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Arni Sholihah, Erwan Delrieu-trottin, Tedjo Sukmono, Hadi Dahruddin, Juliette Pouzadoux, et al.. Limited dispersal and in situ diversification drive the evolutionary history of Rasborinae fishes in Sundaland. *Journal of Biogeography*, 2021, 48 (9), pp.2153-2173. 10.1111/jbi.14141 . hal-03370830

HAL Id: hal-03370830

<https://hal.science/hal-03370830v1>

Submitted on 17 Nov 2021

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1 **Research article: Limited dispersal and *in situ* diversification drive the evolutionary**
2 **history of Rasborinae fishes in Sundaland**

3

4 **Running title: Diversification of Sundaland's Rasborinae**

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31 **Funding information:**

32 This study was supported by IRD through annual allocations (2012-2020) and incentive funds
33 (2012-2013), the Ministry of Foreign Affairs and International Development through a BIO-
34 Asia grant (BIOSHOT 2016-2017) managed by Campus France, the “Institut Français

35 d'Indonésie” through a “Science et impacts” grant (2016-5758) and the European
36 Commission through a grant from the Southeast Asia – Europe Joint Funding scheme for
37 Research and Innovation program (FRESHBIO, 307943/00). AS benefited from a PhD
38 scholarship from the Indonesian Endowment Fund for Education (LPDP). The Indonesian
39 ministry of research and technology approved this study.
40

41 **Abstract**

42 **Aim:** Sea level changes have long been put forward to explain the colonization of Southeast
43 Asian islands by freshwater aquatic organisms. We examined the relative impact of
44 Sundaland geology since the Oligocene and of Pleistocene Eustatic Fluctuations on the
45 mitochondrial lineage diversification of a species-rich subfamily of freshwater fishes widely
46 distributed in Southeast Asia. We specifically tested if the expansion of exposed lands and
47 increased island connectivity during Pleistocene low sea levels (the Paleoriver hypothesis)
48 induced bursts of diversification.

49 **Location:** Sundaland

50 **Taxon:** Rasborinae (Actinopterygii, Cypriniformes, Danionidae)

51 **Methods:** We aggregated 1,017 cytochrome oxidase I sequences and 79 mitogenomes to
52 delineate Molecular Operational Taxonomic Units (MOTUs) and further reconstruct a time-
53 calibrated phylogeny of Rasborinae. Ancestral area estimations were conducted using both
54 island and paleoriver partitioning to examine the impact of island connectivity during
55 Pleistocene sea level changes on dispersal. Temporal trends of diversification are explored
56 through statistical selection of best-fit models.

57 **Results:** The origin of Sundaland mitochondrial lineages is dated at ca. 33 Ma and four major
58 clades are identified, which diversified between ca. 31 and 22 Ma. The Island of Borneo and
59 North Sunda paleoriver are identified as the source of Sundaland Rasborinae. Geographical
60 patterns of lineage divergence indicate that most divergence events occurred within islands
61 and diversification under constant birth rate models are the most likely for all clades.

62 **Conclusions:** The geographical and historical context of diversification of mitochondrial
63 lineages in Rasborinae provides little support for the Paleoriver Hypothesis. The onset of
64 isolation of Borneo from mainland Asia triggered the initial diversification of the group (ca.
65 31-22 Ma). The late colonization of Java and Sumatra occurred through several independent
66 dispersal events, poorly explained by Pleistocene sea level changes, and frequently followed
67 by *in situ* diversification.

68

69 **KEYWORDS**

70 Ancestral areas estimation, Cryptic diversity, Dispersal pathways, Diversification models,
71 Historical biogeography, Mitogenomes, Pleistocene climatic fluctuations, Phylogenetic
72 reconstructions, Sea levels.

73

74 1. INTRODUCTION

75 Sundaland has long attracted the attention of evolutionary biologists. From his
76 observations in the 19th century, Alfred Wallace already deduced the biological uniqueness of
77 the “Indo-Malay Islands” compared to neighbouring continental Asia and Celebes (Wallace,
78 1869). It is now acknowledged that Sundaland’s diversity and endemism occur in an area
79 where the geological history is intricate (Hall, 2009, 2013; Lohman et al., 2011). Including
80 the Malay Peninsula and the islands of Borneo, Sumatra, Java and Bali, Sundaland emerged
81 since the Paleocene, ca. 60 million years ago (Ma), until the middle Oligocene ca. 30 Ma, as a
82 promontory at the southern end of Eurasia (Fig. 1A). Complex tectonic movements during
83 the Miocene triggered the formation of Borneo between 20 and 10 Ma (Figs. 1B & 1C) and
84 the subsequent emergence of Sumatra and Java between 10 and 5 Ma (Figs. 1C & 1D).
85 Insular Sundaland remained partially connected until entering the Pliocene (5.33-2.58 Ma).
86 Upon entering early Quaternary (2.6 Ma), Pleistocene Climatic Fluctuations (PCFs) led to
87 global variations of average temperature (Westerhold et al., 2020; Zachos, Dickens, & Zeebe,
88 2008) and sea levels (Miller et al., 2005). Geology and Pleistocene eustasy interacted in
89 Sundaland (Husson, Boucher, Sarr, Sepulchre, & Cahyarini, 2020; Sarr, Sepulchre, &
90 Husson, 2019; Sathiamurthy & Voris, 2006; Voris, 2000; Woodruff, 2010). During
91 Pleistocene glacial periods, sea level dropped between -60m and -120m and created
92 connections between Sundaland’s islands (Fig. 1D). These exposed land areas likely had
93 freshwater drainage systems that extended between modern islands, and this is central to the
94 Palaeoriver Hypothesis with respect to fish species dispersal (Kottelat, Whitten, Kartikasari,
95 & Wirjoatmodjo, 1993; Voris, 2000). Four major paleorivers occurred in Southeast Asia: (1)
96 East Sunda, (2) North Sunda, (3) Malacca straits, and (4) Siam (Fig. 1D). These paleorivers
97 likely impacted the dispersal of Sundaland’s freshwater biotas and their evolutionary history
98 (de Bruyn et al., 2013).

99 A high proportion of Sundaland contemporary freshwater diversity corresponds to
100 cryptic lineages with Pleistocene origins (Dahrudin et al., 2017; de Bruyn et al., 2014;
101 Hubert, Kadarusman, et al., 2015; Hubert et al., 2019; Hutama et al., 2017; Kusuma,
102 Ratmuangkhwang, & Kumazawa, 2016; Farhana et al., 2018; Sholihah et al., 2021, 2020).
103 Several studies detected congruence between the distribution of some freshwater lineages and
104 the boundaries of paleoriver watersheds (Beck et al., 2017; de Bruyn et al., 2013; Dodson,
105 Colombani, & Ng, 1995; Tan, Jamsari, & Siti Azizah, 2012). The timing of speciation across
106 clades during the Pleistocene indicates that PCFs may have triggered bursts of species
107 proliferation in Sundaland through sea level changes (Fig. 2), a mechanism already suggested

108 in other areas (Barraclough & Nee, 2001; Cannon, Morley, & Bush, 2009; Condamine et al.,
109 2015; Hubert & Renno, 2006; Mittelbach et al., 2007; Nores, 1999; Wiens & Donoghue,
110 2004). Nevertheless, other factors likely contributed to the build-up of Sundaland diversity,
111 including: (1) pre-Pleistocene geology (Beck et al., 2017; Condamine, Toussaint, et al., 2013;
112 de Bruyn et al., 2014; Dodson et al., 1995); (2) dynamic interactions between insular and
113 paleoriver watershed boundaries (Brown et al., 2013; Esselstyn & Brown, 2009;
114 Papadopoulou & Knowles, 2015a, 2015b; Sholihah et al., 2021); (3) varying dispersal
115 abilities as a consequence of life history traits influencing abilities to colonize novel
116 environments, and pass biotic and abiotic filters (Beck et al., 2017; Esselstyn, Timm, &
117 Brown, 2009; Hubert, Calcagno, Etienne, & Mouquet, 2015; Logue, Mouquet, Hannes,
118 Hillebrand, et al., 2011; Patel, Weckstein, Patane, Bates, & Aleixo, 2011; Pouyaud, Sudarto,
119 & Paradis, 2009); and (4) habitat rearrangements during PCFs (Bird, Taylor, & Hunt, 2005;
120 Heaney, 1992; Wurster, Rifai, Zhou, Haig, & Bird, 2019). By contrast to the Last Glacial
121 Maximum (LGM) ca. 17,000 years ago, which housed the maximal extension of paleoriver
122 watersheds, Sundaland is currently considered in a refugial state. This statement underlines
123 the importance to understand the impact of PCFs on diversity patterns in Sundaland for
124 effective conservation efforts. Sundaland is one of the most threatened biodiversity hotspots
125 in Southeast Asia, (Hoffmann et al., 2010; Mittermeier, Turner, Larsen, Brooks, & Gascon,
126 2011; Myers, Mittermeier, Mittermeier, da Fonseca, & Kent, 2000), mostly due to its
127 alarming rate of deforestation during the last decades (Gaveau et al., 2014; Imai, Furukawa,
128 Tsujino, Kitamura, & Yumoto, 2018; Laumonier et al., 2010), in conjunction with water
129 contamination (Garg, Hamilton, Hochard, Kresch, & Talbot, 2018) and watershed
130 fragmentation through the development of dams for irrigation and hydroelectric powerplants
131 (Mulligan, van Soesbergen, & Sáenz, 2020).

132 Freshwater fishes are tightly dependent of watershed dynamics and constitute model
133 systems to trace historical watershed dynamics (Bernatchez & Wilson, 1998; de Bruyn et al.,
134 2013; Durand, Persat, & Bouvet, 1999; Hubert et al., 2007). Sundaland hosts several species-
135 rich groups that are particularly suited to explore the consequences of PCFs on freshwater
136 diversity patterns (Hubert, Kadarusman, et al., 2015). One of these groups is the Rasborinae
137 (Cypriniformes, Danionidae), a subfamily of iconic and highly diversified, small-size species
138 widely distributed in Sundaland (Brittan, 1972; Dahrudin et al., 2017; Hubert et al., 2019;
139 Kusuma et al., 2016; Liao, Kullander, & Fang, 2011; Sholihah et al., 2020; Tan &
140 Armbruster, 2018). Rasborinae comprises eleven genera variously distributed in Asia, of
141 which seven are endemic of Sundaland or much more diverse here than in adjacent areas

142 (Sholihah et al., 2020). These include *Boraras*, *Brevibora*, *Kottelatia*, *Pectenocypris*,
143 *Rasbora*, *Trigonopoma* and *Trigonostigma* (Sholihah et al., 2020; Tan & Armbruster, 2018).
144 The systematics of the subfamily is still confused due to the lack of robust phylogenetic
145 hypothesis of intrarelationships (Brittan, 1972; Hui & Chian, 2020; Kottelat & Vidthayanon,
146 1993; Kottelat & Witte, 1999; Liao, Kullander, & Fang, 2010; Liao et al., 2011). However,
147 the monophyly of Rasborinae is supported by both molecular and morphological characters
148 (Saitoh et al., 2006; Stout, Tan, Lemmon, Lemmon, & Armbruster, 2016; M. Tan &
149 Armbruster, 2018; K. L. Tang et al., 2010). Rasborinae encompasses ca. 80 species in
150 Sundaland (Sholihah et al., 2020), representing ca. 75% of Rasborinae diversity (Eschmeyer,
151 Fricke, & van der Laan, 2018; Froese & Pauly, 2020). Recent genetic reappraisals of
152 Rasborinae species diversity in Sundaland confirmed species boundaries and distribution
153 ranges, along with the recognition of a substantial amount of cryptic diversity (Dahrudin et
154 al., 2017; Hubert et al., 2019; Sholihah et al., 2020). Most cryptic lineages identified have
155 very narrow, non-overlapping distribution ranges, suggesting landscape fragmentation mostly
156 contributed to generate this diversity (Sholihah et al., 2020). However, the origin and
157 underlying evolutionary dynamics of this diversity remain largely unexplored. In particular,
158 the historical connectivity between Sundaland and the continent during the isolation of
159 Borneo (ca. 20-30 Ma), and the subsequent emergence of Sumatra (ca. 20-10 Ma) and Java
160 (ca. 10-5 Ma), questions the dynamics of colonization of Sundaland by Rasborinae. Several
161 potential scenarios can be predicted, ranging from an origin through *in situ* lineage
162 proliferation initiated in Borneo after its isolation (ca. 20-30 Ma) to multiple immigrations
163 events from the continent during the emergence of Sundaland islands (ca. 30-5 Ma) (Sholihah
164 et al., 2021; Šlechtová, Musilova, Tan, Kottelat, & Bohlen, 2021).

165 Here, we explore the phylogenetic relationships of Sundaland's Rasborinae through
166 mitochondrial genome skimming (Dodsworth, 2015; Straub et al., 2012), with the aim to
167 examine the potential impacts of Sundaland geology and Pleistocene sea level changes on
168 mitochondrial lineage proliferation of this species-rich group. We addressed the following
169 questions: (1) Did Rasborinae diversify (a) through *in situ* radiation in Sundaland (i.e.
170 monophyly of Sundaland Rasborinae) once Borneo isolated from Mainland (ca. 30-20 Ma) or
171 (b) through multiple colonization events from Mainland followed by *in situ* diversification
172 (i.e. polyphyly of Sundaland lineages) during the emergence of Sundaland (ca. 30-5 Ma)? (2)
173 Did paleorivers serve as dispersal pathways between islands during Pleistocene low sea levels
174 and enabling the colonization of Sundaland islands? (3) Did paleoriver watersheds prompt
175 allopatric divergence across their boundaries? (4) Did PCF affect rates of mitochondrial

176 lineage diversification? Through a dense taxonomic, spatial and mitochondrial genomic
177 sampling, Rasborinae phylogenetic intrarelationships were inferred and mitochondrial
178 divergence events dated to explore dynamics of lineage proliferation through ancestral area
179 estimations and statistical selection of best-fit diversification models.

180

181 **2. MATERIALS AND METHODS**

182 **2.1 Analytical procedure and sampling**

183 The species diversity of the subfamily Rasborinae has been recently revisited in
184 Sundaland through standardized mitochondrial DNA-based approaches (Dahrudin et al.,
185 2017; Hubert et al., 2019; Sholihah et al., 2020). Here, the objective is to take advantage of
186 this updated cytochrome oxidase I (i.e. DNA barcode) reference library to explore the
187 Rasborinae intrarelationships and guide taxon sampling for further mitogenome skimming
188 (Dodsworth, 2015; Straub et al., 2012). As the earliest branching events and intrarelationships
189 are still unknown in Rasborinae (Brittan, 1972; Liao et al., 2010), mitogenomes were first
190 used to reconstruct a backbone phylogeny and identify major clades. Then, mitogenomes
191 were combined to all DNA barcodes available to reconstruct phylogenetic relationships
192 within each clade based on a dense taxon sampling. Sampling and collection management is
193 as described in Sholihah et al. (2020). Specimens were captured using gears such as
194 electrofishing, seine nets, cast nets and gill nets across sites that encompass the diversity of
195 freshwater lentic and lotic habitats in Sundaland (Fig. 1). Specimens were identified
196 following original descriptions where available, as well as monographs (Kottelat, 2013;
197 Kottelat et al., 1993) and further validated through DNA barcodes by including records from
198 type localities (Hubert et al., 2019; Sholihah et al., 2020). Species names were further
199 validated using several online catalogues (Eschmeyer et al., 2018; Froese & Pauly, 2020).
200 Specimens were photographed, individually labelled, and voucher specimens were preserved
201 in a 5% formalin solution. Prior to fixation a fin clip or a muscle biopsy was taken and fixed
202 separately in a 96% ethanol solution for further genetic analyses. Both tissues and voucher
203 specimens were deposited in the national collections at the Museum Zoologicum Bogoriense
204 (MZB), Research Center for Biology (RCB), and Indonesian Institute of Sciences (LIPI).

205

206 **2.2 Mitogenomes skimming**

207 Genomic DNA was extracted using a MINIPREP SIGMA extraction kit following
208 manufacturer's specifications. A 651-bp segment from the 5' region of the cytochrome
209 oxidase I gene (COI) was amplified as described in Sholihah et al. (2020). PCR

210 amplifications were done using the primers cocktails C_FishF1t1/C_FishR1t1 including M13
211 tails (Ivanova, Zemlak, Hanner, & Hébert, 2007) in a final volume of 10.0µl containing 5.0µl
212 Buffer 2X, 3.3µl ultrapure water, 1.0µl each primer (10µM), 0.2µl enzyme Phire Hot Start II
213 DNA polymerase (5U) and 0.5µl of DNA template (~50 ng). Amplifications were conducted
214 as followed: initial denaturation at 98°C for 5 min followed by 30 cycles denaturation at 98°C
215 for 5s, annealing at 56°C for 20s and extension at 72°C for 30s, followed by a final extension
216 step at 72°C for 5 min. The PCR products were purified with ExoSap-IT (USB Corporation,
217 Cleveland, OH, USA) and sequenced in both directions. The sequences and collateral
218 information are available in BOLD (Ratnasingham & Hebert, 2007) in the data set DS-
219 BIFRA (Table S1, dx.doi.org/10.5883/DS-BIFRA).

220 Genomic libraries for mitogenome skimming were prepared following the protocol
221 developed by Tilak et al. (2015) for multiplexed Illumina sequencing. Genomic DNA was
222 physically fragmented through ultrasound (35 kHz) for a duration varying between 10 and 20
223 min using an ultrasonic cleaning unit (Elmasonic One). We followed the Illumina library
224 preparation procedure with blunt-end repair, adapter ligation, adapter fill-in and indexing
225 PCR steps (13 cycles) developed by Meyer and Kircher (Meyer & Kircher, 2010). Each step
226 was followed by a purification using SPRI bead suspensions (Agencourt® AMPure® XP),
227 adding 1.7 volume of Agencourt® AMPure® XP reagent per volume of sample and eluted in
228 25µl of ultra-pure water. Quantification of DNA libraries was done with a Nanodrop ND-800
229 spectrophotometer (Nanodrop technologies). Indexed libraries were pooled using their
230 relative concentrations to ensure equimolarity and a single pool was single-read sequenced
231 (150 bp long reads) on Illumina HiSeq 2500 at MGX (Montpellier, France). Mitogenomes
232 were then assembled on Unipro UGENE (Okonechnikov et al., 2012) by reference to the
233 closest mitogenome available among the 10 Rasborinae mitogenomes available in GenBank.
234 Complete mitogenomes were then annotated using the online tool MitoAnnotator (Iwasaki et
235 al., 2013) available at mitofish.aori.u-tokyo.ac.jp. Annotated mitogenomes are accessible in
236 GenBank (Table S1).

237

238 **2.3 Reconstructing a backbone phylogeny of Rasborinae with mitogenomes**

239 The Most Recent Common Ancestor (MRCA) of Rasborinae has been previously
240 estimated at 43 Ma (Betancur-R et al., 2017). Thus, tRNAs and control region were trimmed
241 for phylogenetic reconstructions due to their fast substitution rates, and likely high levels of
242 homoplasy. Protein and ribosomal RNA (rRNA) coding regions were retained and

243 individually partitioned in subsequent phylogenetic reconstructions. First, a maximum
244 likelihood (ML) tree was reconstructed using a partitioned model for each protein and rRNA
245 coding regions with a GTR+I+ Γ model as implemented in RAxML-HPC Blackbox (Miller,
246 Pfeiffer, & Schwartz, 2010) with RAxML 8 (Stamatakis, 2014). Topological support was
247 estimated with 5,000 non-parametric bootstrap replicates. Second, a calibrated tree was
248 reconstructed using Bayesian inferences as implemented in BEAST 2.6.2 (Bouckaert et al.,
249 2014; Heled & Drummond, 2010). The most likely substitution models were jointly
250 determined for all partitions using ModelFinder (Kalyaanamoorthy, Minh, Wong, von
251 Haeseler, & Jermin, 2017) as implemented in the IQTREE online webserver (Nguyen,
252 Schmidt, Von Haeseler, & Minh, 2015) at <http://iqtree.cibiv.univie.ac.at>. The selected models
253 were further used to conduct a Bayesian partitioned analysis based on a Yule model (uniform
254 birth rate), relaxed clock with log normal distribution, and standardized site models as
255 implemented in the SSM package in BEAST 2.6.2. Two Monte Carlo Markov Chains
256 (MCMC) of 50 million generations (burnin of 10%) were conducted to check for
257 convergence and to check that ESS estimates reached 200 using Tracer 1.7.1 (Drummond,
258 Suchard, Xie, & Rambault, 2012). Two clock rates were jointly estimated for rRNA and
259 protein-coding regions along tree topology. MCMCs were initiated with a 0.3% of divergence
260 per million years (Myrs) for rRNA (Hardman & Lundberg, 2006; Orti, 1997) and 1.2% per
261 Myrs for protein-coding regions (Bermingham, McCafferty, & Martin, 1997). The two runs
262 were then combined with LogCombiner 2.6.2 (Bouckaert et al., 2014) and the maximum
263 clade credibility tree, median age estimates and corresponding 95% highest posterior density
264 (HPD) were summarized using TreeAnnotator 2.6.2 (Bouckaert et al., 2014). This analysis
265 was repeated with a birth-death model of diversification to assess the potential influence of
266 the branching process prior on divergence time estimates (Ritchie, Lo, & Ho, 2017). Both
267 ML and Bayesian inferences were rooted using an assortment of mitogenomes (Table S1)
268 available for several closely related subfamilies of Danionidae as well as other Cypriniformes
269 families following previously published phylogenetic hypotheses (Betancur-R et al., 2017;
270 Chang, Rabosky, Smith, & Alfaro, 2019; Rabosky et al., 2018; K. L. Tang et al., 2010).

271

272 **2.4 DNA barcodes, mitochondrial lineage delimitation and clade-specific** 273 **phylogenetic inferences**

274 Once major clades were identified within the subfamily, all DNA barcodes available
275 from previous studies were compiled (Table S1). DNA barcode sequences were selected
276 according to a preliminary screening of their phylogenetic affinities and robustness of the

277 phylogenetic inferences. A Neighbour Joining (NJ) was first reconstructed for the 1,097 DNA
278 barcodes from Sholihah et al. (2020) and branching support was estimated through 5,000
279 bootstrap replicates using PAUP 4.0a (Swofford, 2001). Only DNA barcode records related
280 to species with mitogenomes available, with bootstrap proportions (BP) above 80% were
281 retained. Genetic delimitation of species follows the protocol described in Sholihah et al.
282 (2020). Four different sequence-based methods of species delimitation were used to
283 delimitate Molecular Operational Taxonomic Units (MOTUs) (Blaxter et al., 2005) using the
284 1,097 DNA barcodes dataset. These methods were: (1) Refined Single Linkage (RESL) as
285 implemented in BOLD and used to generate Barcode Index Numbers (BIN) (Sujeewan
286 Ratnasingham & Hebert, 2013), (2) Automatic Barcode Gap Discovery (ABGD) (Puillandre,
287 Lambert, Brouillet, & Achaz, 2012), (3) Poisson Tree Process (PTP) in its multiple rates
288 version (mPTP) as implemented in the stand-alone software mptp_0.2.3 (Zhang, Kapli,
289 Pavlidis, & Stamatakis, 2013), and (4) General Mixed Yule-Coalescent (GMYC) in its
290 multiple rate version (mGMYC) as implemented in the R package ‘Splits’ 1.0-19 (Fujiwasa
291 & Barraclough, 2013). RESL and ABGD used DNA alignments as input files, while a ML
292 tree was used for mPTP and a Bayesian Chronogram based on a strict-clock model using a
293 1.2% of genetic distance per Myrs for mGMYC. The ML tree for mPTP was reconstructed
294 using RAxML 8 using a GTR+ Γ substitution model (Stamatakis, 2014) and the ultrametric
295 and fully resolved tree for mGMYC was reconstructed using BEAST 2.6.2 with two
296 independent Markov chains of 50 million generations each including a Yule pure birth model
297 tree prior, a strict-clock model and a GTR+I+ Γ substitution model. Both runs were combined
298 using LogCombiner 2.6.2 and the maximum clade credibility tree was constructed using
299 TreeAnnotator 2.6.2. Duplicated haplotypes were pruned for further species delimitation
300 analyses.

301 Once DNA barcodes were selected and MOTUs delimited, DNA barcode and
302 mitogenome alignments were concatenated for each of the major clades identified.
303 Phylogenetic relationships within clades were reconstructed using the Bayesian analysis
304 implemented in the StarBEAST2 package (Ogilvie, Bouckaert, & Drummond, 2017) from the
305 BEAST 2.6.2 suite (Bouckaert et al., 2014). This approach implements a mixed-model
306 including a coalescent component within MOTU and a diversification component between
307 MOTU that allows accounting for variations of substitution rates within and between MOTUs
308 (Ho & Larson, 2006; Ritchie et al., 2017). StarBEAST2 jointly reconstruct and optimize gene
309 trees and MOTU trees, and as such requires the designation of MOTUs, which were
310 determined using the majority rule consensus of the lineage delimitation analyses. After

311 preliminary analyses, phylogenetic reconstructions were conducted using a single partition
312 including rRNA and protein-coding regions, GTR+I+ Γ substitution model, uncorrelated log-
313 normal species tree model (UCLN), and MCMCs of 60 million generations. Age of each
314 clade MRCA estimated from the backbone phylogeny was used as a calibration point with a
315 normal distribution and a sigma of 1.0. Clock rate was estimated and an initial value of 0.8 %
316 of divergence per Myrs was used according to the initial BEAST 2.6.2 analysis of the
317 mitogenome dataset. Independent runs were combined using LogCombiner 2.6.2 (Bouckaert
318 et al., 2014). Gene and MOTU maximum clade credibility trees, median age estimates and
319 corresponding 95% HPD were summarized using TreeAnnotator 2.6.2 (Bouckaert et al.,
320 2014). All phylogenetic reconstructions were performed using CIPRES (Miller et al., 2010),
321 and phylogenetic trees and alignments have been deposited in Dryad
322 (doi.org/10.5061/dryad.tb2rbp00g).

323

324 **2.5 Diversification rates estimation**

325 Lineages through time (LTT) were plotted using the MOTU trees of each major
326 clades with the R-package ‘ape’ (Paradis & Schliep, 2019). Confidence intervals were
327 computed using 1,000 dated trees sampled along the StarBEAST2 MCMC. To test the impact
328 of past environmental dynamics on diversification, we relied on a ML framework with five
329 diversification models (constant-rate, time-dependent, temperature-dependent, sea-level-
330 dependent, and diversity-dependent models) and their variants (Condamine, Rolland, &
331 Morlon, 2019, 2013). In total, we fitted 17 diversification models (Table S2) using the R-
332 packages ‘RPANDA’ 1.3 (Morlon et al., 2016) and ‘DDD’ 3.7 (Etienne et al., 2012). We
333 accounted for potential missing lineages in the phylogeny in the form of global sampling
334 fraction, i.e. the ratio of sampled lineages diversity over the total described lineages, and ran
335 these analyses for sampling fractions of 100% and 90%. In ‘RPANDA’, we first fitted two
336 constant-rate models as initial references, namely: BCST (speciation rate constant through
337 time with no extinction) and BCSTDCST (speciation and extinction rates constant through
338 time). Second, we fitted four time-dependent models: BtimeVar (speciation rate varying
339 through time with no extinction), BtimeVarDCST (speciation rate varying through time with
340 constant extinction), BCSTDtimeVar (constant speciation and extinction rate varying through
341 time) and BtimeVarDtimeVar (both speciation and extinction rates varying through time).
342 Lastly, we fitted eight models with speciation and extinction rates varying according to
343 external environmental variables: BtemperatureVar and Bsea-levelVar (speciation varying in

344 function of the environmental variable), BtemperatureVarDCST and Bsea-levelVarDCST
345 (speciation varying in function of the variable with constant extinction rate),
346 BCSTDtemperatureVar and BCSTDsea-levelVar (extinction rate varying in function of the
347 variable and constant speciation rate) and BtemperatureVarDtemperatureVar and Bsea-
348 levelVarDsea-levelVar (both speciation and extinction rates varying in function of the
349 variable).

350 Exponential dependence with time, temperature or sea level and diversification rates
351 are chosen for its robustness and flexibility depending on the strength and direction of the
352 dependence to the fitted variable. Speciation (λ) and extinction (μ) rates are parameterized as
353 follows. When λ and μ are exponential functions of sea level (S) through time (t), the
354 equations are $\lambda(S_{(t)}) = \lambda_0 \times e^{\alpha S(t)}$ and $\mu(S_{(t)}) = \mu_0 \times e^{\beta S(t)}$, where λ_0 and μ_0 are
355 respectively the expected λ and μ at $S = 0$ meter, while α and β are coefficients that measure
356 the strength and the sign of the relationship with sea level (e.g. $\alpha > 0$ and $\beta > 0$ respectively
357 indicate λ and μ increase with sea level high stands). Similar parameterisation can be used for
358 exponential relationship between temperature (T) through time (t) and λ as well as μ rates in
359 which $\lambda(T_{(t)}) = \lambda_0 + \alpha T_{(t)}$ or $\lambda(T_{(t)}) = \lambda_0 \times e^{\alpha T(t)}$, where $T(t)$ is the temperature at time t
360 and λ_0 is speciation rate at $T = 0^\circ\text{C}$.

361 The last three diversity-dependent ML models were fitted using ‘DDD’ package in
362 which λ and μ vary as linear functions of number of lineages within each clade (Etienne et
363 al., 2012). The diversity-dependent models are parameterised by λ_0 , μ_0 (respectively
364 indicating λ and μ at the absence of competing lineage), K (carrying capacity, representing
365 asymptotic clade size). All λ and μ were constrained to be positive. The results were then
366 compiled with the previous 14 models in ‘RPANDA’ and all are compared using corrected
367 Akaike Information Criterion (AICc) and Akaike weights (AIC ω). The model with the lowest
368 AICc and highest AIC ω was considered as the best fitting model for the phylogeny.

369

370 **2.6 Ancestral areas estimation**

371 To explore dispersal and vicariance history based on the Paleoriver Hypothesis, we
372 reconstructed ancestral distribution of Sundaland Rasborinae using the R-package
373 ‘BioGeoBEARS’ 1.1.2 (Matzke, 2014; Matzke, 2013) based on the StarBEAST2 MOTU
374 trees. Species presence/absence were compiled (Table S1) for two sets of geographical
375 delimitation based on: (1) paleoriver and (2) contemporary island boundaries. Then,
376 geographical patterns of divergence were recorded as follows: (1) no dispersal, sister lineages

377 co-occur within the same paleoriver and the same island; (2) dispersal between islands within
378 a paleoriver, sister lineages are alternatively distributed on different islands within the same
379 paleoriver; (3) dispersal between paleorivers within the same island, sister lineages are
380 alternatively distributed on different paleorivers within the same islands; and (4) dispersal
381 between islands and between paleorivers, sister lineages are alternatively distributed on
382 different paleorivers and different islands. Ancestral area estimations involving paleorivers
383 were based on the following geographical areas (Fig. 1): (1) the Malacca Straits paleoriver,
384 (2) the East Sunda paleoriver, (3) the North Sunda paleoriver, (4) the Siam paleoriver, (5) the
385 Northern Borneo river system, and (6) the Mekong river system. On the other hand,
386 estimations based on insular delimitation followed geographical divisions of: (1) Sumatra-
387 Bangka-Belitung, (2) Java-Bali-Lombok, (3) Borneo, and (4) Mainland Southeast Asia. For
388 analytical requirements, only MOTUs with known localities that could be associated to both
389 islands and palaeodrainages were used.

390 Inferences of the ancestral areas using ‘BioGeoBEARS’ were conducted using six
391 alternative models including dispersal-extinction cladogenesis (DEC), DEC+J, dispersal-
392 vicariance analysis ML-version (DIVALIKE), DIVALIKE+J, Bayesian biogeographical
393 inference model (BAYAREALIKE) and BAYAREALIKE+J (Matzke, 2014; Van Dam &
394 Matzke, 2016). The inclusion of the parameter J has been recently criticized from a
395 conceptual and statistical perspective (Ree & Sanmartín, 2018). The concept of jumping
396 dispersal has been developed for insular systems to account for the settlement of a new
397 lineage established by colonization without an intermediate widespread ancestor (Clark et al.,
398 2008; Ree & Sanmartín, 2018). Considering the biogeographical scenario of Sundaland and
399 the insularity of the system, jumping dispersal cannot be discarded *a priori* from a conceptual
400 perspective and several studies have previously highlighted the importance of jumping
401 dispersal in insular systems (Beck et al., 2017; Condamine et al., 2015; Cowie & Holland,
402 2006; de Bruyn et al., 2013; Hendriks, Alciatore, Schilthuizen, & Etienne, 2019; Sholihah et
403 al., 2021). Models of ancestral area estimation including the J parameters were thus
404 considered here and the best-fit model was estimated using the AICc.

405

406 3. RESULTS

407 3.1 Mitogenomes skimming

408 Illumina sequencing yielded a number of reads ranging between 4.5 and 12 million
409 per genomic libraries. A total of 58 new mitogenomes were successfully assembled with a
410 minimum coverage of 10X for four genera including three *Brevibora*, one *Pectenocypris*, 45

411 *Rasbora* and seven *Trigonopoma*. Mitogenomes were ca. 16,500 bp long on average and
412 include the coding regions of two rRNA (12S, 16S), 22 tRNA, 13 protein-coding genes and
413 the Control Region (CR). In addition, 10 Rasborinae mitogenomes were retrieved from
414 GenBank including the genera *Amblypharyngodon*, *Horadandia*, *Rasboroides*, *Rasbora* and
415 *Boraras* (Table S1). These 10 mitogenomes were used as reference genomes for assembly
416 and further phylogenetic reconstructions. An additional set of 11 mitogenomes was retrieved
417 from GenBank of Danionidae subfamilies and Cypriniformes families, which were used as
418 outgroups (Table S1). For phylogenetic reconstruction, tRNA coding regions and CR were
419 trimmed. The final alignment included 79 mitogenomes and 13,898 bp consisting of 2,518 bp
420 of rRNA and the 13 protein-coding regions including ND1 (975 bp), ND2 (1,045 bp), COI
421 (1551 bp), COII (691 bp), ATP8 (1655 bp), ATP6 (673 bp), COIII (785 bp), ND3 (349 bp),
422 ND4L (297 bp), ND4 (1,375 bp), ND5 (1,822 bp), ND6 (518 bp), and Cytb (1,134 bp).

423

424 **3.2 Reconstructing the backbone phylogeny of Rasborinae**

425 Phylogenetic reconstructions based on the 79 mitogenomes are well supported with
426 most internal branching events displaying posterior probabilities (PP) of 100% for the
427 Bayesian inference (Fig. 3A) and Bootstrap Proportions (BP) above 90% for the ML
428 reconstruction (Fig. 3B). Bayesian and ML topologies are congruent with continental Asian
429 Rasborinae (*Amblypharingodon*, *Horadandia* and *Rasboroides*) corresponding to the earliest
430 branching events in Rasborinae tree and Sundaland lineages constituting a monophyletic
431 group (Fig. 3). Four major clades are identified within Sundaland: (1) Clade I including the
432 genera *Pectenocypris*, *Boraras*, *Trigonopoma* and *Rasbora kalbarensis*; (2) Clade II
433 including some *Rasbora* species; (3) Clade III including some *Rasbora* species; and (4) Clade
434 IV including some *Rasbora* species and the genera *Brevibora* and *Trigonostigma*. The
435 MRCA of Rasborinae dates back to ca. 46 Ma (95% HPD = 40-51 Ma, Eocene), while the
436 MRCA of the four Sundaland clades is dated at ca. 33 Ma (95% HPD = 30-37 Ma,
437 Oligocene-Eocene transition). The four clades have varying age estimates with the MRCA of
438 Clade I dated at ca. 31 Ma, (95% HPD = 27-34 Ma, Oligocene), the MRCA of Clade II at ca.
439 28 Ma (95% HPD = 24-31 Ma, Oligocene), the MRCA of Clade III at ca. 26 Ma (95% HPD
440 = 23-30 Ma, Oligocene), and the MRCA of Clade IV at ca. 22 Ma (95% HPD = 19.36-24.86
441 Ma, early Miocene). Estimated clock rates ranged between 0.31% per Myrs, with a variance
442 of 0.0017%, for rRNA coding regions and 0.74% per Myrs, with a variance of 0.0048%, for
443 protein-coding regions. Divergence time estimates were very similar with a birth-death model

444 (Fig. S1). The MRCA of Sundaland Rasborinae is dated at ca. 33 Ma (95% HPD = 30-37
445 Ma), and divergence time estimates of descending nodes yielded very similar values.

446

447 **3.3 Mitochondrial lineage delimitation and clade-specific phylogenetic inferences**

448 The four clades have a substantial proportion of cryptic diversity (Fig. 4) as
449 previously reported (Sholihah et al., 2020). COI sequence selection based on 80% BP
450 threshold yielded 1,017 sequences, which together with the 66 Rasborinae mitogenomes sum
451 up to 1,083 sequences for 71 nominal species, 157 MOTUs and 10 genera (Table S1). ML
452 and Bayesian gene trees are congruent for all clades (Fig. 4). Most internal branching events
453 are well supported in the ML gene trees (Figs. 4A, 4C, 4E, 4G), except among some
454 *Trigonopoma* MOTUs within Clade I (Fig. 4A), and the most derived MOTUs of Clade IV
455 (Fig. 4G). Bayesian gene trees were more supported for all clades (Figs. 4B, 4D, 4F, 4H) with
456 most internal branching events supported by PP>0.9. The estimated mitogenome clock rate
457 was 0.55% per Myrs for Clade I, 0.64% per Myrs for Clade II, 0.51% per Myrs for Clade III,
458 and 0.56% per Myrs for Clade IV. According to the backbone phylogeny analysis and
459 subsequent MRCA age calibrations, several clades are identified and labelled as clades I-IV.
460 In clade I, three subclades are observed: (1) *Pectenocypris* spp., with an MRCA dated at ca. 8
461 Ma (95% HPD = 4-13 Ma), (2) *Boraras* spp., with a MRCA dated at ca. 24 Ma (95% HPD =
462 19-28 Ma), and (3) *Trigonopoma* spp., including *Kottelatia britani* and *Rasbora kalbarensis*,
463 with a MRCA dated at ca. 26 Ma (95% HPD = 24-27 Ma). In clade II, two subclades are
464 observed: (1) *R. lacrimula*, *R. semilineata*, *R. hubbsi*, *R. rutteni* and *R. sarawakensis*, with a
465 MRCA dated at ca. 16 Ma (95% HPD = 14-18 Ma), and (2) all remaining species within
466 clade II, with a MRCA dated at ca. 25 Ma (95% HPD = 24-27 Ma). In clade III, two clades
467 can be identified: (1) *R. cephalotaenia* MOTUs, with a MRCA dated at ca. 8 Ma (95% HPD
468 = 5-11 Ma), and (2) all remaining species within clade III, with a MRCA dated at ca. 21 Ma
469 (95% HPD = 19-24 Ma). In clade IV, three subclades can be identified: (1) *Rasbora tornieri*
470 and *R. dusonesis*, with a MRCA dated at ca. 17 Ma (95% HPD = 12-21 Ma), (2) *R. myersi*, *R.*
471 *borapetensis*, *R. sumatrana* and *R. argyrotaenia*, with a MRCA dated at ca. 15 Ma (95%
472 HPD = 13-26 Ma), and (3) all other *Rasbora* species within the clade, starting from *R.*
473 *trilineata*, with a MRCA dated at ca. 19 Ma (95% HPD = 18-20 Ma).

474

475 **3.4 Diversification rates estimation**

476 MOTUs age estimates highlight that nearly half have Pleistocene origins (47.7%) by
477 contrast with only 10.3% of nominal species (Fig. S2). However, this proportion varies

478 among clades with 55% of MOTUs with a Pleistocene origin in Clade IV, 50% in Clade III,
479 41% in Clade I and 36% in Clade II. Best-fit diversification models indicate no clade-specific
480 patterns of diversification (Table S3). The constant speciation rate without extinction (BCST)
481 model is the most likely for all clades (AIC ω of 0.23 for Clades I and II, 0.262 for Clade III,
482 and 0.22 for Clade IV), with both sampling fractions used (Table 1, Table S3). Speciation
483 rates are similar for Clades I, II and III with $\lambda = 0.0898, 0.108, 0.1195$ events/Myr/lineage,
484 respectively (Table 1, Fig. S2). Clade IV, however, shows a higher rate of speciation with $\lambda =$
485 0.147 (Table 1, Fig. S2).

486

487 **3.5 Ancestral areas estimation**

488 A total of 139 MOTUs from 60 nominal species with known geographical distribution
489 were used for ancestral area estimations for the four clades (Fig. 5, Fig. S4). The most likely
490 biogeographical models include the J parameter for all clades and both island-based and
491 paleoriver-based geographical partitioning (Table S4). DEC+J is the most likely model in
492 most cases, except for Clade III with the paleoriver-based partitioning supporting the
493 DIVALIKE+J model. Ancestral area estimations point to Borneo as the most likely origin of
494 Clades II and IV and subclades of Clade II, with a high probability of Bornean ancestry of
495 their MRCAs (Figs. 5B, 5C, 5D). The insular ancestry of Clade I is not resolved, but the
496 North Sundaland paleoriver is identified as the most likely origin of Clade I (Fig. 5A) as well
497 as Clades II and IV (Figs. 5B, 5D). Ancestral areas estimation indicates a recent colonization
498 of Java during the Pliocene (ca. 4 Ma) by Clade IV (Fig. 5D). *In situ* diversification is
499 observed in all clades, particularly in Borneo (island-based analyses) and North Sunda (in
500 paleoriver-based analyses) as exemplified by the upper group of Clade II (*Rasbora lacrimula*,
501 *R. hubsii*, *R. semilineata*, *R. sarawakensis*, *R. ruttleri*) from Borneo (ca. 16 Ma, 95% HPD =
502 14-18 Ma), as well as *Trigonopoma gracile* MOTU144-MOTU148 (ca. 6 Ma, 95% HPD = 3-
503 9 Ma) and *Trigonopoma pauciperforatum* MOTU154-MOTU157 (ca. 4 Ma, 95% HPD = 2-6
504 Ma) from North Sunda (Fig. 5).

505 Several dispersal pathways are identified between Sundaland and Asia mainland, and
506 within Sundaland (Table 2, Figs. 5 & 6). Between 31-17.5 Ma, two pathways are identified:
507 (a) between Borneo and Asia mainland, and (b) Borneo and Sumatra. Between 17.5-7.5 Ma,
508 four pathways are identified: (a) between Borneo and Asia mainland, (b) between Borneo and
509 Sumatra, (c) between Sumatra and Asia, and (d) between North and East Sunda paleorivers
510 within Borneo. Between 7.5-0 Ma, eight pathways are identified: (a) between Borneo and

511 Asia mainland, (b) between Borneo and Sumatra, (c) between Sumatra and Asia mainland,
512 (d) between North and East Sunda paleorivers within Borneo, (e) between North Sunda and
513 Malacca paleorivers within Sumatra, (f) between Sumatra (North Sunda paleoriver) and Asia
514 mainland, (g) between Sumatra and Java, and (h) between Borneo and Java. Several burst of
515 *in situ* mitochondrial lineage diversification are detected within Borneo since the Early
516 Miocene, and within Sumatra and Java since the early Pliocene (Fig. 6).

517 In total, most mitochondrial lineage diversification events are observed within islands
518 with 59% and between paleorivers with 54% (Table 3, Fig. S3). Most divergence events are
519 associated to dispersal as 66% involve either different islands or different paleorivers, while
520 34% occurred within the same island and the same paleoriver (Table 2). However, these
521 trends vary through time. Most lineage divergence between islands occurs during the last 5
522 Myrs and is mostly associated to dispersal between paleorivers (Fig. S3A). Along the same
523 line, *in situ* divergence within paleoriver occurs mostly within island during the last 5 Myrs
524 (Fig. S3A). Geographical patterns of divergence vary among clades with a spectacular
525 dominance of divergence within islands for Clade II, most frequently occurring within the
526 same paleoriver (Table 2, Fig. S3C). Proportions are more balanced for other clades (Table
527 2), with most divergence events within paleorivers occurring within islands (Fig. S3).

528

529 4. DISCUSSION

530 4.1 Sundaland biogeography

531 Our phylogenetic and biogeographic reconstructions support the hypothesis of mostly
532 *in situ* diversity build-up of Rasborinae within Sundaland, with limited connections between
533 Sundaland and Asia mainland, during a timeframe consistent with geological reconstructions
534 in Southeast Asia (Hall, 2009; Hall, Cottam, & Wilson, 2011; Lohman et al., 2011).
535 Rasborinae lineages from mainland Asia are associated with the earliest branching events at
536 the root of the Rasborinae phylogenetic reconstructions. Our divergence time estimate of
537 Sundaland clades indicates that the four Sundaland lineages started to diversify between ca.
538 31-22 Ma, during the isolation of Borneo from mainland Asia (Fig. 1). These age estimates
539 are consistent with a single origin of Sundaland Rasborinae through *in situ* diversification as
540 evidenced by the phylogenetic reconstructions supporting their monophyly. Ancestral area
541 estimations further confirm this scenario as Borneo is inferred as the most likely origin of
542 most Sundaland clades (Fig. 5) and also the only island supporting early Miocene *in situ*
543 diversification (Fig. 6A: 1). These results suggest Rasborinae of Sundaland originate from
544 mainland Asia in the Oligocene, when Borneo was still part of mainland Asia, and

545 diversification of the four clades started during the isolation of Borneo. This timeframe
546 supports the pre-Pleistocene colonisation of Sundaland by freshwater fishes (de Bruyn et al.,
547 2013; Dodson et al., 1995; Sholihah et al., 2021), as previously reported in insular Southeast
548 Asia (Brown et al., 2013), followed by subsequent dispersal and divergence during the
549 emergence of Sumatra and Java (Fig. 6).

550 Our biogeographic estimations further highlight the importance of the North Sunda
551 paleoriver during the initial freshwater fish diversification in Sundaland (de Bruyn et al.
552 2013, 2014). The North Sunda paleoriver is the most likely centre of origin of most
553 Rasborinae clades (Fig. 4) and also the part of Borneo involved in the highest number of
554 dispersal pathways during the late Miocene (Fig. 6B: a, b and d) and early Pliocene (Fig. 6C:
555 a, b and d). The diversification of Rasborinae mitochondrial lineages further followed
556 Sundaland's geological history with various colonization scenarios for Sumatra and Java.
557 Java is the youngest of Sundaland islands, with a separation that occurred during the last 5
558 Myrs (Fig. 1), which is consistent with our divergence time estimates as none of the MOTUs
559 endemic of Java are older than ca. 4 Myrs (*Rasbora* sp. 2). However, our reconstructions
560 indicate that colonization of Java likely results from at least two distinct immigration events
561 (Fig. 6C: g, h) followed by *in situ* diversification (Fig. 6C: 1). Immigration followed by *in*
562 *situ* lineage diversification has been previously suggested for freshwater fishes in Java,
563 including *Rasbora* (Hubert et al., 2019; Hutama et al., 2017; Kusuma et al., 2016). These
564 divergence events are likely resulting from the intense volcanic activity in Java, which
565 formed several volcanic arches and fragmented rivers into multiple, small and confined
566 watersheds during the Pliocene and Pleistocene. Java is the only island of Sundaland with a
567 predominant influence of volcanic activity during its emergence (Lohman et al., 2011). These
568 rugged aquatic landscapes likely fragmented ancestral lineages, creating local radiations
569 within the island (Nguyen et al. 2008; Pouyaud et al. 2009; Hubert et al. 2015, 2019; Kusuma
570 et al. 2016; Dahrudin et al. 2017; Hutama et al. 2017).

571 This scenario in Java contrasts with Sumatra, which biogeographic estimations
572 suggest a more ancient and intricate scenario of colonization (Fig. 6). Two ancient lineages
573 are detected in Sumatra: *Rasbora kalbarensis* diverged ca. 23 Ma, and *R. jacobsoni* diverged
574 ca. 20 Ma. These lineages occur in the North Sunda or Malacca paleorivers (Fig. 5). The age
575 estimates of these species contrast with most lineages in Sumatra, not exceeding ca. 13 Myrs
576 and mostly tracing back to the Miocene-Pliocene transition ca. 5 Ma. These contrasted
577 patterns suggest two waves of colonization during: (1) the onset of Borneo isolation and the
578 emergence of the first volcanic arches in Sumatra during the early Miocene (Fig. 6A: b), and

579 (2) the final stage of isolation of Sumatra, when land bridges were still connecting the
580 Southern tip of Sumatra, Borneo and West Java during the late Miocene (Fig. 6B: b, c). Cases
581 of *in situ* diversification are also detected in Sumatra during the Pliocene (Fig. 6C: 2).

582

583 **4.2 Dispersal and Pleistocene palaeoenvironments**

584 Our ancestral area estimations and modelling of lineage divergence and dispersal
585 indicate jump dispersal is common in Rasborinae, a result supported by the significant
586 increase of likelihood scores and Akaike weights when the J parameter is included (Table
587 S4). Multiple cases of trans-island dispersal have been reported among Sundaland freshwater
588 fishes (Adamson, Hurwood, & Mather, 2010; Beck et al., 2017; de Bruyn et al., 2013; Lim et
589 al., 2016; Farhana et al., 2018; Pouyaud et al., 2009; Sholihah et al., 2021; Tan & Lim, 2013).
590 However, our reconstructions question Pleistocene sea level changes as a main driver of
591 dispersal between islands. During glacial maxima, sea levels dropped (Miller et al., 2005).
592 The shallow Java Sea has given way to exposed lands, which likely had freshwater drainage
593 systems that extended between modern islands (Voris, 2000; Woodruff, 2010). These
594 paleoriver systems are expected to ease dispersal between islands and promote divergence
595 (Fig. 2). This prediction received little support here. Most mitochondrial divergence events
596 occurred within islands (Table 3) and most divergence events between islands occurred
597 between paleorivers (Fig. S3). The predominance of divergence within islands is likely linked
598 to Rasborinae ecology. Most species in Clades I, II, and III are small-size species inhabiting
599 forested streams and peat swamps (Kottelat, Whitten, Kartikasari, & Wirjoatmodjo, 1993;
600 Sholihah et al., 2020). These species are forest-dependent taxa with limited dispersal abilities.

601 During glacial maxima, climate was cooler and drier. Savanna and seasonal forest
602 corridors expanded through the interior of Sundaland (Bird et al., 2005; Heaney, 1992),
603 enhancing microclimates and diversity of freshwater habitats along the inter-island channels
604 (Bird et al., 2005; Gorog, Sinaga, & Engstrom, 2004; Heaney, 1992; Pouyaud et al., 2009;
605 Wurster et al., 2019). While documented for terrestrial organisms, divergence pattern of
606 Clade II suggests that vegetational changes during glacial maxima also limited dispersal for
607 aquatic, forest-associated organisms. Clade II further exemplifies the intricate interactions
608 between palaeoenvironments and dispersal. Habitat specificity toward forest habitats and peat
609 swamps may have limited dispersal between islands despite the availability of freshwater
610 corridors. These results highlight the dynamic interactions between palaeoenvironments and
611 Pleistocene sea level changes (Esselstyn and Brown 2009; Brown et al. 2013; Papadopoulou
612 and Knowles 2015a, 2015b).

613

614 **4.3 Macroevolutionary drivers of diversification**

615 Pleistocene climatic fluctuations have been frequently invoked to account for
616 Pleistocene increased rates of diversification (Mittelbach et al., 2007; Weir & Schluter,
617 2007). In Sundaland, Pleistocene sea level changes are predicted to induce cycle of dispersal
618 during glacial time and vicariance during interglacial periods (Kottelat et al., 1993; Voris,
619 2000; Woodruff, 2010). An amplification of sea-level fluctuations during the Pleistocene has
620 been observed (Fig. 1) (Miller et al., 2005), which predict increased rates of lineage
621 divergence in the context of Sundaland (Fig. 2). This prediction is not supported here.
622 Constant lineage divergence models of diversification are the most likely for all clades (Fig.
623 S2; Table S3). In a model with a constant probability of divergence per lineage through time,
624 lineage diversity increases linearly over time without levelling off toward the present (Table
625 S2). Thus, the Pleistocene origin of a large proportion of lineages could be a consequence of
626 constant diversification through time. This result might be surprising when considering the
627 vast array of aquatic habitats occupied by Rasborinae in Sundaland: lowland vs. highland,
628 fast vs. slow running waters, peat swamps, lakes, ponds (Brittan, 1972; Hubert et al., 2019;
629 Kottelat et al., 1993; Kusuma et al., 2016; Sholihah et al., 2020). Besides, ecological
630 transitions are scarce in Rasborinae. Clades I, II and III include small-size, forest-associated
631 species while Clade IV include all the large, riverine and open-habitat *Rasbora* species
632 (Kottelat et al., 1993; Liao et al., 2011; Sholihah et al., 2020). This pattern suggests that
633 adaptive habitat-shift had limited impact on the pace of diversification in Rasborinae. Yet,
634 Clade IV has the highest diversification rate of the four clades and is also the only clade that
635 colonized Java. Altogether, the transition between forest and open habitat, which happened
636 during the onset of Clade IV diversification, and higher divergence rate suggest an influence
637 of ecological contingency on Rasborinae diversification. This group of riverine and
638 opportunistic species was successful at colonizing open habitats, a previously non-colonized
639 set of habitats for Rasborinae.

640 Despite the high diversity of mitochondrial lineages in Sundaland Rasborinae, we find
641 no evidence of diversity equilibrium. The diversity-dependent diversification models received
642 little support for all clades, suggesting intra-clade biotic interactions have little influence on
643 either divergence opportunities or probabilities of maintenance of newly emerging lineages
644 (Alonso, Etienne, & McKane, 2006; Hubert, Calcagno, Etienne, & Mouquet, 2015). If
645 considering the ample distribution and abundance of Rasborinae in Sundaland and their
646 presence in all aquatic habitats, this result is surprising. Rasborinae assemblages were likely

647 unsaturated during the diversification of the subfamily (Cornell, 1993). Diversity equilibrium
648 and slowdown of diversification rates implies a shift in divergence/extinction equilibriums
649 once assemblages are saturated (Hubert, Calcagno, et al., 2015; Kisel, McInnes, Toomey, &
650 Orme, 2011; Phillimore & Price, 2008). Here, PCFs might be expected to have cyclically
651 perturbed aquatic assemblages, and regularly disrupted a potential course toward equilibrium.
652 Alternatively, Sundaland ecological carrying capacity might still be far from being reached,
653 despite the staggering species richness of Sundaland ichthyofauna.

654

655 **4.4 Robustness of the inferences and systematic implications**

656 Our study first confirms the monophyly of the subfamily Rasborinae and its
657 distinctiveness from the subfamilies Chedrinae, Danioninae and Esominae (Conway, Chen, &
658 Mayden, 2008; Fang, Norin, Liao, Källersjö, & Kullander, 2009; Mayden et al., 2007; Rüber,
659 Kottelat, Tan, Ng, & Britz, 2007; Tan & Armbruster, 2018; Tang et al., 2010). Our clade-
660 specific phylogenetic reconstructions confirm the monophyly of the genera *Boraras*,
661 *Pectenocypris* and *Trigonostigma*, but also support the paraphyly of the genus *Trigonopoma*,
662 and the polyphyly of the genera *Brevibora* and *Rasbora*. The polyphyly of *Rasbora* is in line
663 with previous molecular and morphology-based phylogenetic studies, which highlighted that
664 *Rasbora* encompasses several lineages of distinct evolutionary origins (Liao et al., 2010,
665 2011; Lumbantobing, 2010; Sholihah et al., 2020; M. Tan & Armbruster, 2018; K. L. Tang et
666 al., 2010). Yet, most *Rasbora* species groups initially described by Brittan (1954, 1972) are
667 recovered. For instance, Clade III matches the delimitation of *R. einthovenii* species group
668 and Clade II matches the boundaries of *R. trifasciata* species group (Brittan, 1972; Liao et al.,
669 2010). We also support the elevation of *R. pauciperforatum* species group to the genus level
670 (*Trigonopoma*) by Liao et al (2010). However, our results indicate *R. kalbarensis* should
671 probably be considered a member of the genus *Trigonopoma*. Likewise, the genus *Boraras*
672 described by Kottelat and Vidthayanon (Kottelat & Vidthayanon, 1993) is supported here.
673 Most of the taxonomic conflicts are concentrated in Clade IV, in which *R. lateristriata* and *R.*
674 *sumatrana* species groups from Brittan (1972), and the genus *Brevibora* from Liao et al
675 (2011) are not monophyletic. The present study warrants further taxonomic works within
676 Rasborinae and highlights the need of an in-depth revision of the genera *Rasbora* and
677 *Brevibora*.

678 The estimated age of the Rasborinae mitochondrial MRCA, dated at ca. 46 Ma (41-53
679 Ma), is consistent with the 44 Myrs reported by Betancur-R et al. (2017) based on one
680 mitochondrial and 20 nuclear genes. However, these results are not concordant with the ray-

681 finned fishes phylogeny of Rabosky et al. (2018) dating the MRCA of Rasborinae at 59 Ma,
682 and the MRCA of Sundaland Rasborinae at 42 Ma. Several differences in the calibration
683 methods and molecular markers may account for these differences. Phylogenetic
684 reconstructions of Rabosky et al. (2018) are based on 20 nuclear markers. Discordances
685 between mitochondrial and nuclear markers might be expected due to the maternal
686 inheritance of mitochondrial genomes, with potential cryptic past introgression events and
687 selective sweeps leading to conflicting phylogenetic reconstructions (Hubert, Torrico,
688 Bonhomme, & Renno, 2007; Ríos, Bouza, & García, 2019; Wallis et al., 2017). Rabosky et
689 al. (2018) and our phylogenetic reconstructions yielded concordant deep phylogenetic
690 relationships, with lineages of Asia mainland (*Amblypharyngodon*, *Horadandia* and
691 *Rasboroides*) placed in basal positions, and Sundaland lineages being equally assorted into
692 the four clades I-IV. However, discordance between mitochondrial and nuclear markers due
693 to past introgression cannot be discarded for shallower phylogenetic scales, hybridization
694 being common in Cypriniformes (Atsumi, Nomoto, Machida, Ichimura, & Koizumi, 2018;
695 Hopkins & Eisenhour, 2008; Tang, Liu, Yu, Liu, & Danley, 2012). Discrepancies in the age
696 estimate of Rasborinae MRCA are most likely due to the use of alternative calibration
697 methods. Rabosky et al. (Rabosky et al., 2018) fossil calibrations are scarce for
698 Cypriniformes, with only three, distantly related from Rasborinae and ancient fossils
699 (†*Amyzon aggregatum* for the North American Catostomidae dated between 49-122 Ma,
700 †*Cyprinus maomingensis* for Eurasia Cyprini dated between 40-98 Ma, and
701 †*Huashancyprinus robustispinus* for Eurasia *Cyprinus* dated between 23-73 Ma). The
702 Rasborinae MRCA age estimate proposed by Rabosky et al. (2018) implies a markedly
703 different biogeographic scenario, with Rasborinae diversification originating much before the
704 isolation of Borneo. This ancient origin is not supported by recent phylogenetic
705 reconstructions among the Cypriniformes genera *Nemacheilus* and *Pangio* in Southeast Asia,
706 which MRCAs were recently dated at ca. 20 Ma according to phylogenetic reconstructions
707 based on both mitochondrial and nuclear markers (Šlechtová et al., 2021). Along the same
708 line, a recent reappraisal of previously published phylogenetic reconstructions support an
709 early to late Miocene origin of several Southeast Asian fish taxa (Sholihah et al., 2021).

710

711 5. CONCLUSION

712 Pleistocene sea level changes had less impact on Rasborinae diversification than
713 expected under the Paleoriver Hypothesis. Geographical patterns of divergence suggest that
714 limited dispersal abilities and *in situ* diversification were predominant during the diversity

715 build-up of Rasborinae in Sundaland. Our phylogenetic and biogeographic reconstructions
716 are in line with the timeframe of geological reconstructions in Southeast Asia. The
717 Rasborinae followed the geological history of Sundaland and tightly matched the onset of
718 isolation of Borneo. In particular, the North Sunda paleoriver is identified as a key aquatic
719 system during the rise of the group and an important source of diversity for the neighbouring
720 river systems. Our study also provides new lines of evidence about dispersal of freshwater
721 organisms in Sundaland. Paleoriver watershed boundaries poorly explain geographical
722 patterns of divergence and dispersal between islands. Surprisingly, our macroevolutionary
723 inferences show no evidence of diversification slowdown and diversity ceiling, despite the
724 exceptional levels of species richness of Sundaland ichthyofauna. This unexpected result
725 further questions the mechanisms underlying these diversification trends. Several alternative
726 scenarios may be invoked, including the impact of PCFs on disturbing speciation/extinction
727 equilibriums. Our study warrants further research on the evolutionary mechanisms underlying
728 diversification in such species-rich tropical systems.

729

730 **Acknowledgements**

731 The authors wish to thank Siti Nuramaliati Prijono, Bambang Sunarko, Witjaksono,
732 Mohammad Irham, Marlina Adriyani, Ruliyana Susanti, Rosichon Ubaidillah, the late Renny
733 K. Hadiaty, Hari Sutrisno and Cahyo Rahmadi at Research Centre for Biology (RCB-LIPI) in
734 Indonesia; Edmond Dounias, Jean-Paul Toutain, Robert Arfi and Valérie Verdier from the
735 ‘Institut de Recherche pour le Développement’; Joel Le Bail and Nicolas Gascoin at the
736 French embassy in Jakarta for their continuous support. We also would like to thank Eleanor
737 Adamson, Hendry Budianto, Tob Chann Aun, Pak Epang, Herman Ganatpathy, Renny K
738 Hadiaty, Sébastien Lavoué, Michael Lo, Hendry Michael, Sopian Sauri, Joshua Siow, Heok
739 Hui Tan, Elango Velautham, Norsham S. Yaakob, and Denis Yong for their help in the field.
740 We are also particularly thankful to Sumanta at IRD Jakarta for his help during the field
741 sampling in Indonesia. The present study and all associated methods were carried out in
742 accordance with relevant guidelines and regulation of the Indonesian Ministry of Research
743 and Technology (Indonesia), the Economic Planning Unit, Prime Minister’s Department
744 (Malaysia), the Forest Department Sarawak (Malaysia), the Vietnam National Museum of
745 Nature (Vietnam) and the Inland Fisheries Research and Development Institute (Cambodia).
746 Field sampling in Indonesia was conducted according to the research permits
747 7/TKPIPA/FRP/SM/VII/2012, 68/EXT/SIP/FRP/SM/VIII/2013,
748 41/EXT/SIP/FRP/SM/VIII/2014, 361/SIP/FRP/E5/Dit.KI/IX/2015,

749 50/EXT/SIP/FRP/E5/Dit.KI/IX/2016, 45/EXT/SIP/FRP/E5/Dit.KI/VIII/2017, and
750 392/SIP/FRP/E5/Dit.KI/XI/2018 for Nicolas Hubert, and, 1/TKPIPA/FRP/ SM/I/2011 and
751 3/TKPIPA/FRP/SM/III/2012 for Lukas Rüber. The Fieldwork in Peninsular Malaysia and
752 Sarawak was conducted under permits issued by the Economic Planning Unit, Prime
753 Minister's Department, Malaysia (UPE 40/200/19/2417 and UPE 40/200/19/2534) and the
754 Forest Department Sarawak (NCCD.970.4.4[V]-43) and were obtained with the help of
755 Norsham S. Yaakob (Forest Research Institute Malaysia, Kepong, Kuala Lumpur, Malaysia).
756 Luong Van Hao and Pham Van Luc (Vietnam National Museum of Nature) helped with
757 arranging research permits in Vietnam and So Nam (Inland Fisheries Research and
758 Development Institute, IFRDI) helped with arranging research permits in Cambodia. All
759 experimental protocols were approved by the Indonesian Ministry of Research and
760 Technology (Indonesia), the Indonesian Institute of Sciences (Indonesia), the Forest
761 Department Sarawak (Malaysia), Economic Planning Unit of the Prime Minister's
762 Department (Malaysia), the Vietnam National Museum of Nature (Vietnam) and the Inland
763 Fisheries Research and Development Institute (Cambodia). This publication has ISEM
764 number 2021-062 SUD.

765

766 **Data availability statement**

767 DNA barcodes are available in the Barcode of Life Data System ([dx.doi.org/110.5883/DS-](https://dx.doi.org/110.5883/DS-BIFRA)
768 [BIFRA](https://dx.doi.org/110.5883/DS-BIFRA)) and GenBank (see Table S1 for accession numbers). Mitogenomes are available in
769 GenBank (see Table S1 for accession numbers). Phylogenetic reconstructions and DNA
770 sequence alignments are available in Dryad (doi.org/10.5061/dryad.tb2rbp00g).

771

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- 1200

1201 **Biosketch**

1202 Arni Sholihah is a lecturer at Institut Teknologi Bandung (Indonesia), and obtained her PhD
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1204 biogeography and conservation of Southeast Asian biotas. The team consists in evolutionary
1205 biologists and/or specialists of Southeast Asian freshwater biotas interested in mechanisms of
1206 diversity build-up and conservation.

1207

1208 **Editor: Jonathan Waters**

1209

1210 **Author contributions:** AS, DW, LR and NH conceived the study. AS, TS, HD, DW, LR and
1211 NH conducted sampling. AS, EDT, JP, MKT, YF, JFA, LR and NH conducted the
1212 sequencing. AS, EDT, FC, LR and NH analysed the data. AS and NH drafted the initial
1213 version of the manuscript, and all authors further contributed to draft and approved the final
1214 version.

1215

1216 **Appendices**

1217 **Figure S1** Bayesian maximum clade credibility tree of Rasborinae based on 14 partitions (13
1218 protein coding and one rRNA coding partitions), two prior clock rates (0.3% per Myrs for
1219 rRNA partition, 1.2% per Myrs for the 13 protein coding partitions) and a birth-death
1220 diversification model. Node circles indicate posterior probabilities (PP) and node bars
1221 represent 95% highest posterior density (HPD) of age estimates.

1222

1223 **Figure S2** Lineage through time plots for each clade and distribution of the species and
1224 MOTUs age estimates (A), speciation rates through time according to BCST model for each
1225 clade (B), sea-levels (C, following Miller et al. 2005).

1226

1227 **Figure S3** Geographic pattern of speciation in Rasborinae. The plots show the numbers of
1228 speciation events associated to the four geographic patterns of speciation as follows: between
1229 islands and within paleorivers, between islands and between paleorivers, within islands and
1230 within paleorivers, and within islands and between paleorivers. Each bar shows the number
1231 of speciation events for each category for all clades (A), Clade I (B), Clade II (C), Clade III
1232 (D), and Clade IV (E).

1233

1234 **Figure S4** Mitochondrial MOTU trees reconstructed using StarBEAST2. A to D, Bayesian
1235 maximum credibility species trees for Clades I, II, III and IV, respectively, including
1236 posterior probabilities (PP, node circles) and 95% highest posterior density (HPD, node bars).

1237

1238 **Table S1** List of DNA sequences used in present study, including systematic (Order, family,
1239 genus, species and updated species names), field numbers (BOLD), GenBank accession
1240 numbers for COI and Complete Mitochondrial Genomes (CMG), OTU numbers assigned,
1241 locality, geographic distribution (Locality, island and paleoriver) and phylogenetic status
1242 (ingroup, outgroup).

1243

1244 **Table S2** Description of the 17 diversification models tested including acronym, rate
1245 variation, number of parameters and parameters involved (see material and methods section
1246 for details).

1247

1248 **Table S3** Likelihood scores for each diversification model for each group. Description of
1249 each model can be found in Table S1.

1250

1251 **Table S4** Log likelihood scores and Akaike Information Criterion values for DEC, DEC+J,
1252 DIV, DIV+J, BAY and BAY+J as calculated using BioGeoBEARS for island-based and
1253 paleoriver-based partitioning.

1254

1255 **Figures and Tables captions**

1256 **Figure 1** Geological reconstructions of the Indo-Australian archipelago since the middle
1257 Oligocene (modified from Lohman et al. 2011), paleoriver reconstruction in the Pleistocene
1258 (modified from Voris, 2000 and Woodruff, 2010) and sea levels fluctuations (adapted from
1259 Miller et al. 2005). A, middle Oligocene *ca.* 30 Ma. B, early Miocene *ca.* 20 Ma. C, late
1260 Miocene *ca.* 10 Ma. D, early Pliocene *ca.* 5 Ma. E, modern including limits of exposed land
1261 during -60 m and -120 m sea level drops, contour of the paleoriver watersheds and sampling
1262 sites. F, sea level reconstructions over the last 15 Myr.

1263

1264 **Figure 2** Mechanisms of lineage dispersal and proliferation through eustasy (Paleoriver
1265 hypothesis). During interglacial times, sea-level highstands induce a fragmentation of
1266 watersheds into multiple tributaries further connected during sea-level lowstands of glacial
1267 times. *In situ* radiation panel depicts a scenario of watershed colonisation during glacial times

1268 from an initial ancestor (a), further fragmented during sea-level highstand and resulting in a
1269 locally radiating lineage (a1-a8). Jump dispersal and *in situ* radiation panel depicts a scenario
1270 of watershed colonisation during glacial times from two ancestors (a, b), further fragmented
1271 during sea-level highstands and resulting in multiple local radiations (b1-b2, a1-a6).

1272

1273 **Figure 3** Phylogenetic reconstructions in Rasborinae based on 79 mitogenomes with
1274 Rasborinae taxa in black, outgroups in grey and four major clades labelled Clade I to Clade
1275 IV. A, Bayesian maximum clade credibility tree based on 14 partitions (13 protein coding and
1276 one rRNA coding partitions), two prior clock rates (0.3% per Myrs for rRNA partition, 1.2%
1277 per Myrs for the 13 protein coding partitions) and a Yule diversification model. Node circles
1278 indicate posterior probabilities (PP) and node bars represent 95% highest posterior density
1279 (HPD) of age estimates. B, Maximum likelihood phylogenetic tree based on 14 partitions (13
1280 protein coding and one rRNA coding partitions). Node circles indicate bootstrap proportion
1281 (BP).

1282

1283 **Figure 4** Mitochondrial gene trees of Rasborinae Clades I, II, III and IV. Maximum
1284 likelihood trees and bootstrap proportions (BP, node circles) are in panels A, C, E, and G, or
1285 Clades I, II, III and IV, respectively. Bayesian maximum clade credibility trees, posterior
1286 probabilities (PP, node circles) and 95% highest posterior density (HPD, node bars) are in
1287 panels B, D, F, and H for Clades I, II, III, and IV, respectively. All ML trees were rooted
1288 using *A. mola*, *R. vaterifloris* and *H. atukorali*, Clade I ML tree (A) included additional extra-
1289 groups as follows: *R. cephalotaenia*, *R. einthovenii*, *R. sumatrana*, *R. dusonensis*, *R.*
1290 *aprotaenia*, *R. semilineata*, *R. rutteni*, *R. bankanensis*, and *R. borneensis*. Clade II ML tree
1291 (C) included additional extra-groups as follows: *R. cephalotaenia*, *R. einthovenii*, *R.*
1292 *sumatrana*, *R. dusonensis*, *R. aprotaenia*, *B. maculatus*, *T. n sp*, and *P. balaena*. Clade III ML
1293 tree (E) included additional extra-groups as follows: *B. maculatus*, *T. n sp*, *P. balaena*, *R.*
1294 *borneensis*, *R. bankanensis*, *R. semilineata*, *R. rutteni*, *R. sumatrana*, *R. dusonensis*, and *R.*
1295 *aprotaenia*. Clade IV ML tree (G) included additional extra-groups as follows: *B. maculatus*,
1296 *T. n sp*, *P. balaena*, *R. borneensis*, *R. bankanensis*, *R. semilineata*, *R. rutteni*, *R.*
1297 *cephalotaenia*, and *R. einthovenii*.

1298

1299 **Figure 5** Mitochondrial ancestral area estimations of Rasborinae Clades I, II, III, and IV. A
1300 to D, ancestral area estimations for Clades I, II, III, and IV, respectively, according to an

1301 island-based (left) or paleoriver-based (right) geographical partitioning. Nodes labelling is
1302 temporally ordered and referred in the text.

1303

1304 **Figure 6** Dispersal pathways and *in situ* diversification among Sundaland Rasborinae
1305 between 31-17.5 Ma (A, Early Miocene), 17.5-7.5 Ma (B, Late Miocene) and 7.5 Ma-present
1306 (C, Early Pliocene). Arrows represent dispersal pathways according to ancestral area
1307 estimations (Table 2) and stars indicates *in situ* diversification.

1308

1309 **Table 1** Summary statistics of the most likely diversification models for Rasborinae Clades I,
1310 II, III, and IV including acronym, rate variation, number of parameters (NP), speciation rates
1311 (λ), corrected Akaike Information Criterion (AICc) and Akaike weight (AIC ω).

1312

1313 **Table 2** Freshwater dispersal pathways and associated clades through time.

1314

1315 **Table 3** Summary statistics of geographical patterns of lineage divergence for Rasborinae
1316 Clades I, II, III, and IV.

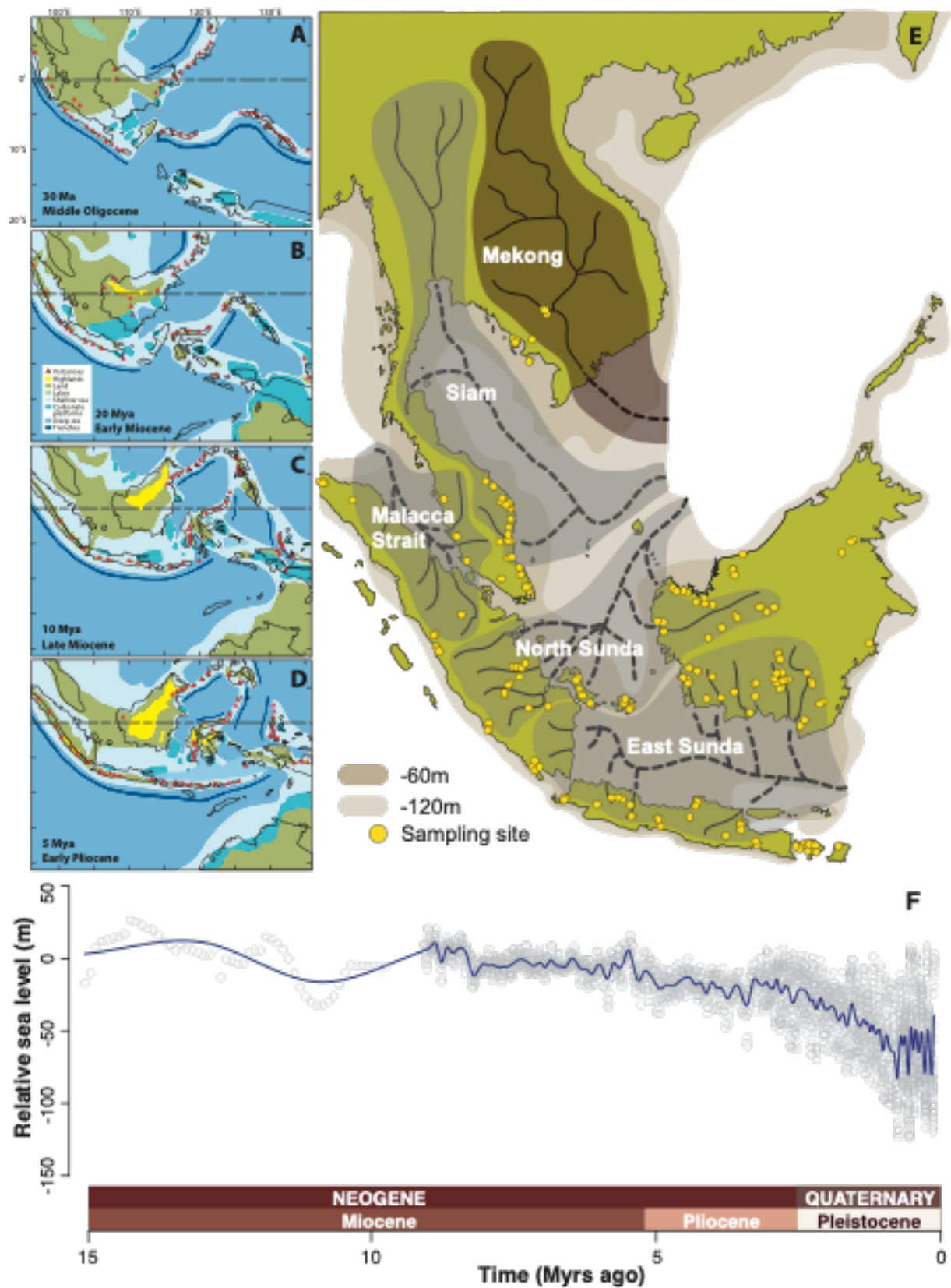


Fig. 1

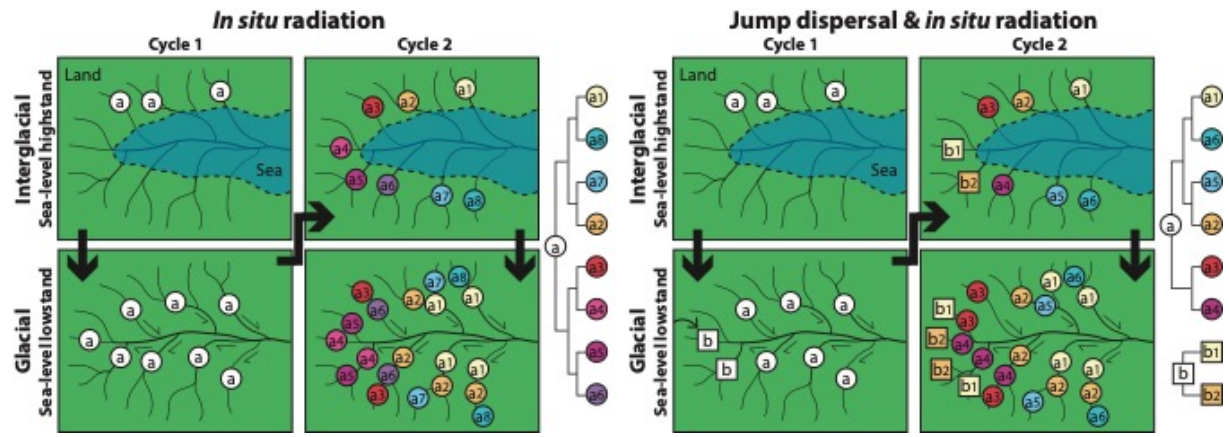


Fig. 2

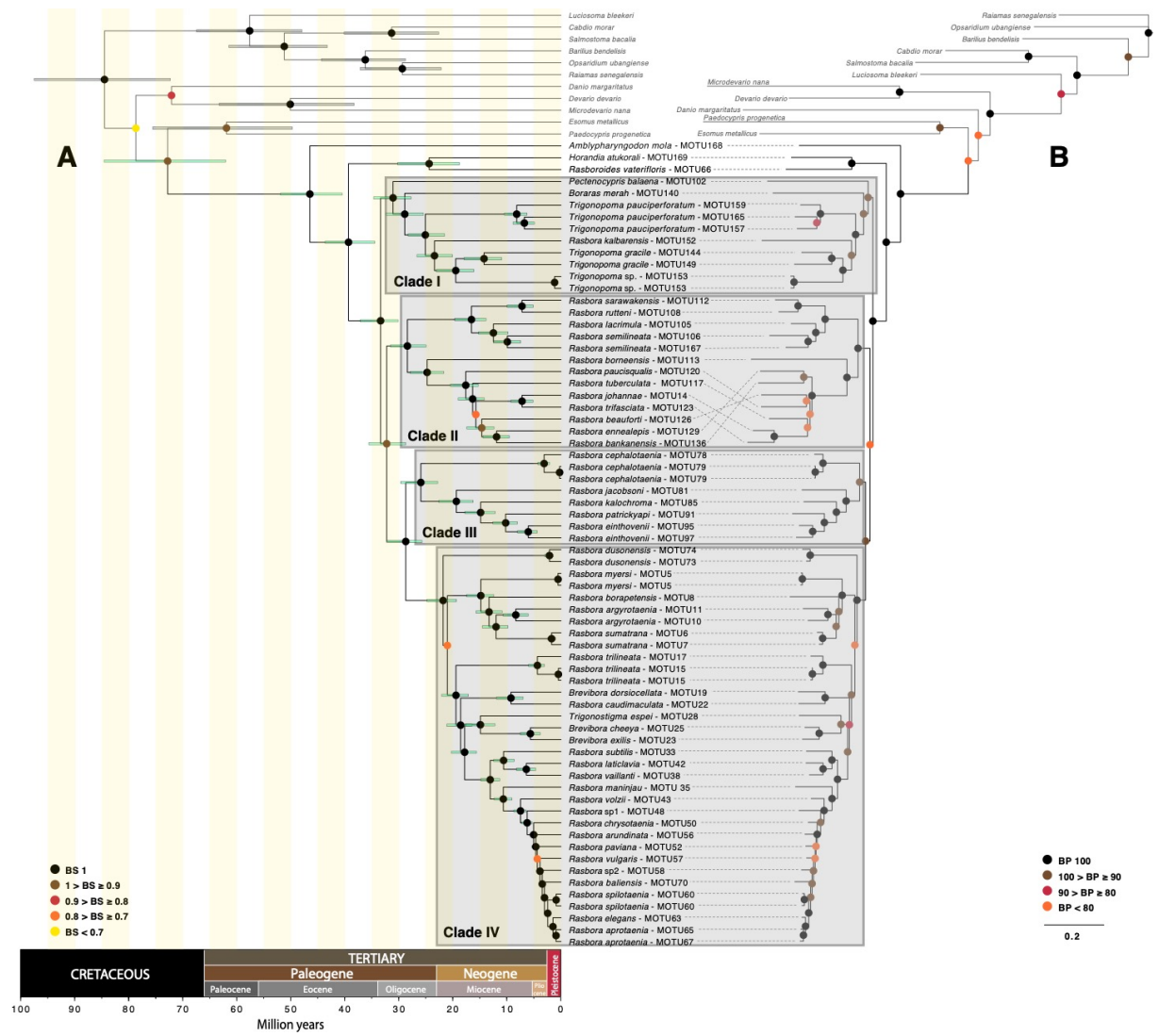


Fig. 3

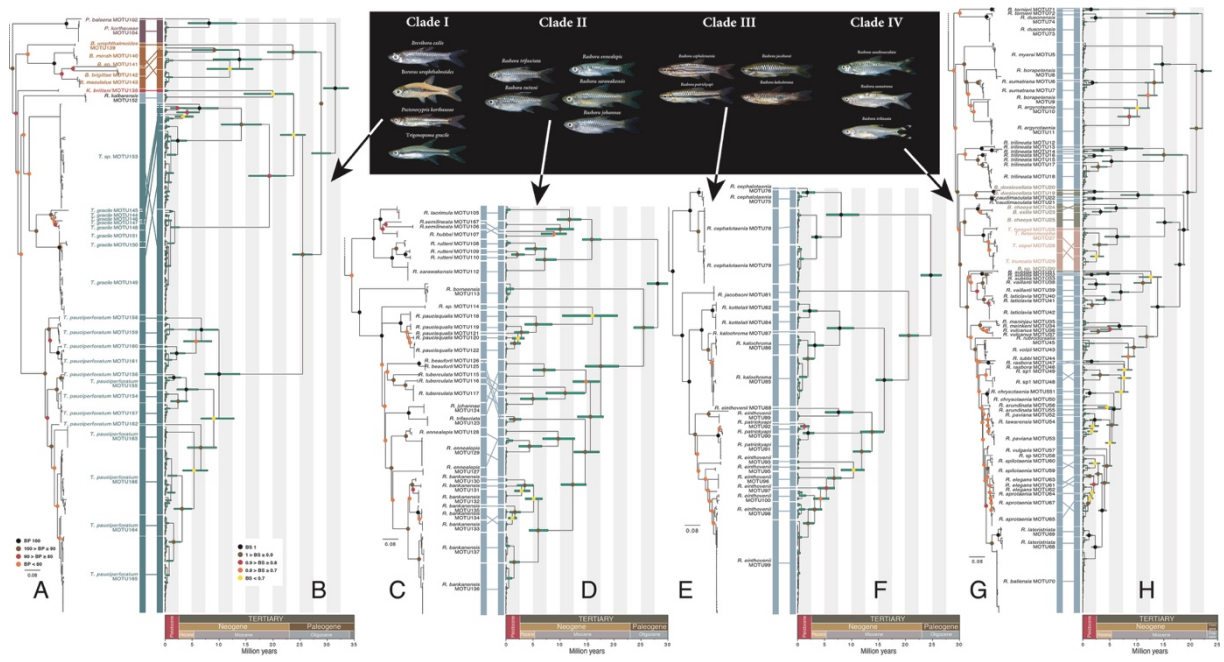


Fig. 4

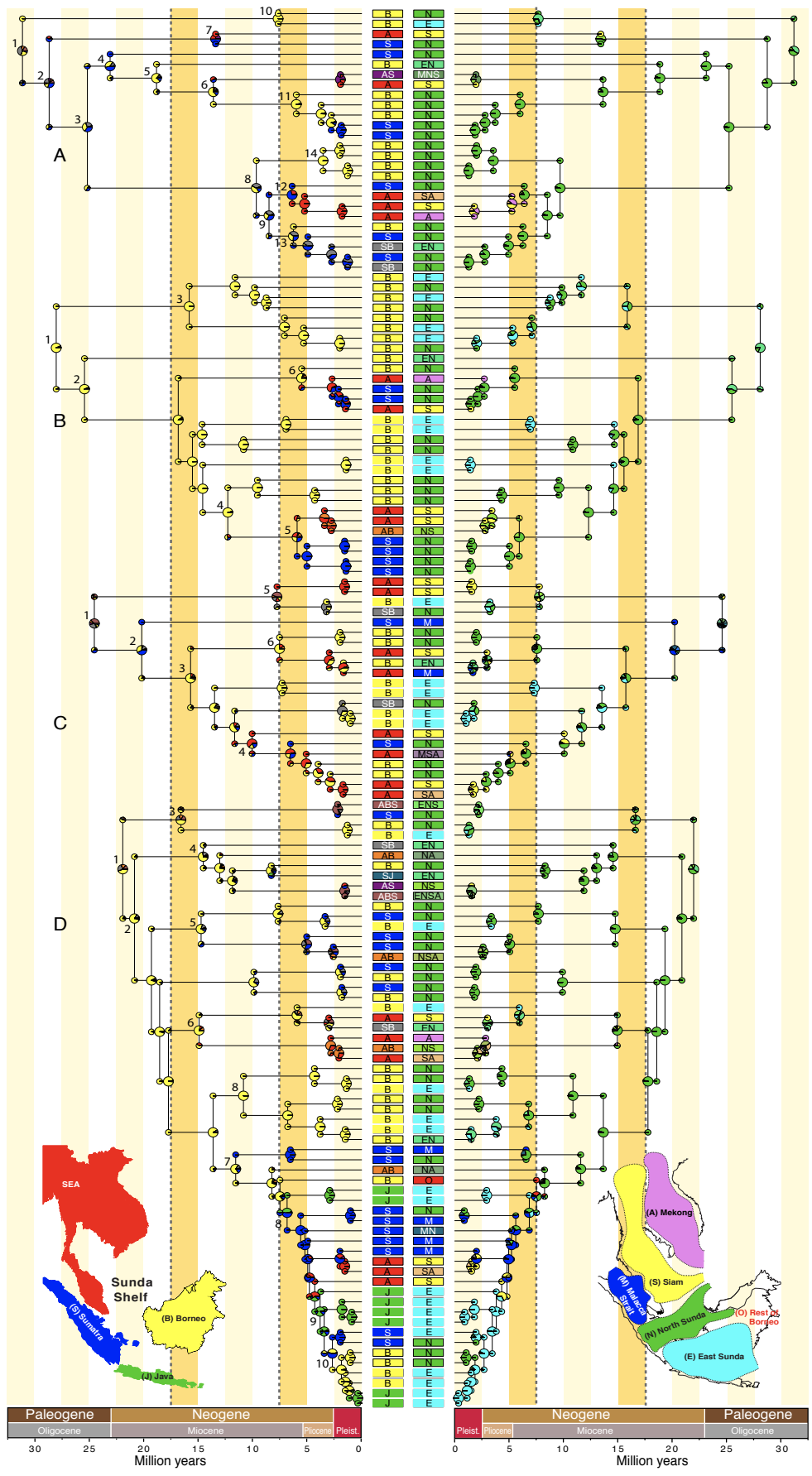


Fig. 5

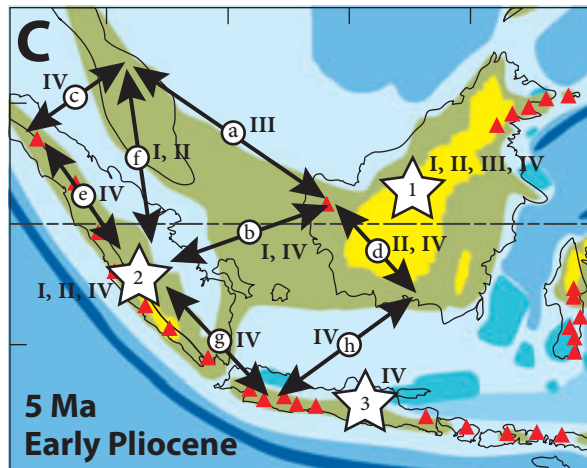
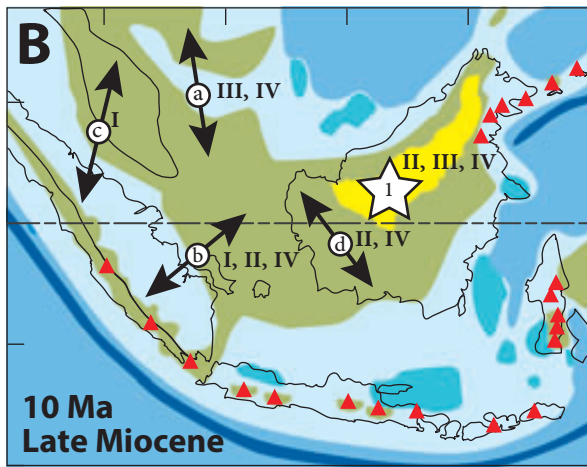
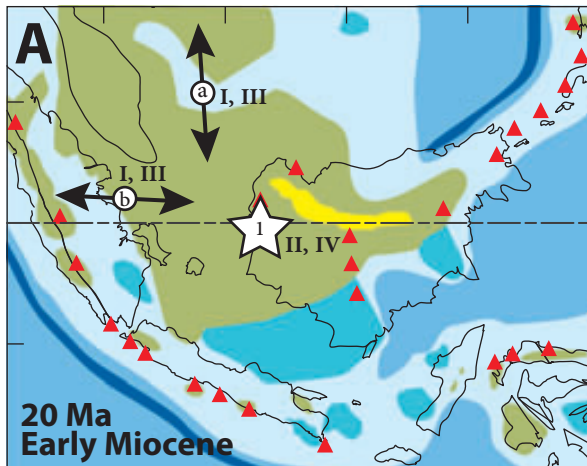


Fig. 6