Eukaryotic biodiversity and ecological networks from the surface to the mesopelagic in the Northwest Atlantic Slope Water

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1. ABSTRACT

The diversity and interactions among mesopelagic organisms are difficult to study and as a result, are insufficiently unaccounted for in food web and biogeochemical models. This knowledge gap hinders our ability to model and forecast ecosystem function and formulate effective policies for conservation and management in the face of growing interest in exploiting midwater living resources. We used multi-marker metabarcoding of environmental DNA (eDNA) samples collected from Northwest Atlantic Slope Water to resolve patterns of eukaryotic community composition spanning taxonomically across protists (microbial eukaryotes),

invertebrates, and vertebrates and vertically from the ocean surface to the base of the mesopelagic zone. With statistical network analyses, we explored cross-kingdom associations including trophic interactions such as food web dynamics and evaluate network robustness to biodiversity loss. We found depth-specific communities of distinct protist, invertebrate, and vertebrate assemblages. Ecological networks for the epipelagic, upper mesopelagic, and lower mesopelagic suggest that protists are keystone taxa and important mediators of trophic interactions; they increase network complexity and contribute to network stability. We also identified metazoans including copepods, gelatinous taxa (cnidarians, tunicates), and mesopelagic fish as important components of network interactions. Our study demonstrates a holistic approach to generate insights on mesopelagic biodiversity and implications for ecosystem resilience that can inform future conservation and management efforts.

2. INTRODUCTION

Diverse ecological communities underpin ecosystem function and critical ecosystem services (Oliver et al., 2015; Sala et al., 2021; Nauta and De Domenico, 2024). In the vast mesopelagic region of the ocean from the base of the sunlit zone to 1000 m deep (Buesseler et al., 2020), a wide variety of life supports important hunting grounds for commercially and ecologically relevant fish including sharks, tuna, and billfish (Braun et al., 2023; Iglesias et al., 2023; Willis et al., 2025). This region is also a significant reservoir of organic carbon (Arístegui et al., 2009) and biogeochemical processes that occur at these depths determine flux into deeper waters and subsequent long-term sequestration (Mazuecos et al., 2015; Cavan et al., 2019; Nguyen et al., 2022).

Despite the recognized importance of the deep sea, studies have primarily focused on coastal surface or epipelagic (surface) ecosystems, leaving the mesopelagic both undersampled and understudied (St. John et al., 2016). These knowledge gaps are largely driven by challenges associated with accessing and sampling a vast ecosystem that spans considerable horizontal and vertical spatial scales (Sutton et al., 2017). Difficulty acquiring logistical resources and expertise for deep sea exploration and research are also major contributing factors (Tolochko and Vadrot, 2021; Amon et al., 2022). Furthermore, many studies focus on specific groups of organisms in isolation, such as those exclusively examining microbes or metazoans (Yang et al., 2024), which greatly skews our understanding of biodiversity, ecological interactions, and functional roles.

Environmental DNA (eDNA) approaches have emerged as reliable tools to assess biodiversity at scale (McClenaghan et al., 2020; Chavez et al., 2021; Holman et al., 2021; Yeh and Fuhrman, 2022; Govindarajan et al., 2023a; Dan et al., 2024). Recent studies employing multiple marker metabarcoding approaches resolve diversity patterns across the domains of life – from prokaryotes to top predators (Djurhuus et al., 2020; Holman et al., 2021). Using statistical and network analyses, these studies have documented key predator-prey interactions, identified potential keystone taxa, and uncovered unexplored trophic connections that may serve as

64 indicators of ecosystem function in a changing ocean. As growing interest in mesopelagic
65 fisheries for aquaculture and nutraceuticals (Martin et al., 2020; Bisson et al., 2023) and deep sea
66 mining activities (Drazen et al., 2020) threaten overexploitation and habitat destruction, a more
67 complete understanding of biodiversity and ecological dynamics is needed to inform the
68 sustainable management of mesopelagic resources.

69 Collectively, microbially catalyzed biogeochemical transformations and animal feeding
70 behaviors, including diel vertical migration, are core processes that influence carbon dynamics in
71 the surface and deep ocean. In the epipelagic ocean (~0 m-200 m), phytoplankton harness energy
72 from the sun to convert carbon dioxide into organic carbon. Zooplankton grazing and senescence
73 of primary production can export organic carbon out of the surface ocean, providing a food source
74 for life in the deep ocean (Cawley et al., 2021; Hemsley et al., 2023) and contributing to the largest
75 reservoir of organic carbon on earth (Arístegui et al., 2009). In the mesopelagic, the balance
76 between microbial remineralization of organic carbon to carbon dioxide and assimilation into
77 biomass within the food web impacts carbon flux into deeper waters where carbon can be
78 sequestered for variable time periods (e.g., 10-1000 years) (Mazuecos et al., 2015; Cavan et al.,
79 2019; Nguyen et al., 2022). For these reasons, organismal interactions including food web
80 dynamics in the epipelagic and mesopelagic zones are interconnected and play a determinant
81 role in the fate of carbon in the ocean (Robinson et al., 2010; Herndl and Reinthaler, 2013; Giering
82 et al., 2014).

83 Few multi-marker metabarcoding studies have been conducted in deep pelagic
84 ecosystems and existing studies tend to emphasize organismal diversity and distribution rather
85 than interactions among taxa (Giner et al., 2020; Laroche et al., 2020a; Govindarajan et al., 2021;
86 Holman et al., 2021; Govindarajan et al., 2023b). A more holistic approach would facilitate our
87 ability to effectively understand how community composition and organismal interactions across
88 the tree of life influence crucial ecosystem processes. We aimed to investigate patterns of
89 biodiversity and their interactions to better understand ecosystem structure and stability from the

surface to the base of the mesopelagic in the Northwest Atlantic Slope Water region. We applied an eDNA metabarcoding approach with two markers to resolve the eukaryotic community, inclusive of microeukaryotes (protists), invertebrates, and vertebrates, and calculated diversity indices to determine depth-specific biodiversity patterns. We then performed covariance network analyses on multi-marker metabarcoding data, constructing depth-specific networks for metazoans (invertebrates and vertebrates), protists, and all taxa combined across the epipelagic (10 m, 100 m), upper mesopelagic (300 m, 500 m), and lower mesopelagic (800 m, 1000 m) depth zones.

Network topologies revealed depth-specific trends of network complexity determined by the total number of nodes (ASVs), edges (interactions or links), and link density (edge-to-node ratio) (Landi et al., 2018). We explored the influence of complexity across depth zones on network stability, determined by sequentially removing ASVs from the networks (node connectivity and robustness) and edges (edge connectivity) (Iyer et al., 2013; Tipton et al., 2018). Collectively, these analyses revealed insights on the role of marine protists as keystone taxa, especially at mesopelagic depths. A diverse protistan community contributes to network stability and facilitates a significant proportion of trophic interactions involving invertebrate and vertebrate taxa, suggesting their vital role in food web dynamics and ecosystem resilience.

3. MATERIALS & METHODS

3. 1. Sample Collection

Bulk water samples were collected in Northwest Atlantic Slope Water in March 2020 on the *R/V* Armstrong (AR43) at six discrete depths (10 m, 100 m, 300 m, 500 m, 800 m, and 1000 m) at three sampling stations (Figure 1). Sampling spanned surface depths to the base of the mesopelagic and included the deep scattering layer (~500 m) as determined by a broadband Simrad EK80 split beam echosounder system on the *R/V* Armstrong (Supplementary Figure S1, Supplementary Methods). Water was collected with a 24-Niskin CTD rosette across three casts

at sampling sites with similar water column characteristics (Figure 1). Two casts (001 and 007) were collected at midnight while cast 002 was collected at mid-day. At each depth, four replicates were collected for a total of 72 samples. For each sample, ~5 L of water was pumped through sterile 0.2 µm PES Sterivex (MilliporeSigma, Burlington, MA, USA) filters, sealed with Luer lock caps, and stored at -80°C. Sample collection carboys and filtration tubing were bleach-sterilized and rinsed with Milli-Q water prior to filtration with a Masterflex L/S peristaltic pump system following established protocols (Govindarajan et al., 2021, 2022).

The AR43 expedition coincided with high densities of the salp *Salpa aspera*, gelatinous zooplankton that are known to periodically "bloom" in the Northwest Atlantic Slope Water (Wiebe et al., 1979; Madin et al., 2006). From analysis of in situ high speed (15 Hz) image data, we estimated densities of 5-10 individuals m^{-3} in surface waters at night (Supplementary Figure S2, Supplementary Methods), which are in the typical range for bloom densities (e.g., 3.5 individuals m^{-3} and higher) (Groeneveld et al., 2020).

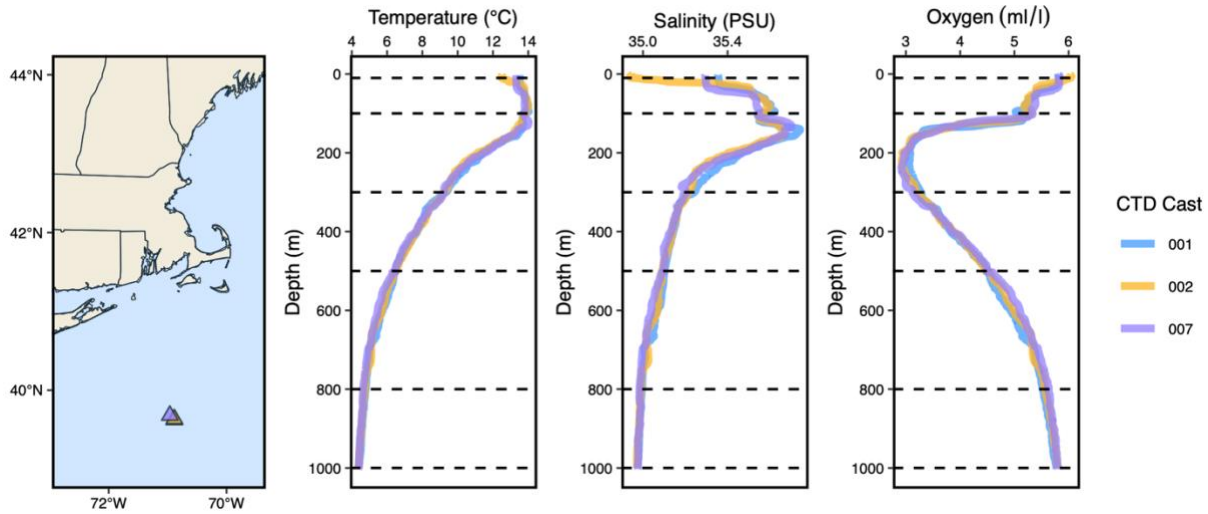


Figure 1. Sampling location and CTD profiles for eDNA collection. Temperature, salinity, and oxygen profiles for each CTD cast (001, 002, and 007) where eDNA samples were collected are shown. Dashed black lines indicate the depths where samples were collected (10 m, 100 m, 300 m, 500 m, 800 m, and 1000 m).

134 **3.2. DNA Extractions and PCR**

135 DNA was extracted with a Qiagen DNEasy Blood & Tissue extraction kit (Qiagen,
136 Germantown, MD, USA) following manufacturer's protocols with modifications for Sterivex filters
137 (Govindarajan et al., 2021). Extracted DNA was stored at -20°C prior to metabarcoding. All
138 samples were metabarcoded for portions of the 18S and 12S rRNA genes (see below), except
139 for one sample collected on CTD cast 007 at 1000 m which did not have enough DNA template
140 for 12S rRNA metabarcoding. All lab surfaces and equipment were cleaned with a 10% sodium
141 hypochlorite solution (household bleach) and extractions were performed in a dedicated
142 laboratory space away from sources of concentrated DNA such as post-PCR or tissue samples.

143 The 18S V9 hypervariable region was amplified using the 1380F/1510R primer set with
144 CS1/CS2 Fluidigm adapters and following a two-step PCR protocol (Amaral-Zettler et al., 2009;
145 Govindarajan et al., 2021). The initial PCR cycling program began with a denaturation step at
146 95°C for 3 min, 25 cycles at 95°C for 30 sec, 55°C for 30 sec, and 72°C for 30 sec, followed by
147 an elongation step at 72°C for 5 min. PCR reactions (25 µl) consisted of 2.5 µl of DNA template,
148 0.5 µl of each primer, 12.5 µl of 2x KAPA HiFi HotStart ReadyMix (Kapa Biosystems; Wilmington,
149 MA, USA), and 9 µl of molecular-grade water. Duplicate PCR reactions were run for each sample,
150 pooled, and sent to the Genome Research Core at the University of Illinois at Chicago (UIC) to
151 complete a second PCR amplification to add unique tags using MyTaq HS 2X Master Mix and the
152 Access Array Barcode Library for Illumina (Fluidigm, South San Francisco, CA, USA). The PCR
153 cycling program was as follows: 95°C for 5 min followed by 18 cycles of 95°C for 30 sec, 60°C for
154 30 sec, 72°C for 30 sec, and 72°C for 7 min. Amplicon libraries were purified using AMPure XP
155 beads (Beckman Coulter, Indianapolis, IN, USA). Amplicon sequencing with a targeted
156 sequencing depth of 100000 reads per sample was done on an Illumina MiSeq (2x250 bp)
157 (Govindarajan et al., 2022).

158 The hypervariable 12S region of the mitochondrial rRNA gene was amplified using MiFish
159 primers (Miya et al., 2015) appended with Illumina adapter overhang nucleotide sequences and

160 a modified two-step PCR protocol with a touch-down PCR program for the first PCR (Pitz et al.,
161 2020). The initial PCR cycling program began with a denaturation step at 95°C for 15 min; 13
162 cycles of 94°C for 30 sec, 69.5°C for 30 sec (decreasing 1.5°C with each cycle), and 72°C for 90
163 sec; 25 cycles of 94°C for 30 sec, 50°C for 30 sec, and 72°C for 45 sec; followed by an elongation
164 step at 72 °C for 10 min. PCR reactions (25 µl) consisted of 2.5 µl of DNA template, 1 µl of each
165 primer, 12.5 µl of 2x KAPA HiFi HotStart ReadyMix, and 8 µl of molecular-grade water. Duplicate
166 PCR products were pooled and sent to the Center for Genome Innovation at the University of
167 Connecticut for size selection, a second round of PCR, and sequencing. Amplicons from the
168 pooled PCR products were visualized with the Agilent 4200 TapeStation electrophoresis system
169 using the High Sensitivity DNA D1000 assay (Agilent Technologies, Santa Clara, CA). Size-
170 selection for targeted amplicons (215bp-335bp) was conducted using the Sage Science
171 PippinPrep HT gel cassette (2% Agarose, PippinHT). Illumina barcodes were added to each
172 amplicon using a second PCR amplification. The PCR cycling program was as follows: 95°C for
173 3 min followed by 12 cycles of 95°C for 15 sec, 60°C for 30 sec, and 72°C for 90 sec. Amplicon
174 libraries were purified using AMPure XP beads and assessed for quality and adapter dimer
175 content on the Agilent 4200 TapeStation using a D1000 assay. Amplicon sequencing with a
176 targeted sequencing depth of 100000 reads per sample was done on an Illumina MiSeq
177 (2x250bp) with 20–30% PhiX added (Illumina, San Diego, CA).
178 For both 18S and 12S primer sets, PCR runs included field controls of filtered Milli-Q water
179 (1 L for each CTD cast) as well as PCR negative (without DNA template) and positive controls.
180 The PCR positive control was included to determine the quality of sequencing results and
181 consisted of previously extracted 1ng/µl sample of *Fundulus heteroclitus*, an estuarine fish that
182 would not be found in the environmental samples.
183
184 **3.3 Multi-marker metabarcoding bioinformatics**

185 Demultiplexed sequencing reads were imported into and processed in QIIME 2 with
186 default settings (v2022.11.1) (Bolyen et al., 2019). Adapters and primers were trimmed from the
187 reads with Cutadapt (Martin, 2011). Reads were quality-filtered, trimmed to the primer region 120
188 bp (18S) and 150 bp (12S), denoised, and merged into amplicon sequence variants (ASVs) with
189 DADA2 (Callahan et al., 2016). For both gene markers, taxonomy was assigned by a naïve Bayes
190 classifier at an 80% confidence threshold (Pedregosa et al., 2011); the classifier was trained on
191 reference databases curated and evaluated with the REference Sequence annotation and
192 CuRatIon Pipeline (RESCRIPt) QIIME 2 plugin (Robeson et al., 2021).
193 The 18S sequencing reads were annotated with two different databases: one for protists
194 and one for metazoans. The protist (18S) classifier was trained with the Protistan Ribosomal
195 Reference (PR2) database (v5.0.1) (Guillou et al., 2013) that was updated with 9 taxonomic levels
196 including the replacement of kingdom with domain and the addition of a new subdivision level.
197 The metazoan (18S) classifier was trained with the SILVA SSURef_NR99 (v138.1) database
198 (Pruesse et al., 2007; Quast et al., 2013). A new 12S classifier was created by combining a
199 custom reference database of 12S sequences for 80 species of mesopelagic fish from the
200 Northwest Atlantic (Govindarajan et al., 2023b) with the MetaZooGene database (v2023-m07-15)
201 in Mode-A (most inclusive option) for vertebrates (O'Brien et al., 2024). For 18S sequences,
202 taxonomy assignments were first assigned with PR2 and protist sequences were selected as the
203 subset where phylum was not classified as "Metazoa". This subset will be referred to as the protist
204 dataset. Sequences where phylum was classified as "Metazoa" were subsequently classified with
205 the SILVA-based classifier. Metazoan 18S reads were classified predominantly as invertebrate
206 taxa and will be referred to as the invertebrate dataset (Govindarajan et al., 2021). Likewise,
207 metazoan 12S reads were classified as vertebrates (mainly fish) and will be referred to as the
208 vertebrate dataset. For downstream bioinformatic and statistical analyses, the 18S reads were
209 processed separately as two individual datasets representing protist and invertebrate reads, while
210 12S reads represented the standalone vertebrate dataset.

211 After taxonomic classification, 142 of 399 invertebrate ASVs remained unassigned at the
212 phylum level or were unassigned sequences from the phylum Arthropoda, which represented
213 18.4% of all sequences in the invertebrate dataset. Of those 142 ASVs, one ASV represented
214 ~13% of invertebrate reads and comprised of ~48% of reads at 100 m (Supplementary Figure
215 S3A). These unassigned sequences were manually classified with Geneious Prime 2025.0.3 with
216 a BLAST search and NCBI's new BLAST core nucleotide database (core_nt). The top match was
217 selected from the assigned grade score at a 95% cut-off. This approach annotated 67 of the 142
218 unassigned invertebrate ASVs, which reduced the total number of unassigned reads to 0.35%.
219 Most unassigned reads were classified to Order Calanoida (calanoid copepods). Similarly, 345 of
220 677 vertebrate ASVs remained unassigned with > 80% of ASVs classified as Unassigned
221 Actinopterygii (ray-finned fishes). Altogether, unassigned ASVs comprised 12.9% of reads.
222 Following the BLAST process described for invertebrates, 117 vertebrate ASVs were successfully
223 classified, reducing the unassigned read percentage to ~1% (Supplementary Figure S3B).
224 Taxonomy, ASV count, and metadata files were imported into R (v4.3.2) with qiime2R
225 (v0.99.6) (https://github.com/jbisanz/qiime2R) and merged with phyloseq (v1.46.0) (McMurdie
226 and Holmes, 2013) to generate phyloseq objects for protists, invertebrates, and vertebrates.
227 Potential contaminants were identified and removed with the R package decontam and a
228 conservative threshold of 0.5, which identifies all sequences more prevalent in negative controls
229 than samples as contaminants (Davis et al., 2018). In total, decontam identified and removed 44
230 protist, 19 invertebrate, and 17 vertebrate ASVs. Additional decontamination of the datasets was
231 conducted manually and detailed in Supplementary Methods. Samples with less than 15000
232 reads (protists), 6000 reads (invertebrates), and 3000 reads (vertebrates) were removed,
233 resulting in 69 samples (protists), 70 samples (invertebrates), and 61 samples (vertebrates) out
234 of 72 total samples.
235 Alpha diversity indices (richness, Shannon Index, evenness) were calculated from a
236 rarefaction approach with iterative subsampling (1000 iterations) and a subsampling threshold

determined by the minimum read count of 27865 (protists), 6076 (invertebrates), and 3183 (vertebrates) in the sample set (Schloss, 2024). Diversity indices reflect the mean index value for each depth after rarefaction and statistical significance was computed by one-way ANOVA with Tukey's HSD post-hoc analysis (p value < 0.05).

Depth-specific community composition was assessed with principal component analyses conducted with the rda function in vegan v2.6.4 (Oksanen et al., 2022) on centered log-ratio (CLR) transformed ASV counts (Aitchson, 1986; Coenen et al., 2020). Zero-value data were replaced with the "const" method which replaces zeros with 65% of the next lowest value (Bastiaanssen et al., 2022). Statistical significance was determined with permutational multivariate analysis of variance (PERMANOVA) with the adonis2 function in vegan on Euclidean distance matrices. Pairwise comparisons were conducted with the pairwise.adonis2 function from the pairwiseAdonis package v0.4 (Arbizu, 2020). ASVs were grouped into relevant taxonomic groups of ecological and functional significance for taxa bar plots to show the proportion of ASV composition and relative abundance. UpSet plots were used to visualize ASV overlap across depths, with a matrix format that shows which ASVs are shared or unique to specific depths. Taxa with low relative abundance (< 1%) were grouped to streamline visualizations with additional details provided in Supplementary Materials (Supplementary Tables S1-S3).

3.4 Network Analyses

Network analysis from Sparse InversE Covariance Estimation for Ecological Association inference (SPIEC-EASI) was applied to protist, invertebrate, and vertebrate compositional datasets to assess ASV-ASV co-occurrence patterns with depth across these datasets (Kurtz et al., 2015; Tipton et al., 2018). SPIEC-EASI identifies statistically significant relationships while accounting for issues inherent to compositional metabarcoding datasets (Kurtz et al., 2015). ASV count tables are CLR-transformed and a graphical model inference framework is used to identify

262 direct associations between ASVs while minimizing indirect correlations and reducing the
263 detection of spurious relationships.

264 Samples were grouped into three depth zones: epipelagic (10 m and 100 m), upper
265 mesopelagic (300 m and 500 m), and lower mesopelagic (800 m and 1000 m). Out of a possible
266 total of 24 samples in each depth zone, only samples that contained protist, invertebrate, and
267 vertebrate ASVs were retained for network analysis, resulting in a total of 15 epipelagic samples,
268 21 upper mesopelagic samples, and 22 lower mesopelagic samples. ASVs were filtered on
269 abundance (> 50 reads) and prevalence (present in at least 10% of samples in each depth zone)
270 to minimize dense networks and focus the analyses on prevalent and abundant ASVs.

271 Undirected networks were generated for each depth zone for metazoan-only (invertebrate
272 and vertebrate) ASVs, protist-only ASVs, and all ASVs (All Taxa) for a total of nine networks. In
273 each network, edges (links) represent signed associations (positive or negative) between nodes
274 (ASVs). The SpiecEasi v1.1.1 package was used to construct these networks on WHOI's high-
275 performance computing cluster in R v4.4.3, applying the Meinshausen–Buhlmann's neighborhood
276 selection method with an optimal sparsity threshold (lambda min ratio) of 1e-3, and 100
277 subsampling replicates (rep.num = 100) (Kurtz et al., 2015). Networks were then exported into
278 RStudio to assess network topology and robustness with igraph v2.0.2 in R (Csárdi and Nepusz,
279 2006).

280 Although ecological networks can be built from species-level or other taxonomic groups,
281 we built networks from ASVs, the lowest genetic unit, to render an appropriate comparison across
282 the three datasets generated from two markers of varying taxonomic resolution. For example,
283 18S V9 reliably resolves taxonomy to the order level while 12S MiFish can resolve to species
284 level. To show this, we evaluated the three naïve Bayes classifiers referenced in this study with
285 the evaluate-fit-classifier function in the QIIME 2 RESCRIPt plugin (Robeson et al., 2021) to test
286 the classifiers' performance on the same sequences it was trained with. The F-measure score,
287 which reflects the balance between precision and recall, for the 18S V9 classifiers drops below

288 ~0.95 after Order while the 12S classifier has a high F-measure up to species-level classification
289 (Supplementary Figure S4). After networks were generated, ASVs were grouped into relevant
290 taxonomic groups of ecological and functional significance for downstream network analyses.
291
292 **3.5 Visualizations**
293 Unless otherwise specified, figures were generated with ggplot2 v3.5.1 (Wickham, 2016).
294 UpSet plots were generated with ComplexUpset v1.3.3. Networks were visualized with ggnetwork
295 v0.5.13 (Tyner et al., 2017). When necessary, visualizations were compiled with minimal editing
296 for aesthetics with the creative software, Affinity Designer 2 (Serif, Europe).
297
298 **4. RESULTS**
299 **4.1 Patterns of diversity from 18S and 12S metabarcoding**
300 Metabarcoding of the 18S V9 rRNA gene generated ASVs for protists and invertebrates
301 while the 12S MiFish metabarcoding generated ASVs for vertebrates (predominately fish). The
302 18S dataset ranged from 70-90% protist sequences with the proportion of invertebrate sequences
303 decreasing with depth (Supplementary Figure S5). Protist and invertebrate sequences were
304 parsed from the 18S dataset and assessed separately. Following decontamination and rarefaction
305 of metabarcoding reads, a total of 8112 ASVs were recovered across both markers with 7046
306 (86.9%) for protists, 399 (4.9%) for invertebrates, and 667 (8.2%) for vertebrates. The numbers
307 of observed ASVs (or ASV richness) for protists and invertebrates were generally higher in the
308 mesopelagic than the epipelagic with relatively constant richness across mesopelagic depths
309 (Figure 2). For vertebrates, higher richness was observed at 10 m and 500 m than at other depths.
310 For invertebrates, Shannon diversity indices were significantly different between surface (10 m)
311 and all other depths ($p < 0.01$) while Pielou's evenness indices varied significantly at depth,
312 especially between 100 m and select mesopelagic depths ($p < 0.05$). For vertebrates, average
313 Shannon and Pielou's indices followed similar patterns as observed for ASV richness, although

no significant differences were observed between depths (Supplementary Tables S4-S6). For protists however, Shannon and Pielou indices exhibited patterns that contrasted with those for richness. The highest Shannon diversity and Pielou evenness indices occurred at 100 m and then decreased with depth down to 500 m before increasing again to 1000 m.

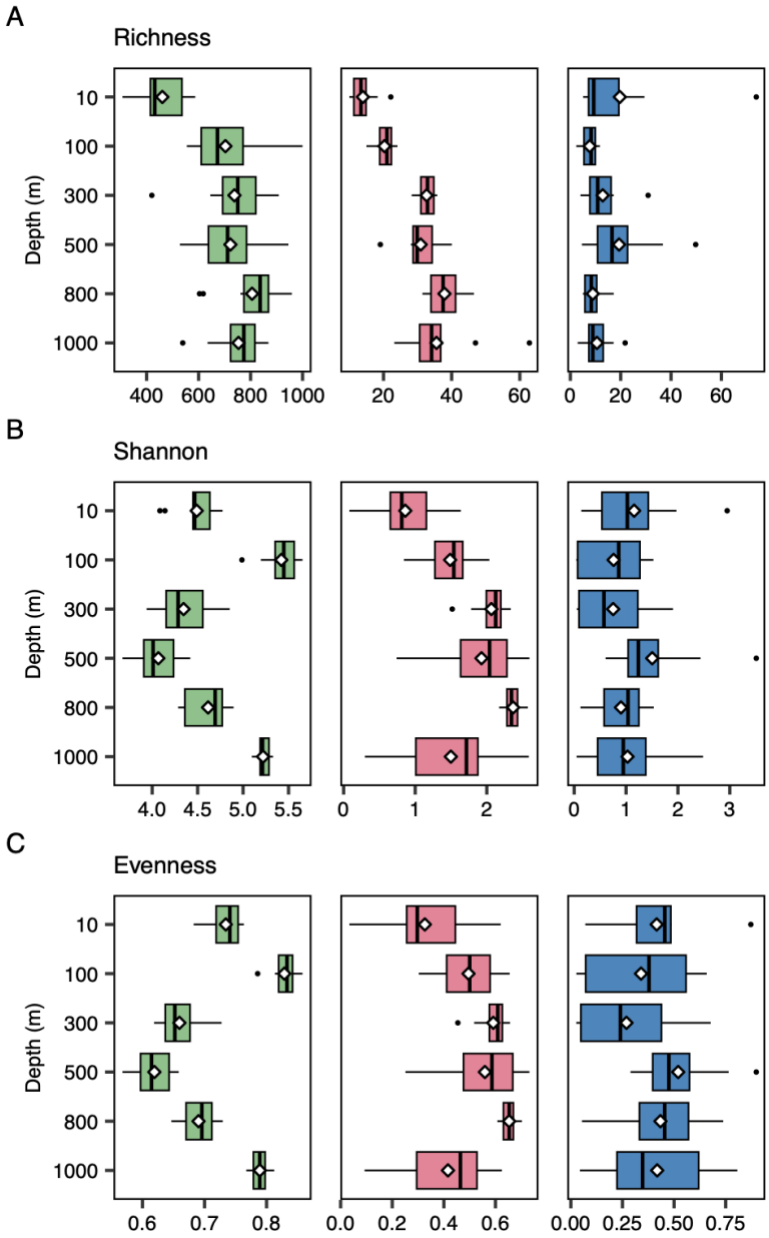


Figure 2. Patterns of alpha diversity with depth for A) Richness (observed ASVs), B) Shannon Diversity Index, and C) Pielou's Evenness Index across all samples for protists (n=69), invertebrates (n=70), and vertebrates (n=61). Boxplots show the variation in diversity indices at each depth between samples divided into quartiles with outlier values indicated by black points. A white diamond indicates the mean value at each depth.

Protistan diversity in epipelagic waters was comprised of mostly alveolates (dinoflagellates, Syndiniales, and ciliates) and stramenopiles (e.g., diatoms) (Supplementary Figure S6A). Alveolate ASVs increased in mesopelagic waters, as did rhizarian (e.g., radiolarians) and excavate ASVs, with these three groups representing a significant portion of protistan diversity (Supplementary Figure S6D). Invertebrate diversity was driven mainly by taxonomic groups with relative read abundance < 1% (rare reads), including Trachymedusae and Narcomedusae (Cnidaria) (Supplementary Figure S6B, Supplementary Table S2). Orders Calanoida (calanoid copepods) and Siphonophorae (Cnidaria; siphonophores), as well as unassigned metazoan ASVs, also represented a significant portion of diversity (Supplementary Figure S6E). Fish were the main category of vertebrate ASVs detected (Supplementary Figure S6C), with a significant portion attributed to deep sea fish taxa including Melamphidae (bigscales), Myctophidae (lanternfish), and Gonostomatidae (bristlemouths). Similar to the invertebrates, rare taxonomic groups (low read count) contributed significantly to vertebrate diversity (Supplementary Figure S6F). Five mammalian ASVs were also detected, comprising ~0.038% of the total dataset. These included ASVs assigned to whales and dolphins known to occur at the study site, including two ASVs from the genus *Balaenoptera* (whales) and three ASVs for dolphins in the genera *Delphinus*, *Stenella*, and *Grampus* (Supplementary Table S3).

4.2 Depth structuring of the eukaryotic community

Principal component analysis (PCA) and PERMANOVA of rarefied, center-log ratio (CLR) transformed protist and invertebrate reads from all samples revealed significant depth clustering ($p < 0.001$) (Figure 3). Moreover, pairwise comparison showed that communities at each depth were significantly different from other depths ($p < 0.001$). For vertebrate communities, significant differences were observed between surface (10 m) and mesopelagic depths ($p < 0.01$). Differences were also found between 500 m and all other depths ($p < 0.05$). Clustering by CTD cast, which reflected the time of sampling, was not statistically significant ($p > 0.05$). Given the

lack of significant diel patterns in this dataset, samples across all three casts were combined at each depth for subsequent analyses.

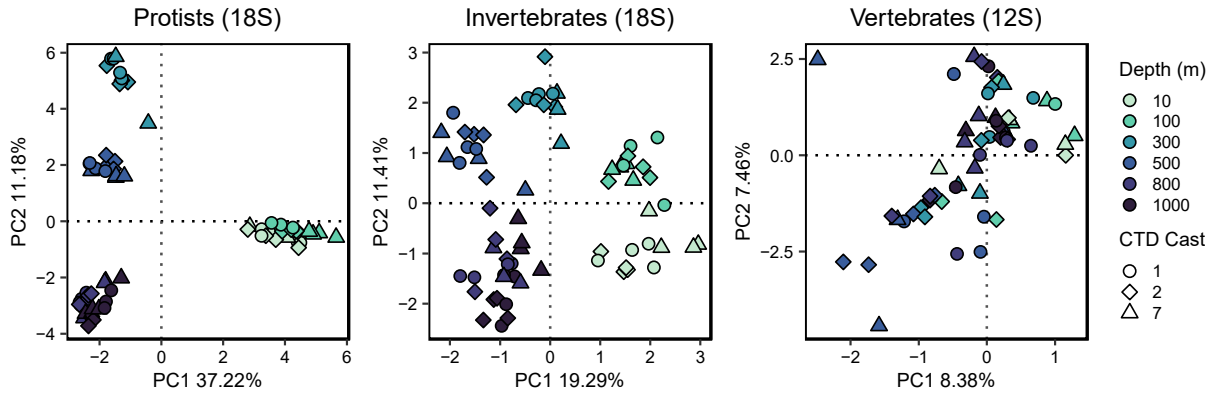


Figure 3. Principal component analysis (PCA) of center-log ratio-transformed reads for protists (n=69), invertebrates (n=70), and vertebrates (n=60). Each point represents one sample. The shape and color of each point indicates the CTD cast and the sampling depth, respectively, of each sample. CTD cast here can also reflect diel sampling with casts 1 and 7 sampled at midnight and cast 2 sampled during mid-day. One outlier (10 m, PC1 = ~10) from the vertebrate dataset was removed for visualization purposes (see Supplementary Figure S7).

Sequenced reads were aggregated by depth to generate relative abundance profiles that reflect the overall water column community structure (Figure 4). For protists, epipelagic (< 200 m) community structure was dominated by photosynthetic taxa including dinoflagellates, diatoms and other stramenopiles, and chlorophytes. The relative abundance of the parasitic taxon Syndiniales, as well as radiolarians, increased with depth and were the dominant taxa in the mesopelagic (> 200 m). Excavates were also relatively more abundant in deeper waters. For invertebrates, calanoid copepods (Arthropoda) exhibited higher relative abundance in both the epipelagic and lower mesopelagic (1000 m), while siphonophores (Cnidaria) were also relatively abundant, especially in the upper mesopelagic. At surface depths, salps were relatively abundant compared to other invertebrate taxa.

Key taxonomic groups were comprised of ASVs that were only detected at one specific depth (unique ASVs), detected at two or more depths (shared ASVs), or detected at all depths (cosmopolitan ASVs) (Supplementary Figure S8). Unique, shared, and cosmopolitan protist ASVs included a mix of both photosynthetic and non-photosynthetic taxa across all depths with deeper

waters harboring a higher number of unique ASVs than near the surface (10 m). Unique invertebrate ASVs were greater at mesopelagic depths and dominated by taxa with low relative abundance (< 1%), while unique vertebrate ASVs were highest at 10 m and 500 m. Across the three organismal groups, unique ASVs were proportionally higher than shared and cosmopolitan ASVs, especially for invertebrates (68.4%) and vertebrates (89.2%) compared to protists (56.6%).

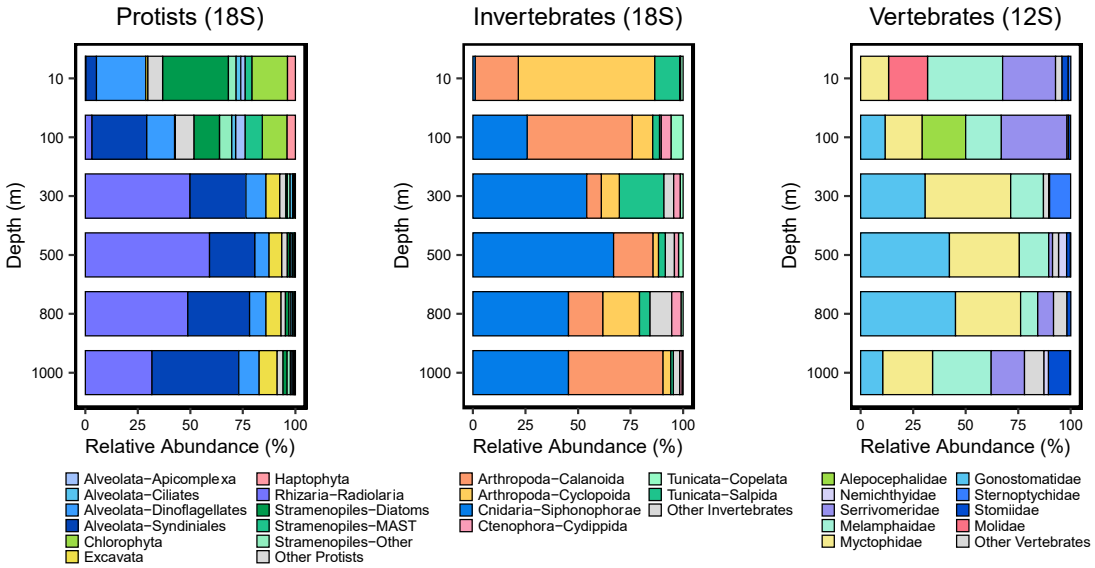
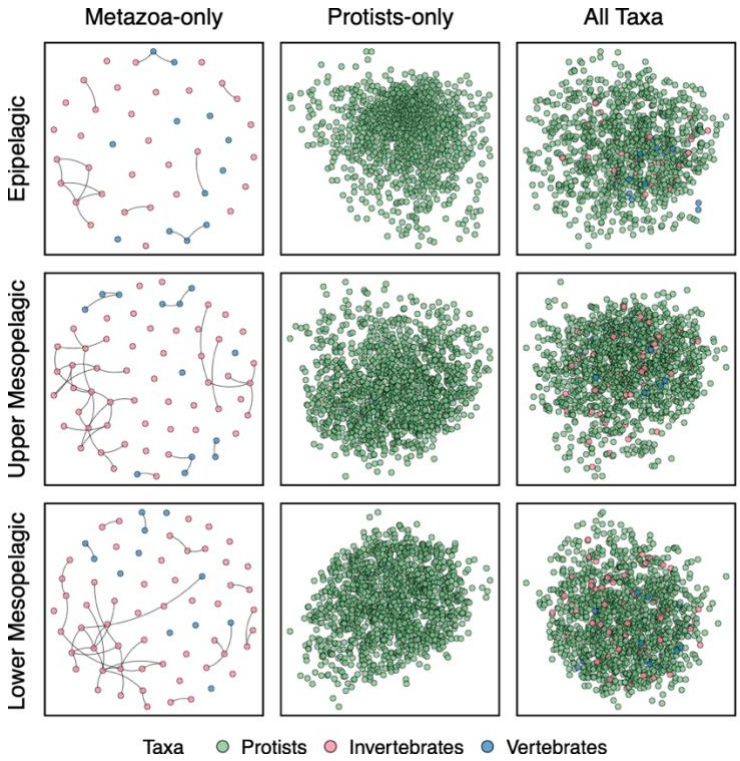


Figure 4. Depth profiles of relative read abundance (%) for protists, invertebrates, and vertebrates calculated from samples aggregated across three CTD casts. Bar plots show taxonomic groups in the order of decreasing relative abundance. In the legend, taxonomic groups within protists (Supergroup and/or Division or Subdivision) and invertebrates (Phylum and Order) are colored and listed in alphabetical order. Vertebrate families were grouped at the Order level in alphabetical order: Alepocephalidae (Alepocephaliformes); Nemichthyidae, Serrivomeridae (Anguilliformes); Melamphidae (Beryciformes); Myctophidae (Myctophiformes); Gonostomatidae, Sternoptychidae, Stomiidae (Stomiiformes); and Molidae (Tetraodontiformes). For each group, only taxa with overall relative abundance > 1% are displayed, with all other taxa combined in "Other". For a full list of "Other" taxa, see Supplementary Tables S1-S3.

Shared and cosmopolitan ASVs for invertebrates and vertebrates may signal animal migration behaviors throughout the water column. For invertebrates, shared and cosmopolitan ASVs included representatives from Orders Calanoida (Arthropoda), Siphonophorae (Cnidaria), Cydippida (Ctenophora), as well as Copelata and Salpida (Tunicata) (Supplementary Figure S9). For vertebrates (Supplementary Figure S10), shared and cosmopolitan ASVs were observed from

395 mesopelagic fish species including *Benthosema glaciale* (Myctophidae), *Cyclothone microdon*,
396 (Gonostomatidae), *Scopeloberyx opisthopterus* (Melamphaidae), and *Serrivomer beanii*
397 (Serrivomeridae).
398
399 **4.3 Depth-specific eukaryotic networks**
400 We generated single-taxon and multi-trophic networks of protists, invertebrates, and
401 vertebrates for the epipelagic (10 m and 100 m), upper mesopelagic (300 m and 500 m), and
402 lower mesopelagic (800 m and 1000 m). Associations between "Metazoa-only" (invertebrates and
403 vertebrates), "Protists-only", and All Taxa (all groups) for each depth zone were inferred with
404 SPIEC-EASI to assess the contribution of broad eukaryotic groups to network connectivity and
405 stability.
406 Metazoa-only networks were small and fragmented, consisting of multiple components
407 including singleton and doubleton associations that resulted in lower complexity networks
408 compared to Protist-only and All Taxa networks (Figure 5, Supplementary Table S7). In contrast,
409 Protist-only networks and All Taxa networks were fully connected such that a link existed between
410 any two nodes in the network. Across all networks, the epipelagic had lower complexity (fewer
411 nodes and edges) and decreased edge density (edge-to-node ratio) compared to the mesopelagic
412 depths.
413 For each network, we assessed resilience and stability to the loss of ASVs (genetic
414 diversity). Node and edge connectivity, the minimum threshold for node or edge removal that
415 fragments a connected network, increased with depth for All Taxa networks (Supplementary
416 Table S7). The lower mesopelagic had the highest threshold for node and edge connectivity for
417 both All Taxa and Protist networks. For the already fragmented Metazoa-only networks,
418 connectivity was zero across all depth zones. We evaluated attack robustness, which measures
419 the size of the network (remaining subnetwork) as nodes are sequentially removed based on
420 betweenness (putative bottlenecks or keystone taxa), degree (highly connected ASVs or hubs),

421 and at random (Iyer et al., 2013; Tipton et al., 2018). Metazoa-only networks were the least robust,
422 especially in the mesopelagic. Protists-only and All Taxa networks had comparable robustness
423 with higher robustness in mesopelagic networks (Supplementary Figure S11).



424

425 **Figure 5**. Depth-specific networks for Metazoa-only (invertebrate and vertebrates), Protists-only,
426 and All Taxa (all ASVs). All nodes are shown as points with color indicating the broad taxonomic
427 classification of protists, invertebrates, and vertebrates. Edges are shown for the Metazoa-only
428 network to show the fragmented nature of the network with singleton nodes. The Protists-only
429 and All Taxa networks are connected networks and edges are not shown. All networks include
430 predicted positive and negative interactions.
431

432 **4.4 Ecological interactions from the surface to the mesopelagic**

433 Positive and negative interactions were separated from the combined networks to explore
434 ecological interactions, especially trophic dynamics across depth. Epipelagic and upper
435 mesopelagic networks averaged 58 and 57% positive interactions, respectively, while the lower
436 mesopelagic network was ~53% positive (Supplementary Table S8). On average, the edge
437 density of positive networks was 7.9 compared to 6.4 for negative networks, suggesting that
438 positive networks are more complex. Nodes were compartmentalized into modules that

delineated subsets of ASVs that interact more frequently or have stronger interactions than with other ASVs (modularity). Average modularity across the three depth zones was higher for positive networks compared to negative networks (Supplementary Table S9). For both positive and negative networks, modularity decreased with depth. Node and edge connectivity for negative networks averaged 1.67 compared to an average of 3 for positive networks. Negative networks were also less robust than positive networks, especially in the epipelagic networks (Supplementary Figure S12).

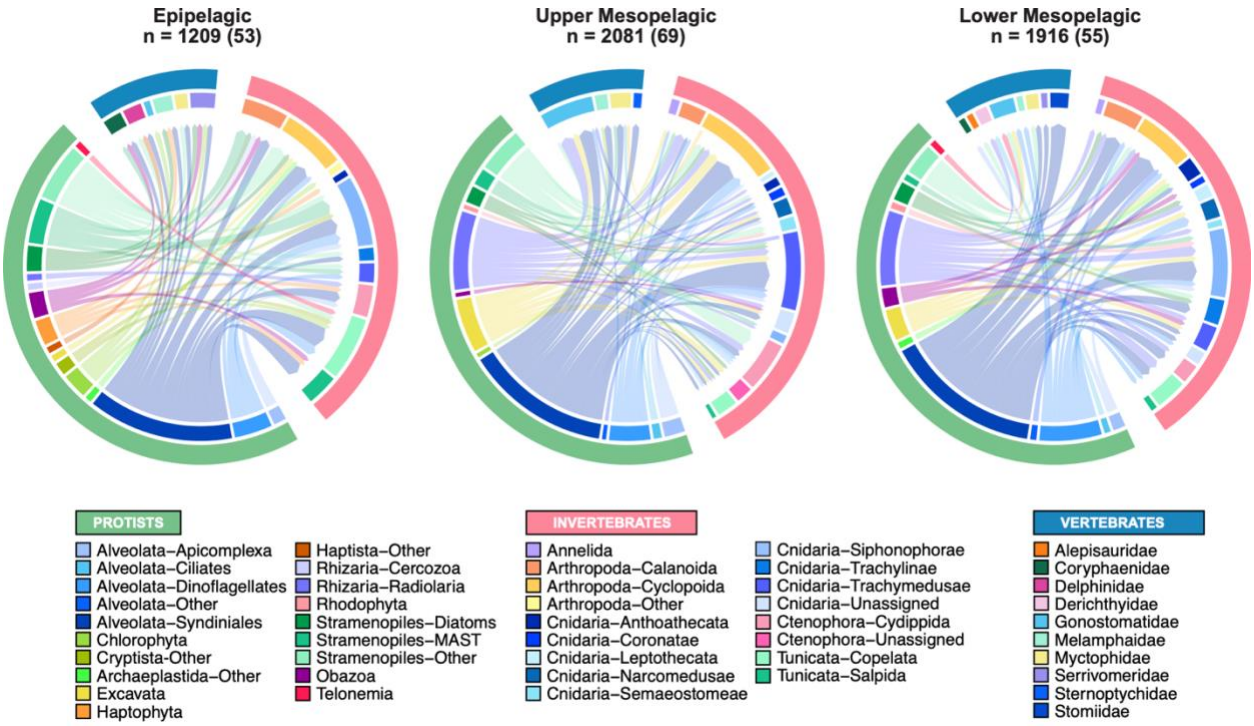
Nodes with the highest edge weights (90th percentile), indicating the strongest interactions, were isolated from the positive and negative networks to explore key ASV associations in each network (Supplementary Figure S13). In both positive and negative subnetworks, the top ranking ASVs based on node degree (number of connections) and betweenness centrality were predominantly protistan taxa, especially Syndiniales (Alveolata) (Supplementary Figures S14-S15). Top ranking invertebrate ASVs included copepods (both calanoid and cyclopoid), siphonophores (cnidarians), and ctenophores while vertebrate ASVs included mesopelagic fish. Notably, *Grampus griseus* (Risso's dolphin) was a top-ranking ASV in the positive network, while salps (tunicates) and *Coryphaena hippurus* (common dolphinfish) were high-ranking ASVs in the negative network.

Trophic interactions were assessed by assuming a simple food web from the negative network where protists are at the bottom, invertebrates are intermediate, and vertebrates are top predators. In general, the total number of pair-wise associations (protist-invertebrate, protist-vertebrate, and invertebrate-vertebrate) were highest in the mesopelagic, with 2081 and 1916 associations in the upper and lower mesopelagic, respectively, compared to 1209 associations in the epipelagic (Figure 6). We narrowed focus to the strongest interactions at each depth zone by selecting ASV-ASV associations with the top 10% of edge weights. Many of these strongest relationships featured protist associations with both invertebrates and vertebrates and highlighted known interactions such as zooplankton grazing of phytoplankton, predator-prey dynamics

465 between zooplankton and mesopelagic fish, as well as putative parasitic interactions between

466 alveolates and various metazoans (Figure 6).

467



468

469 **Figure 6**. Chord diagrams indicate the number of strong pairwise interactions in the negative
470 network and the taxonomic groups involved at each depth zone. Interactions were selected by
471 removing all ASV-ASV linkages below the 90th percentile threshold for edge weight (so that only
472 the strongest interactions remained). Only protist-invertebrate, protist-vertebrate, and
473 invertebrate-vertebrate interactions were considered. The total number of pairwise associations
474 for each network is listed (n) with the number of strong associations in parentheses. Colors along
475 the circumference (track) of the diagram indicate taxonomic groupings. The outer track shows
476 protists in green, invertebrates in pink, and vertebrates in blue. The inner track further divides
477 these taxa into broad functional groups. Each link between two ASVs (or interaction) is depicted
478 as a directional arrow that starts from the ASV in a lower trophic level and points towards the ASV
479 at the higher trophic level. The arrows are also colored based on the lower trophic level ASV.
480 Trophic levels are simplified and ordered as protist > invertebrate > vertebrate. The size of each
481 inner track segment indicates the relative number of ASVs under each functional group within a
482 chord diagram.
483

484 **5. DISCUSSION**

485 **5.1 Protists and metazoans exhibit contrasting diversity patterns**

Based on current knowledge of the deep sea, we lack consensus on broad diversity trends due to prevailing gaps across spatial, temporal, and taxonomic scales (Haddock and Choy, 2024; Yang et al., 2024). Traditional midwater assessments often rely on net-based trawls, which sample few depths and regions and can underrepresent taxa that avoid capture or are too fragile (Kaartvedt et al., 2012; Gold et al., 2021; Suarez-Bregua et al., 2022). As such, deep sea studies that span the eukaryotic community from microeukaryotes to metazoans remain scarce. Since we applied multi-marker metabarcoding to eDNA, this study has generated new insights into eukaryotic biodiversity and ecology from the surface down to the base of the mesopelagic.

A key finding of our study is that alpha diversity increased in the mesopelagic compared to the epipelagic. We found this for both genetic diversity (ASV richness) and Shannon diversity in the Northwest Atlantic Slope Water, especially for protists and invertebrates. This observation counters the existing perspective of decreasing diversity in midwater ecosystems compared to epipelagic waters generated from the global Ocean Biodiversity Information System (OBIS) database (Costello and Chaudhary, 2017). However, Costello and Chaudhary did note a diversity maximum at ~400-500 m, which aligns with our findings, especially for vertebrates (Figure 2). A recent survey of more than two decades of ROV-generated data revealed taxa-specific patterns in the eastern North Pacific such as higher species richness for crustaceans and fishes in the mesopelagic compared to the epipelagic (Haddock and Choy, 2024).

While our findings generally show increasing alpha diversity with depth (Figure 2), we observed low indices for protists between 300 m and 800 m with a minimum at 500 m. We attributed the lower diversity in this depth zone to a small number of ASVs associated with Syndiniales (Dinoflagellata) and Radiolaria (Rhizaria) that are highly abundant relative to other ASVs (Supplementary Figure S14). Through the upper mesopelagic, this trend is generally in line with previous studies that reported a protist diversity maximum at the base of the euphotic zone followed by decreasing diversity in the mesopelagic (Laroche et al., 2020b; Blanco-Bercial et al.,

2022). In contrast, other studies have found increasing diversity in the mesopelagic, which we also observed in our dataset at 1000 m (Giner et al., 2020; Ollison et al., 2021).

We also found higher richness in the mesopelagic for invertebrates, which is similar to diversity metrics reported for other areas of the North Pacific (Matthews and Blanco-Bercial, 2023) as well as the southeast Pacific (González et al., 2023), but contrasting with diversity patterns reported off Hawaii (Laroche et al., 2020b). These studies showed that arthropods (especially copepods) and cnidarians are significant contributors to metazoan diversity. In addition, we found vertebrate diversity assessed with the 12S biomarker detected mainly fish. As with previous studies (Canals et al., 2021; Govindarajan et al., 2023b), a significant portion of sequencing reads were associated with deep sea fish (Supplementary Figure S6).

For invertebrates and vertebrates, Shannon diversity was high across mesopelagic depths with the highest ASV richness at 500 m for vertebrates, which corresponded with the deep scattering layer detected at 38 kHz (Supplementary Figure S1), a region of the midwater with strong acoustic backscatter from mesopelagic fish and invertebrates (Barham, 1966; Aksnes et al., 2017). Taxonomic groups with low relative abundance (< 1%) or “rare” taxa typically contributed significantly to alpha diversity for protists, invertebrates, and vertebrates (Supplementary Figure S6 and S8). While our study was not explicitly focused on the role of these low abundance taxa, these rare taxa may exert considerable influence over ecosystem function and stability (Lyons et al., 2005; Mouillot et al., 2013; Logares et al., 2014; Lynch and Neufeld, 2015; Jousset et al., 2017).

There are various factors that may contribute to some of the differences reported across metabarcoding studies. There are differences in methodology (e.g., primer selection, volume filtered, filter pore size or size fractionation, and number of samples), as well as study site (e.g., Atlantic or Pacific) and seasonal timing of sampling linked to varied environmental conditions that shape the community (Govindarajan et al., 2023a). For example, our study was conducted in the productive Northwest Atlantic Slope Water region and consisted of bulk water sampling (no size

fractionation) in March 2020, while the Blanco-Bercial et al. study (2022) was conducted monthly over the course of one year and the Giner et al. study (2020) used size-fractionated water samples (0.2-3 μm).

Moreover, the chance encounter of a salp bloom during our sampling (see Methods) contributed to high relative abundance of salp sequences in surface waters (Figure 4) compared to other studies (Govindarajan et al., 2022; González et al., 2023; Matthews and Blanco-Bercial, 2023). Although we were unable to sample outside of the bloom to assess their impact on community composition, it is possible that diversity trends we observed may have been influenced by high salp densities. For example, previous studies suggest that salp blooms may impact biodiversity by substantially reducing phytoplankton biomass (Zeldis et al., 1995; Décima et al., 2023) and outcompeting other planktonic organisms for food (Paffenhöfer et al., 1995; Perissinotto and A. Pakhomov, 1998; Stukel et al., 2021).

Going forward, the maturation of multi-marker metabarcoding for deep sea studies will benefit from improved reference libraries taxonomic assignments, increased spatial and temporal sampling, and standardization of sampling technologies, wet lab processes, and bioinformatics pipelines (McClenaghan et al., 2020; Patin and Goodwin, 2022; Kelly et al., 2023).

5.2 Eukaryotic community structure is depth-dependent

Eukaryotic communities were depth-dependent with differing community composition for protists, invertebrates, and vertebrates (Figure 3). Protist community composition was highly influenced by depth with distinct communities at each of our sampled depths and a notable shift in dominant taxa between epipelagic and mesopelagic depth zones. Invertebrate communities were also depth-specific, although there was more overlap across the communities with samples clustering into three depth bands for the epipelagic (< 200 m), upper mesopelagic (300-500 m), and lower mesopelagic (> 500 m). Vertebrate communities were less structured with depth with samples at 500 m exhibiting a significant difference between epipelagic and lower mesopelagic

563 samples. Depth-dependency of eukaryotic communities, especially for protists, has been
564 established previously, with a distinct transition in community composition between the sunlit
565 surface and the deep (Ollison et al., 2021; Blanco-Bercial et al., 2022; Yeh and Fuhrman, 2022;
566 Sun et al., 2023; Anderson et al., 2024). For protists, a high relative abundance of photosynthetic
567 taxa including stramenopiles and chlorophytes transitions into dominance by alveolates,
568 especially Syndiniales and radiolarians.

569 Similar to other metazoan studies, we found high relative abundance of calanoid copepods
570 (Order Calanoida) in the water column, as well as a subsurface abundance of Siphonophorae
571 and Ctenophora (e.g., comb jellies) (Laroche et al., 2020b; Govindarajan et al., 2021). For
572 vertebrates, we detected high relative abundance of mesopelagic fish from families Myctophidae
573 and Gonostomatidae, which were also present in other metabarcoding studies (Canals et al.,
574 2021; Govindarajan et al., 2023b; Dan et al., 2024). In epipelagic waters, additional taxa occurred
575 in high relative abundance including the families Serrivomeridae (sawtooth eels), Molidae (molas),
576 and Alepocephalidae (slickheads).

577 The eukaryotic community at each depth was further shaped by a combination of unique,
578 shared, and cosmopolitan ASVs (Supplementary Figure S8). The detection of unique ASVs could
579 indicate niche specialization to different environmental conditions within a given taxonomic group
580 (Ollison et al., 2021; Anderson et al., 2024). Unexpectedly, we found unique ASVs for diatoms
581 and chlorophytes in deep waters. Rather than niche specialization of these photosynthetic taxa
582 to aphotic conditions, we hypothesize that these sequences indicate export of primary producers
583 out of the euphotic zone as sinking particles (Mestre et al., 2018; Durkin et al., 2022).

584 Animals shed DNA as they move through the water column, and we hypothesize that
585 unique ASVs represent cohorts of animals that are non-migratory while shared and cosmopolitan
586 ASVs reflect migratory cohorts. One possible explanation for the high occurrence of unique
587 invertebrate and vertebrate ASVs may be due to under-sampling of metazoan biodiversity, which
588 tend to be patchily distributed in the water column. Environmental factors that influence eDNA

shedding, persistence, and transport in combination with low-volume (~1-5 L) sampling efforts impact eDNA recovery for metazoan detection (Govindarajan et al., 2022, 2023a). While these volumes may be adequate for microbial studies, they likely underestimate metazoan biodiversity in deep sea ecosystems (Govindarajan et al., 2022), which can lead to a skewed perspective of their vertical and horizontal distribution. However, unique and cosmopolitan ASVs can be used to probe DVM behaviors, which may be useful to better understand the ecology of these otherwise elusive taxa that warrant further study.

We detected invertebrate and vertebrate ASVs that appeared at multiple sampling depths (shared and cosmopolitan ASVs), which included representatives from known migratory invertebrate taxa including copepods, cnidarians, and tunicates (Bianchi and Mislan, 2016; Romero-Romero et al., 2019; Easson et al., 2020), as well as mesopelagic fish including lanternfish and bristlemouths. Most of these fish are considered migratory except for *Cyclothone microdon* (bristlemouth) and *Scopeloberyx opisthopterus* (bigscale), which are lower mesopelagic and bathypelagic dwelling (Sutton, 2013; Govindarajan et al., 2023b; Richards et al., 2023). However, our study detected one ASV each of *C. microdon* (15 ASVs total) and *S. opisthopterus* (97 ASVs total) with a relatively high abundance in epipelagic waters, especially during the day. While studies have indicated that juvenile stages of mesopelagic fish may occur at shallower depths (Olivar and Beckley, 2022), it remains unclear whether the driving mechanism is ontogenetic migration or other drivers such as niche expansion that require further study (Sutton et al., 2008; Cook et al., 2013; Granata et al., 2023).

5.3 Protists increase ecosystem complexity and stability

Diversity (nodes or ASVs), connectivity (edges or interactions) and edge density (edge-to-node ratio) are core determinants of network complexity (Landi et al., 2018; Espinoza et al., 2020). Increasing biological diversity and their interactions increases ecosystem complexity, which often correlates with enhanced stability or resilience (McCann, 2000; Dunne et al., 2002;

615 Carpentier et al., 2021; Nauta and De Domenico, 2024). Our ecological network analyses from
616 multi-marker metabarcoding of the eukaryotic community showed that protistan taxa play a key
617 role in mediating trophic interactions and ecosystem function. While metazoan networks were
618 fragmented, the addition of protistan ASVs increased diversity and interactions (Supplementary
619 Table S7), producing fully connected networks at all depths with protist nodes facilitating
620 interactions between previously unconnected metazoan nodes (Figure 5). Increased protistan
621 diversity may stabilize connectivity by enhancing the likelihood that biological communities are
622 resilient to environmental fluctuations and can compensate the loss of functionally important taxa
623 (functional redundancy) (Naeem and Li, 1997; Naeem, 1998; McCann, 2000).

624 Alternatively, our fragmented ecological networks may reflect the more heterogenous
625 distributions of metazoan taxa that reduce co-occurrences and interactions, especially in the vast
626 and deep pelagic ocean where food is scarce (Robison, 2004; Ramirez-Llodra et al., 2010).
627 Fragmented networks may also reflect sampling biases associated with low-volume samples,
628 which may not provide a comprehensive snapshot of metazoan diversity and distribution
629 compared to more easily sampled protistan taxa (Anderson and Thompson, 2022; Govindarajan
630 et al., 2022). Significant knowledge gaps on metazoan eDNA further complicate our interpretation
631 of metazoan eDNA signatures due in part to unknown rates of DNA shedding across different
632 taxa and the varying impacts of environmental parameters on eDNA persistence (Allan et al.,
633 2021a, 2021b; McCartin et al., 2022; Govindarajan et al., 2023a). Nevertheless, molecular tools
634 like multi-marker metabarcoding and increasing availability of large-volume autonomous
635 samplers are revolutionizing biodiversity research and provide important multi-trophic insights that
636 are otherwise difficult to obtain, especially in the deep sea (Govindarajan et al., 2023a; Dan et al.,
637 2024; Haddock and Choy, 2024; Yang et al., 2024).

638

639 **5.4 Protists are key mediators of ecological interactions**

640 Positive interactions represent putative mutualistic or commensal relationships while
641 negative interactions reflect antagonistic relationships including competition, predation, and
642 parasitism (Landi et al., 2018). The balance of positive and negative interactions shapes
643 community interactions and ecosystem processes and in turn, ecological stability and resilience
644 to environmental change (Travis et al., 2005; Losapio et al., 2021). In our networks, there were
645 more positive interactions than negative interactions across all depth zones (Supplementary
646 Table S8), indicating an important role for mutualistic or facilitative relationships in marine
647 communities (Stachowicz, 2001; Deutschmann et al., 2024). The proportion of negative
648 interactions increased with depth, suggesting that competition or predation dynamics may
649 increase in importance in the relatively resource-scarce mesopelagic.

650 Positive networks were also more robust to node loss than negative networks and for both
651 network types, mesopelagic networks were more robust (Supplementary Figure S12). This may
652 be a result of the higher complexity found in the positive networks that can enhance network
653 stability. Moreover, positive networks had higher modularity, suggesting increased
654 compartmentalization of ASVs with potential niche partitioning and functional specialists
655 (Supplementary Table S8), which may also have a moderately stabilizing effect on networks. This
656 trend did not apply to depth-specific networks where positive and negative networks in the
657 epipelagic had higher modularity but lower robustness than mesopelagic networks. In our study,
658 decreased complexity in the epipelagic relative to mesopelagic depths is likely a stronger driver
659 of network stability. These dynamics suggest that negative-type interactions (e.g., key predator-
660 prey relationships), particularly in the epipelagic, may be more vulnerable to fragmentation or loss
661 of keystone taxa.

662 Top-ranking nodes indicating keystone taxa are highly connected ASVs that are important
663 facilitators of resource transfer (i.e., carbon and energy) throughout a network. A majority of the
664 top-ranking nodes in our study were protists (Supplementary Figures S14-S15), which included a
665 high number of ASVs belonging to the marine alveolate Syndiniales, suggesting an important role

666 for parasitism in the marine environment (Guillou et al., 2008; de Vargas et al., 2015; Anderson
667 et al., 2024). Copepod ASVs as well as various gelatinous taxa (cnidarians, ctenophores, and
668 salps), mesopelagic fish, and top predators (such as Risso's dolphin and common dolphinfish)
669 were also identified as keystone taxa (Supplementary Figures S14-15). Our findings highlight
670 protists as keystone taxa while also underscoring the importance of maintaining biodiversity
671 across trophic levels and functional groups to sustain ecosystem function and stability.

672 We identified known and previously unobserved trophic interactions in our simplified food
673 web analysis that featured protist associations with both invertebrates and vertebrates (Figure 6).
674 Protist-based associations were more common than invertebrate-vertebrate associations and
675 likely play a key role in carbon export out of the surface ocean and through deep sea food webs.
676 For example, sinking particles and marine snow harbor microbial communities comprised of
677 senescent primary producers and diverse microbial communities. Thus, our finding of protist-
678 dominated interactions, especially in mesopelagic networks, aligns with the consensus that
679 marine snow is an important food source in the deep sea (Dilling and Brzezinski, 2004; Choy et
680 al., 2015; Cawley et al., 2021). Additionally, these putative interactions may not reflect direct
681 feeding relationships between protists and metazoans, but rather highlight trophic dynamics in
682 the environment that contribute to overall ecosystem function and warrant further study (Djurhuus
683 et al., 2020; Holman et al., 2021)

684

685 **6. Conclusions**

686 Mesopelagic studies that integrate both microorganisms and metazoans are rare, yet
687 growing anthropogenic pressures underscore the need for more holistic research on this critical
688 ocean realm. Our study applied a multi-marker metabarcoding approach to survey mesopelagic
689 biodiversity in the Northwest Atlantic Slope Water region and construct ecological networks to
690 examine mesopelagic diversity, organismal interactions, and ecosystem stability. Our findings
691 revealed depth-specific structuring of the eukaryotic community, spanning protists, invertebrates,

692 and vertebrates. Notably, ecological networks that included all eukaryotic groups were more
693 robust than metazoan-only networks, with the incorporation of protist ASVs enhancing network
694 complexity and stability. The higher diversity of protistan ASVs likely conferred resilience to taxa
695 loss across mesopelagic networks compared to the epipelagic network.

696 Additionally, we found that negative trophic interactions were more vulnerable to taxa loss
697 than positive interactions, with implications for carbon and energy transfer within food webs and
698 deep-sea carbon sequestration. While mesopelagic networks appear more structurally stable, it
699 is crucial to recognize that surface and deep-sea ecosystems are intrinsically linked through the
700 biological carbon pump and vertically migrating organisms. Therefore, a more complete
701 understanding of biodiversity, species interactions, and their impact on ecosystem function across
702 spatial, temporal, and taxonomic scales is essential for effective mesopelagic conservation and
703 resource management. Future work incorporating a cross-domain lens, inclusive of bacteria and
704 archaea, and biogeochemical processes such as carbon flux (Guidi et al., 2016; Nguyen et al.,
705 2022; McMonagle et al., 2024) will help us better understand the role of biodiversity and their
706 interactions in facilitating carbon cycling and other critical ecosystem services.

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