

Supplementary Materials for

Evolutionary history of Chinese cavefishes parallels paleogeoclimatic and river capture processes

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Supplementary Note 1

(1) Supplementary Data 2: *Sinocyclocheilus* clade (Cypriniformes, Cyprinidae)

We reanalyzed the mitochondrial genome data from Wen et al.¹, and additionally we collected mitochondrial fragments *16S*, *Cyt b*, *ND5*, *ND4*, and *COI*. The combined dataset totaled 15,671 bases (bp). In the absence of a reference fossil calibration, we refer to Wen et al.¹ and Yang et al.²: (1) *Sinocyclocheilus* originated at 43.96 million years (Ma) (sigma=2.8); (2) the most recent common ancestor of *Sinocyclocheilus* occurred at 32.13 Ma (sigma=2.8); (3) the divergence of the *S. angularis* species group and the *S. tingi* + *S. cyphotergous* species groups occurred at about 26.3 Ma (sigma = 4.2). BEAST analyses were run for 40 million generations under an uncorrelated relaxed clock model and a Yule tree prior, sampled every 5000 generations. All calibrations were performed using a normal prior and monophyly.

(2) Supplementary Data 3: *Karstsinnectes-Micronemacheilus-Oreonectes-Paranemachilus-Guinemachilus-Eonemachilus-Yunnanilus-Troglonectes-Triplophysa* clade (Cypriniformes, Nemacheilidae)

We collected nuclear genes *EGR1*, *EGR2B*, *EGR3*, *IRBP*, *RAG1*, *RH1*, and *MYH6* for divergence time assessment. We used six secondary calibrations and one fossil calibration from the family Cobitidae to assess ages: (1) the root age of the family Gyrinocheilidae was ca. 75.3 million years ago (Ma)³; (2) the stem age for the Botidae was ca. 61.3 Ma³; (3) the stem age for the Vaillantellidae was ca. 56.3 Ma³; (4) the stem age for the Cobitidae was ca. 49.9 Ma³; (5) the stem age for the Balitoridae was ca. 45.5 Ma³; (6) the fossil from the middle Miocene, *Cobitis centrochir* (13.8–15.9 Ma)⁴, was set to the stem age of the genus *Cobitis*; and (7) the divergence between *Triplophysa* and *Barbatula* occurred at ca. 23.5 Ma⁵. BEAST analysis was run for 200 million generations and sampled every 2000 generations. All calibrations used a normal prior, monophyly, and standard deviation values of 2.2 (for the first five), 0.55 (for the sixth), and 1.6 (for the seventh).

(3) Supplementary Table 2: *Neolissochilus* clade (Cypriniformes, Cyprinidae)

We collected mitochondrial *COI*, *Cyt b*, *ND4*, and *16S* for divergence time assessment. The combined dataset totaled 5754 bp. We refer to Rabosky et al.⁶ for the reconstruction of the fish tree of life, setting two secondary calibration points: 20.82 Ma (sigma=1.0) for the root age and 17.69 Ma (sigma=1.0) for the age of the most recent common ancestor of *Tok-Neolissochilus-Puntius*). BEAST analyses were run for 10 million generations under an uncorrelated relaxed clock model and a Yule tree prior, sampled every 1000 generations. All calibrations were performed using a normal prior and monophyly.

(4) Supplementary Table 3: *Eidinemacheilus-Schistura* clade (Cypriniformes, Nemacheilidae)

We collected mitochondrial *COI*, *Cyt b*, and *16S* for divergence time assessment. The combined dataset totaled 4406 bp. We refer to Hirt et al.³ and Zhou⁴, setting two secondary calibration points and a fossil calibration point: (1) 87.2 Ma (sigma=10) for the root age of the Cypriniformes; (2) 75.3 Ma (sigma=10) for the root age of the Cobitoidei; and (3) The fossil calibrations of the genus *Cobitis* were recorded as 13.8–15.9Ma (mean= 14.85, sigma=2.5). BEAST analyses were run for 10 million generations under an uncorrelated relaxed clock model and a Yule tree prior, sampled every 1000 generations. All calibrations were performed using a normal prior and monophyly.

(5) Supplementary Table 7: *Bibarba-Protocobitis* clade (Cypriniformes, Cobitidae)

We collected mitochondrial *COI*, *Cyt b*, and *16S* and the nuclear gene *RAG1* for divergence time assessment. The combined dataset totaled 5916 bp. We refer to Hirt et al.³ and Zhou⁴, setting two secondary calibration points and a fossil calibration point: (1) 87.2 Ma (sigma=10) for the root age of the Cypriniformes; (2) 75.3 Ma (sigma=10) for the root age of the Cobitoidei; and (3) The fossil calibrations of the genus *Cobitis* were recorded as 13.8–15.9Ma (mean= 14.85, sigma=2.5). BEAST analyses were run for 10 million generations under an

uncorrelated relaxed clock model and a Yule tree prior, sampled every 1000 generations. All calibrations were performed using a normal prior and monophyly.

(6) Supplementary Table 5: *Balitora* clade (Cypriniformes, Balitoridae)

We collected mitochondrial *COI* and *Cyt b* and the nuclear genes *RAG1*, *IRBP*, and *EGR2B* for divergence time assessment. The combined dataset totaled 5829 bp. We refer to Hirt et al.³ and Zhou⁴, setting a secondary calibration points and a fossil calibration point: (1) 56.3 Ma (sigma=6.15) for the root age; and (2) The fossil calibrations of the genus *Cobitis* were recorded as 13.8–15.9Ma (mean= 14.85, sigma=2.5). BEAST analyses were run for 20 million generations under an uncorrelated relaxed clock model and a Yule tree prior, sampled every 1000 generations. All calibrations were performed using a normal prior and monophyly.

(7) Supplementary Table 6: *Xiurenbagrus* clade (Siluriformes, Amblycipitidae)

We collected mitochondrial *COI*, *Cyt b*, and *ND4* and the nuclear gene *RAG2* for divergence time assessment. The combined dataset totaled 5103 bp. We refer to Rabosky et al.⁶ for the reconstruction of the fish tree of life, setting two secondary calibration points: 58.07 Ma (sigma=2.5) for the root age and 51.42 Ma (sigma=2.5) for the age of the most recent common ancestor of *Liobagrus*-*Xiurenbagrus*-*Acrochordonichthys*-*Breitensteinia*-*Amblyceps*). BEAST analyses were run for 20 million generations under an uncorrelated relaxed clock model and a Yule tree prior, sampled every 1000 generations. All calibrations were performed using a normal prior and monophyly.

(8) Supplementary Table 7: *Horaglanis* (Siluriformes, Siluridae)

We collected mitochondrial *Cyt b*, *COI*, *16S*, and *12S* for divergence time assessment. The combined dataset totaled 5386 bp. We refer to Rabosky et al.⁶ for the reconstruction of the fish tree of life, setting two secondary calibration points: *Chaca* originated at 67.7 Ma (sigma=2.5) and *Silurus* Originated at 44.04 Ma (sigma=2.5). BEAST analyses were run for 50 million generations under an uncorrelated relaxed clock model and a Yule tree prior, sampled every 1000 generations. All calibrations were performed using a normal prior and monophyly.

(9) Supplementary Data 4: *Pseudocrossocheilus*-*Longanalus*-*Hongshuia* clade (Cypriniformes, Cyprinidae)

We collected mitochondrial *COI*, *Cyt b*, *16S*, *ND4*, and *ND5* and the nuclear genes *RAG1*, *RHOD*, *EGR2B*, and *IRBP2* for divergence time assessment. The combined dataset totaled 5386 bp. In the absence of a reference fossil calibration, we refer to Rabosky et al.⁶: (1) the divergence of the *Nipponocyprissieboldii* and the *Zaccoplatus* occurred at about 24.37 million years ago (Ma) (stdev=2.5); (2) *Pseudocrossocheilus* originated at 10.69 Ma (stdev=2.5). BEAST analyses were run for 100 million generations under an uncorrelated relaxed clock model and a Yule tree prior, sampled every 1000 generations.

(10) Supplementary Table 8: *Homatula* clade (Cypriniformes, Nemacheilida)

We collected mitochondrial *Cyt b* for divergence time assessment. The dataset totaled 1140 bp. We refer to Rabosky et al.⁶ for the reconstruction of the fish tree of life, setting two secondary calibration points: (1) the divergence of the *Tracatichthys* and the *Homatula* + *Schistura* occurred at about 39.09 million years ago (Ma) (stdev=2.5); (2) *Schistura* originated at 34.71 Ma (stdev=2.5). BEAST analyses were run for 10 million generations under an uncorrelated relaxed clock model and a Yule tree prior, sampled every 1000 generations. All calibrations were performed using a normal prior and monophyly.

Supplementary Table 1. Primers used in PCR and sequencing in this study.

Marker	Primer name and sequence (5'-3')	Annealing temp (°C)	Source
<i>16S</i>	16Sp1F: CTTACACCGAGAARACATC 16Sp1R: CTTAAGCTCCAAAGGGTC	53	Li et al. ⁷
<i>COI</i>	COI-L5956: CACAAAGACATTGGCACCCT COI-H6855: AGTCAGCTGAAKACTTTTAC	50	Peng et al. ⁸
<i>Cyt b</i>	Ver-L14724: GACTTGAAAAACCACCGTTG Ver-H15915: CTCCGATCTCCGGAT TACAAGAC	52	Xiao et al. ⁹
<i>ND4</i>	F: CCWAAGGCSCATGTWGARGC R: GAAGAGTTTTTGGTTCCTAAG	50	Saitoh et al. ¹⁰
<i>ND5</i>	L13058-ND5: CTCGCTATGGAGGGYCKAC H13393-ND5: CCCTATTTTKCGGATGTCTTGYTC	52	Miya et al. ¹¹
<i>EGR1</i>	E1 290F b: TMTCTTACACAGGCCGYTTCAC E1 1126Rb: CTTTYTCTGCTTTCTTGTCCTTCT E1 228F c: GAAATTTCCATGGASAAACCTCT E1 1389Rc: AGAACTGTAGATGTTGCTGRCCAC E1 333Fd: CAGYAACAGTCTRTGGGCTGAG E1 1104Rd CGCAGGTGGATCTTRGTGTG E2B 278Fb: AGTTTTCCATCGACTCSCAGTA E2B 1117Rb: AGGTGGATTTTGGTGTGTCTYTT	55	Chen et al. ¹²
<i>EGR2B</i>	E2B 205Fc: ACTTRTCCTATYCCAGCAGCTT E2B 1108Rd: TTTTGTGTGTCTCTTTCTYTCGTC E2B 287Fd: TTGACTCSCAGTATCCAGGTAAC E3 161Fb: AATATCATGGACYTGGGNATGG	55	Chen et al. ¹²
<i>EGR3</i>	E3 1136Rb: GGYTTCTTGTCTTCTGTTTSAG E3 254Fd: GTCACCTAYYTGGGSAAGTTT IRBP101Fd: TCMTGGACAAYTACTGCTCACC	55	Chen et al. ¹²
<i>IRBP2</i>	IRBP1001Rb: GGAAATGCATAGTTGTCTGCAA IRBP155F: TKCTCACCAGAAARACTCACRGG IRBP1021R: AGTTGTCTGCAACMAGTGYSGC	52	Liu et al. ¹³
<i>MYH6</i>	myh6_F507: GGAGAATCARTCKGTGCTCATCA myh6_R1322: CTCACCACCATCCAGTTGAACAT	52	Liu et al. ¹³
<i>RAG1</i>	F1: GCTGCAGTCAGTACCACAAGATGT R1: GATACTTGGAGGTGTAGAGCCAGT	53	Chen et al. ¹²
<i>RHOD</i>	RH1F: CATACGAATATCCCCAGTACTACC RH1R: GCTTGTTTCATGCAGATGTAGATGC	52	Liu et al. ¹³

Supplementary Table 2. Species and their GenBank accession numbers used for molecular analysis in this study, for *Neolissochilus*. Red indicates cave-dwelling species

ID	Species	<i>COI</i>	<i>Cyt b</i>	<i>ND4</i>	<i>16S</i>
1	<i>Neolissochilus pnar</i>	OQ351362	OQ349707		OQ357609
2	<i>Neolissochilus baoshanensis</i>	KJ994640	KJ994692	KJ994744	KJ994588
3	<i>Neolissochilus benasi</i>	KJ994638	KJ994690	KJ994742	KJ994586
4	<i>Neolissochilus benasi</i>	MN598560	MN598560	MN598560	MN598560
5	<i>Neolissochilus hexagonolepis</i>	KU380329	KU380329	KU380329	KU380329
6	<i>Neolissochilus kaladanensis</i>	MG518431			
7	<i>Neolissochilus nigrovittatus</i>	LC189740			
8	<i>Neolissochilus qiaojiensis</i>	KJ994613	KJ994665	KJ994728	KJ994561
9	<i>Neolissochilus soroides</i>	OM203154	OM203154	OM203154	OM203154
10	<i>Neolissochilus stracheyi</i>	OM203155	OM203155	OM203155	OM203155
11	<i>Neolissochilus wynaadensis</i>	KP712095	KP712195	KP712316	KP712652
12	<i>Neolissochilus hendersoni</i>	NC_062665	NC_062665	NC_062665	NC_062665
13	<i>Neolissochilus heterostomus</i>	KJ994661	KJ994713	KJ994765	KJ994609
14	<i>Neolissochilus hexastichus</i>	NC_056297	NC_056297	NC_056297	NC_056297
15	<i>Neolissochilus stracheyi2</i>	NC_031555	NC_031555	NC_031555	NC_031555
16	<i>Tor yingjiangensis</i>	KJ994660	KJ994712	KJ994764	KJ994608
17	<i>Tor khudree</i>	NC_027617	NC_027617	NC_027617	NC_027617
18	<i>Puntius chelynoides</i>	MH626062	OM918740		JQ435839
19	<i>Hypselobarbus periyarensis</i>	HM010717	HM010729	HM010741	HM010705

Supplementary Table 3. Species and their GenBank accession numbers used for molecular analysis in this study, for *Eidinemacheilus* and *Schistura*.

ID	Species	<i>COI</i>	<i>Cyt b</i>	<i>16S</i>
1	<i>Eidinemacheilus smithi</i>	KX429660		
2	<i>Eidinemacheilus smithi</i>	OP310814		
3	<i>Eidinemacheilus proudlovei</i>	KX774390		
4	<i>Schistura jarutanini</i>	NC_031584	NC_031584	NC_031584
5	<i>Schistura sijuensis</i>	MK388817	MK732337	MK726134
6	<i>Aborichthys elongatus</i>	NC_031582	NC_031582	NC_031582
7	<i>Acanthocobitis botia</i>	AP012139	AP012139	AP012139
8	<i>Afronemacheilus abyssinicus</i>	ON997077		
9	<i>Barbatula barbatula</i>	KP715096	KP715096	KP715096
10	<i>Claea dabryi</i>	KT906089	KT906089	KT906089
11	<i>Dzihunia amударjensis</i>	MW649537		
12	<i>Eonemachilus longidorsalis</i>	OM732331	OM732331	OM732331
13	<i>Homatula wenshanensis</i>	NC_063102	NC_063102	NC_063102
14	<i>Indoreonectes evezardi</i>	MW464180	KY497109	
15	<i>Lefua nikkonis</i>	AP011300	AP011300	AP011300
16	<i>Mesonoemacheilus triangularis</i>	AP011406	AP011406	AP011406
17	<i>Micronemacheilus cruciatus</i>	AP012142	AP012142	AP012142
18	<i>Mustura bella</i>	OL191130	OL191242	
19	<i>Nemacheilus masyai</i>	AP011444	AP011444	AP011444
20	<i>Nemachilichthys rueppelli</i>	NC_031583	NC_031583	NC_031583
21	<i>Nemacheilus pallidus</i>	NC_031639	NC_031639	NC_031639
22	<i>Oreonectes platycephalus</i>	NC_031579	NC_031579	NC_031579
23	<i>Oxyonemacheilus amanos</i>	AP011233	AP011233	AP011233
24	<i>Paracanthocobitis mooreh</i>	MW074285	KT005615	
25	<i>Paracobitis malapterura</i>	KJ723515	MG229881	
26	<i>Paranemachilus genilepis</i>	MT845213	MT845213	MT845213
27	<i>Paraschistura montana</i>	HQ219198	FJ711438	
28	<i>Petruichthys brevis</i>	NC_031637	NC_031637	NC_031637
29	<i>Physoschistura shanensis</i>	OL191098	OL191222	
30	<i>Pteronemacheilus lucidorsum</i>	OL191117	OL191215	
31	<i>Sasanidus kermanshahensis</i>	KU928289		
32	<i>Schistura robertsi</i>	OL191034	MK887044	
33	<i>Sectoria heterognathos</i>	MG238203	MG238297	
34	<i>Schistura disparizona</i>	MG238158	MG238252	
35	<i>Schistura shuangjiangensis</i>	MG238191	MG238285	
36	<i>Schistura balteata</i>	AB242172	AB242172	AB242172
37	<i>Schistura aurantiaca</i>	OL191121	MK886950	
38	<i>Seminemacheilus lendlii</i>	MT077005	KP738578	
39	<i>Traccatichthys pulcher</i>	NC_073140	NC_073140	NC_073140
40	<i>Triplophysa baotianensis</i>	NC_056365	NC_056365	NC_056365
41	<i>Triplophysa tibetana</i>	NC_030483	NC_030483	NC_030483

42	<i>Troglocobitis starostini</i>	ON997078		
43	<i>Troglonectes furcicaudalis</i>	NC_073138	NC_073138	NC_073138
44	<i>Tuberoschistura baenzigeri</i>	NC_031641	NC_031641	NC_031641
45	<i>Turcinoemacheilus kosswigi</i>	KJ179265	KU180216	
46	<i>Yunnanilus sichuanensis</i>	NC_042209	NC_042209	NC_042209
47	<i>Misgurnus anguillicaudatus</i>	DQ026434	DQ026434	DQ026434
48	<i>Cobitis takatsuensis</i>	AP011290	AP011290	AP011290
49	<i>Gyrinocheilus aymonieri</i>	AB242164	AB242164	AB242164
50	<i>Gyrinocheilus pennocki</i>	AP011226	AP011226	AP011226
51	<i>Catostomus commersonii</i>	AB127394	AB127394	AB127394

Supplementary Table 4. Species and their GenBank accession numbers used for molecular analysis in this study, for *Bibarba* and *Protocobitis*. Bold type indicates sequences obtained through sequencing by the authors.

ID	Species	<i>Cyt b</i>	<i>COI</i>	<i>16S</i>	<i>RAG1</i>
1	<i>Bibarba bibarba</i>	KT585706			KT585690
2	<i>Bibarba bibarba</i>	KT585705			KT585689
3	<i>Bibarba bibarba</i>	KT585704			KT585688
4	<i>Bibarba bibarba</i>	KT585703			KT585687
5	<i>Bibarba bibarba</i>	MG710539			MG710543
6	<i>Bibarba parvovulus</i>	KT585699			KT585683
7	<i>Bibarba parvovulus</i>	KT585698			KT585682
8	<i>Bibarba parvovulus</i>	MG710541			
9	<i>Bibarba parvovulus</i>	MG710540			
10	<i>Acantopsis choirorhynchus</i>	AB242161	AB242161	AB242161	AB531314
11	<i>Acanthopsoides gracilentus</i>	AP013298	AP013298	AP013298	EF508600
12	<i>Canthophrys gongota</i>	NC_031576	NC_031576	NC_031576	FJ650414
13	<i>Cobitis lutheri</i>	NC_022717	NC_022717	NC_022717	EU670830
14	<i>Cobitis takatsuensis</i>	AP009306	AP009306	AP009306	EU409616
15	<i>Iksookimia yongdokensis</i>	MN581868	MN581868	MN581868	EU670838
16	<i>Kichulchoia multifasciata</i>	AP011337	AP011337	AP011337	KM818297
17	<i>Koreocobitis rotundicaudata</i>	AP011339	AP011339	AP011339	EU670841
18	<i>Kottelatlimia pristis</i>	AP011343	AP011343	AP011343	EF508640
19	<i>Lepidocephalichthys guntea</i>	AP011338	AP011338	AP011338	KY356514
20	<i>Lepidocephalus macrochir</i>	AP011342	AP011342	AP011342	
21	<i>Microcobitis misgurnoides</i>	KP161131			EF508616
22	<i>Misgurnus anguillicaudatus</i>	LC532168	LC532168	LC532168	EU670842
23	<i>Niwaella delicata</i>	AP011230	AP011230	AP011230	KT585692
24	<i>Pangio kuhlii</i>	NC_031599	NC_031599	NC_031599	EF056331
25	<i>Paralepidocephalus yui</i>	NC_068240	NC_068240	NC_068240	
26	<i>Paramisgurnus dabryanus</i>	AP012124	AP012124	AP012124	JN177188
27	<i>Sabanejewia radnensis</i>	AP011229	AP011229	AP011229	
28	<i>Protocobitis longicostatus</i>	PX733120	PX733120	PX733120	
29	<i>Protocobitis longibarba</i>	PP868402	PP866712		
30	<i>Protocobitis anteroventris</i>	PQ591769			
31	<i>Protocobitis longicostatus</i>	OP948913	OP948913		
32	<i>Protocobitis typhlops</i>	OR713096	OR713096		
33	<i>Ellopostoma mystax</i>	AP011447	AP011447	AP011447	FJ650417
34	<i>Bhavana australis</i>	AP013303	AP013303	AP013303	MT002575
35	<i>Micronemacheilus pulcher</i>	NC_031581	NC_031581	NC_031581	EU409611
36	<i>Vaillantella maassi</i>	AB242173	AB242173	AB242173	EU711132
37	<i>Gyrinocheilus aymonieri</i>	AB242164	AB242164	AB242164	EU292682
38	<i>Catostomus commersonii</i>	AB127394	AB127394	AB127394	EU409612

Supplementary Table 5. Species and their GenBank accession numbers used for molecular analysis in this study, for *Balitora*. Bold type indicates sequences obtained through sequencing by the authors.

ID	Species	<i>Cyt b</i>	<i>COI</i>	<i>RAG1</i>	<i>IRBP</i>	<i>EGR2B</i>
1	<i>Hemimyzon yaotianensis</i>	JN176994		JN177053		
2	<i>Sinogastromyzon szechuanensis</i>	MN241814	MN241814			
3	<i>Sinogastromyzon hsiashiensis</i>	JN176997	JN177109	JN177054		
4	<i>Lepturichthys dolichopterus</i>	GU084245	JN177091	JN177029		
5	<i>Lepturichthys fimbriata</i>	GU084229	JN177102	JN177182	JN177272	JN177251
6	<i>Sinogastromyzon nantaiensis</i>		KU943003			
7	<i>Sinogastromyzon puliensis</i>	FJ605359	FJ605359			
8	<i>Metahomaloptera omeiensis</i>	JN177000	JN177080	JN177041		
9	<i>Sinogastromyzon sichangensis</i>	JN176998	JN177078	JN177040	KP695068	KP694496
10	<i>Sinogastromyzon sichangensis</i>	OQ754146		OQ754160	OQ754156	OQ754151
11	<i>Jinshaia sinensis</i>	JN176985	JN177117	JN177044		
12	<i>Jinshaia abbreviata</i>	JN176992	JN177228	JN177180	JN177274	JN177249
13	<i>Lepturichthys fimbriata</i>	JN176942	JN177139	JN177020	JN177273	
14	<i>Hemimyzon formosanus</i>	AY392484	KU943001		KP695096	
15	<i>Hemimyzon taitungensis</i>	KX056121				
16	<i>Balitora ludongensis</i>	OQ754141				
17	<i>Balitora ludongensis</i>	OQ754142				
18	<i>Balitora ludongensis</i>	MT157616	MT157616			
19	<i>Balitora anlongensis</i>	OQ754144		OQ754158	OQ754154	OQ754149
20	<i>Balitora anlongensis</i>	OQ754145		OQ754159	OQ754155	OQ754150
21	<i>Balitora anlongensis</i>	OQ754143		OQ754157	OQ754152	OQ754148
22	<i>Sinogastromyzon wui</i>	JN177001	JN177076			
23	<i>Balitora nujiangensis</i>		KM610757			
24	<i>Balitora nujiangensis</i>		KM610756			
25	<i>Sinogastromyzon tonkinensis</i>	JN177002	JN177074	JN177056	JN177277	JN177247
26	<i>Balitora brucei</i>	MK732323	MK388804			
27	<i>Balitora brucei</i>		KJ774109			
28	<i>Balitora annamitica</i>			EF056359		
29	<i>Balitora mysorensis</i>	KU378018	KU378005			
30	<i>Balitora mysorensis</i>	KU378019	KU378006			
31	<i>Balitora chipkali</i>	KU378016	KU378003			
32	<i>Balitora chipkali</i>	KU378017	KU378004			
33	<i>Balitora jalpalli</i>		MT216524			
34	<i>Balitora laticauda</i>	KU378007	KU377994			
35	<i>Balitora laticauda</i>	KU378008	KU377995			
36	<i>Balitora elongata</i>	DQ105218				
37	<i>Balitora elongata</i>	DQ105217				
38	<i>Balitora meridionalis</i>			KP322550		
39	<i>Balitora kwangsiensis</i>	JN177004		JN177060		
40	<i>Balitora kwangsiensis</i>	OQ754147		OQ754161	OQ754153	
41	<i>Balitora elongata</i>			KP695617	KP695065	

42	<i>Balitora kwangsiensis</i>	JN177006	JN177071	JN177058		
43	<i>Balitora kwangsiensis</i>	JN177005	JN177072	JN177059	JN177276	JN177248
44	<i>Balitora kwangsiensis</i>	DQ105216				
45	<i>Homaloptera bilineata</i>			KP322549		
46	<i>Homaloptera confuzona</i>	NC_033955	NC_033955	KP322543		
47	<i>Homaloptera parclitella</i>	NC_031634	NC_031634	EU409610	EU409668	EU409732
48	<i>Homaloptera ocellata</i>	NC_033953	NC_033953	KP322539		
49	<i>Homaloptera ogilviei</i>	NC_031635	NC_031635			
50	<i>Pseudohomaloptera leonardi</i>	AB242165	AB242165	EU711130	FJ197076	AB531164
51	<i>Pseudohomaloptera sexmaculata</i>		ON903153	KP322545		
52	<i>Balitoropsis ophirolepis</i>		KR052868	KP322540		
53	<i>Balitoropsis zollingeri</i>		KR052865	KP322535		
54	<i>Bhavana australis</i>	MT002547	MT002512	MT002571		
55	<i>Travancoria elongata</i>		MT216535			
56	<i>Travancoria jonesi</i>		MT216539			
57	<i>Ghatsa montana</i>		MT216529			
58	<i>Ghatsa santhamparaiensis</i>		MT216532			
59	<i>Ghatsa pillaii</i>		MT216530			
60	<i>Homalopteroides smithi</i>	NC_033957	NC_033957	KP322546		
61	<i>Homalopterula gymnogaster</i>			KP322554		
62	<i>Neohomaloptera johorensis</i>	NC_033952	NC_033952			
63	<i>Vanmanenia caldwelli</i>	JN177011	JN177232	JN177178	JN177280	JN177252
64	<i>Ellopostoma mystax</i>	AP011447	AP011447	FJ650417	FJ650489	FJ650448
65	<i>Misgurnus anguillicaudatus</i>	DQ026434	DQ026434	AB531306	JN177287	AB531185
66	<i>Cobitis takatsuensis</i>	AP011290	AP011290	EU409616		EU409739
67	<i>Vaillantella maassi</i>	AB242173	AB242173	EU711132	FJ197080	FJ650453
68	<i>Myxocyprinus asiaticus</i>	AB223007	AB223007	JN177063	JX488937	JN177263

Supplementary Table 6. Species and their GenBank accession numbers used for molecular analysis in this study, for *Xiurenbagrus*.

ID	Species	<i>Cyt b</i>	<i>COI</i>	<i>ND4</i>	<i>RAG2</i>
1	<i>Xiurenbagrus dorsalis</i>	NC_060563	NC_060563	NC_060563	
2	<i>Xiurenbagrus xiurenensis</i>	EU490939	EU490890	EU490842	EU491015
3	<i>Xiurenbagrus xiurenensis</i>	DQ192464	EU490889	DQ192416	DQ192456
4	<i>Xiurenbagrus xiurenensis</i>	DQ192465		DQ192417	DQ192457
5	<i>Xiurenbagrus gigas</i>	EU490936	EU490887	EU490839	EU491012
6	<i>Amblyceps apangi</i>	EU490922	EU490873	EU490825	EU490999
7	<i>Amblyceps arunchalensis</i>		MN587190		
8	<i>Amblyceps foratum</i>	EU490924	EU490875	EU490826	
9	<i>Amblyceps laticeps</i>		KY290130		
10	<i>Amblyceps mangois</i>	DQ119364	DQ508067		DQ508037
11	<i>Amblyceps mucronatum</i>	EU490925	EU490876	EU490827	EU491001
12	<i>Amblyceps serratum</i>	EU490923	EU490874	EU490828	EU491000
13	<i>Liobagrus aequilabris</i>	KY653629	KY653521		
14	<i>Liobagrus andersoni</i>	KX767082	KX767082	KX767082	
15	<i>Liobagrus anguillicauda</i>	DQ192463	KY653538	DQ192415	DQ192455
16	<i>Liobagrus chengduensis</i>	ON638208			
17	<i>Liobagrus formosanus</i>		KU943004		
18	<i>Liobagrus huaiheensis</i>	ON638214			
19	<i>Liobagrus hyeongsanensis</i>	MZ066608	MZ066608	MZ066608	
20	<i>Liobagrus kingi</i>	NC_020337	NC_020337	NC_020337	
21	<i>Liobagrus marginatoides</i>	EU490929	EU490880	EU490832	EU491005
22	<i>Liobagrus marginatus</i>	DQ192462	EU490881	DQ192414	DQ192454
23	<i>Liobagrus mediadiposalis</i>	NC_027167	NC_027167	NC_027167	
24	<i>Liobagrus nigricauda</i>	NC_021407	NC_021407	NC_021407	
25	<i>Liobagrus obesus</i>	NC_008232	NC_008232	NC_008232	
26	<i>Liobagrus pseudostyani</i>	ON638210			
27	<i>Liobagrus reinii</i>	AP012015	AP012015	AP012015	
28	<i>Liobagrus somjinensis</i>	MN756661	MN756661	MN756661	
29	<i>Liobagrus styani</i>	EU490932	EU490883	EU490835	EU491008
30	<i>Acrochordonichthys rugosus</i>	DQ119410	DQ508027	EU490802	DQ508032
31	<i>Breitensteinia cessator</i>	EU490900	DQ508070	EU490803	DQ508040
32	<i>Pseudecheneis sulcata</i>	DQ192469	KF742428	DQ192412	DQ192451

Supplementary Table 7. Species and their GenBank accession numbers used for molecular analysis in this study, for *Horaglanis*.

ID	Species	<i>Cyt b</i>	<i>COI</i>	<i>16S</i>	<i>12S</i>
1	<i>Horaglanis krishnai</i>	MZ802974	MZ820774		
2	<i>Horaglanis krishnai</i>	MZ802975	MZ820775		
3	<i>Horaglanis populi</i>	OP832204	OP825096	OP824387	OP824404
4	<i>Horaglanis populi</i>	OP832205	OP825097	OP824388	OP824405
5	<i>Horaglanis abdulkalami</i>	OP832203	OP825094	OP824386	OP824403
6	<i>Horaglanis abdulkalami</i>		OP825093	OP824385	OP824402
7	<i>Horaglanis alikunhii</i>	HG937614	HE819391		
8	<i>Horaglanis alikunhii1</i>	HG937613	HE819393		
9	<i>Horaglanis krishnai2</i>	OP832208	OP825103	OP824393	OP824411
10	<i>Horaglanis krishnai3</i>	OP832210	OP825106	OP824396	OP824414
11	<i>Belodontichthys truncatus</i>	DQ119456	MK448174		
12	<i>Ceratoglanis scleronema</i>	MH633760	MH633777		
13	<i>Hemisilurus mekongensis</i>	DQ119392	MK448161		
14	<i>Kryptopterus bicirrhys</i>	DQ119480	MH732875		MH688299
15	<i>Ompok bimaculatus</i>	NC_036233	NC_036233	NC_036233	NC_036233
16	<i>Phalacrodon apogon</i>	DQ119409	EF609377		
17	<i>Pterocryptis anomala</i>	NC_051505	NC_051505	NC_051505	NC_051505
18	<i>Silurichthys schneideri</i>	DQ119430			
19	<i>Silurus meridionalis</i>	NC_014866	NC_014866	NC_014866	NC_014866
20	<i>Wallago attu</i>	NC_063564	NC_063564	NC_063564	NC_063564
21	<i>Chaca bankanensis</i>	AP012008	AP012008	AP012008	AP012008
22	<i>Horabagrus brachysoma</i>	NC_030188	NC_030188	NC_030188	NC_030188
23	<i>Pimelodus yuma</i>	NC_061908	NC_061908	NC_061908	NC_061908
24	<i>Heteropneustes fossilis</i>	AP012013	AP012013	AP012013	AP012013
25	<i>Pseudecheneis sulcata</i>	MK843301	MK843301	MK843301	MK843301
26	<i>Diplomystes nahuelbutaensis</i>	NC_015823	NC_015823	NC_015823	NC_015823
27	<i>Helogenes marmoratus</i>	AP012014	AP012014	AP012014	AP012014
28	<i>Platydoras armatulus</i>	NC_025585	NC_025585	NC_025585	NC_025585
29	<i>Bunocephalus coracoideus</i>	NC_015811	NC_015811	NC_015811	NC_015811

Supplementary Table 8. Species and their GenBank accession numbers used for molecular analysis in this study, for *Homatula*.

ID	Species	Cyt b
1	<i>Homatula dotui</i>	OK230029
2	<i>Homatula dotui</i>	OK230030
3	<i>Homatula wuliangensis</i>	HM010517
4	<i>Homatula pycnolepis</i>	HM010541
5	<i>Homatula pycnolepis</i>	KF041000
6	<i>Homatula pycnolepis</i>	HM010549
7	<i>Homatula acuticephala</i>	HM010527
8	<i>Homatula potanini</i>	JF340395
9	<i>Homatula variegata</i> ,	HM010520
10	<i>Homatula longidorsalis</i>	HM010550
11	<i>Homatula longidorsalis</i>	HM010519
12	<i>Homatula variegata</i> ,	HM010489
13	<i>Schistura macrotaenia</i>	JN837655
14	<i>Schistura caudofurca</i>	JN837651
15	<i>Schistura callichroma</i>	JN837652
16	<i>Schistura cryptofasciata</i>	JF340401
17	<i>Schistura fasciolata</i>	HM010565
18	<i>Schistura bucculenta</i>	JN837654
19	<i>Sectoria heterognathos</i>	DQ105200
20	<i>Schistura latifasciata</i>	JN837653
21	<i>Schistura amplizona</i>	JN837656
22	<i>Traccatichthys pulcher</i>	DQ105198
23	<i>Tuberoschistura baenzigeri</i>	NC_031641

Supplementary Table 9. Evaluation results of cave-dwelling fishes within the *Sinocyclocheilus* at the species levels for ancestral areas using the R package BioGeoBEARS. The best model is indicated in bold. Abbreviations: LnL=log-likelihood; d =dispersal rate per million years along branches; e =extinction rate per million years along branches; j = likelihood of founder-event speciation at cladogenesis; AIC= Akaike information criterion.

ID	Model	LnL	Number of parameters	d	e	j	AIC	AIC model weight
1	DEC	-145.7	2	0.003	0.006	0.000	295.3	0.000
2	DEC+J	-118.3	3	0.000	0.000	0.020	242.6	0.890
3	DIVALIKE	-145.0	2	0.004	0.002	0.000	294.1	0.000
4	DIVALIKE+J	-145.0	2	0.004	0.002	0.000	294.1	0.000
5	BAYAREALIKE	-185.2	2	0.005	0.057	0.000	374.3	0.000
6	BAYAREALIKE+J	-120.4	3	0.000	0.000	0.020	246.8	0.110

Supplementary Table 10. Evaluation results of cave-dwelling fishes within the Nemacheilidae at the species levels for ancestral areas using the R package BioGeoBEARS. The best model is indicated in bold. Abbreviations: LnL=log-likelihood; d =dispersal rate per million years along branches; e =extinction rate per million years along branches; j = likelihood of founder-event speciation at cladogenesis; AIC= Akaike information criterion.

ID	Model	LnL	Number of parameters	d	e	j	AIC	AIC model weight
1	DEC	-265.7	2	0.003	0.012	0.000	535.40	0.000
2	DEC+J	-197.8	3	0.000	0.000	0.022	401.50	0.880
3	DIVALIKE	-257.0	2	0.003	0.005	0.000	517.90	0.000
4	DIVALIKE+J	-257.0	2	0.003	0.005	0.000	517.90	0.000
5	BAYAREALIKE	-320.4	2	0.005	0.062	0.000	644.80	0.000
6	BAYAREALIKE+J	-199.8	3	0.000	0.000	0.022	405.60	0.120

Supplementary Table 11. Evaluation results of cave-dwelling fishes within the Nemacheilidae at the species levels for ancestral areas using the R package BioGeoBEARS. The best model is indicated in bold. Abbreviations: LnL=log-likelihood; d =dispersal rate per million years along branches; e =extinction rate per million years along branches; j = likelihood of founder-event speciation at cladogenesis; AIC= Akaike information criterion.

ID	Model	LnL	Number of parameters	d	e	j	AIC	AIC model weight
1	DEC	-265.7	2	0.003	0.012	0.000	535.40	0.000
2	DEC+J	-197.8	3	0.000	0.000	0.022	401.50	0.880
3	DIVALIKE	-257.0	2	0.003	0.005	0.000	517.90	0.000
4	DIVALIKE+J	-257.0	2	0.003	0.005	0.000	517.90	0.000
5	BAYAREALIKE	-320.4	2	0.005	0.062	0.000	644.80	0.000
6	BAYAREALIKE+J	-199.8	3	0.000	0.000	0.022	405.60	0.120

Supplementary Table 12. The ages of different features of the diversification dynamics. Bold font indicates a higher possibility.

Features of the diversification dynamics	Observations (99% confidence interval) (Ma)
Dispersal events (MDisE)	
Origination of MDisE	33.56 (33.90–30.90)
Peak of MDisE	16.66 (16.8–16.5), 5.89 (6.9–5.7) , 4.36 (4.8–4.2)
Valley of MDisE	13.80 (13.8–13.8), 8.16 (9.0–7.5) , 17.62 (17.7–17.1)
Breakpoints of MDisE	23.45(24.55–22.36), 14.24 (15.05–13.44), 4.23(4.49–3.97)
<i>In situ</i> diversification (MDivE)	
Origination of MDivE	43.20 (45.00–34.50)
Peak of MDivE	8.27 (8.70–7.80), 2.53 (3.30–2.10) , 1.45 (1.50–0.90)
Valley of MDivE	24.95 (25.20–24.11), 13.68(13.80–1.20), 3.40 (3.00–3.90)
Breakpoints of MDivE	35.29 (38.02–32.56), 18.05(20.00–16.10), 6.35 (6.95–5.75)
Migration into caves (MCE)	
Origination of MCE	44.48 (45.00–36.00)
Peak of MCE	32.70 (32.70–32.70) , 13.46 (13.50–13.20), 26.04 (26.40–25.80)
Valley of MCE	10.66 (11.10–10.20) , 16.20 (16.20–16.20), 28.35 (28.50–28.20)
Breakpoints of MCE	42.75 (46.50–39.00), 9.00 (10.02–7.98)
Lineage divergences (MDE)	
Origination of MDE	39.45 (34.20–40.80)
Peak of MDE	2.48 (2.70–2.10) , 1.43 (1.80–0.90), 9.00 (9.60–8.40)
Valley of MDE	3.35 (3.90–3.00) , 13.64 (13.80–12.90), 24.71 (25.20–24.00)
Breakpoints of MDE	35.6(38.59–32.61), 15.14 (16.95–13.34), 5.81 (6.31–5.32)
Pearl River to Yangtze River (PTY)	
Origination of PTY	24.05 (26.10–17.40)
Peak of Pearl PTY	~13.0 [#] , 16.4 (16.5–16.3)*, 0.60 (0.60 - 0.60)**, ~2.0 [#] ,
Valley of PTY	4.3 [#] , 15.50 (15.50 - 15.50)*, 0.90 (0.90 - 0.90)**,
Breakpoints of PTY	21.74(22.95–20.53), 13.24(13.64–12.84), 8.61(9.59–7.62)
Yangtze River to Pearl River (YTP)	
Origination of YTP	13.01 (13.50–10.00)
Peak of YTP	~5.0 [#] , 4.6 (4.7–4.3)
Breakpoints of YTP	9.6 (10.27–8.93), 5.47(5.71–5.22)

Note: *Time window size: 0.5 Ma; **Time window size: 0.5 Ma; [#]Observation from Figure 3C.

Supplementary Table 13. The ages and 95% confidence intervals for different features of *in situ* diversification of cave fishes in different basins.

River	Origination	Peak	Valley	Breakpoints
Hongshui	39.91 (40.80–31.50)	1.22 (0.60–1.50), 2.54 (2.40–3.00), 6.05 (6.90–5.70)	21.60 (21.60–21.60), 13.80 (13.80–13.80), 8.70 (8.70–8.70)	9.88 (11.49–8.28), 16.93 (19.39–14.47), 35.95 (40.99–30.92)
Guijiang–Hejiang	37.74 (45.00–12.90)	NA	0.77 (0.90–0.60)	7.86 (8.27–7.46), 13.80 (14.57–13.03), 35.43 (43.18–27.68)
Nanpanjiang	33.60 (33.30–31.20)	4.07 (34.5–0.90), 8.82 (9.30–8.40)	7.07 (8.10–6.90), 18.25 (18.60–18.00), 5.29 (5.40–4.80)	1.94 (2.55–1.32), 10.16 (11.83–8.49), 31.36 (45.62–17.11)
Zuojiang–Youjiang	33.29 (34.20–23.40)	12.00 (12.00–12.00), 2.66 (2.40–3.60)	11.10 (11.10–11.10), 13.80 (13.80–13.80), 3.19 (3.60–2.70)	8.36 (8.81–7.91), 13.70 (15.28–12.11), 24.30 (27.51–21.09)
Liujiang	27.61 (29.10–23.91)	0.90 (1.50–0.60), 2.60 (2.70–2.10), 16.02 (16.50–15.90)	3.91 (4.50–3.60), 7.61 (8.10–7.50), 2.11 (2.40–1.50)	3.60 (5.25–1.95), 13.17 (14.17–12.17), 20.76 (22.65–18.88)
Upper Yangtze–Wujiang	22.41 (27.60–13.20)	2.27 (2.70–2.10), 4.58 (4.80–4.50), 7.65 (7.80–7.50)	3.34 (3.60–3.00)	2.03 (2.39–1.68)
Yuanjiang	11.39 (11.70–8.10)	NA	NA	5.66 (6.19–5.14), 9.14 (10.34–7.93)
Jinshajiang	11.91 (13.50–9.30)	2.91 (3.30–2.70), 0.90 (0.90–0.90)	3.42 (3.60–3.00)	5.19 (5.53–4.86), 9.87 (10.49–9.26)
Panlongjiang	11.54 (12.90–3.30)	0.60 (0.60–0.60)	NA	0.92 (1.09–0.74), 8.85 (9.53–8.18)
Beipanjiang	9.13 (7.80–9.90)	NA	2.30 (2.40–1.80)	3.00 (4.47–1.53), 7.20 (7.57–6.83), 7.91 (8.43–7.40)

Supplementary Table 14. Summary of the number of cavefish dispersal events between the Yangtze River and the Pearl River. Respective lineages/species, lower and upper bounds of the 95% intervals for the age.

Lineages/species	Lower	Upper	Event type
<i>Troglonectes duanensis</i> - <i>Troglonectes translucens</i>	0.09	0.39	Pearl→Yangtze
<i>Sinocyclocheilus sanxiaensis</i> - <i>Sinocyclocheilus cyphotergous</i>	0.87	4.22	Pearl→Yangtze
<i>Sinocyclocheilus anophthalmus</i> - <i>Sinocyclocheilus huizeensis</i>	8.27	17.31	Pearl→Yangtze
<i>Triplophysa tianeensis</i> - <i>Triplophysa guizhouensis</i>	9.16	14.98	Pearl→Yangtze
<i>Triplophysa</i> _ <i>baishuijiangensis</i> - <i>Triplophysa qiubeiensis</i>	10.8	17.33	Pearl→Yangtze
<i>Sinocyclocheilus qujingensis</i> - <i>Sinocyclocheilus huizeensis</i>	11.72	20.63	Pearl→Yangtze
<i>Sinocyclocheilus zhenningensis</i> - <i>Sinocyclocheilus donglanensis</i>	16.18	25.98	Pearl→Yangtze
<i>Sinocyclocheilus punctatus</i> - <i>Sinocyclocheilus guiyang</i>	1.06	7.24	Yangtze→Pearl
<i>Sinocyclocheilus tingi</i> - <i>Sinocyclocheilus grahami</i>	1.28	6.37	Yangtze→Pearl
<i>Sinocyclocheilus punctatus</i> - <i>Sinocyclocheilus cyphotergous</i>	2.85	9.56	Yangtze→Pearl
<i>Triplophysa qini</i> - <i>Triplophysa guizhouensis</i>	3.35	7.95	Yangtze→Pearl
<i>Sinocyclocheilus qujingensis</i> - <i>Sinocyclocheilus lateristriatus</i>	4.2	13.35	Yangtze→Pearl
<i>Triplophysa baishuijiangensis</i> - <i>Triplophysa_xuanweiensis</i>	4.41	12.98	Yangtze→Pearl

Supplementary Table 15. Summary of the paleoelevation results from the Himalaya–Tibetan Plateau.

Unit	Age_min_Ma	Age_max_Ma	Elev_min_km	Elev_max_km	Age	Paleoelevation (m)	Source
Himalaya and India–Asia suture (IAS)	60	60	0	0	~60Ma	0	14
Himalaya and India–Asia suture (IAS)	54	58	0	1800	56 Ma	900 ± 900 m	15
Himalaya and India–Asia suture (IAS)	19	21	1400	3200	21–19 Ma	2300 ± 900 m	15
Himalaya and India–Asia suture (IAS)	22	25	1500	2900	25–22 Ma	1500–2900 m	16
Himalaya and India–Asia suture (IAS)	21	24	1270	2721	24–21 Ma	2080 (+641/–810) m	17
Himalaya and India–Asia suture (IAS)	19	21	3417	4587	21–19 Ma	4057 (+530/–640) m	17
Himalaya and India–Asia suture (IAS)	19	20	3883	5740	26–19 Ma	4863 (+ 877/–980) m	17
Himalaya and India–Asia suture (IAS)	20	20	4000	5000	26–21 Ma	Low elevation	18,19
Himalaya and India–Asia suture (IAS)	16	18	5100	5400	~17 Ma	5100–5400 m	20,21
Himalaya and India–Asia suture (IAS)	9.6	11	3320	4280	11–9.6 Ma	3800 ± 480 m	22,23
Himalaya and India–Asia suture (IAS)	9.6	11	5550	6250	11–9.6 Ma	5900 ± 350m	22,23
Himalaya and India–Asia suture (IAS)	7	7	4070	4930	<7 Ma	4500 ± 430 m	22,23
Himalaya and India–Asia suture (IAS)	7	7	5970	6630	<7 Ma	6300 ± 330m	22,23
Himalaya and India–Asia suture (IAS)	9.6	11	5370	7650	11–9.6 Ma	6240 (+1410/–870) m	24
Himalaya and India–Asia suture (IAS)	7	7	4970	7110	<7 Ma	5700 (+1410/–730) m	24
Himalaya and India–Asia suture (IAS)	1.7	7	5120	7260	~7–1.7 Ma	5850 (+1410/–730) m	24
Himalaya and India–Asia suture (IAS)	9	10	5200	5900	9.2 to <1 Ma	decrease in the mean watershed elevation of 1 to 1.5 km since the Late Miocene	25
Himalaya and India–Asia suture (IAS)	1	9.2	6200	7000	9.2 to <1 Ma	6600 ± 400 m (catchment)	25,26
Himalaya and India–Asia suture (IAS)	1	9.2	4900	5900	9.2 to <1 Ma	5400 ± 500 m (basin floor)	25,26
Himalaya and India–Asia suture (IAS)	3.2	7.2	5000	7400	~7.2–3.2 Ma	6300 (+1100/–1300) m	
Himalaya and India–Asia suture (IAS)	3.2	7.2	1700	3300	~7.2–3.2 Ma	Lake surface 2500 ± 800 m	27,28
Himalaya and India–Asia suture (IAS)	3.2	7.2	3000	3900	~7.2–3.2 Ma	surrounding mountains 3600 m ± 600 m	
Himalaya and India–Asia suture (IAS)	3	5	1800	3400	9.2 to <1 Ma	decrease in the mean watershed	29

					elevation of 1 to 1.5 km since the		
					<47.5 Ma	Late Miocene 1500 ± 900 m	
Lhasa–Qiangtang suture Valley	46.8	48.2	600	2400	(47.5 ± 0.7 Ma)		30
Lhasa–Qiangtang suture Valley	46	46	1680	3320	46 Ma	2590 (+730/–910) m	31
Lhasa–Qiangtang suture Valley	40	50	1000	2600	50–40 Ma	1700 (+900/–700) m	32
Lhasa–Qiangtang suture Valley	29	37	3700	4500	37–29 Ma	4100 ± 400 m	32
Lhasa–Qiangtang suture Valley	33.9	41.2	3600	4100	Eocene	3600 to 4100 m	33
Lhasa–Qiangtang suture Valley	5.333	23.03	4500	4900	Miocene	4500 to 4900 m	33
Lhasa–Qiangtang suture Valley	35.7	39.4	50	650	39.4–35.7 Ma	close to sea level	34
Lhasa–Qiangtang suture Valley	30	40	2830	5470	Eocene	4050 (+1420/–1220) m	35
Lhasa–Qiangtang suture Valley	30	40	3415	6480	Late Eocene to Oligocene (35 ± 5 Ma)	4850 (+1630/–1435) m	35
Lhasa–Qiangtang suture Valley	15	23.03	3685	4735	Miocene	4260 (+475/–575) m	35
Lhasa–Qiangtang suture Valley	23.5	26.2	4500	5000	~26 Ma	4500–5000 m	36
Lhasa–Qiangtang suture Valley	23	26	3090	3290	25.5–19.8 Ma	3190 ± 100 m	37
Lhasa–Qiangtang suture Valley	19.8	25.5	2240	3300	25.5–19.8 Ma44	2770 ± 530 m	38
Lhasa–Qiangtang suture Valley	19.8	25.5	2480	3600	25.5–19.8 Ma44	3040 ± 560 m	38
Lhasa–Qiangtang suture Valley	12	15	3100	3600	12–15Ma	3100-3600	39
Eastern Tibet	50	54	-200	1500	54–50 Ma	700 (+800/–900) m	40
Eastern Tibet	40	44	2700	4600	44–40 Ma	3800 (+800/–1100) m	40

Eastern Tibet	35.5	37.9	2800	3800	Middle Miocene	3300 ± 500 m	41
Eastern Tibet	35.5	37.9	2850	3750	Late Miocene	3300 ± 450 m	41
Eastern Tibet	35.5	37.9	2350	2950	~37 Ma	2650 ± 300 m	41
Eastern Tibet	33.9	37.7	1800	3200	Late Eocene	2500 ± 700 m	42
Eastern Tibet	36	36	2300	3500	~36 Ma	2900 ± 600 m	42
Eastern Tibet	37	38	1900	4100	38–37 Ma	3000 ± 1100 m	43
Eastern Tibet	35	36	2000	3800	36–35 Ma	2900 ± 900 m	44
Eastern Tibet	33	35	3000	4800	35–33 Ma	3900 ± 900 m	44
Eastern Tibet	16	23	2200	4900	~23–16 Ma	3800 (+1100/–1600) m	45
Eastern Tibet	40	45	2.4	3	Estimated value	Estimated value	14
Eastern Tibet	5	7	2360	4540	Latest Miocene–Pliocene	2100–4280 m	46

Supplementary Table 16. Original sediment budget data for the Pearl River/South China basins, compiled from Figure 3E in Clift⁴⁷.

Time_start_Ma	Time_end_Ma	Rate_min	Rate_max
45	33	4	6
33	29	6	9
29	18	7.5	11
18	12	13.5	20.5
12	6	5	8
6	0	8	12

Supplementary Table 17. Data used to plot the idealized evolution of the Asian monsoon from 45 Ma to present, extracted from Figure 1B of Farnsworth et al.⁴⁸.

Time_Ma	Precipitation (m/year)
44.5	1.25
39.5	1.65
35.9	1.72
31	1.68
25.6	1.75
27.7	1.7
18.2	1.72
14.9	1.7
12.7	1.9
9.4	2.15
6.3	2
4.5	2.12
3.1	1.72
2.2	1.48
0	1.5

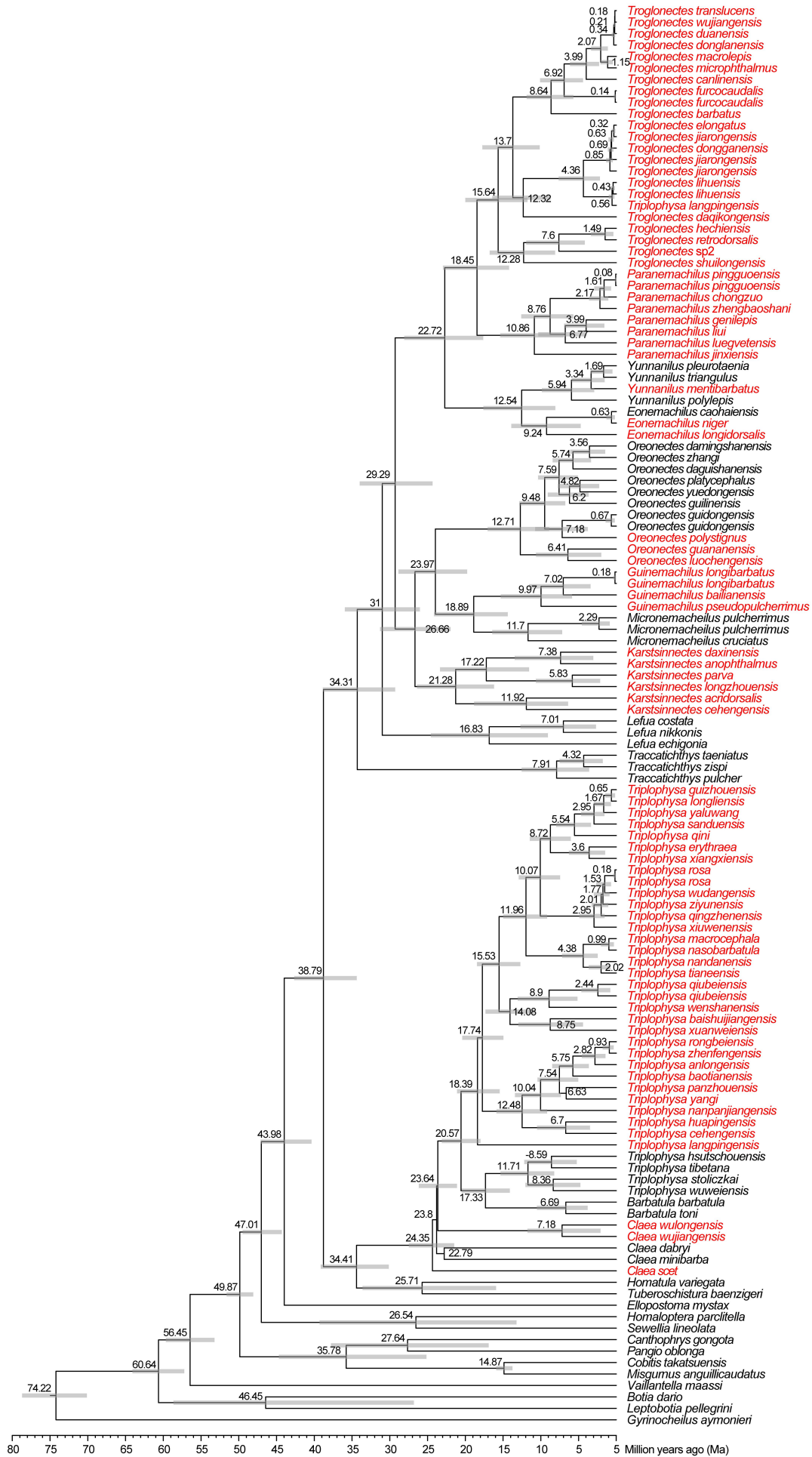
Supplementary Table 18. Mean values, confidence intervals, and statistical test results for the 16 dataset breakpoints detected.

Dataset	Breakpoint_ID	Breakpoint_Time	Breakpoint_95%CI_Lower	Breakpoint_95%CI_Upper	Breakpoint_SE	Breakpoint_t	Breakpoint_p-value	Significance
Dispersal	1	4.23	3.97	4.49	0.13	31.67	0	****
Dispersal	2	14.24	13.44	15.05	0.41	34.68	0	****
Dispersal	3	23.45	22.36	24.55	0.56	42.08	0	****
<i>In situ</i> diversification	1	6.35	5.75	6.95	0.30	20.84	0	****
<i>In situ</i> diversification	2	18.05	16.10	20.00	1.00	18.12	0	****
<i>In situ</i> diversification	3	35.29	32.56	38.02	1.39	25.32	0	****
Migration into caves	1	9.00	7.98	10.02	0.52	17.22	0	****
Migration into caves	2	42.75	39.00	46.50	1.91	22.36	0	****
Lineage divergence	1	5.81	5.32	6.31	0.25	23.01	0	****
Lineage divergence	2	15.14	13.34	16.95	0.92	16.46	0	****
Lineage divergence	3	35.60	32.61	38.59	1.52	23.36	0	****
Guijiang-Hejiang	1	7.86	7.46	8.27	0.21	37.98	0	****
Guijiang-Hejiang	2	13.80	13.03	14.57	0.39	35.22	0	****
Guijiang-Hejiang	3	35.43	27.68	43.18	3.95	8.96	0	****
Beipanjiang	1	3.00	1.53	4.47	0.75	4.00	6.29E-05	****
Beipanjiang	2	7.20	6.83	7.57	0.19	38.31	0	****
Beipanjiang	3	7.91	7.40	8.43	0.26	30.07	0	****
Hongshui	1	9.88	8.28	11.49	0.82	12.05	0	****
Hongshui	2	16.93	14.47	19.39	1.25	13.50	0	****
Hongshui	3	35.95	30.92	40.99	2.57	13.99	0	****
Jinshajiang	1	5.19	4.86	5.53	0.17	30.11	0	****
Jinshajiang	2	9.87	9.26	10.49	0.31	31.49	0	****
Liujiang	1	3.60	1.95	5.25	0.84	4.28	1.86E-05	****
Liujiang	2	13.17	12.17	14.17	0.51	25.91	0	****
Liujiang	3	20.76	18.88	22.65	0.96	21.64	0	****
Nanpanjiang	1	1.94	1.32	2.55	0.32	6.13	8.53E-10	****

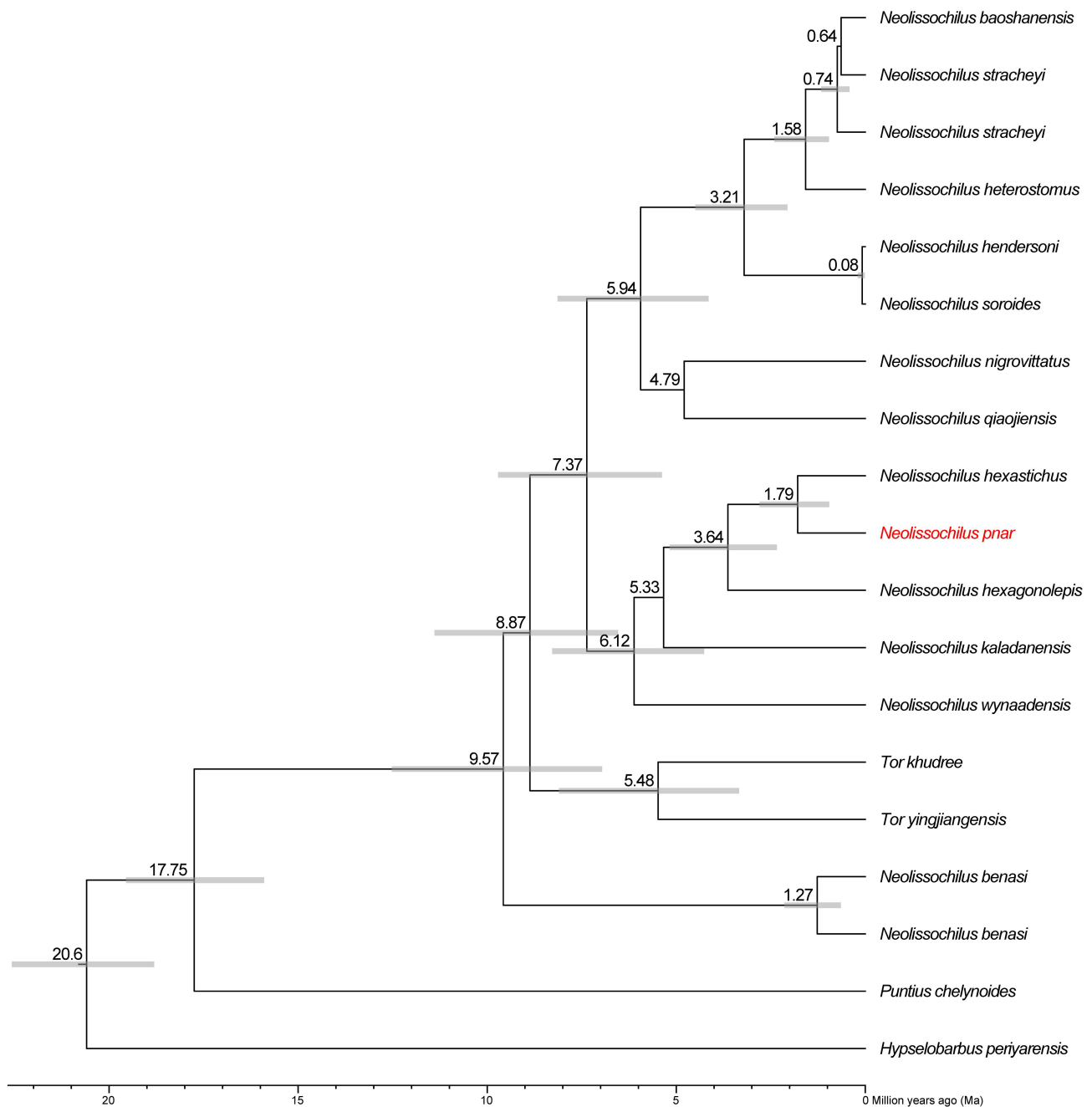
Nanpanjiang	2	10.16	8.49	11.83	0.85	11.92	0	****
Nanpanjiang	3	31.36	17.11	45.62	7.27	4.31	1.61E-05	****
Panlongjiang	1	0.92	0.74	1.09	0.09	10.35	0	****
Panlongjiang	2	8.85	8.18	9.53	0.35	25.63	0	****
Upper Yangtze-Wujiang	1	2.03	1.68	2.39	0.18	11.11	0	****
Yuanjiang	1	5.66	5.14	6.19	0.27	21.22	0	****
Yuanjiang	2	9.14	7.93	10.34	0.61	14.88	0	****
Zuojiang-Youjiang	1	8.36	7.91	8.81	0.23	36.60	0	****
Zuojiang-Youjiang	2	13.70	12.11	15.28	0.81	16.91	0	****
Zuojiang-Youjiang	3	24.30	21.09	27.51	1.64	14.85	0	****
Pearl →Yangtze	1	8.61	7.62	9.59	0.50	17.11	0	****
Pearl →Yangtze	2	13.24	12.84	13.64	0.20	64.71	0	****
Pearl →Yangtze	3	21.74	20.53	22.95	0.62	35.25	0	****
Yangtze→Pearl	1	5.47	5.22	5.71	0.13	43.30	0	****
Yangtze→Pearl	2	9.60	8.93	10.27	0.34	28.05	0	****



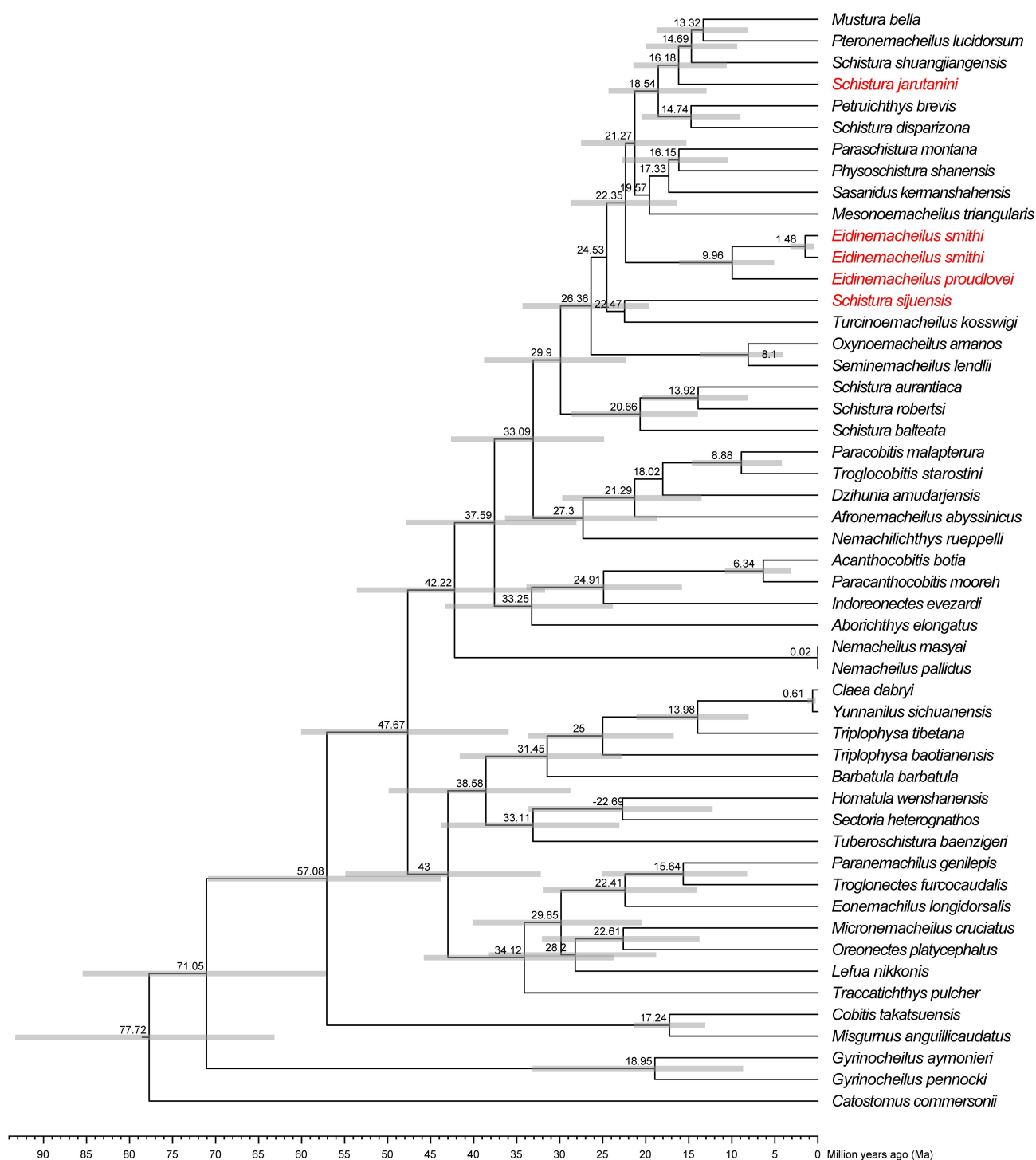
Supplementary Figure 1. Divergence time estimation of *Sinocyclocheilus* cavefish species based on mitochondrial data using BEAST v.2.4.7. Gray bars represent 95% confidence intervals, and node values indicate median divergence times. Species names in red denote cave-dwelling species.



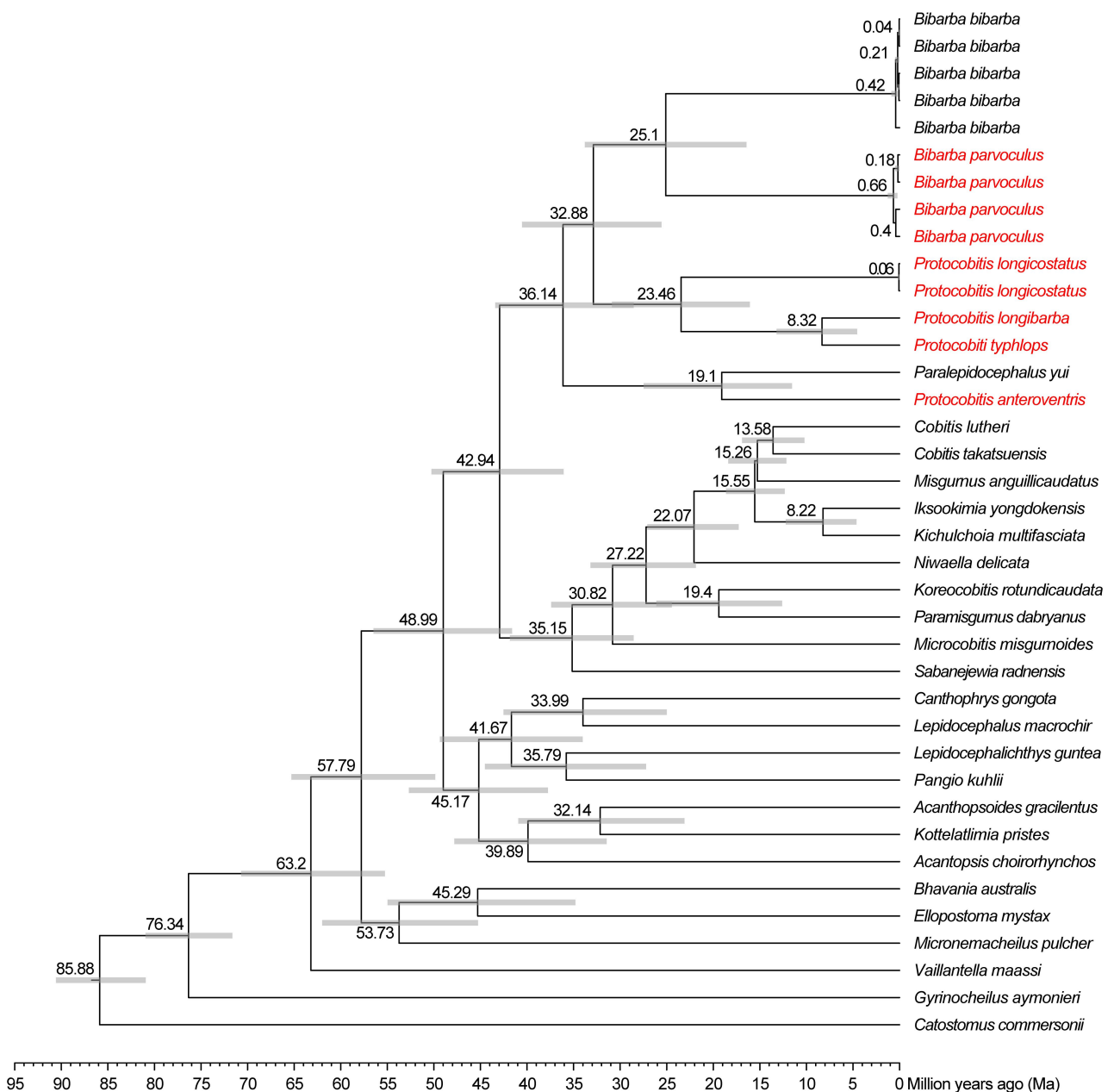
Supplementary Figure 2. Divergence time estimation of Chinese Nemacheilids cavefish species (*Karstsinnectes-Micronemacheilus-Oreonectes-Paranemachilus-Guinemachilus-Eonemachilus-Yunnanilus-Troglo nectes-Triplophysa*) based on mitochondrial data using BEAST v.2.4.7. Gray bars represent 95% confidence intervals, and node values indicate median divergence times. Species names in red denote cave-dwelling species.



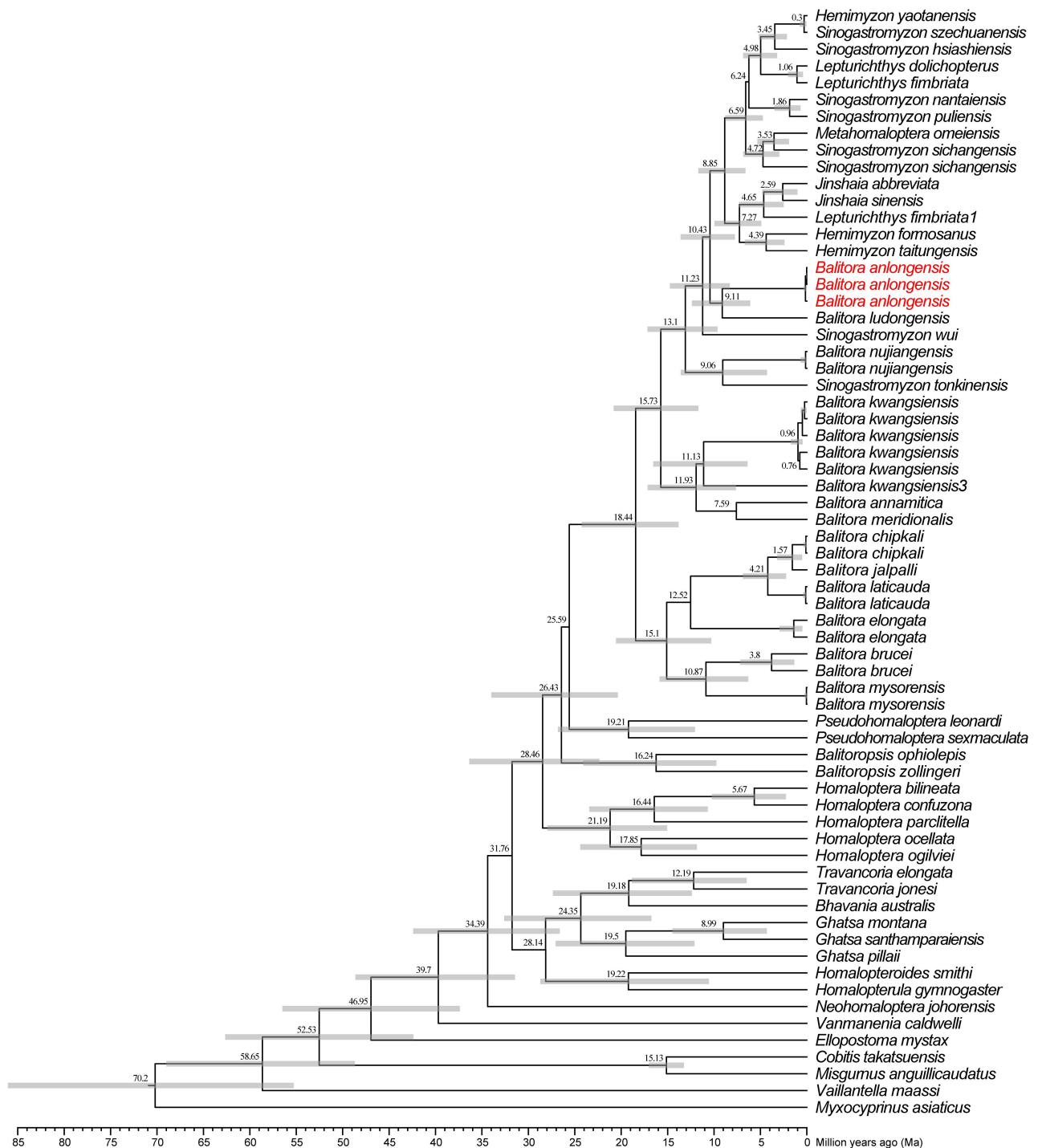
Supplementary Figure 3. Divergence time estimation of *Neolissochilus* cavefish species based on mitochondrial data using BEAST v.2.4.7. Gray bars represent 95% confidence intervals, and node values indicate median divergence times. Species names in red denote cave-dwelling species.



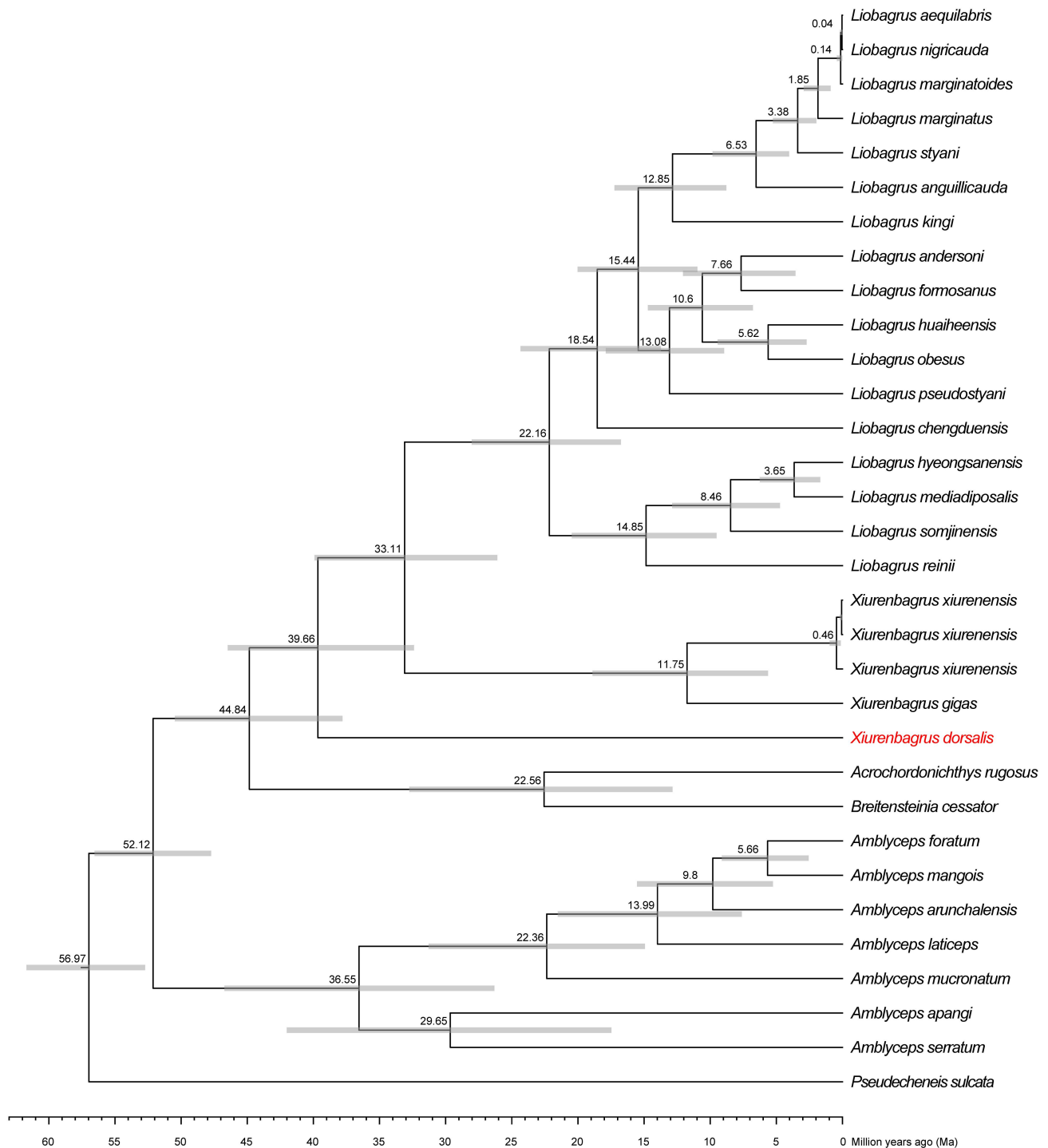
Supplementary Figure 4. Divergence time estimation of *Eidinemacheilus*-*Schistura* cavefish species based on mitochondrial data using BEAST v.2.4.7. Gray bars represent 95% confidence intervals, and node values indicate median divergence times. Species names in red denote cave-dwelling species.



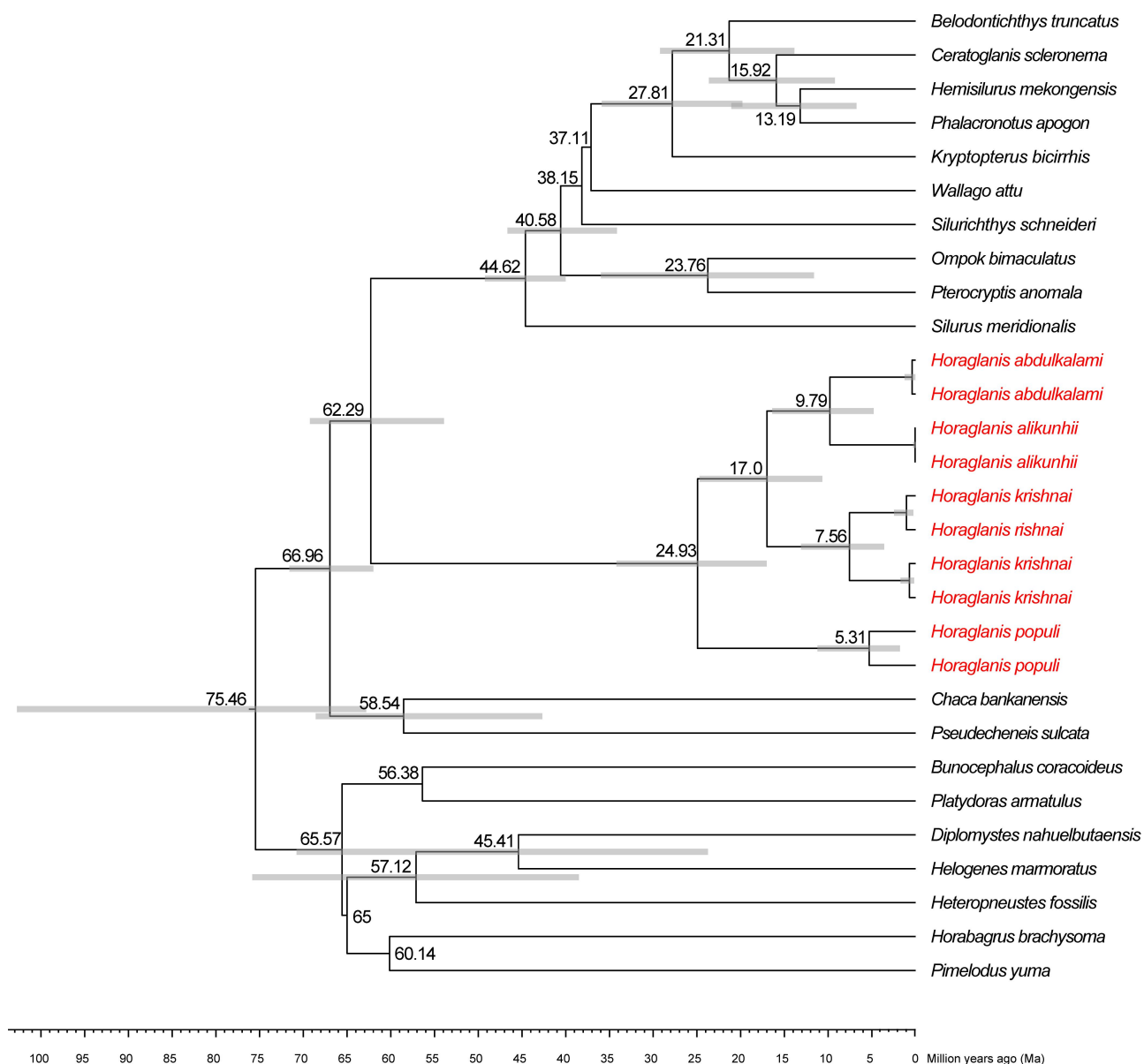
Supplementary Figure 5. Divergence time estimation of *Bibarba*-*Protocobitis* cavefish species based on mitochondrial data using BEAST v.2.4.7. Gray bars represent 95% confidence intervals, and node values indicate median divergence times. Species names in red denote cave-dwelling species.



Supplementary Figure 6. Divergence time estimation of *Balitora* cavefish species based on mitochondrial data using BEAST v.2.4.7. Gray bars represent 95% confidence intervals, and node values indicate median divergence times. Species names in red denote cave-dwelling species.



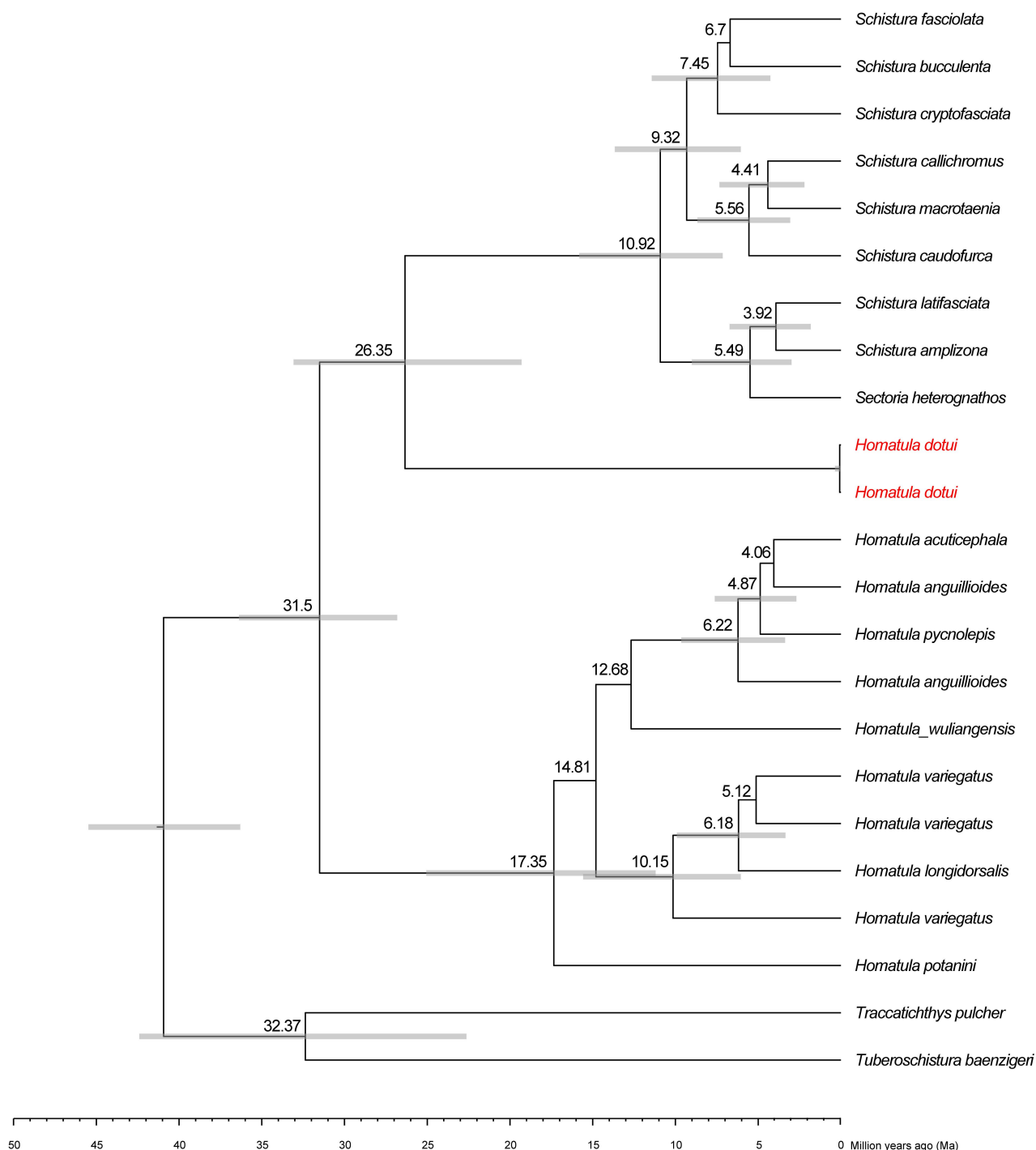
Supplementary Figure 7. Divergence time estimation of *Xiurenbagrus* cavefish species based on mitochondrial data using BEAST v.2.4.7. Gray bars represent 95% confidence intervals, and node values indicate median divergence times. Species names in red denote cave-dwelling species.



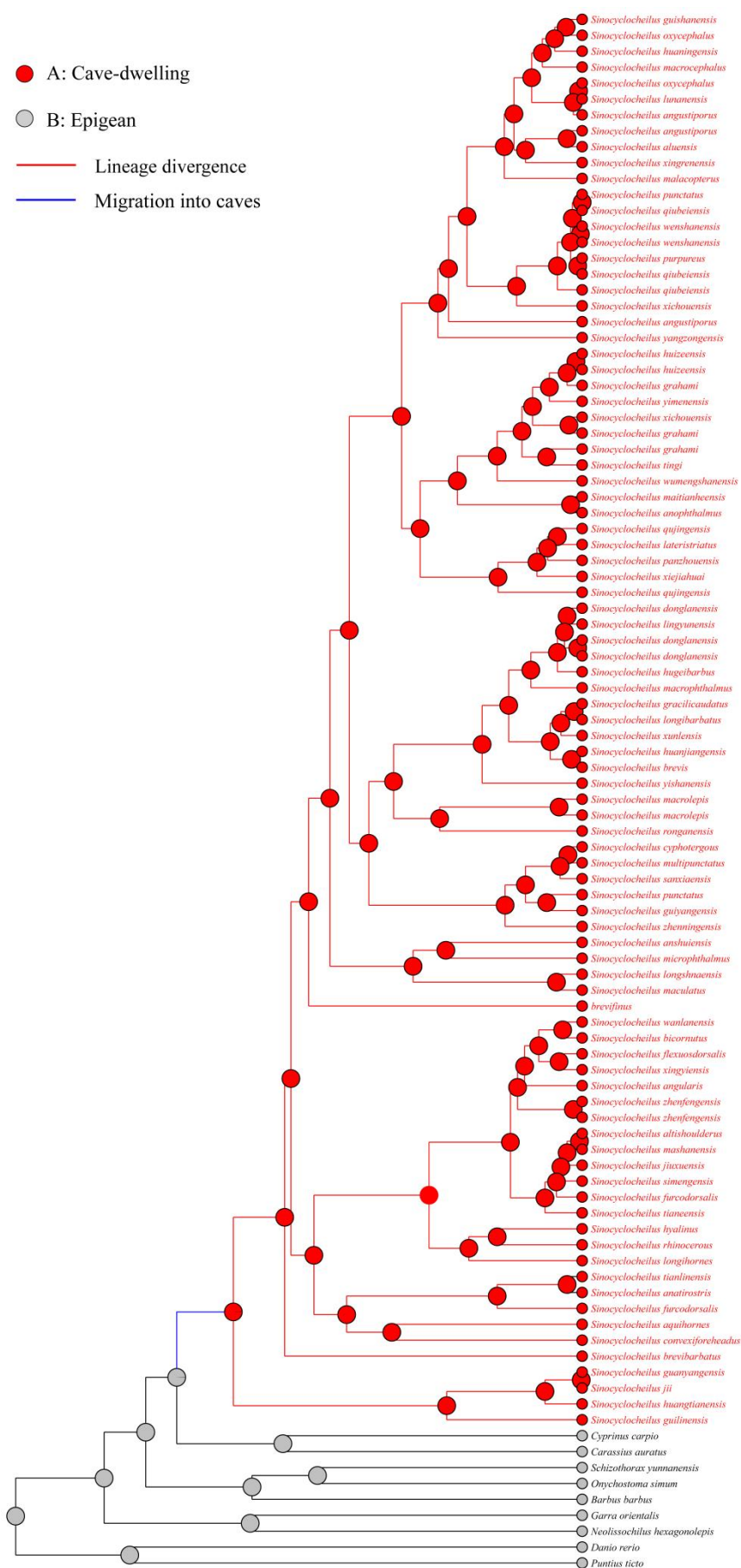
Supplementary Figure 8. Divergence time estimation of *Horaglanis* cavefish species based on mitochondrial data using BEAST v.2.4.7. Gray bars represent 95% confidence intervals, and node values indicate median divergence times. Species names in red denote cave-dwelling species.



Supplementary Figure 9. Divergence time estimation of *Pseudocrossocheilus*-*Longanalus*-*Hongshuia* cavefish species based on mitochondrial data using BEAST v.2.4.7. Gray bars represent 95% confidence intervals, and node values indicate median divergence times. Species names in red denote cave-dwelling species.

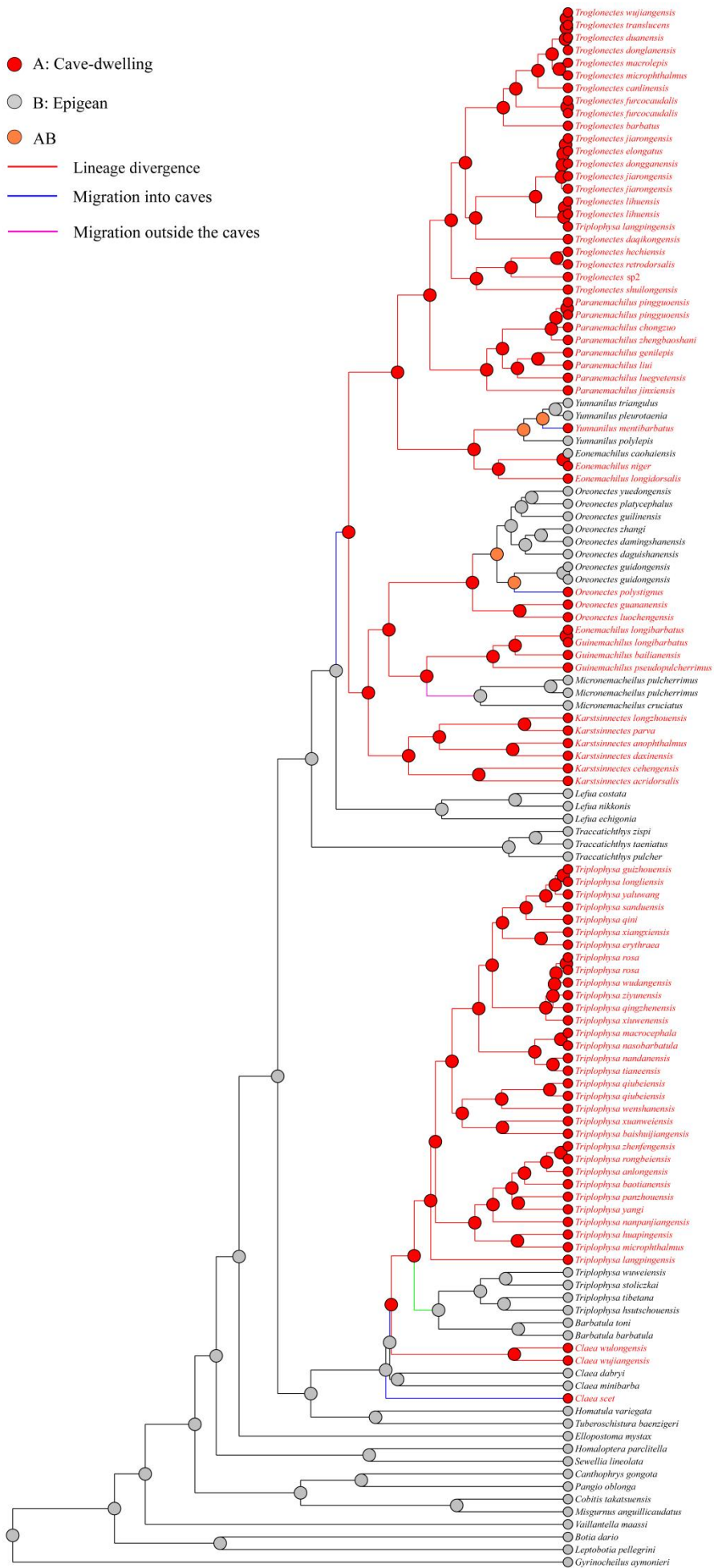


Supplementary Figure 10. Divergence time estimation of *Homatula* cavefish species based on mitochondrial data using BEAST v.2.4.7. Gray bars represent 95% confidence intervals, and node values indicate median divergence times. Species names in red denote cave-dwelling species.

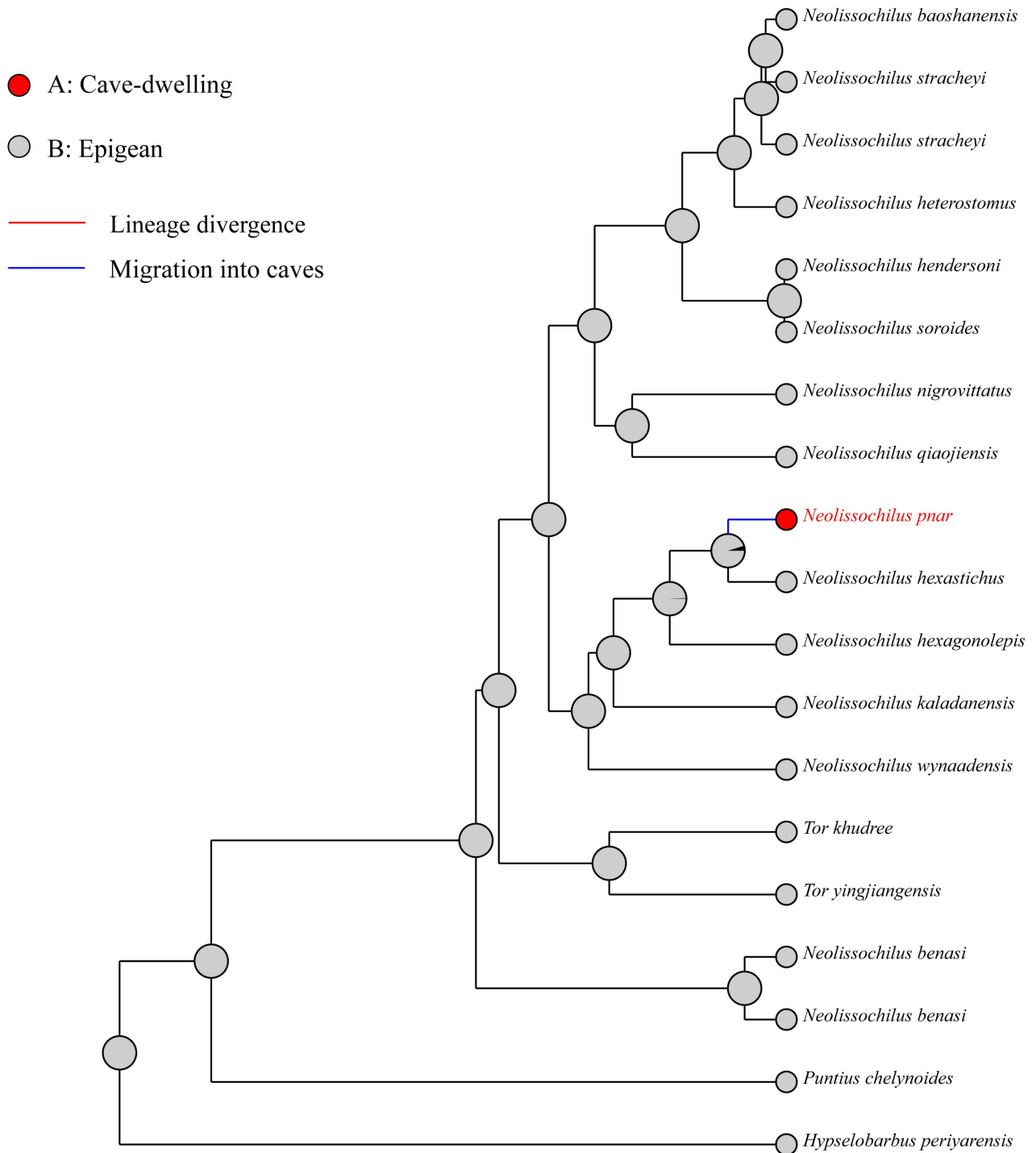


Supplementary Figure 11. Ancestral habitat reconstructions of *Sinocyclocheilus* cavefish species based on time tree using RASP. Species names in red denote cave-dwelling species.

- A: Cave-dwelling
- B: Epigean
- AB
- Lineage divergence
- Migration into caves
- Migration outside the caves



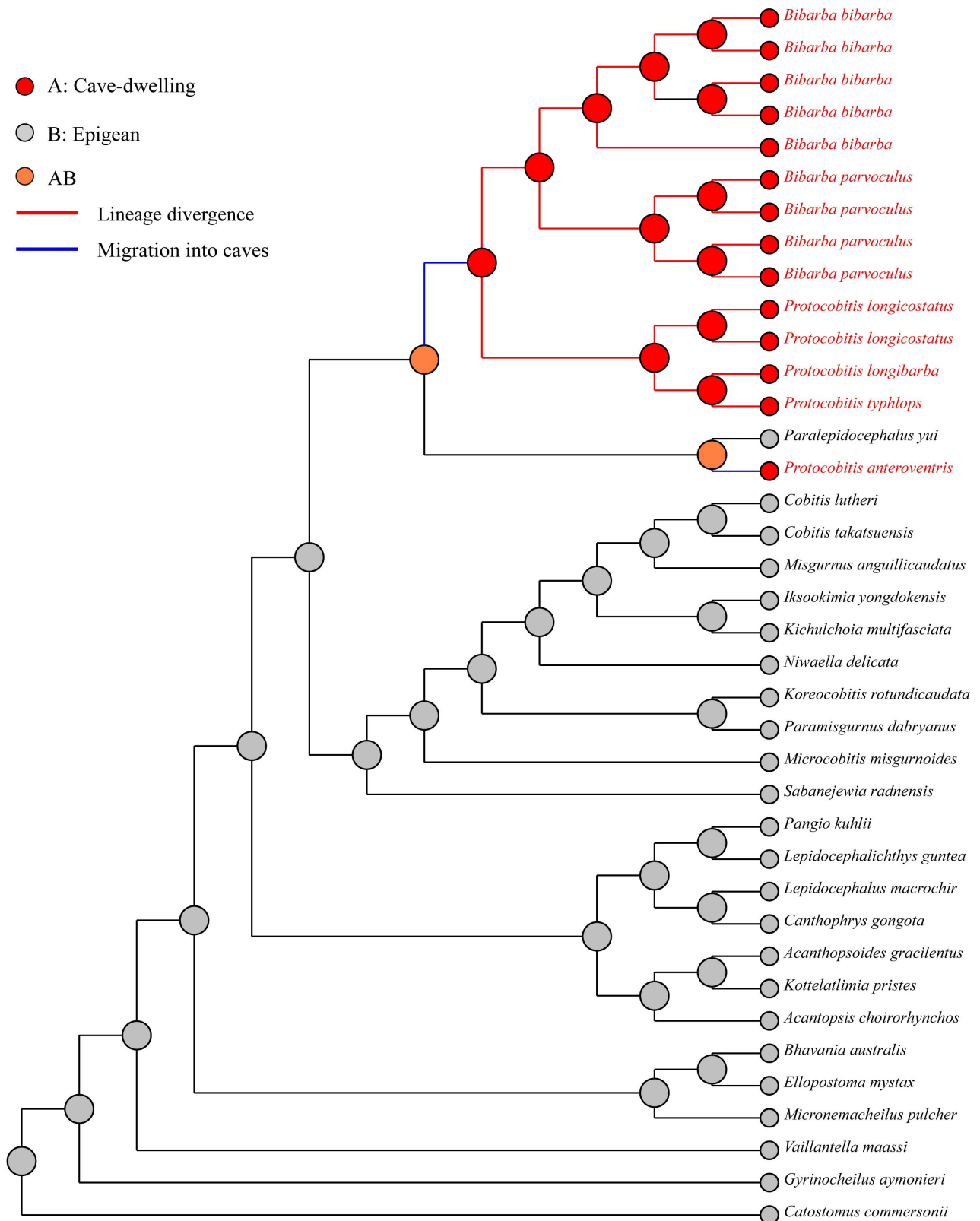
Supplementary Figure 12. Ancestral habitat reconstructions of Nemacheilids cavefish species (*Karstsinnectes*-*Micronemacheilus*-*Oreonectes*-*Paranemacheilus*-*Guinemacheilus*-*Eonemacheilus*-*Yunnanilus*-*Troglo nectes*-*Triplophysa*) based on time tree using RASP. Species names in red denote cave-dwelling species.



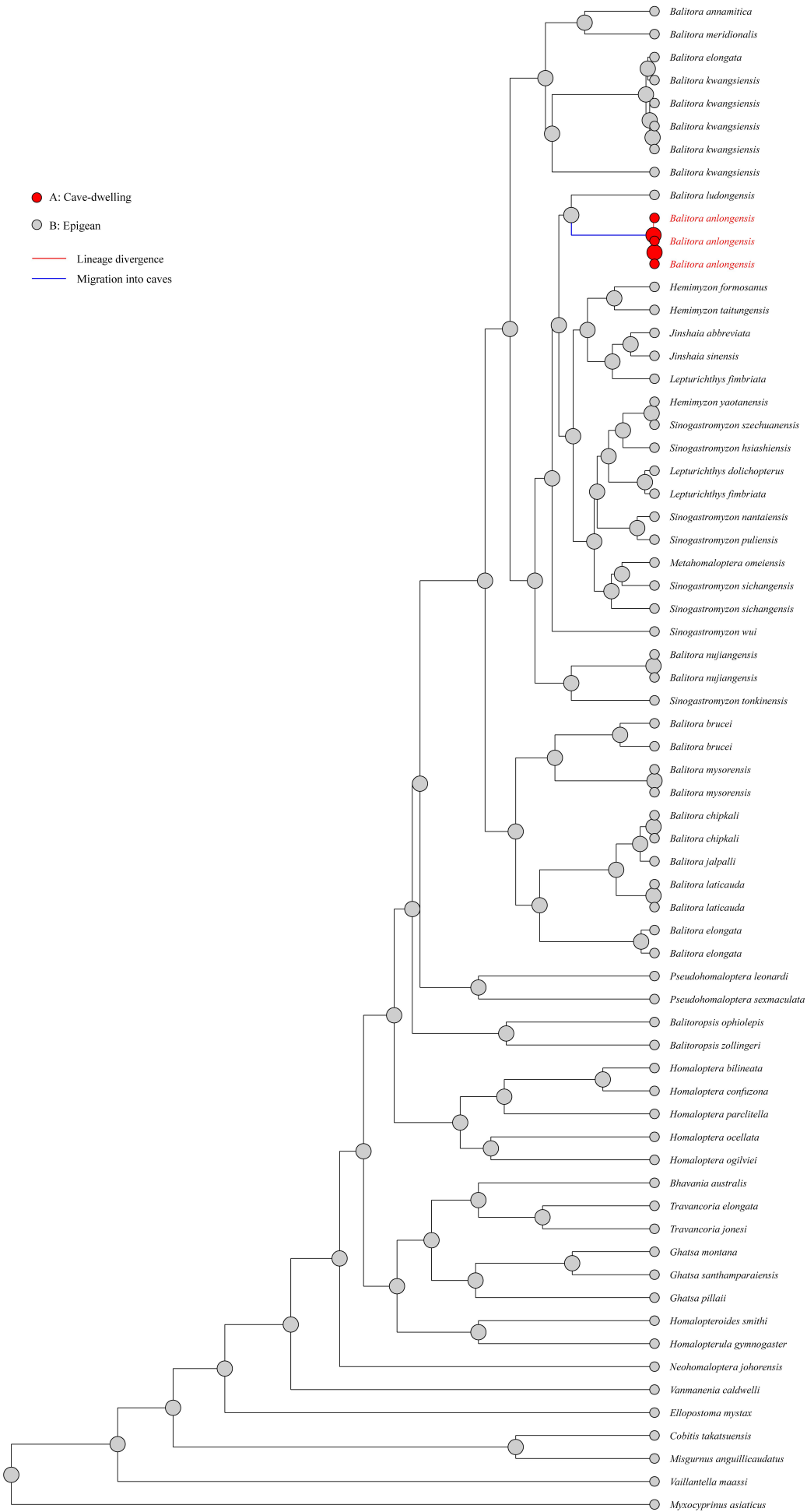
Supplementary Figure 13. Ancestral habitat reconstructions of *Neolissochilus* cavefish species based on time tree using RASP. Species names in red denote cave-dwelling species.



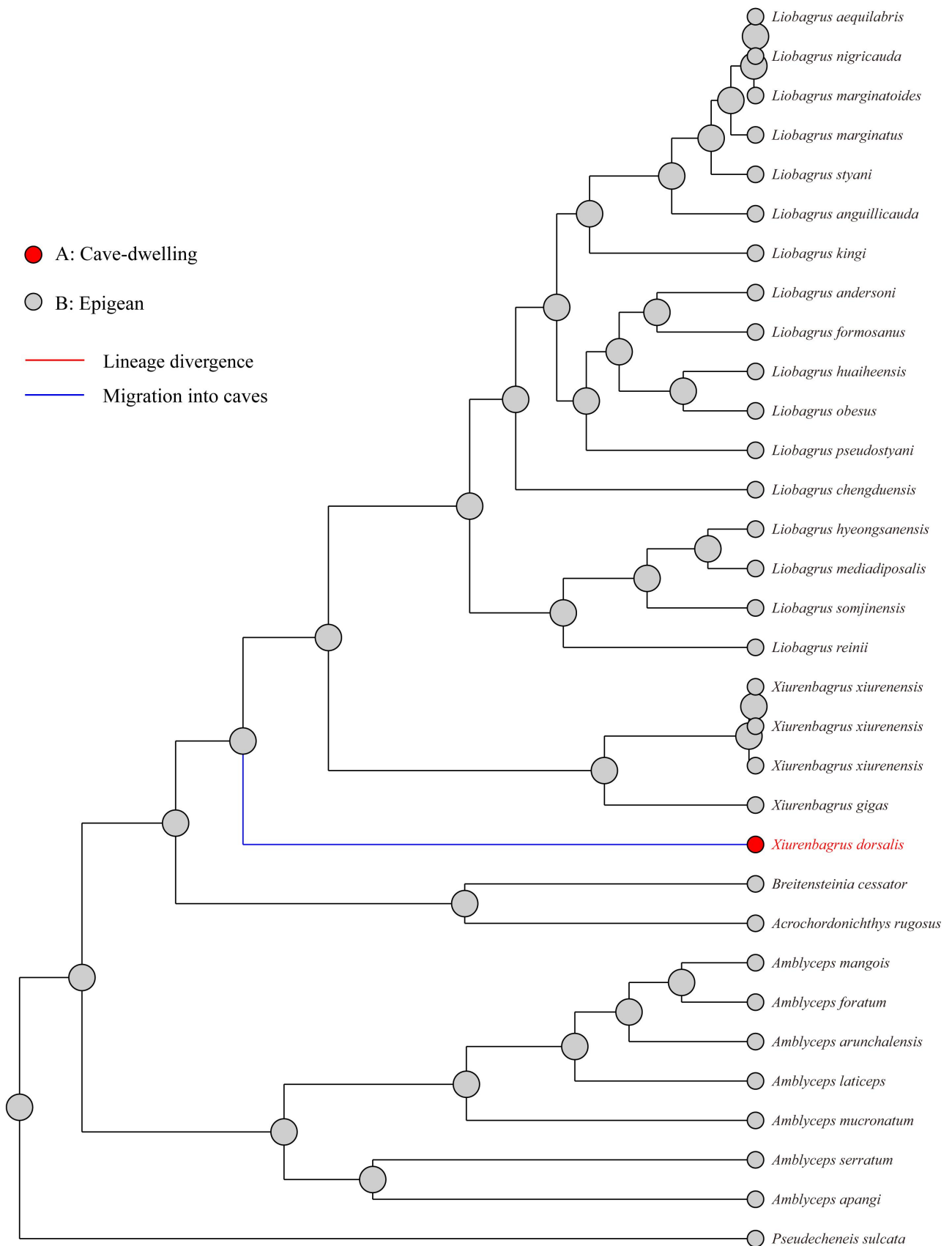
Supplementary Figure 14. Ancestral habitat reconstructions of *Eidinemacheilus-Schistura* cavefish species based on time tree using RASP. Species names in red denote cave-dwelling species.



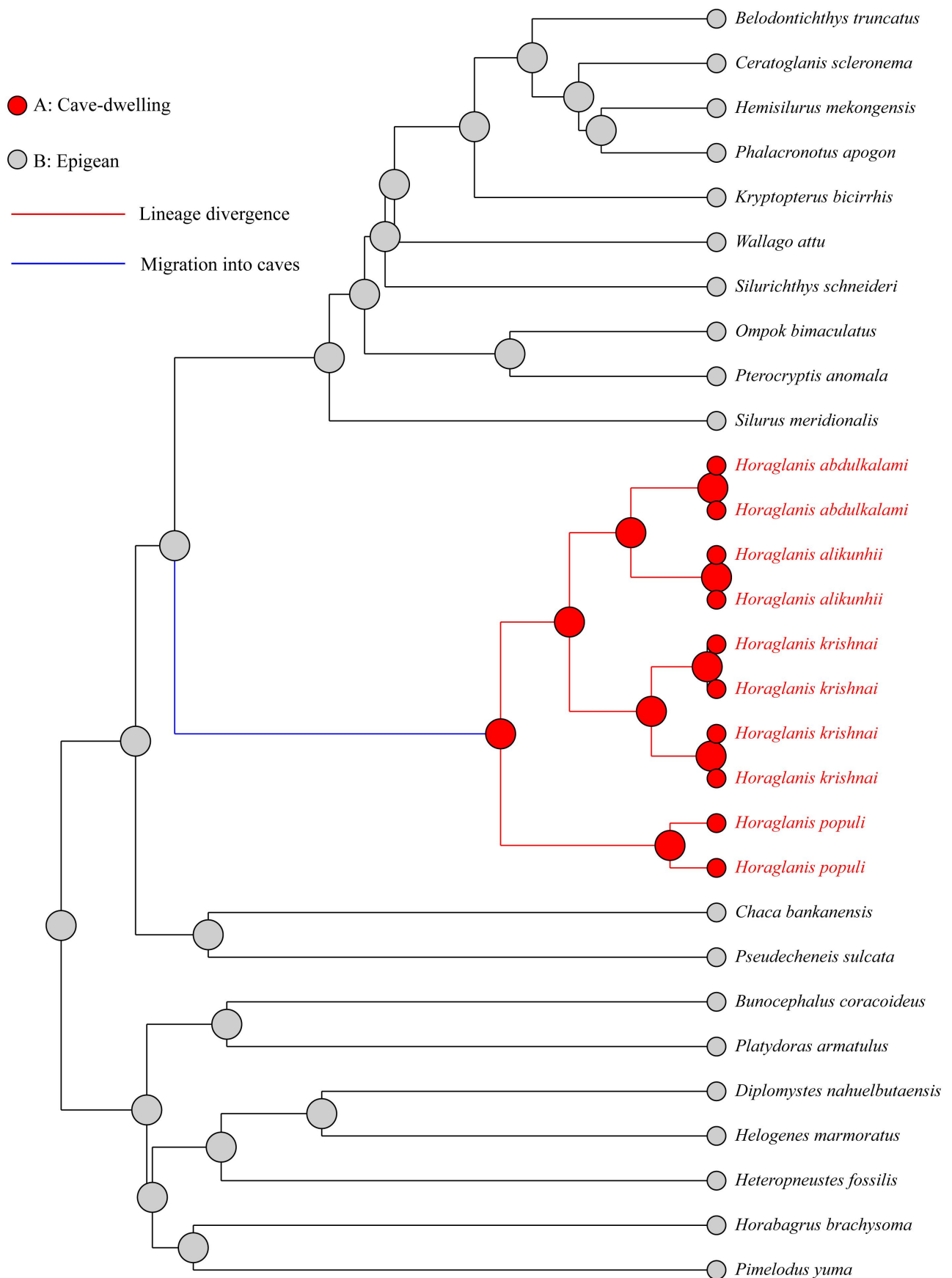
Supplementary Figure 15. Ancestral habitat reconstructions of *Bibarba-Protocobitis* cavefish species based on time tree using RASP. Species names in red denote cave-dwelling species.



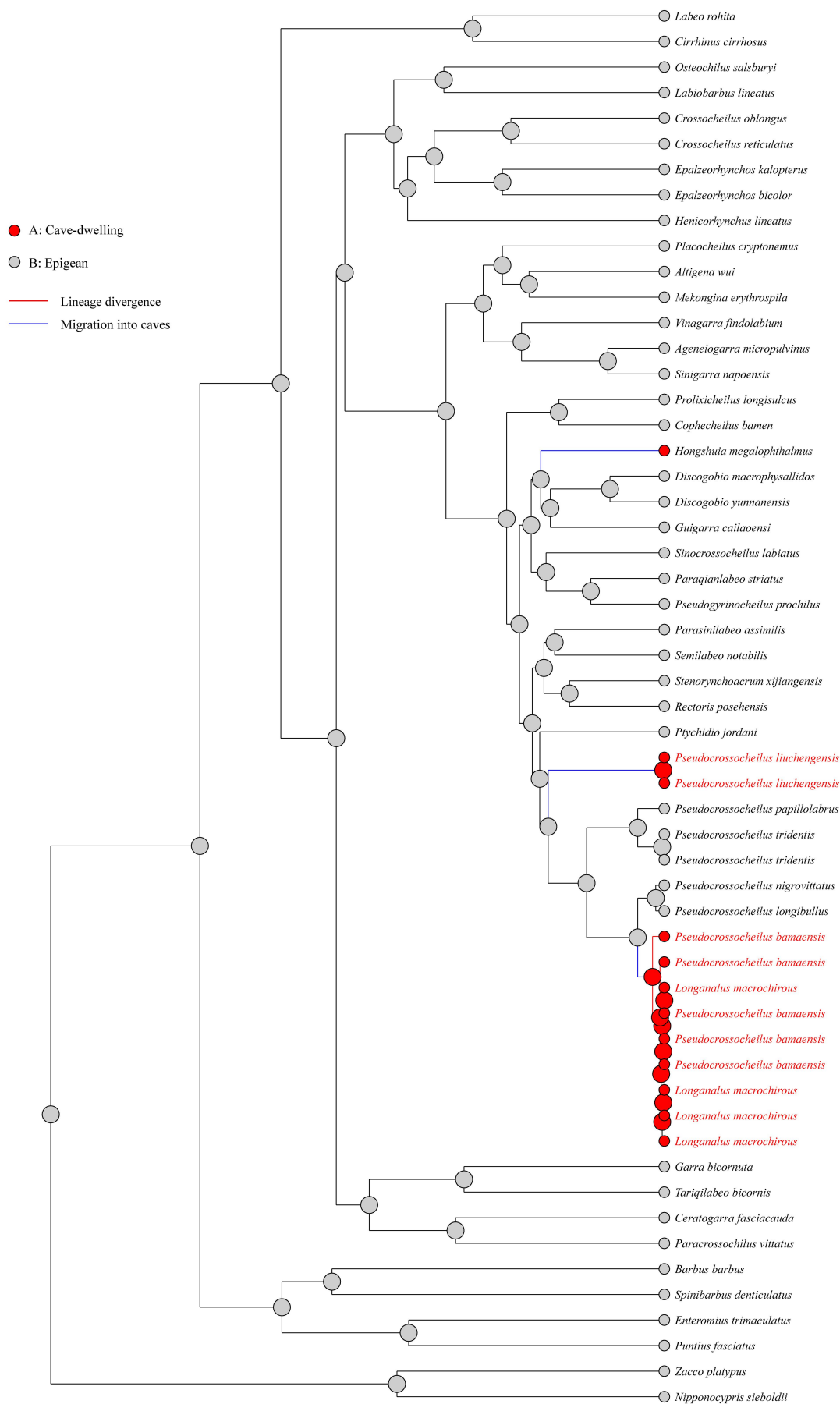
Supplementary Figure 16. Ancestral habitat reconstructions of *Balitora* cavefish species based on time tree using RASP. Species names in red denote cave-dwelling species.



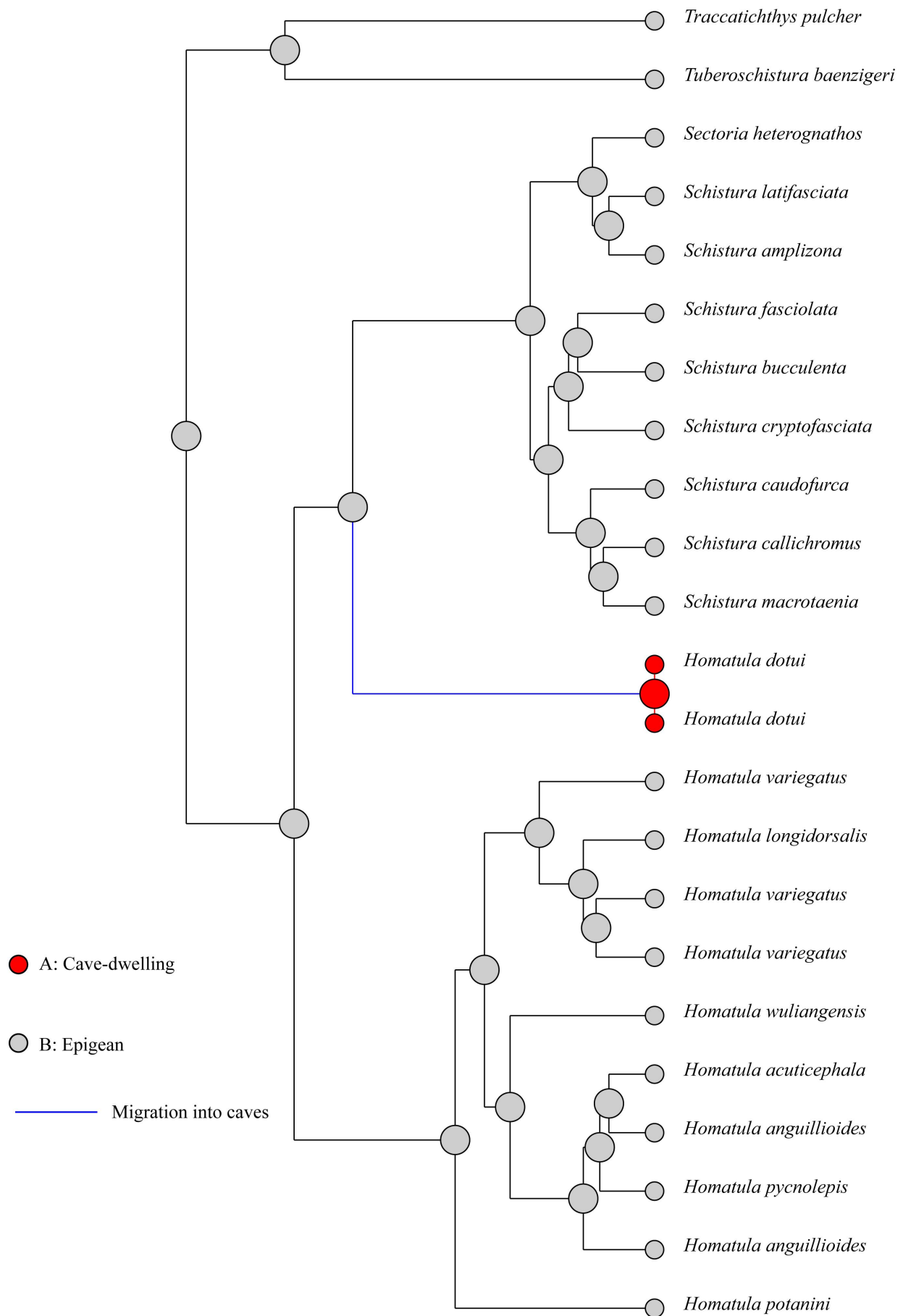
Supplementary Figure 17. Ancestral habitat reconstructions of *Xiurenbagrus* cavefish species based on time tree using RASP. Species names in red denote cave-dwelling species.



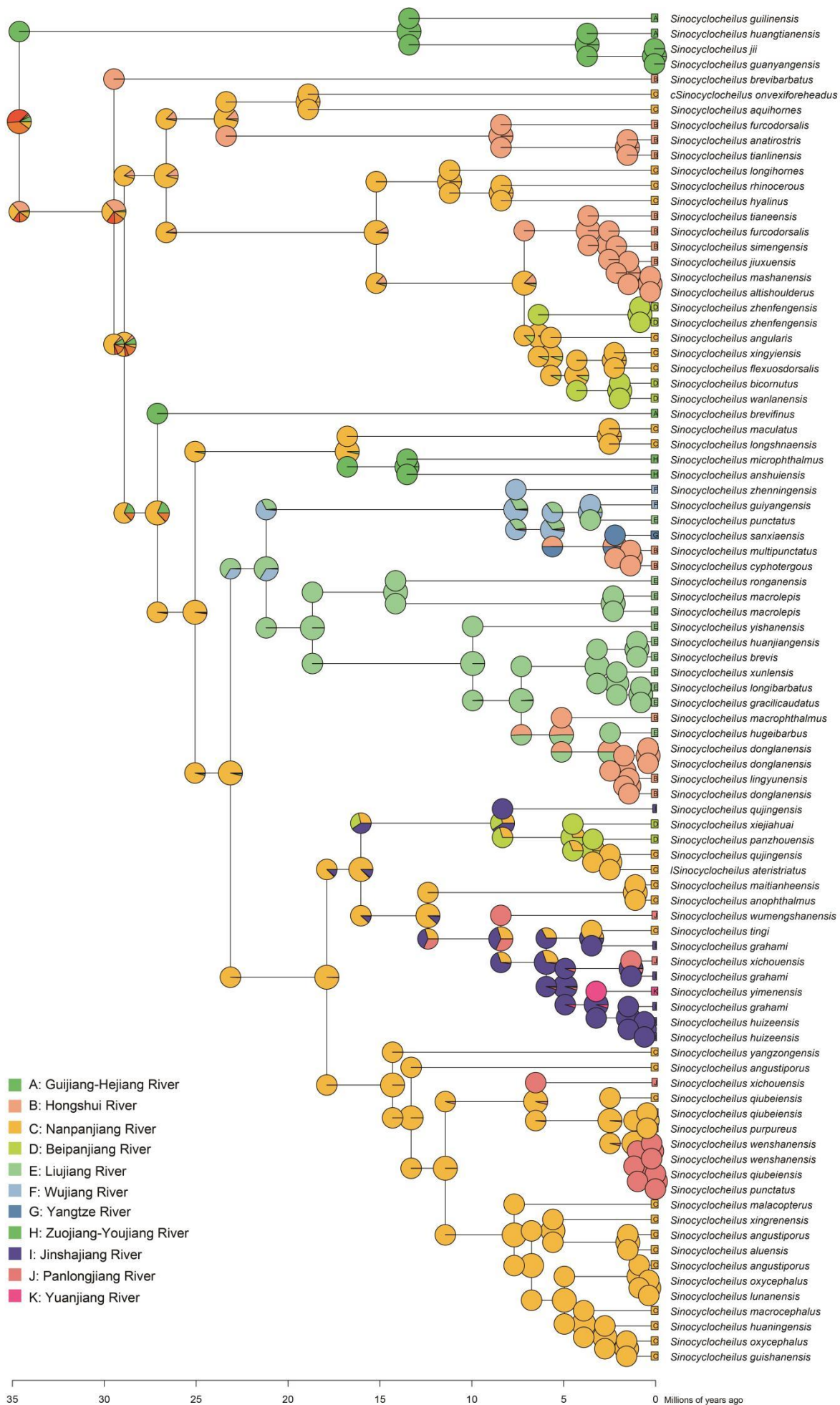
Supplementary Figure 18. Ancestral habitat reconstructions of *Horaglanis* cavefish species based on time tree using RASP. Species names in red denote cave-dwelling species.



Supplementary Figure 19. Ancestral habitat reconstructions of *Pseudocrossocheilus*-*Longanalus*-*Hongshuiacavefish* species based on time tree using RASP. Species names in red denote cave-dwelling species.

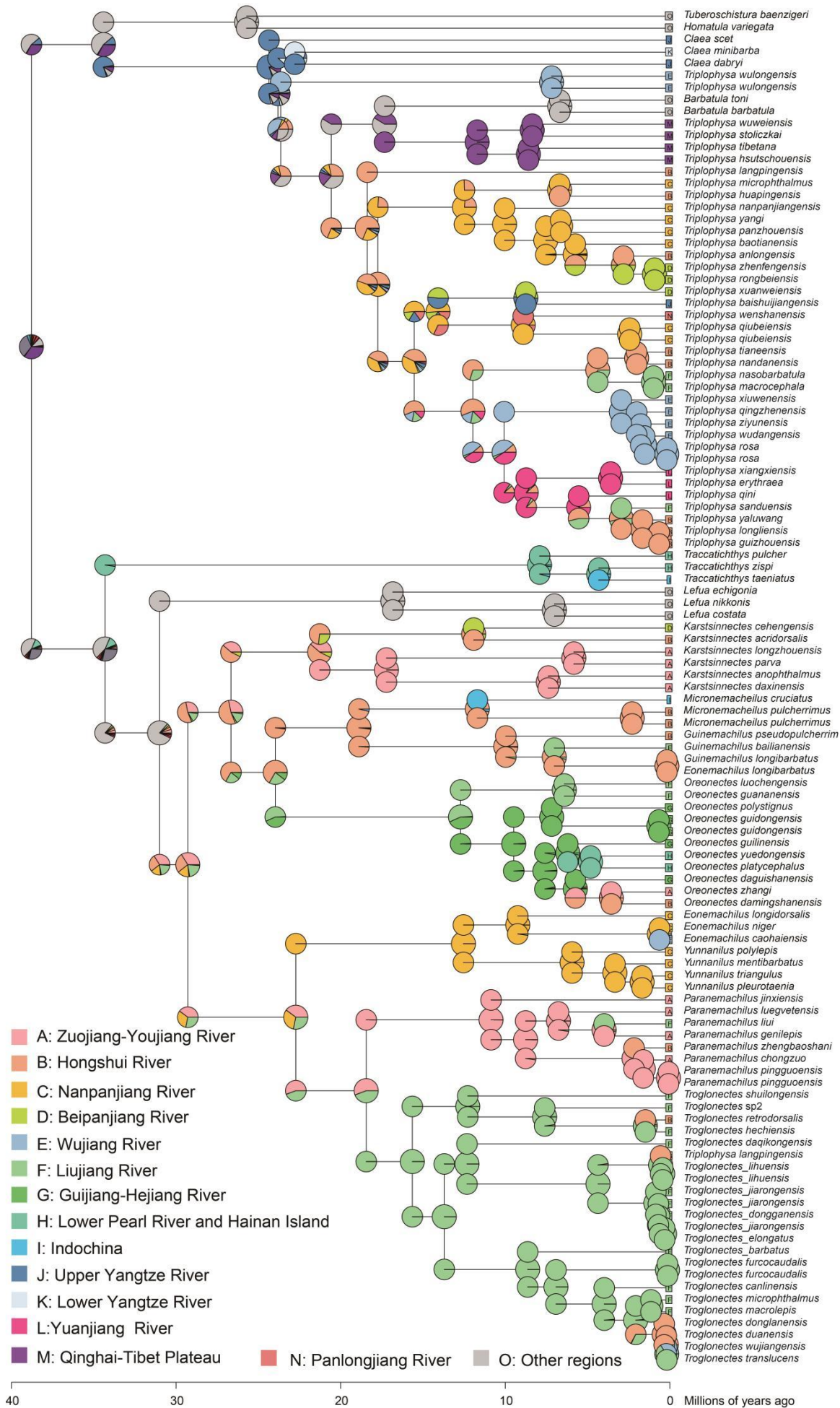


Supplementary Figure 20. Ancestral habitat reconstructions of *Homatula* cavefish species based on time tree using RASP. Species names in red denote cave-dwelling species.

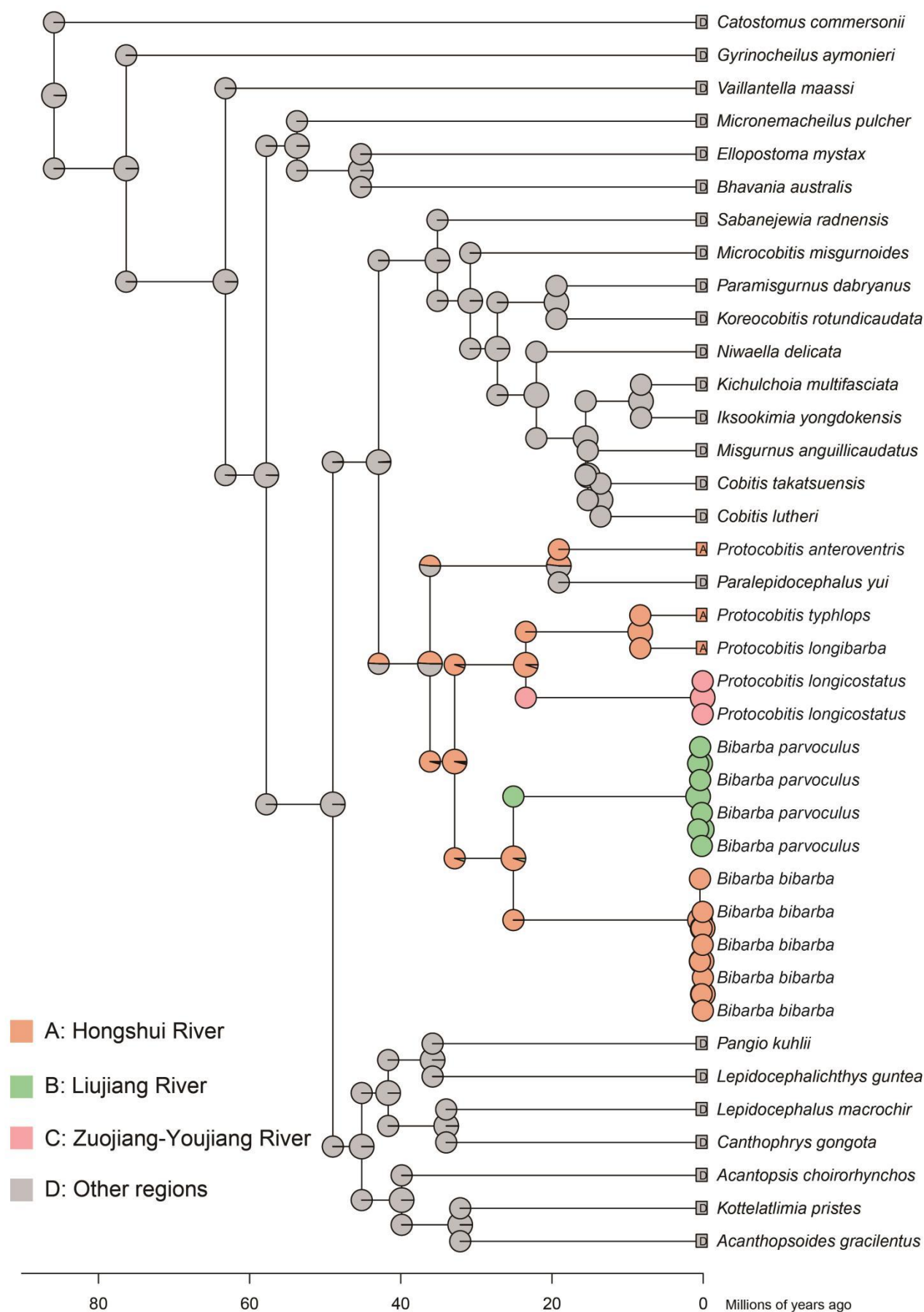


35 30 25 20 15 10 5 0 Millions of years ago

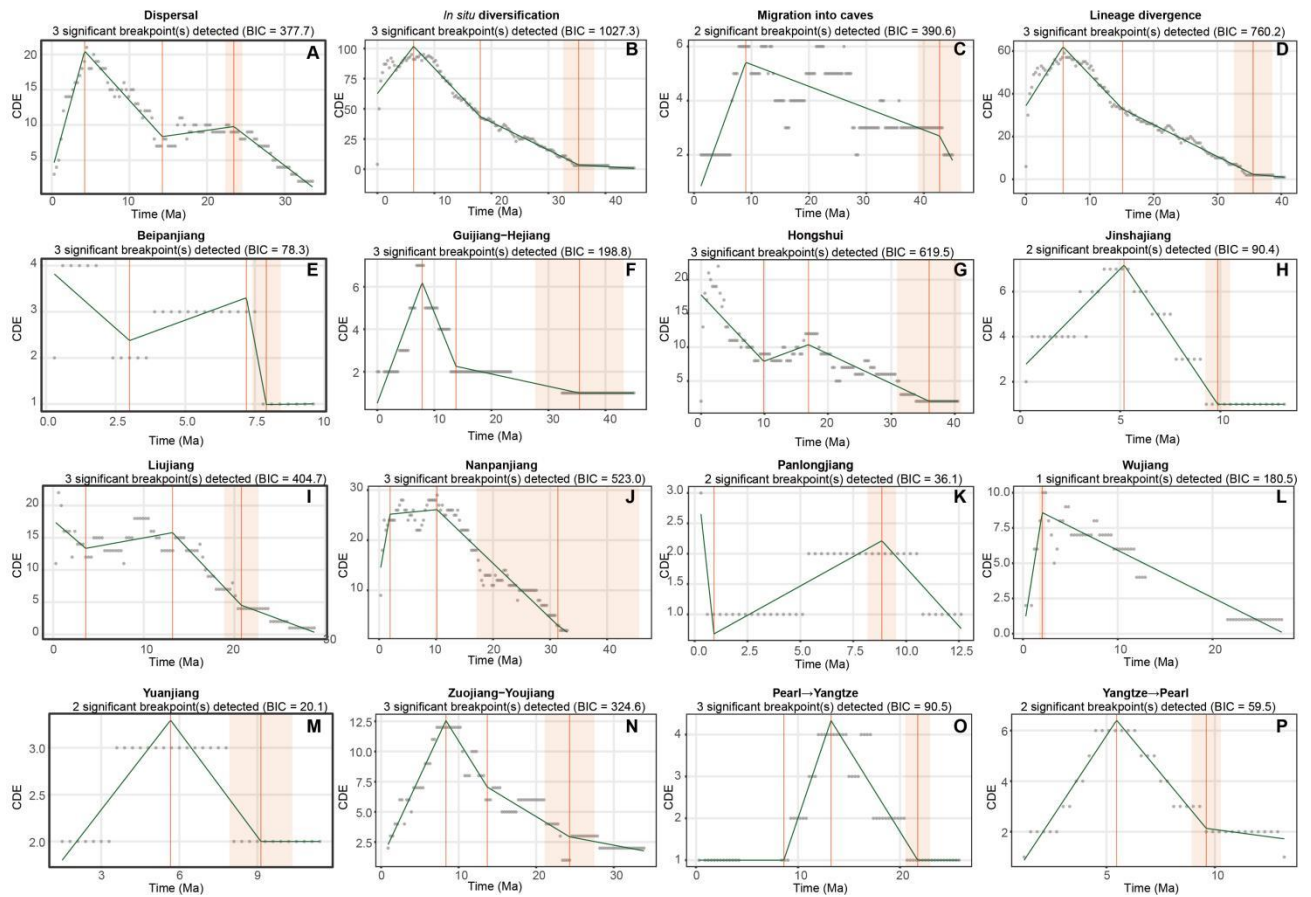
Supplementary Figure 21. Ancestral range reconstructions of *Sinocyclocheilus* cavefish species based on time tree using BioGeoBEARS.



Supplementary Figure 22. Ancestral range reconstructions of Chinese Nemacheilids cavefish species (*Karstsinnectes*-*Micronemacheilus*-*Oreonectes*-*Paranemachilus*-*Guinemachilus*-*Eonemachilus*-*Yunnanilus*-*Troglonectes*-*Triplophysa*) based on time tree using BioGeoBEARS.



Supplementary Figure 23. Ancestral range reconstructions of *Bibarba*-*Protocobitis* cavefish species based on time tree using BioGeoBEARS.



Supplementary Figure 24. Timing of rate shifts associated with 16 dataset diversification breakpoints. Orange vertical lines indicate the detected breakpoints and their corresponding ages. (A) Dispersal. (B) *In situ* diversification. (C) Migration into caves. (D) Lineage divergence, (E) Beipanjiang. (F) Guijiang-Hejiang. (G) Hongshui. (H) Jinshajiang. (I) Liujiang. (J) Nanpanjiang. (K) Panlongjiang. (L) Wujiang. (M) Yuanjiang. (N) Zuojiang-Youjiang. (O) Pearl→Yangtze. (P) Yangtze→Pearl. Abbreviation: CDE, Concurrent Diversification Events.

Supplementary References

1. Wen, H. *et al.* Molecular phylogeny and historical biogeography of the cave fish genus *Sinocyclocheilus* (Cypriniformes: Cyprinidae) in southwest China. *Integr. Zool.* **17**, 311–325 (2022).
2. Yang, J. *et al.* The *Sinocyclocheilus* cavefish genome provides insights into cave adaptation. *BMC Biol.* **14**, 1–13 (2016).
3. Hirt, M. V. *et al.* Effects of gene choice, base composition and rate heterogeneity on inference and estimates of divergence times in cypriniform fishes. *Biol. J. Linn. Soc.* **121**, 319–339 (2017).
4. Zhou, J. A new cobitid from the middle Miocene of Shanwang, Shandong. *Vertebr. Palasiat.* **30**, 71–76 (1992).
5. Wang, Y. *et al.* Mitogenomic perspectives on the origin of Tibetan loaches and their adaptation to high altitude. *Sci. Rep.* **6**, 29690 (2016).
6. Rabosky, D. L. *et al.* An inverse latitudinal gradient in speciation rate for marine fishes. *Nature* **559**, 392–395 (2018).
7. Li, J. *et al.* Variation patterns of the mitochondrial 16S rRNA gene with secondary structure constraints and their application to phylogeny of cyprinine fishes (Teleostei: Cypriniformes). *Mol. Phylogenet. Evol.* **47**, 472–487 (2008).
8. Peng, J., Wang, X., Wang, D. & He, S. Application of DNA barcoding based on the mitochondrial COI gene sequences in classification of Culter (Pisces: Cyprinidae). *Acta Hydrobiol. Sin.* **33**, 271–276 (2009).
9. Xiao, W., Zhang, Y. & Liu, H. Molecular Systematics of Xenocyprinae (Teleostei: Cyprinidae): Taxonomy, Biogeography, and Coevolution of a Special Group Restricted in East Asia. *Mol. Phylogenet. Evol.* **18**, 163–173 (2001).
10. Sevilla, R. G. *et al.* Primers and polymerase chain reaction conditions for DNA barcoding teleost fish based on the mitochondrial cytochrome b and nuclear rhodopsin genes. *Mol. Ecol. Notes* **7**, 730–734 (2007).
11. Miya, M., Saitoh, K., Wood, R., Nishida, M. & Mayden, R. L. New primers for amplifying and sequencing the mitochondrial ND4/ND5 gene region of the Cypriniformes (Actinopterygii: Ostariophysi). *Ichthyol. Res.* **53**, 75–81 (2006).
12. Chen, W. J., Miya, M., Saitoh, K. & Mayden, R. L. Phylogenetic utility of two existing and four novel nuclear gene loci in reconstructing Tree of Life of ray-finned fishes: the order Cypriniformes (Ostariophysi) as a case study. *Gene* **423**, 125–134 (2008).
13. Liu, S. Q. *et al.* Phylogenetic relationships of the Cobitoidea (Teleostei: Cypriniformes) inferred from mitochondrial and nuclear genes with analyses of gene evolution. *Gene* **508**, 60–72 (2012).
14. Ding, L. *et al.* Timing and mechanisms of Tibetan Plateau uplift. *Nat. Rev. Earth Environ.* **3**, 652–667 (2022).
15. Ding, L. *et al.* Quantifying the rise of the Himalaya orogen and implications for the South Asian monsoon. *Geology* **45**, 215–218 (2017).
16. Ai, K. *et al.* The uppermost Oligocene Kailas flora from southern Tibetan Plateau and its implications for the uplift history of the southern Lhasa terrane. *Palaeogeogr. Palaeoclimatol. Palaeoecol.* **515**, 143–151 (2019).
17. Xu, Q. *et al.* Stable isotopes reveal southward growth of the Himalayan-Tibetan Plateau since the Paleocene. *Gondwana Res.* **54**, 50–61 (2018).
18. DeCelles, P., Kapp, P., Quade, J. & Gehrels, G. Oligocene–Miocene Kailas basin, southwestern Tibet: Record of postcollisional upper-plate extension in the Indus-Yarlung suture zone. *Bulletin* **123**, 1337–1362 (2011).
19. DeCelles, P. G. *et al.* Oligocene–Miocene Great Lakes in the India–Asia Collision Zone. *Basin Res.* **30**, 228–247 (2018).
20. Gébelin, A. *et al.* The miocene elevation of Mount Everest. *Geology* **41**, 799–802 (2013).
21. Gébelin, A. *et al.* Infiltration of meteoric water in the South Tibetan Detachment (Mount Everest, Himalaya): When and why? *Tectonics* **36**, 690–713 (2017).
22. Garzzone, C. N., Dettman, D. L., Quade, J., DeCelles, P. G. & Butler, R. F. High times on the Tibetan Plateau: Paleoelevation of the Thakkhola graben, Nepal. *Geology* **28**, 339–342 (2000).

23. Garzione, C. N., Quade, J., DeCelles, P. G. & English, N. B. Predicting paleoelevation of Tibet and the Himalaya from $\delta^{18}\text{O}$ vs. altitude gradients in meteoric water across the Nepal Himalaya. *Earth Planet. Sci. Lett.* **183**, 215–229 (2000).
24. Rowley, D. B., Pierrehumbert, R. T. & Currie, B. S. A new approach to stable isotope-based paleoaltimetry: implications for paleoaltimetry and paleohypsometry of the High Himalaya since the Late Miocene. *Earth Planet. Sci. Lett.* **188**, 253–268 (2001).
25. Saylor, J. *et al.* The late Miocene through present paleoelevation history of southwestern Tibet. *Am. J. Sci.* **309**, 1–42 (2009).
26. Huntington, K. W., Saylor, J., Quade, J. & Hudson, A. M. High late Miocene–Pliocene elevation of the Zhada Basin, southwestern Tibetan Plateau, from carbonate clumped isotope thermometry. *Bulletin* **127**, 181–199 (2015).
27. Chen, C. *et al.* Lower-altitude of the Himalayas before the mid-Pliocene as constrained by hydrological and thermal conditions. *Earth Planet. Sci. Lett.* **545**, 116422 (2020).
28. YUE, L. P. *et al.* Paleomagnetic Chronology and Record of Himalayan Movements in the Longgugou Section of Gyirong-Oma Basin in Xizang (Tibet). *Chin. J. Geophys.* **47**, 1135–1142 (2004).
29. Murphy, M. A., Saylor, J. E. & Ding, L. Late Miocene topographic inversion in southwest Tibet based on integrated paleoelevation reconstructions and structural history. *Earth Planet. Sci. Lett.* **282**, 1–9 (2009).
30. Su, T. *et al.* A Middle Eocene lowland humid subtropical “Shangri-La” ecosystem in central Tibet. *Proceedings of the National Academy of Sciences* **117**, 32989–32995 (2020).
31. Xu, Q., Ding, L., Hetzel, R., Yue, Y. & Rades, E. F. Low elevation of the northern Lhasa terrane in the Eocene: Implications for relief development in south Tibet. *Terra Nova* **27**, 458–466 (2015).
32. Xiong, Z. *et al.* The rise and demise of the Paleogene Central Tibetan Valley. *Sci. Adv.* **8**, eabj0944.
33. Polissar, P. J., Freeman, K. H., Rowley, D. B., McInerney, F. A. & Currie, B. S. Paleoaltimetry of the Tibetan Plateau from D/H ratios of lipid biomarkers. *Earth Planet. Sci. Lett.* **287**, 64–76 (2009).
34. Wei, Y. *et al.* Low palaeoelevation of the northern Lhasa terrane during late Eocene: Fossil foraminifera and stable isotope evidence from the Gerze Basin. *Sci. Rep.* **6**, 27508 (2016).
35. Rowley, D. B. & Currie, B. S. Palaeo-altimetry of the late Eocene to Miocene Lunpola basin, central Tibet. *Nature* **439**, 677–681 (2006).
36. DeCelles, P. G. *et al.* High and dry in central Tibet during the Late Oligocene. *Earth Planet. Sci. Lett.* **253**, 389–401 (2007).
37. Sun, J. *et al.* Palynological evidence for the latest Oligocene–early Miocene paleoelevation estimate in the Lunpola Basin, central Tibet. *Palaeogeogr. Palaeoclimatol. Palaeoecol.* **399**, 21–30 (2014).
38. Jia, G., Bai, Y., Ma, Y., Sun, J. & Peng, P. a. Paleoelevation of Tibetan Lunpola basin in the Oligocene–Miocene transition estimated from leaf wax lipid dual isotopes. *Global Planet. Change* **126**, 14–22 (2015).
39. Sun, J. *et al.* Middle Miocene paleoenvironmental change and paleoelevation of the Lunpola Basin, Central Tibet. *Global Planet. Change* **220**, 104009 (2023).
40. Xiong, Z. *et al.* The early Eocene rise of the Gonjo Basin, SE Tibet: From low desert to high forest. *Earth Planet. Sci. Lett.* **543**, 116312 (2020).
41. Hoke, G. D., Liu-Zeng, J., Hren, M. T., Wissink, G. K. & Garzione, C. N. Stable isotopes reveal high southeast Tibetan Plateau margin since the Paleogene. *Earth Planet. Sci. Lett.* **394**, 270–278 (2014).
42. Wu, J. *et al.* Paleoelevations in the Jianchuan Basin of the southeastern Tibetan Plateau based on stable isotope and pollen grain analyses. *Palaeogeogr. Palaeoclimatol. Palaeoecol.* **510**, 93–108 (2018).
43. Li, L. *et al.* Carbonate stable and clumped isotopic evidence for late Eocene moderate to high elevation of the east-central Tibetan Plateau and its geodynamic implications. *GSA Bulletin* **131**, 831–844 (2019).
44. Su, T. *et al.* Uplift, climate and biotic changes at the Eocene–Oligocene transition in south-eastern Tibet. *Natl. Sci. Rev.* **6**, 495–504 (2019).

45. Li, S., Currie, B. S., Rowley, D. B. & Ingalls, M. Cenozoic paleoaltimetry of the SE margin of the Tibetan Plateau: Constraints on the tectonic evolution of the region. *Earth Planet. Sci. Lett.* **432**, 415–424 (2015).
46. Huang, Y.-J. *et al.* Higher palaeoelevation in the Baoshan Basin: Implications for landscape evolution at the southeastern margin of the Tibetan Plateau. *J. Palaeogeogr.* **13**, 563–580 (2024).
47. Clift, P. D. Controls on the erosion of Cenozoic Asia and the flux of clastic sediment to the ocean. *Earth Planet. Sci. Lett.* **241**, 571-580 (2006).
48. Farnsworth, A. *et al.* Past East Asian monsoon evolution controlled by paleogeography, not CO₂. *Sci. Adv.* **5**, eaax1697 (2019).