**Appendices:**

**Appendix A:** Additional tables and figures from methods and results

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Figure A1: Map showing sampling locations of individual collected and amplified during the course of the study. Colors have to be used for this figure in print.



Figure A2: Results of divergence dating analysis and ancestral range estimation using DIVALIKE+*j* model following PTP analysis. Discrete areas are color coded as shown in the map. Most probable range inheritance scenarios are mapped on the tree as colored circles. Tips represent the present distribution of extant taxa included in the analysis. Multiple colored areas stand for distribution across different subdivisions. Colors have to be used for this figure in print. The horizontal bars at the nodes of the phylogeny represent 95% HPD of the divergence dates at respective nodes. The numbers next to node refer to node numbers in Appendix A Table A6. Colors have to be used for this figure in print.

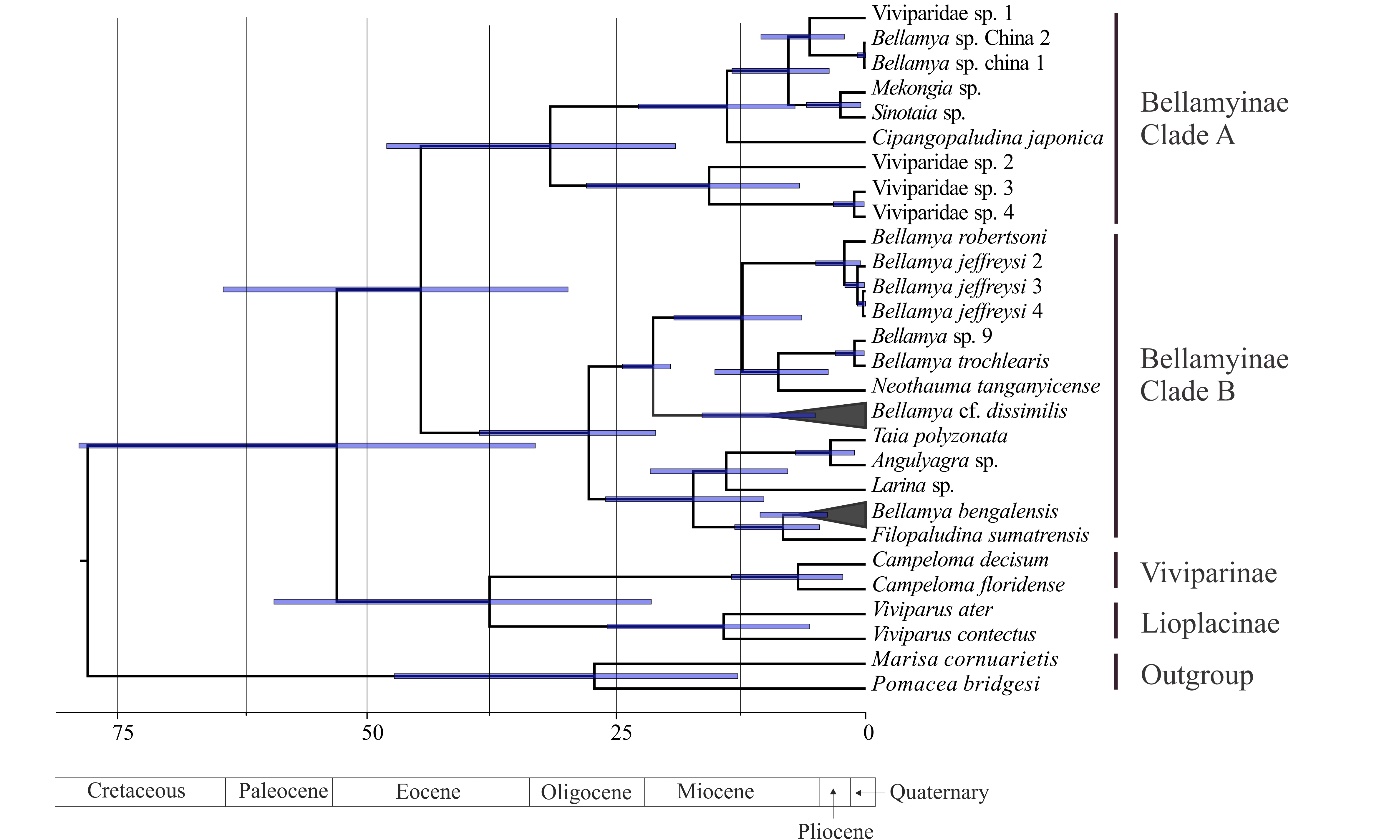


Figure A3: Results of divergence dating analysis using the dataset excluding ambiguous regions in noncoding genes. The horizontal bars at the nodes of the phylogeny represent 95% HPD of the divergence dates at respective nodes.

Table A1: A list of specimens from India used in the study with the sampling location

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species and individuals | Biogeographic subregion | Sample ID | Location | COI | 16S rRNA | 18S rRNA | 28S rRNA | Histone H3 |
| *Bellamya bengalensis* 1 | IS | CES151289.1 | Bhavanisagar | # | # | # | # | # |
| *Bellamya bengalensis* 2 | IS | CES 151222.2 | Mirzapur | # | # | # | # | # |
| *Bellamya bengalensis* 3 | IS | CES 151252.2 | Swaimadhopur | # | # | # | # | # |
| *Bellamya bengalensis* 4 | IS | CES 16383.1 | Barwani | # | # | # | # | # |
| *Bellamya bengalensis* 5 | IS | CES 151115.1 | Krishnagiri | # | # | # | # | # |
| *Bellamya bengalensis 6* | IS | CES 151180.1 | Adilabad | # | # | # | # | # |
| *Bellamya bengalensis 7* | SEA | CES 16543.1 | Meleng | # | # | # | # | # |
| *Bellamya bengalensis 8* | IS | M56 | Aurangabad | # | # | # | # | # |
| *Bellamya bengalensis 9* | IS | ARS2 | Singampatti | # | # | # | # | # |
| *Bellamya bengalensis 10* | SEA | 43 | Imphal | # | # | # | # | # |
| *Bellamya bengalensis 11* | SEA | Chun2 | Kohima | # | # | # | # | # |
| *Bellamya bengalensis 12* | SEA | Chun3 | Kohima | # | # | # | # | # |
| *Bellamya* cf*. dissimilis 1* | IS | S.Sen | Coorg | # | # | # | # | # |
| *Bellamya* cf. *dissimilis 2* | IS | CES 151209.2 | Mirzapur | # | # | # | # | # |
| *Bellamya* cf. *dissimilis 3* | IS | CES 16321.1 | Baripada | # | # | # | # | # |
| *Bellamya* cf. *dissimilis 4* | IS | CES 16389.1 | Mangod | # | # | # | # | # |
| *Bellamya* cf. *dissimilis 5* | IS | CES 16516.1 | Pandharpur | # | # | # | # | # |
| *Bellamya* cf. *dissimilis 6* | IS | 16523.1 | Beed | # | # | # | # | # |
| *Bellamya* cf. *dissimilis 7* | IS | CES 16531.1 | Nagpur | # | # | # | # | # |
| *Bellamya* cf. *dissimilis 8* | SEA | CES 16559.1 | Meleng | # | # | # | # | # |
| *Bellamya* cf. *dissimilis 9* | IS | ARK1 | Konaje | # | # | # | # | # |
| *Bellamya* cf. *dissimilis 10* | IS | ARS1 | Singmpatti | # | # | # | # | # |
| Viviparidae sp. 3 | SEA | Chun1 | Kohima | # | # | # | # | # |
| Viviparidae sp. 4 | SEA | ARM1 | S. Vanlaiphai | # | # | # | # | # |

# sequences are yet to be submitted

Table A2: Sequences downloaded from genebank with accession numbers.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Species | Country | COI | 16S | 18S | 28S | H3 |
| Species distributed in SEA and IS | | | | | | |
| *Bellamya bengalensis* | India | FJ405822 | FJ405724 | FJ405677 | FJ405622 | FJ405766 |
| Species distributed in SEA | | | | | | |
| *Angulyagra* sp | Vietnam | FJ405819 | FJ405723 | FJ405675 | FJ405628 | FJ405769 |
| *Bellamya* sp. | China | FJ405824 | FJ405725 | - | - |  |
| *Bellamya* sp. | China | FJ405826 | FJ405726 | - | - | FJ405776 |
| *Cipangopaludina japonica* | USA\* | FJ405821 | FJ405736 | FJ405639 | FJ405621 | FJ405777 |
| *Filopaludina sumatrensis* | Singapore | FJ405834 | - | - | FJ405633 | FJ405770 |
| *Larina* sp. | Australia | FJ405829 | FJ405733 | FJ405681 | FJ405626 | FJ405764 |
| *Mekongia* sp. | Vietnam | FJ405820 | FJ405722 | FJ405676 |  | FJ405767 |
| *Sinotaia* sp. | Vietnam | FJ405832 | FJ405728 | FJ405688 | FJ405631 | FJ405768 |
| Taia polyzonata | Singapore | FJ405833 | FJ405727 | FJ405679 | FJ405632 | FJ405771 |
| Viviparidae sp. 1 | China | FJ405831 | FJ405729 | FJ405687 | FJ405629 | - |
| Viviparidae sp. 2 | China | FJ405825 | FJ405730 | FJ405686 | - | FJ405775 |
| Species distributed in Africa | | | | | | |
| *Bellamya* sp. 9 | Uganda | FJ405790 | FJ405703 | FJ405652 | FJ405611 | FJ405740 |
| *Bellamya jeffreysi* 2 | Tanzania | FJ405804 | FJ405702 | FJ405656 | FJ405583 | FJ405761 |
| *Bellamya jeffreysi* 3 | Tanzania | FJ405812 | FJ405700 | FJ405654 | FJ405584 | FJ405762 |
| *Bellamya jeffreysi* 4 | Tanzania | FJ405806 | FJ405701 | FJ405651 | FJ405585 | FJ405763 |
| *Bellamya robertsoni* | Malawi | FJ405802 | - | FJ405638 | FJ405581 | FJ405747 |
| *Bellamya trochlearis* | Uganda | FJ405816 | FJ405691 | FJ405637 | FJ405603 | FJ405741 |
| *Neothauma tanganyicense* | Zambia | FJ405788 | FJ405709 | FJ405643 | FJ405598 | FJ405739 |
| Species distributed in the holarctic region | | | | | | |
| *Viviparus ater* | Switzerland | FJ405830 | FJ405734 | FJ405683 | FJ405630 | FJ405774 |
| *Viviparus contectus* | Denmark | FJ405778 | FJ405692 | FJ405635 | FJ405634 | FJ405737 |
| *Campeloma floridens* | USA | FJ405827 | FJ405731 | FJ405684 | FJ405624 | FJ405772 |
| *Campeloma decisum* | USA | FJ405828 | FJ405732 | FJ405680 | FJ405625 | FJ405773 |
| Outgroup | | | | | | |
| *Marisa cornuarietis* | South America | FJ439657 | EU274493 | EU274545 | EU274527 | EU274511 |
| *Pomacea bridgesii* | South America | FJ439658 | EU274500 | EU274553 | EU274532 | EU274514 |

\**Cipangopaludina japonica* is introduced to the USA.

- No information can be found

Table A3: Partition schemes and models of sequence of evolution used for different analyses

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| RAxML | | MrBayes | | Beast | |
| partitions | models | partitions | models | partitions | models |
| 18S rRNA | GTR+I | 18S rRNA | JC | 18S rRNA, 28S rRNA | TrNef+G |
| H3 codon position 1, H3 codon position 2, COI codon position 2 | GTR+I | H3 codon position 1, H3 codon position 2, COI codon position 2 | JC | H3 codon position 1, H3 codon position 2, COI codon position 2 | K80 |
| H3 codon position 3 | GTR+I | H3 codon position 3 | HKY+G | H3 codon position 3 | HKY+G |
| 16S rRNA | GTR+I | 16S rRNA | GTR+G | 16S rRNA | GTR+G |
| 28S rRNA, COI codon position 1 | GTR+I | 28S rRNA, COI codon position 1 | GTR+G | COI codon position 1 | TrNef+I |
| COI codon position 3 | GTR+I | COI codon position 3 | HKY+I+G | COI codon position 3 | HKY+I+G |

Table A4: Results of species delimitation analysis:

|  |  |  |  |
| --- | --- | --- | --- |
| Method | Species | individuals | Support |
| PTP | Species 1 | *B. bengalensis* 2, *B. bengalensis* 3, *B. bengalensis* 4, *B. bengalensis* 5, *B. bengalensis* 8 | 0.36 |
| Species 2 | *B. bengalensis* 12 | 0.89 |
| Species 3 | *B. bengalensis* 1 | 0.74 |
| Species 4 | *B. bengalensis* 7 | 0.42 |
| Species 5 | *B. bengalensis* 10 | 0.42 |
| Species 6 | *B. bengalensis* 5, *B. bengalensis* 9 | 0.58 |
| Species 7 | *B. bengalensis* 11 | 0.69 |
| Species 8 | *B. bengalensis* (from Sengupta et al., 2009; see Table A2) | 0.69 |
|  | | | |
| PTP | Species 1 | *Bellamya* cf. *dissimilis* 3 | 0.88 |
| Species 2 | *Bellamya* cf. *dissimilis* 2, *Bellamya* cf. *dissimilis* 4, *Bellamya* cf. *dissimilis* 7 | 0.58 |
| Species 3 | *Bellamya* cf. *dissimilis* 5, *Bellamya* cf. *dissimilis* 6 | 0.59 |
| Species 4 | *Bellamya* cf. *dissimilis* 1, *Bellamya* cf. *dissimilis* 9 | 0.35 |
| Species 5 | *Bellamya* cf. *dissimilis* 8 | 0.7 |
| Species 6 | *Bellamya* cf. *dissimilis* 10 | 0.81 |

Table A5: Model comparison for BioGeoBears analyses; significant P values, the highest log Likelihood score, the best AIC score, and the respective model are shown in bold:

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Alternative | Null | Alt Likelihood | Null likelihood | Alt AIC | Null AIC | P value |
| BioGeoBears analyses following mPTP results | | | | | | |
| DEC+J | DEC | -26.6 | -30.18 | 59.16 | 64.36 | **0.0074** |
| **DIVALIKE+J** | DIVALIKE | **-24.64** | -25.82 | **55.27** | 55.65 | 0.12 |
| BAYAREALIKE+J | BAYAREALIKE | -27.55 | -36.75 | 66.11 | 77.52 | **1.8e-05** |
| BioGeoBears analyses following PTP results | | | | | | |
| DEC+J | DEC | -35.71 | -52.4 | 77.41 | 108.9 | **7.1e-09** |
| **DIVALIKE+J** | DIVALIKE | **-34.78** | -47.47 | **75.56** | 98.94 | **4.7e-07** |
| BAYAREALIKE+J | BAYAREALIKE | -36.83 | -70.79 | 79.67 | 145.6 | **1.7e-16** |

Table A6: Probability of the estimated ranges at relevant nodes:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Node | Highest probability | Range | Second highest probability | Range |
| BioGeoBears analyses following mPTP results | | | | |
| 1 | SEA | 0.98 | SEA-IS | 0.009 |
| 2 | SEA | 0.78 | SEA-IS | 0.20 |
| 3 | SEA-IS | 0.66 | IS | 0.14 |
| 4 | SEA | 0.98 | SEA-IS | 0.018 |
| BioGeoBears analyses following PTP | | | | |
| 1 | SEA | 0.92 | India | 0.05 |
| 2 | SEA | 0.87 | India | 0.12 |
| 3 | India | 0.98 | Africa | 0.0095 |
| 4 | India | 0.94 | SEA | 0.06 |
| 5 | SEA | 0.73 | India | 0.26 |
| 6 | SEA | 0.72 | India | 0.28 |
| 7 | India | 0.50 | SEA | 0.49 |
| 8 | India | 0.50 | SEA | 0.49 |
| 9 | India | 0.75 | SEA | 0.25 |
| 10 | India | 0.71 | SEA | 0.29 |
| 11 | SEA | 1 | India | 1.15e-24 |

**Appendix B: Details on usage of fossil calibrations**

1. The oldest *Bellamya bengalensis* fossil, unearthed from the late Pliocene deposits in Jammu (Kundal, 2013), was used to calibrate the stem lineage of *B. bengalensis*. There are reports of *B. bengalensis* fossils from contemporary or slightly younger deposits from elsewhere in the IS such as Chandigarh (Bhatia & Mathur, 1973), Saketi (Mathur, 1998), Narmada valley (Prashad, 1928). Thus, it can be safely assumed that this lineage existed in IS at that specific period. A lognormal calibration with an offset of 2.2 mya was used because the lineage could not be younger than the age of the fossil (Ho and Phillips, 2009). The stem lineage was calibrated instead of the crown because the stem lineage might have existed much before the extant crown lineages started diversifying and the fossil could have belonged to any point in the stem lineage from the split from its sister group to the beginning of diversification in the crown. Calibrating the stem will make sure all these uncertainties will be taken into consideration. To allow for the uncertainty in time estimate of the age of the stem lineage the prior was given a broad enough range (2.2–8 mya). The upper age is based on a previous dating attempt that the authors have undertaken using the substitution rate of the COI gene.
2. The oldest African Bellamyinid fossil, unearthed from the Iriri member of the Napak formation and is dated to early Miocene (~19 mya) (Pickford, 2004). A previous study on African Viviparids used this fossil to calibrate the root node of the phylogeny consisting of African Bellamyinid species (Schultheib et al., 2014). Here we used the same logic as before that the African lineage cannot be younger than 19 mya, and the fossil can belong to the stem lineage instead of the crown. Hence, we calibrated the stem African lineage with a lognormal prior and the offset was placed at 19 mya. The upper age of the distribution was 40 mya: the time when Africa collided with Eurasia (Van Yperen et al., 2005).

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