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1 **Cross-ocean patterns and processes in fish biodiversity on coral reefs through the lens**
2 **of eDNA metabarcoding**

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41 **Abstract**

42 Increasing speed and magnitude of global change threaten the world's biodiversity and particularly
43 coral reef fishes. A better understanding of large-scale patterns and processes on coral reefs is
44 essential to prevent fish biodiversity decline but it requires new monitoring approaches. Here, we
45 use environmental DNA metabarcoding to reconstruct well-known patterns of fish biodiversity on
46 coral reefs and uncover hidden patterns on these highly diverse and threatened ecosystems. We
47 analyzed 226 eDNA seawater samples from 100 stations in 5 tropical regions (Caribbean, Central
48 and Southwest Pacific, Coral Triangle and Western Indian ocean) and compared those to 2,047
49 underwater visual censuses from the Reef Life Survey (RLS) in 1,224 stations. Environmental
50 DNA reveals a higher (16%) fish biodiversity, with 2,650 taxa, and 25% more families than
51 underwater visual surveys. By identifying more pelagic, reef-associated and crypto-benthic
52 species, eDNA offers a fresh view on assembly rules across spatial scales. Nevertheless, RLS
53 identified more species than eDNA in 47 shared families, which can be due to incomplete sequence
54 assignment, possibly combined with incomplete detection in the environment, for some species.
55 Combining eDNA metabarcoding and extensive visual census offers novel insights on the spatial
56 organization of the richest marine ecosystems.

1. Introduction

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Coral reefs host the highest fish diversity on earth despite covering less than 0.1% of the ocean's surface (1,2). They are also severely threatened (3), with near future outlooks predominantly pessimistic (4). Data syntheses over decades of surveys estimate the total number of coral reef fishes from 2,400 to 8,000 species (5,6), distributed among approximately 100 families (7). Typically, coral reef biodiversity displays clear spatial patterns, including longitudinal and latitudinal gradients outwards the Indo-Australian Archipelago (8,9), also known as the 'Coral Triangle', hosting the world's highest level of marine biodiversity (10). The exceptional biodiversity in the Coral Triangle has recently been suggested to strongly relate to higher diversity among fish families that feed on plankton (11). Other trophic groups are also very important on coral reefs but are often undetected because they are transient or hidden (12,13). Intriguingly, the proportions of fish species among families are shown to be strongly conserved across the Indo-Pacific (8). The spatial patterns of coral reef fishes are also marked by strong variations in taxonomic composition (species turnover or β diversity), often due to isolation (14). Many species on coral reefs are geographically localized, but can sometimes be locally abundant, while others are widespread (15).

Coral reef fishes have evolved in a physically complex environment and present a wide range of forms and functions (16). Small cryptic species, hereafter called crypto-benthic, that live inside the reef structure, can be very difficult to sample or survey using non-destructive methods (17), yet represent half of the fish diversity on coral reefs (13). Even though fishes are among the best-studied taxa inhabiting coral reefs (18), our knowledge of their biodiversity is only partial (19), the taxonomy is complex, uncertain for many species (5), and countless species remain undescribed.

81 Environmental DNA (eDNA) metabarcoding, a method retrieving and analyzing DNA naturally
82 released by organisms in their environment (20), provides an opportunity to not only better
83 understand classical biodiversity patterns, but also uncover novel ones hidden by our incomplete
84 taxonomic and biogeographic coverage (21). Environmental DNA is particularly powerful in
85 aquatic ecosystems (22) and is now well established for marine microorganisms (23,24). By
86 contrast, its potential to provide an integrated biodiversity assessment of macroorganisms,
87 including vertebrates of all trophic levels (from crypto-benthic to large pelagic fish species), is
88 only shown at local (25) and regional (26–30) scales but not yet at spatial scales including more
89 than one biogeographic region or multiple ocean basins.

90 Here, we investigate how a cross-ocean basin snapshot of eDNA sampling could describe the
91 distribution of fish biodiversity on coral reefs, reveal unknown patterns, and challenge well-
92 established assembly rules. From 226 eDNA seawater samples (2,712 PCR replicates) collected
93 in 100 stations at 26 sites covering five tropical regions (Southeast Polynesia, Tropical
94 Northwestern Atlantic, Tropical Southwestern Pacific, Western Indian Ocean and Western Coral
95 Triangle) across the Indian, Pacific and Atlantic Oceans (figure S1-S2), we produced a final dataset
96 of 189,350,273 mitochondrial 12S rRNA gene sequence reads (see Methods), clustered into 2,023
97 molecular operational taxonomic units (MOTUs), and assigned to Actinopterygii (bony fishes)
98 and Chondrichthyes (cartilaginous fishes) taxa (tables S1- S2). We then compared fish biodiversity
99 patterns obtained from eDNA to those observed from 2,047 standardized visual surveys of reef
100 fishes in 1224 stations at 219 sites within 24 tropical regions (31).

101

102 **2. Results**

103 **(a) Global estimates of fish biodiversity on coral reefs**

104 We estimated total fish diversity on coral reefs using the asymptote of a multi-model accumulation
105 curve for both eDNA MOTUs (32) and visual census species (Methods). The asymptote estimated
106 from 100 eDNA stations distributed in five regions sampled over a 28-month period reaches 2,650
107 MOTUs (figure 1a). This detectable fish MOTUs diversity, including also MOTUs unassigned at
108 the species-level, is 16% higher than the estimate from visual census data, which reaches an
109 asymptote at 2,268 fish species from 2,047 tropical transects surveyed during 13 years (figure 1b).
110 The asymptotic estimation of family richness obtained with eDNA reaches 147 families, 25% more
111 than the asymptotic number of families estimated with visual census data (118 families, figure 1c-
112 d). Among the 71 families shared between both datasets, 24 have a higher number of MOTUs from
113 eDNA survey than species from visual survey while 47 have more species from visual survey than
114 MOTUs from eDNA survey (figure 1e). Families with more taxa identified using eDNA include
115 those often associated with reef-adjacent habitats such as mangroves or soft sediments like
116 Mugilidae (e.g. *Mugil rubrioculus*), Elopidae and Gerreidae (33, e.g. *Gerres oyena*), and crypto-
117 benthic species that live hidden in crevices (e.g. Gobiidae) or nocturnal fish species (34, e.g.
118 Congridae). Families with more taxa with visual census include Acanthuridae, Chaetodontidae,
119 Blenniidae, Labridae, Pomacentridae and Scaridae. Fifty-five families are detected only with
120 eDNA, including Myctophidae, Engraulidae, Atherinidae and Exocoetidae, while 24 families are
121 detected only by visual census, including Caesionidae, Chaenopsidae, Labrisomidae and
122 Microdesmidae. Environmental DNA estimates a diversity of crypto-benthic species 13% higher
123 than with visual census, and, among many others, includes species such as the elegant firefish
124 (*Nemateleotris decora*), which lives on the outer reef slope between 25 to 70 m (figure 2a). Yet,
125 the difference in fish diversity assessment between the two methods is the strongest for pelagic
126 and wide-ranging species, for which eDNA reveals more than 7 times higher richness than with

127 visual census. These species mainly belong to Scombridae (e.g. *Katsuwonus pelamis*), Clupeidae,
128 Carcharhinidae (e.g. *Carcharhinus leucas*, *Sphyrna lewini*) and Belonidae (figure 2b).

129

130 MOTU richness per fish family retrieved with eDNA is strongly correlated with fish species
131 richness within families recorded in visual census data (Pearson correlation = 0.84, $p < 0.001$, $n =$
132 71, figure 1e). Highly diverse families seen on coral reefs are also well represented in eDNA
133 samples, with Gobiidae, Labridae and Pomacentridae containing more than 100 MOTUs each,
134 together representing about 20% of MOTUs (figure 1f, figures S3- S4). The slope of the log-log
135 relationship between MOTUs richness per family and species richness per family is equal to 0.8
136 showing that the relationship is not proportional but saturating. The richest fish families contain
137 more MOTUs detected with eDNA than species detected with visual surveys.

138

139 (b) Biogeography of eDNA sequences

140 The spatial distribution of MOTUs follows clear biogeographic patterns, with a peak in the coral
141 triangle and lower values of MOTU richness toward Southeast Polynesia (figure S5). The richest
142 region (West Papua, Indonesia, Western Coral Triangle) contains ~50% of the global pool of fish
143 MOTUs while the poorest region (Fakarava, French Polynesia, Southeast Polynesia) contains only
144 9% of the global pool (figures S6-S7 and table S2). Distance-based Redundancy Analysis
145 (dbRDA) was performed on fish family proportions at each site (i.e. number of MOTUs or species
146 assigned to each family in each site, see Methods) for eDNA and visual surveys with the region
147 and the site MOTU/species richness as explanatory variables, including their interaction (figure 3,
148 table S3). For eDNA, the dbRDA explains up to 42% of variation in family proportions between
149 pairs of sites with region and MOTU/species richness both having significant effects ($F = 4.1$ and
150 5.7, respectively, $p < 0.001$), but no significant interaction ($F = 1.99$, $p > 0.05$). The partial dbRDA

151 on eDNA showed a significant effect of region while controlling for MOTU richness ($F = 2.79$, p
152 < 0.001). The first axis explains 17.2% of variation in family proportions and separates the Western
153 Coral Triangle from other regions (figure 3*a-b*). The first axis shows a higher proportion of
154 Lutjanidae but lower proportions of Labridae and Gobiidae in sites of the Western Coral Triangle.
155 It also confirms the longitudinal diversity gradient from the Coral Triangle. The second axis
156 explains 11.2% of variation and discriminates the Tropical Northwestern Atlantic from the
157 Western Indian Ocean, due to a higher proportion of Clupeidae and Carangidae in the Atlantic
158 Ocean and a higher proportion of Acanthuridae in the Indian Ocean. The dbRDA performed on
159 visual census data explained greater variation ($R^2 = 0.5$, $p < 0.001$) and the region also had a
160 significant, albeit weaker than for MOTUs, effect on fish family proportions ($F = 17.7$, $p < 0.01$),
161 while species richness and interaction between the two variables also had significant effects ($F =$
162 6.28 and 2 , $p < 0.01$ respectively). The first axis explains 41.6% of variance in family proportions
163 and separates the Tropical Northwestern Atlantic from the other regions with a higher proportion
164 of Gobiidae and Serranidae. The second axis explains 5.7% of variance in family proportions and
165 separates the Southeast Polynesia from Indo-Pacific regions, and is mostly driven by the higher
166 proportion of Pomacentridae in the Indo-Pacific (figure 3*c-d*).

167

168 (c) **Global patterns of fish turnover and rarity**

169 Our eDNA survey shows that a majority of MOTUs are geographically restricted, with 85% of the
170 MOTUs detected in only one region (figure 4*a*), and 35% in only one site (figure S8). Geographic
171 restriction is one aspect of species rarity but is shown to play a primary role in determining
172 extinction risk while local abundance and habitat specialization have secondary roles (35). We
173 hierarchically partitioned the global MOTU diversity (γ_{global}) into additive diversity components

174 (i.e. dissimilarity) due to difference between regions ($\beta_{inter-region}$), mean difference between
175 sites within regions ($\bar{\beta}_{inter-site}$), mean difference between stations within sites ($\bar{\beta}_{inter-station}$)
176 and mean station diversity ($\bar{\alpha}_{station}$) (36). As a consequence of the geographic restriction of most
177 MOTUs to one region, the total fish MOTU (γ) diversity is mainly due to inter-region β -diversity
178 (~74%) followed by inter-site (14.8%) and inter-station (5.9%) β -diversity (figure 4b). The same
179 partitioning using different site delineations (10 and 20 km) provides similar results (table S4).
180 Diversity partitioning of crypto-benthic fish MOTUs only or pelagic fish MOTUs only reveals
181 similar patterns (table S5). The partitioning diversity of species detected by visual census also
182 revealed similar patterns but with a stronger effect of $\beta_{inter-region}$ (84%) and lower (3x)
183 $\bar{\beta}_{inter-site}$ and $\bar{\beta}_{inter-station}$ (table S5, figure S9).

184

185 Beyond the hierarchical partitioning of diversity, we compared the distribution of fish MOTUs
186 and species visual occurrences independently of the survey method and sampling effort using
187 global species abundance distributions (gSAD) (37). We fitted the fish MOTU and species visual
188 occurrences to three distributions (log-series, Pareto and Pareto with exponential finite adjustment,
189 *i.e.* Pareto Bended, see Methods) and estimated the parameters by maximum likelihood. For the
190 visual census gSAD, the best fit was obtained with the log-series and Pareto distributions (table
191 S6) with a slope of -0.95 (confidence interval at 95% [-0.98;-0.92]) (figure S10). This suggests a
192 distribution of geographically restricted or rare species close to the neutral theory (β close to -1).
193 By contrast, the best fit for fish MOTUs was obtained with the Pareto Bended distribution with a
194 slope $\beta = -0.76$ (confidence interval at 95% [-0.85;-0.65]) and then with the log-series distribution,
195 suggesting a lower prevalence of rarity than under the neutral theory, in agreement with previous
196 tests based on species distributions on coral reefs (38).

197

3. Discussion

199 Environmental DNA allows the detection and identification of more taxa than traditional
200 techniques (26,39), but further offers novel insights on the spatial organization of the richest
201 marine ecosystem at large scale. Over a timespan of 2.3 years, in major tropical ocean basins,
202 eDNA metabarcoding reveals a higher proportion of crypto-benthic, pelagic and soft-sediment-
203 associated fishes on coral reefs than detected in the most extensive visual census over 13 years.
204 We found a high local MOTU turnover, but we were not able to conclude if it is due to an
205 insufficient sampling at the station level, or if it suggests that differences in fish species
206 composition may exist between adjacent reefs that are not detected by visual surveys (40), so that
207 fish biodiversity is more patchy than previously thought on coral reefs.

208

209 We were also able to retrieve well-known patterns of fish diversity on coral reefs such as the
210 biogeographic boundaries between the Atlantic and Pacific oceans, the longitudinal diversity
211 gradient from the center of the Coral Triangle, with Southeast Polynesia being the least diverse
212 region and Western Coral Triangle the richest, and that Gobiidae, Labridae, Pomacentridae and
213 Apogonidae are the most diverse fish families on coral reefs (8). We found a lower proportion of
214 rare MOTUs than expected under the neutral theory with eDNA, which is in agreement with the
215 findings of a previous study from coral reefs in the Indo-Pacific (38), while visual census data
216 suggests higher rarity close to that predicted from the neutral theory. More surprising, our study
217 calls into question the pattern of fish family stability composition across the Indo-Pacific that was
218 revealed more than 20 years ago (8), and the recent finding that planktivore families drive fish
219 biodiversity patterns on coral reefs (11). We found significant effects of species richness and
220 region on family composition, which appears less stable than previously thought.

221
222 Environmental DNA identified many pelagic, deepwater and crypto-benthic species not seen by
223 divers. Among the pelagic species identified with eDNA, many belong to the Scombridae and
224 Carcharhinidae families, which likely avoid divers or are not permanent residents on coral reefs
225 so can be missed in visual surveys (41). Some crypto-benthic or reef-associated species, hidden in
226 the reef, can also be missed by divers so were also more represented in eDNA than in visual
227 surveys. Crypto-benthic species also have a crucial role for coral reef functioning, by promoting
228 biomass production and fueling the reef trophodynamics (42), but their diversity has been
229 underestimated so far (13). Transient, pelagic and deep-water species may be very important for
230 reef functioning, through pelagic larval stages or nocturnal migration up the reef slope (12,43,44),
231 but their presence and role need further investigation. In contrast, visual census also detected many
232 families not detected, or not identified, by eDNA, such as Acanthuridae, Blenniidae, Caesionidae,
233 Chaenopsidae, Chaetodontidae, Labrisomidae, Labridae or Microdesmidae. This limited
234 identification by eDNA can be due to the very low representation of these families in 12S reference
235 databases (between 0 and 12%), or to the low resolution of the teleo marker for species of these
236 families, so several species can share the same sequence and be grouped under the same MOTU.
237 Environmental DNA may also be inappropriate to detect these species in the environment.

238
239 The finding of a strong regional effect on both species composition (figure 3) and species
240 differentiation (figure 4) at a large scale is in agreement with visual surveys and previous
241 knowledge (45), while the suggestion of a strong turnover at the local scale may be an unexpected
242 result for coral reef fishes. This predominant role of large-scale bioregional differentiation explains
243 the exceptional fish diversity on coral reefs, probably associated with long-term geological
244 isolation (2). Overall, the Tropical Northwestern Atlantic region has a very distinct MOTU

245 composition compared to the four other regions (figure 3) with only 1.2% of MOTUs being shared
246 between the Tropical Northwestern Atlantic and any other region, while 20% of MOTUs are
247 shared between at least two Indo-Pacific regions (figure 4a). The isolation of the Tropical
248 Northwestern Atlantic region can be explained by the hard vicariant barrier of the Isthmus of
249 Panama (14,46), and a limited suitable area for coral reefs during the past quaternary glaciation.
250 By contrast, the Indo-Pacific maintained extensive coral reef refuges that have served as centers
251 of survival during ice-age periods (9).

252 The greater local compositional dissimilarity of reef fishes among adjacent stations with eDNA
253 than with visual census may correspond to local environmental or habitat differences, to stochastic
254 or random processes (47), or may be due to an insufficient sampling at the station level
255 (Supplementary Analyses Fig. 6). A higher number of replicates per station would be necessary to
256 characterize exhaustively the diversity at the station level and more confidently conclude on the
257 local turnover hypothesis.

258

259 While our results confirm the potential of eDNA to monitor biodiversity in marine ecosystems,
260 some limitations should be addressed in the future to fully exploit this potential. Completing public
261 reference databases would improve the accuracy of taxonomic assignment, which is essential for
262 a better estimation of biodiversity patterns. At such a large spatial scale, reference databases are
263 far from exhaustive with only up to 13% of fish species sequenced on our marker (52), preventing
264 assignment to the species level for 81% of our eDNA sequences. Using multiple markers is an
265 alternative to the database limitation (53,54), but it is much more expensive. For these reasons, we
266 used MOTUs curated by a combination of a clustering algorithm and conservative abundance-
267 based post-clustering filters. While un-curated MOTUs are prone to overestimate real diversity
268 (55) and a given MOTU can represent several species within one cluster or several MOTUs

269 belonging to one species, MOTUs with conservative curation have been shown to reflect the true
270 level of fish diversity across scales in streams (56,57). Additionally, some species share the same
271 barcode sequence due to insufficient genetic differentiation on such a small mitochondrial marker
272 (54). This lack of taxonomic resolution combined with a conservative curated MOTUs pipeline
273 can underestimate MOTUs richness. Moreover, some crypto-benthic or rare fish families are still
274 underrepresented in public databases, and their diversity is potentially underestimated with eDNA
275 (i.e. Blenniidae, Gobiococidae, Chaenopsidae, Aploactinidae).

276 Differences in sampling method and in sample size might influence the detected biodiversity with
277 eDNA. The lower volume of water sampled in the Western Coral Triangle region (2L per sample,
278 so 4L per station using point-sampling instead of 2-km transect with 30L elsewhere), could
279 underestimate fish biodiversity. However, previous studies show that MOTU accumulation curves
280 based on this dataset were close to the total fish diversity reported in this region (32). Furthermore,
281 β -diversity between samples within stations in each region indicates that dissimilarity between
282 samples is not greater in the Western Coral Triangle than in other regions (figure S11). To account
283 for differences in sample size and obtain a balanced design, we performed sensitivity analyses by
284 rarefying our complete dataset to i) 4 stations for all sites and ii) 4 sites per region after removing
285 the lowest sampled region (Southeast Polynesia) (Supplementary Analyses Fig. 1-4). We obtained
286 similar patterns even after subsampling stations or sites. However, our site-based and station-based
287 accumulation curves do not reach plateaus suggesting that our sampling effort was not sufficient
288 to exhaustively estimate fish biodiversity for each site (Supplementary Analyses Fig. 5) and station
289 (Supplementary Analyses Fig. 6). Twenty-five replicates (so, 12 stations in case of field
290 duplicates) could accurately estimate biodiversity regionally due to high local turnover (58). A
291 higher number of eDNA samples would be necessary here to reach MOTU accumulation per site
292 and station.

293 The transport and degradation of eDNA can also impact species detection. As some evidence
294 suggests that eDNA from pelagic fishes degrades slower than from inshore species (59), we cannot
295 exclude that eDNA from pelagic and deep-water families (*e.g.* Myctophidae) might disperse
296 sufficiently with sea currents such that species living close to reef habitats are detected.
297 Environmental DNA transport could also explain the detection of some freshwater fish families
298 (*i.e.* Centrarchidae, Osphronemidae or Channidae) in a few samples located near an estuary or in
299 an enclosed bay with freshwater inputs.

300

301 Better understanding and anticipating the effects of multiple threats to the marine environment
302 depends on the temporal and spatial extent of our monitoring capacity in the vast ocean.
303 Environmental DNA is a powerful tool to investigate biodiversity patterns at large scale and
304 monitor biodiversity, but still benefits from the combination with complementary approaches as
305 visual methods for an exhaustive biodiversity survey across space and time to keep pace with
306 ongoing changes.

307

308 **4. Methods**

309 **(a) Environmental DNA collection and sample processing**

310 Environmental DNA seawater samples were collected between 2017 and 2019, following a
311 hierarchical pattern. A total of 226 eDNA samples (filters) were collected in 100 stations
312 (gathering of replicates at the same location) located in 26 sites (groups of stations separated by at
313 least 35 km) distributed across five tropical regions (figure S1-S2). Three different sampling
314 methods were used comprising a 2km-long sampling transect of 30L (surface or bottom depth) or
315 point samples of 2L (table S7 and Methods S1), and between 12 and 64 samples were collected by

316 region. Filtration was performed with Polyethersulfone (PES) filters, 0.2 µm pore size. For each
317 sampling campaign, a strict contamination control protocol was followed in both field and
318 laboratory stages (39). Negative field controls were performed in multiple sites, and revealed no
319 contamination from the boat or samplers.

320

321 **(b) eDNA extraction, amplification and sequencing**

322 DNA extraction was performed in a dedicated DNA laboratory (SPYGEN, www.spygen.com)
323 equipped with positive air pressure, UV treatment and frequent air renewal. Decontamination
324 procedures were conducted before and after all manipulations. Detailed protocols of DNA
325 extraction, amplification and sequencing can be found in Method S2 and in (32,39). A teleost-
326 specific 12S mitochondrial rRNA primer pair (teleo, forward primer -
327 ACACCGCCCGTCACTCT, reverse primer – CTTCCGGTACTTACCATG (39)) was used
328 for the amplification of metabarcode sequences. As we analysed our data using MOTUs as a proxy
329 for species to overcome genetic database limitations, we chose to amplify only one marker. Teleo
330 marker has been shown to be the most appropriate for fish, owing to its high interspecific
331 variability, and its short size allowing us to detect rare and degraded DNA reliably (39,54,60,61).
332 Twelve DNA amplifications PCR per sample were performed.

333

334 **(c) Bioinformatic analysis**

335 Following sequencing, reads were processed using clustering and post-clustering cleaning to
336 remove errors and estimate the number of species using Molecular Operational Taxonomic Units
337 (MOTUs) (56). First, reads were assembled using *VSEARCH* (62), then demultiplexed and
338 trimmed using *CUTADAPT* (63) and clustering was performed using *SWARM* v.2 (64) with a

339 minimum distance of 1 mismatch between clusters. Taxonomic assignment of MOTUs was carried
340 out using the Lower Common Ancestor (LCA) algorithm *ecotag* implemented in the OBITOOLS
341 toolkit (65) and the European Nucleotide Archive (ENA) as a reference database (release 143,
342 March 2020). Details on the bioinformatics analysis can be found in Methods S3. Taxonomic
343 assignments obtained from the LCA algorithm at the species level were accepted if the percentage
344 of similarity with the reference sequence was 100%, at the genus level if the similarity was between
345 90 and 99%, and at the family level if the similarity was > 85% following previous studies (32,66).
346 If these criteria were not met, the MOTU was left unassigned. Only 21% of assigned MOTUs are
347 assigned to the family level with a similarity between 85 and 90% (Table S8).

348

349 **(d) Visual census data**

350 The visual census survey data used here is a subset (2047 transects, in 219 sites, figure S1) of the
351 complete visual census data (3027 transects) provided by the RLS (31), and comprises all species
352 observed on standardized 50 m surveys at sites in tropical biogeographic realms between 2006 and
353 2017 (Methods S4) (67). We selected only the most recent survey for each station and only
354 transects with more than five percent of coral cover. Two different sampling protocols were
355 adapted to detect both reef and crypto-benthic fishes.

356

357 **(e) Statistical analysis**

358 More details on the statistical analysis are available in Methods S5.

359 Accumulation curves were calculated for species per 500 m² transect, MOTUs per eDNA sample,
360 and families per transect and sample. We used the functions “specaccum” and “fitspecaccum”
361 from the R package “vegan” which calculates the expected species accumulation curve using a

362 sample-based rarefaction method and fit a nonlinear accumulation model. In order to assess the
363 impact of the irregular sampling on the estimates measured with accumulation curves, we subset
364 randomly half of the transects in the 3 most sampled regions in Australia, and calculated again the
365 accumulation curves for species and families (figure S12). The results were unchanged.

366 Linear regression models were fitted between the number of MOTUs per family in the eDNA
367 dataset and the number of species per family in the visual census dataset, after $\log(x+1)$
368 transformation (figure 1e).

369 Accumulation curves were also calculated by sub-setting MOTUs belonging to crypto-benthic
370 orders, or to pelagic families, for both datasets (figure 2). The asymptote was calculated as
371 described above.

372 We performed distance-based Redundancy Analysis (dbRDA) on family proportions, with *region*
373 and *site richness* as explanatory variables, using the function *capscale* from the *vegan* package.
374 We subset the Visual Census to select only the 68 sites that fell into the 5 regions in common with
375 the eDNA dataset. Total dbRDA provided the effects of each of the variables and their interaction.
376 We then calculated partial dbRDA to measure the effect of the Region while correcting for the
377 effect of site richness (figure 3, table S3).

378 We applied an additive partitioning framework (68) to separate the total MOTUs diversity at the
379 global scale (γ global) into contributions at smaller scales from regions to local richness : $\gamma_{global} =$
380 $\beta_{inter-region} + \text{mean } \beta_{inter-site} + \text{mean } \beta_{inter-station} + \text{mean } \bar{\alpha}_{station}$. In this additive framework, the three
381 levels of biodiversity (69) (i.e. α , β and γ) are expressed with the same unit and consequently the
382 contribution of α and β diversity to total diversity (γ) can be directly compared (70).

383 We analyzed the distribution of fish MOTU and species occurrences using global species
384 abundance distribution (gSAD) which plots, on a log-log scale, the number of species as a function
385 of the number of observations (37).

386

387

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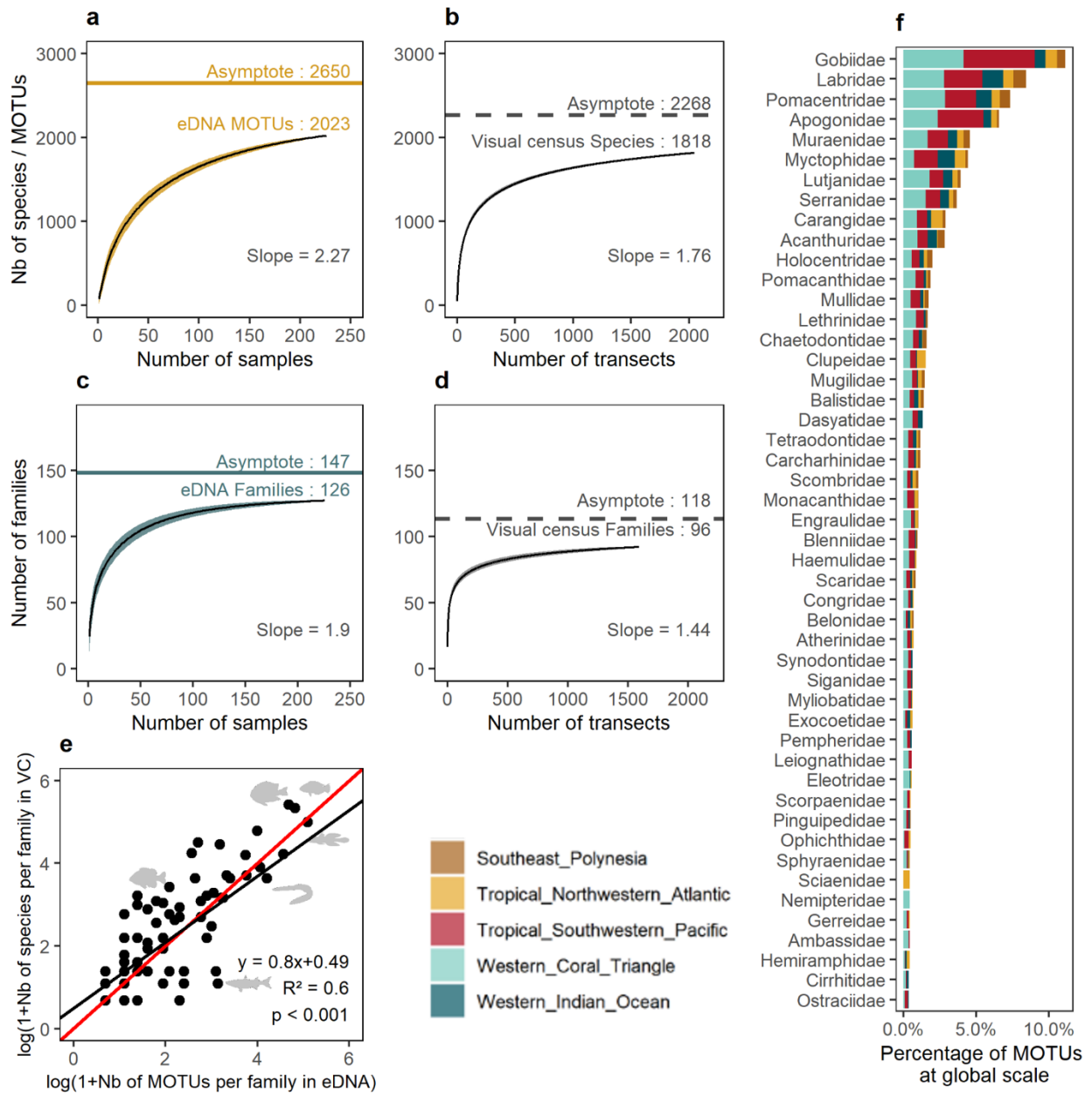
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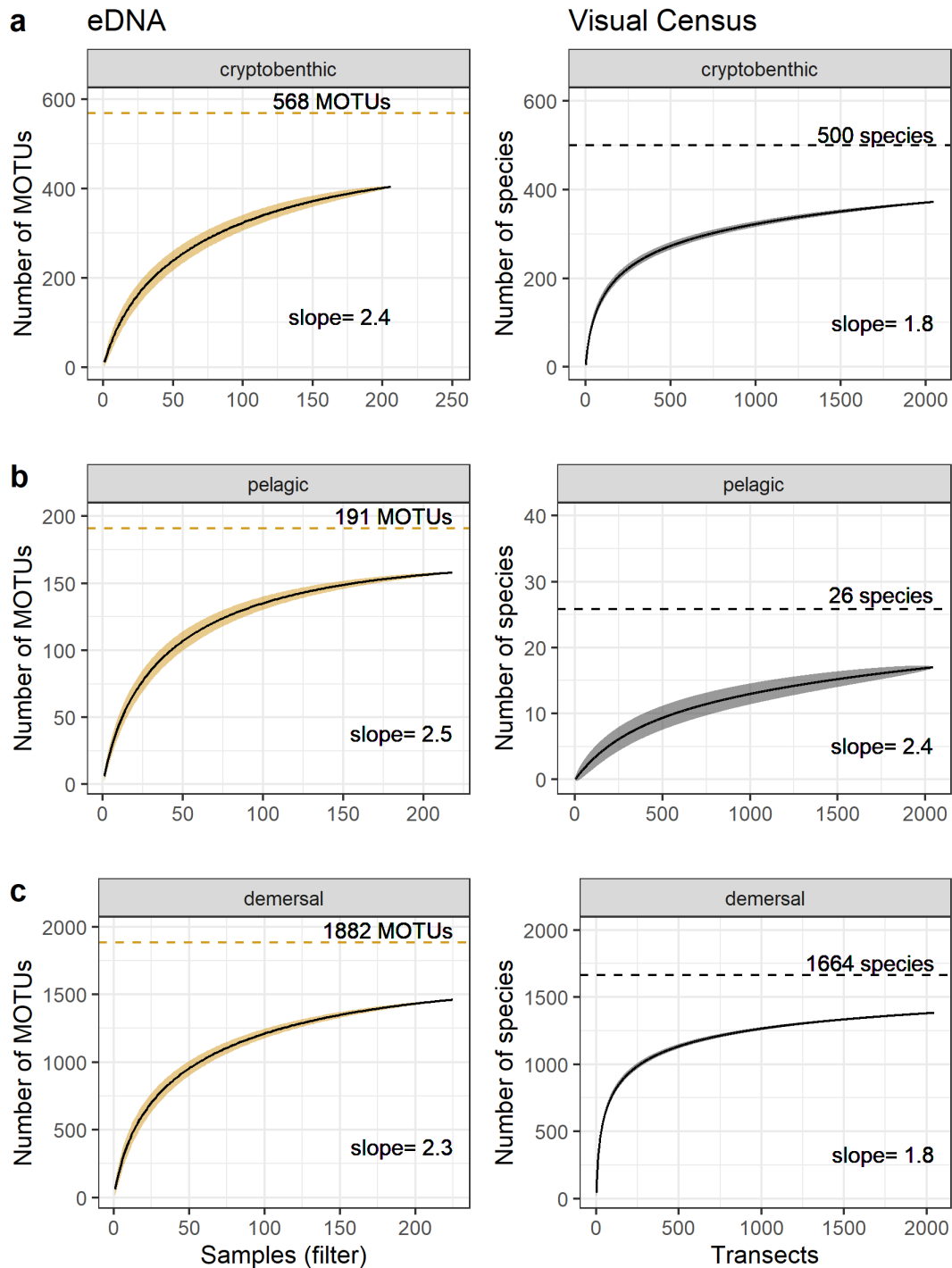
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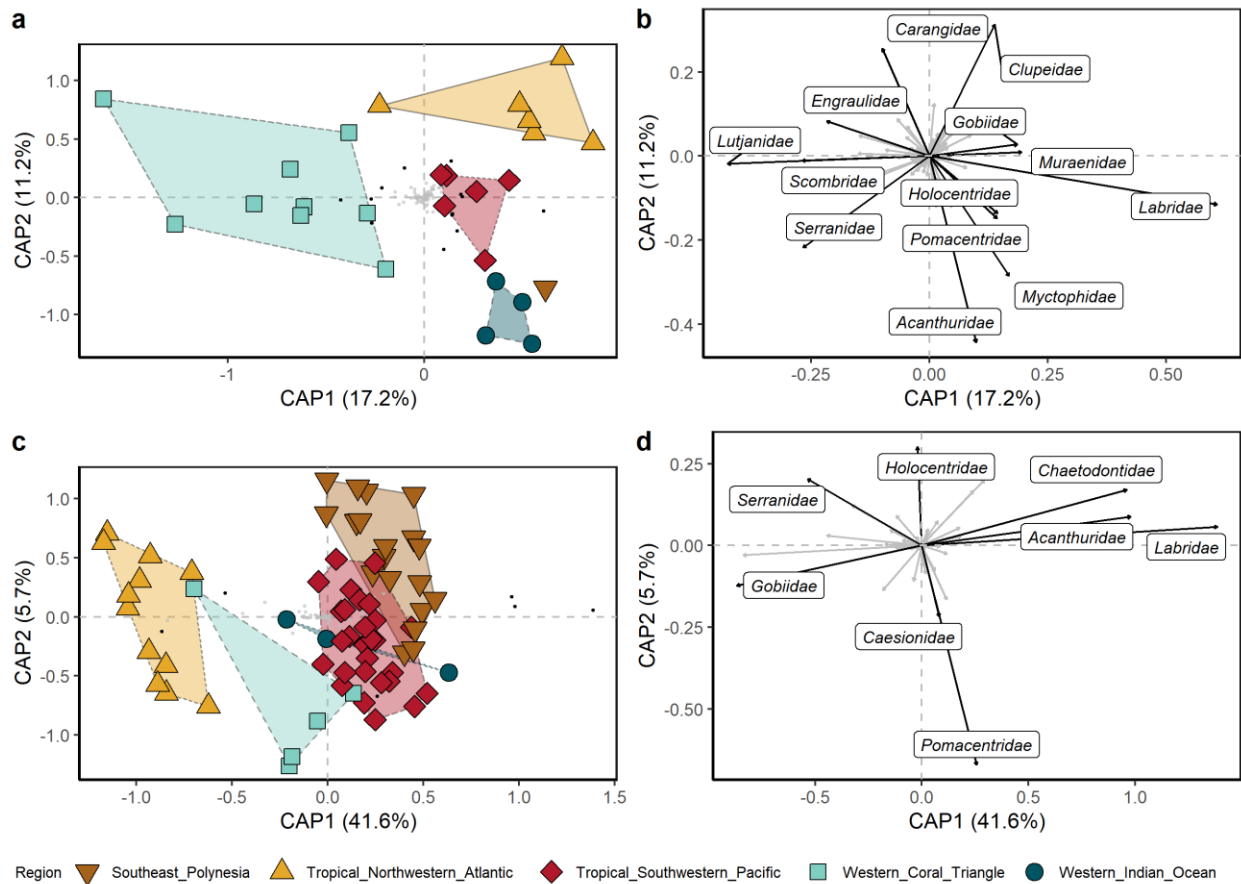
570 **Figure 1. Estimates of overall fish richness from environmental DNA (eDNA) and visual**
 571 **census.** (a) accumulation curve of molecular operational taxonomic units from eDNA (eDNA
 572 MOTUs), (b) accumulation curve of species from the visual census database, (c) accumulation
 573 curve of eDNA families, (d) accumulation curve of visual census families. For (a-d), Species
 574 accumulation model is fitted according to Lomolino method (see methods). (e) linear regression
 575 (black line) between the number of species per family in visual census data and the number of
 576 MOTUs per family in eDNA (log(x+1) transformation) over $n = 77$ families. Each point is a
 577 family. Red line is $x=y$. (f) percentage of MOTUs assigned to each family at global scale, and
 578 proportion in each region.



579

580 **Figure 2. Estimates of overall fish richness from eDNA and visual census across habitat**
 581 **categories.** (a) accumulation curve of crypto-benthic eDNA MOTUs (left) and visual census
 582 species (right), (b) accumulation curve of pelagic MOTUs (left) and visual census species (right),
 583 c, accumulation curve of demersal MOTUs (left) and visual census species (right). Accumulation
 584 model is fitted with a nonlinear Lomolino model (see Methods).

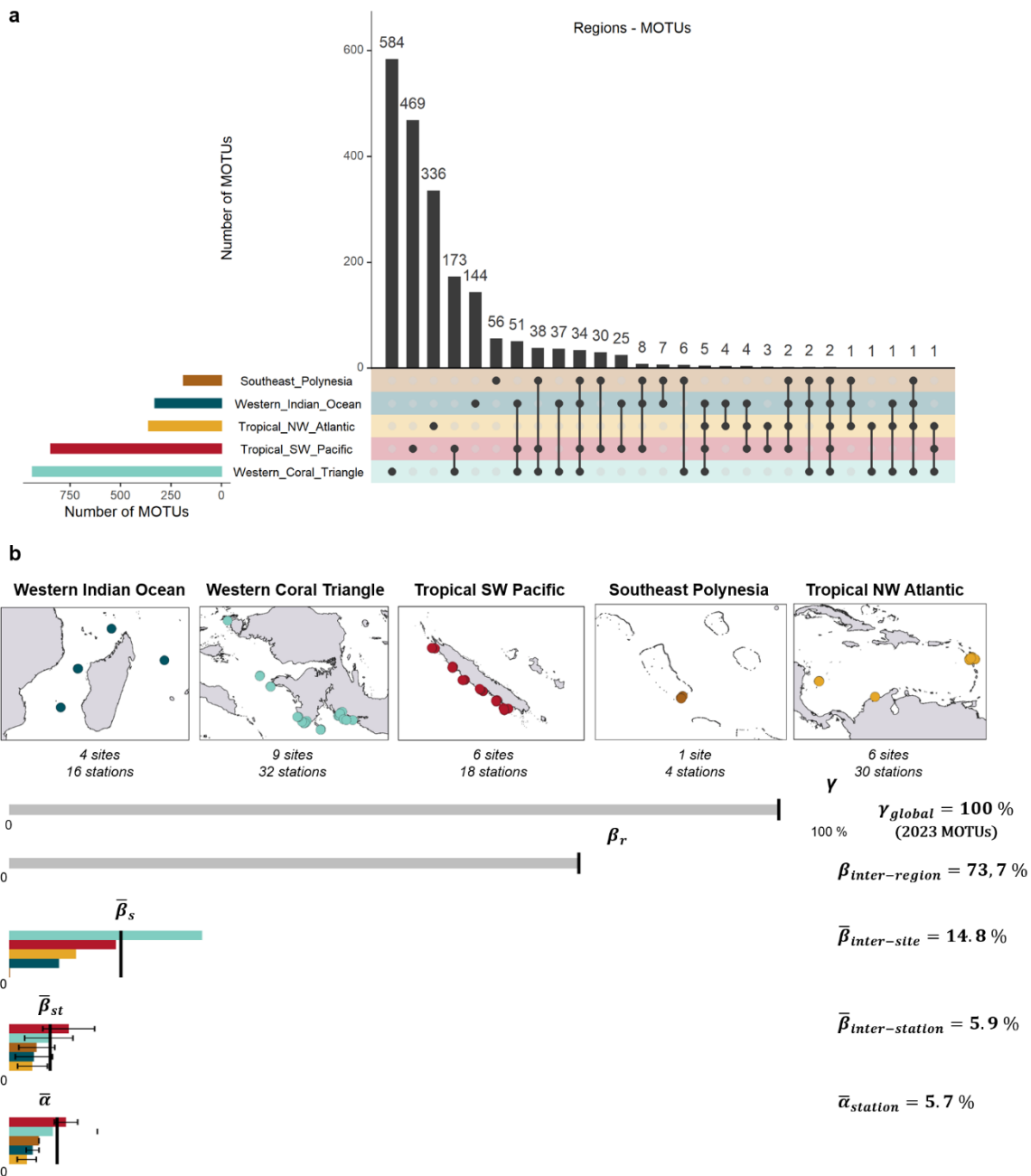
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587 **Figure 3. Partial Distance-based Redundancy analysis of MOTU proportions of each family**
 588 **in each site.** (a) dbRDA on eDNA dataset, with 133 families in 26 sites ($R^2=0.21$, $F=3.11$,
 589 $p=0.001$), (b) families with scores > 95% of scores distribution on each axis for eDNA, (c) dbRDA
 590 on a subset of Visual Census dataset to select only the sites in the same regions as in the eDNA
 591 dataset, with 76 families in 68 sites ($R^2=0.5$, $F=15.8$, $p=0.001$), (d) families with scores > 95% of
 592 scores distribution on each axis for Visual Census. Axis labels indicate the percentage of variance
 593 explained by the 2 first dbRDA dimensions (CAP1 and CAP2).

594



595

596 **Figure 4. Hierarchical partitioning of MOTU occurrences across spatial scales.** (a) Number
 597 of MOTUs found in only one region, or shared between 2, 3, 4 or all 5 regions. Histograms indicate
 598 the number of MOTUs present in all the regions identified by the dots in the lower part. (b) Global
 599 fish diversity (γ_{global}) is partitioned into $\beta_{inter-region}$ + mean $\beta_{inter-site}$ + mean $\beta_{inter-station}$ + mean $\bar{\alpha}_{station}$.
 600 Mean values at global scales are indicated with the black vertical segments. For $\beta_{inter-site}$, $\beta_{inter-station}$
 601 and $\bar{\alpha}_{station}$, mean values are given for each region (colored bars) with the standard errors. $\beta_{inter-region}$
 602 contributes the highest to gamma global (73.7%).
 603