityus riverai</i>	-	-	-	KY982270	KY981984	KY982080	-
<i>Tityus sastrei</i>	-	-	-	OK561897	OK493252	-	OK493234
<i>Tityus soratensis</i>	-	-	-	KY674500	KY674460	-	KY674482
<i>Tityus trivittatus</i>	-	-	-	KY674501	KY674461	-	-
<i>Uroplectes emiliae</i>	-	-	-	ON255653	ON262674	-	ON259253
<i>Uroplectes fischeri</i>	-	-	-	ON255654	ON262675	ON259161	ON259254
<i>Uroplectes flavoviridis</i>	-	-	-	-	ON262676	ON259162	ON259255
<i>Uroplectes gracilior</i>	-	-	-	ON255655	ON262677	ON259163	ON259256
<i>Uroplectes otjimbinguensis</i>	-	-	-	ON255656	ON262678	-	ON259257
<i>Zabius sp. 1 R007MACr36495</i>	-	-	-	KY674505	KY674465	-	KY674487
<i>Zabius sp. 2 R010MACr36496</i>	-	-	-	KY674506	KY674466	-	KY674488
<i>Zabius sp. 3 R034MACr36497</i>	-	-	-	KY674507	KY674467	-	KY674489
<i>Zabius sp. 4 R035MACr36498</i>	-	-	-	KY674508	KY674468	-	KY674490
<i>Brachistosternus paposo</i>	-	-	-	KT446990	KT446655	KT446767	KT446879

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## ModelFinder results

Best-fit DNA partition scheme obtained with ModelFinder and employed in IQ-TREE for estimating tree topology and branch lengths. PI = number of parsimony-informative sites, IS = number of invariant sites.

Partition	Number of taxa	Length (bp)	PI	IS	Model
18S rRNA	154	1752	115	1554	TNe+G4
28S rRNA	196	235	50	171	TNe+G4
16S rRNA (mtDNA)	234	265	169	79	GTR+F+G4
COI 1st position	253	195	75	110	TN+F+G4
COI 2nd position	253	195	24	146	GTR+F+G4
COI 3rd position	253	194	191	1	GTR+F+G4

## Calibration points

Calibration points used for node age estimation in buthid scorpions are detailed below. Each label corresponds to a calibration point, as shown on the phylogeny illustrated on the following page. Minimum and maximum node ages were applied to convert the maximum likelihood tree, generated using IQ-TREE v.2.3.2, into an ultrametric tree through penalized maximum likelihood. Node ages in the resulting ultrametric tree were then estimated using Bayesian inference in BEAST v1.10.4, employing lognormal priors. The 2.5% and 97.5% quantiles (Qs) of these priors aligned with the minimum and maximum ages for each calibration point.

Label	Split	Node age (My)			Prior specification		
		Min.	Max.	Source	meanlog	sdlog	2.5%-97.5% Qs
a	Buthus group	44.00	53.29	Ojanguren-Affilastro et al. 2017	3.88	0.049	44.07-53.46
b	Ananteris sp./A. balzanii	2.12	7.20	Ojanguren-Affilastro et al. 2017	1.36	0.310	2.14-7.4
c	Greater Antilles clade of Centruroides (fossil record)	17.00	20.00	Esposito and Prendini 2019	2.91	0.040	17.02-20.06
d	Greater Antilles/Chortis Maya clade of Centruroides	23.00	26.00	Esposito and Prendini 2019	3.20	0.030	23.02-26.06
e	Chortis Maya clade of Centruroides (fossil record)	15.00	23.00	Esposito and Prendini 2019	2.92	0.110	15.06-23.17
f	Centruroides/Heteroctenus	26.00	30.00	Esposito and Prendini 2019	3.33	0.040	26.03-30.07
g	Tityus group	26.04	42.17	Ojanguren-Affilastro et al. 2017	3.50	0.120	26.15-42.52
h	Tityus (Archeotityus) group	7.16	15.89	Ojanguren-Affilastro et al. 2017	2.37	0.200	7.21-16.11
i	Zabius spp.	3.29	7.38	Ojanguren-Affilastro et al. 2017	1.60	0.210	3.31-7.48







## R Function for defining lognormal priors

The `get_lognormal` R function is designed to define lognormal priors for node age estimation in BEAST. It performs parameter optimization using the L-BFGS-B protocol to find the `meanlog` ( $\mu$ ) and `sdlog` ( $\sigma$ ) parameters of a lognormal distribution, ensuring that the 2.5% and 97.5% quantiles align with the target quantiles – i.e., the prior belief about the respective node age. The objective function within `get_lognormal` aims to minimize the squared difference between the target quantiles and the actual quantiles for the given `meanlog` and `sdlog` values. It is defined as:

$$f(\mu, \sigma) = \sum_{i=1}^n (Q(p_i; \mu, \sigma) - T_i)^2$$

where:

- $f(\mu, \sigma)$  is the objective function,
- $Q(p_i; \mu, \sigma) = \exp(\mu + \sigma \cdot \Phi^{-1}(p_i))$  is the lognormal quantile function,
- $\mu$  is the `meanlog` (logarithmic mean of the distribution),
- $\sigma$  is the `sdlog` (logarithmic standard deviation),
- $p_i$  are the quantile probabilities (e.g., 0.025 and 0.975),
- $T_i$  are the target quantiles (see the example below),
- $\Phi^{-1}(p)$  is the inverse of the CDF of the standard normal distribution.

### Instructions

Simply copy the code provided on the next page and paste it into your R console. Press Enter, and you will see the `get_lognormal` function appear in your Environment panel (assuming you are using RStudio).

```

# Function to find optimal values for meanlog and sdlog

get_lognormal <- function(target_quantiles, quantile_probs, seed_number) {

  # Define the objective function
  objective_function <- function(params) {
    meanlog <- params[1]
    sdlog <- params[2]

    # Calculate the actual quantiles for the given meanlog and sdlog
    actual_quantiles <- qlnorm(quantile_probs, meanlog, sdlog)

    # Calculate the sum of squared differences between target and actual quantiles
    sum((actual_quantiles - target_quantiles)^2)
  }

  # Set initial guesses for meanlog and sdlog
  initial_guess <- c(log((target_quantiles[1] + target_quantiles[2]) / 2), 0.5)

  # Use optim to find the best meanlog and sdlog
  result <- optim(initial_guess,
    objective_function,
    method = "L-BFGS-B",
    lower = c(-Inf, 0.01),
    upper = c(Inf, Inf)
  )

  # Extract the optimal meanlog and sdlog
  optimal_meanlog <- result$par[1]
  optimal_sdlog <- result$par[2]

  # Generate samples using the optimal parameters
  set.seed(seed_number)
  n_samples <- 1000
  samples <- rlnorm(n_samples, optimal_meanlog, optimal_sdlog)

  # Return the results

  return(
    cat(
      "Optimal meanlog:", round(optimal_meanlog, 3), "\n",
      "Optimal sdlog:", round(optimal_sdlog, 3), "\n",
      "Quantiles of 1000 simulated values:",
      round(quantile(samples, probs = quantile_probs), 3)
    )
  )
}

```

## Usage

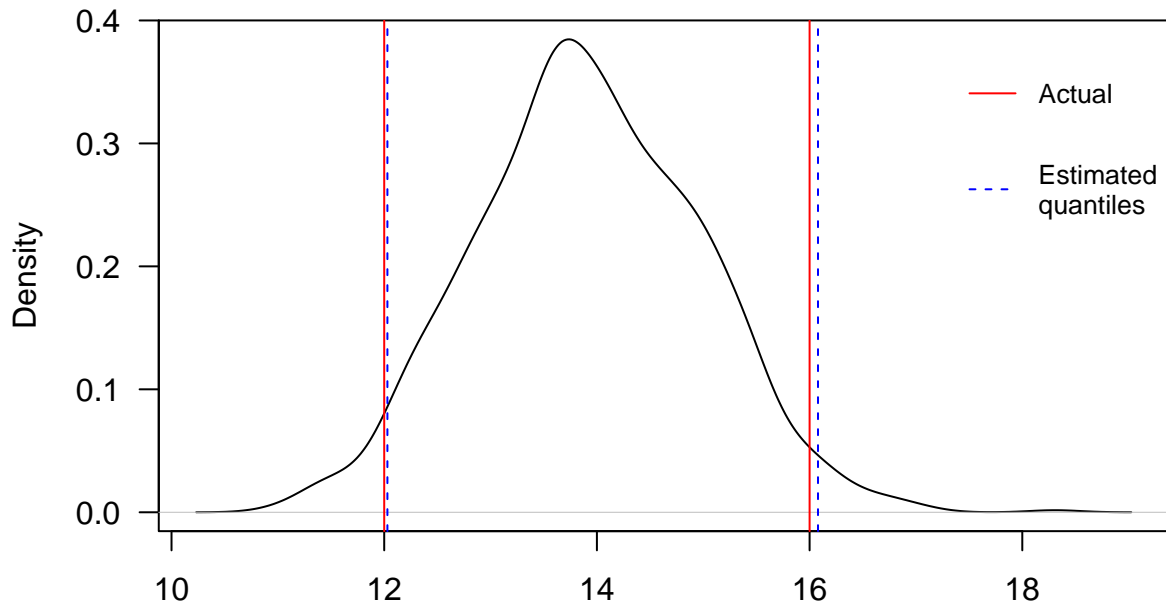
Let's say we have a fossil record for a specific node in our phylogeny, with an estimated age between 12 and 16 million years. We want to set a lognormal prior for this node so that the 2.5% and 97.5% quantiles of the lognormal distribution approximate this age range. In other words, we aim for the referred quantiles to be as close as possible to 12 and 16 million years. To achieve this, we will use the `get_lognormal` function to determine the `meanlog` and `sdlog` parameters of the lognormal distribution. The main arguments in the `get_lognormal` function are `target_quantiles`, which should include the minimum and maximum ages from our fossil record (12 and 16 million years in this case), and `quantile_probs`, which represent the quantiles of the lognormal distribution that should correspond to the values provided in `target_quantiles`. We also need to provide a seed number to ensure reproducibility (it can be any number). Thus, all we need to do is the following:

```
get_lognormal(  
  target_quantiles = c(12, 16),  
  quantile_probs = c(0.025, 0.975),  
  seed_number = 10  
)
```

```
## Optimal meanlog: 2.629  
## Optimal sdlog: 0.073  
## Quantiles of 1000 simulated values: 12.03 16.079
```

The function returns the optimal values for `meanlog` (2.629) and `sdlog` (0.073) for a lognormal distribution, ensuring that the 2.5% and 97.5% quantiles closely match the values provided via `target_quantiles`. We can generate and plot a lognormal distribution using the optimal `meanlog` and `sdlog`:

```
a <- rlnorm(n = 1000, meanlog = 2.629, sdlog = 0.073)  
plot(density(a), main = NA, las = 1)  
abline(v = 12, col = "red")  
abline(v = 16, col = "red")  
abline(v = 12.03, col = "blue", lty = "dashed")  
abline(v = 16.079, col = "blue", lty = "dashed")  
legend("topright",  
  legend = c("Actual", "Estimated\nquantiles"),  
  col = c("red", "blue"),  
  lty = c("solid", "dashed"),  
  bty = "n", cex = 0.8,  
  y.intersp = 2.5  
)
```



N = 1000 Bandwidth = 0.2391

## Interaction models

### Context

This is a set of complementary analyses designed to test for sex-specific differences in the slope parameters of linear measurements used to predict total length and carapace length in buthid scorpions. To assess these differences, an interaction term between sex and each predictor was added to the models. The regression models were built using a Bayesian framework with the R package `MCMCglmm` (Hadfield 2010) accounting for the phylogenetic relationships among species. In essence, these are phylogenetic mixed linear models fitted for trait data with repeated measures (i.e., the species), which were used as the random factor in the analyses. The dataset included natural logarithm values of linear measurements from 195 species. Abbreviations for the traits are provided in the table below.

Trait abbreviation:

Trait	Abbreviation
Total length	ToL
Carapace length	CarL
Chela length	CheL
Chela width	CheW
Length of metasomal segment V	Met5L
Width of metasomal segment V	Met5W
Telson length	TeL
Telson width	TeW

### Interactions with sex were not statistically significant when predicting total length

The table below presents the interaction terms between sex and each predictor, using total length as the response variable. The models were specified with species included as a random factor to account for repeated measures (i.e., one measurement per sex). All analyses considered the phylogenetic dependence of trait values (see the main text for further details). ESS = effective sample size.

Model	Parameter	Posterior Mean	Lower 95% CI	Upper 95% CI	ESS
M1	Intercept	2.1067	1.9907	2.2011	1000
	carL	1.0333	0.9881	1.0772	900
	sexm	0.0367	-0.0295	0.1062	816
	carL:sexm	0.0149	-0.0247	0.0520	863
M2	Intercept	2.3406	2.1305	2.5767	900
	cheL	0.6968	0.6367	0.7581	999
	sexm	-0.0847	-0.1700	0.0055	900
	cheL:sexm	0.0326	-0.0060	0.0728	900
M3	Intercept	3.4082	3.2306	3.5734	836
	cheW	0.6405	0.5808	0.7105	900
	sexm	-0.0148	-0.0531	0.0245	900
	cheW:sexm	-0.0204	-0.0626	0.0254	900
M4	Intercept	2.1614	2.0517	2.2747	900
	met5L	0.9480	0.9016	0.9922	900
	sexm	-0.0424	-0.1040	0.0241	900
	met5L:sexm	-0.0158	-0.0481	0.0214	900
M5	Intercept	3.1300	2.9011	3.3314	900
	met5W	0.7158	0.6437	0.7938	1002
	sexm	0.0097	-0.0448	0.0677	900
	met5W:sexm	-0.0206	-0.0746	0.0258	900
M6	Intercept	2.3378	2.2198	2.4567	940
	teL	0.8932	0.8516	0.9409	900
	sexm	-0.0261	-0.0847	0.0336	900
	teL:sexm	0.0166	-0.0192	0.0507	900
M7	Intercept	3.2794	3.1353	3.4318	992
	teW	0.8140	0.7608	0.8611	900
	sexm	0.0005	-0.0300	0.0275	900
	teW:sexm	0.0279	-0.0041	0.0646	900

### Interactions with sex were mostly non significant when predicting carapace length

The table below presents the interaction terms between sex and each predictor, using carapace length as the response variable. The models were specified with species included as a random factor to account for repeated measures (i.e., one measurement per sex). All analyses considered the phylogenetic dependence of trait values (see the main text for further details). Only the interaction with metasomal segment V (`ln_met5L:sexm`) was statistically significant. ESS = effective sample size.

Model	Parameter	Posterior Mean	Lower 95% CI	Upper 95% CI	ESS
M1	Intercept	0.4280	0.1693	0.6841	996
	cheL	0.5755	0.5257	0.6271	950
	sexm	-0.1089	-0.1644	-0.0581	900
	cheL:sexm	0.0136	-0.0087	0.0404	900
M2	Intercept	1.2761	1.1072	1.4480	900
	cheW	0.5668	0.5081	0.6272	900
	sexm	-0.0656	-0.1014	-0.0363	805
	cheW:sexm	-0.0337	-0.0696	0.0005	900
M3	Intercept	0.2023	0.0624	0.3322	900
	met5L	0.8267	0.7681	0.8760	900
	sexm	-0.0493	-0.1160	0.0234	900
	met5L:sexm	-0.0420	-0.0755	-0.0001	900
M4	Intercept	1.0414	0.8626	1.2410	900
	met5W	0.6400	0.5778	0.6975	900
	sexm	-0.0725	-0.1088	-0.0367	900
	met5W:sexm	0.0006	-0.0321	0.0315	900
M5	Intercept	0.3500	0.2297	0.4848	1083
	teL	0.7830	0.7414	0.8263	1212
	sexm	-0.0804	-0.1240	-0.0290	862
	teL:sexm	0.0107	-0.0160	0.0378	874
M6	Intercept	1.1788	1.0365	1.3087	900
	teW	0.7154	0.6698	0.7572	793
	sexm	-0.0591	-0.0795	-0.0379	818
	teW:sexm	0.0205	-0.0036	0.0467	900



## Phylogenetic multiple regressions

### Context

The results of several multiple regression models analyzed using a Bayesian phylogenetic approach are presented below. These models were designed to evaluate whether including a secondary predictor improves the accuracy of predictions for total length and carapace length in buthid scorpions - remember that in the previous analyses (main text), **Met5L** and **TeL** appeared as the best single predictor (lowest RMSE values) of total length and carapace length, respectively. The multiple regression models were built using a Bayesian framework with the R package **MCMCg1mm** (Hadfield 2010) accounting for the phylogenetic relationships among species. In essence, these are phylogenetic mixed linear models fitted for trait data with repeated measures (i.e., the species), which were used as the random factor in the analyses. The dataset included natural logarithm values of linear measurements from 195 species.

### Multiple regression for predicting total length

The multiple regression analyses revealed that while adding a second predictor improves the accuracy of total length predictions, the improvement is modest. The RMSE for the model using **Met5L** as the sole predictor was 6.42 mm, corresponding to an average relative error of 13% (with the mean total length in the dataset being 51.28 mm). In comparison, the RMSE for the best multiple regression model, which combines **Met5L** with **CheW**, is 5.13 mm, leading to an average relative error of 10%. Therefore, the addition of a second predictor enhances the accuracy of total length predictions by only 3% at most. ESS = effective sample size.

Model	RMSE (mm)	Parameter	Posterior Mean	Lower 95% CI	Upper 95% CI	ESS
M4	5.129	Intercept	2.331	2.245	2.413	900
		met5L	0.767	0.722	0.820	900
		cheW	0.196	0.157	0.233	900
M3	5.147	Intercept	2.497	2.393	2.614	1066
		met5L	0.619	0.558	0.681	1045
		teW	0.344	0.279	0.395	992
M5	5.220	Intercept	2.235	2.137	2.330	900
		met5L	0.783	0.729	0.833	900
		met5W	0.204	0.157	0.251	900
M1	5.451	Intercept	2.165	2.063	2.247	900
		met5L	0.472	0.400	0.552	900
		teL	0.491	0.415	0.561	900
M2	5.637	Intercept	2.041	1.936	2.130	900
		met5L	0.739	0.683	0.803	900
		cheL	0.218	0.170	0.269	900

## Multiple regression for predicting carapace length

Similarly, for the multiple regression models predicting carapace length, adding a secondary predictor improved accuracy by only up to 2% at most. The mean carapace length in the dataset was 5.6 mm. ESS = effective sample size.

Model	RMSE (mm)	Parameter	Posterior Mean	Lower 95% CI	Upper 95% CI	ESS
M5	0.559	Intercept	0.337	0.249	0.432	665
		teL	0.653	0.602	0.703	900
		met5W	0.224	0.173	0.273	900
M3	0.571	Intercept	0.576	0.465	0.680	900
		teL	0.493	0.425	0.561	900
		teW	0.362	0.296	0.428	900
M4	0.577	Intercept	0.390	0.306	0.484	817
		teL	0.681	0.633	0.733	900
		cheW	0.172	0.134	0.220	900
M2	0.622	Intercept	0.147	0.046	0.252	900
		teL	0.702	0.640	0.760	900
		cheL	0.150	0.102	0.210	900
M1	0.656	Intercept	0.188	0.071	0.282	900
		teL	0.727	0.647	0.815	900
		met5L	0.131	0.035	0.219	900

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