SUPPLEMENTARY MATERIAL

Brief Discussion of Fossils not Used for Calibration

Several fossils have not been included in the present study, because of their doubful taxonomic affinities and poor stratigraphic constraints. Relevant examples include:

†*Viviparus* (?) *albascopularis* was described from the Australian Wallumbilla Formation (Early Cretaceous, Aptian, c. 125-112 Myr) by Etheridge (1902) representing the earliest record of a freshwater gastropod from Australia. Kear et al. (2003) later re-assessed this fossil and placed it within *Notopala* based on comparative morphology and morphometry. However, the single available specimen lacks its protoconch and lacks an intact aperture and thus several diagnostic traits cannot be assessed. Moreover, it has been found in marine deposits and was therefore reworked.

Fossils described by Hislop (1860) from the Indian Deccan Plateau Formation (Late Cretacous, Maastrichtian, 70-65 Myr) have tentatively been assigned to the genus *Bellamya* (Hartman et al. 2008). Whereas these shells resemble the general habitus of smooth-shelled viviparids, they are much smaller than is typical for the family. Moreover, their preservation does not allow to evaluate diagnostic features which renders their placement within the Viviparidae is questionable.

Fossil viviparids have been also found in South America, namely †*Viviparus wichmanni* from the Late Cretaceous of Argentina (Doello-Jurado 1922) and †*Paludina araucana* from the Tertiary of Chile (Philippi 1887). However, their assignment to the Viviparidae remains questionable due to non-characteristic descriptions as already indicated by Prashad (1928). Moreover, the colonization of South America out of Laurasia during the Cretaceous is very unlikely according to Prashad (1928) and our palaeogeographical reconstructions (Fig. S6).

The North American *Tulotomops* (only known from the Upper Cretaceous) and *Lioplacodes* cannot be unambiguously assigned to Viviparidae.

Remarks on Habitat Types for the Five Fossils Used to Time-Calibrate the Phylogeny

Inference of the habitat of fossil taxa requires accurate knowledge of the depositional environment and relevant taphonomic processes. Moreover, the local occurrence of fossil assemblages may only poorly reflect the total geographical range of the taxon in question. We therefore took a conservative approach when inferring habitat types for fossil taxa.

†*Viviparus langtonensis* (CP1) – **habitat type: uncertain ('LeA/LoA')**

Freshwater-brackish (lagoon-like) habitat

†*Campeloma harlowtonense* (CP2) – **habitat type: probably lotic ('LoA')**

According to (Yen 1950), the associated fauna suggests that the origin of the Kootenai Formation was likely fluviatile. He also compared the Kootenai mollusc assemblage with the recent mollusc fauna of the Great Falls of the Potomac River, near Washington, D.C., USA and found several similarities. Although Yen (1950) further notes that a lacustrine origin should also be considered, a riverine origin seems most likely.

†*Margarya nanningensis* (CP3) – **habitat type: probably lentic ('LeC')**

Paleo-Lake Nanning

Bellamya cf. *unicolor* (CP4) – **habitat type: probably lotic ('LoA')**

Pickford (2004) suggested the Iriri Member of the Napak formation to be fluvio-paludal (i.e., slow-flowing or standing water) based on sedimentology, but interpreted the fossils as indicating a riverine environment rather than paludal conditions based on the presence of *Etheria*, the river oyster, which, however, can live in both fluvial and lacustrine conditions.

†*Neothauma hattinghi* (CP5) – **habitat type: uncertain ('LeB/LoB')**

Neothauma hattinghi was considered to have evolved in a large and probably shallow lake according to Van Damme and Pickford (1999). However, the habitat type was inferred based on the sculpture of the specimens only, and no other sedimentological evidence was provided. To avoid circular reasoning, we did not constrain the habitat type of this species.

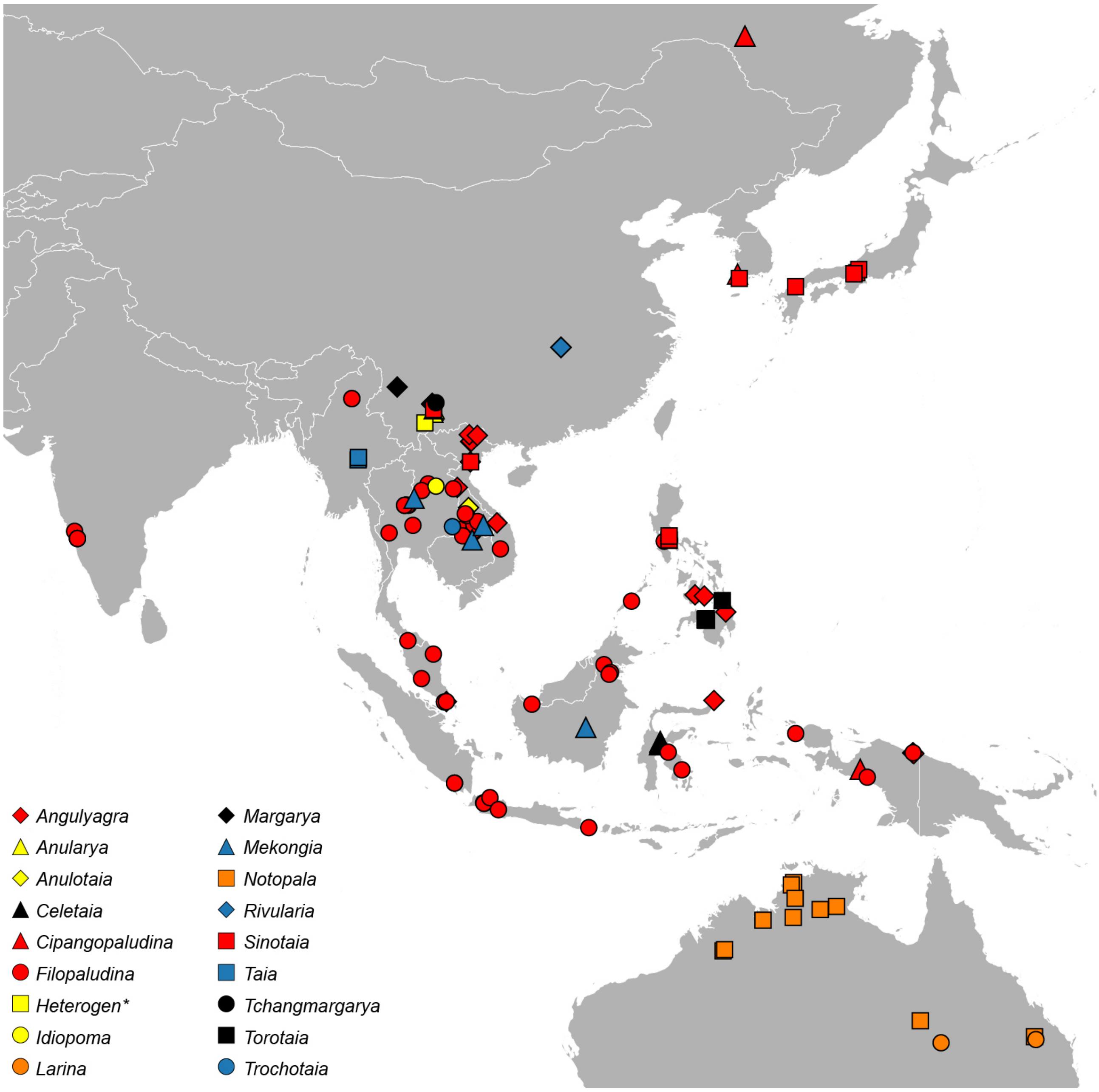

FIGURE S1. Distribution map of samples of Viviparidae collected in Asia/Australia. Note that a recent study has suggested to synonymize *Heterogen* with *Cipangopaludina* (Hirano et al. 2015).

FIGURE S2. Best Maximum Likelihood phylogram based on a RAxML analysis of the complete dataset (193 sequences). Numbers on branches indicate bootstrap values based on 456 replicates. See main text for details.

FIGURE S3. Bayesian consensus phylogram based on a MrBayes analysis of the complete dataset (193 sequences). Numbers on branches indicate posterior probabilities. See main text for details.

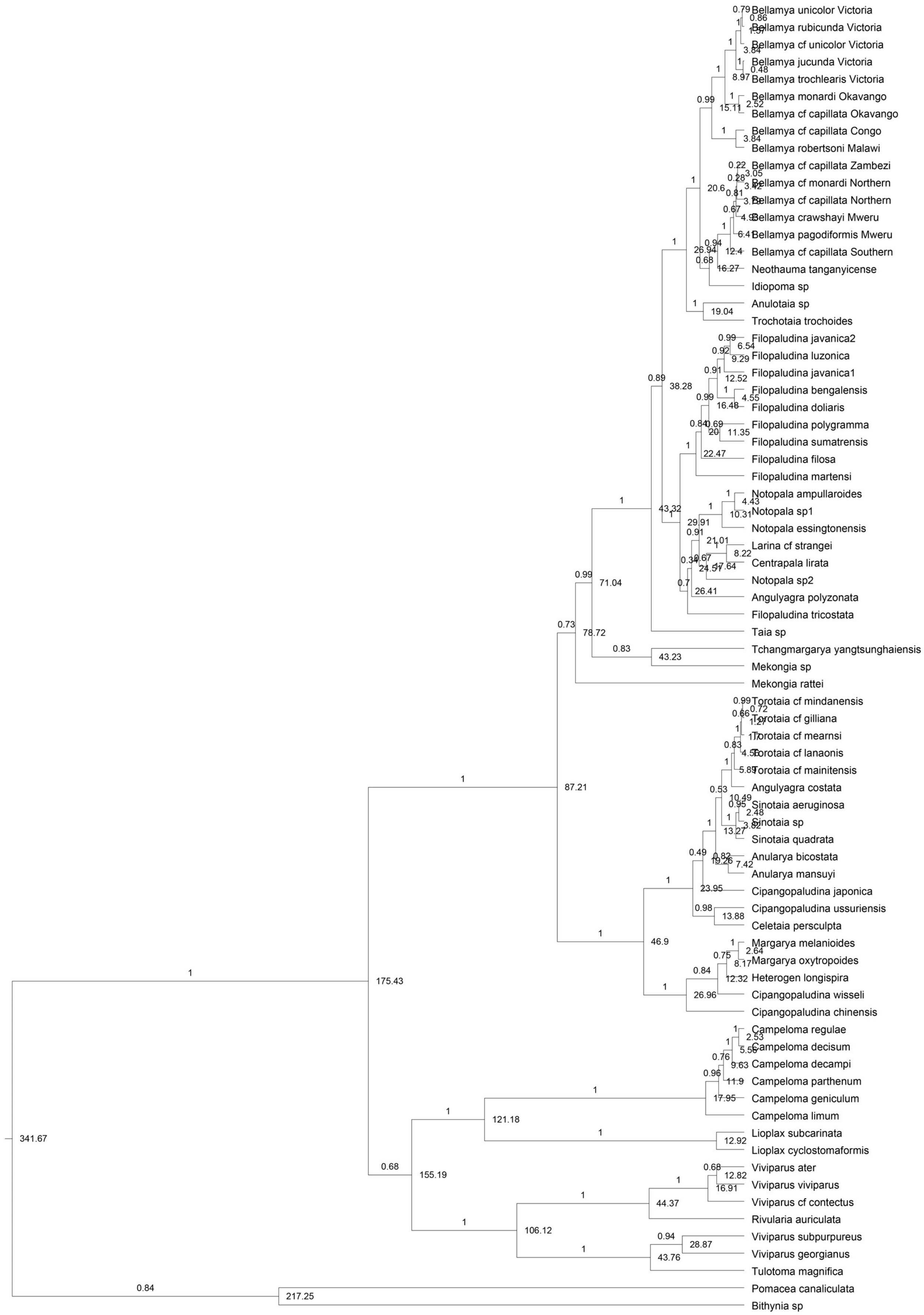

FIGURE S4. Maximum-clade credibility (MCC) tree based on a BEAST analysis of the reduced dataset (76 sequences) using five fossil-calibration points. Numbers on branches indicate posterior probabilities; numbers at nodes denote mean ages. See main text for details.

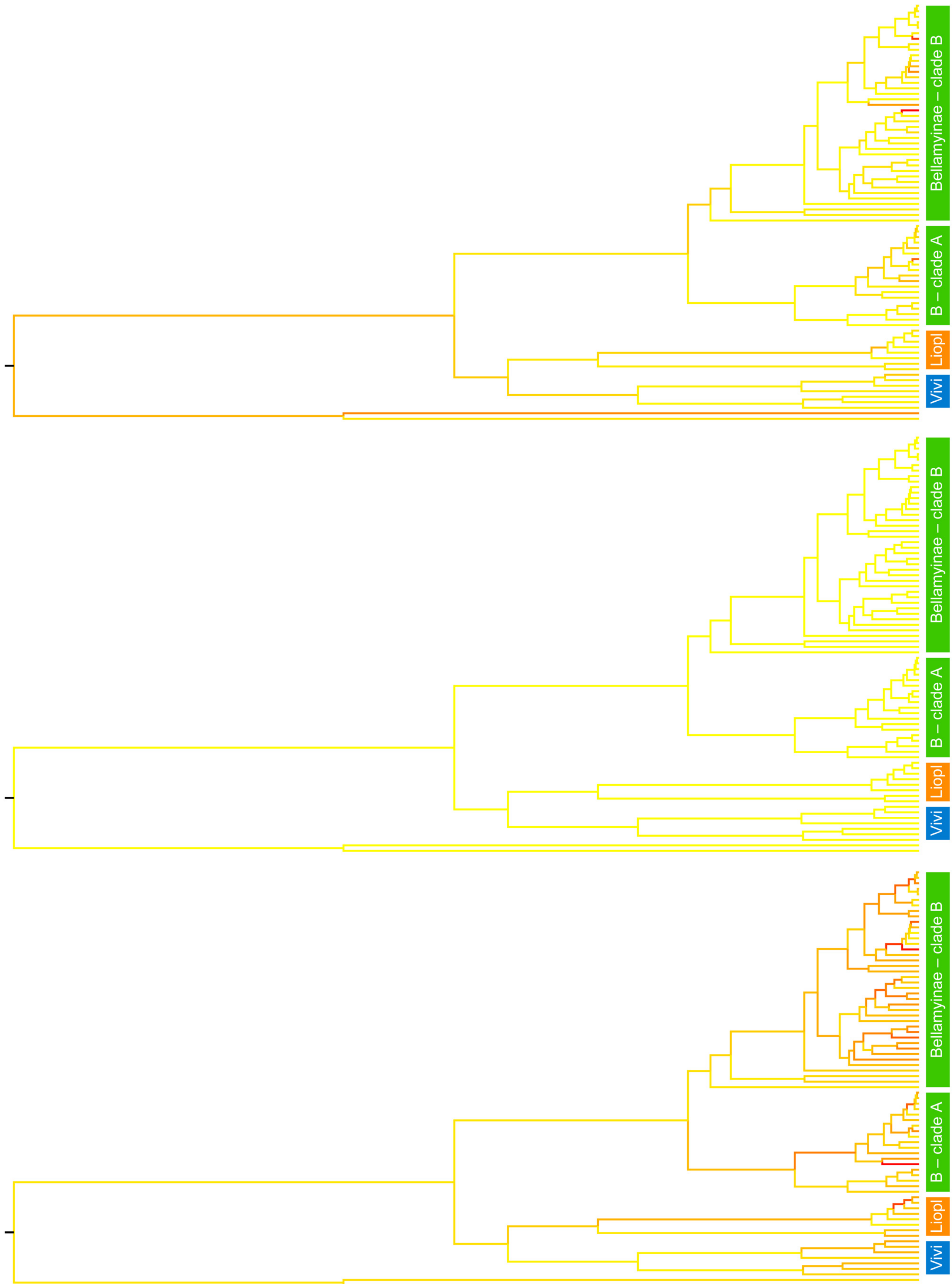

FIGURE S5. Brach-specific rates for nuclear 28S rRNA (upper panel), nuclear H3 (middle), and mitochondrial COI (lower panel) based on the BEAST MCC tree visualized in FigTree 1.4.2. The colour gradient across the branches denotes low (yellow) or high (red) mean rates. See Figure S4 for details.

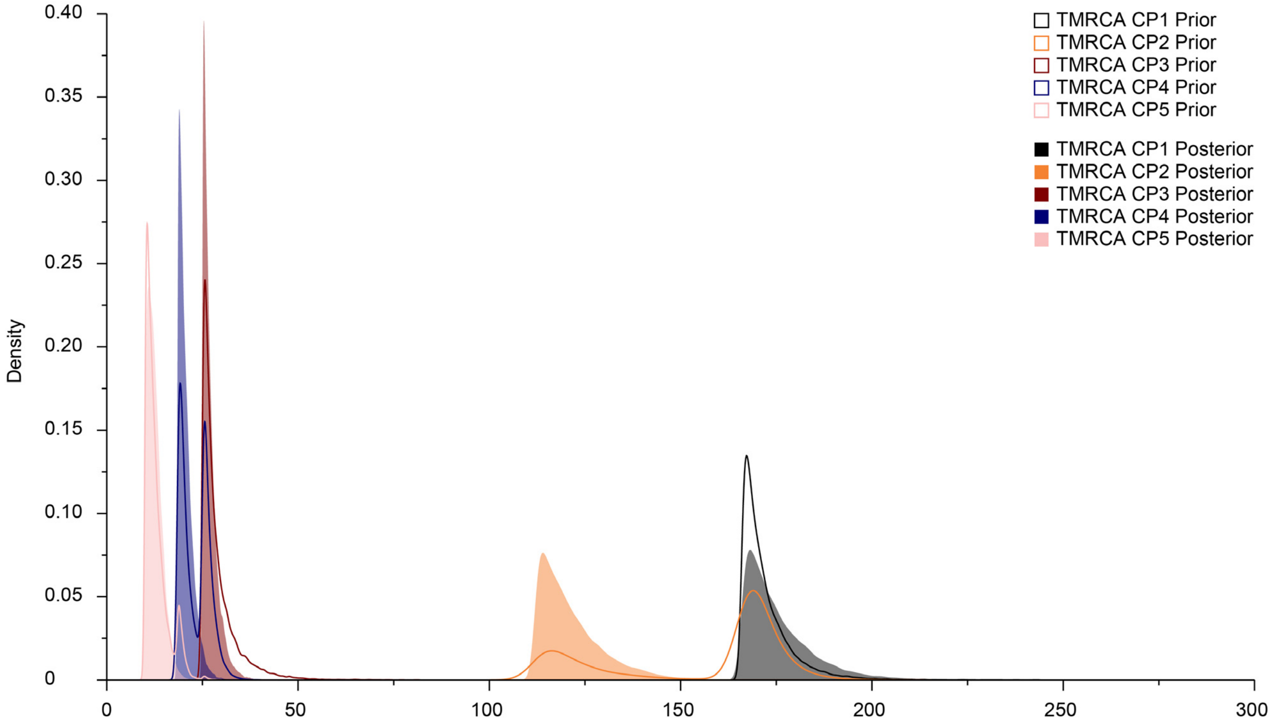

FIGURE S6. Comparison of posterior distributions obtained from the default BEAST analysis (using calibration points CP1-CP5) and the full prior distribution obtained the 'sample from prior only' analysis visualized in TRACER 1.5. See main text for details.

FIGURE S7. General shell morphology of Viviparidae. Voucher specimens of each representative operational taxonomic unit (OTU) shown in the OTU-based tree of Viviparidae (see Table S1). Additional image sources: *Anularya bicostata*, *Margarya oxytropoides* and *Tchangmargarya yangtsunghaiensis* from Zhang et al. (2015); *Bellamya crawshayi* from Sengupta et al. (2009), *Cipangopaludina ussuriensis* from Gerstfeldt (1859); *Cipangopaludina japonica* from Van Bocxlaer and Strong (2016); and *Cipangopaludina longispira* from Hirano et al. (2015). *Bellamya* species were assigned to biogeographical clades identified in the study of Schultheiß et al. (2014).

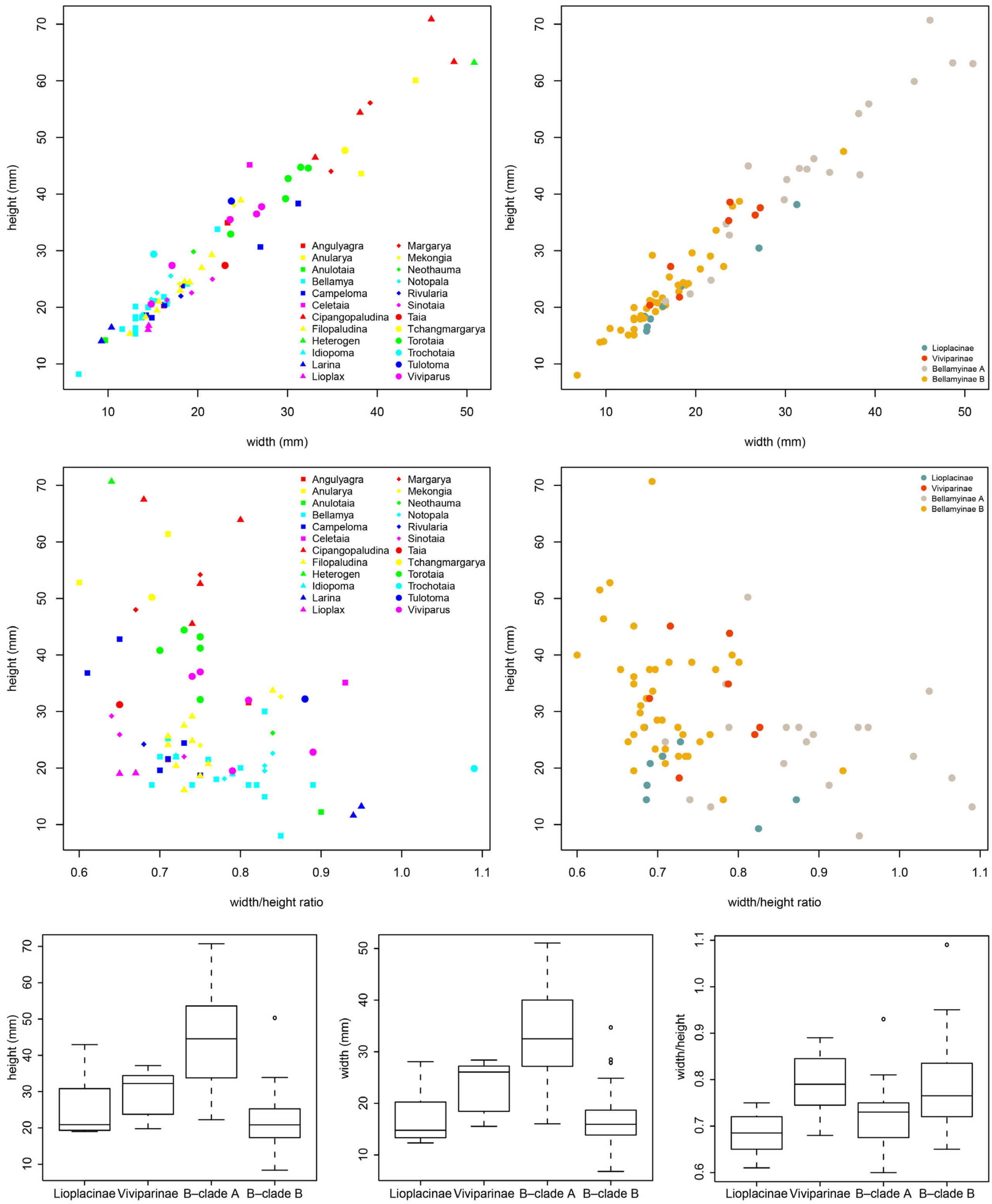

FIGURE S8. Genus- and clade-specific comparisons of standard shell measurements (height, width, and width-height ratio) obtained from the voucher images for each of the 74 OTUs shown in Fig. S6. Upper panels: width vs. height, middle panels: width-height ratio vs. height, and lower panels: boxplots per clade.

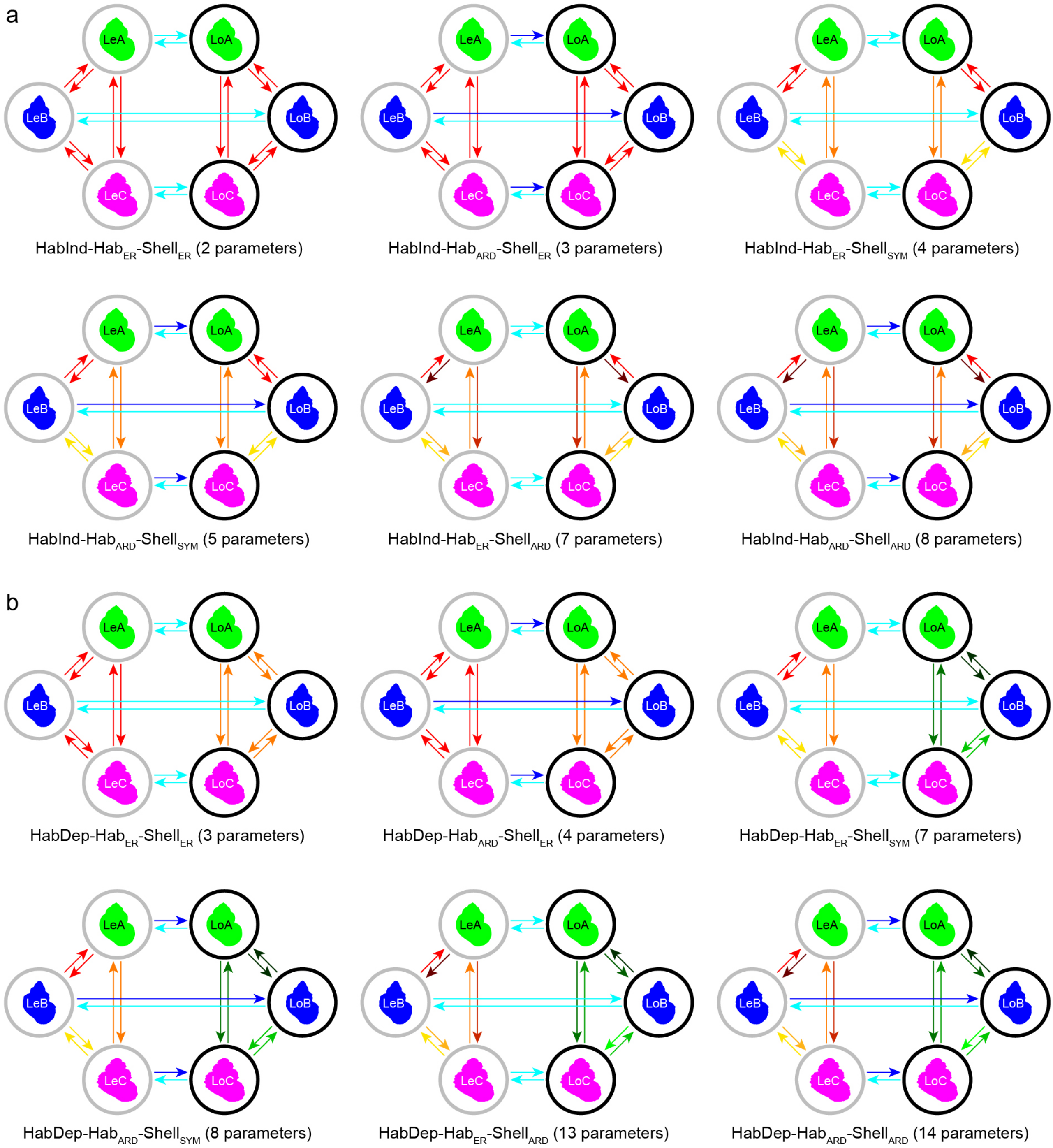

FIGURE S9. Illustration of transition matrices used to identify the best-fit model for habitat and shell transitions. a) Matrices for habitat-independent shell transitions; b) Matrices for habitat-dependent shell transitions. Note that transitions implementing both a habitat and shell shift (e.g., 'LeA'→'LoB') were not allowed *a priori*. Character states: 'LeA' = lentic with shell type A ('absent'), 'LeB' = lentic with shell type B ('fine'), 'LeC' = lentic with shell type C ('coarse'), 'LoA' = lotic with shell type A ('absent'), 'LoB' = lotic with shell type B ('fine'), and 'LoC' = lotic with shell type C ('coarse'). Model specifications: 'HabDep' = habitat-dependent, 'HabInd' = habitat-independent, 'Hab' = habitat transition rate, 'Shell' = shell transition rate, 'ARD' = all rates different, 'ER' = equal rates, and 'SYM' = symmetric rates.

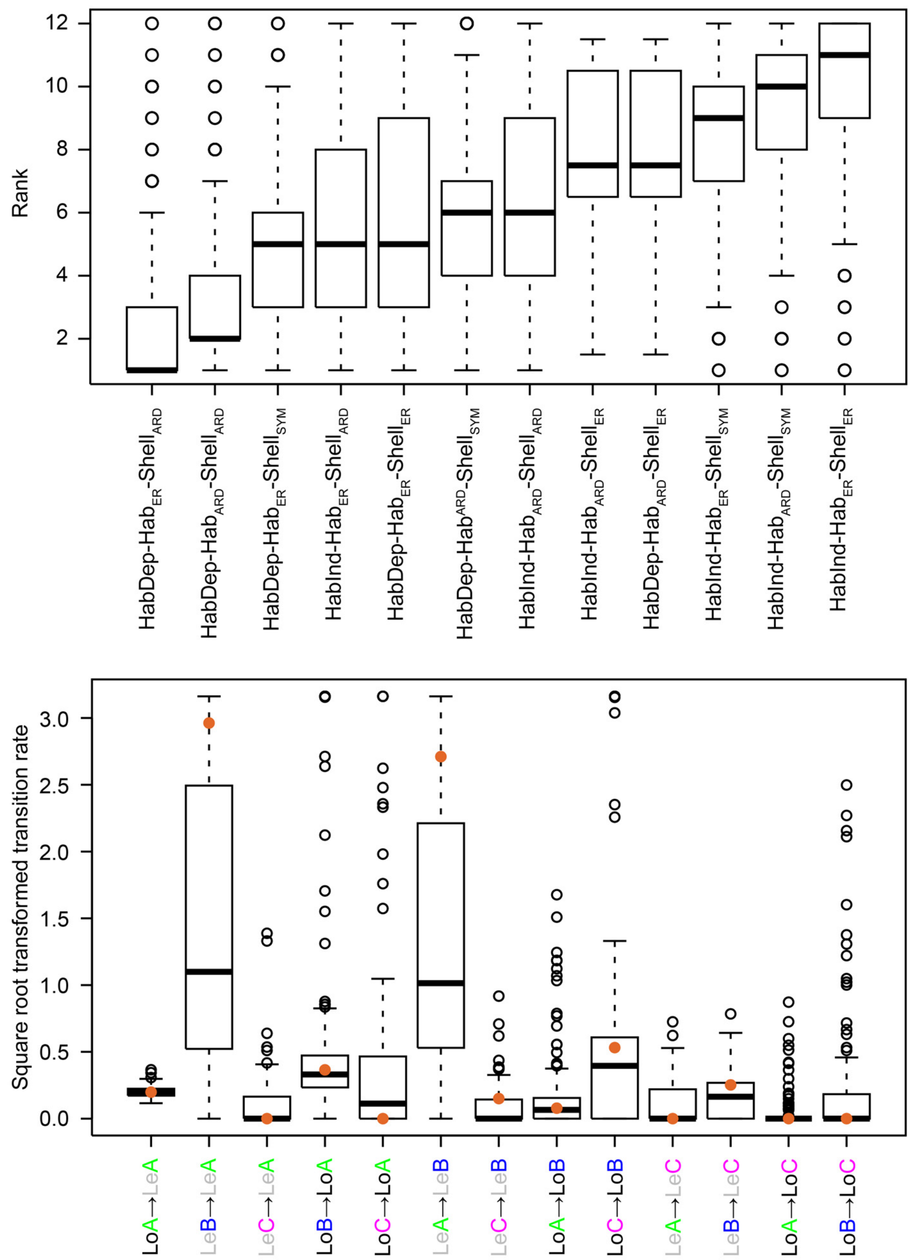

FIGURE S10. Evaluation of taxon sampling on model robustness based on 250 replicates (see main text for details). Upper panel: ranked model-fit comparision of habitat-shell evolution models according to AIC values (see also Fig. S9 and Table S8). Lower panel: estimated transition rates for the prevailing model of habitat-dependent asymmetric shell transition rates. Orange dots represent the transition rates estimated for the best-fit model in the unconstrained analysis that were used for simulations (see Table S8).

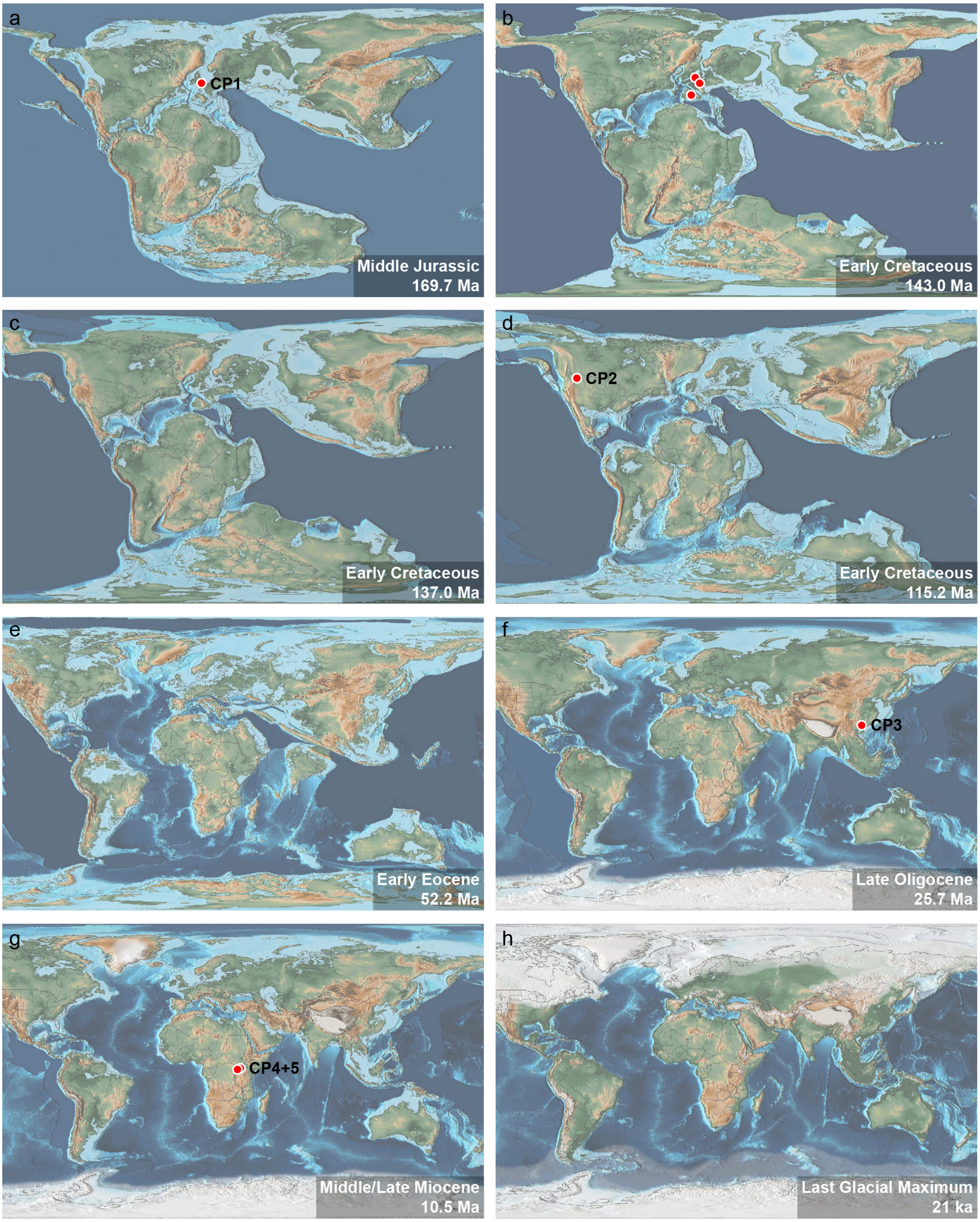

FIGURE S11. Palaeogeographical maps including selected fossil representatives mentioned in the main text. a) †*Viviparus langtonensis* (calibration point, CP1); b) †*Viviparus* spp.; c) Valanginian stage during which the colonization of Laurasia intensified; d) †*Campeloma harlowtonense* (CP2); e) onset of India-Asia collision; f) onset of Asia-Australia collision, †*Margarya nanningensis* (CP3); g) *Bellamya* cf. *unicolor* (CP4, Early Miocene) and †*Neothauma hattinghi* (CP5); and h) the Last Glacial Maximum and the related global low sea level stand led to the interconnection of Southeast Asian islands. Modified from Scotese (2014a, 2014b, 2014c, 2014d).

TABLE S1. Material examined including locality information, assigned OTUs, predefined BIOGEOBEARS areas and GenBank accession numbers. *Bellamya* species were assigned to biogeographical clades identified in the study of (Schultheiß et al. 2014). BIOGEOBEARS areas: (A) = North America, (B) = Africa, (C) = Europe, (D) = East Asia (China, Far East Russia, Japan, and South Korea), (E) = India, (F) = Indochina (incl. the Thai-Malay Peninsula and Singapore), (G) = Sumatra, (H) = Philippines, (J) Palawan, (K) = Borneo, (L) = Java (incl. Bali), (M) = Sulawesi, and (N) = 'East of Wallacea' (Australia and New Guinea). COI sequences marked with an asterisk were sequenced on a Roche 454 GS FLX Titanium platform (see main text and Table S2 for details). Specimens displayed in Fig. S7 are indicated with a camera icon.

Taxon/Specimen (incl. collection number)	OTU (BIOGEOBEARS)	BIOGEOBEARS area	Latitude	Longitude	GenBank acc. no. COI	28S rRNA	H3
Angulyagra costata ZMB 107071-1 Sulawesi	Angulyagra_costata	H, M, N	1.49255	124.86733	MN997886	MN999555	MN997713
Angulyagra costata ZMB 113429-1 Cebu			9.79963	123.37553	MN997887*	MN999556	MN997714
Angulyagra costata ZMB 113431-1 Bohol			9.71163	124.10770	MN997888	MN999557	MN997715
Angulyagra costata ZMB 127100-1 LakeSentani			-2.62132	140.52718	MN997889	MN999558	MN997716
Angulyagra costata ZMB 127101-1 LakeSentani			-2.63322	140.49260	MN997890	MN999559	MN997717
Angulyagra costata ZMB 127109-1 LakeSentani 📷			-2.68998	140.58362	MN997891	MN999560	MN997718
Angulyagra costata ZMB 230163-2 Mindanao			8.45128	125.79404	MH319893	MN999561	MN997719
Angulyagra polyzonata ZMB 114132-1 VNM	Angulyagra_polyzonata	F	20.25765	105.70833	MN997892	MN999562	MN997720
Angulyagra polyzonata ZMB 114171-1 VNM			21.84767	105.73150	MN997893	MN999563	MN997721
Angulyagra polyzonata ZMB 114175-1 VNM 📷			21.88203	105.77450	MN997894	MN999564	MN997722
Angulyagra polyzonata ZMB 114189-1 VNM			22.40165	105.62417	MN997895	MN999565	MN997723
Angulyagra polyzonata ZMB 114202-1 VNM			22.33333	106.25833	MN997896	MN999566	MN997724
Angulyagra polyzonata ZMB 114403-1 VNM			15.46183	107.80183	MN997897	MN999567	MN997725
Angulyagra polyzonata ZMB 114411-1 LAO			18.24450	104.68683	MN997898	MN999568	MN997726
Angulyagra polyzonata ZMB 192077-1 SGP			1.40100	103.82150	MN997899	MN999569	MN997727
Anularya bicostata ZMB 193469-1 CHN	Anularya_bicostata	D	24.43150	102.86500	MN997900*	MN999570	MN997728
Anularya mansuyi ZMB 193466-3 CHN	Anularya_mansuyi	D	24.32967	102.76950	MN997901*	MN999571	MN997729
Anularya mansuyi ZMB 193466-5 CHN			24.32967	102.76950	MN997902	MN999572	MN997730
Anularya mansuyi ZMB 193467-1 CHN			24.16417	102.75883	MN997903*	MN999573	MN997731
Anularya mansuyi ZMB 193467-5 CHN			24.16417	102.75883	MN997904*	MN999574	MN997732
Anulotaia sp. ZMB 114963-1 LAO 📷	Anulotaia_sp	F	16.65800	105.56383	MN997905	MN999575	MN997733
Bellamya cf. *capillata* 16985 'Congo' 📷	Bellamya_cf_capillata_Congo	B	2.09981	22.66347	JX489246	JX489315	JX489284
Bellamya cf. *capillata* 9473 'Northern' 📷	Bellamya_cf_capillata_Northern	B	-9.04567	29.04460	HQ012725	HQ012692	JX489259
Bellamya cf. *capillata* 17554 'Okavango' 📷	Bellamya_cf_capillata_Okavango	B	-17.75630	25.18654	JX489255	JX489359	JX489293
Bellamya cf. *capillata* 16566 'Southern'	Bellamya_cf_capillata_Southern	B	-14.38287	23.23285	JX489243	JX489312	JX489279
Bellamya cf. *capillata* 16567 'Southern'			-14.38287	23.23285	JX489244	JX489313	JX489280
Bellamya cf. *capillata* 16569 'Southern'			-15.08967	22.84252	JX489245	JX489314	JX489281
Bellamya cf. *capillata* 17539 'Southern'			-15.19352	22.95794	JX489251	JX489319	JX489289
Bellamya cf. *capillata* 17544 'Southern'			-16.24204	23.24116	JX489252	JX489320	JX489290
Bellamya cf. *capillata* 17545 'Southern'			-16.24204	23.24116	JX489253	JX489321	JX489291
Bellamya cf. *capillata* 17549 'Southern' 📷			-16.65075	23.56652	JX489254	JX489322	JX489292
Bellamya cf. *capillata* 17053 'Zambezi' 📷	Bellamya_cf_capillata_Zambezi	B	-13.55640	23.09447	JX489250	JX489318	JX489288

Bellamya cf. *monardi* 16987 ‘Northern’	Bellamya_cf_monardi_Northern	B	-14.81798	26.04066	JX489248	JX489316	JX489286
Bellamya cf. *monardi* 16995 ‘Northern’			-14.70344	26.10316	JX489249	JX489317	JX489287
Bellamya cf. *unicolor* 15745 ‘Victoria’	Bellamya_cf_unicolor_Victoria	B	1.84843	30.47826	JX489240	JX489310	JX489277
Bellamya crawshayi GB ‘Mweru’	Bellamya_crawshayi_Mweru	B	-8.99556	28.71611	FJ405844	FJ405695	FJ405746
Bellamya jucunda 15321 ‘Victoria’	Bellamya_jucunda_Victoria	B	0.03892	32.49402	JX489231	JX489302	JX489269
Bellamya monardi 9489 ‘Okavango’	Bellamya_monardi_Okavango	B	-18.12071	21.58754	HQ012800	HQ012686	JX489263
Bellamya pagodiformis 9477 ‘Mweru’	Bellamya_pagodiformis_Mweru	B	-9.34801	28.73133	HQ012720	HQ012688	JX489261
Bellamya robertsoni 6597 ‘Malawi’	Bellamya_robertsoni_Malawi	B	-14.08923	34.93017	HQ012797	HQ012704	JX489257
Bellamya rubicunda 15312 ‘Victoria’	Bellamya_rubicunda_Victoria	B	1.58649	31.10057	JX489230	JX489301	JX489268
Bellamya rubicunda 15482 ‘Victoria’			1.81842	31.32021	JX489233	JX489304	JX489271
Bellamya rubicunda 15483 ‘Victoria’			1.81842	31.32021	JX489234	JX489305	JX489272
Bellamya trochlearis 15192 ‘Victoria’	Bellamya_trochlearis_Victoria	B	0.16176	33.58264	JX489227	JX489298	JX489265
Bellamya trochlearis 15193 ‘Victoria’			0.16176	33.58264	JX489228	JX489299	JX489266
Bellamya trochlearis 15494 ‘Victoria’			0.03892	32.49402	JX489235	JX489339	JX489273
Bellamya unicolor 15261 ‘Victoria’	Bellamya_unicolor_Victoria	B	0.14067	33.60258	JX489229	JX489300	JX489267
Bellamya unicolor 15476 ‘Victoria’			2.45933	31.50487	JX489232	JX489303	JX489270
Bellamya unicolor 15707 ‘Victoria’			1.09002	32.93648	JX489238	JX489307	JX489275
Bellamya unicolor 15733 ‘Victoria’			1.69255	32.09473	JX489239	JX489309	JX489276
Bithynia sp. ZMB 191552-1 Sulawesi	Bithynia_sp	N.A. (outgroup)	-1.89580	120.66565	KY574006	N.A.	KY574014
Campeloma decampi USNM 1292572 USA	Campeloma_decampi	A	34.68917	-86.82861	MN997906	MN999576	MN997734
Campeloma decampi USNM 1292573 USA		A	34.74278	-87.08444	MN997907	MN999577	MN997735
Campeloma decisum USNM 1292574 USA	Campeloma_decisum	A	35.60389	-86.87528	MN997908	MN999578	MN997736
Campeloma decisum USNM 1292575 USA		A	34.75833	-87.81306	MN997909	MN999579	MN997737
Campeloma geniculum USNM 1292576 USA	Campeloma_geniculum	A	31.00778	-87.16222	MN997910	MN999580	MN997738
Campeloma limum NCSM 27484 USA	Campeloma_limum	A	32.44167	-81.83333	MN997911	MN999581	MN997739
Campeloma parthenum NCSM 45096 USA	Campeloma_parthenum	A	31.42573	-88.45760	MN997912	MN999582	MN997740
Campeloma regulae USNM 1292577 USA	Campeloma_regulae	A	32.89639	-86.43472	MN997913	MN999583	MN997741
Campeloma regulae USNM 1292580 USA		A	33.16806	-87.02139	MN997914	MN999584	MN997742
Celetaia persculpta ZMB 190992-1 Sulawesi	Celetaia_persculpta	M	-1.98372	120.58513	MN997915	MN999585	MN997743
Celetaia persculpta ZMB 190993-5 Sulawesi			-1.96547	120.67560	MN997916	MN999586	MN997744
Celetaia persculpta ZMB 191078-5 Sulawesi			-1.92128	120.67135	MN997917	MN999587	MN997745
Celetaia persculpta ZMB 192209a-1 Sulawesi			-1.82850	120.63593	MN997918*	MN999588	MN997746
Celetaia persculpta ZMB 192210a-1 Sulawesi			-1.74285	120.65202	MN997919	MN999589	MN997747
Celetaia persculpta ZMB 192211a-1 Sulawesi			-1.77105	120.62488	MN997920	MN999590	MN997748
Celetaia persculpta ZMB 192213a-1 Sulawesi			-1.77323	120.63878	MN997921	MN999591	MN997749
Cipangopaludina ussuriensis UGSB 23018 RUS	Cipangopaludina_ussuriensis	D	53.73392	127.30203	MN997923	MN999593	MN997751
Cipangopaludina ussuriensis UGSN23019 RUS	Cipangopaludina_ussuriensis		53.75181	127.30603	MN997924	MN999594	MN997752
Cipangopaludina chinensis ZMB 192694-1 KOR	Cipangopaludina_chinensis	D	35.03267	126.72100	MN997925*	MN999595	MN997753
Cipangopaludina japonica USNM 1296945 USA	Cipangopaludina_japonica	D	38.81370	-77.03800	MN997926	MN999596	MN997754
Cipangopaludina wisseli ZMB 127112a LakePaniai	Cipangopaludina_wisseli	N	-3.91975	136.36817	MN997927	MN999597	MN997755
Filopaludina bengalensis ZMB 113662-2 IND	Filopaludina_bengalensis	E	14.79633	74.59083	MN997928	MN999598	MN997756

Filopaludina bengalensis ZMB 113664-1 IND			14.22833	74.81200	MN997929	MN999599	MN997757
Filopaludina bengalensis ZMB 113664-3 IND			14.22833	74.81200	MN997930	MN999600	MN997758
Filopaludina bengalensis ZMB 113664-4 IND			14.22833	74.81200	MN997931	MN999601	MN997759
Filopaludina decipiens ZMB 127091-1 WestPapua	Filopaludina_javanica2	K, L, M, N	-1.10817	131.29255	MN997932	MN999602	MN997760
Filopaludina decipiens ZMB 127107-1 WestPapua			-4.54932	136.92412	MN997933	MN999603	MN997761
Filopaludina doliaris ZMB 113665-4 MMR	Filopaludina_doliaris	F	25.23383	96.39000	MN997934	MN999604	MN997762
Filopaludina doliaris ZMB 113665-5 MMR			25.23383	96.39000	MN997935	MN999605	MN997763
Filopaludina filosa ZMB 114012-1 THA	Filopaludina_filosa	F	16.86687	100.63167	MN997936*	MN999606	MN997764
Filopaludina filosa ZMB 114049-1 THA			16.84375	100.85672	MN997937	MN999607	MN997765
Filopaludina filosa ZMB 192078-1 SPG			1.37198	103.66118	MN997938	MN999608	MN997766
Filopaludina javanica ZMB 112753-1 Sarawak	Filopaludina_javanica2	K, L, M, N	1.19733	110.54733	MN997939	MN999609	MN997767
Filopaludina javanica ZMB 127093-1 Kalimantan			4.30733	116.21750	MN997943	MN999613	MN997771
Filopaludina javanica ZMB 127096-1 Kalimantan			3.68967	116.73050	MN997944	MN999614	MN997772
Filopaludina javanica ZMB 127098-1 Kalimantan			3.55188	116.62385	MN997945	MN999615	MN997773
Filopaludina javanica ZMB 191097-1 Sulawesi			-2.57760	121.26892	MN997946	MN999616	MN997774
Filopaludina javanica ZMB 191406-1 Bali			-8.51243	115.02283	MN997948	MN999618	MN997776
Filopaludina javanica ZMB 127082-1 Java	Filopaludina_javanica1	G, L, M	-6.55548	106.74945	MN997940	MN999610	MN997768
Filopaludina javanica ZMB 127085-1 Java			-6.60083	106.79867	MN997941	MN999611	MN997769
Filopaludina javanica ZMB 127086-1 Java			-6.59800	106.77773	MN997942	MN999612	MN997770
Filopaludina javanica ZMB 191398-3 Sulawesi			-3.96495	122.34565	MN997947	MN999617	MN997775
Filopaludina javanica ZMB 191702-2 Sumatra			-5.00882	104.46482	MN997949	MN999619	MN997777
Filopaludina javanica ZMB 191702-3 Sumatra			-5.00882	104.46482	MN997950	MN999620	MN997778
Filopaludina javanica ZMB 192080-1 Java			-6.15330	107.24835	MN997951	MN999621	MN997779
Filopaludina luzonica FLMNH 113451 Palawan	Filopaludina_luzonica	H, J	9.30000	118.38333	MN997952	MN999622	MN997780
Filopaludina luzonica ZMB 113414-1 Luzon			14.11340	121.36477	MN997953	MN999623	MN997781
Filopaludina luzonica ZMB 113417-1 Luzon			14.01517	120.95417	MN997954	MN999624	MN997782
Filopaludina luzonica ZMB 113437-1 Luzon			14.10620	121.37590	MN997955	MN999625	MN997783
Filopaludina luzonica ZMB 113438-1 Luzon			14.11730	121.36842	MN997956*	MN999626	MN997784
Filopaludina luzonica ZMB 113439-1 Luzon			14.12242	121.33663	MN997957*	MN999627	MN997785
Filopaludina martensi ZMB 113166-1 LAO	Filopaludina_martensi	F	14.72450	105.95150	MN997958	MN999628	MN997786
Filopaludina martensi ZMB 113176-1 THA			14.95217	105.00917	MN997959*	MN999629	MN997787
Filopaludina martensi ZMB 113178-2 LAO			14.80833	105.92000	MN997960*	MN999630	MN997788
Filopaludina martensi ZMB 114000-1 THA			15.26433	101.19367	MN997961	MN999631	MN997789
Filopaludina martensi ZMB 114019-1 THA			16.83783	100.53017	MN997962*	MN999632	MN997790
Filopaludina martensi ZMB 114036-1 THA			16.84567	100.75027	MN997963	MN999633	MN997791
Filopaludina martensi ZMB 114120-1 THA			16.83967	100.53863	MN997964	MN999634	MN997792
Filopaludina martensi ZMB 114412-1 LAO			18.14417	104.37533	MN997965	MN999635	MN997793
Filopaludina martensi ZMB 114951-1 THA			14.66750	99.31833	MN997966*	MN999636	MN997794
Filopaludina martensi ZMB 193437-1 LAO			18.52762	102.39233	MN997967	MN999637	MN997795
Filopaludina polygramma ZMB 113167-1 LAO	Filopaludina_polygramma	F	15.33533	105.98183	MN997968	MN999638	MN997796
Filopaludina polygramma ZMB 113170-1 LAO			16.03100	105.43867	MN997969	MN999639	MN997797
Filopaludina polygramma ZMB 114948-1 LAO			15.56417	106.29150	MN997970	MN999640	MN997798

Filopaludina polygramma ZMB 114959-1 LAO			16.17433	105.30850	MN997971	MN999641	MN997799
Filopaludina sumatrensis ZMB 113175-1 THA	Filopaludina_sumatrensis	F, L	14.43517	105.10500	MN997972*	MN999642	MN997800
Filopaludina sumatrensis ZMB 113444-1 MYS			5.13745	102.80230	MN997973	MN999643	MN997801
Filopaludina sumatrensis ZMB 113446 MYS			3.21073	101.86743	MN997974	MN999644	MN997802
Filopaludina sumatrensis ZMB 113447b-1 MYS			6.18982	100.79600	MN997975	MN999645	MN997803
Filopaludina sumatrensis ZMB 114070-1 THA			18.00122	101.88633	MN997976*	MN999646	MN997804
Filopaludina sumatrensis ZMB 114405 VNM			13.40900	108.07483	MN997977	MN999647	MN997805
Filopaludina sumatrensis ZMB 191654 Java			-7.10020	107.91727	MN997978	MN999648	MN997806
Filopaludina sumatrensis ZMB 192076 SGP			1.40100	103.82150	MN997979	MN999649	MN997807
Filopaludina tricostata ZMB 127114-1 LakeSentani	Filopaludina_tricostata	N	-2.62132	140.52718	MN997980	MN999650	MN997808
Heterogen longispira GB CHN	Heterogen_longispira	D	23.67000	102.57000	GU198809	KJ867091	N.A.
Idiopoma sp. ZMB 113172-1 LAO	Idiopoma_sp	F	18.34667	103.00933	MN997981	MN999651	MN997809
Idiopoma sp. ZMB 192469-1 MMR	Idiopoma_sp		N.A.	N.A.	MN997982	MN999652	MN997810
Larina cf. *strangei* ZMB 192393 AUS	Larina_cf_strangei	N	-25.18025	150.18370	MN997983	MN999653	MN997811
Larina lirata ZMB 192040 AUS	Larina_lirata	N	-25.43667	142.72700	MN997922	MN999592	MN997750
Lioplax cyclostomaformis USNM 1292582 USA	Lioplax_cyclostomaformis	A	33.16806	-87.02139	MN997984	MN999654	MN997812
Lioplax subcarinata NCSM 40332-1 USA z	Lioplax_subcarinata	A	35.81510	-77.54652	MN997985	MN999655	MN997813
Lioplax subcarinata USNM 1292583 USA		A	34.75833	-87.81306	N.A.	MN999656	MN997814
Margarya melanioides ZMB 193463-2 CHN	Margarya_melanioides	D	24.80050	102.67133	MN997986*	MN999657	MN997815
Margarya melanioides ZMB 193463-7 CHN			24.80050	102.67133	MN997987	MN999658	MN997816
Margarya melanioides ZMB 193463-8 CHN			24.80050	102.67133	MN997988*	MN999659	MN997817
Margarya melanioides ZMB 193468-1 CHN			26.14683	99.95250	MN997989	MN999660	MN997818
Margarya oxytropoides GB CHN	Margarya_oxytropoides	D	24.86694	102.71332	KJ636775	KJ867094	N.A.
Mekongia rattei ZMB 114062-1 THA	Mekongia_rattei	F	17.39268	101.28417	MN997990	MN999661	MN997819
Mekongia rattei ZMB 114956-1 LAO			14.11667	105.85500	MN997991*	MN999662	MN997820
Mekongia rattei ZMB 114958-1 LAO			15.25600	106.73550	MN997992*	MN999663	MN997821
Mekongia sp. ZMB 192085-1 Kalimantan	Mekongia_sp	K	-0.63083	114.78783	MN997993	MN999664	MN997822
Neothauma tanganyicense 6992 7033 Tanganyika	Neothauma_tanganyicense	B	-4.78543	29.69946	HQ012717	HQ012707	MN997823
Neothauma tanganyicense ZMB 107101-1 Tanganyika			-8.72467	31.13300	MN997994	MN999665	MN997824
Notopala ampullaroides ZMB 106669-1 AUS	Notopala_ampullaroides	N	-14.07067	131.25093	MN997995	MN999666	MN997825
Notopala ampullaroides ZMB 106691-1 AUS			-15.79215	128.71755	MN997996	MN999667	MN997826
Notopala essingtonensis ZMB 106602-1 AUS	Notopala_essingtonensis	N	-12.83803	131.13330	MN997997	MN999668	MN997827
Notopala essingtonensis ZMB 106638-1 AUS			-14.71337	134.50790	MN997998	MN999669	MN997828
Notopala essingtonensis ZMB 106647-1 AUS			-13.02193	130.95155	MN997999	MN999670	MN997829
Notopala essingtonensis ZMB 192707-1 AUS			-14.95263	133.22150	MN998000	MN999671	MN997830
Notopala sp. ZMB 106620-1 AUS	Notopala_sp1	N	-15.58103	131.10237	MN998001	MN999672	MN997831
Notopala sp. ZMB 106694-1 AUS			-18.21088	125.57900	MN998002	MN999673	MN997832
Notopala sp. ZMB 106695-1 AUS			-18.10868	125.69818	MN998003	MN999674	MN997833
Notopala sp. ZMB 192042-1 AUS	Notopala_sp2	N	-23.70367	141.09583	MN998004	MN999675	MN997834
Notopala sp. ZMB 192392-1 AUS			-24.95695	150.07405	MN998005	MN999676	MN997835
Pomacea canaliculata ZMB 191395a Sulawesi	Pomacea_canaliculata	N.A. (outgroup)	-5.35915	119.47758	KY574007	KY573999	KY574015

Rivularia auriculata ZMB 116176-1 CHN	Rivularia_auriculata	D	29.26350	112.83800	KY574008	KY574000	KY574016
Rivularia auriculata ZMB 116176-2 CHN			29.26350	112.83800	KY574009	KY574001	KY574017
Rivularia auriculata ZMB 116176-3 CHN			29.26350	112.83800	KY574010	KY574002	KY574018
Sinotaia aeruginosa ZMB 114131-1 VNM	Sinotaia_aeruginosa	F	20.25765	105.72500	MN998006	MN999677	MN997836
Sinotaia quadrata ZMB 113413-1 Luzon	Sinotaia_quadrata	D, H	14.07825	121.34230	MN998007	MN999678	MN997837
Sinotaia quadrata ZMB 113416-1 Luzon			14.11377	121.33817	MN998008*	MN999679	MN997838
Sinotaia quadrata ZMB 113442-1 Luzon			14.42767	121.33700	MN998009*	MN999680	MN997839
Sinotaia quadrata ZMB 192692-1 JPN			35.13542	136.09883	MN998010	MN999681	MN997840
Sinotaia quadrata ZMB 192730-1 JPN			35.38333	136.25333	MN998011	MN999682	MN997841
Sinotaia quadrata ZMB 192731-1 JPN			34.04167	131.28333	MN998012	MN999683	MN997842
Sinotaia quadrata ZMB 192732-1 KOR			34.68567	126.86167	MN998013	MN999684	MN997843
Sinotaia quadrata ZMB 192735-1 JPN			35.05333	135.87500	MN998014*	MN999685	MN997844
Sinotaia sp. ZMB 193457-2 CHN	Sinotaia_sp	D	24.37622	102.81633	MN998015	MN999686	MN997845
Sinotaia sp. ZMB 193457-5 CHN			24.37622	102.81633	MN998016*	MN999687	MN997846
Taia sp. ZMB 113650-1 MMR	Taia_sp	F	20.55900	96.90300	MN998017	MN999688	MN997847
Taia sp. ZMB 113654-4 MMR			20.42100	96.88667	MN998018	MN999689	MN997848
Taia sp. ZMB 113654-7 MMR			20.42100	96.88667	MN998019	MN999690	MN997849
Taia sp. ZMB 113660-4 MMR			20.60750	96.90350	MN998020	MN999691	MN997850
Taia sp. ZMB 113660-7 MMR			20.60750	96.90350	MN998021	MN999692	MN997851
Taia sp. ZMB 113660-8 MMR			20.60750	96.90350	MN998022	MN999693	MN997852
Taia sp. ZMB 113660-9 MMR			20.60750	96.90350	MN998023	MN999694	MN997853
Tchangmargarya yangtsunghaiensis GB CHN	Tchangmargarya_yangtsunghaiensis	D	24.90944	103.00444	KJ636773	KJ867100	N.A.
Torotaia cf. gilliana UGSB 18385 Lanao	Torotaia_cf_gilliana	H	7.87518	124.18552	MH319885	MN999695	MN997854
Torotaia cf. *lanaonis* UGSB 18372 Lanao	Torotaia_cf_lanaonis	H	7.80100	124.19423	MH319881	MN999696	MN997855
Torotaia cf. *lanaonis* UGSB 18377 Lanao			7.80100	124.19423	MH319883	MN999697	MN997856
Torotaia cf. *lanaonis* UGSB 18387 Lanao			7.87518	124.18552	MH319886	MN999698	MN997857
Torotaia cf. *lanaonis* UGSB 18399 Lanao			7.79040	124.27493	MH319891	MN999699	MN997858
Torotaia cf. *mainitensis* ZMB 230165-1 Mindanao	Torotaia_cf_mainitensis	H	9.34755	125.52062	MH319896	MN999700	MN997859
Torotaia cf. *mearnsi* UGSB 18390 Lanao	Torotaia_cf_mearnsi	H	7.93712	124.23564	MH319887	MN999701	MN997860
Torotaia cf. *mearnsi* UGSB 18391 Lanao			7.93712	124.23564	MH319888	MN999702	MN997861
Torotaia cf. *mindanensis* UGSB 18380 Lanao	Torotaia_cf_mindanensis	H	7.83259	124.15815	MH319884	MN999703	MN997862
Trochotaia trochoides ZMB 113179-1 THA	Trochotaia_trochoides	F	15.16100	104.29950	MN998024	MN999704	MN997863
Tulotoma magnifica USNM 1292584 USA	Tulotoma_magnifica	A	32.86556	-86.32556	MN998025	MN999705	MN997864
Tulotoma magnifica USNM 1292586 USA		A	33.42889	-86.35278	MN998026	MN999706	MN997865
Viviparus ater GB CHE	Viviparus_ater	C	47.31667	8.58333	FJ405882	FJ405630	FJ405774
Viviparus cf. *contectus* GB MKD	Viviparus_cf_contectus	C	41.10222	20.80222	KY574011	KY574003	KY574019
Viviparus georgianus USNM 1292587 USA	Viviparus_georgianus	A	34.07306	-87.07306	MN998027	MN999707	MN997866
Viviparus subpurpureus USNM 1292588 USA	Viviparus_subpurpureus	A	34.75833	-87.81306	N.A.	MN999708	MN997867
Viviparus viviparus GB DEU	Viviparus_viviparus	C	52.84167	14.11583	KY574013	KY574005	KY574021

TABLE S2. Main sequencing information for all COI sequences that were obtained by amplicon sequencing on a Roche 454 GS FLX Titanium platform as indiciated with an asterisk in Table S1 (see main text for details).

Taxon/Specimen (incl. collection number)	**Number or reads**	**Coverage**
Angulyagra costata ZMB113429-1 Cebu	55	15-55
Anularya bicostata ZMB193469-1 CHN	54	7-51
Anularya mansuyi ZMB193466-3 CHN	68	15-65
Anularya mansuyi ZMB193467-1 CHN	14	4-14
Anularya mansuyi ZMB193467-5 CHN	19	6-19
Celetaia persculpta ZMB192209a-1 Sulawesi	81	37-79
Cipangopaludina chinensis ZMB192694-1 KOR	174	35-75
Filopaludina filosa ZMB114012-1 THA	27	4-23
Filopaludina luzonica ZMB113438-1 Luzon	95	14-62
Filopaludina luzonica ZMB113439-1 Luzon	120	15-94
Filopaludina martensi ZMB113176-1 THA	14	5-13
Filopaludina martensi ZMB113178-2 LAO	36	16-34
Filopaludina martensi ZMB114019-1 THA	123	5-112
Filopaludina martensi ZMB114951-1 THA	33	6-32
Filopaludina sumatrensis ZMB113175-1 THA	23	7-22
Filopaludina sumatrensis ZMB114070-1 THA	17	1-17
Margarya melanioides ZMB193463-2 CHN	22	6-22
Margarya melanioides ZMB193463-8 CHN	16	5-16
Mekongia rattei ZMB114956-1 LAO	44	12-43
Mekongia rattei ZMB114958-1 LAO	25	5-24
Sinotaia quadrata ZMB113416-1 Luzon	52	6-51
Sinotaia quadrata ZMB113442-1 Luzon	66	7-58
Sinotaia quadrata ZMB192735-1 JPN	16	4-15
Sinotaia sp. ZMB193457-5 CHN	118	27-111

TABLE S3. Fossils used to calibrate the molecular phylogeny (see also 'Brief Discussion of Fossils not Used for Calibration' above).

Calibration point	**Fossil species**	**Locality Formation**	**Stratigraphic age (Myr)**	**Reference**
CP1	†*Viviparus langtonensis*	England, UK Inferior Oolite (Middle Jurassic, Bathonian)	174-166	Hudleston (1896); Tracey et al. (1993)
CP2	†*Campeloma harlowtonense*	Montana, USA Kootenai Formation (Early Cretaceous, Aptian)	121-112	Stanton (1903); Yen (1950)
CP3	†*Margarya nanningensis*	Guangxi, China Yongning Formation (Early? Oligocene)	30-25	Quan et al. (2016); Tian et al. (2018)
CP4	*Bellamya* cf. *unicolor*	Napak, Uganda Iriri Member (Early Miocene)	20-18.5	Pickford (2004)
CP5	†*Neothauma hattinghi*	Albertine Rift Valley, Uganda Kakara and Lower Oluka Formation (Middle/Late Miocene)	11-10	Van Damme and Pickford (1999)

TABLE S4. Synapomorphic shell features for the fossils used to calibrate the molecular phylogeny.

Calibration point	**Fossil species**	**Synapomorphic shell features**	**Reference**
CP1	†*Viviparus langtonensis*	Shells of Viviparidae possess a high shell spire and a thick periostracum and thus differ from those of Ampullariidae and Cyclophoridae (all belonging to the Architaenioglossa)	Simone (2004)
CP2	†*Campeloma harlowtonense*	Shells of Lioplacinae are thick and turreted with an outer lip being subangulated, sinuous or incurved at the base. In *Campeloma*, the outer lip of the aperture is nearly straight in lateral profile (as the fossil), whereas it is strongly sinuous in *Lioplax*	Gill (1863); Thompson (1999)
CP3	†*Margarya nanningensis*	Shells of *Margarya* have a produced, '*Melania*'-like spire, are composed of scalariform and rapidly increasing whorls and are sculptured with prominent spiral ribs (keels)	Nevill (1877)
CP4	*Bellamya* cf. *unicolor*	Protoconchs of *Bellamya* are pointed and carinated	Van Damme and Pickford (1999)
CP5	†*Neothauma hattinghi*	Protoconchs of *Neothauma* are smooth and obtuse	Van Damme and Pickford (1999)

TABLE S5. Comparison of divergence time estimates for the nodes corresponding to the five fossil calibration points obtained from the original and modified BEAST analyses using a reduced set of CPs. Grey-marked divergence times refer to nodes that were not fossil-constrained.

Fossil calibration point	Full set of CPs (CP1-CP5)	Reduced set of CPs (CP1 only)	Reduced set of CPs (CP3-CP5 only)
CP1 mean (95% HPD)	175.4 (166.0, 192.9) My	174.9 (166.0, 192.8)	155.6 (84.0, 239.2) My
CP2 mean (95% HPD)	121.2 (112.0, 137.9) My	101.1 (53.7, 147.2) My	99.2 (49.2, 164.2) My
CP3 mean (95% HPD)	27.0 (25.0, 31.0) My	8.9 (3.0, 16.7) My	26.9 (25.0, 30.7) My
CP4 mean (95% HPD)	20.6 (18.5, 24.3) My	24.8 (12.3, 40.0) My	20.4 (18.5, 24.0) My
CP5 mean (95% HPD)	12.4 (10.0, 15.7) My	12.1 (4.3, 21.2) My	12.3 (10.0, 15.4) My

TABLE S6. BIOGEOBEARS results table. Best-fit models are printed in bold. 'LnL' = log likelihood, 'Nparams' = number of parameters, 'd' = dispersal rate, 'e' = extinction rate (i.e., range contraction), 'j' = jump dispersal weights, 'AIC' = Akaike information criterion.

Analysis	Model	LnL	Nparams	d	e	j	AIC	ΔAIC
unconstrained	**DEC+J**	**-141.0**	**3**	**0.0005**	**0**	**0.0071**	**288.0**	**0**
	DIVALIKE+J	-142.2	3	0.0006	0	0.0081	290.4	2.4
	BayAreaLIKE+J	-146.8	3	0.0004	0	0.0122	299.6	11.6
	DEC	-148.0	2	0.0009	0.0008	0	300.0	12.0
	DIVALIKE	-151.3	2	0.0010	0	0	306.6	18.6
	BayAreaLIKE	-181.5	2	0.0008	0.0099	0	367.0	79.0
fossil-constrained	**DEC+J**	**-151.8**	**3**	**0.0006**	**0**	**0.0097**	**309.6**	**0**
	DIVALIKE+J	-152.8	3	0.0006	0	0.0098	311.6	2.0
	BayAreaLIKE+J	-153.3	3	0.0004	0	0.0138	312.6	3.0
	DIVALIKE	-162.8	2	0.0012	0.0015	0	329.6	20.0
	DEC	-172.5	2	0.0020	0.0110	0	349.0	39.4
	BayAreaLIKE	-194.9	2	0.0017	0.0114	0	393.8	84.2

TABLE S7. Standard shell parameters for each voucher specimen shown in Fig. S7 as well as shell and habitat type assigned to each OTU and fossil species used to time-calibrate the phylogeny. Shell types: A = 'sculpture absent', B = 'fine', C = 'coarse' including noduled spirals. Habitat type: 'Le' = lentic and 'Lo' = lotic.

Species (OTU)	**Height (mm)**	**Width (mm)**	**Width/height**	**Shell type**	**Habitat type**
Angulyagra_costata	31.6	25.6	0.81	B	Le/Lo[1]
Angulyagra_polyzonata	21.5	15.3	0.71	B	Le/Lo[1]
Anularya_bicostata	61.4	43.3	0.71	C	Le
Anularya_mansuyi	52.8	31.7	0.60	C	Le
Anulotaia_sp	12.2	11.0	0.90	B	Lo
Bellamya_cf_capillata_Congo	14.9	12.4	0.83	A	Lo
Bellamya_cf_capillata_Northern	25.2	18.0	0.71	A	Lo
Bellamya_cf_capillata_Okavango	17.0	13.7	0.81	A	Lo
Bellamya_cf_capillata_Southern	17.0	13.9	0.82	A	Lo
Bellamya_cf_capillata_Zambezi	18.0	13.8	0.77	A	Lo
Bellamya_cf_monardi_Northern	22.0	15.9	0.72	A	Lo
Bellamya_cf_unicolor_Victoria	8.0	6.8	0.85	A	Le
Bellamya_crawshayi_Mweru	21.5	16.4	0.76	B	Le
Bellamya_jucunda_Victoria	22.0	15.5	0.70	A	Le
Bellamya_monardi_Okavango	17.0	15.2	0.89	A	Lo
Bellamya_pagodiformis_Mweru	20.0	15.9	0.80	B	Le
Bellamya_robertsoni_Malawi	30.0	24.8	0.83	A	Le
Bellamya_rubicunda_Victoria	19.0	15.1	0.79	A	Le
Bellamya_trochlearis_Victoria	17.0	11.8	0.69	B	Le
Bellamya_unicolor_Victoria	17.0	12.5	0.74	A	Le
Campeloma_decampi	36.8	22.6	0.61	A	Lo
Campeloma_decisum	21.6	15.4	0.71	A	Lo
Campeloma_geniculum	18.7	14.1	0.75	A	Lo
Campeloma_limum	24.4	17.8	0.73	A	Lo
Campeloma_parthenum	42.8	28.0	0.65	A	Lo
Campeloma_regulae	19.6	13.8	0.70	A	Lo
Celetaia_persculpta	35.1	32.8	0.93	C	Le
Cipangopaludina_ussuriensis	45.5	33.7	0.74	B	Lo
Cipangopaludina_chinensis	52.6	39.3	0.75	A	Lo
Cipangopaludina_japonica	67.5	45.6	0.68	A	Lo
Cipangopaludina_wisseli	63.9	50.9	0.80	A	Le
Filopaludina_bengalensis	24.1	17.2	0.71	A	Lo
Filopaludina_decipiens_javanica	25.6	18.2	0.71	A	Le/Lo[1]
Filopaludina_doliaris	16.1	11.8	0.73	A	Le
Filopaludina_filosa	20.4	14.7	0.72	A	Lo
Filopaludina_javanica	24.8	18.3	0.74	A	Le/Lo[1]
Filopaludina_luzonica	29.1	21.6	0.74	B	Le
Filopaludina_martensi	33.7	28.4	0.84	B	Lo
Filopaludina_polygramma	20.7	15.8	0.76	A	Lo
Filopaludina_sumatrensis	18.6	13.9	0.75	A	Le/Lo[1]
Filopaludina_tricostata	27.5	20.0	0.73	B	Le
Heterogen_longispira	70.7	45.5	0.64	B	Le
Idiopoma_sp	22.0	15.9	0.72	A	Lo
Larina_cf_strangei	11.6	10.9	0.94	A	Lo
Larina_lirata	13.2	12.6	0.95	B	Lo
Lioplax_cyclostomaformis	19.0	12.3	0.65	A	Lo
Lioplax_subcarinata	19.1	12.8	0.67	A	Lo
Margarya_melanioides	48.0	32.0	0.67	C	Le
Margarya_oxytropoides	54.2	40.5	0.75	C	Le
Mekongia_rattei	24.0	18.0	0.75	A	Lo
Mekongia_sp	32.6	27.8	0.85	A	Lo
Neothauma_tanganyicense	26.2	22.0	0.84	A	Le
Notopala_ampullaroides	22.6	19.0	0.84	A	Lo
Notopala_essingtonensis	19.5	16.1	0.83	A	Lo
Notopala_sp1	20.4	16.9	0.83	A	Lo
Notopala_sp2	18.1	14.2	0.78	A	Lo
Rivularia_auriculata	24.2	16.5	0.68	A	Le
Sinotaia_aeruginosa	22.0	16.0	0.73	A	Le
Sinotaia_quadrata	29.2	18.6	0.64	A	Le/Lo[1]
Sinotaia_sp	25.9	16.9	0.65	B	Lo
Taia_sp	31.2	20.3	0.65	C	Le
Tchangmargarya_yangtsunghaiensis	50.2	34.6	0.69	C	Le
Torotaia_cf_gilliana	40.8	28.6	0.70	B	Le
Torotaia_cf_lanaonis	32.1	24.2	0.75	B	Le
Torotaia_cf_mainitensis	41.2	31.1	0.75	C	Le
Torotaia_cf_mearnsi	43.2	32.5	0.75	B	Le
Torotaia_cf_mindanensis	44.4	32.4	0.73	A	Le
Trochotaia_trochoides	19.9	21.7	1.09	B	Le
Tulotoma_magnifica	32.2	28.3	0.88	C	Lo
Viviparus_ater	37.0	27.6	0.75	A	Le
Viviparus_cf_contectus	32.0	26.0	0.81	A	Le
Viviparus_georgianus	22.8	20.3	0.89	A	Lo
Viviparus_subpurpureus	19.5	15.5	0.79	A	Lo
Viviparus_viviparus	36.2	26.7	0.74	A	Lo
†*Viviparus langtonensis* (CP1)	–	–	–	A	Le/Lo[2] | Le/Lo[2]
†*Campeloma harlowtonense* (CP2)	–	–	–	A	Le/Lo[2] | Lo[2]
†*Margarya nanningensis* (CP3)	–	–	–	C	Le/Lo[2] | Le[2]
Bellamya cf. *unicolor* (CP4)	–	–	–	A	Le/Lo[2] | Lo[2]
†*Neothauma hattinghi* (CP5)	–	–	–	B	Le/Lo[2] | Le/Lo[2]

[1] species found in both habitat types, [2] ambiguous; see also 'Remarks on Habitat Types for the Five Fossils Used to Time-Calibrate the Phylogeny' above.

TABLE S8. AIC comparison of shell-habitat estimation based on the transition models shown in Fig. S9. Model specifications: 'HabDep' = habitat-dependent, 'HabInd' = habitat-independent, 'Hab' = habitat transition rate, 'Shell' = shell transition rate, 'ARD' = all rates different, 'ER' = equal rates, and 'SYM' = symmetric rates.

Analysis	Model	LnL	Nparams	AIC	ΔAIC
unconstrained	**HabDep-Hab$_{ER}$-Shell$_{ARD}$**	**-97.7**	**13**	**221.4**	**0.0**
	HabDep-Hab$_{ARD}$-Shell$_{ARD}$	-97.1	14	222.2	0.8
	HabDep-Hab$_{ER}$-Shell$_{SYM}$	-104.9	7	223.9	2.5
	HabDep-Hab$_{ARD}$-Shell$_{SYM}$	-104.4	8	224.9	3.5
	HabInd-Hab$_{ER}$-Shell$_{ARD}$	-106.6	7	227.2	5.8
	HabInd-Hab$_{ARD}$-Shell$_{ARD}$	-105.8	8	227.5	6.1
	HabDep-Hab$_{ER}$-Shell$_{ER}$	-111.5	3	228.9	7.6
	HabDep-Hab$_{ARD}$-Shell$_{ER}$	-110.9	4	229.9	8.5
	HabInd-Hab$_{ER}$-Shell$_{SYM}$	-113.0	4	234.0	12.6
	HabInd-Hab$_{ARD}$-Shell$_{SYM}$	-112.1	5	234.3	12.9
	HabInd-Hab$_{ER}$-Shell$_{ER}$	-119.8	2	243.7	22.3
	HabInd-Hab$_{ARD}$-Shell$_{ER}$	-119.0	3	244.0	22.6
fossil-constrained	**HabDep-Hab$_{ER}$-Shell$_{ARD}$**	**-105.3**	**13**	**236.6**	**0.0**
	HabDep-Hab$_{ARD}$-Shell$_{ARD}$	-104.7	14	237.4	0.8
	HabInd-Hab$_{ER}$-Shell$_{ARD}$	-114.0	7	242.1	5.5
	HabInd-Hab$_{ARD}$-Shell$_{ARD}$	-113.2	8	242.5	5.9
	HabDep-Hab$_{ER}$-Shell$_{SYM}$	-114.8	7	243.6	7.0
	HabDep-Hab$_{ARD}$-Shell$_{SYM}$	-114.0	8	243.9	7.3
	HabDep-Hab$_{ARD}$-Shell$_{ER}$	-121.1	4	250.2	13.6
	HabDep-Hab$_{ER}$-Shell$_{ER}$	-122.1	3	250.2	13.6
	HabInd-Hab$_{ER}$-Shell$_{SYM}$	-123.9	4	255.8	19.2
	HabInd-Hab$_{ARD}$-Shell$_{SYM}$	-123.1	5	256.1	19.5
	HabInd-Hab$_{ER}$-Shell$_{ER}$	-131.1	2	266.3	29.7
	HabInd-Hab$_{ARD}$-Shell$_{ER}$	-130.3	3	266.6	30.0
fossil-constrained (uncertain habitats)	**HabDep-Hab$_{ER}$-Shell$_{ARD}$**	**-106.6**	**13**	**239.2**	**0.0**
	HabDep-Hab$_{ARD}$-Shell$_{ARD}$	-105.9	14	239.9	0.7
	HabInd-Hab$_{ER}$-Shell$_{ARD}$	-114.4	7	242.7	3.6
	HabInd-Hab$_{ARD}$-Shell$_{ARD}$	-113.5	8	243.0	3.9
	HabDep-Hab$_{ER}$-Shell$_{SYM}$	-116.0	7	246.0	6.9
	HabDep-Hab$_{ARD}$-Shell$_{SYM}$	-115.2	8	246.5	7.3
	HabDep-Hab$_{ER}$-Shell$_{ER}$	-123.3	3	252.5	13.3
	HabDep-Hab$_{ARD}$-Shell$_{ER}$	-122.4	4	252.7	13.6
	HabInd-Hab$_{ER}$-Shell$_{SYM}$	-124.2	4	256.4	17.2
	HabInd-Hab$_{ARD}$-Shell$_{SYM}$	-123.4	5	256.7	17.5
	HabInd-Hab$_{ER}$-Shell$_{ER}$	-131.4	2	266.9	27.7
	HabInd-Hab$_{ARD}$-Shell$_{ER}$	-130.6	3	267.2	28.0

TABLE S9. Transition rates obtained for the best-fit models (see Table S6 for details). Elevated transition rates are marked in grey, transition rates marked with a '–' were not allowed *a priori*. Character states: 'LeA' = lentic with shell type A ('absent'), 'LeB' = lentic with shell type B ('fine'), 'LeC' = lentic with shell type C ('coarse'), 'LoA' = lotic with shell type A, 'LoB' = lotic with shell type B, and 'LoC' = lotic with shell type C.

Analysis		Transition rates					
unconstrained		**LeA**	**LoA**	**LeB**	**LoB**	**LeC**	**LoC**
HabDep-Hab$_{ER}$-Shell$_{ARD}$	**LeA**	-7.39	0.04	**7.35**	–	0	–
	LoA	0.04	-0.05	–	0.01	–	0
	LeB	**8.78**	–	-8.88	0.04	0.06	–
	LoB	–	**0.13**	0.04	-0.17	–	0
	LeC	0	–	0.02	–	-0.06	0.04
	LoC	–	0	–	**0.28**	0.04	-0.32
fossil-constrained		**LeA**	**LoA**	**LeB**	**LoB**	**LeC**	**LoC**
HabDep-Hab$_{ER}$-Shell$_{ARD}$	**LeA**	-4.05	0.03	**4.02**	–	0	–
	LoA	0.03	-0.06	–	0.03	–	0
	LeB	**4.64**	–	-4.75	0.03	0.08	–
	LoB	–	**0.26**	0.03	-0.29	–	0
	LeC	0	–	0.03	–	-0.07	0.03
	LoC	–	0	–	**0.27**	0.03	-0.31
fossil-constrained (uncertain habitat)		**LeA**	**LoA**	**LeB**	**LoB**	**LeC**	**LoC**
HabDep-Hab$_{ER}$-Shell$_{ARD}$	**LeA**	-8.36	0.04	**8.32**	–	0	–
	LoA	0.04	-0.06	–	0.02	–	0
	LeB	**10.00***	–	-10.11	0.04	0.07	–
	LoB	–	**0.23**	0.04	-0.27	–	0
	LeC	0	–	0.03	–	-0.07	0.04
	LoC	–	0	–	**0.25**	0.04	-0.29

* Note that the maximum value for rates was fixed to 10 to fit the models in the fossil-constrained analyses.

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