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## Limited dispersal and in situ diversification drive the evolutionary history of Rasborinae fishes in Sundaland

Arni Sholihah, Erwan Delrieu-trottin, Tedjo Sukmono, Hadi Dahruddin, Juliette Pouzadoux, Marie-ka Tilak, Yuli Fitriana, Jean-françois Agnèse, Fabien L. Condamine, Daisy Wowor, et al.

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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**

5

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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 19<sup>th</sup> 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](https://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](http://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+ $\Gamma$  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) (Sujeevan  
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+ $\Gamma$  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+ $\Gamma$  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+ $\Gamma$  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](https://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 ( $\lambda$ ) and extinction ( $\mu$ ) rates are parameterized as  
353 follows. When  $\lambda$  and  $\mu$  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  $\lambda_0$  and  $\mu_0$  are  
355 respectively the expected  $\lambda$  and  $\mu$  at  $S = 0$  meter, while  $\alpha$  and  $\beta$  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  $\lambda$  and  $\mu$  increase with sea level high stands). Similar parameterisation can be used for  
358 exponential relationship between temperature ( $T$ ) through time ( $t$ ) and  $\lambda$  as well as  $\mu$  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  $\lambda_0$  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  $\lambda$  and  $\mu$  vary as linear functions of number of lineages within each clade (Etienne et  
363 al., 2012). The diversity-dependent models are parameterised by  $\lambda_0$ ,  $\mu_0$  (respectively  
364 indicating  $\lambda$  and  $\mu$  at the absence of competing lineage),  $K$  (carrying capacity, representing  
365 asymptotic clade size). All  $\lambda$  and  $\mu$  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 $\omega$ ). The model with the lowest  
368 AICc and highest AIC $\omega$  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 $\omega$  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

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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](https://doi.org/10.5061/dryad.tb2rbp00g)).

771

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1201 **Biosketch**

1202 Arni Sholihah is a lecturer at Institut Teknologi Bandung (Indonesia), and obtained her PhD  
1203 at the doctoral school GAIA (Université de Montpellier). She is interested in the  
1204 biogeography and conservation of Southeast Asian biotas. The team consists in evolutionary  
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1206 diversity build-up and conservation.

1207

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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 ( $\lambda$ ), corrected Akaike Information Criterion (AICc) and Akaike weight (AIC $\omega$ ).

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.

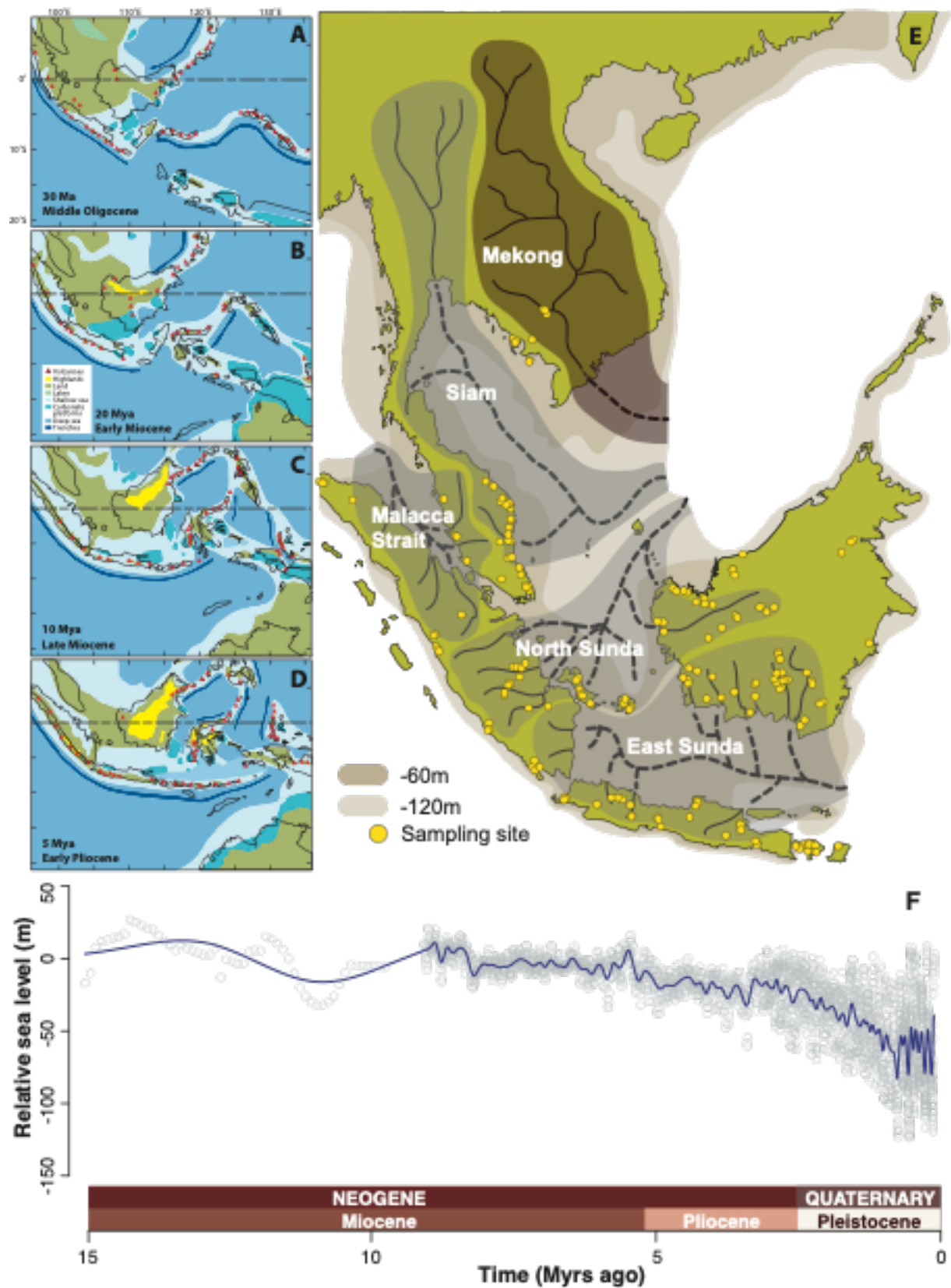


Fig. 1

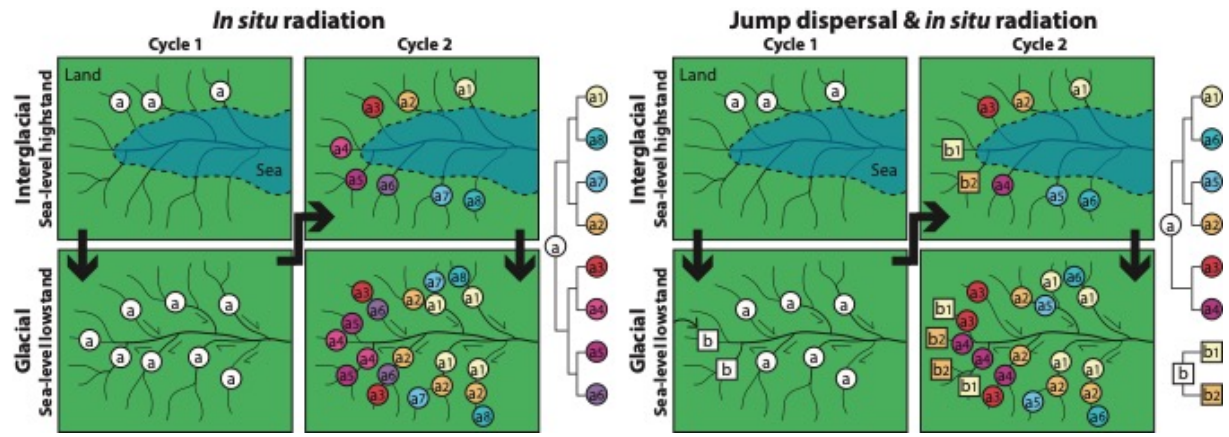


Fig. 2

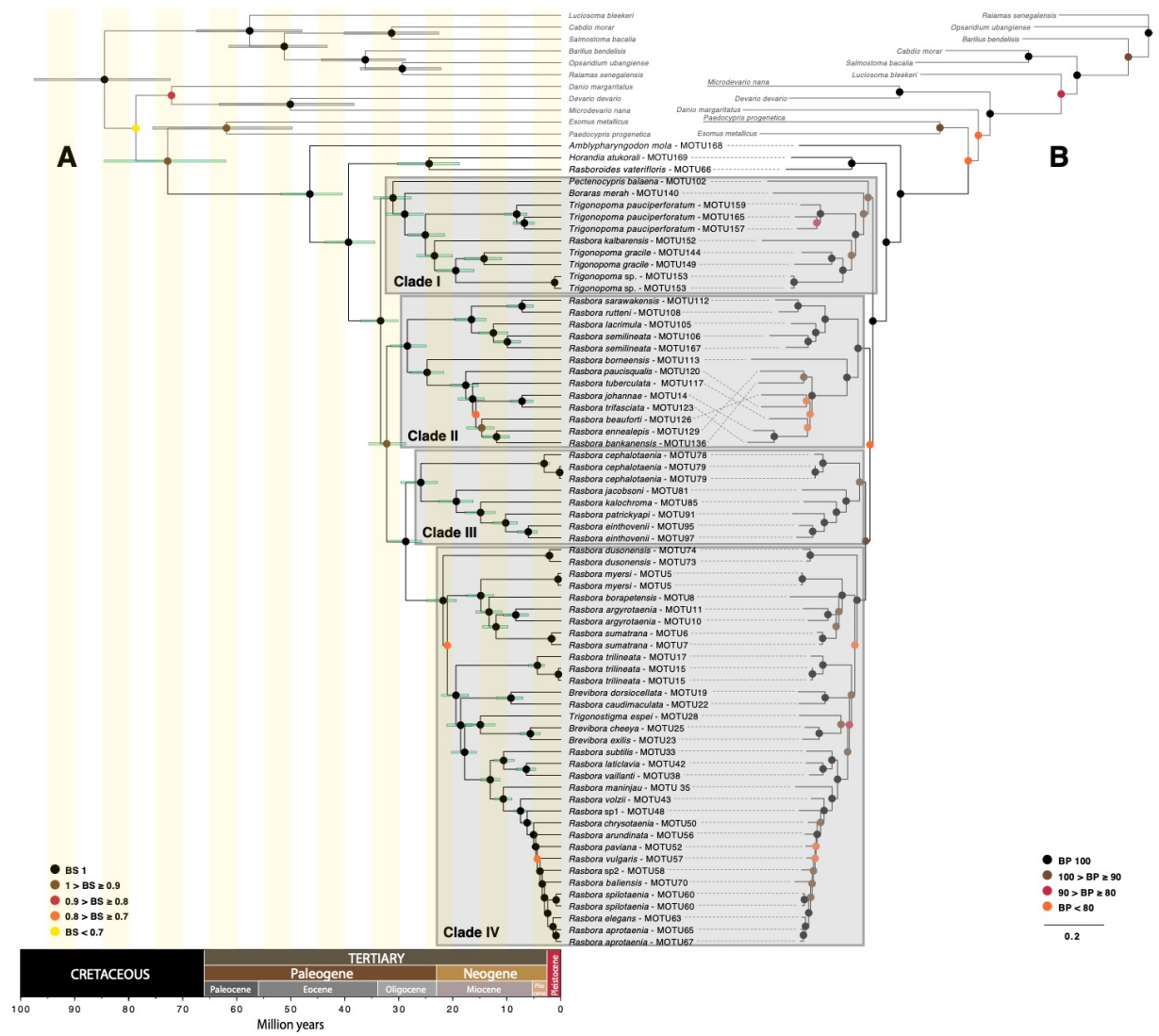


Fig. 3







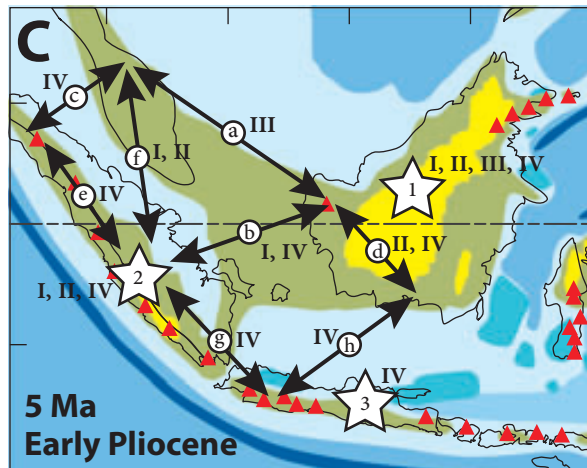
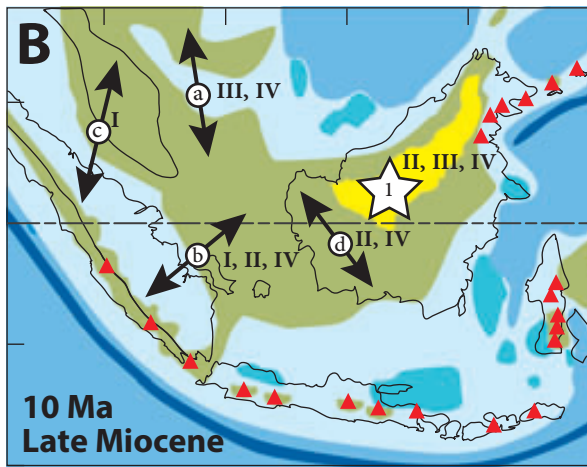
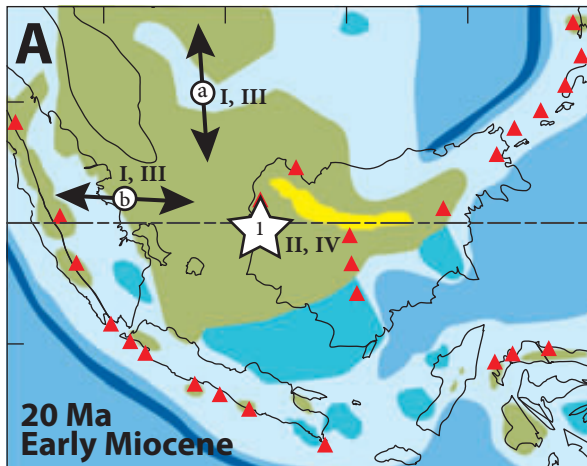


Fig. 6