Sponge distribution and the presence of photosymbionts in Moorea, French Polynesia

Christopher J Freeman, Cole G Easson

Photosymbionts play an important role in the ecology and evolution of diverse host species within the marine environment. Although sponge-photosymbiont interactions have been well described from geographically disparate sites worldwide, our understanding of these interactions from shallow water systems within French Polynesia is limited. We surveyed diverse habitats around the north coast of Moorea, French Polynesia and screened sponges for the presence of photosymbionts. Overall sponge abundance and diversity were low, with <1% cover and only eight putative species identified by 28S barcoding from surveys at 21 sites. Of these eight species, seven were found predominately in shaded or semi-cryptic habitats under overhangs or within caverns. *Lendenfeldia chondrodes* was the only species that supported a high abundance of photosymbionts and was also the only species found in exposed, illuminated habitats. Interestingly, *L. chondrodes* was found at 3 distinct sites, with a massive, fan shaped growth form at two of the lagoon sites and a thin, encrusting growth form within a bay site. These two growth forms differed in their photosymbiont abundance, with massive individuals of *L. chondrodes* having higher photosymbiont abundance than encrusting individuals from the bay. We present evidence that some sponges from French Polynesia support abundant photosymbiont communities and provide initial support for the role of these communities in host ecology.

1   Sponge distribution and the presence of photosymbionts in Moorea, French Polynesia

2   Christopher J. Freeman[1,2] and Cole G. Easson[3,4]

3   [1]Smithsonian Marine Station, Fort Pierce, Florida, USA

4   [2]IRCP, Institute for Pacific Coral Reefs, Labex Corail, BP1013 Papetoai, 98729 Moorea,

5   French Polynesia

6   [3]Nova Southeastern University, Halmos College of Natural Science and Oceanography, Dania

7   Beach, Florida, USA

8   [4]Department of Biology, University of Alabama at Birmingham, Birmingham, Alabama, USA

9   **Abstract**

10   Photosymbionts play an important role in the ecology and evolution of diverse host species

11   within the marine environment. Although sponge-photosymbiont interactions have been

12   well described from geographically disparate sites worldwide, our understanding of these

13   interactions from shallow water systems within French Polynesia is limited. We surveyed

14   diverse habitats around the north coast of Moorea, French Polynesia and screened sponges

15   for the presence of photosymbionts. Overall sponge abundance and diversity were low, with

16   <1% cover and only eight putative species identified by 28S barcoding from surveys at 21

17   sites. Of these eight species, seven were found predominately in shaded or semi-cryptic

18   habitats under overhangs or within caverns. *Lendenfeldia chondrodes* was the only species

19   that supported a high abundance of photosymbionts and was also the only species found in

20   exposed, illuminated habitats. Interestingly, *L. chondrodes* was found at 3 distinct sites, with

21   a massive, fan shaped growth form at two of the lagoon sites and a thin, encrusting growth

22   form within a bay site. These two growth forms differed in their photosymbiont abundance,

23   with massive individuals of *L. chondrodes* having higher photosymbiont abundance than

24   encrusting individuals from the bay. We present evidence that some sponges from French

25   Polynesia support abundant photosymbiont communities and provide initial support for the

26   role of these communities in host ecology.

27   **Introduction**

28   In the marine environment, symbiotic interactions fuel high species diversity in

29   otherwise nutrient poor systems like hydrothermal vents and coral reefs (Steinert,

30   Hentschel & Hacker, 2000; Venn, Loram & Douglas, 2008). On tropical reefs, the mutualism

31   between the dinoflagellate symbiont *Symbiodinium* and reef building corals has long

32   epitomized such an interaction (Muscatine & Cernichiari, 1969; Muscatine & Porter; 1977),

33   but recent research has explored the functional role of photosynthetic microbes within

34   other dominant benthic fauna like octocorals (Baker et al., 2015) and sponges (Freeman et

35   al., 2013). Although autotrophic nutrition supplied by these photosymbionts can provide

36   more than enough C to compensate for holobiont (microbial symbiont and host)

37   metabolism (Venn, Loram & Douglas, 2008; Usher, 2008), there is substantial variation in

38   the structure and function of these interactions across groups and species (Thacker &

39   Freeman, 2012).

40   While reef building corals and octocorals host diverse communities of metabolically

41   distinct microbes (Knowlton & Rohwer, 2003), many species of sponges support a microbial

42   diversity that rivals that found in other eukaryotic hosts (Thacker & Freeman, 2012). The

43   structure of these interactions also varies across species, with high host specificity in

44   microbial community composition across sympatric host species (Thacker & Freeman,

45   2012; Easson & Thacker, 2014). This, coupled with the fact that host sponge identity

46   accounts for over 70 % of the variation in the placement of an individual sponge within

47   bivariate (δ^{13}C and δ^{15}N) isotopic "niche space", implies that microbial community

48   composition also plays an important role in the functional placement of a species in its

49   ecosystem (Freeman, Easson & Baker, 2014).

50   By allowing sponge hosts to utilize inorganic sources of C and N, abundant

51   photosymbiont communities also play a crucial role in sponge metabolism and impact the

52   overall nutritional benefit of these interactions to the host (Freeman & Thacker, 2011;

53   Freeman et al., 2013; Freeman, Easson & Baker, 2014). Although sponge-photosymbiont

54   interactions have been widely reported in disparate geographic areas ranging from the

55   Great Barrier Reef (Wilkinson, 1983), Palau and Guam (Ridley, Faulkner & Haygood, 2005;

56   Usher, 2008), Western Australia (Lemloh et al., 2009), Africa (Steindler, Beer & Ilan, 2002),

57   the Red Sea and Mediterranean (Wilkinson & Fay, 1979; Usher, 2008), and the Caribbean

58   (Erwin & Thacker, 2007; Freeman & Thacker, 2011; Easson & Thacker, 2014), limited data

59   exists on the prevalence of these interactions in other locations. For instance, despite the

60   fact that over 75 species of sponges have been previously reported in the Society and

61   Marquesas Islands of French Polynesia, the presence of photosymbiont hosting species is

62   largely based on anecdotal evidence that many of the species catalogued are from orders

63   dominated by "phototrophic" species (Hall et al., 2013). In addition, such assertions may not

64   be accurate, as the presence of photosymbionts can be variable even among species within a

65   genus and may thus vary substantially at higher taxonomic levels (Erwin & Thacker, 2007).

66   To identify sponge species hosting photosymbiont communities in Moorea, French

67   Polynesia and describe the general habitat in which they are found, we conducted surveys

68   across diverse habitats and environmental conditions in bays, lagoons, and along the reef

69   slope on the northern coast of Moorea. Surveys included both man-made and natural

70   substrates, as well as under overhangs and semi-cryptic habitats. Sponges were identified

71   by obtaining a partial 28S rRNA gene sequence (Thacker et al., 2013, Erpenbeck et al., 2015)

72   and screened for the abundance of photosymbionts by chlorophyll *a* analysis (Erwin &

73   Thacker, 2007).

74   **Materials and Methods**

75   *Sample collection*

76   We surveyed 21 sites along the northern coast of Moorea, French Polynesia (see

77   Schrimm, Buscail & Adjeroud, 2004 for a detailed description of the island) using a

78   combination of SCUBA and snorkeling (Figure 1). Sites included locations previously

79   reported to support sponge communities (Adjeroud & Salvat, 1996; Adjeroud, 1997;

80 Desmet, 2009; Hall et al., 2013) and also sites that were selected haphazardly by satellite

81 images and word of mouth from local researchers. To include both diverse habitats and

82 substrate types, we surveyed bay and lagoon sites, including the motu (an independent set

83 of islands within the lagoon), reef crest, channel openings, near beaches, reef slopes, and

84 docks/man-made structures (Figure 1; Table 1). Initial transects revealed that average

85 sponge cover was < 1%, with coral or bare rock as the most common substrate. To

86 adequately sample sponge species in this area, we therefore adapted our methods and

87 surveyed sites by a two-diver swimming census method. Using this method, when a sponge

88 was observed, a small (3-6 cm^3) sample was collected using a sharp dive knife and placed

89 into an individual sealed bag. Once on the boat, samples were stored on ice for transit back

90 to the Centre de Recherches Insulaires et Observatoire de L'Environment (CRIOBE) research

91 station. At CRIOBE, samples were photographed and two subsamples were taken. The first

92 subsample was preserved in 95% EtOH for taxonomic identification via 28S barcoding. The

93 use of 28S barcoding for sponge molecular taxonomy has increased in recent years (Thacker

94 et al., 2013, Erpenbeck et al., 2015), and while species-level taxonomic resolution may be

95 limited using this marker, it is not uncommon for sponges of French Polynesia to be

96 identified to only genus via morphological characters alone (Adjeroud & Salvat, 1996;

97 Adjeroud, 1997; Desmet, 2009; Hall et al., 2013). We therefore propose that 28S barcoding

98 provides comparable taxonomic resolution to morphology-based studies in this area and,

99 importantly, also provides a comparatively rapid, effective, and objective comparison of

100 specimens collected across sites that may have slightly different morphologies. Because of

101 this, we have intentionally restricted our identifications to 28S barcoding. The second

102 subsample was frozen for chlorophyll *a* analysis. Permits for sponge collection and export

103 were obtained from the Institute for Pacific Coral Reefs (IRCP) and the Haut-commissariat

104   de la République en Polynésia Francaise. Representative vouchers of these sponges are

105   stored at the Smithsonian Marine Station in Fort Pierce, Florida.

106   *DNA extraction, PCR amplification, and sequencing*

107   A total of 40 collected specimens were sequenced to obtain a molecular barcode.

108   Genomic DNA was extracted from ethanol-preserved samples using the PowerSoil DNA

109   extraction kit (MoBio), following the manufacturer's protocol. The oligonucleotide primers

110   SP635F and SP1411R were used to amplify a portion of the 28S ribosomal subunit (Thacker

111   et al., 2013), yielding an approximately 650bp fragment. PCR reaction products were gel-

112   purified and cleaned using the Wizard PCR Preps DNA Purification System (Promega).

113   Forward and reverse sequencing reactions were performed at the University of Alabama at

114   Birmingham (UAB) Center for AIDS Research (CFAR) DNA Sequencing Core Facility. Forward

115   and reverse sequences were then compared to ensure the accuracy of sequencing reactions

116   in CodonCode Aligner software (CodonCode) and Geneious (version 6.1.8, Biomatters

117   Limited), yielding a final consensus sequence for each voucher specimen A representative

118   sequence for each species is archived in GenBank under accession numbers KU746954 to

119   KU746961.

120   *Phylogenetic analyses and species identification*

121   Phylogenetic relatedness among surveyed sponge species was assessed using a

122   phylogeny constructed from a partitioned alignment of gene sequences from 40 collected

123   specimens and 44 GenBank sequences coding for the large (28S) nuclear ribosomal

124   subunits, which is a common marker used for molecular identification of sponge species

125   (Thacker et al., 2013). Sequences were aligned using the default options of MAFFT 7.245

126   (Katoh et al., 2002). We implemented a relaxed-clock model in MrBayes version 3.2.1

127   (Ronquist et al., 2012), using the CIPRES computational resources (Miller, Pfeiffer &

128   Schwartz, 2010) and constrained sponges in the class *Calcarea* as an outgroup using the

129   independent gamma rate relaxed clock model with a birth-death process (Aris-Brosou &

130   Yang 2003). We included three parallel runs of 10 million generations, each using four

131   Markov chains and sampling every 100 generations. A consensus phylogeny of the three

132   parallel runs was summarized following a burn-in of 25 %. Sponge specimens were

133   ultimately identified to the lowest possible taxonomic level using the 28S genetic marker.

134   *Chlorophyll* a *analysis*

135   At the Smithsonian Marine Station, frozen sponge samples were lyophilized overnight,

136   ground to a fine powder, and weighed to the nearest 0.001g. To quantify photosymbiont

137   abundance, chlorophyll *a* (chl *a*) analysis was carried out as in Erwin & Thacker (2007) and

138   Freeman, Easson & Baker (2014). In short, dried sponge tissue was extracted in 90 %

139   acetone overnight at 4 °C and the concentration of chl *a* was quantified by measuring the

140   absorbance of these extracts at 750, 664, 647, and 630 nm and applying equations from

141   Parsons, Maita & Lalli (1984). Chlorophyll *a* values were not obtained for *Dysidea* sp. from

142   Kaveka dock because these sponge individuals were too small to allow for both taxonomic

143   vouchers and chl *a* samples to be taken. We compared differences in mean chl *a*

144   concentrations using an Analysis of Variance (ANOVA; Systat, v. 11). Pairwise comparisons

145   of mean chl *a* concentrations between the three *L. chondrodes* populations and between *L.*

146   *chondrodes* and the low chl *a* samples were carried out using the Fisher's least significant

147   difference (LSD) post hoc test.

148   **Results**

149   Almost all specimens were from the class Demospongiae, with only one species from

150   Calcarea that closely matched *Leucetta* sp. Within Demospongiae, sequenced specimens

151   spanned all three subclasses (Heteroscleromorpha, Keratosa, Verongimorpha), and 5

152   sponge orders within these subclasses (Hadromerida, Spirophorida, Haplosclerida,

153   Verongida, Dictyoceratida). Many of these specimens were genetically similar to members

154   of genera previously reported in French Polynesia. For instance, CB# 1 to 5 (Cooks Bay,

155   Figures 1 and 2) were similar to species from the genus *Leucetta* sp. (Adjeroud & Salvat,

156   1996; Adjeroud, 1997; Hall et al., 2013; Figure 3), OB2# 1 (Opunohu Bay 2, Figures 1 and 2)

157   was similar to *Cinachyrella* sp. (Hall et al., 2013; Figure 3), IC# 1 to 3 and KD# 3 and 4

158   (Intercontinental Lagoon and Kaveka Dock; Figures 1 and 2), were identified as a *Haliclona*

159   *sp.* (Adjeroud, 1997; Hall et al., 2013; Figure 3), and KD# 1 and 2 (Kaveka dock, Figure 1)

160   were most similar to a species within the genus *Dysidea* (Adjeroud & Salvat, 1996;

161   Adjeroud, 1997; Hall et al., 2013; Figure 3). Other specimens were genetic matches to

162   sponges within the orders Verongida (S&G# 6 to 9), Dictyoceratida (S&G# 1 to 5), and the

163   subclass Heteroscleromorpha (OB1#1 and 2) (Figures 1-3).

164   One species included several individuals of variable growth forms collected from

165   different locations (an encrusting growth form in Opunohu Bay [OB3# 1 to 6] and a massive

166   fan-shaped growth form in the Motu Channel [MC# 1 to 5] and Intercontinental Reef [ICR#

167   1 to 5]; Figures 1 and 2) that were shown to all be genetically identical (Figure 3). BLAST

168   results in GenBank revealed that these samples most closely matched *Fasciospongia*

169   *chondrodes* (also known as *Lendenfeldia chondrodes*). Histological comparisons indicated

170   internal fiber structure and thickness consistent with *L. chondrodes* (C. Diaz, personal

171   communication), and 16S and ITS cloning of all three morphotypes (Freeman & Easson, in

172   prep) showed the presence of both *Oscillatoria spongeliae* and *Synechocystis* sp. symbionts,

173   a composition unique to *L. chondrodes* (as in *L. chondrodes* from Ridley, Faulkner & Haygood,

174   2005). These three separate observations offer compelling evidence that these represent

175   different morphotypes of the same species.

176   Most sponge species were found in shaded or otherwise semi-cryptic habitats,

177   except for *Lendenfeldia chondrodes*, which was found in exposed locations at all three sites.

178   Interestingly, there was a wide range of chlorophyll *a* values across sponge samples

179   (Analysis of Variance [ANOVA]: F=65.270, p<0.001; Figure 4), with six of the seven species

180   having low (<125 µg chl *a* [g sponge tissue]$^{-1}$; Erwin & Thacker, 2007) values and all three

181   populations of *Lendenfeldia chondrodes* having significantly higher (~300-675 µg chl *a* [g

182   sponge tissue]$^{-1}$) chl *a* values than any of the other species (ANOVA followed by LSD

183   multiple pairwise comparisons: p<0.05; Figure 4). Chlorophyll *a* values of *L. chondrodes*

184   varied across the three sites (ANOVA followed by LSD multiple pairwise comparisons:

185   p<0.05), with the encrusting, smooth growth form in Opunohu Bay having the lowest

186   photosymbiont abundance and the two massive, fan-shaped growth forms from the Motu

187   and the Intercontinental reef having chl *a* values over 550 µg chl *a* (g sponge tissue)$^{-1}$

188   (Figure 4). The highest chl *a* values were found in the massive, fan shaped growth form from

189   the Intercontinental reef.

190   **Discussion**

191   This study expands our understanding of sponge distribution in Moorea, French

192   Polynesia and provides initial quantitative evidence that some sponges in French Polynesia

193   host abundant photosymbiont communities. The overall sponge diversity throughout the

194   Society Islands has previously been shown to be around 40 species (identified as operation

195   taxonomic units [OTUs]; Hall et al., 2013), with up to 17 species across sites in Moorea (10

196   species: Adjeroud & Salvat, 1996; 17 species: Adjeroud, 1997; 7 species: Desmet, 2009; 12

197   species: Hall et al., 2013). Variation in overall sponge diversity reported from Moorea likely

198   reflects the fact that some studies survey deep sites (18-39 m; Hall et al., 2013), while

199   others restrict collections to bays (Adjeroud & Salvat, 1996) or survey a wide variety of

200   habitats and depths (Adjeroud, 1997). To search for photosymbiont-hosting sponges, our

201   surveys were generally restricted to shallow (<10 m deep) environments, but we sampled

202   across diverse environmental conditions in bays, lagoons, and channel openings (Adjeroud

203   & Salvat, 1996; Adjeroud, 1997; Schrimm, Buscail & Adjeroud, 2004).

204   Our qualitative estimates of <1 % sponge cover on shallow substrates around

205   Moorea approaches the lower range reported from other locations in the Pacific. For

206   instance, the abundance of individual sponge species was from <1% to ~10 % in the

207   Wakatobi region of Indonesia, and the percent cover of the whole sponge community in this

208   region ranged from 10% to over 50 %, (Bell & Smith, 2004; Bell et al., 2010), with over 100

209   sponges per m^2 at some sites (Powell et al., 2014). Likewise, the total number of individual

210   sponges observed across a depth gradient from 5 to 40 m on Davies Reef on the Great

211   Barrier Reef (GBR) ranged from 25 to well over 2000 at a single site, with over ten

212   individuals per m^2 at some sites (Wilkinson & Evans, 1989) and between 0.5 to ten sponge

213   individuals per m^2 at sites across the entire GBR reef tract (Wilkinson, 1987). Sponge

214   abundance in Moorea is also substantially lower than that observed from most sites in the

215   Caribbean, where the percent cover of sponges above 15 m depth ranges from 0.6 % to over

216   20 % (Pawlik et al., 2015).

217   We found interesting trends in the distribution of sponges across sites. Species with

218   low photosymbiont abundance were found in semi-cryptic habitats underneath overhangs

219   and in caverns. In addition, the *Haliclona* sp. was found in high abundances on artificial

220   substrates surrounding the Intercontinental Hotel and on the pilings of the Hotel Kaveka

221   within Cooks Bay, and rarely on reefs. Whether this species preferentially settles on artificial

222   substrates or favors areas with potentially elevated nutrient levels remains to be tested. In

223   contrast, the three growth forms of *Lendenfeldia chondrodes* were all found on exposed

224   substrates in generally well-lit environments. Together this certainly suggests that

225   environmental conditions are playing a role in the distribution of sponges in Moorea.

226   The distribution of sponges on Pacific reefs is commonly ascribed to environmental

227   conditions. In particular, across the Great Barrier Reef, the overall biomass of sponges

228   decreases as you move offshore and the presence of phototrophic sponges (obtaining at

229   least 50 % of their energy requirements from photosynthetic symbionts) increases, with up

230   to 90 % of sponges from offshore reefs being phototrophic (Wilkinson, 1987). Although we

231   found three sponges in the order Dictyoceratida (Hall et al., 2013), only *Lendenfeldia*

232   *chondrodes* had chl *a* concentrations that were high enough to suggest that it might be

233   phototrophic.

234   Unlike phototrophic sponges on the GBR, *L. chondrodes* was found at relatively

235   pristine lagoon sites, at a more turbid site close to development (Intercontinental Reef), and

236   within bays that are impacted by terrestrial sources of nutrients (Adjeroud & Salvat, 1996;

237   Adjeroud, 1997; Schrimm, Buscail & Adjeroud, 2004). In addition, while phototrophic

238   sponges in the Pacific typically have foliose, flattened plate or cup like growth forms to

239   maximize light exposure (Wilkinson, 1987), individuals of *L. chondrodes* in Moorea were

240   either thinly encrusting or encrusting with abundant vertical fingers, giving the sponge a

241   fan-shaped growth form (similar to *L. chondrodes* in Ridley et al., 2005; Figure 2). These two

242   growth forms appear to be intermediate along the continuum encompassing foliose plate

243   sponges from the GBR, encrusting and finger-like projections in sponges from Palau and

244   Guam, and some of the encrusting and generally amorphous or fan-shaped sponges that

245   host photosymbionts in the Caribbean (Thacker & Starnes, 2003; Ridley et al., 2005;

246   Freeman & Thacker, 2011; Freeman et al., 2013; Pawlik et al., 2015).

247   *Lendenfeldia chondrodes* has been previously shown to host photosymbionts,

248   including the sponge-specific filamentous cyanobacteria *Oscillatoria spongeliae*, as well as

249   *Synechocystis* sp. (Ridley, Faulkner & Haygood, 2005). This, coupled with our data showing

250   high photosymbiont abundance within individuals of *L. chondrodes* in Moorea, suggests that

251   this sponge is likely benefitting from this association. Additional work is underway to assess

252   the productivity of this species and determine if their internal photosymbionts are indeed

253   capable of more than compensating for host and symbiont metabolism (Freeman et al.,

254   2013; Pawlik et al., 2015). Regardless of its status as a phototrophic species, *L. chondrodes*

255   was one of the dominant species across sites, suggesting that the presence of

256   photosymbionts may allow this species to survive and grow across more diverse habitats

257   than species that do not host photosymbionts and are largely restricted to refugia.

258   It is important to mention that cyanobacteria may acclimate to local conditions by

259   increasing or decreasing the chl *a* concentrations within each cell (Six et al., 2014). Despite

260   this, we anticipate that it is unlikely that variation in chl *a* concentration per cell is

261   structuring the vast differences between *Lendenfeldia chondrodes* and the other species in

262   this study that have chl *a* values ranging from 1.5 % to 28 % of the chl *a* values of *L.*

263   *chondrodes* from Opunohu Bay and 0.7 to 13.5 % of the chl *a* values of *L. chondrodes* from

264   the Intercontinental Reef site. In addition, while cyanobacterial cell counts performed in

265   conjunction with traditional chl *a* pigment analyses may allow for a more robust estimate of

266   chl *a* per cell, the difficulty in resolving and counting individual cells within the filaments of

267   *Oscillatoria spongeliae* via fluorescent microscopy has been demonstrated previously (Flatt

268   et al., 2005). Ongoing research is therefore aimed at determining how symbiont metabolism

269   varies across *Lendenfeldia chondrodes* collected from these three sites, and whether this

270   variation is correlated with these differences in chl *a* concentration.

271   A recent study by Wecker et al. (2015) identified dinoflagellates from the genera

272   *Symbiodinium* and *Dinophysis*, as well a member of the order Dinophyceae within three

273   sponge species from Moorea and Tahiti. Wecker et al. (2015) identified *Symbiodinium* and

274   other dinoflagellates by PCR screening, but without quantifying the abundance of these

275   symbionts via chl *a* analyses or microscopy, it is difficult to resolve whether their presence

276   reflects a true symbiosis or just reflects a low abundance of these microbes in the sponge at

277   the time of sampling. In contrast, *L. chondrodes* from our study has been shown by

278   amplification of the 16S rRNA gene and transmission electron microscopy to host abundant

279   communities of sponge-specific cyanobacteria (Ridley, Faulkner & Haygood, 2005). We thus

280   anticipate that elevated chl *a* values in this species predominately reflect cyanobacterial

281   symbiont abundance and not *Symbiodinium* or other dinoflagellates.

282   In summary, photosymbionts may allow sponges like *L. chondrodes* to compete for

283   space in well-illuminated reef habitats, filling niches that are unavailable to other sponge

284   species (Freeman, Easson & Baker, 2014). In Moorea, these sponges may also expand into

285   niches recently vacated by coral die-offs from crown-of thorns outbreaks (Kayal et al.,

286   2012). Manipulative shading experiments and reciprocal transplants among these sites may

287   help to elucidate this further (Thacker & Freeman, 2012). With recent evidence that the

288   functional placement of a sponge individual within an ecosystem may be driven by the

289   overall microbial community composition, however, additional work is needed to

290   investigate variation in the microbiomes of sponges from across French Polynesia.

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408 **Table 1:** Sites supporting sponge communities around Moorea, French Polynesia. Site

409 abbreviations correspond to labeled red markers in Figure 1

Site	Name	GPS Coordinates	Description	Sponge Species
S&G	Spur and Groove	17°30'7.21"S 149°55'36.98"W	6-8 m deep, hardbottom, high-energy	Verongid sp. and Dictyoceratida sp.
MR	Motu Reef	17°29'16.50"S 149°55'7.73"W	1-2 m deep, coral heads, hardbottom, sandy habitat	*Lendenfeldia chondrodes* (De Laubenfels, 1954) massive fan morph
MC	Motu Channel	17°29'20.37"S 149°54'52.47"W	2-4 m deep, sandy bottom, occasional coral head and hard substrate, high current	*Lendenfeldia chondrodes* (De Laubenfels, 1954) massive fan morph
ICR	Intercontinental Reef	17°29'17.21"S 149°53'47.82"W	2-3 m deep, vertical wall in channel, hard substrate, moderate current	*Lendenfeldia chondrodes* (De Laubenfels, 1954) massive fan morph
ICL	Intercontinental Lagoon Wall	17°29'25.97"S 149°53'32.56"W	1 m deep, artificial concrete substrate	*Haliclona* sp.
OB 3	Opunohu Bay Site 3	17°29'48.71"S 149°51'46.03"W	2-10 m deep, hard substrate, overhangs and high vertical relief, moderate current	*Lendenfeldia chondrodes* (De Laubenfels, 1954) encrusting, smooth morph, *Leucetta* sp., Heteroscleromorpha sp, *Cinachyrella* sp.
OB 2	Opunohu Bay Site 2	17°29'53.60"S 149°51'42.36"W	2-10 m deep, hard substrate, overhangs and high vertical relief, moderate current	*Lendenfeldia chondrodes* (De Laubenfels, 1954) encrusting, smooth morph, *Cinachyrella* sp.
OB 1	Opunohu Bay Site 1	17°30'19.68"S 149°51'29.17"W	3-5 m deep, hard substrate, overhangs	*Lendenfeldia chondrodes* (De Laubenfels, 1954) encrusting, smooth morph, Heteroscleromorpha sp., *Cinachyrella* sp., *Leucetta* sp.
CB	Cooks Bay	17°29'32.09"S 149°49'34.26"W	2-5 m deep, hard substrate, overhangs	*Lendenfeldia chondrodes* (De Laubenfels, 1954) encrusting, smooth morph, *Leucetta* sp., Heteroscleromorpha sp.
KD	Kaveka Hotel Dock	17°29'23.59"S 149°49'8.37"W	1-2 m deep, artificial concrete substrate	*Haliclona* sp., *Leucetta* sp., *Dysidea* sp.

410 **Figure 1:** Map of sites surveyed along the northern coast of Moorea, French Polynesia.

411 Sponges were observed at sites represented by a red marker, while white markers denote

412 sites in which sponges were not observed. Abbreviations on red markers correspond to site

413 names in Table 1. Map data: Google, Digital Globe Image NASA and CNES/Astrium
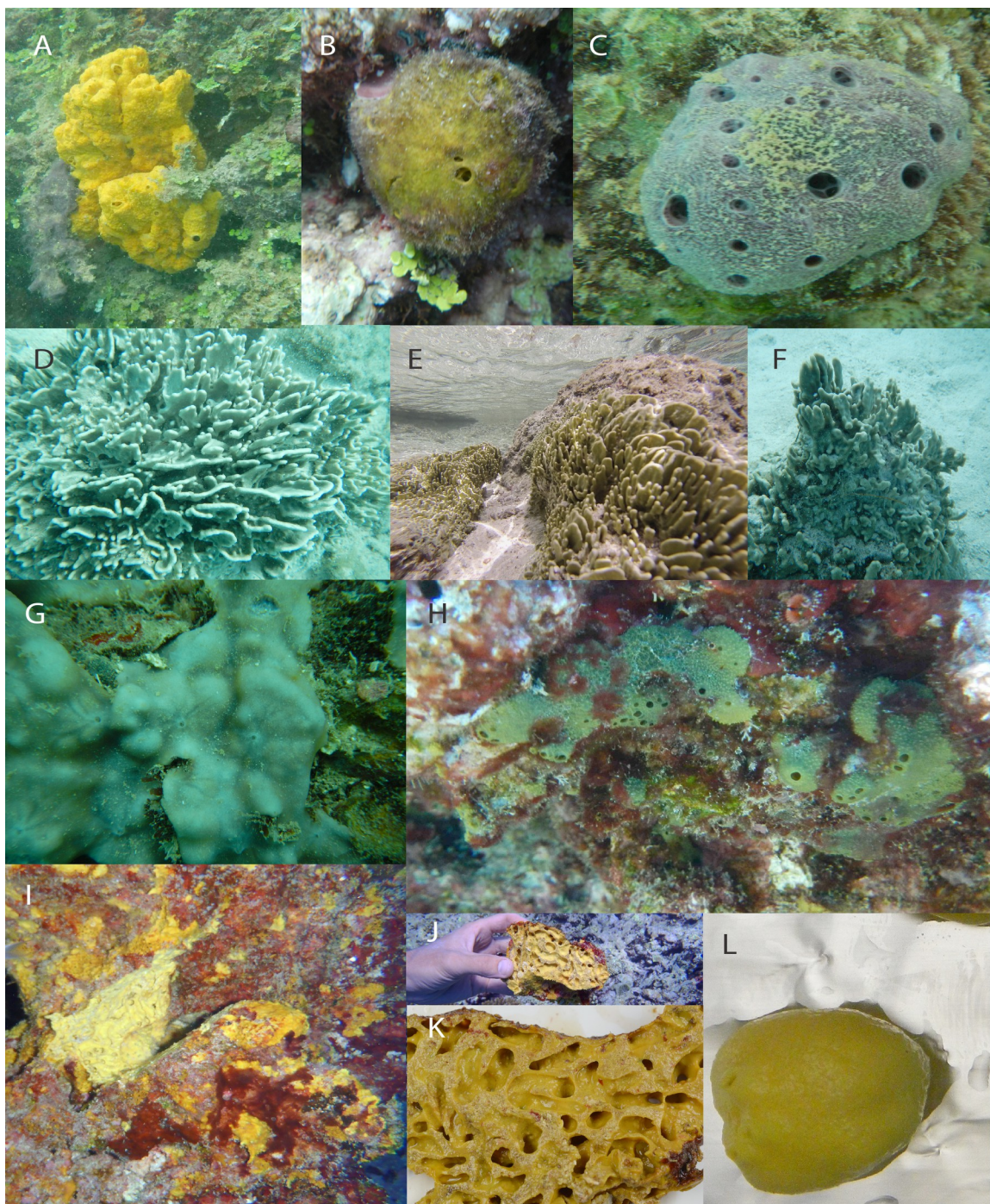
Figure 2: Photographs of sponges from Moorea, French Polynesia: Heteroscleromorpha sp.

from Opunohu Bay site #1 (A); *Cinachyrella* sp. from Opunohu Bay site #2 (B); *Haliclona* sp.

from Intercontinental Lagoon Wall (C); *Lendenfeldia chondrodes* from Intercontinental Reef

(D), Motu Channel (E and F), and Opunohu Bay Site #3 (G); Dictyoceratida sp. from the Spur

418   and Groove site (H); Verongid sp. from Spur and Groove Site (I, J, and K); *Leucetta* sp. from

419   Cooks Bay (L). Photographs of *Dysidea* sp. from Kaveka Hotel Dock were not taken.

420 **Figure 3**: Bayesian 28S phylogeny of relationships among collected specimens and closely

421 related, previously sequenced specimens from GenBank. Scale bar indicates 0.06

422 substitutions per site. Posterior probabilities are shown for each node.
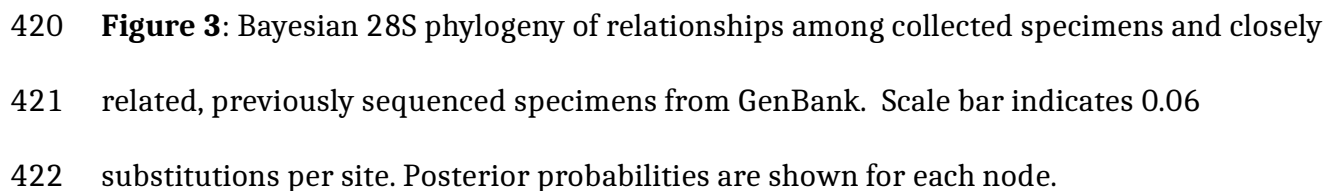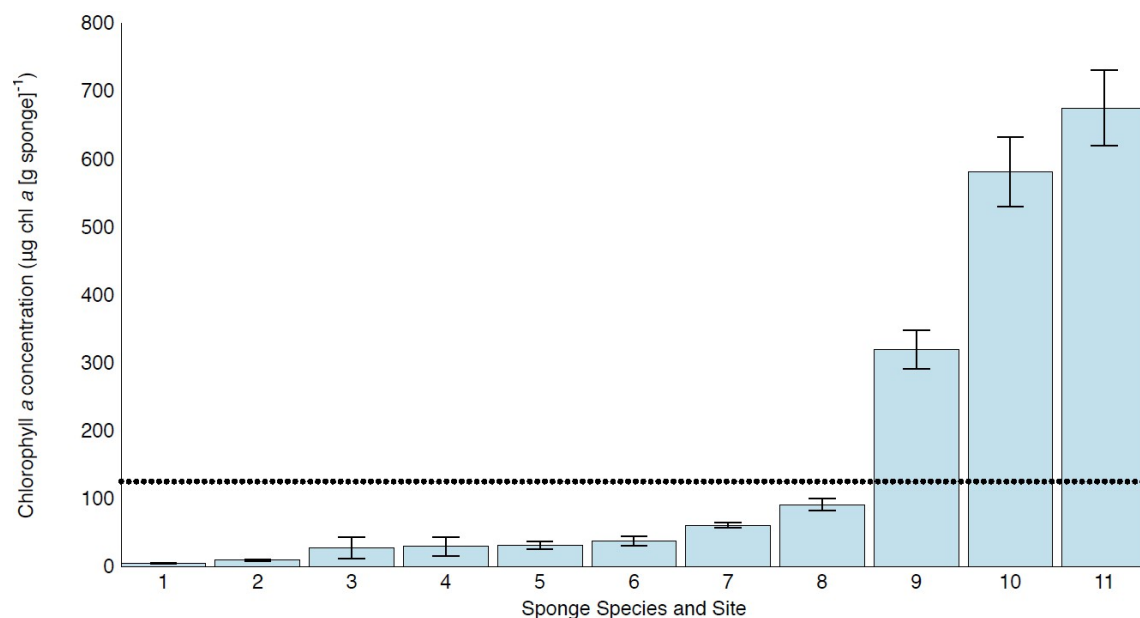
Figure 4: Mean (±) SE chlorophyll a concentration (μg chl a [g sponge tissue]$^{-1}$) across

seven sponge species from habitats around Moorea, French Polynesia. The dotted line at

125 μg chl a (g sponge tissue)$^{-1}$ denotes the separation between sponges hosting high (>

125) and low (< 125) photosymbiont communities (established by Erwin & Thacker, 2007).

Sponge identifications and sites are: 1: *Leucetta* sp. from Kaveka Dock (KD), 2: *Leucetta* sp.

from Cooks Bay (CB), 3: Dictyoceratida sp. from Spur and Groove (S&G), 4:Verongid sp. from

Spur and Groove (S&G), 5: *Cinachyrella* sp. from Opunohu Bay (OB), 6: Heteroscleromorpha

sp. from Opunohu Bay (OB), 7: *Haliclona* sp. from Kaveka Dock (KD), 8: *Haliclona* sp. from

Intercontinental Lagoon (ICL), 9: *Lendenfeldia chondrodes* from Opunohu Bay (OB), 10:

Lendenfeldia chondrodes from Motu Channel (MC) and 11: *Lendenfeldia chondrodes* from

Intercontinental Reef (ICR).