

Supporting Online Material

Effects of light attenuation on the sponge holobiont- implications for dredging management

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Figure S1. Sponges under different light treatments. Sponge health at the end of the 28 d exposure period, in the phototrophic species (A) *C. orientalis*, (B) *C. foliascens* and (C) *C. coralliophila*, and in the heterotrophic species (D) *S. flabelliformis* and (E) *I. basta*. From left to right, representative sponges exposed to the 0, 0.8, 3.2, 8.1 mol photons $\text{m}^{-2} \text{d}^{-1}$ treatments and natural light (NL, 3.2–6.5 mol photons $\text{m}^{-2} \text{d}^{-1}$).



Figure S2. Area change of all sponges. Percentage of area change (mean $\pm$ SE) for all species and treatments (0, 0.8, 3.2, 8.1 mol photons $\text{m}^{-2} \text{d}^{-1}$ and natural light (3.2–6.5 mol photons $\text{m}^{-2} \text{d}^{-1}$)) during the 28 d exposure period and 14 d observational period.

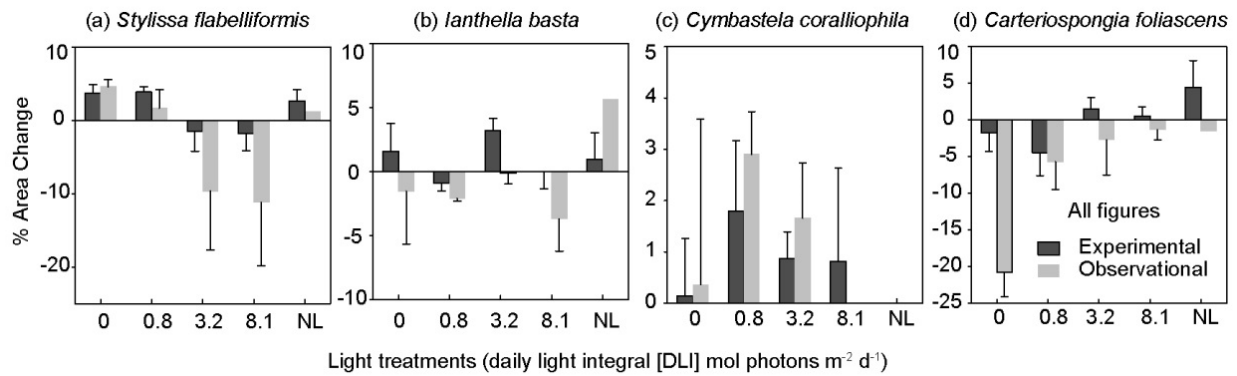


Figure S3. Non-metric Multi-Dimensional Scaling plots on pigments data. nMDS of all photopigments retrieved by A) Spectrophotometry (Chl a, Chl b, Chl c, Chl d, Total Chl and Carotenoids) and B) UPLC (Total Chl a, Total Chl, Total Xanthophylls, Total Carotenoids, Chl c2, Peridinin, Neoxanthin, Violaxanthin, Diadinoxanthin, Dincoxanthin, Zeaxanthin, Chl b, Chl a, Chl a epimer, Pheophytin a, α -carotene and β -carotene). Symbols correspond to species: triangles for *C. coralliophila*, inverted triangles for *C. foliascens*, and squares for *C. orientalis*. Colours represent light treatments: grey for low light intensity treatment (0.8 mol photons $\text{m}^{-2} \text{d}^{-1}$), black for 0 mol photons $\text{m}^{-2} \text{d}^{-1}$ and white for natural light control.



Figure S4. Non-metric Multi-Dimensional Scaling plots on microbial OTU data. nMDS of microbial communities for all 5 sponge species and the environmental control (seawater).

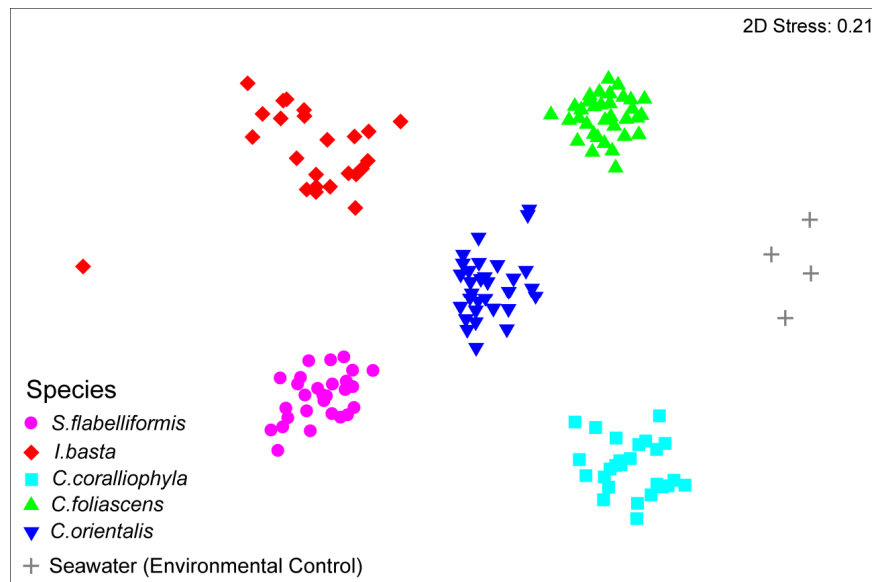


Table S1. SIMPER results on *C. foliascens* and *C. orientalis*. Similarity Percentage Analysis (SIMPER) for 30 most significant OTUs driving differences between Natural Light and the 0 mol photons m⁻² d⁻¹ light treatment at 28d and on the species that showed significant differences according to the PERMANOVA analysis (Table 3C).

OTU	Average relative abundance (%)		Contribution (%)	Taxonomic ID
	Natural Light	0		
C. foliascens				
Otu000006	5.39	0.04	6.62	Cyanobacteria
Otu000013	3.7	1.76	2.4	Gammaproteobacteria
Otu000033	0	1.33	1.66	Alphaproteobacteria
Otu000015	1.7	3	1.61	Gammaproteobacteria
Otu000023	1.01	2.05	1.38	Bacteroidetes
Otu000019	2.12	1.84	1.36	Alphaproteobacteria
Otu000034	1.25	1.84	1.34	Gammaproteobacteria
Otu000032	0.96	2.01	1.32	Gammaproteobacteria
Otu000016	1.29	2.04	1.09	Bacteroidetes
Otu000026	1.58	2.37	1.09	Bacteroidetes
Otu000017	2.06	2.86	1.01	Alphaproteobacteria
Otu000059	0.29	0.75	0.81	Alphaproteobacteria
Otu000007	4.28	4.36	0.76	Bacteroidetes
Otu000050	0.57	0.75	0.74	Gammaproteobacteria
Otu000064	0.81	1.25	0.66	Alphaproteobacteria
Otu000048	0.68	0.82	0.63	Gammaproteobacteria
Otu000070	0	0.51	0.63	Alphaproteobacteria
Otu000029	1.65	2.14	0.61	Gammaproteobacteria
Otu000204	0.04	0.53	0.61	Gammaproteobacteria
Otu000073	0.37	0.36	0.6	Gammaproteobacteria
Otu000185	0.04	0.51	0.58	Deltaproteobacteria
Otu000173	0.44	0	0.55	Cyanobacteria
Otu000113	0.17	0.59	0.51	Chloroflexi
Otu000047	0	0.41	0.51	Bacteroidetes
Otu000156	0.11	0.43	0.49	Gammaproteobacteria
Otu000170	0.39	0	0.48	Gammaproteobacteria
Otu000209	0.07	0.45	0.47	Gammaproteobacteria
Otu000077	0.24	0.28	0.44	Alphaproteobacteria
Otu000176	0.18	0.5	0.4	Gammaproteobacteria
Otu000090	0.78	0.47	0.4	Gammaproteobacteria
C. orientalis				
Otu000070	0.08	1.24	1.28	Alphaproteobacteria
Otu000061	1.04	0	1.07	Cyanobacteria
Otu000075	0.14	1.12	1.03	Gammaproteobacteria
Otu000088	1.06	0.11	1.02	Bacteroidetes
Otu000078	0.18	0.99	0.87	Gammaproteobacteria
Otu000083	0.1	0.88	0.84	Gammaproteobacteria
Otu000058	0.57	1.33	0.81	Unclassified Bacteria
Otu000001	9.08	8.42	0.78	Alphaproteobacteria
Otu000104	0.7	0	0.76	Bacteroidetes
Otu000285	0.69	0	0.74	SBR1093
Otu000067	0.11	0.65	0.65	Alphaproteobacteria
Otu000107	0.07	0.56	0.65	Alphaproteobacteria
Otu000124	0	0.58	0.62	Alphaproteobacteria
Otu000253	0.57	0	0.57	Alphaproteobacteria
Otu000110	0.59	0.18	0.57	Cyanobacteria

Otu000141	0.5	0	0.52	SBR1093
Otu000335	0.49	0	0.5	Gammaproteobacteria
Otu000123	0.04	0.47	0.45	Alphaproteobacteria
Otu000091	0.17	0.57	0.43	Gammaproteobacteria
Otu000159	0.45	0.04	0.42	Alphaproteobacteria
Otu000339	0.06	0.39	0.38	Gammaproteobacteria
Otu000286	0	0.41	0.37	Crenarchaeota
Otu000259	0.35	0	0.37	Alphaproteobacteria
Otu000261	0	0.36	0.37	Chlamydiae
Otu000276	0.35	0	0.37	Alphaproteobacteria
Otu000445	0.33	0.1	0.37	Chloroflexi
Otu000273	0.04	0.37	0.36	Chloroflexi
Otu000115	0.06	0.38	0.36	Alphaproteobacteria
Otu000593	0.27	0.19	0.36	Deltaproteobacteria
Otu000079	0.36	0.04	0.35	Alphaproteobacteria

Table S2. Sponge sampling details. List of species, morphologies, nutritional mode and sampling location.

Species Name (Author)	Functional Morphology	Primary Nutritional Mode	Sampling Location
<i>Cymbastela coralliophila</i> (Hooper & Bergquist, 1992)	Encrusting (thick) Cup (table)	Phototrophic ¹	Davies Reef (central Offshore GBR) S 18°49.354', E147°38.253'
<i>Carteriospongia foliascens</i> (Pallas, 1766)	Cup (wide cup)	Phototrophic ²	Fantome Island (Palm Islands) S 18°41.028', E 146° 30.706'
<i>Cliona orientalis</i> (Thiele, 1900)	Encrusting (bioeroding)	Phototrophic ³	Pelorus Island (Palm Islands) S 18°32.903', E 146° 29.172'
<i>Stylissa flabelliformis</i> (Hentschel, 1912)	Erect (laminar)	Heterotrophic ⁴	Pelorus Island (Palm Islands) S 18°32.903' E 146°9.172'
<i>Ianthella basta</i> (Pallas, 1976)	Erect (laminar)	Heterotrophic ⁵	Davies Reef S 18°49.354' 147°38.253'

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