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1 Transcriptomic responses of sponge 2 holobionts to in situ, seasonal anoxia 3 and hypoxia

4
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17 **inverse was used on a previous paper. Both authors have the right to list their name first on their**
18 **CVs.**

19 **Abstract**

20 Deoxygenation can be fatal for many marine animals; however, some sponge species are
21 tolerant of hypoxia and anoxia. Indeed, two sponge species, *Eurypon* sp. 2 and *Hymeraphia*
22 *stellifera*, survive seasonal anoxia for months at a time. To understand their tolerance
23 mechanisms, we performed differential gene expression analyses on the sponges, their
24 mitochondria and their microbial symbionts under *in situ* conditions of normoxia, hypoxia and
25 anoxia. Each species possessed a unique microbiome, but the microbiomes of each species
26 were dominated by a species-specific *Thaumarchaeon* and a *Gammaproteobacterium*.
27 Holobiont gene expression was species- and oxygen-level dependent, though there were some
28 shared interspecific responses to deoxygenation. In general, few changes occurred in the
29 expression of sponge metabolic genes as a function of oxygenation level, indicating that they
30 may remain metabolically active under anoxia. However, ATP synthesis genes were
31 significantly upregulated under hypoxia when compared to normoxia, and genes for DNA
32 replication were downregulated. Mitochondrial gene expression was effectively unchanged
33 under both hypoxia and anoxia. Nevertheless, both anoxia and hypoxia caused upregulation of
34 heat shock proteins (HSPs), indicating cellular level adaptations to deoxygenation stress. A
35 meta-analysis demonstrated that sponge transcriptional responses to anoxia were distinct from
36 those displayed by other invertebrates while dormant, and the hypothesis of sponge dormancy
37 under anoxia was not supported. *Thaumarchaeota* symbionts also upregulated stress response
38 genes in hypoxia, while maintaining expression of oxygen-dependent metabolic pathways under
39 hypoxia and anoxia. *Gammaproteobacteria* symbionts showed relatively few noteworthy
40 changes in gene expression in response to anoxia but decreased metabolic gene expression in
41 hypoxia. There was no clear evidence of upregulated anaerobic respiration in the
42 transcriptomes of the sponge holobionts under anoxia or hypoxia. The tolerance of some
43 sponges to prolonged anoxia warrants further investigation and could give them an advantage
44 in future oceans following climate change as well as in ancient oceans when oxygen
45 concentrations were lower than at present.

46 Introduction

47
48 Ocean oxygen levels are predicted to decline by 1–7% over the next century (Keeling,
49 Körtzinger, and Gruber 2010). Climate change is expanding marine oxygen-minimum zones,
50 while enhanced nutrient runoff is causing coastal eutrophication and subsequent deoxygenation
51 (Kirchman 2021). Deoxygenation is expected to negatively affect the physiology, metabolism
52 and survival of many marine organisms (Diaz and Rosenberg 2008). As a result of
53 deoxygenation and other anthropogenic stressors, we are facing large scale habitat and
54 biodiversity losses, but the full effects of these stressors are still unknown.

55
56 Sessile organisms that cannot move or migrate in response to deoxygenation are particularly
57 vulnerable. Sponges (Phylum: Porifera Grant, 1836), sessile, ecologically important filter-
58 feeding animals, are hypothesized to suffer from increasing hypoxic/anoxic areas worldwide
59 (Breitburg et al. 2018; Levin 2018; Stramma et al. 2008), and some *in situ* mortality of sponges
60 (along with other taxa) following deoxygenation has been reported (Altieri et al. 2017;
61 Stachowitsch 1984). However, species-specific responses to deoxygenation in Porifera are
62 variable, and some species are tolerant of hypoxia. Lab experiments have shown that the
63 demosponge *Halichondria (Halichondria) panicea* Pallas, 1766 can survive low oxygen levels
64 down to 0.5–4% of air saturation (a.s.) (Mills et al. 2014), and *Tethya wilhelma* can survive down
65 to 0.25–2% a.s. for 4 days and <0.05% a.s. for at least one hour (Mills et al. 2018). Additional
66 demosponge species that tolerate similar levels of hypoxia include *Geodia barretti* Bowerbank,
67 1858 with 7% a.s. (20 $\mu\text{M O}_2$, Leys and Kahn 2018) and *Haliclona pigmentifera* Dendy, 1905
68 (0.50-0.68% a.s., Gunda and Janapala 2009). In a recent experimental study, four
69 taxonomically distinct sponge species (*Cliona celata* Grant, 1826, *Suberites carnosus* Johnston,
70 1842, *Polymastia crocea* Kelly-Borges and Bergquist, 1997 and *Suberites australiensis*
71 Bergquist, 1968) were exposed to various levels of hypoxia (1.5–40% a.s., 0.13–3.3 $\text{mg O}_2 \text{ L}^{-1}$)
72 in aquaria. These sponges exhibited species-specific physiological, morphological and
73 behavioral responses to deoxygenation. Sub-lethal oxygen thresholds for these sponges were
74 in the range of 6–20% a.s. (0.48–1.56 $\text{mg O}_2 \text{ L}^{-1}$) while mortality was only observed in one of the
75 two species (*P. crocea*) exposed to severe hypoxia lower than 5% a.s. (0.13 $\text{mg O}_2 \text{ L}^{-1}$)
76 (Micaroni et al. 2021a). The sponge species most sensitive to deoxygenation in controlled
77 experiments, *P. crocea*, had a median lethal time (time until death, LT50) of 286 h at ~1.5% a.s.
78 (0.13 $\text{mg O}_2 \text{ L}^{-1}$, (Micaroni et al. 2021a), which was still longer than most marine organisms
79 under comparable conditions (reviewed in Micaroni et al. 2021a and Hughes et al. 2020).

80
81 Few studies have investigated the deoxygenation tolerance of sponges *in situ*. Bayer et al.
82 (2020) found that the glass sponge *Vazella pourtalesii* Schmidt, 1870 lives in reduced oxygen
83 conditions (< 4 mL/L) on the Scotian Shelf, Canada. Schuster et al. (2021) reported at least nine
84 encrusting demosponge species of the orders Axinellida Lévi, 1953 and Poecilosclerida
85 Topsent, 1928 that tolerate seasonal anoxia in a Marine Lake in Lough Hyne, Ireland for ~three
86 months at a time in the summer, and there are more sponge species at this site (Bell and
87 Barnes 2000). The anoxia-tolerant sponges of Lough Hyne therefore have LT50s that exceed
88 their ca. three month exposure to anoxia, and, compared to other animals, their tolerance is
89 rivaled only by the anemone *Bunodosoma cavernatum* Bosc, 1802 (LT50 in anoxia >1.5
90 months, (Ellington 1982). Moreover, the abundance (percent cover) of encrusting sponges in

91 the seasonally anoxic site of Lough Hyne only slightly decreased over 30 years despite
92 widespread sponge losses in the well oxygenated parts of the lough (Micaroni et al. 2021b),
93 indicating that these sponges are uniquely suited to their seasonally anoxic niche.

94
95 Many invertebrates exposed to harsh conditions like anoxia or hypoxia have evolved molecular
96 response pathways to survive in these environments. For instance, under anoxia, marine
97 mollusks shift from lipid, carbohydrate and amino acid metabolism to carbohydrate catabolism
98 as the primary fuel for ATP generation (Larade and Storey 2009). Some mollusks also maximize
99 anoxic survival time (mollusc LT50s at 0 mg L⁻¹: 360–672 h, see Micaroni, Strano, et al. 2021b)
100 by building up a fixed reserve of internal fuels (primarily glycogen) to increase ATP output and
101 to reduce acidity. A small suite of upregulated genes also plays a critical role in cell
102 preservation, facilitating long-term viability under hypoxia (Larade and Storey 2009). Some
103 anemones may even have elements of a facultative anaerobic metabolism (Sassaman and
104 Mangum 1972).

105
106 Only one study has investigated the transcriptomic response of a sponge to hypoxia. After four
107 days of exposure to hypoxia (0.25–2% a.s.), 128 genes within the sponge *T. wilhelma* were
108 differentially expressed compared to controls, but none of these genes were clearly related to
109 metabolic or stress responses (Mills et al. 2018). However, one hour exposure to near anoxia
110 (<0.05% a.s., 105 nM O₂) elicited stress responses in *T. wilhelma*'s transcriptome (Mills et al.
111 2018), demonstrating that transcriptomic responses were mostly observed under very low
112 oxygen levels.

113
114 In most metazoans, the hypoxia-inducible factor (HIF) pathway is essential for maintaining
115 oxygen homeostasis in response to hypoxia (Samenza 2007). However, in sponges and
116 ctenophores, the likely sister-lineages to other metazoans (Feuda et al. 2017), key components
117 of the HIF pathway, including orthologs for HIFa and HIFb, are absent (Mills et al. 2018). HIFa is
118 a transcription factor responsible for triggering metabolic adaptation to deoxygenation in most
119 metazoans (Samenza 2007). Due to the absence of HIFa in sponges, the mechanisms of
120 tolerance to hypoxia and anoxia are largely unknown (Mills et al. 2018).

121
122 The sponge microbiome may play a role in sponge deoxygenation tolerance. Sponges can host
123 diverse microbiomes that perform vital functions and can constitute large portions of their
124 biomass (Wilkinson 1978). The host and microbiome together are referred to as a 'holobiont'
125 (Webster and Taylor 2012). Some sponge symbionts have anaerobic capabilities, including
126 sulfate reduction (Hoffmann et al. 2005), denitrification, and anaerobic ammonium oxidation
127 (anammox) (Hoffmann et al. 2009). In *V. pourtalesii*, the microbial community is thought to be
128 specialized for the low-oxygen conditions in which it lives (Bayer et al. 2020).

129
130 A previous study has shown that the microbiomes of anoxia-tolerant sponges from Lough Hyne
131 were unchanged under anoxia, hypoxia and normoxia despite drastic changes in the microbial
132 communities of the water and sediment, indicating that the holobiont as a whole is tolerant to
133 deoxygenation (Schuster et al., 2021). Specifically, the microbiomes of the anoxia-tolerant
134 sponge species *Eurypon* sp. 2 and *Hymenaphia stellifera* Bowerbank, 1864 were both
135 dominated by two microbes – one *Thaumarchaeon* and one *Gammaproteobacterium*, though

136 each sponge hosted a different species from each clade. *Eurypon* sp. 2 harbors the
137 *Thaumarchaeon* OTU1 (closest related isolate: *Nitrosopumilus adriaticus* strain NF5), and *H.*
138 *stellifera* harbors OTU3 (closest related isolate: *Nitrosopumilus oxycliniae* strain HCE1). For the
139 *Gammaproteobacteria*, *Eurypon* sp. 2 contains OTU2 (closest related isolate: *Arenicella*
140 *chitinivorans* strain ALEN 1); whereas *H. stellifera* contains OTU7 (closest related isolate: *A.*
141 *chitinivorans* strain ALEN 1, (Schuster et al. 2021). Although their location within Lough Hyne
142 sponges has not yet been determined, *Gammaproteobacteria* and *Thaumarchaeota* symbionts
143 are abundant and widely distributed throughout the sponge tissue in other species (Moeller et
144 al. 2019). These symbionts also participate in integrated metabolic processes with their host
145 species (Moitinho-Silva et al. 2017).

146
147 Schuster et al. (2021) hypothesized potential metabolic pathways within these two symbiont
148 taxa that might function under deoxygenation. Based on the genomes of their close relatives,
149 the *Thaumarchaeota* in these sponges were hypothesized to have components of a facultatively
150 anaerobic metabolism, including fumarate, nitrite, and sulfite respiration and the ability to
151 ferment (Bayer et al. 2020), which could aid in deoxygenation tolerance. A recent study
152 demonstrated that another close *Thaumarchaeota* relative, *Nitrosopumilus maritimus*, can
153 produce trace levels of oxygen (100–200 nM) under environmental anoxia (Kraft et al. 2022).
154 The pathway of oxygen production and the genes involved are not currently known. However,
155 comparative proteomics suggested that proteins upregulated during oxygen production included
156 some AsnC family proteins and nitroreductases (Kraft et al. 2021). We therefore hypothesized
157 that nitroreductases and AsnC family proteins would be upregulated under hypoxia and anoxia
158 in sponge *Thaumarchaeota*. *Gammaproteobacteria* symbionts were hypothesized to use sulfide
159 or thiosulfate as an electron donor anaerobically coupled to nitrate reduction, removing
160 exogenous, toxic sulfide from the holobiont under anoxia (Schuster et al. 2021).

161
162 To understand the mechanisms of sponge holobiont tolerance and survival under extended
163 anoxia, we performed differential gene expression analysis of the sponges *Eurypon* sp. 2 and *H.*
164 *stellifera* as well as their respective mitochondria and microbial symbionts including
165 *Thaumarchaeota* and *Gammaproteobacteria*. Sponges were collected from Lough Hyne under
166 *in situ* normoxia, hypoxia and anoxia. Since neither of these holobionts are established model
167 species, we generated reference transcriptomes for the sponges and assembled the genomes
168 of their symbionts and mitochondria from metagenomic sequences. Additionally, we performed
169 a meta-analysis of the sponge differential expression data to determine if the responses of
170 Lough Hyne sponges to deoxygenation are similar to those of *T. wilhelma* under deoxygenation,
171 other invertebrates under heat stress (Dixon et al. 2015), in a dauer state (Sinha et al. 2012),
172 and during diapause (Gong et al. 2013). Finally, we considered the implications of sponge
173 deoxygenation tolerance for future oceans as well as early animal evolution under low
174 atmospheric oxygen concentrations.

175

176 **Materials and Methods**

177

178 **Sampling**

179 Sponges were sampled between July 2018 and August 2019 at Labhra Cliff (Lough Hyne
180 Nature Reserve, Ireland; N51°30.05309 W9°18.17679) as described in Schuster et al. (2021)

181 under permit no. R23-27/2018 issued by the Irish Department of Environment, Heritage, and
182 Local Governments. Samples were taken under various *in situ* oxygen conditions that were
183 categorized as follows: normoxic (5.3–12 mg L⁻¹, 49.3–111% a.s.), hypoxic (1.30–3.56 mg L⁻¹,
184 12.1–33.1% a.s.), and anoxic (0.00–0.01 mg L⁻¹, 0.00–0.93% a.s., i.e. instrument detection
185 limit). All samples were frozen in liquid nitrogen within ~15 minutes of collection and kept at
186 liquid nitrogen temperatures in a dry shipper until returned to the laboratory where samples
187 were stored in a -80°C freezer until extraction. The sponges were identified using molecular
188 barcodes (see Schuster et al. 2021) as *Eurypon* sp. 2 and *H. stellifera*.

189

190 **DNA/RNA extraction**

191 Total RNA was isolated using TRIzol™ Reagent from Invitrogen (ThermoFisher Scientific,
192 Denmark). For RNA sequencing (RNAseq), eight samples of *H. stellifera* (anoxic = 2, hypoxic =
193 5, normoxic = 1) were taken, and sixteen samples of *Eurypon* sp. 2 (anoxic = 2, hypoxic = 7,
194 normoxic = 7) were collected (n = 24 in total). Metadata for individual samples, including oxygen
195 concentration, season, depth and collection date are included in Supplemental Table 1. Since
196 these two species are indistinguishable *in situ*, the samples taken for each species were
197 unequal in number. Remaining DNA in the RNA extracts were removed using the DNase MAX
198 kit (Qiagen).

199

200 Additionally, high molecular weight (HMW) DNA was extracted from one individual of each
201 species using the protocol from Vargas et al. (2021) for metagenomic sequencing. The *Eurypon*
202 sp. 2 sample used for metagenomic sequencing was taken under anoxia (DC24), and RNA was
203 also sequenced from this sample. Due to limited availability of samples and DNA, a sample of
204 *H. stellifera* that was not included in the RNAseq (DC297, sampled under normoxia) was used
205 for metagenome sequencing. DNA and RNA yields were determined using a Qubit™ (Thermo
206 Fisher Scientific) and a NanoDrop™ spectrophotometer (Thermo Fisher Scientific). RNA quality
207 was evaluated on an Agilent TapeStation using an RNA ScreenTape (Agilent Technologies).

208

209 **Reference transcriptomes and metatranscriptomes**

210 All RNA samples were sequenced twice with two different library preps - one for polyadenylated
211 (poly A) messenger RNA (mRNA, from eukaryotes) and one for total RNA (to also capture
212 prokaryotic RNA). Library preparation for the eukaryotic (sponge) RNA was done using
213 NEBNext® Ultra™ II Directional RNA Library Prep Kit for Illumina (New England Biolabs, USA).
214 For the prokaryotic RNAseq, the supernatant from the poly A enrichment was treated with
215 NEBNext® rRNA Depletion Kit (Bacteria) and then NEBNext® rRNA Depletion Kit
216 (Human/Mouse/Rat, New England Biolabs, USA) to eliminate ribosomal RNA (rRNA) that
217 causes sequence biases. This combination of poly A exclusion and rRNA depletion eliminated
218 the most rRNA compared to other combinations of methods (or single methods in isolation) in
219 preliminary tests, yielding sequences with only ~25% rRNA. For the eukaryotic (n = 24) and
220 prokaryotic (n = 24) RNA samples, library preparation was completed using the NEBNext Ultra II
221 Directional RNA library preparation kit (New England Biolabs, Denmark). Libraries pooled in
222 equimolar concentrations were sequenced (5M reads per sample, 2 x 50 bp) at the Center for
223 Functional Genomics and Tissue Plasticity (ATLAS) at SDU, using a NovaSeq 6000 (Illumina,
224 USA).

225

226 To ensure good coverage for the final reference transcriptomes, two samples from each species
227 were sequenced deeper in additional runs. For *H. stellifera*, the sample for deeper sequencing
228 (DC129, sampled under normoxia) was also present in the sample set above. In contrast, for
229 *Eurypon* sp. 2 another sample (DC128, sampled under normoxia) was used due to the limited
230 availability of sample tissue. As in the sequencing above, two libraries were created and
231 sequenced for each sample - one with eukaryotic RNA and one with prokaryotic RNA. For this
232 deeper sequencing, mRNA in the sponge transcriptomes was purified using the NucleoTrap
233 mRNA kit (Macherey-Nagel, Germany). Prokaryotic RNA was rRNA depleted using the Ribo-
234 zero Magnetic kit (Illumina, USA). An additional purification step was performed for all RNA
235 samples using the standard protocol for the CleanNGS kit (CleanNA, Netherlands) before
236 sequencing preparation using the NEBNext Ultra II Directional RNA library preparation kit (New
237 England Biolabs, Denmark). Samples were diluted in equimolar concentrations, pooled and
238 sequenced (2 x 150 bp) on a HiSeq X platform (Illumina, USA) by DNASense ApS (Aalborg,
239 Denmark).

240
241 For the eukaryotic RNA, shallow (2 x 50 bp) sequencing generated 9.20×10^8 and 4.38×10^8
242 reads for *Eurypon* sp. 2 and *H. stellifera*, respectively, across all sampled sponges, and deeper
243 sequences (2 x 150 bp) generated 2.05×10^8 and reads 3.45×10^8 for each sponge of the two
244 species, respectively. For the prokaryotic RNA, shallow sequencing yielded 1.27×10^9 and 6.68
245 $\times 10^8$ reads for *Eurypon* sp. 2 and *H. stellifera*, respectively. The deeper prokaryotic sequencing
246 generated 1.52×10^8 and 1.20×10^8 for *Eurypon* sp. 2 and *H. stellifera*, respectively (totals are
247 shown in Supplemental Table 2).

248
249 To obtain reference transcriptomes for each sponge species without prokaryotic symbionts, all
250 eukaryotic RNA sequences were combined into a single file. These sequences were trimmed for
251 quality control using public scripts (Matz 2015; Meyer 2016) and assembled with Trinity v 2.8.5
252 (Grabherr et al. 2011). This assembly was filtered for contaminants and annotated using egg-
253 NOG mapper (Huerta-Cepas et al. 2019). The final sponge transcriptomes included only genes
254 with metazoan annotations or no annotations. For a detailed description of all filtering and
255 assembly steps, see Strehlow et al. (2020) and (<https://zenodo.org/badge/latestdoi/573040118>)
256 for all scripts used in the current paper. Sponge reference transcriptomes fit within the expected
257 range of size, gene number, and N50 (Supplemental Table 2) of published sponge
258 transcriptomes (Strehlow et al. 2020; Riesgo et al. 2014). Additionally, sponge reference
259 transcriptomes were effectively complete based on Benchmarking Universal Single-Copy
260 Orthologs (BUSCO) analysis (Supplemental Table 2, Simão et al. 2015) and were therefore
261 suitable for use for subsequent differential expression analysis (see below). Sponge reference
262 transcriptome assemblies are available through NCBI under BioProject number PRJNA89319.

263 264 **Reference Metagenomes**

265 Two reference metagenomes were sequenced for *Eurypon* sp. 2 and *H. stellifera* at DNASense
266 ApS (Aalborg, Denmark). DNA was fragmented to ~550 bp (M220 Focused-ultrasonicator,
267 Covaris, USA) and used for library preparation following the NEBNext Ultra II DNA library
268 preparation kit. The DNA library was paired-end sequenced (2 x 150 bp) on a NovaSeq platform
269 (Illumina, USA).

270

271 Sequences were assembled using Megahit v.1.2.9 (Li et al. 2016). The final contig fasta files
272 were used to plot GC (%) vs. mean coverage of mapped reads to identify individual bins. For
273 this, we used the custom python scripts spadescontigstocovgc.py (Francis 2020a) as well as the
274 R script contig_gc_coverage.R (Francis 2020b) to extract bins for the *Thaumarchaeota* and
275 *Gammaproteobacteria* symbiont of each sponge species. Final statistics for each genome are
276 shown in Supplemental Table 2. Raw sequences are available from NCBI under BioProject
277 number PRJNA893197. Metagenome assemblies are available on
278 <https://github.com/bstrehlow/Sponge-transcriptomic-responses-to-seasonal-anoxia>.

279

280 **Mitogenomes**

281 Using only the deep sequences of total ('prokaryotic') RNA, the mitochondrial genomes of single
282 individuals of *Eurypon* sp. 2 (DC128) and *H. stellifera* (DC129) were assembled following the
283 pipeline in Plese et al. (2019).

284

285 For future utilization, single contigs that likely represent the mitochondrial genomes of *Eurypon*
286 sp. 2 and *Hymeraphia stellifera* were retrieved from the reference metagenome in addition to
287 the coding regions used for differential expression below. The assembled contigs for each
288 metagenome were blasted against the mitochondrial genome of DC128 (*Eurypon* sp. 2) using
289 blastn, with an e-value cutoff of 1×10^{-50} for *Eurypon* sp. 2 (DC97) and 1×10^{-30} for *Hymeraphia*
290 *stellifera* (DC297). In general, there was only a single hit for each protein coding gene,
291 confirming a single contig as the mitochondrial genome for each sample. Based on the blast,
292 these two contigs contained all protein coding genes retrieved from the transcriptome that were
293 the focus of this analysis. These 'mitogenomes' can be accessed here:

294 <https://zenodo.org/badge/latestdoi/573040118>.

295

296 **Differential Expression Analysis**

297 Trimmed reads from the shallow sequencing for each individual were mapped back to their
298 respective reference transcriptome or genome using bowtie2 (version 2.3.5.1, Langmead and
299 Salzberg 2012) and mapped reads were counted for each contig using samcount.pl (see Matz
300 2015). Eukaryotic reads were mapped to the sponge reference transcriptome for each species.
301 Prokaryotic reads were mapped to their respective metagenomic bins - metagenome assembled
302 genomes (MAGs), i.e. *Thaumarchaeota* or *Gammaproteobacteria*, within each sponge species.
303 The mitochondrial reference was broken into its 14 genes and prokaryotic (total RNA) reads
304 from both species were mapped to their matching mitochondrial reference and counted as
305 above.

306

307 Analyses were performed to compare the gene expression of each target (sponge species,
308 symbiont species, and mitochondria; n=8) under the three different oxygen conditions (anoxia,
309 hypoxia and normoxia). Differential gene expression analysis was performed with the package
310 DESeq2 v. 1.22.2 (Love et al. 2016) in R (R Core Team 2016) with (RStudio Team 2020). Three
311 pairwise comparisons of oxygen condition (normoxia vs. hypoxia, normoxia vs. anoxia, and
312 anoxia vs. hypoxia) were computed from DESeq2 results. Significantly differentially expressed
313 genes between each of these pairwise comparisons were identified using a false discovery rate
314 (FDR) adjusted p-value threshold of 0.1. The ReportingTools software package (Huntley et al.
315 2013) was used to create PDF pages displaying 4 plots of significantly differentially expressed

316 genes and their annotations in various oxygen conditions, as well as box plots, p-values, and
317 LFCs (<https://zenodo.org/badge/latestdoi/573040118>). These files are searchable in case
318 particular genes are of interest to future studies. We note that comparisons to *H. stellifera* under
319 normoxia were made with only one normoxic sample due to sampling restrictions. Despite this
320 sampling limitation, the normoxic data for *H. stellifera* are still shown as a baseline and
321 reference. For each sponge species, log fold changes (LFC, from DESeq2) in all genes were
322 calculated so that positive LFCs were upregulated and negative values were downregulated in
323 hypoxia or anoxia relative to normoxia. For the comparisons between hypoxia and anoxia,
324 positive LFCs were upregulated in anoxia and vice versa.

325
326

327 **KOG analysis**

328 EuKaryotic Orthologous Groups (KOG class) assignments were used to compare large scale
329 trends and potential correlations in differential gene expression between Lough Hyne sponges
330 under varied oxygen conditions and external gene expression data from other species and
331 conditions. Delta-ranks, a measure of each KOG class enrichment with up or downregulated
332 genes, were calculated from LFC data using the KOGMWU package in R (Dixon et al. 2015),
333 and delta-ranks were plotted using the package pheatmap (Kolde 2013). While it is also
334 possible to calculate delta-ranks with signed p-values (see KOGMWU supporting
335 documentation), LFC was used here to include changes between normoxia and other conditions
336 for *H. stellifera*. Since there was only one normoxic replicant for this species, LFC was a more
337 appropriate metric than signed p values. Within each pairwise comparison (i.e. hypoxic, anoxic,
338 and anoxic vs hypoxic), significantly enriched KOGs were also calculated using KOGMWU
339 (FDR-adjusted $p < 0.05$).

340

341 These KOG enrichments were also compared to those calculated from the sponge *Tethya*
342 *wilhelma* after four days of exposure to hypoxia and one hour of exposure to anoxia (Mills et al.
343 2018). To test whether KOG enrichment in sponges exposed to variable oxygen conditions was
344 correlated with gene expression in other invertebrate stress responses, delta rank data was
345 included from adult *Acropora millepora* coral exposed to heat stress (31.5 °C for three days,
346 (Dixon et al. 2015). Similarly, to test the similarity of the sponge data to noted decreases in
347 metabolic activity in invertebrates, KOGs enriched in the dauer (dormant) state in
348 *Caenorhabditis elegans* (Sinha et al. 2012) and the diapause state of the midge *Sitodiplosis*
349 *mosellana* (Gong et al. 2013) were added using delta rank tables calculated by Strader et al.
350 (2016). Correlations between the KOG delta ranks in different datasets were performed using
351 Pearson's Correlation in KOGMWU. Within the significantly enriched KOGs 'replication,
352 recombination and repair' and 'energy production and conversion,' genes that were significantly
353 differentially expressed were plotted in heatmaps to further investigate sponge transcriptomic
354 responses to deoxygenation at the gene level in Lough Hyne sponges.

355

356 KOG enrichment analysis was performed as above for each of the two major symbionts within
357 the two sponge species; however, Clusters of Orthologous groups (COGs) were used since
358 they are designed for prokaryotes rather than eukaryotic KOGs and are fewer in number.

359

360 **Gene ontology (GO) term enrichment analysis**

361 Log fold changes calculated above were used for rank-based gene ontology (GO) analysis with
362 adaptive clustering (GO_MWU, Wright et al. 2015) to determine what GO terms were
363 significantly enriched under various oxygen conditions. These analyses were run individually for
364 each pairwise comparison of oxygen condition in both sponge species. These analyses were
365 not completed for the two symbiont types because GO terms were not available for these
366 microbes.

367

368 **Phylogenetic positions of nitroreductase proteins**

369 To determine if nitroreductases in sponge symbionts are related to genes that may be involved
370 in oxygen production in *N. maritimus*, nitroreductase proteins from the *Thaumarchaeota*
371 symbionts of *H. stellifera* and *E. sp. 2* were extracted using annotations assigned by egg-NOG.
372 Phylogenetic position of nitroreductase proteins from *H. stellifera* and *E. sp. 2* were investigated
373 by aligning them to other known nitroreductase proteins from Genbank using Mafft v7 (Kato
374 and Standley 2013). The ModelTest-NG v.0.1.7 function (Edler et al. 2020) implemented within
375 RaxmlGUI 2.0 was used to calculate the evolutionary model. According to AIC, LG+I+G was
376 chosen as the best-fitting model. Maximum Likelihood (ML) phylogeny was then reconstructed
377 using raxmlGUI v.2.0.6 (Edler et al. 2020) with 100 (rapid) bootstraps. The resulting protein tree
378 was rendered by FigTree v.1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree/>).

379

380 **Results**

381

382 **Sponge differential expression**

383 There were three pairwise comparisons for significantly differentially expressed genes - hypoxia
384 vs. normoxia, anoxia vs. normoxia, and anoxia vs. hypoxia. The number of significantly
385 differentially expressed genes in these comparisons for sponges, their mitochondria and their
386 symbionts are summarized in Table 1. In the sponge *Eurypon* sp. 2, 737, 1,376 and 1,090
387 genes were significantly differentially expressed under hypoxia (vs. normoxia), anoxia (vs.
388 normoxia), and anoxia vs. hypoxia, respectively ($p < 0.1$, Table 1). The differentially expressed
389 genes under each oxygen condition ranged between 1.5–2.8% of the genes of the *Eurypon* sp.
390 2 reference transcriptome, and 41–48% of these genes are annotated, which reflects the overall
391 annotation percentage of 39.7% for the whole transcriptome (Supplemental Table 2). In
392 hypoxia, the majority of these differentially expressed genes were upregulated (68%). Under
393 anoxia, on the other hand, the majority of genes were downregulated (60%). In anoxia vs.
394 hypoxia, 57% of genes were upregulated in anoxia compared to hypoxia in *Eurypon* sp. 2
395 (Table 1).

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Table 1. Number of significantly differentially expressed genes (DEGs) under deoxygenation in the sponge holobionts summarized per reference genome or transcriptome. The direction (up or down) within each paired oxygen condition comparison is relative to normoxia or in the case of anoxia vs. hypoxia, hypoxia. The number of annotated genes is shown in parentheses.

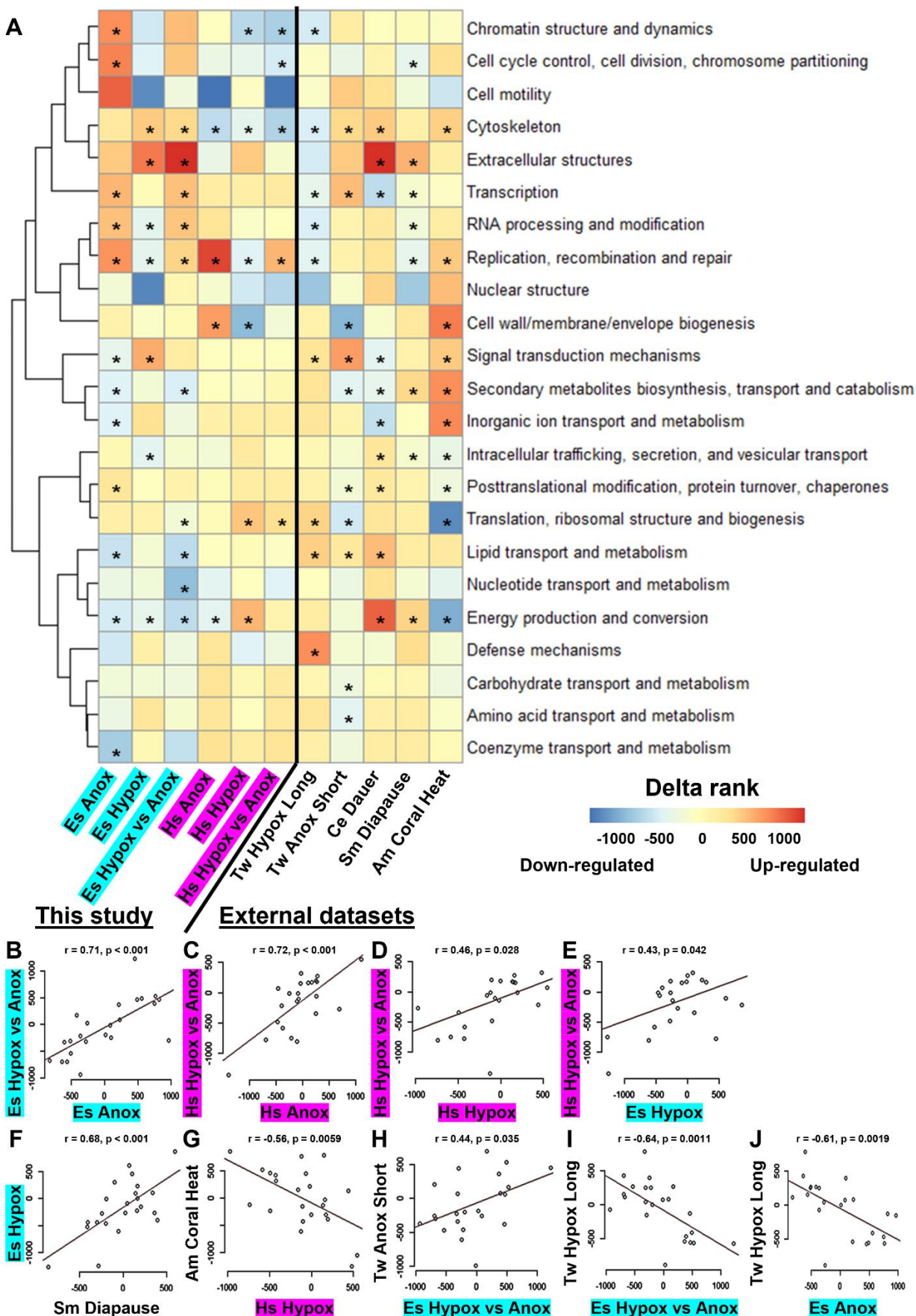
Sponge	Reference	Total genes in Reference	Hypoxia		Anoxia		Anoxia vs hypoxia	
			Up	Down	Up	Down	Up	Down
<i>Eurypon</i> sp. 2	sponge	49,911	499 (239)	238 (112)	551 (228)	825 (340)	622 (273)	468 (205)
<i>H. stellifera</i>	sponge	62,494	465 (125)	58 (9)	40 (11)	244 (87)	1531 (438)	623 (286)
<i>Eurypon</i> sp. 2	mitochondria	14	0 (0)	0 (0)	0 (0)	0 (0)	1 (1)	0 (0)
<i>H. stellifera</i>	mitochondria	14	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
<i>Eurypon</i> sp. 2	<i>Thaumarchaeota</i>	1,556	19 (14)	1 (1)	3 (3)	0 (0)	0 (0)	0 (0)
<i>H. stellifera</i>	<i>Thaumarchaeota</i>	1,551	17 (12)	0 (0)	0 (0)	0 (0)	1 (0)	27 (20)
<i>Eurypon</i> sp. 2	<i>Gammaproteobacteria</i>	2,751	3 (3)	29 (29)	0 (0)	0 (0)	0 (0)	0 (0)
<i>H. stellifera</i>	<i>Gammaproteobacteria</i>	3,057	0 (0)	0 (0)	0 (0)	0 (0)	20 (20)	416 (401)

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In the sponge *H. stellifera*, 523, 284, and 2,154 genes were significantly differentially expressed in hypoxia, anoxia, and in anoxia vs. hypoxia, respectively ($p < 0.1$, Table 1). Differentially expressed genes in the different oxygen conditions corresponded to 0.42-3.4% of the total number of genes in the *H. stellifera* transcriptome. Approximately 25-37% of the differentially expressed genes were annotated, which, as in the other sponge species, roughly corresponded to the global percentage (37.0%) of genes annotated within the *H. stellifera* reference transcriptome. Under hypoxia in this species, the vast majority of differentially expressed genes (89%) were upregulated. As in *Eurypon* sp. 2, the majority of differentially expressed genes (84%) were downregulated in anoxia in *H. stellifera*. The majority of differentially expressed genes between anoxia and hypoxia were upregulated in anoxia (71%, Table 1).

KOG enrichments in sponges

418 The global gene expression patterns of Lough Hyne sponges in response to deoxygenation
419 were compared across the two species by assessing up and down regulation of KOG classes
420 (broad functional annotations assigned to genes). Within these sponges, KOG expression in
421 response to hypoxia and anoxia (versus normoxia) were largely distinct in both species (Figure
422 1A). However, KOG expression in *H. stellifera* in hypoxia vs. anoxia was significantly positively
423 correlated, i.e. similar, to that of *Eurypon* sp. 2 under hypoxia ($r = 0.43$, $p < 0.05$, Figure 1E), but
424 global expression patterns were only similar between the two species in this single case.
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430 **Figure 1.** KOG expression profiles of sponges under varied oxygen concentrations compared to each
431 other and external datasets. A. Clustered heatmap (based on correlation) of KOG class (rows)
432 enrichments for upregulated or downregulated genes. Highlighted columns correspond to data
433 generated in this study (Purple: *Hymeraphia stellifera* [Hs], Cyan: *Eurypon* sp. 2 [Es]). Unhighlighted
434 columns represent external datasets. Up or down regulation with respect to normoxia is indicated in
435 'Hypox' (hypoxia) and 'Anox' (anoxia) columns, and differential regulation with respect to hypoxia is
436 shown in 'Hypox vs. Anox' columns, i.e. upregulated KOGs (red delta ranks) are upregulated in anoxia
437 with respect to hypoxia. Within each column on the heatmap, KOGs that are significantly enriched (FDR-
438 adjusted $p < .05$) are marked with asterisks. KOG enrichments from the sponge *Tethya wilhelma* after
439 four days exposure to hypoxia (Tw Hypox Long) and one hour exposure to anoxia (Tw Anox Short), the
440 coral *Acropora millepora* after three days of exposure to heat stress (Am Coral Heat), *Caenorhabditis*
441 *elegans* in a dauer state (Ce Dauer), and the midge *Sitodiplosis mosellana* in diapause (Sm Diapause)
442 from external studies were included for comparative purposes. B-E. Significant ($p < 0.05$) correlations
443 between the KOG enrichments for different species and oxygen levels from this study. F-J. Significant
444 correlations between KOG enrichments in this study and those of external datasets. All other possible
445 comparisons between the various datasets were not significant.

446
447 Within *Eurypon* sp. 2, KOG class expression patterns in hypoxia vs. anoxia were significantly
448 positively correlated to those of hypoxia ($r = 0.71$, $p < 0.01$, Figure 1B). Similarly, in *H. stellifera*,
449 KOG enrichment in hypoxia vs. anoxia was positively correlated to that of hypoxia ($r = 0.72$, $p <$
450 0.001 , Figure 1C) and anoxia ($r = 0.46$, $p < 0.05$, Figure 1D). All significant correlations between
451 datasets are shown in (Figure 1B-J), and all relationships that were not significantly correlated
452 are not shown.

453
454 At the level of individual KOGs, the KOG class 'replication recombination and repair' (RRR) was
455 significantly enriched in all pairwise comparisons of oxygen conditions for both sponge species
456 ($P_{adj} < 0.05$), though in different directions depending on oxygen. It was significantly upregulated
457 in anoxia and anoxia vs. hypoxia but downregulated in hypoxia in both species (Figure 1A).

458
459 In *Eurypon* sp. 2, five genes with RRR KOG annotations were significantly upregulated in
460 hypoxia, e.g. HELZ and HELZ2 transcription associated helicases, and 11 genes were
461 significantly downregulated ($p < 0.1$, Supplemental Figure 4A), including five genes from the
462 minichromosome maintenance (MCM) protein complex. In anoxia, two genes were significantly
463 upregulated within RRR in this species - 'siz regulation of ARF protein signal transduction' and
464 DNA polymerase epsilon catalytic subunit ($p < 0.1$, Supplemental Figure 4B). The majority of
465 significantly differentially expressed RRR genes (five) were downregulated in anoxia ($p < 0.1$,
466 Supplemental Figure 4B). The majority of RRR genes (nine) were also downregulated in anoxia
467 vs. hypoxia, with only two significantly upregulated in anoxia (Supplemental Figure 4B). The
468 genes NBN and RFC1 were downregulated in anoxia compared to both normoxia and hypoxia
469 (Supplemental Figure 4B,C). Similarly, the gene 'siz regulation of ARF protein signal
470 transduction' was upregulated in anoxia compared to both normoxia and hypoxia (Supplemental
471 Figure 4B,C).

472

473 In *H. stellifera*, three genes were significantly differentially expressed in the RRR KOG class in
474 hypoxia, and all were upregulated ($p < 0.1$, Supplemental Figure 4D). No genes within this class
475 were significantly differentially expressed in anoxia (vs. normoxia). Eleven genes were
476 upregulated and eight genes were downregulated in anoxia vs. hypoxia (Supplemental Figure
477 4E). Similar to *Eurypon* sp. 2, HELZ2 was downregulated in anoxia vs. hypoxia in *H. stellifera*.
478 In contrast to *Eurypon* sp. 2 a distinct MCM gene (MCM6) was downregulated in anoxia vs.
479 hypoxia. Additionally, four genes from the structural maintenance of chromosomes protein 6
480 (SMC6) complex were downregulated in anoxia vs. hypoxia.

481
482 Like RRR, the KOG class 'energy production and conversion' (EPC) was significantly enriched
483 ($P_{\text{adj}} < 0.05$) between all conditions except for anoxia vs. hypoxia in *H. stellifera* ($P_{\text{adj}} = 0.07$).
484 EPC was significantly upregulated in hypoxia in *H. stellifera* but downregulated in all remaining
485 conditions in both sponge species (Figure 1A).

486
487 Within *Eurypon* sp. 2 specifically, four genes were significantly downregulated and twelve genes
488 were upregulated within the EPC class in hypoxia ($p < 0.1$, Supplemental Figure 5A). Various
489 nuclear genes for processes in the mitochondria were differentially expressed in hypoxia.
490 SLC25A27 (a mitochondrial membrane uncoupling protein), ndufs8 (a NADH dehydrogenase
491 core subunit in the mitochondrial membrane - complex I), and Surf1 (part of the complex that
492 regulates cytochrome c oxidase assembly) were downregulated in hypoxia (Supplemental
493 Figure 5A). However, other nuclear mitochondrial genes were upregulated, including four
494 subunits of ATP synthase and two additional genes with annotations corresponding to ATP
495 synthesis (Supplemental Figure 5A). In anoxia, fourteen genes were upregulated and five genes
496 were downregulated in the EPC class (Supplemental Figure 5B).

497
498 As in hypoxia, ndufs8 was downregulated, but no other significant DEGs were shared across
499 the two oxygen levels. The following genes were also downregulated in anoxia: mitochondrial
500 sulfite oxidase (SUOX), malate dehydrogenase (MDH1), and two genes belonging to the ATP
501 gaunido phosphatase family (Supplemental Figure 5B). Conversely, four genes involved in
502 phosphoenolpyruvate carboxykinase activity were significantly upregulated in anoxia ($p < 0.1$,
503 Supplemental Figure 5B). Additionally, three mitochondrial membrane transporter proteins from
504 the SLC family, two CYB5R4 cytochrome reductase genes, a mitochondrial carrier protein, and
505 fdx1 cytochrome reductase were upregulated in anoxia. In anoxia vs. hypoxia in *Eurypon* sp. 2,
506 ten genes were upregulated in anoxia (Supplemental Figure 5C). Upregulated genes included
507 all of the same genes that were significantly upregulated in anoxia, except for the
508 phosphoenolpyruvate carboxykinase associated genes. Six genes were significantly
509 downregulated in anoxia vs. hypoxia. Of these, three were also downregulated in anoxia (vs.
510 normoxia) and two genes were significantly upregulated in anoxia (Supplemental Figure 5A-C).
511 It is noteworthy, however, that all of the upregulated genes in anoxia vs. normoxia and hypoxia
512 were only strongly upregulated in one of the two anoxia replicates (DC56, Supplemental Figure
513 5 B,C).

514
515 In *H. stellifera*, eight genes were upregulated and two genes were downregulated in hypoxia. As
516 in *Eurypon* sp. 2, the ATP5A1 ATP synthase subunit was upregulated in hypoxia. An additional
517 ATP synthase subunit (ATP6V0C) that was not significantly upregulated in *Eurypon* sp. 2 was

518 upregulated in *H. stellifera* in hypoxia ($p < 0.1$, Supplemental Figure 5D). Mitochondrial
519 sulfide:quinone oxidoreductase (SQRDL), three genes associated with phosphoenolpyruvate
520 carboxykinase, and a histone demethylase (KDM6A) were also significantly upregulated in
521 hypoxia in *H. stellifera*. Conversely, PCK1 (also associated with phosphoenolpyruvate
522 carboxykinase) and MDH1 were significantly downregulated in hypoxia ($p < 0.1$, Supplemental
523 Figure 5D). In anoxia in *H. stellifera*, ATP5A1 was significantly upregulated, and ATP6V0C,
524 PCK1, and MDH1 were significantly downregulated (Supplemental Figure 5E). Comparing
525 anoxia vs. hypoxia, eight genes were upregulated and five genes were downregulated
526 (Supplemental Figure 5F).

527
528 As in hypoxia, SQRDL, four genes associated with phosphoenolpyruvate carboxykinase activity,
529 and KDM6A were upregulated in anoxia vs. hypoxia. Additionally, two unshared genes,
530 including the mitochondrial Succinyl-CoA:3-ketoacid coenzyme A transferase 1 (OXCT1) and a
531 mitochondrial carrier protein, were upregulated in anoxia vs. hypoxia (Supplemental Figure 5F).
532 Five genes were downregulated in anoxia vs. hypoxia in *H. stellifera*. Two of these four only
533 exhibited high expression levels in one hypoxic sample (DC105) that drove the observed
534 difference (Supplemental Figure 5F). The other three downregulated genes in anoxia vs.
535 hypoxia were mitochondrial creatine kinase (CKMT2), NAD P transhydrogenase (NNT), and
536 proto-oncogene tyrosine-protein kinase (Src).

537
538 The 'cytoskeleton' KOG class was also significantly enriched ($P_{\text{adj}} < 0.01$) in all but one oxygen
539 condition – anoxia in *Eurypon* sp. 2 ($P_{\text{adj}} = 0.1$). Interestingly, enrichment patterns in this KOG
540 were species specific, being significantly upregulated in hypoxia and anoxia vs. hypoxia in
541 *Eurypon* sp. 2 and downregulated in all conditions for *H. stellifera*.

542
543 The other twenty KOG classes were only significantly enriched in Lough Hyne sponges under a
544 few (or no) different oxygen conditions and patterns of significant enrichment were generally
545 condition and species-specific (Figure 1A). With the exception of EPC, KOGs pertaining to
546 metabolic processes were rarely significantly enriched. Expression of the KOG classes
547 'carbohydrate metabolism' and 'amino acid transport and metabolism' were not significantly
548 changed under any oxygen condition ($P_{\text{adj}} > 0.05$). There was some significant enrichment of
549 metabolic KOGs, but only in *Eurypon* sp. 2. 'Coenzyme transport and metabolism' and
550 'inorganic ion transport and metabolism' were both downregulated in anoxia, and 'nucleic acid
551 transport metabolism' was downregulated in hypoxia vs. anoxia. For both these conditions
552 (anoxia and hypoxia vs. anoxia), 'Lipid transport and metabolism' and 'Secondary metabolites
553 biosynthesis, transport and catabolism' were significantly downregulated. However, the
554 transcription of the majority of genes labeled with metabolic KOGs remained unchanged under
555 anoxia and hypoxia.

556
557 Comparing the Lough Hyne dataset with external datasets of invertebrate KOG expression in
558 response to stress, only two positive correlations were found. In *Eurypon* sp. 2, expression
559 patterns under anoxia vs. hypoxia were comparable to those of *T. wilhelma* under short-term
560 anoxia ($r = 0.44$, $p < 0.05$, Figure 1H). The hypoxic response of *Eurypon* sp. 2 resembled that of
561 diapause in *S. mosellana* ($r = 0.68$, $p < 0.001$, Figure 1F), but this was the only correlation found
562 between Lough Hyne sponge data and diapause or dauer states. Importantly, KOG enrichments

563 under anoxia (versus normoxia) were not positively correlated to any other external datasets for
564 either sponge species.

565
566 Three significant negative correlations, which corresponded to opposing KOG expression
567 patterns, were observed between Lough Hyne sponges and external datasets. Hypoxia
568 responses in *H. stellifera* were negatively correlated with those of *A. millepora* under heat stress
569 ($r = -0.56$, $p < 0.01$, Figure 1G). The long exposure of *T. wilhelma* to hypoxia was negatively
570 correlated to both anoxia ($r = -0.64$, $p < 0.01$, Figure 1J) and hypoxia vs. anoxia ($r = -0.61$, $p <$
571 0.01 , Figure 1I) in *Eurypon* sp. 2.

572
573 GO term enrichments in sponges

574
575 Generally, significantly enriched GO terms between the different treatments were not shared
576 between the two sponge species (Supplemental Figures 1-3). The strongest upregulated GO
577 enrichments ($p < 0.01$) in hypoxia in *Eurypon* sp. 2 were cellular signaling and 'lipoprotein
578 particle receptor binding' (Supplemental Figure 1A). For *H. stellifera*, on the other hand, the
579 strongest upregulated enrichments ($p < 0.01$) in hypoxia included the terms 'protein tyrosine
580 kinase binding,' 'molecular adaptor,' 'structural molecule,' and 'structural constituent of
581 ribosome'; whereas the downregulation of the term 'motor' was strong ($p < 0.01$, Supplemental
582 Figure 1B).

583
584 Under anoxia, strong upregulation of the 'proteasome binding' term was observed in *Eurypon*
585 sp. 2 ($p < 0.01$), and the terms 'phosphoenolpyruvate carboxykinase,' 'carbohydrate kinase,'
586 monovalent inorganic cation transmembrane transporter,' and 'sodium ion transmembrane
587 transporter' were highly downregulated ($p < 0.01$, Supplemental Figure 2A). In *H. stellifera*
588 under anoxia, the terms 'damaged DNA binding' and 'calcium-dependent phospholipid binding'
589 were highly upregulated, and four terms associated with various aspects of the cytoskeleton
590 were downregulated ($p < 0.01$, Supplemental Figure 2B).

591
592 In *Eurypon* sp. 2 under anoxia vs. hypoxia, the terms 'lipoprotein receptor binding' and
593 'proteasome binding' were strongly upregulated in anoxia, but no terms were strongly
594 downregulated in anoxia versus hypoxia ($p < 0.01$, Supplemental Figure 3A). The former term
595 was also upregulated under anoxia vs. normoxia. Conversely, the strongest enrichments in *H.*
596 *stellifera* in anoxia vs. hypoxia were downregulated in anoxia and were composed of three of
597 the four cytoskeletal binding GO terms that were also downregulated in anoxia vs. normoxia
598 (see above, $p < 0.01$, Supplemental Figure 3B), but no strong upregulation of GO terms was
599 observed.

600
601 Considering GO enrichments at lower significance levels ($0.01 < p < 0.1$), within *Eurypon* sp. 2,
602 the GO terms 'proteasome binding,' 'lipoprotein particle receptor binding,' and 'Hsp70 binding'
603 (HSP: Heat shock protein) were significantly upregulated in all cases of decreased oxygen albeit
604 at varied significance levels ($p < 0.05$, Supplemental Figures 1–3A). Between only two levels,
605 the terms 'transmembrane signaling receptor,' 'secondary active transmembrane transporter,'
606 and 'molecular transducer' were upregulated in hypoxia but downregulated in anoxia. However,
607 the term lipoprotein particle receptor binding was downregulated in anoxia and upregulated in

608 hypoxia ($p < 0.1$, Supplemental Figures 1,2A). Additionally, the term 'structural constituent of
609 ribosome' was upregulated in anoxia but downregulated in anoxia vs. hypoxia ($p < 0.1$,
610 Supplemental Figures 1,3A). No additional GO terms other than the three present in all oxygen
611 levels for *Eurypon* sp. 2 were enriched in both the pairwise comparison of anoxia and anoxia vs.
612 hypoxia.

613
614 No GO terms were significantly up or downregulated in all three levels of oxygen conditions for
615 *H. stellifera*. However, some GO terms were significantly enriched in two levels. The term
616 'ATPase, coupled to transmembrane movement of ions, rotational mechanism' was
617 downregulated in hypoxia but upregulated in anoxia ($p < 0.1$, Supplemental Figures 1B, 2B
618 respectively). The GO terms 'I-SMAD binding', 'thioesterase binding,' and 'ubiquitin-like protein
619 ligase binding' were all upregulated in hypoxia (vs. normoxia) and anoxia vs. hypoxia, while the
620 'motor' term was downregulated ($p < 0.1$, Supplemental Figures 1B, 3B).

621
622 There were only two shared GO enrichments between both sponge species for any given
623 oxygen condition. The terms 'protein tyrosine kinase binding' and 'structural constituent of the
624 ribosome' were upregulated in both species in hypoxia ($p < 0.1$, Supplemental Figure 1),
625 although they were enriched to different degrees of significance. No significantly enriched GO
626 terms were shared between species in normoxia vs. anoxia or hypoxia vs. anoxia.

627
628 At the gene level, significantly differentially expressed heat shock proteins (Hsps) in both
629 sponges are shown in Supplemental Figure 8. In *Eurypon* sp. 2, one Hsp gene
630 (DNAJC8/Hsp40) was downregulated in hypoxia ($p < 0.01$), but four Hsp genes (HSPA8, two
631 genes for HSP90B1, and Hsp70) were significantly upregulated in hypoxia ($p < 0.1$,
632 Supplemental Figure 8A). Additionally, HSPA8 and C11orf73 (Hsp70 binding protein) were
633 upregulated in anoxia vs normoxia ($p < 0.05$, Supplemental Figure 8A). Another Hsp70 gene
634 was also significantly downregulated in anoxia vs. hypoxia ($p < 0.05$, Supplemental Figure 8A).
635 In *H. stellifera*, HSP90A1 was upregulated in hypoxia and anoxia ($p < 0.1$, Supplemental Figure
636 8B). Two additional Hsp genes (both for HSP90B1) were also upregulated in anoxia. Finally, the
637 two HSP90B1 genes were upregulated in anoxia vs. hypoxia, but HSPA5 was downregulated in
638 anoxia vs. hypoxia ($p < 0.05$, Supplemental Figure 8B).

639

640 **Mitochondrial gene expression**

641 All 14 coding genes from the sponge mitochondria were transcribed in both species and in all
642 oxygen conditions. There was only one mitochondrial gene (*nad2*) that was significantly
643 differentially expressed but only in *Eurypon* sp. 2. This gene was significantly upregulated ($p <$
644 0.1) in anoxia vs hypoxia (Supplemental Figure 6A, Table 1). Similar counts for each individual
645 mitochondrial gene across both sponge species and all oxygen conditions were found. For
646 instance, counts for *atp6* were consistently twice as high as counts for *atp8* (Supplemental
647 Figure 6).

648

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650

651

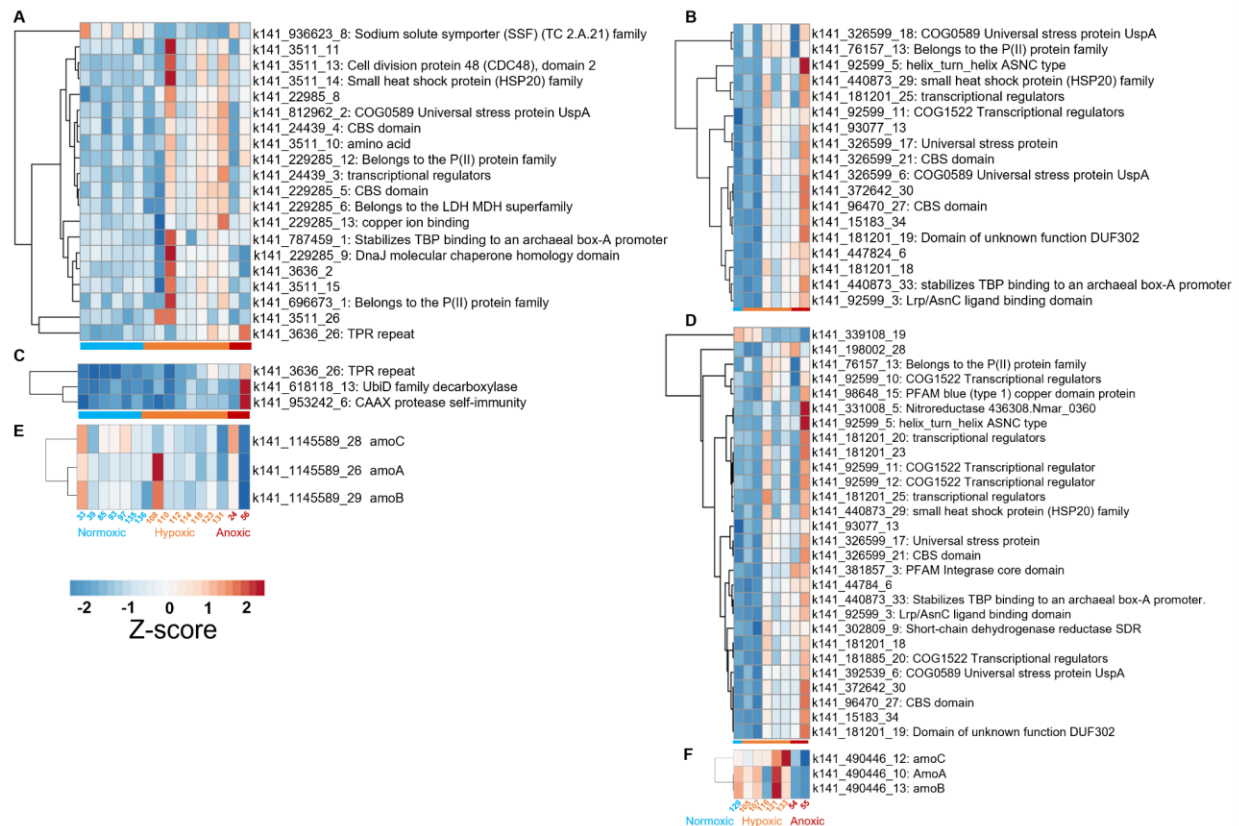
652 Prokaryotic differential expression

653

654 *Thaumarchaeota* gene expression

655 For the *Thaumarchaeota* associated with *Eurypon* sp. 2, 20, 3 and 0 genes were differentially
 656 expressed in hypoxia, anoxia, and hypoxia vs. anoxia, respectively ($p < 0.1$, Table 1). These
 657 genes accounted for 0-1.3% of this *Thaumarchaeota* genome, and 75-100% of the differentially
 658 expressed genes were annotated (Table 1), compared to 69.2% annotated in the entire
 659 reference genome. All but one of the differentially expressed genes in hypoxia were upregulated
 660 (Table 1, Figure 2A). The downregulated gene belonged to the sodium solute symporter family
 661 (SSF, TC 2.A.21, Figure 2A). The upregulated genes in hypoxia included three stress response
 662 genes (COG0589 Universal stress protein [UspA], small heat shock protein [HSP20], and DnaJ
 663 molecular chaperone homology domain), two CBS domains, a member of the lactate/malate
 664 dehydrogenase (LDH MDH) superfamily, a tetratricopeptide (TPR) repeat, two transcription
 665 regulators, and a PII signal transduction protein.

666



667

668 **Figure 2.** A-D. All significantly differentially expressed genes for the *Thaumarchaeota* in both sponge
 669 species (left: *E. sp. 2*, right: *H. stellifera*). For *Thaumarchaeota* associated with *E. sp. 2*, only two pairwise
 670 comparisons of oxygen conditions had significant differences: A. hypoxia vs. normoxia and C. anoxia vs.
 671 normoxia. In symbionts associated with *H. stellifera*, there were significantly differentially expressed
 672 genes in hypoxia vs. normoxia (B) and anoxia vs. hypoxia (D). There were no significant differences in the
 673 three genes involved in ammonia oxidation (AmoA, B and C) in either symbiont, but their heatmaps are
 674 shown in E and F for *E. sp. 2* and *H. stellifera*, respectively.

675

676 Only three genes were significantly differentially expressed in anoxia in *Eurypon* sp. 2's
677 *Thaumarchaeota*, and all were upregulated (Table 1, Figure 2C). The upregulated genes in
678 anoxia were a UbiD family decarboxylase, CAAX protease self-immunity, and the same TPR
679 repeat that was also upregulated in hypoxia. There were no significantly differentially expressed
680 genes between anoxia and hypoxia in this *Thaumarchaeota* (Table 1). The genes necessary for
681 ammonia oxidation, i.e. subunits A, B and C of ammonia monooxygenase (Amo), were present
682 in this *Thaumarchaeota*, but they were not differentially expressed under deoxygenation (Figure
683 2E).

684
685 In the *Thaumarchaeota* symbiont of *H. stellifera*, 17, 0 and 28 genes were significantly
686 differentially expressed in hypoxia, anoxia and hypoxia vs. anoxia, respectively. Similar to the
687 symbiont of *Eurypon* sp. 2, all 17 differentially expressed genes in the *H. stellifera* symbiont
688 were upregulated in hypoxia. These genes included the stress response genes 'universal stress
689 protein, an HSP20 family protein, and two copies of UspA. HSP20 and UspA were also
690 upregulated in the *Eurypon* sp. 2 holobiont. Similarly, a PII signal transduction protein, CBS
691 domain, and two transcription regulators (one identical: TBP stabilizer, and one distinct to *H.*
692 *stellifera* symbionts) were upregulated in both *Thaumarchaeota* species in hypoxia. Unlike in
693 *Eurypon* sp. 2, the *Thaumarchaeota* in *H. stellifera* upregulated a helix turn helix ASNC type
694 domain and a Lrp/AsnC ligand binding domain (Figure 2B). No genes were significantly
695 differentially expressed in anoxia in this *Thaumarchaeon*.

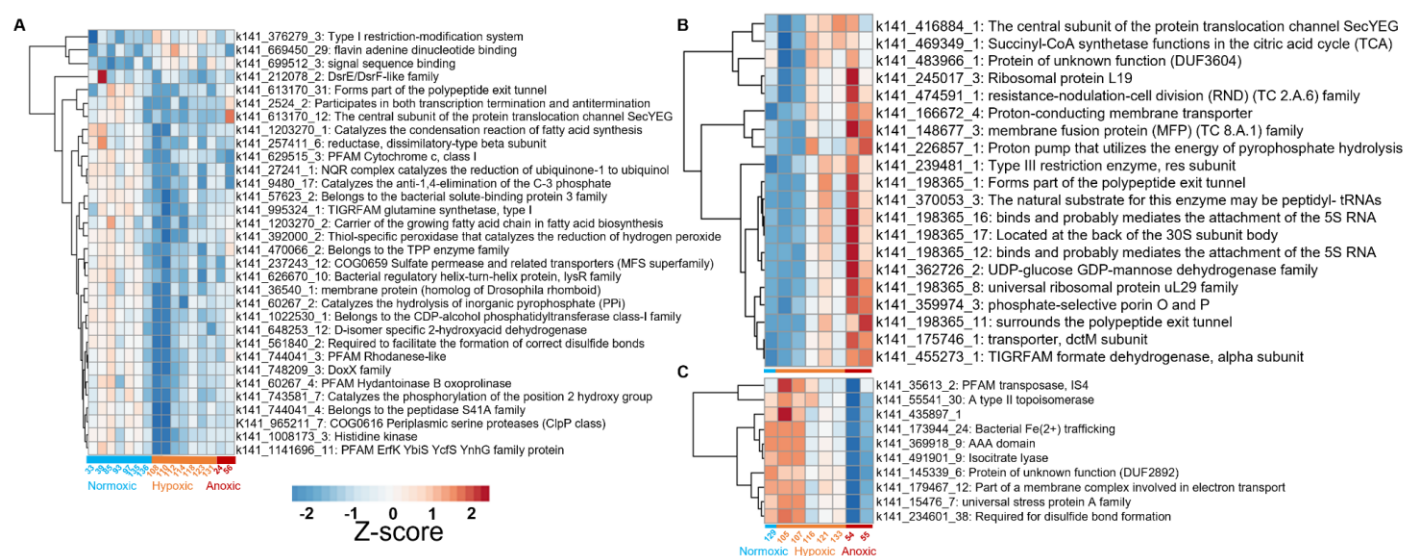
696
697 As in the other holobiont species, *Thaumarchaeota* genes for ammonia oxidation were not
698 significantly differentially expressed with *H. stellifera* symbionts (Figure 2F). Twenty-seven
699 genes were upregulated and one gene (K141_339108_19, unannotated) was downregulated in
700 anoxia vs. hypoxia in the *Thaumarchaeota* within *H. stellifera* (Figure 2D). Most of the
701 upregulated genes in anoxia vs. hypoxia were also upregulated in hypoxia. Upregulated genes
702 in anoxia vs. hypoxia unique to the *H. stellifera* holobiont included additional transcriptional
703 regulators, an integrase domain, and a putative nitroreductase. The phylogenies of this
704 upregulated nitroreductase and all nitroreductases from the studied holobionts as well as
705 publicly available nitroreductase sequences from other *Thaumarchaeota* are shown in
706 Supplemental Figure 9.

707
708 For both *Thaumarchaeota*, only two COGs ('signal transduction mechanisms' and
709 'transcription') were significantly enriched ($P_{\text{adj}} < 0.05$, Supplemental Figure 7A). These two
710 COGs were both downregulated in hypoxia and anoxia vs. hypoxia within *H. stellifera*
711 symbionts. All other COG classes were comparable in their expression levels regardless of
712 holobiont species or oxygen concentration (Supplemental Figure 7A).

713 714 *Gammaproteobacteria* gene expression

715 The *Gammaproteobacteria* associated with *Eurypon* sp. 2 only exhibited significant differential
716 expression under hypoxia but not in any other oxygen condition (Table 1). In hypoxia, three
717 genes were upregulated: type 1 restriction-modification system, flavin adenine dinucleotide
718 binding, and signal sequence binding (Figure 3A). The 29 downregulated genes in hypoxia
719 included two genes involved in sulfur processing (k212078_2, k237243_12), cytochrome c
720 (class I), a gene associated with the assembly of the periplasmic c-type cytochromes

721 (k561840_2), a NQR complex gene, various genes involved in pore formation, a Rhodanese-
 722 like gene, glutamine synthetase (type I), and YbiS YcfS YnhG family protein.
 723
 724
 725



726
 727 **Figure 3.** All significantly differentially expressed genes for the *Gammaproteobacteria* in both
 728 sponge species (A: *Eurypon* sp 2, B: *H. stellifera*. For *Gammaproteobacteria* associated with
 729 *Eurypon* sp. 2, there were only significant differences between hypoxia vs. normoxia (A). In
 730 symbionts associated with *H. stellifera*, there were only significantly differentially expressed
 731 genes in anoxia vs. hypoxia (B,C). All downregulated genes in anoxia vs. hypoxia are shown in B.
 732 There were 402 genes that were downregulated in anoxia vs. hypoxia in *Gammaproteobacteria*
 733 from *H. stellifera*, so only the top 10 based on p value are shown (C).

734
 735 In the *Gammaproteobacteria* associated with *H. stellifera*, genes were only significantly
 736 differentially expressed between anoxia and hypoxia (436 genes, $p < 0.1$, Table 1, Figure 3B,C).
 737 Twenty genes were upregulated in anoxia vs. hypoxia and all were annotated (Figure 3B).
 738 Upregulated genes in anoxia vs. hypoxia included five genes associated with the ribosome
 739 (k141_198365_15, k141_198365_8, k141_198365_17, and k141_245017_3), various genes for
 740 molecular transport, a transmembrane proton pump (k141_226857_1), succinyl-CoA
 741 synthetase, and formate dehydrogenase (alpha subunit). There were also 416 genes that were
 742 significantly downregulated in anoxia vs. hypoxia (Table 1). The top ten upregulated genes
 743 (lowest p values) are exhibited in Figure 3C.

744
 745 *Gammaproteobacterial* COG expression is shown in Supplemental Figure 7B. Only one COG
 746 class, 'translation, ribosomal structure and biogenesis,' was significantly enriched in
 747 *Gammaproteobacteria* under the different oxygen conditions ($P_{adj} < 0.05$). This COG class was
 748 downregulated in *Gammaproteobacteria* associated with *Eurypon* sp. 2 under hypoxia as well
 749 as those of *H. stellifera* in anoxia vs. hypoxia (Figure 7B).

750

751 Discussion

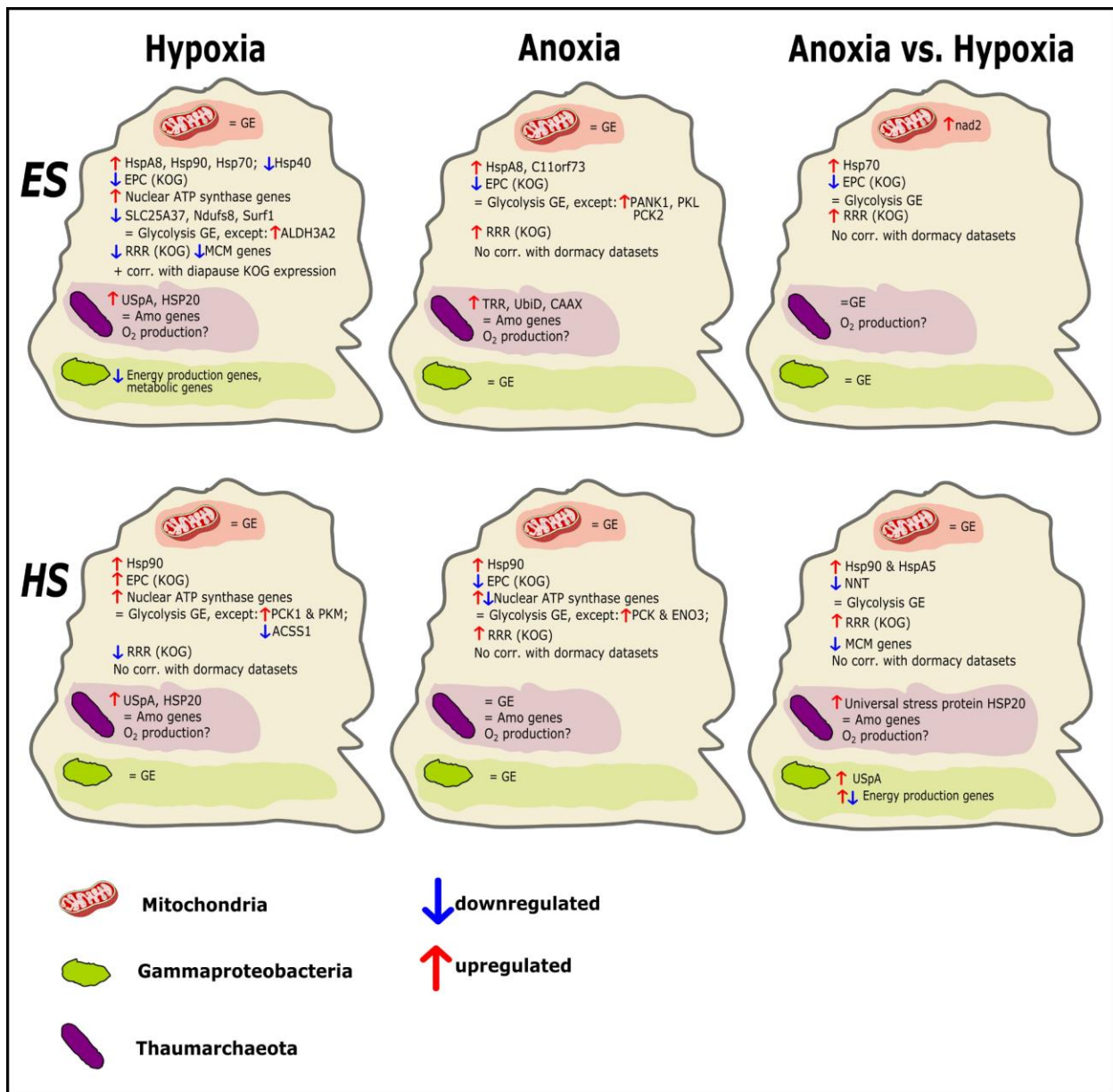
752

753 Sponge holobiont gene expression was significantly changed by exposure to deoxygenation in
754 situ, though responses were generally species-specific, dependent on oxygen level, and varied
755 across holobiont members. The potential functions of this differential expression are discussed
756 below for each member of the two holobionts: sponge, sponge mitochondria, *Thaumarchaeota*
757 and *Gammaproteobacteria*. The implications of this study for past and future oceans are
758 considered.

759

760 Differential expression in sponges during deoxygenation

761 Cellular stress responses were observed in the expression of HSPs, a group of stress response
762 genes that have been widely studied in marine invertebrates. These proteins are molecular
763 chaperones involved in protein folding, unfolding, transport and the assembly of protein
764 complexes, and they are present in nearly all organisms (Li and Srivastava 2004). Both Lough
765 Hyne sponges upregulated HSP genes in response to hypoxia and anoxia (vs normoxia),
766 though there was downregulation of some HSP genes in deoxygenation as well. *Eurypon* sp. 2
767 and *H. stellifera* both upregulated Hsp90 genes in hypoxia, but they upregulated different HSPs
768 in anoxia: HSPA8 and Hsp90 for *Eurypon* sp. 2 and *H. stellifera*, respectively. It should be noted
769 that Hsp90 upregulation in *H. stellifera* in anoxia was driven by only one replicate. However, in
770 the pairwise comparison with the highest replication in this study, hypoxia vs. normoxia in
771 *Eurypon* sp. 2, Hsp90 genes were significantly upregulated in hypoxia. Hsp90 expression was
772 also higher in anoxia than normoxia for *Eurypon* sp. 2, but this was not significant. Based on
773 these trends, it is possible that increased replication would result in a clearer upregulated signal
774 from Hsp90 genes, since false negatives in gene expression analyses decrease with more
775 replication (Schurch et al., 2016). *Eurypon* sp. 2 also upregulated HSPA8 and Hsp70 in hypoxia
776 but downregulated Hsp40. In long term hypoxia, *T. wilhelma* exhibited a similar HSP expression
777 pattern, upregulating Hsp90 but downregulating Hsp70 (Mills et al. 2018). Sponges under heat
778 stress also upregulate Hsp70 (López-Legentil et al. 2008; Guzman and Conaco 2016; Webster
779 et al. 2013) and HSP90 (Guzman and Conaco 2016). Pollutants such as lead and zinc can also
780 stimulate the upregulation of HSPs in sponges (Efremova et al. 2002; Schröder et al. 2006).
781 HSPs are therefore crucial to sponge stress response. HSP expression patterns and other key
782 transcriptomic responses of the sponge holobionts are outlined in Figure 4.



783
 784 **Figure 4.** Summary of sponge holobiont responses to deoxygenation presented in a tabular
 785 format with species on the left (*Es*: *Euryyon* sp. 2, *Hs*: *H. stellifera*) and oxygen condition on the
 786 top (hypoxia, anoxia, and hypoxia vs. normoxia). The major components of the holobiont are
 787 illustrated as follows: sponge cell (tan), mitochondria (red), *Gammaproteobacteria* (green), and
 788 *Thaumarchaeota* (purple). Upregulated and downregulated genes and KOGs are indicated with
 789 red and blue arrows, respectively. Unchanged gene expression (GE) is noted by the = sign.
 790 Correlations (corr.) with external dormancy datasets are indicated along with the direction of
 791 the correlation (+ or -).

792

793 In metazoans with a complete HIF pathway, Hsp90 also serves to stabilize HIFa and therefore
 794 plays an important role in hypoxia tolerance (Semenza 2007). In the absence of HIFa in

795 sponges, Hsp90 may play a greater role in oxygen homeostasis given that it is upregulated
796 under hypoxia in all sponges that have been examined transcriptomically to date, i.e. *Eurypon*
797 sp. 2, *H. stellifera* and *T. wilhelma*, and that Hsp90 is upregulated in *H. stellifera* under anoxia.
798 Hsp90 could stabilize currently unknown proteins that are involved in sponge oxygen regulation
799 or modulate transcription factors other than HIFa. Further research is needed to determine the
800 exact role of Hsp90 in sponge oxygen homeostasis, but it presents a good candidate for a gene
801 underlying sponge tolerance to deoxygenation.

802 Patterns of species and oxygen-condition-dependent expression of GO terms were observed in
803 sponges in response to deoxygenation. GO terms such as 'proteasome binding' and 'Hsp70
804 binding' were upregulated in all cases of decreased oxygen in *Eurypon* sp. 2, suggesting that
805 the species-specific response to deoxygenation in *Eurypon* sp. 2 may center around repairing or
806 degrading damaged proteins. In *H. stellifera*, on the other hand, upregulated GO terms related
807 to DNA repair in anoxia, including 'damaged DNA binding', 'DNA binding,' and 'catalysis of DNA
808 and RNA,' so DNA repair may be more central to the deoxygenation tolerance of this species.
809 Both protein and DNA repair upregulation might be a response to reactive oxygen species
810 (ROS), which can become more abundant under hypoxia due to imbalances in the
811 mitochondrial electron transport chain (Görlach et al. 2015). If there is any oxygen present in the
812 sponges under environmental anoxia, e.g. oxygen produced by *Thaumarchaeota* (see Kraft et
813 al. 2022, [Thaumarchaeota gene expression](#) below), then ROSs could cause cellular stress in
814 anoxia. Otherwise, the presence of sulfide in the water under anoxia (Schuster et al. 2021) or
815 ROSs other than superoxide (O₂⁻) could damage proteins and DNA in anoxic conditions.

816 The EPC KOG class was significantly downregulated in all oxygen conditions in both sponges
817 except for hypoxia and hypoxia vs. anoxia in *H. stellifera*, when it was significantly upregulated
818 and unchanged, respectively (Figure 1, 4). Within the EPC class, however, there were species-
819 specific responses to anoxia and hypoxia at the level of individual differentially expressed
820 genes. Most nuclear ATP synthase genes were upregulated in hypoxia in *Eurypon* sp. 2 but
821 were unchanged under anoxia. Similarly, two ATP synthase subunits (ATP5A1 and ATP6V0C)
822 were upregulated in hypoxia in *H. stellifera*. In anoxia, ATP5A1 was also upregulated, but
823 ATP6V0C was downregulated. Additionally, downregulation of SLC25A27 in *Eurypon* sp. 2 in
824 hypoxia may increase the coupling across the mitochondrial membrane to improve ATP
825 synthesis. We note that the electron transport chain genes Ndufs8 and Surf1 were also
826 downregulated in hypoxia *Eurypon* sp. 2. The NNT gene, also involved in electron transport,
827 was downregulated in anoxia vs. hypoxia in *H. stellifera*. Nevertheless, most of the genes
828 associated with the respiration electron transport chain were not differentially expressed, and
829 electron transport likely continued under deoxygenation. Sponges may therefore have increased
830 ATP production under hypoxia but not under anoxia. In a similar way, mollusks may upregulate
831 mitochondrial electron transport system activity and ATP synthesis capacity to improve
832 respiration efficiency under hypoxia (Hochachka and Lutz 2001).

833 Glycolysis, which can produce ATP and NADH without oxygen (Stryer 1995), was expected to
834 increase under anoxia. However, relatively few genes directly or indirectly involved in glycolysis
835 were differentially expressed in our sponges under deoxygenation. In *Eurypon* sp. 2,
836 pantothenate kinase 1 (PANK1), ATP-dependent 6-phosphofructokinase (PFKL) and
837 Phosphoenolpyruvate carboxykinase 2 (PCK2) were significantly upregulated in anoxia, and

838 only aldehyde dehydrogenase 3 family, member a2 (ALDH3A2) was significantly upregulated in
839 hypoxia (see Supplemental Reports, Supplemental Figure 5). In *H. stellifera*, acetyl-coenzyme A
840 synthetase 1 (ACSS1) was significantly downregulated in hypoxia, but PCK1 and pyruvate
841 kinase (PKM) were upregulated in hypoxia. In anoxia for *H. stellifera*, beta-enolase (ENO3) and
842 PCK1 were upregulated. Based on these results, it is unlikely that glycolysis rates increased
843 under anoxia and hypoxia in either species. It is more probable that glycolysis continued under
844 anoxia and hypoxia at normal rates in both species, since gene expression in the other ~70
845 genes associated with glycolysis was not significantly changed under deoxygenation (Figure 4).
846 Either way, the sponges would have at least some access to anaerobically generated ATP
847 through glycolysis during environmental deoxygenation.

848 In the KOG class 'replication, recombination and repair' (RRR), there was significant
849 upregulation in anoxia and anoxia vs. hypoxia, but downregulation in hypoxia (vs. normoxia) for
850 both sponge species. In *Eurypon* sp. 2, many MCM genes involved in the initiation of DNA
851 replication were downregulated in hypoxia but remained unchanged in anoxia. Certain aspects
852 of DNA replication, e.g. the DNA polymerase epsilon catalytic subunit, may even be upregulated
853 in anoxia. The pattern was less clear in *H. stellifera*, but MCM genes were downregulated in
854 anoxia compared to hypoxia (Figure 4). These data indicated that DNA replication may
855 decrease under hypoxia but remain stable during anoxia, possibly due to increased oxidative
856 stress under hypoxia compared to normoxia (see above). This pattern of a 'stronger' response
857 to hypoxia than anoxia mirrored that of nuclear ATP synthesis genes.

858 Between the two study species, there was only one significant, positive correlation of KOG class
859 expression between hypoxia in *Eurypon* sp. 2 and hypoxia vs. anoxia in *H. stellifera*,
860 demonstrating the general species-specific responses of most KOGs to deoxygenation. Within a
861 single sponge species, no correlations were seen between KOG enrichments in anoxia or
862 hypoxia (vs. normoxia), highlighting the transcriptomic differences between responses to
863 hypoxia and anoxia. KOG enrichments in hypoxia *versus* anoxia, on the other hand, were
864 positively correlated with those of anoxia in *Eurypon* sp. 2 and both anoxia and hypoxia in *H.*
865 *stellifera*.

866 When quantitatively compared to transcriptomic datasets from the sponge *T. wilhelma* using
867 KOGMWU, transcriptomic responses in Lough Hyne sponges were only positively correlated
868 between *T. wilhelma* under short-term anoxia and *Eurypon* sp. 2 in hypoxia vs. anoxia (Figure
869 1H). This positive correlation could indicate similar transcription patterns demonstrated by *T.*
870 *wilhelma* and *Eurypon* sp. 2 transitioning from hypoxia to anoxia. However, no further
871 similarities between the responses of *T. wilhelma* and Lough Hyne sponges to deoxygenation
872 were observed. In fact, the long-term exposure of *T. wilhelma* to hypoxia was negatively
873 correlated to KOG enrichments for both anoxia vs. hypoxia and normoxia vs. anoxia in *Eurypon*
874 sp. 2 (Figure 1I, J), meaning that KOG expression was generally opposite between these two
875 species for these conditions in terms of up and down regulation. The physiological responses of
876 *T. wilhelma* and *Eurypon* sp. 2 to deoxygenation are presumably very different. These results
877 demonstrate that large-scale transcriptomic responses to deoxygenation depend on both the
878 studied species and oxygen concentration.

879

880 Based on KOG correlation analyses, the hypothesis that sponges are dormant, i.e. temporarily
881 ceasing growth, development, and physical activity, under anoxia was not supported (Figure 4).
882 Sponge gene expression under anoxia did not correlate to either diapause or a dauer state in *C.*
883 *elegans* (Sinha et al. 2012) or *S. mosellana* (Gong et al. 2013), respectively. Although these
884 dormancy datasets come from distantly related invertebrates, Strader et al. (2016)
885 demonstrated a correlation between the KOG expression patterns of a specific phenotype of
886 coral larvae and diapause in *S. mosellana*, hypothesizing that this potential functional analog of
887 dormancy could serve to increase larval dispersal. Therefore, the sponges of Lough Hyne could
888 only be considered dormant under anoxia if their transcriptional method of dormancy was
889 distinct from that of an insect, nematode and coral, which is possible but not parsimonious given
890 that animals are monophyletic (Feuda et al. 2017). Nevertheless, it was inconclusive whether or
891 not sponges are pumping water or feeding during anoxia, but sponges were definitively pumping
892 under hypoxia (Schuster et al. 2021). Sponge pumping and filtering activity remain to be
893 quantified under anoxia and hypoxia in situ.

894 Paradoxically, *Eurypon* sp. 2 responses to hypoxia were positively correlated to diapause in *S.*
895 *mosellana* (Figure 1F, 5). Therefore, the hypoxic response in *Eurypon* sp. 2 species, rather than
896 the anoxic response, was similar to diapause in terms of global KOG expression patterns. The
897 RRR kog was also downregulated in *Eurypon* sp. 2 under hypoxia as well as in *S. mosellana*
898 under diapause, which may partially explain the correlation between these datasets. Despite the
899 correlation, the EPC expression patterns between the two species were opposing. EPC was
900 significantly downregulated in hypoxia in *Eurypon* sp. 2 and upregulated in diapause in *S.*
901 *Mosellana*. These KOG enrichments are calculated from thousands of genes, so any individual
902 gene within a KOG class might still be upregulated even if the KOG class is significantly
903 downregulated. Therefore, it is possible that ATP production increased in hypoxia based on the
904 upregulation of ATP synthase genes, in spite of the downregulation of the EPC KOG. Diapause
905 can be associated with the reduction of cell division (MacRae 2010), which may occur in
906 sponges under hypoxia but not anoxia based on MCM gene expression. In comparison, KOG
907 enrichments under anoxia were not positively correlated to any external datasets for either
908 sponge species (Figure 1), indicating that sponge transcriptomic responses to anoxia are
909 relatively novel compared to those of other taxa in response to various factors in the existing
910 literature (Dixon et al. 2015; Strader et al. 2016).

911

912 **Sponge mitochondrial gene expression during deoxygenation**

913

914 A high degree of transcriptional stability under deoxygenation was observed in sponge
915 mitochondria. Only one of the 14 mitochondrial protein-coding genes, *nad2*, was significantly
916 differentially expressed in the different oxygen conditions, where it was upregulated in anoxia
917 vs. hypoxia in *Eurypon* sp 2 (Figure 4). Both of the sponge species had higher expression of
918 *nad2* in anoxia than in normoxia or hypoxia, but this difference was only significant in *Eurypon*
919 sp. 2.

920

921 Surprisingly little is known about differential gene expression in mitochondria, even within
922 humans. In the limited studies available, mitochondrial gene expression was significantly
923 different between human cancer cells and normal cells (Reznik et al. 2017) as well as between
924 different populations of healthy pancreas tissue (Medini et al. 2021). In these studies, *nad2* was

925 significantly downregulated in most studied cancers, though it was still significantly upregulated
926 in a few cancer types, and *nad2* was also significantly differentially expressed between
927 pancreas cell populations. Based on the general upregulation of nuclear genes associated with
928 respiration in hypoxia, mitochondrial gene upregulation was expected in hypoxia when
929 compared to normoxia and anoxia, but the opposite was true for *nad2* in *Eurypon* sp. 2 in the
930 current study. The other six *nad* genes, which code for parts of the same membrane respiratory
931 chain complex (complex 1, NADH dehydrogenase), however, were not significantly differentially
932 expressed in either species. In both human studies, when one mitochondrial gene was
933 significantly differentially expressed, most other mitochondrial genes were significantly
934 differentially expressed in the same direction (Reznik et al. 2017; Medini et al. 2021). The
935 physiological meaning (if any) of this single, significantly differentially expressed mitochondrial
936 gene in sponges remains to be determined.

937
938 Compared to that of humans, even less is known about mitochondrial gene expression in
939 marine invertebrates. Mitochondrial gene expression is usually excluded from differential
940 expression analyses due to the differences in library preparation potentially needed for
941 sequencing mitochondrial RNA and/or the exclusion of mitochondrial RNA from reference
942 transcriptomes (*sensu* Meyer 2016). This dearth is partly due to the nature of mitochondrial
943 transcription, which generates a single continuous transcript. Following transcription, however,
944 mitochondrial transcripts are broken up into individual coding mRNA, tRNA or rRNA (D'Souza
945 and Minczuk 2018). After the breakup, the levels of mRNAs from specific genes are controlled
946 post-transcriptionally (D'Souza and Minczuk 2018). It is therefore possible to have different
947 counts between the different mitochondrial genes despite their single transcript origin
948 (Supplemental Figure 6). The consistent 'expression' of transcripts across oxygen conditions for
949 each mitochondrial protein-coding gene following continuous transcription are likely to be
950 necessary for the maintenance of mitochondrial function.

951
952 It remains unclear how sponge mitochondria maintain this transcription from an energetic
953 standpoint under anoxia. Within the mitochondrial electron transport chain, oxygen is used as
954 the terminal electron acceptor and is crucial for the generation of ATP through oxidative
955 phosphorylation. Theoretically, anoxia should cause electron transport and oxidative
956 phosphorylation in the mitochondria to cease (Chandel and Schumacker 2000). If the
957 mitochondria are transcribing solely to maintain oxidative phosphorylation machinery until
958 oxygen returns, then they would need to use at least enough energy (~2 ATP per base) to
959 transcribe for months at a time without oxygen (Lynch and Marinov 2015), and this energetic
960 requirement would apply to the transcription of sponge nuclear genes as well. Glycolysis may
961 provide some anaerobic ATP production, even if it is not upregulated in anoxia or hypoxia.
962 Alternatively, to maintain ATP production through aerobic respiration, the sponges of Lough
963 Hyne might have access to oxygen produced by their *Thaumarchaeota* symbionts, a topic
964 explored in more detail below.
965

966 **Microbiome gene expression during deoxygenation**

967 *Thaumarchaeota* gene expression

968 *Thaumarchaeota* symbionts from both sponge species exhibited significant differential gene
969 expression under hypoxia. Only the *Thaumarchaeota* from *Eurypon* sp. 2 (OTU1) exhibited
970 differential gene expression under anoxia, and only those of *H. stellifera* (OTU3) differentially
971 expressed genes under anoxia vs. hypoxia. Though there were some species-specific
972 responses, overall gene expression in both *Thaumarchaeota* was similar, supporting the
973 hypothesis from Schuster et al. (2021) that these taxonomically similar symbionts between two
974 sponge species might have similar functional roles.

975 Relatively few genes involved in anaerobic metabolism were expressed in *Thaumarchaeota*
976 symbionts under any oxygen condition. Lactate/malate dehydrogenase, which could be involved
977 in fermentation (Bayer et al. 2020), was upregulated in *Eurypon* sp. 2 *Thaumarchaeota*, but only
978 in hypoxia. Genes for the other anaerobic pathways suggested by Bayer et al. 2020, i.e.
979 succinate dehydrogenase/ fumarate reductase, nitrite reductase and sulfite reductase, were
980 present in both *Thaumarchaeota* genomes in the present study but were not significantly
981 differentially expressed under different oxygen conditions. The genes for nitrite reductase
982 exhibited low expression across all samples (0–20 counts) in both *Thaumarchaeota*, and so did
983 the dehydrogenase/ fumarate reductase gene in the *Thaumarchaeota* of *H. stellifera*. Therefore,
984 these genes with low expression may not be used under the conditions of this study. Only three
985 genes in the *Thaumarchaeota* of *Eurypon* sp. 2 under anoxia were significantly differentially
986 expressed, and none of these were involved in anaerobic metabolism. No genes were
987 differentially expressed in *H. stellifera* *Thaumarchaeota* under anoxia. Therefore, there was no
988 transcriptomic evidence for the upregulation of anaerobic metabolism within *Thaumarchaeota* in
989 anoxia.

990 Transcription of ammonium monooxygenase (AMO) genes did not significantly change under
991 anoxia or hypoxia, even though the ammonia oxidation pathway is oxygen dependent. Like the
992 sponge mitochondria, the *Thaumarchaeota* are therefore either transcribing AMO genes to be
993 ready when oxygen returns, or they are obtaining trace oxygen for this pathway by synthesizing
994 oxygen themselves (Kraft et al. 2022). If sponge *Thaumarchaeota* symbionts are also able to
995 produce oxygen under anoxic conditions like their relative *N. maritimus*, then they should
996 express amo genes under anoxia as well as normoxia. The proposed pathway for oxygen
997 production in *N. maritimus* involves the reduction of nitrite to nitric oxide that is dismutated into
998 oxygen and nitrous oxide (Kraft et al. 2022). Water sampled for nitrite concentrations in Lough
999 Hyne using established methods (Grasshoff et al. 1999) revealed that nitrite concentrations
1000 under anoxia ranged from 0.2–1.2 μM (Supplemental Table 3), increasing with depth below the
1001 thermocline. Therefore, the conditions in Lough Hyne would theoretically allow for
1002 *Thaumarchaeota* to produce oxygen under anoxia.

1003 AsnC family proteins and nitroreductase expression was upregulated during oxygen production
1004 in *N. maritimus* (Kraft et al. 2021). In *Archaea*, AsnC proteins can regulate metabolic processes,
1005 including the switch between aerobic and anaerobic metabolisms (Lemmens et al. 2019).
1006 Similarly, nitroreductases can have a wide range of metabolic functions (Akiva et al. 2017).

1007 *Thaumarchaeota* within *H. stellifera* upregulated a Lrp/AsnC ligand binding domain under
1008 hypoxia and in anoxia vs. hypoxia. Another AsnC type protein was also upregulated under
1009 hypoxia, and a nitroreductase was upregulated under anoxia vs. hypoxia. However, these
1010 proteins did not directly correspond to those upregulated in *N. maritimus* during oxygen
1011 production (Supplemental Figure 9), and the latter proteins are not definitively known to be
1012 involved in oxygen production, since the pathway remains unknown.

1013 In hypoxia, both *Thaumarchaeota* upregulated the stress response genes USpA and a protein
1014 from the HSP20 family (Figure 4). It was surprising that *Thaumarchaeota* may be stressed by
1015 hypoxia since free-living thaumarchaeal Nitrosopumilales can be found in high abundances in
1016 oxygen-minimum zones (OMZs) where oxygen is either at low concentrations or below
1017 detection (Löscher et al. 2012), though some *Thaumarchaeota* OTUs decrease in abundance in
1018 suboxic and anoxic zones (Sollai et al. 2019). Members of the genus *Nitrosopumilus*, however,
1019 increase their absolute abundance in suboxic regions, but then decrease in abundance with
1020 depth in the anoxic zone (Sollai et al. 2019), indicating a preference for suboxic environments. If
1021 suboxia is also the preferred niche of sponge *Thaumarchaeota* symbionts, the upregulation of
1022 stress response genes in response to hypoxia may correspond to a rise in intracellular oxidative
1023 stress following an increase in metabolic activity in hypoxia, like their sponge hosts.

1024

1025 *Gammaproteobacteria* gene expression

1026 Gene expression in the *Gammaproteobacteria* was species and oxygen-condition dependent. In
1027 *Eurypon* sp. 2, *Gammaproteobacteria* downregulated genes in hypoxia that were associated
1028 with respiration and energy production, including cytochrome c and associated genes (Welchen
1029 et al. 2016). The *Gammaproteobacteria* also downregulated key metabolic genes in hypoxia
1030 such as glutamine synthetase and structural genes like YbiS YcfS YnhG family protein, which is
1031 involved in cell wall production (Magnet et al. 2008). So unlike sponges or *Thaumarchaeota*,
1032 *Gammaproteobacteria* in *Eurypon* sp. 2 (OTU2) may decrease metabolic activity under hypoxia,
1033 though this is likely not the case in *H. stellifera* symbionts (OTU7).

1034 *Gammaproteobacteria* in *H. stellifera* downregulated hundreds of genes in anoxia vs. hypoxia,
1035 including USpA, so, like other members of the holobiont, hypoxia requires a stronger
1036 transcriptomic response and, therefore, may be more stressful than anoxia for these
1037 *Gammaproteobacterial* symbionts. The few upregulated genes in anoxia vs. hypoxia included
1038 genes for energy production, e.g. a transmembrane proton pump, succinyl-CoA synthetase (part
1039 of the citric acid cycle), and formate dehydrogenase (alpha subunit), although other genes
1040 associated with energy production were downregulated. Formate dehydrogenase can function
1041 in both aerobic respiration and in anaerobic respiration (Jormakka, et al. 2003), but this enzyme
1042 was not significantly upregulated in anoxia compared to normoxia or in the
1043 *Gammaproteobacteria* of *Eurypon* sp. 2 under any condition. So, it is unlikely that this anaerobic
1044 pathway is active in sponge-associated *Gammaproteobacteria* under anoxia.

1045 *Gammaproteobacteria* symbionts were previously hypothesized to oxidize sulfide under anoxia
1046 (Schuster et al. 2021). Although they are not present in OTU2, OTU7 from *H. stellifera* has the
1047 sulfur oxidation genes soxA, soxY, and soxZ, which could oxidize sulfide, as well as the nitrate
1048 reductase gene NAP. However, the sox genes were not expressed in any samples in the

1049 current study, and NAP was expressed at very low levels across all samples (2-28 counts).
1050 Moreover, neither symbiont exhibited significant differential gene expression in anoxia versus
1051 normoxia. Consequently, there was very little transcriptomic evidence that the anaerobic
1052 pathways in these *Gammaproteobacteria* were activated during environmental anoxia.

1053 **Summary of potential adaptations of sponge holobionts to low oxygen**

1054 Metabolically, sponge transcription under anoxia was surprisingly similar to normoxia throughout
1055 the holobiont members, and there was no evidence of dormancy within the holobionts in anoxia
1056 (Figure 4). No clear anaerobic respiration responses were observed in the transcriptomes of
1057 sponges, their mitochondria or their two microbial symbionts under environmental anoxia. The
1058 limited significant differential expression of glycolysis genes could indicate that this metabolic
1059 process continues to comparable degrees under normoxia, hypoxia, and anoxia. Therefore, in
1060 the sponges and their microbes, glycolysis could potentially provide ATP without oxygen (Figure
1061 4).

1062 Hypoxia, rather than anoxia, elicited upregulation in energy production machinery such as ATP
1063 synthase (Figure 4). These potential metabolic increases suggest that within the hypoxic limits
1064 studied here (1.30-3.56 mg L⁻¹), sponges perform optimally. Indeed, these limits are above
1065 those at which mortality or substantial physiological changes have been observed for sponges
1066 (Micaroni et al. 2021; Kumala et al. 2021; Mills et al. 2014). This increased energy production
1067 could be stressful, however, and the diversion of resources could limit cell division in hypoxia
1068 (Figure 4). Somewhere between the lower limit of hypoxia (1.37 mg L⁻¹) and the full anoxia
1069 studied here, sponges may no longer attempt to increase energy efficiency, and therefore
1070 elevated transcription of ATP synthase genes was not observed in anoxia.

1071 For both the sponges and their *Thaumarchaeota* symbionts, cellular stress responses were
1072 evident under deoxygenation. Both sponge species upregulated HSP genes under anoxia and
1073 hypoxia. These genes may be crucial for sponge deoxygenation tolerance in these species
1074 (Figure 4). We hypothesize that Hsp90 plays a role in sponge oxygen homeostasis, but this
1075 needs to be tested. The *Thaumarchaeota* symbionts upregulated HSP20 and other stress
1076 response genes in anoxia and hypoxia for *H. stellifera* and hypoxia within *E. sp. 2* (Figure 4). In
1077 hypoxia, archaeal and host upregulation of stress response genes may have been a response
1078 to oxidative stress following increased metabolic activities. In anoxia, cellular stress response
1079 might result from the presence of sulfide. Additionally, post-transcriptional, metabolic changes
1080 may play a role in deoxygenation tolerance, and proteomic and metabolomic changes should be
1081 examined in future studies.

1082 Given the largely unchanged metabolic gene expression patterns under hypoxia or anoxia in
1083 these sponges, the production of oxygen by *Thaumarchaeota* could also be crucial to holobiont
1084 survival (noted with a question mark in Figure 4). Although any oxygen produced would be at
1085 extremely low concentrations, it would have a short path of diffusion to the sponge cells, as
1086 *Thaumarchaeota* symbionts maintain high cell densities within sponges (Moeller et al. 2019). In
1087 addition, mitochondria in general can utilize very low concentrations of oxygen (500 nM) without
1088 changing their oxygen consumption rate, and cells can still respire below that threshold albeit at
1089 a lower rate (Chance 1965; Longmuir 1957; Wilson et al. 1979). In culture, oxygen generated by

1090 *Thaumarchaeota* reached 100-200 nM (Kraft et al., 2022). If sponge *Thaumarchaeota* produce
1091 oxygen at similar levels under anoxia, cellular respiration could continue in sponges under
1092 anoxia, though likely at lower respiration rates when compared to normoxia. However, given
1093 that the genes responsible are still unknown, the production of oxygen by sponge
1094 *Thaumarchaeota* needs to be verified experimentally.

1095 **Relevance to future ocean deoxygenation**

1096
1097 Sponges are predicted to be the ‘winners’ over other benthic organisms in the future due to their
1098 tolerance of ocean warming and acidification associated with climate change (Bell et al. 2018).
1099 Indeed, sponges have already increased in abundance in some locations while corals have
1100 decreased due to altered carbon and nutrient cycling (Pawlik et al. 2016). The additional
1101 stressor of deoxygenation that comes with climate change and coastal eutrophication has been
1102 relatively overlooked compared to ocean warming and acidification. In other marine taxa, a
1103 meta-analysis demonstrated that the incorporation of deoxygenation as a factor along with
1104 warming could substantially decrease survival times of marine organisms compared to warming
1105 alone (Vaquer-Sunyer and Duarte 2011). Since sponges may be more tolerant than other taxa
1106 to changes in all three stressors of temperature, pH and oxygen, they could indeed become
1107 more abundant in a changing ocean. However, even sponges can be lethally affected by
1108 warming, acidification (Bennett et al. 2017) and deoxygenation (Micaroni et al. 2021) in
1109 scenarios that might occur with climate change, since tolerance to these stressors is species-
1110 specific. So, surviving sponge species in a warmed, acidified, and deoxygenated ocean might
1111 be abundant, but their abundance, and diversity would likely be lower than at present. The
1112 effects of all three of these stressors together need to be understood on a much wider range of
1113 organisms to accurately predict the composition of future oceans. More importantly, the causes
1114 and effects of anthropogenic climate change need to be ameliorated as soon as possible to
1115 avoid such diversity loss.

1116 **Relevance for animal evolution**

1117 Assuming that the first metazoans were more like an adult sponge than a ctenophore, based on
1118 morphology (Nielsen 2008) and phylogeny (Feuda et al. 2017), then some species of early
1119 sponges or proto-animals could have tolerated low environmental oxygen levels and at least
1120 some periods of benthic anoxia and euxinia in the Neoproterozoic Era (~538.8–1,000 million
1121 years ago) when early animals, including sponges, first evolved (Dohrmann and Wörheide
1122 2017). Lough Hyne sponges are a valuable model system for understanding early animal
1123 evolution. Early sponges could have survived under low and variable oxygen levels using
1124 mechanisms like those of Lough Hyne sponges. Therefore, contrary to longstanding
1125 hypotheses, the evolution of animals probably did not require high and stable levels of
1126 environmental oxygen.

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1135 **Conflict of interest disclosure**

1136 The authors declare that they comply with the PCI rule of having no financial conflicts of interest
1137 in relation to the content of the article.

1138 **Data, scripts, code, and supplementary information availability**

1139 Raw sequence data as well as genome and transcriptome assemblies are available at NCBI
1140 under BioProject number PRJNA893197
1141 (<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA893197>). Scripts, code, and additional data
1142 are available here: <https://zenodo.org/badge/latestdoi/573040118>. Supplemental figures and
1143 tables are available on BioRxiv under 'Supplementary material.'

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