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HAL Authorization

1 **Similar trait structure and vulnerability in pelagic fish faunas on two remote island**  
2 **systems**

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6  
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8

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29 **Abstract**

30 The link between biodiversity and ecosystem functioning has been the topic of  
31 considerable research, but it remains unclear how biodiversity decline is compromising  
32 ecosystem functionality, particularly in the pelagic realm. Here, we explore how pelagic fish  
33 species diversity relates to functional diversity by sampling two locations, which, on the  
34 basis of biogeography, environmental conditions, and human pressures, were expected to  
35 host pronounced differences in species composition and abundances, and therefore  
36 functionality. Strings of five drifting mid-water Baited Remote Underwater Video Systems  
37 were used to survey pelagic vertebrate diversity and abundance in two isolated oceanic  
38 island systems, the Malpelo Fauna and Flora Sanctuary – a large, 25-year-old marine  
39 protected area – and an unprotected area in Cape Verde. Functional diversity, which offers  
40 insight into a community’s resilience against disturbance, was analysed using six key  
41 functional traits of marine fishes. Abundance was recorded as MaxN, the maximum  
42 number of individuals of a given species in a single frame during the 2-hour deployment  
43 time. Cape Verde showed high overall abundance (Total MaxN 873) and low biomass (3,559  
44 kg), with a predominance of smaller fishes. Malpelo showed high biomass (7,839 kg) but  
45 lower abundance (Total MaxN 465), with a predominance of large species. Species and  
46 functional diversity were marginally different between locations. Multivariate analysis of  
47 species relative abundances showed significant divergence between locations, although  
48 community functional traits overlapped strongly, suggesting that both communities share  
49 a similar structure and vulnerability. The existence of a common functional ‘backbone’ in  
50 diverging species communities across the oceans, under different productivity regimes,  
51 and under different protection levels, suggests that although pelagic communities may  
52 differ considerably in terms of species composition, this does not translate into a differing  
53 functional structure and resilience potential. Whether this vulnerability is a common  
54 feature of pelagic communities and how this contrasts with benthic systems warrants  
55 further research.

56

57

58 Key words: Biodiversity, Functional diversity, Pelagic fish, Islands, Mid-water BRUV

59 **Introduction**

60 The pelagic realm is the world's largest habitat, covering 71% of Earth's surface (1368.10<sup>6</sup>  
61 km<sup>2</sup>), and providing millions of tons of fish biomass annually (Chassot et al. 2010). Pelagic  
62 systems have a massive influence on global nutrient cycling, food production, and climate  
63 change, each of which may be influenced by the abundance and composition of pelagic  
64 communities (Duffy & Stachowicz 2006, Sala et al. 2021). Yet, the vast pelagic area with  
65 dynamic environmental conditions (Breitburg et al. 2018)) and heterogeneous distribution  
66 of animals (Denderen et al. 2018) make it difficult to monitor and understand pelagic  
67 faunas (Briscoe et al. 2016), challenging the design of marine protected areas (Sala et al.  
68 2021) and the appropriate management of fisheries (Pons et al. 2018).

69 Pelagic ecosystems hold unique characteristics compared to the benthos, with likely  
70 implication for vulnerability and resilience. While pelagic diversity is considered relatively  
71 low compared with that of demersal fish communities (Tittensor et al. 2010), pelagic  
72 communities may show high local diversity, as a function of biogeography, bathymetry, and  
73 productivity (Bouchet et al. 2020). Oceanic islands, banks, and seamounts are notable  
74 hotspots of species richness (Letessier et al. 2019), which predictably aggregate fish  
75 biomass, including mobile predators, by acting as navigation points and reliable feeding  
76 grounds (Hosegood et al. 2019). Because prey density in the open ocean is generally low,  
77 predators need to forage over a wide range to fulfil their energetic requirements, leading  
78 to resource translocation from other habitats and promoting food web connectivity  
79 (Heupel et al. 2014).

80 Ecosystem functioning and resilience are increasingly assessed using trait-based analyses  
81 (McLean et al. 2019), an approach that determines which functional roles are being filled  
82 and by which species (Mouillot et al. 2013). At the community level, functional traits explain  
83 differences of vulnerability between species: for example, predators and large individuals  
84 may be preferentially targeted by fishing (Mbaru et al. 2020). In the face of increasing  
85 fisheries pressure and environmental change, a trait-based approach may capture novel  
86 aspects of pelagic community vulnerability missed by classic community-based analyses.  
87 However, it remains unclear to which degree different pelagic systems are similarly

88 vulnerable, due in part because of limited pelagic sampling methodologies (Letessier et al.  
89 2017).

90 Here, we use mid-water Baited Remote Underwater Video Systems (BRUVS, Bouchet &  
91 Meeuwig 2015) to assess how pelagic fish communities differ taxonomically and  
92 functionally. Our study took place in Malpelo Island and in Cape Verde, two remote tropical  
93 island systems located in different biogeographical provinces (Kulbicki et al. 2013), which  
94 are exposed to contrasting levels of both environmental conditions and human pressures.  
95 We hypothesise that species community differences in taxonomy and relative abundance  
96 at each location may lead to trait dissimilarity, with implication for resilience and  
97 vulnerability.

98 Our objectives were to 1) describe and contrast species communities on each island using  
99 mid-water BRUVS and multivariate analyses, and 2) assess the extent to which any species  
100 dissimilarity translates into functional dissimilarity, using multivariate trait-based analyses,  
101 and then (3) make general inference concerning pelagic vulnerability.

102

## 103 **Materials and Methods**

### 104 *Study locations*

105 Our study aimed to target features such as islands and seamounts known to provide key  
106 habitat for top predators and migratory species. In Malpelo Island, BRUVS were  
107 deployment at four sites around the island, located within 3°57'5.184" to 4°1'46.704" N,  
108 and 81°40'8.256" to 81°35'47.4" W, with seabed depths ranging from 25 m to 1500 m (Fig.  
109 1). In Cape Verde, BRUVS deployments focusing on the areas southwest of the island of  
110 Boa Vista, and on the João Valente Bank seamount between 15°47'40.452" to 16°0'25.2"  
111 N, and 23°12'17.316" to 22°56'11.148" W, with seabed depths ranging from 25 to 500 m  
112 (Fig. 1).

113 Malpelo is a remote oceanic island located in the Tropical Eastern Pacific, approximately  
114 500 km west of Buenaventura, Colombia. The interaction of multiple seasonal currents  
115 results in distinct cold and warm water seasons at Malpelo (Bessudo et al. 2011). The survey  
116 at Malpelo was conducted between 18 and 28 March 2018, 8:00 AM to 5:00 PM local time,

117 during the cold season, which occurs between January and April and is characterized by a  
118 shallow thermocline – around 15 m depth – decreased visibility due to high primary  
119 production caused by upwelling, and an average sea surface temperature of about 25° C  
120 (Soler et al. 2013). An area of 8,575 km<sup>2</sup> surrounding Malpelo is designated as the Malpelo  
121 Flora and Fauna Sanctuary, a marine protected area (MPA) since 1995 (UNESCO 2019).  
122 Though it is a no-take MPA, some illegal, unreported, and unregulated (IUU) fishing activity  
123 is believed to occur (Bessudo et al. 2011).

124 The Republic of Cape Verde is an archipelago nation located around 600 km west of  
125 Senegal, with a population of approximately 550,000 (United Nations 2019). It falls within  
126 the Tropical Eastern Atlantic biogeographic region and is subject to the seasonal influences  
127 of both the Canary Current and the North Equatorial Countercurrent (Wirtz et al. 2008).  
128 The survey in Cape Verde took place from 27 September to 1 October 2017, 9:00 AM to  
129 4:30 PM local time, in the warmer months, during which average sea-surface temperature  
130 is around 27°C (Stobberup et al. 2004). Domestic artisanal and commercial fishing occur  
131 throughout the area, including vessels flagged from the European Union and China (Medina  
132 et al. 2015). Substantial IUU fishing also contributes to overall fisheries landings (Medina  
133 et al. 2015). Pelagic target species include tuna, billfish and mackerel scad, with sharks as  
134 important bycatch (Santos et al. 2013).

### 135 *Sampling protocol*

136 The pelagic community in each location was assessed using drifting mid-water BRUVS  
137 (Bouchet & Meeuwig 2015). Each rig consisted of a metal frame with two GoPro cameras  
138 in underwater housings mounted on a bar perpendicular to an arm supporting a bait  
139 canister filled with 1 kg of crushed fish (tuna and mackerel). The two cameras were  
140 intended to be used for stereo measurements, but could not be calibrated in the field, so  
141 only footage from the right-hand camera of each rig was used for analysis. The rigs were  
142 suspended from buoys at a depth of 10 m (Bouchet & Meeuwig 2015). BRUVS rigs were  
143 deployed in groups of five – hereafter referred to as “strings” – with each rig connected to  
144 the next one by a 200 m line. This distance was a trade-off between field practicalities and  
145 maximising the distance between rigs (Bouchet et al. 2018). The strings were allowed to

146 drift for approximately two hours, an effective duration for mid-water BRUVS (Bouchet et  
147 al. 2018).

#### 148 *Data analyses*

149 The BRUVS footage was analysed using the video analysis software VidSync (Neuswanger  
150 et al. 2016). Analysis began when the camera settled underwater and ended when the  
151 duration of the recording reached two hours. Species were identified to the lowest possible  
152 taxonomic level using information and photographs available from reference books and  
153 FishBase (Froese & Pauly 2019, Humann & DeLoach 2004, Humann & DeLoach 2014).  
154 Where species-level identifications could not be made, genus or family names were used.  
155 For each species, we recorded MaxN, the maximum number of individuals present in a  
156 single frame, thereby preventing double-counting (Priede et al. 1994). Due to the proximity  
157 between each rig, abundance for each species was reported at the level of the string, using  
158 the maximum MaxN value across each rig (Bouchet et al. 2018). We opted for this approach  
159 as 200 m separation between rigs is probably not sufficient to guarantee independence,  
160 certainly not for large sharks, which can cover more than this distance during the 2-hour  
161 soak time. In the absence of stereo measurements, the biomass of each species was  
162 computed using common lengths and Bayesian length-weight coefficients available from  
163 FishBase and scaled by abundance (Table S1). These biomass estimates are speculative  
164 since they are based on calculations from FishBase rather than true measurements. The  
165 conclusions on biomass patterns from this study are therefore rough estimates. Future  
166 studies should include stereo measurements to more accurately assess patterns in fish  
167 biomass.

168 Total abundance and biomass by deployment or site were analysed using PERMANOVA.  
169 Biomass was reported by species, but was not analysed further. The differences between  
170 species communities at each site were tested with an analysis of similarities (ANOSIM) on  
171 Bray-Curtis dissimilarity between all pairs of communities. A similarity percentage (SIMPER)  
172 analysis using Bray-Curtis dissimilarity and 1,000 permutations were used to compare  
173 species groups by site. Species community abundance were illustrated using non-metric  
174 multidimensional scaling (NMDS).

175 Each species was functionally described using a set of 6 complementary traits describing  
176 their key ecological features (Mouillot et al. 2014, Villéger et al. 2017). The traits were size,  
177 mobility, period of activity, schooling, position in water column, and diet (Table S2). Values  
178 for the adult stage of each species were gathered from FishBase and other literature  
179 (Supplementary material). A multidimensional functional space was calculated following  
180 the methods of Maire et al. (2015). First, a dissimilarity matrix quantifying the functional  
181 distance between species was computed using Gower's distance, which is able to  
182 accommodate categorical traits. A Principal Coordinates Analysis (PCoA) was performed  
183 with this matrix, and the mean squared deviation (mSD) was used to select the best quality  
184 functional space. The mSD quantifies the "mean squared deviation between the initial  
185 functional distance and the scaled distance in the functional space" and – when using  
186 Gower's distance – ranges from 0 to 1, the closest value to zero indicating the most robust  
187 functional space (Maire et al. 2015). The four-dimensional space – or the space using the  
188 first four axes of the PCoA – was the highest quality space with an mSD of 0.0026 (Fig. S1).

189 Three complementary functional diversity indices were calculated using species position in  
190 the multidimensional space: functional richness (FRic), functional evenness (FEve), and  
191 functional divergence (FDiv) (Villéger et al. 2008). These metrics are favoured for functional  
192 diversity analysis because they can work with multiple traits. FRic measures how much  
193 functional space is filled by a species community and accounts only for species position in  
194 the multidimensional range. FEve and FDiv account for species abundance and measure  
195 regularity and variance within the occupied space, respectively (Villéger et al. 2008). To  
196 further explore functional overlap between communities, functional beta-diversity and its  
197 percentage due to species turnover were computed using Jaccard's dissimilarity index  
198 (Villéger et al. 2013). All analyses were performed in R statistical software (R Core Team  
199 2018), including the *mFD* package for computation of functional space and functional  
200 diversity indices (<https://cmlmagneville.github.io/mFD/>).

201

## 202 **Results and discussion**

203 Eight strings, a total of 40 individual rigs (80 video hours in total), were deployed in Malpelo  
204 and nine strings, a total of 44 individual rigs as one string had only 4 rigs (88 video hours in  
205 total), were deployed in Cape Verde. In line with expectations, we observed distinct species  
206 compositions between locations. BRUVS observations yielded 29 fish species, one juvenile  
207 group (Carangidae) and one mammal (family Delphinidae), with 18 species present in  
208 Malpelo and 19 species present in Cape Verde (Fig. 2A). Species ubiquitous to both sites  
209 were wahoo (*Acanthocybium solandri*), silky shark (*Carcharhinus falciformis*), mackerel  
210 scad (*Decapterus sp.*), amberjack (*Seriola sp.*), and juveniles of family Carangidae. Strings  
211 recorded on average fewer species in Cape Verde ( $5.22 \pm 2.11$  SD per string) than in Malpelo  
212 ( $6.25 \pm 2.19$  SD), albeit not significantly (PERMANOVA  $F_{1,15} = 0.3011$ , p-value = 0.773).  
213 Abundance was higher in Cape Verde (873 individuals total, mean  $97 \pm 128.9$  SD per string),  
214 than in Malpelo (465 individuals total, mean  $58.1 \pm 59.9$  SD per string), whereas biomass in  
215 Malpelo (7,838 kg total, mean  $979.8 \pm 506.3$  SD per string) far exceeded the biomass  
216 observed in Cape Verde (3,558 kg total, mean  $395.44 \pm 563.1$  SD per string, Fig. 2B). An  
217 ANOSIM test revealed significantly dissimilar clusters between locations ( $R = 0.5$ ,  $p = 0.001$ ,  
218 Fig. 3A and B). Fifteen species were responsible for 95% of the dissimilarity between sites  
219 (Table S3, SIMPER). Mackerel scad (*Decapterus sp.*), rainbow runner (*Elagatis bipinnulata*),  
220 yellowfin tuna (*Thunnus albacares*), and little tunny (*Euthynnus alletteratus*) cumulatively  
221 contributed 55% of the difference in abundance between Cape Verde and Malpelo, while  
222 rainbow runner, yellowfin tuna, scalloped hammerhead (*Sphyrna lewini*), and cornetfish  
223 (*Fistularia sp.*) contributed significantly to ( $p < 0.05$ ).

224 In contrast with expectations, communities from the two locations filled the same amount  
225 of the functional space (functional richness Malpelo: 0.542, Cape Verde: 0.452), and species  
226 abundance were similarly distributed in the filled space (functional divergence: Malpelo:  
227 0.833, Cape Verde 0.913) in both locations. While the volume of the overall space occupied  
228 by each location was relatively high, the majority of the species were densely distributed  
229 in one area of the space, displaying low functional evenness (0.425 for Cape Verde, and  
230 0.346 for Malpelo). The first two dimensions showed most species clustered on the right-  
231 hand side (Fig. 3C), defined by mobility, whereas the outliers on the left side of the space  
232 had a more restricted range (Fig. S2A). Highly mobile species, clustered into two groups,

233 one characterised by purely pelagic species of very small, and medium size, and with a  
234 planktivorous or omnivorous diet and one by large or very large, benthopelagic species  
235 living solitary or in small groups, and with either a piscivorous or invertivorous diet. The  
236 third and fourth dimensions of the functional space showed some of the same stratification  
237 observed on the first two dimensions. However, the species which diverged from the main  
238 group were planktivores and invertivores which fed on mobile prey (Fig. 3D), with loose  
239 grouping according to different daily activity patterns (Fig. S2B).

240 Functional divergence and functional evenness are indices of the variance and regularity of  
241 species' distribution within the functional space, respectively, weighted by abundance  
242 (Villéger et al. 2008). A highly divergent and minimally even community is one in which  
243 some functional roles are much better represented and insured than others, which leaves  
244 points of exposure to disturbance, particularly when – as was the case here - dominant and  
245 common species are sensitive (McLean et al. 2019). The most dominant species overall  
246 across either location, the Atlantic horse mackerel (*Trachurus trachurus*) is listed as  
247 Vulnerable (Smith-Vaniz et al. 2015). The most abundant by weight, yellowfin tuna  
248 (*Thunnus albacares*), was at the time of sampling listed as Near Threatened, although has  
249 since been listed as Least Concern (Collette et al. 2021). Furthermore, ecologically  
250 important top predators like the silky shark and scalloped hammerhead that were  
251 ubiquitous in both locations are listed as Vulnerable (Rigby et al. 2017) and Critically  
252 Endangered (Rigby et al. 2019), respectively.

253 Overall functional beta-diversity between the locations was 0.6, to which species turnover  
254 contributed 90.3%. The remaining proportion arose from distinct trait combinations, often  
255 between confamilials like the triggerfishes (mobile in Malpelo, and reef-associated in Cape  
256 Verde), surgeonfishes (large in Malpelo and small in Cape Verde) and jacks (large and  
257 piscivorous in Malpelo, and medium and invertivore in Cape Verde). Fishing remains the  
258 primary threat to pelagic elasmobranchs and teleosts (Pacoureau et al. 2021). Although the  
259 bulk of the functional space was similar between locations, the presence of such unique  
260 trait combinations suggests that some nuanced differences in sensitivity may still render  
261 certain locations more or less resilient (Villéger et al. 2013). Future research should aim to  
262 identify pelagic systems which overperform compared to expectations, in order to identify

263 unique resilient traits associated with either positive or negative ecosystem outcomes  
264 (Cinner et al. 2016).

265 Our survey included different biogeographical provinces and covers contrasting ends of  
266 environmental and human pressure gradients, although -due to time constraints, is limited  
267 to a snap-shot view of the species diversity and abundance. Nevertheless our results  
268 presents preliminary evidence that pelagic ecosystems may share a common ‘backbone’ of  
269 functional traits related to mobility and predatory diet. Such a backbone of 21 common  
270 traits has already been documented to exist within global reef ecosystems (McLean et al.  
271 2021). Since ecological disturbance is likely to affect species with identical functional traits  
272 in similar ways (Mouillot et al. 2013), low trait diversity within pelagic ecosystems may  
273 make the pelagic faunas particularly vulnerable to disturbance. A lack of fish length stereo-  
274 measurements means our biomass estimates must be interpreted with caution. We  
275 propose that further study specifically aims to determine whether this is a consistent  
276 feature of the pelagic realm, and the degree to which it may affect the resilience of mid-  
277 water communities.

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## 283 **Declarations**

284

### 285 **Fundings**

286 Field activities were funded by Monaco Explorations. The Bertarelli Foundation funded  
287 TBL’s salary

288

### 289 **Conflict of interest**

290 We declare no conflict of interest

291

### 292 **Ethics approval**

293 As none of the authors are resident in Cape Verde, research there was conducted under  
294 authorization No. 08/GP-CA.AMP/2017.

295

### 296 **Data/Code availability**

297 All code is referenced in the text

298

299 Author's contribution

300 MS conceived and conducted the analysis, and as part of her MSc thesis. TBL supervised  
301 and managed the study, and co-wrote the first draft together with MS. TBL and JB  
302 coordinated the BRUVS deployment, with assistance from RH, LP, CP, AP, and VM. DM and  
303 SV advised on the functional analysis. DM is the PI of the Monaco Exploration 'Megafauna'  
304 team. All authors helped revise the manuscript.

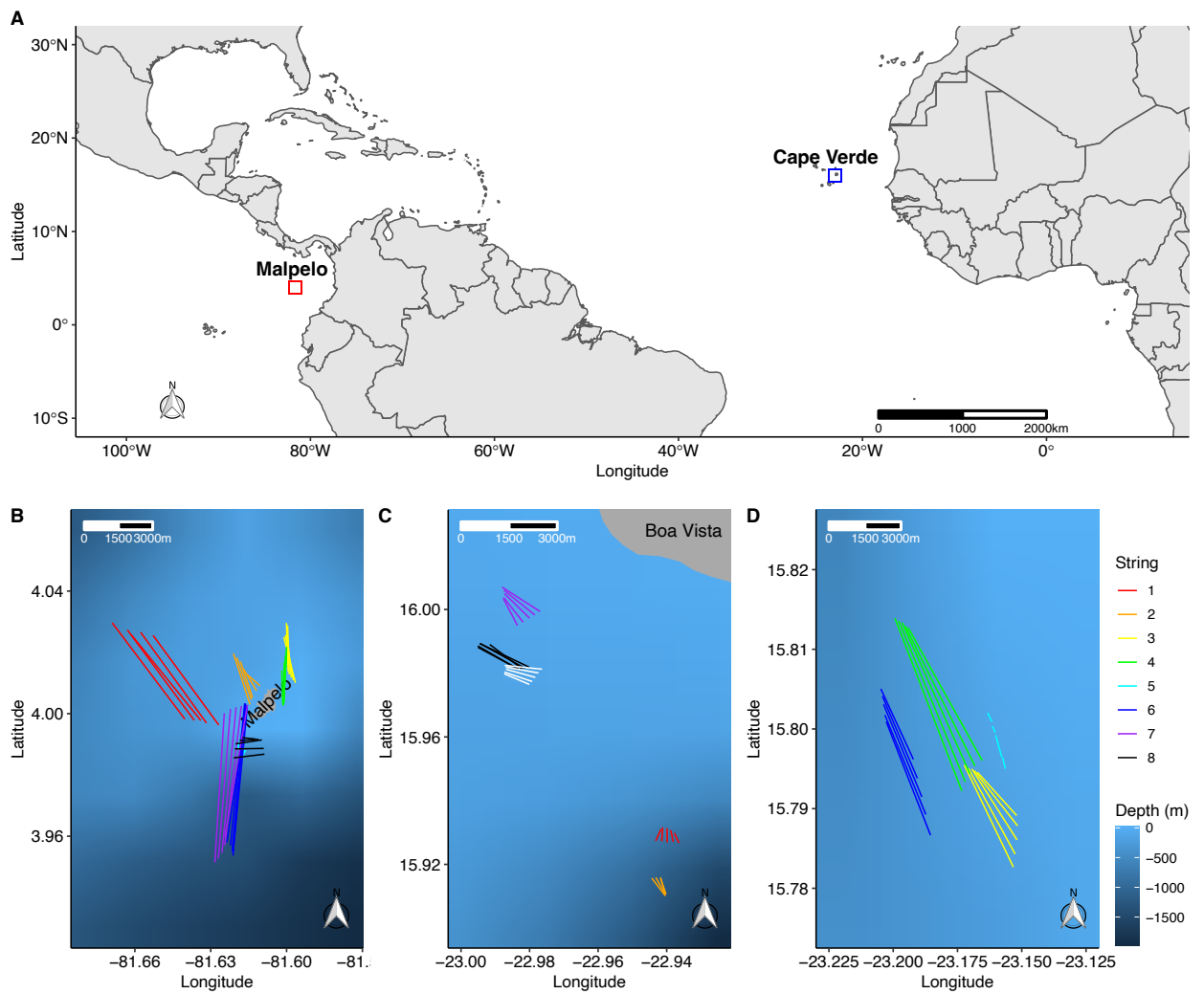
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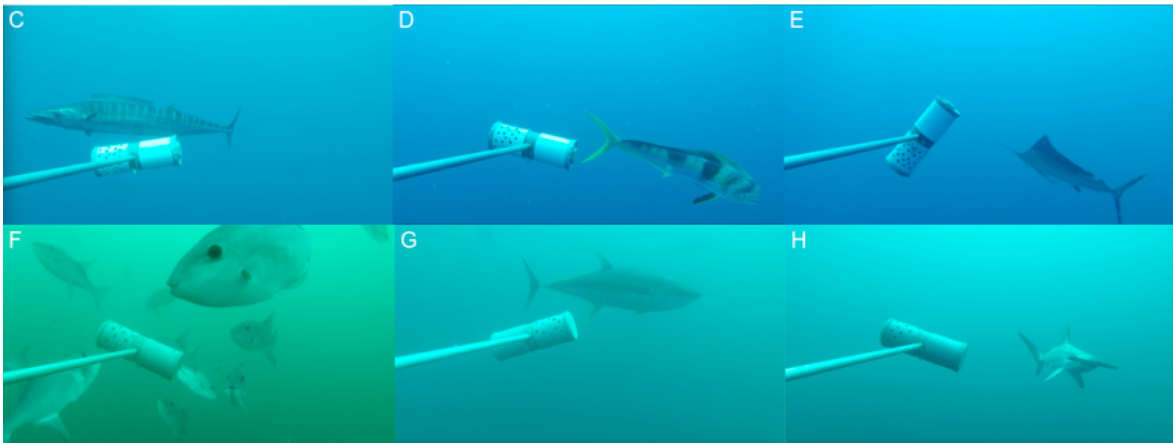
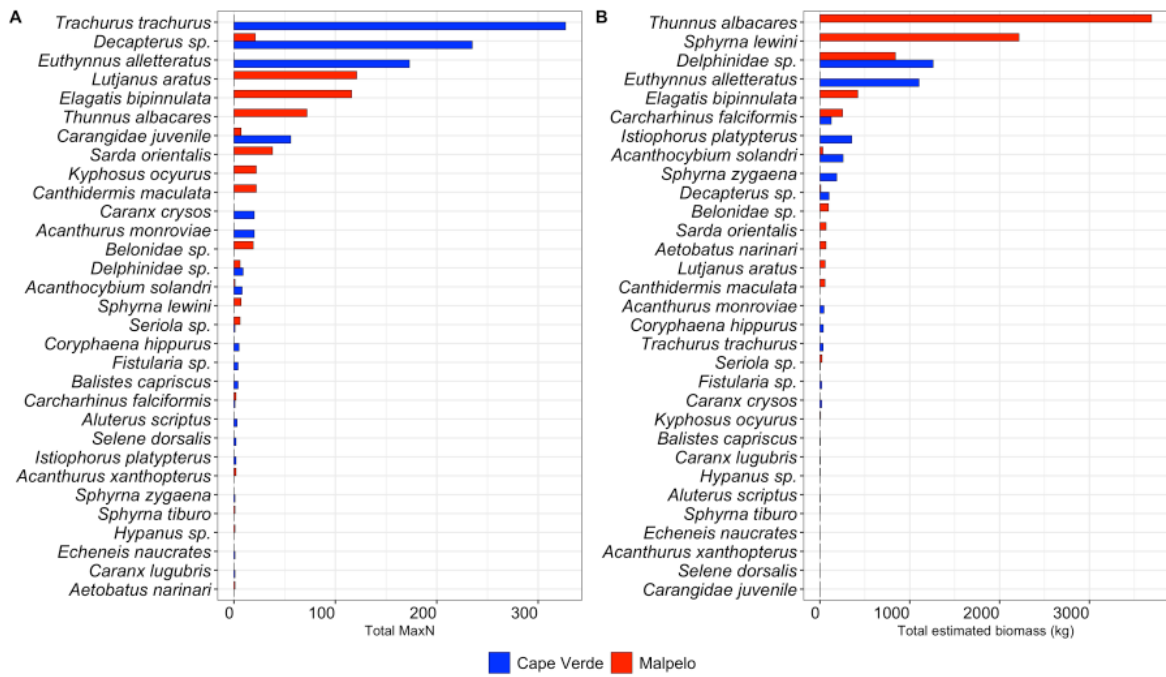
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## Figures

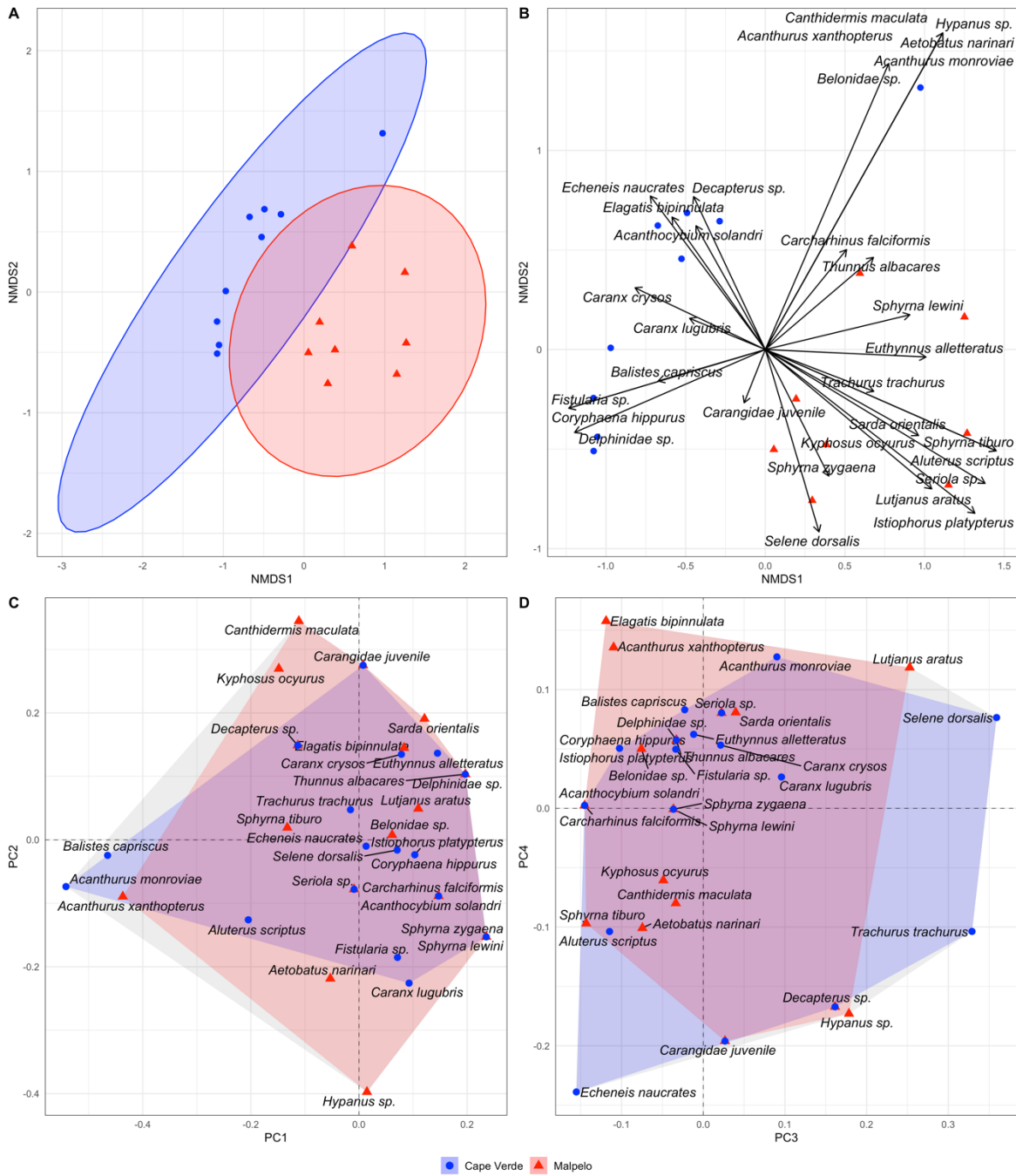


310

311 **Fig. 1** Sampling locations and deployment sites. Sampling locations (A) and BRUVS  
312 deployment sites in Malpelo (B) and Cape Verde (C, D). Line segments indicate BRUVS  
313 trajectories and are color-coded by string, with each line representing an individual rig.



314  
 315 **Fig. 2** Fish community composition in Malpelo and Cape Verde. Ranked abundance (A) and  
 316 biomass (B) of species recorded in either location, and examples of species observed using  
 317 BRUVS. Stills (C) through (E) are from Cape Verde: (C) *Acanthocybium solandri* – Wahoo;  
 318 (D) *Coryphaena hippurus* – Common dolphinfish; (E) *Istiophorus platypterus* – Indo-Pacific  
 319 sailfish [This identification reflects the increasingly common belief that there is only one  
 320 pantropic species of sailfish (e.g Collette et al. 2011), rather than *I. albicans* in the Atlantic  
 321 and *I. platypterus* in the Indo-Pacific]. Stills (F) through (H) are from Malpelo: (F)  
 322 *Canthidermis maculata* – Rough triggerfish; (G) *Thunnus albacares* – Yellowfin tuna; (H)  
 323 *Sphyrna lewini* – Scalloped hammerhead.



324

325 **Fig. 3** Species community differences and functional similarity in Malpelo and Cape Verde.  
 326 Two-dimensional NMDS ordination plot with 95% confidence level ellipses based on  
 327 ANOSIM results from samples (BRUVS strings) from Cape Verde and Malpelo (A). NMDS  
 328 plot of samples with vectors showing species correlation (B). Distribution of species in the  
 329 first and second (C) and third and fourth (D) dimensions of the functional space. Grey hull  
 330 indicates overall volume of the functional space on the two axes shown. Red (Malpelo) and  
 331 blue (Cape Verde) hulls contain positions of all species found at each site.

332

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