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Author(s): Petersen, H. C.; Sapkota., R.; Hiillos, A.-L.; Hansen, B. W.; Banta, G. T.; Knott, K. E.

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1 **Spatial and temporal dynamics of coastal benthic microbial**
2 **communities along a salinity gradient**

3
4 **Authors**

5 H. Cecilie Petersen^{1,2,*}, Rumakanta Sapkota³, Anna-Lotta Hiillos², Benni W. Hansen¹, Gary T.
6 Banta⁴, K. Emily Knott².

7 ¹Department of Science and Environment, Roskilde University, DK-4000 Roskilde, Denmark,

8 ²Department of Biological and Environmental Science, University of Jyväskylä, FI-40014 Jyväskylä,

9 Finland, ³Department of Environmental Science, Aarhus University, DK-4000 Roskilde, Denmark,

10 ⁴Department of Biology, University of Southern Denmark, DK-5238 Odense M, Denmark.

11 * Corresponding author: Universitetsvej 1, DK-4000 Roskilde, Denmark. Tel: +4529930595, Email:

12 haidiceciliepetersen@gmail.com

13 **Abstract**

14 The Baltic Sea is a unique brackish water ecosystem studied for decades; however, knowledge about
15 the diversity of the benthic communities of bacteria and microbial eukaryotes within this system is
16 sparse. Using an amplicon sequencing approach, we evaluated the diversity of shallow water coastal
17 microbial sediment communities and their relation to several environmental factors, on both a large
18 spatial scale in the Baltic Sea and the adjacent North Sea, as well as on a temporal scale at selected
19 sites along the salinity gradient in the Baltic Sea. We found salinity to be among the strongest drivers
20 of both bacterial and eukaryote communities' species diversity, and that community network structure
21 appeared to change between sites of different salinity. However, for the communities in the poly- to
22 mesohaline sections of the study area, diversity seems affected to a higher degree by temperature,
23 nutrient, and sediment characteristics.

24 **Keywords**

25 Baltic Sea, benthic bacteria, benthic protists, brackish microbiology, benthic microbial diversity,
26 microbial networks

27 **Introduction**

28 Interactions between bacteria and microbial eukaryotes in aquatic environments have been reported
29 in pelagic systems over the last decades (e.g., Miki & Jacquet 2008), and as a result of these
30 interactions the communities of these two taxonomic groups may co-vary. A positive correlation may
31 indicate both non-causal relations such as similar preferred conditions, or interactions through
32 commensalism or mutualism. They may however also result in negative correlations reflecting effects
33 of parasitism (Anderson & Harvey 2020), grazing or competition for common resources (Chow et al.
34 2014). These interactions between bacteria and eukaryotes may shape diversity for both groups, by
35 applying selection pressure and contribute to the evolution and maintenance of high diversity of
36 microbes (Hiltunen & Becks 2014, Ramanan et al. 2016), and thus shape the community structure of
37 each other besides other ecosystem components e.g., viruses (Chow et al. 2014).

38 Besides biotic interactions, microbial communities are also affected by environmental factors. In
39 marine environments especially salinity is a known driver of changes in diversity (e.g. Herlemann et
40 al. 2011; Campbell & Kirchman 2013). The Baltic Sea is one of the largest brackish water seas in the
41 world, resembling a large estuary with its characteristic mixing of marine and freshwater (Leppäkoski
42 et al. 2009). Due to the physio-chemical properties of the Baltic Sea, its microbial communities are
43 suspected to be uniquely adapted to the brackish water ecosystem (Ininbergs et al. 2015). The salinity
44 gradient in the Baltic Sea has shown to be a strong driver of community structure for both
45 phytoplankton (Olli et al. 2019), planktonic bacteria (Herlemann et al. 2011, Lindh & Pinhassi 2018,
46 Camarena-Gómez et al. 2021) and microbial eukaryotes (Telesh et al. 2011, Hu et al. 2016). Although
47 the first studies of the microbial communities in the Baltic Sea were conducted more than a decade
48 ago (Riemann et al. 2008), and despite the few studies examining the benthic microbial communities
49 (Klier et al. 2018, Salonen et al. 2018), little is known of the diversity patterns of the benthic bacteria
50 and eukaryote communities of the littoral zone. Salinity is nevertheless known to affect bacterial
51 diversity in the sublittoral zone (Pavloudi et al. 2016, Klier et al. 2018, Li et al. 2021). Benthic
52 bacterial communities have even shown contradictory trends in diversity over salinity gradients,
53 compared to bacterioplankton communities (Campbell & Kirchman 2013, Pavloudi et al. 2016, Klier
54 et al. 2018, Vidal-Durà et al. 2018). However, other physico-chemical driving factors, including
55 seasonal changes in temperature and nutrient availability, could also have a significant influence on
56 the composition of benthic microbial communities, both for bacteria (Vetterli et al. 2015, Lv et al.
57 2016), and microbial eukaryotes (Massana et al. 2015, Salonen et al. 2018, Anderson & Harvey 2020).

58 Microbial communities, including bacteria and eukaryotes, are important components of
59 decomposition and nutrient recycling, and are fundamental for all ecosystems. The use of genetic
60 tools, such as metabarcoding and next generation sequencing for documenting uncultured microbes
61 has widened our knowledge of the composition of these communities particularly in the marine
62 environment. However, the focus of such studies has been primarily on marine pelagic microbial
63 communities, and only within the last decade has widened to include microbial communities in
64 sediments (Edgcomb et al. 2011, Bik et al. 2012, Forster et al. 2016), especially in estuaries and
65 brackish water systems (Chariton et al. 2010, Campbell & Kirchman 2013, Klier et al. 2018).

66 In this study, we monitored changes in diversity and community structure in shallow coastal benthic
67 bacteria and microbial eukaryote communities along a salinity gradient in the Baltic Sea and adjacent
68 North Sea, covering both a large spatial and local temporal scale. These communities may be affected
69 by the species composition and their interactions, which may also be affected by external factors. By
70 assessing associations between bacteria and microbial eukaryotes along the Baltic Sea, we aim to
71 provide a first insight to the interactions, and potential keystone species in the benthic microbial
72 communities of this brackish water sea. Furthermore, we assessed whether and to what extent selected
73 abiotic factors besides salinity (sediment mean grain size, sorting, sediment water content, porosity,
74 C/N ratio, organic content, and sediment temperature) influenced the observed diversity patterns. We
75 hypothesised that the microbial community composition is strongly driven by salinity, and that the
76 microbial diversity changes between sites along the Baltic Sea salinity gradient. Thus, other
77 environmental factors are of less importance in shaping the communities. Because of the expected
78 decrease in diversity along the Baltic Sea we also expected to see a decrease in complexity of
79 interactions between microbial species in these communities as salinity falls. Testing this hypothesis
80 is realised by presenting networks at three selected sites covering a part of the salinity gradient. We
81 expected larger differences among the microbial communities (sites) than among temporal sampling
82 points within the same site.

83

84 **Materials and methods**

85 *Sediment sampling*

86 Samples for assessing spatial variation in microbial community diversity were collected during
87 August 2018, at seven study sites representing a decrease in salinity (List, Saltö, Herslev, Gollwitz,
88 Öland, Tvärminne, Pori) in the North Sea and Baltic Sea (Fig. 1). At three of the sampling sites in the

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89 Baltic Sea with profound differences in salinity (Saltö, Herslev, Öland), samples for assessing
90 temporal variation were collected at four time points (August 2018, November 2018, April 2019,
91 August 2019). All sites were sampled from the coast at water depth 0-0.80 m, except Tvärminne
92 where sampling was performed by SCUBA at 3.8-5.0 m depth. Sediment was collected in three
93 replicate cores (5 cm diameter, min. 15 cm depth). After draining, two technical replicates were
94 collected from each core. Samples were taken from the central region of the core (avoiding the core
95 liner walls) by scraping off the top 5 mm of sediment (approx. 1.5 g), using sterile razor blades and
96 placed in sterile 1.5 ml microcentrifuge tubes. The sediment was preserved in 99% EtOH (Harry et
97 al. 2000) and kept frozen at -18°C until DNA extraction.

98 *Analysis of environmental factors*

99 Temperature was measured using handheld field thermometer (Frederiksen Scientific), salinity was
100 measured using ATACO handheld refractometer (resolution of 0.5 salinity units) and sediment
101 characteristics were recorded for each sampling point. Sediment characteristics (including water
102 content, porosity, organic content, carbon and nitrogen content, grain size and sorting) were
103 determined from three replicate cores per sampling station and analysed following Petersen et al., in
104 review.

105 *DNA extraction and amplification*

106 In this study three sampling replicates represent each sampling site/time, except for samples
107 Tvärminne, Gollwitz, Saltö August 2019, Herslev August 2018, and Öland November 2018, these
108 samples are represented by two sampling replicates and one technical replicate.

109 DNA from 250 mg of sediment per sample was extracted with DNeasy Powerlyzer PowerSoil Kit
110 (Qiagen) according to the manufacturer's protocol. Samples were lysed in Bead Ruptor Elite (OMNI
111 International) at 2500 rpm for 45 s with 750 µl of PowerBead solution (Qiagen). DNA concentration
112 was quantified using a Qubit 4.0 fluorometer with 1X dsDNA HS Assay Kit (Thermo Fisher,
113 Cambridge, UK). Bacterial 16S rRNA gene V1-V2 hypervariable regions were amplified using the
114 universal primers 27F (Ludwig et al. 1993) and 338R (Suzuki & Giovannoni 1996). To assess
115 diversity of the microbial eukaryotic community V4 hypervariable regions was chosen to amplify the
116 eukaryotic 18S rRNA gene. For this we used primer set UNonMetF and UNonMetR (Bower et al.
117 2004), combined with primers E572 and E1009R (Comeau et al. 2011). For primer details see
118 Supplementary Table 1. Reactions were performed in 25 µl volumes containing 12.5 µl of iQ™
119 SYBR® Green Supermix (2X) (Bio-Rad), 200 nM of each primer, 5.5-9.5 µl of nuclease-free water

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120 and 3 ng of template DNA or PCR product from UNonMet primer pair amplification for E572 forward
121 and E1009R reverse primers. All amplifications were performed in a CFX96 Touch™ Real-Time
122 PCR Detection System (Bio-Rad). Thermocycling protocols are shown in Supplementary Table 2.

123 *Library preparation*

124 A fusion PCR was performed to add the Ion Torrent PGM sequencing adapters: barcoded M13-tailed
125 IonA adapter, target specific P1 adapter and a target specific M13- linker primer (following Mäki et
126 al. 2016) (see Supplementary Table 3). Amplification was achieved with the following conditions:
127 95°C/5 min, (94°C/45 s, 53°C/1 min, 72°C/1 min)*13, followed by final elongation of 72°C/5 min.
128 Reactions (25 µl) consisted of 12.5 µl iQ™ SYBR® Green Supermix (2X) (Bio-Rad), 400 nM of
129 fusion primers (IonA forward and P1 reverse), 40 nM of target specific M13- linker primer, 8.5 µl of
130 nuclease-free water and 1 µl of PCR product from the 16S or 18S rRNA amplification step. Libraries
131 were purified with Quanta SparQ PureMag Beads system (Quantabio). Quality and molarity were
132 determined with Agilent 2200 TapeStation before pooling in equimolar concentration (22 pM). The
133 library pool was sequenced with Ion PGM system using an Ion 318 Chip Kit version 2 (Ion Torrent,
134 Life Technologies) at the University of Jyväskylä.

135 *Analysis of sequencing data*

136 Single-end raw sequence reads were sorted by barcode prior to exporting from the Ion Torrent Suite™
137 Software and trimmed to remove sequencing adapters using Cutadapt (version 1.18, Martin 2011).
138 Length filtering was performed using Cutadapt as follows: 16S: min. 150 bp, max. 400 bp; 18S: min.
139 32 bp max. 400 bp. Quality filtering was performed using FASTX toolkit (Gordon & Hannon 2010),
140 with a minimum quality score of 20 for a minimum of 80% of the bases in each read. Dereplication,
141 singleton and chimera filtering were performed using VSEARCH (version 2.15.1, Rognes et al.
142 2016). All datasets were aligned to the SILVA database (version 138, Yilmaz et al. 2014) using
143 Mothur (version 1.44.3, Schloss et al. 2009) before clustering using greedy 97% similarity threshold
144 in VSEARCH. Amplicon sequence variants (ASVs) were mapped using VSEARCH, at a similarity
145 of 95-97.5%. 16S datasets were classified to the SILVA SEED database (version 138, Yilmaz et al.
146 2014) using the Wang method (Wang et al. 2007) with 8 kmer and 80% similarity in Mothur. 18S
147 dataset was classified to the PR2 database (version 4.12.0, Guillou et al. 2013; del Campo et al. 2018)
148 using the BLAST method with 80% similarity in Mothur.

149 We used universal primers, standardised protocols and well curated public databases in order to
150 minimize potential technical biases such as PCR error, sequencing error, sequencing depth,

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151 bioinformatics analysis, and unassigned classification of the organisms (Guillou et al. 2013, Yilmaz
152 et al. 2014, del Campo et al. 2018). Nevertheless, the 16S spatial dataset generated 7.7% unclassified
153 OTUs, 16S temporal dataset generated 9.0% unclassified OTUs, 18S spatial dataset generated 27.1%
154 unclassified OTUs, 18S temporal dataset generated 34.1% unclassified OTUs at phylum/division
155 level. All unclassified OTUs at domain/kingdom were removed prior to further analyses. In addition,
156 in the 16S dataset, all OTUs assigned to “Chloroplast” at the order level, and in the 18S dataset, all
157 OTUs classified to phylum Metazoa, Rhodophyta and class Embryophyceae were removed.

158 *Statistical analysis*

159 All statistical analyses were performed in R version 3.6.3 (2020.02.29). To compensate for large
160 differences in read depth between the samples, all datasets were transformed by rarefaction to an even
161 read depth by repeatable random subsampling (read depth after rarefying in datasets: 16S spatial:
162 9773, 16S temporal: 15497, 18S spatial: 10957, 18S temporal: 7588), using the package ‘phyloseq’
163 (version 1.30.0, McMurdie and Holmes 2013). OTU table plots were made using ‘phyloseq’ package.
164 Alpha diversity (based on OTU richness and Shannon index) and beta diversity (based on Bray-Curtis
165 dissimilarity) measures, dbRDA and ENVFIT analyses based environmental variables were
166 performed in R using ‘vegan’ package (version 2.5-7, Oksanen et al. 2017). Redundant (i.e., highly
167 correlated) variables (water content and mean grain size) were removed on basis of ENVFIT analysis.
168 All plots were made using ‘ggplot2’ (version 3.3.0, Wickham 2016). Significant differentially
169 diversity matrices were detected using the Kruskal-Wallis test followed by Tukey HSD test for pair
170 wise comparison. Salinity gradient test on community structure was performed by subjecting Bray-
171 Curtis dissimilarity matrices in bacterial and microbial eukaryotic communities using the ‘adonis’
172 test from the ‘vegan’ package.

173 Network analysis was performed to show bacterial-eukaryote correlations and network properties
174 were computed using the “igraph” package (Csardi & Tamas Nepusz 2006) as described earlier
175 (Sapkota et al. 2020). We used only temporal datasets with high salinity (all temporal datasets from
176 Saltö), medium salinity (all temporal datasets from Herslev) and low salinity (all temporal datasets
177 from Öland). Spatial datasets representing lower number of replicates per salinity level (high,
178 medium, and low) were excluded. The bacterial and eukaryote OTU table was trimmed for low
179 abundant OTUs (<50 reads) and normalized as relative abundance counts per million using the
180 “edgeR” package (Robinson et al. 2010). Correlations on all OTU pairs were computed using rcorr
181 function from ‘Hmisc’ package and only highly significant ($p < 0.001$) correlated OTUs with
182 spearman’s rank correlations > 0.7 for positive correlations and < -0.7 for negative correlations, were

183 used for network graphics using a Fruchterman-Reingold layout with 999 permutations. In the
184 network, OTUs were set as nodes and the correlation as edges. Nodes (OTUs) with the highest number
185 of connections were used as keystone species in the network analysis. For the figures the 10 most
186 connected OTUs represent keystone species, and tables show the 5% of OTUs with most connections.

187 **Results**

188 *Environmental characteristics*

189 Salinity ranged between 33 and 6 among sites in the spatial study, highest at List and lowest at Pori.
190 For the temporal dataset, salinity ranged between 26 and 7, highest at Saltö and lowest at Öland. In
191 addition to salinity, most variation among spatial sites was seen in sediment temperature, water
192 content, and C/N variables; whereas temperature and C/N variables showed most variation among
193 the temporal samples. For details of environmental characteristics for the spatial and temporal
194 samplings see Supplementary table 4.

195 *Bacterial diversity*

196 In the spatial study, the observed number of OTUs per sample for the bacterial communities (16S)
197 ranged between 1300 and 735, highest at Saltö and lowest at List (Fig. 2A), and Shannon index for
198 each sampling site ranged between 6.2 and 4.3, highest at Saltö and lowest in Öland (Fig. 2A,
199 Supplementary Table 5a). Proteobacteria was the most dominant phylum at all sites, followed by
200 Cyanobacteria and Bacteroidota (Fig. 2C) except for the euhaline site List. At List, Patescibacteria
201 was the second relative abundant phylum, and for both List and Saltö this group was generally more
202 relatively abundant than at the remaining sites (Fig. 2C). The relative abundance of Cyanobacteria
203 was also high at all sites, however lowest at Saltö, and it was the second most relative abundant
204 phylum at Herslev, Gollwitz and Öland (Fig. 2C). Chloroflexi had highest relative abundance at
205 Öland, Tvärminne and Pori (Fig. 2C), compared with other sites. Relative abundance of
206 Gemmatimonadota was generally very low at all sites except for Pori (Fig. 2C).

207 Considering alpha diversity for the spatial dataset, only Shannon diversity was related to salinity,
208 according to both an ANOVA test (Supplementary table 6) and Pearson correlation (Supplementary
209 figure 1). Beta diversity was correlated with all environmental factors (Table 1), however when
210 represented by dbRDA (Fig. 3A), List and Saltö clustered closest together with a positive relation to
211 sorting, salinity and C/N ratio, and negative relation to water content explaining their placement.
212 Herslev and Gollwitz formed a discrete cluster, and Öland and one replicate of Tvärminne clustered
213 together but not as closely, while the remaining replicates of Tvärminne and Pori were placed within

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214 proximity to each other along the same axis. Herslev and Gollwitz were grouped by high organic
215 matter and temperature, and the Öland and Tvärminne cluster was grouped by high water content,
216 well sorted sediment, and low salinity and C/N ratio (Fig. 3A). Pori and the two replicates of
217 Tvärminne were characterised by low organic matter and low temperature at the time of sampling
218 (Fig. 3A). Analysis of distance-decay, which tests if communities become more dissimilar with
219 increasing distance, for bacterial communities along the extent of the Baltic Sea covered in the spatial
220 part of the study showed a strong relationship (Supplementary figure 2A, B & C).

221 In the temporal study, observed OTUs in bacterial communities (16S) ranged between 2122 and 1058
222 (Fig. 4A). Shannon index ranged between 6.5 and 4.5 and Öland showed significant lower diversity
223 compare to Saltö and Herslev (Fig. 4A, Supplementary table 5B). As seen in the spatial part of the
224 study, Proteobacteria was the most dominant phylum at all sampling sites, followed by
225 Cyanobacteria and Bacteroidota, except for Saltö where Patescibacteria had a higher relative
226 abundance (Fig. 4C). Generally, the distribution and relative abundance of phyla followed the same
227 patterns at each sampling time for each sampling site, respectively (Fig. 4C). There were, however,
228 some fluctuations in the relative abundance following the seasonal cycle; Proteobacteria showed a
229 peak in relative abundance in the April 2019 sampling at both Saltö (S3) and Herslev (H3), and
230 Actinobacteria was highest in November 2018 at both Herslev (H2) and Öland (Ö2) (Fig. 4C).
231 Additionally, Actinobacteriota was relatively more abundant at Herslev and Öland compared to Saltö
232 at all sampling times. Desulfobacterota had a lower relative abundance in April 2019 at Saltö (S3)
233 compared to the other sampling dates and had lowest relative abundance at Öland at all times
234 compared to the other sites.

235 Considering alpha diversity of the temporal dataset, ANOVA test showed that only Shannon diversity
236 was related to salinity (Supplementary table 6), however Pearson correlation showed that both
237 observed, and Shannon diversity were correlated to salinity (Supplementary figure 1). In the beta
238 diversity analysis, each site formed its own cluster in the dbRDA plot, but temporal samples from
239 Herslev clustered more closely together than did the temporal samples from the other sites (Fig. 3C).
240 Though the beta-diversity of bacterial dataset was correlated to all environmental factors (Table 1),
241 Saltö August 2018 (S1) and 2019 (S4) were best characterised by a positive relation to salinity and
242 sorting, and November 2018 (S2) and April 2019 (S3) were better characterised by higher C/N ratio,
243 water content and lower temperature in the dbRDA (Fig. 3C). Variation between samples at Herslev
244 was related to sediment temperature, water content and C/N ratio, and variation between samples at
245 Öland was related to organic matter (Fig. 3C). Analysis of distance-decay for bacterial communities

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246 along the extent of the Baltic Sea included in the temporal dataset showed a strong relationship
247 (Supplementary figure 2A & B).

248 Analysis of correlation between salinity and bacterial OTUs showed both positive and negative
249 relationships (Supplementary table 7). Especially several OTUs assigned to genus *Candidatus*
250 *Kaiserbacteria*, showed positive correlation to the salinity gradient.

251

252 *Microbial eukaryote diversity*

253 In the spatial study of microbial eukaryote diversity (18S), observed number of OTUs per sample
254 ranged between 619 and 146 (Fig. 2B), and Shannon index ranged between 4.6 and 1.9 (Fig. 2B).
255 Ochrophyta had high average relative abundance and was the most abundant phylum/division at all
256 sites except Herslev and Gollwitz (Fig. 2D). Ciliophora was the highest relative abundant
257 phylum/division at Gollwitz, and in Herslev, Dinoflagellata had highest relative abundance (Fig. 2D).
258 Alveolata, Apicomplexa, and Fungi had highest relative abundance in the mesohaline sites Gollwitz,
259 Öland, Tvärminne and Pori, and these sites, together with Saltö, also had high relative abundance of
260 Ciliophora (Fig. 2D). Abundance of unclassified eukaryotes was high in the datasets from List and
261 Gollwitz. Neither observed richness nor Shannon diversity of the spatial dataset were related to
262 salinity in both ANOVA test and Pearson correlation (Supplementary table 6, Supplementary figure
263 1 & 3). However, beta diversity was correlated to salinity, together with C/N ratio and water content
264 (Table 1). The dbRDA (Fig. 3B) showed List to cluster together with Öland and one replicate from
265 Saltö and was somewhat close to the Herslev samples also, best described by high C/N ratio, water
266 content and organic matter. The remaining samples from Saltö and Gollwitz were placed somewhat
267 close together, characterised by high organic matter, C/N ratio and poor sorting (Fig. 3B). Tvärminne
268 and Pori formed a distinct cluster mainly characterised by low salinity and temperature, and well
269 sorted sediment (Fig. 3B).

270 For the temporal study of eukaryotes (18S), between 711 and 136 OTUs were captured (Fig. 4B), and
271 Shannon index ranged between 5.1 and 1.6 (Fig. 4B, Supplementary table 5B). Ochrophyta was the
272 most relatively abundant phylum/division in the April 2019 and August 2019 samplings for all sites,
273 except for Öland August 2019, where it was the second most relative abundant, exceeded by
274 Dinoflagellata (Fig. 4D). Ochrophyta was also most relative abundant in August 2018 for both Saltö
275 and Öland (S1 and Ö1) (Fig. 4D). Dinoflagellata was the most relatively abundant phylum/division
276 in the samples from Herslev August 2018 (H1) and November 2018 (H2), as well as Saltö November

277 2018 (S2) (Fig. 4D). The most relatively abundant phylum/division at Öland in November 2018 (Ö2)
278 was Fungi (Fig. 4D). Abundance of unclassified eukaryotes was especially high in the datasets from
279 Saltö. Both alpha diversity measures were significantly correlated to salinity (see Supplementary table
280 6). Community structure was influenced by salinity, as well as temperature, C/N ratio, mean grain
281 size and sediment sorting (Table 1). In the dbRDA plot samples were in general scattered with only
282 little clustering of sites, especially for Herslev and Öland (Fig. 3D), indicating more temporal changes
283 than seen in the bacteria communities (Fig. 3C). For most locations, samples from August for two
284 consecutive years were somewhat similar. For example, Saltö August 2018 (S1) and 2019 (S4)
285 samples clustered together characterised by high temperature, organic matter, and poor sorting.
286 Similarly, August 2018 and 2019 for Herslev (H1 and H4) and Öland (Ö1 and Ö4) were placed closely
287 together, somewhat more like the samples from November or April from those stations compared to
288 Saltö (Fig. 3D). For Saltö, samples from November and April formed a distinct cluster described by
289 different environmental factors than those from August samples, specifically high water content and
290 temperature (Fig. 3D). Temperature was an obvious explanatory variable for the observed community
291 patterns, but also salinity, C/N ratio and sediment sorting were important for the differences in
292 eukaryote communities seen in the dbRDA plots. However, analysis of distance-decay for eukaryote
293 communities along the extent of the Baltic Sea covered in this study only showed a weak correlation
294 for the temporal dataset (Supplementary figure 2C).

295 Analysis of correlations between salinity and eukaryote OTUs only revealed five positive correlations
296 and one negative correlation (Supplementary table 7). In our eukaryote datasets, a large proportion
297 of OTUs could not be classified to phylum/division level at 80% similarity. This is most likely due
298 to incomplete microbial eukaryote coverage in the database; since the benthic microbes historically
299 have received less scientific attention than the pelagic ones, a large proportion of benthic microscopic
300 eukaryotes are expected to be missing from the databases (Forster et al. 2016, Zhang et al. 2018).

301 *Microbe-Microbe interactions shown as networks*

302 To explore bacteria-eukaryote interactions in different salinity environments, we used the temporal
303 dataset and visualised co-occurrence at three different salinity levels as network graphs (Fig. 5).
304 Interestingly, we found distinct co-occurrence patterns in networks from the three different salinity
305 levels. At highest salinity level, co-occurrence networks were strongest, having the more connections
306 compared to networks for the other two salinity levels. Similarly, the lowest salinity level showed the
307 least connections revealing fewer eukaryote-bacteria interactions, and co-occurrence network for the
308 medium salinity level was in between the other two. Several bacterial and eukaryote OTUs were

309 identified as the keystone species based on the highest number of connections that they showed in the
310 co-occurrence networks (for details see Supplementary table 8A, B & C). In particular, Raphid-
311 pennate diatoms (Stramenopiles) appeared several times as keystone eukaryotic species in all three
312 networks. Also, bOTU607 (a member of Rhodobacteraceae) appeared as a keystone species in two
313 networks.

314

315 **Discussion**

316 Using amplicon sequencing, we surveyed microbial communities of shallow coastal sediments on
317 both a large spatial scale in the Baltic Sea and the adjacent North Sea, and a temporal scale in a subset
318 of these communities. We examined diversity patterns of bacterial communities as well as among
319 microbial eukaryotes, and the correlations between the two kingdoms. Because the two taxonomic
320 groups could respond differently to environmental factors, we evaluated the relationship of diversity
321 patterns to selected environmental factors, particularly salinity, temperature, and sediment
322 characteristics for both groups. These analyses suggested that salinity is a strong driver of diversity
323 of microbial communities, however, salinity is not the only driver, as sediment characteristics,
324 nutrients, and temperature also were important. In addition, our results revealed significant
325 interactions and relationships among several bacterial and eukaryote OTUs. This study provides a
326 broader description of coastal benthic microbial communities and their interactions at shallow sites
327 in the Baltic.

328 *Baltic Sea salinity gradient affects bacterial and microbial eukaryote communities*

329 Though the ANOVA test showed that OTU richness for bacteria was not affected by
330 salinity for either dataset, Shannon diversity of these communities was significantly affected by
331 salinity. Moreover, we did see a significant positive correlation for both diversity measures using
332 Pearson's correlation on the temporal dataset (Supplementary figure 3). This suggests that the missing
333 correlation between salinity and observed OTUs for the spatial dataset could be due to too few data
334 points. Likewise, distance-decay showed beta-diversity of both bacterial datasets were positively
335 correlated with distance between communities, hence when distance increases the communities
336 become more dissimilar along the gradient (Supplementary figure 1A, B & C). While salinity was a
337 significant driver of beta diversity for bacteria, it might not be an equally strong driver of diversity
338 patterns at all sites. As reflected in the dbRDA (Fig. 3A and C), the communities at the sites with
339 highest salinity (List and Saltö) were described to a higher degree by salinity, however the

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340 communities at lower salinities were not to a high degree described by salinity, except for Öland
341 which was to some degree described by lower salinity. Despite the coarse sampling, we did observe
342 patterns across the salinity gradient: highest diversity was found at the eu- and polyhaline sites (List
343 and Saltö), a diversity minimum at the mesohaline sites (Öland and Tvärminne), followed by a slight
344 increase in diversity at the site with the mesohaline site of lowest salinity (6) (Pori). This suggests
345 that bacterial communities at the sites of highest salinity are more diverse and evenly distributed than
346 communities in the mesohaline. This pattern suggests that estuarine bacterial communities could be
347 adapted to lower salinity. The pattern we observed supported previous findings in the Baltic Sea,
348 where bacterial communities in the mesohaline consisted mainly of bacterial lineages with a broad
349 salinity tolerance (Klier et al. 2018).

350 Although the bacterial taxonomic composition was dominated by the same phyla at all samplings
351 (both spatial and temporal), there were some differences between the salinity extremes.
352 Patescibacteria had highest relative abundance at the eu- and polyhaline sites, List and Saltö,
353 especially genus *Candidatus Kaiserbacteria*, showed several OTUs positively correlated to salinity,
354 indicating better conditions for this group at higher salinities. However, a few OTUs assigned to
355 *Candidatus Kaiserbacteria* also showed a negative correlation to salinity, highlighting the complexity
356 in bacterial diversity. Cyanobacteria generally were abundant at all sites except at the eu- and
357 polyhaline ones (List and Saltö), indicating better conditions for these taxa at lower salinities.
358 However, individual OTUs of Cyanobacteria also showed both positive and negative correlation to
359 salinity, except most OTUs of *Synechococcales* showed a negative correlation, indicating that this
360 group might favour low salinities. The same argument could be made for phylum *Chloroflexi*, which
361 had highest relative abundance at the low salinity sites (Öland, Tvärminne and Pori), a trend also
362 previously observed for sublittoral bacterial communities in the Baltic Sea (Klier et al. 2018). Several
363 OTUs of *Chloroflexi* was negatively correlated to salinity, thus favouring low salinity, especially
364 OTUs of the obligate anaerobe genus *Anaerolinea*, indicating that the low salinity sites are also
365 affected by low oxygen. *Gemmatimonadota* had low abundance at all sites except the one with lowest
366 salinity (Pori), and three OTUs of family *Gemmatimonadaceae* (member of phylum
367 *Gemmatimonadota*) were negatively correlated to salinity, indicating a negative affiliation to salinity.
368 However, other local factors, such as lack of associated phytoplankton (Mujakić et al. 2021) may also
369 have an influence on this particular phylum.

370 The spatial patterns we found for microbial eukaryotes were like those for bacterial communities:
371 salinity played an important role, but it was not the only driver of benthic marine microbial eukaryote

Benthic microbes along salinity gradient

372 community composition and diversity. We observed no clear trends in alpha diversity related to
373 salinity for either eukaryote dataset, but both OTU richness and Shannon diversity of the temporal
374 dataset was significantly affected by salinity (Table 1) in the ANOVA test, although we did not see a
375 correlation for either eukaryote dataset using Pearson's correlation. This suggests the changes were
376 not continuous, but rather in steps. Neither did we see a relation to distance, which could have been
377 expected to follow somewhat the same diversity trend as salinity. We did however observe a weak
378 correlation along the extent of the Baltic Sea when using the temporal samples. There were also some
379 systematic changes in taxonomic composition along the Baltic Sea and its salinity gradient, e.g., while
380 Alveolata, Apicomplexa and Fungi were present at all sites, the three phyla were more abundant in
381 sites with lower salinity. This indicates that lower salinities are a more favourable condition for these
382 taxa, and, for example, supports earlier findings that fungal communities are adversely influenced by
383 salinity (Mohamed & Martiny 2011, Tisthammer et al. 2016). Nevertheless, only one OTU
384 (unclassified Cercozoa) was significantly negatively correlated to salinity. Additionally, only a few
385 OTUs showed a positive correlation to salinity, representing the orders Cercozoa, Bacillariophyta and
386 Apusomonadidae.

387 *Temporal patterns influence microbial assembly*

388 Seasonal fluctuations in the bacterial communities' OTU richness and Shannon diversity were
389 observed at all sampling sites, but with no shared patterns between sites. In the summer samples
390 (August 2018 and 2019), communities were more similar in comparison to other times of the year
391 (Fig. 3C), except for Herslev. Changes in the abundance of several phyla during the seasonal cycle
392 were also described, however, no clear trends were observed common to all sites. These cyclic
393 changes support previous assumptions of seasonal effects on both benthic and planktonic bacterial
394 communities in the Baltic Sea (Vetterli et al. 2015, Herlemann et al. 2016). The inconsistency
395 between sites suggests that the seasonal changes are shaped locally, rather than on a larger regional
396 climatic scale, or that local factors modify a possible common seasonal pattern.

397 In contrast to the bacterial communities, eukaryote communities seem to have more variation in
398 taxonomic composition on a temporal scale, with each site having their own distinctive pattern,
399 supporting previous observations of microbial eukaryote communities on a smaller geographic scale
400 in the Baltic Sea (Salonen et al. 2018). Additionally, fluctuations in richness were observed at all sites
401 over the season. The eukaryote communities potentially cover more functional groups compared with
402 bacteria (Reynolds 2006), some of which could be favoured at different environmental conditions.

Benthic microbes along salinity gradient

403 The bacterial community may therefore be more resilient to environmental fluctuations, which could
404 explain the differences in patterns, especially the variation in species composition, between bacteria
405 and microbial eukaryotes observed here. However, changes in diversity could be present on a lower
406 taxonomic level e.g., genus level, which will not be reflected in our overview at phylum level.
407 Furthermore, some of the organisms may be represented by dormant stages, especially among
408 microbial eukaryotes (Marcus & Boero 1998), or inactive or even dead organisms added from
409 surrounding water masses (Stoeck et al. 2007) which could be evident in the two organismal groups
410 differently. Although temporal fluctuations were observed in the benthic microbial eukaryote
411 communities, there were no consistent seasonal trends in the species composition, such as signal of
412 spring bloom of either pelagic diatoms or dinoflagellates as earlier observed in benthic microscopic
413 eukaryote communities in the north-eastern Baltic Sea (Salonen et al. 2018). However, the eukaryote
414 community at Herslev in August 2018 had lower alpha diversity than other temporal samples, and
415 was dominated by Dinoflagellata and Chlorophyta, which was distinctly different from the other
416 samples that were largely dominated by Ochrophyta, suggesting that the August 2018 community
417 may have been influenced by blooming dinoflagellates in Herslev.

418 *Inter-kingdom networks contributing to community structure*

419 The diversity of communities is likely not only influenced by environmental factors, but also by
420 competition and predation within the communities. These interactions and the structure of the
421 community, in turn, may be affected by changes in community composition and diversity. We found
422 both positive and negative correlations among bacterial and eukaryote OTUs. The most connected
423 OTUs, putatively regarded as the keystone species, belong to both bacteria and eukaryotes. A few
424 keystone eukaryotes did signify their role in microbe-microbe interactions by having several or only
425 negative correlations. Furthermore, the communities of the low salinity site (Öland) were dominated
426 by a few keystone eukaryotes with only negative correlations, which could indicate a top-down
427 regulated system. The communities of high (Saltö) and medium salinity (Herslev) sites exhibited
428 more complex networks (more OTUs) with higher connectivity; also, keystone species of these
429 communities had more connections, compared to those in the site of low salinity (Öland). This suggest
430 that the communities were functionally affected by either salinity, or by distance from the entrance
431 of the Baltic. This network analyses provides a first insight into the bacteria-eukaryote interactions in
432 benthic sediment communities in the Baltic Sea, however, much remains unknown about these
433 community interactions, not least of which the mechanisms and biological nature of these
434 interactions.

435 *Association with environmental factors other than salinity*

436 Apart from salinity, other environmental factors also affected the diversity of microbial benthic
437 communities. Sediment nutrient composition had a strong influence on the bacterial community
438 diversity, with organic matter being an important driver on the spatial scale, together with temperature
439 (at the mesohaline sites Herslev, Gollwitz, Pori and two replicates of Tvärminne) (Fig. 3A). On the
440 temporal scale, seasonal change in temperature was also an important driver between summer
441 (August) communities and communities from colder winter and spring periods (November and April)
442 (Fig. 3C). Changes in sediment characteristics were also important in explaining temporal changes.
443 C/N ratio and sediment characteristics were mainly related to changes in community at the polyhaline
444 site (Saltö), while changes at the mesohaline site Herslev were better characterised by changes in
445 temperature together with C/N ratio. At the other mesohaline site, Öland, the community was more
446 driven by changes in organic matter and sediment characteristics. For eukaryote communities the
447 roles of environmental variables other than salinity have been described previously (Salonen et al.
448 2018, Zhang et al. 2018). Similar patterns were seen in the temporal communities in the present study,
449 where composition over the year was driven to a higher degree by change in temperature, C/N ratio,
450 organic matter and sorting, than it was by temporal changes in salinity. On a spatial scale, we found
451 no clear patterns common to both eukaryote datasets for any of the sites.

452 **Conclusion**

453 This study provides an insight into the diversity of coastal sediment bacterial and microbial eukaryote
454 communities in the Baltic Sea, on a broad spatial scale as well as over a seasonal cycle along the
455 natural salinity gradient. We found salinity to be among the strongest drivers of both bacterial and
456 eukaryote communities; however, not an equally strong factor for all communities; beta-diversity of
457 mesohaline communities was better described by temperature, nutrients, and sediment characteristics.
458 Bacteria and eukaryote communities also differed from each other, and thus, their species diversity
459 respond differently to the same environmental conditions. The communities may however not only
460 be influenced by external environmental factors, but also be affected by competition and predation
461 within the communities. Analysis of bacteria-eukaryote networks provide a first insight into the
462 microbial interactions in benthic sediment communities in the Baltic Sea. We found network
463 complexity and connectivity to be higher in the communities of high salinity, but were functionally
464 affected by salinity, showing distance decay. A more in-depth look at the community composition

465 patterns at genus rather than phylum level could further elucidate bacterial and microbial eukaryote
466 interactions in Baltic Sea sediments.

467

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487

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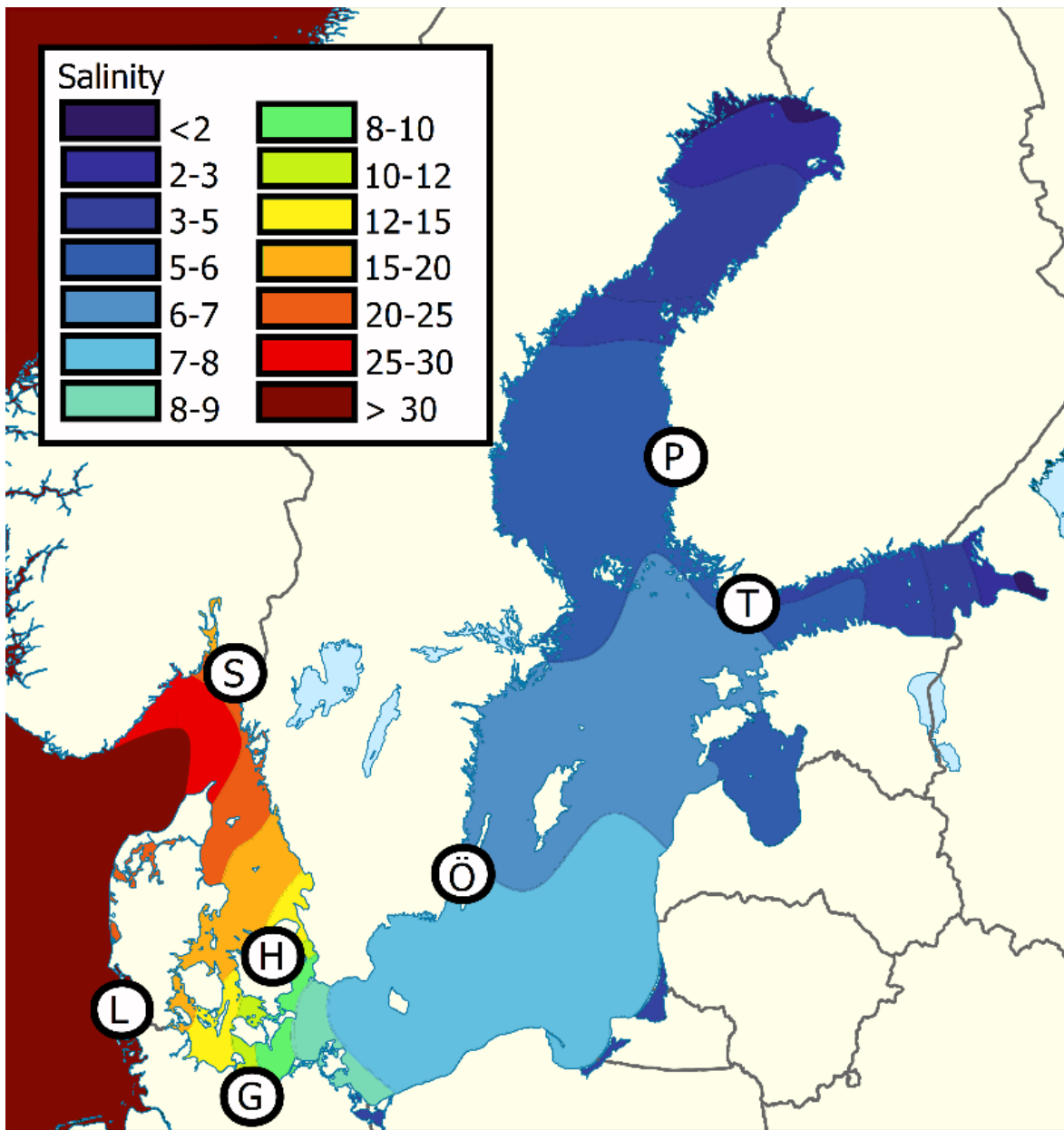
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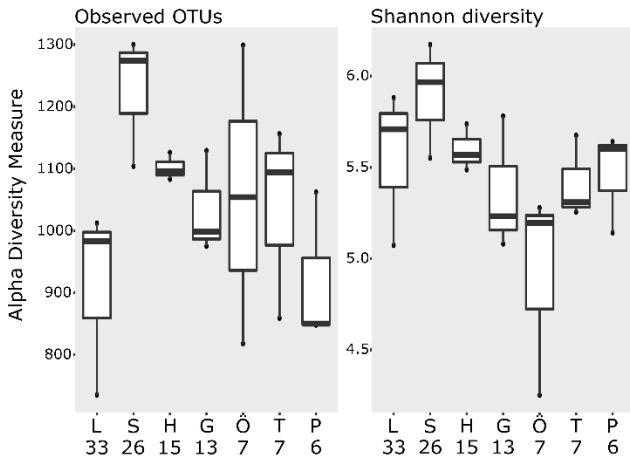
642 **Figure 1.**



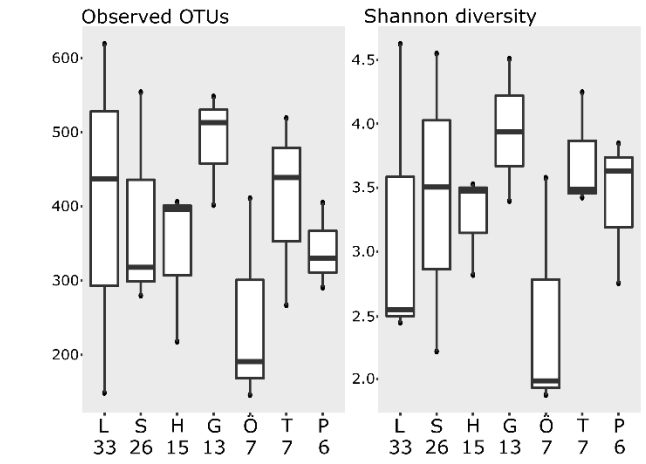
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644 **Figure 2.**

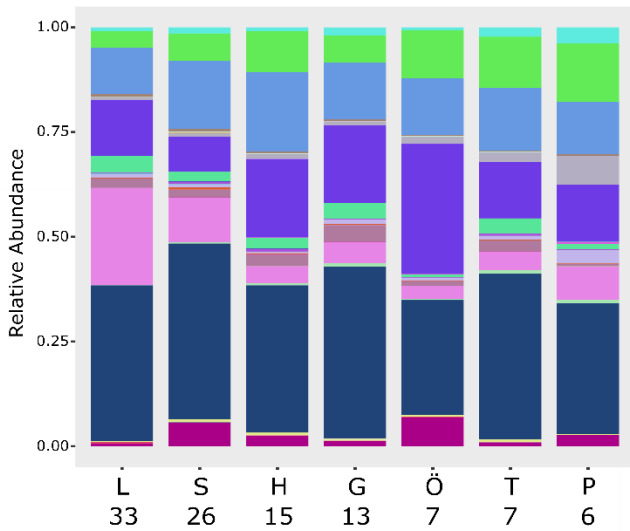
A) Bacteria



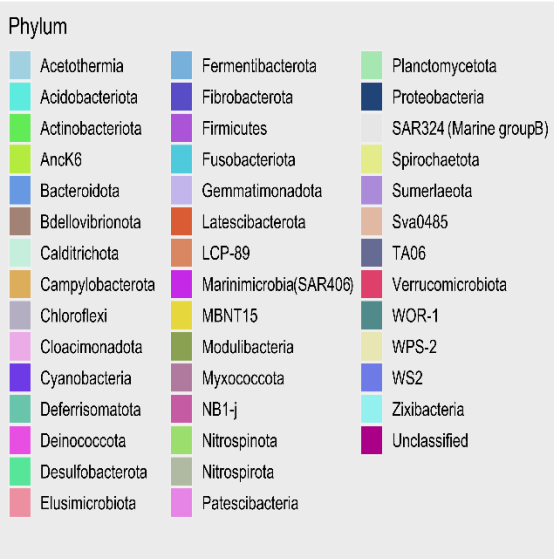
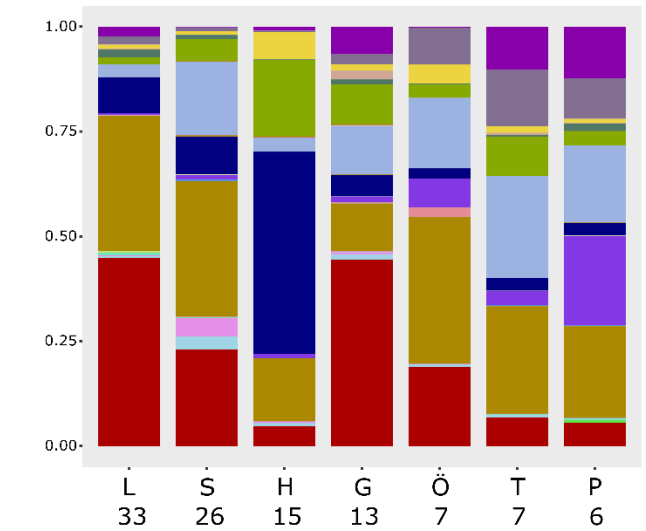
B) Eukaryotes



C) Bacteria

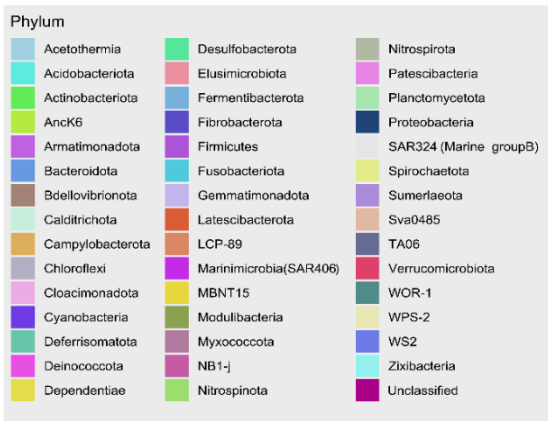
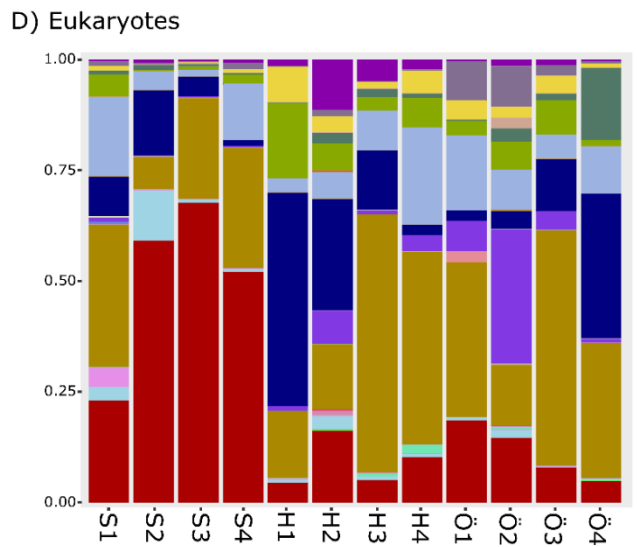
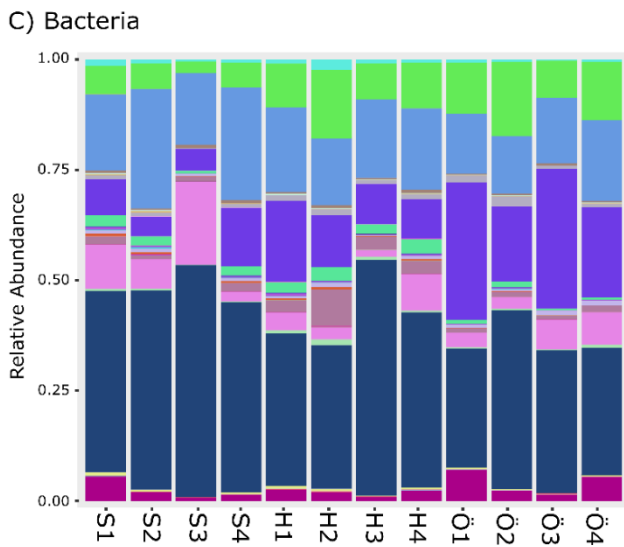
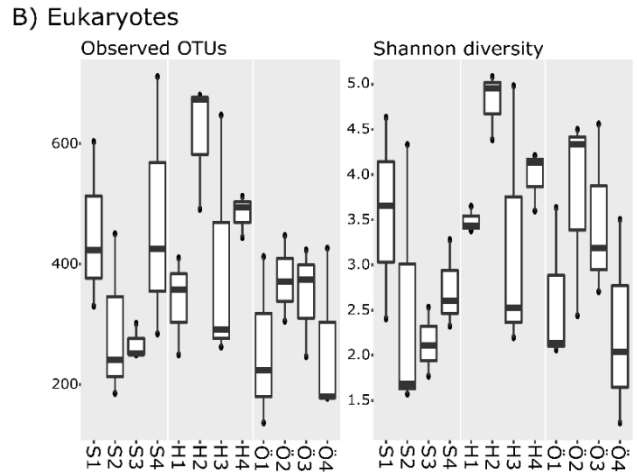
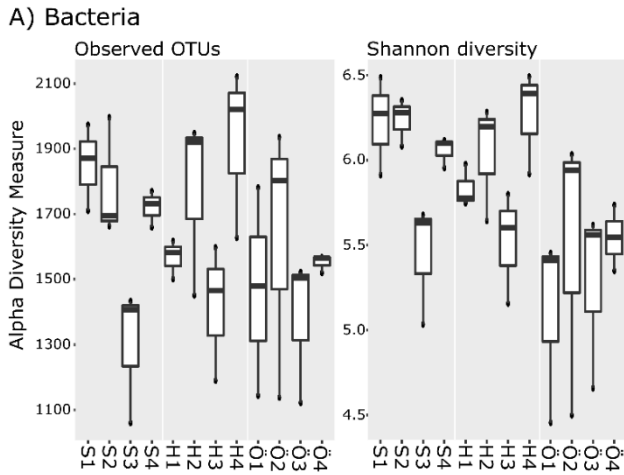


D) Eukaryotes



Benthic microbes along salinity gradient

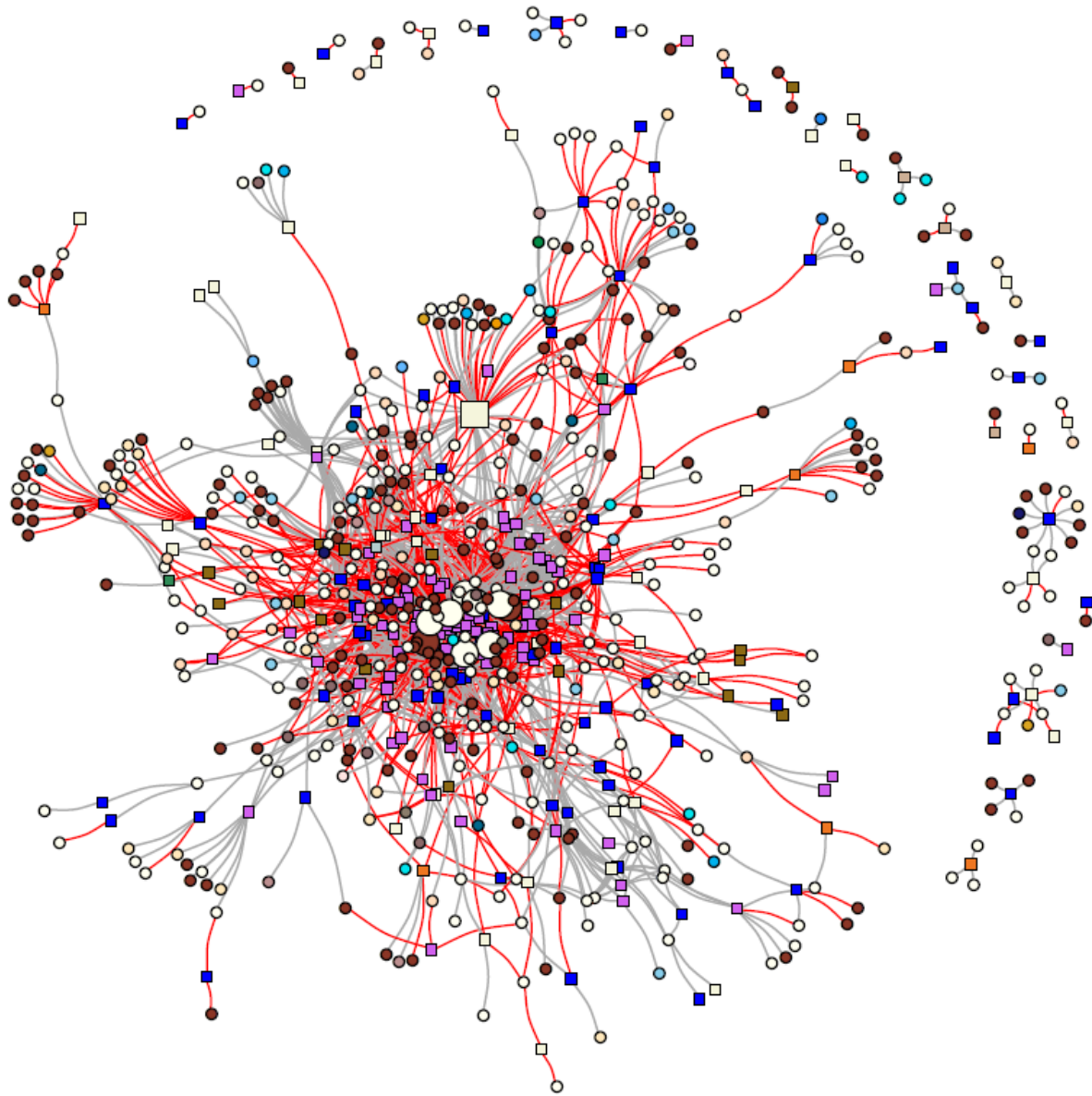
649 **Figure 4.**



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651

652 **Figure 5a.**

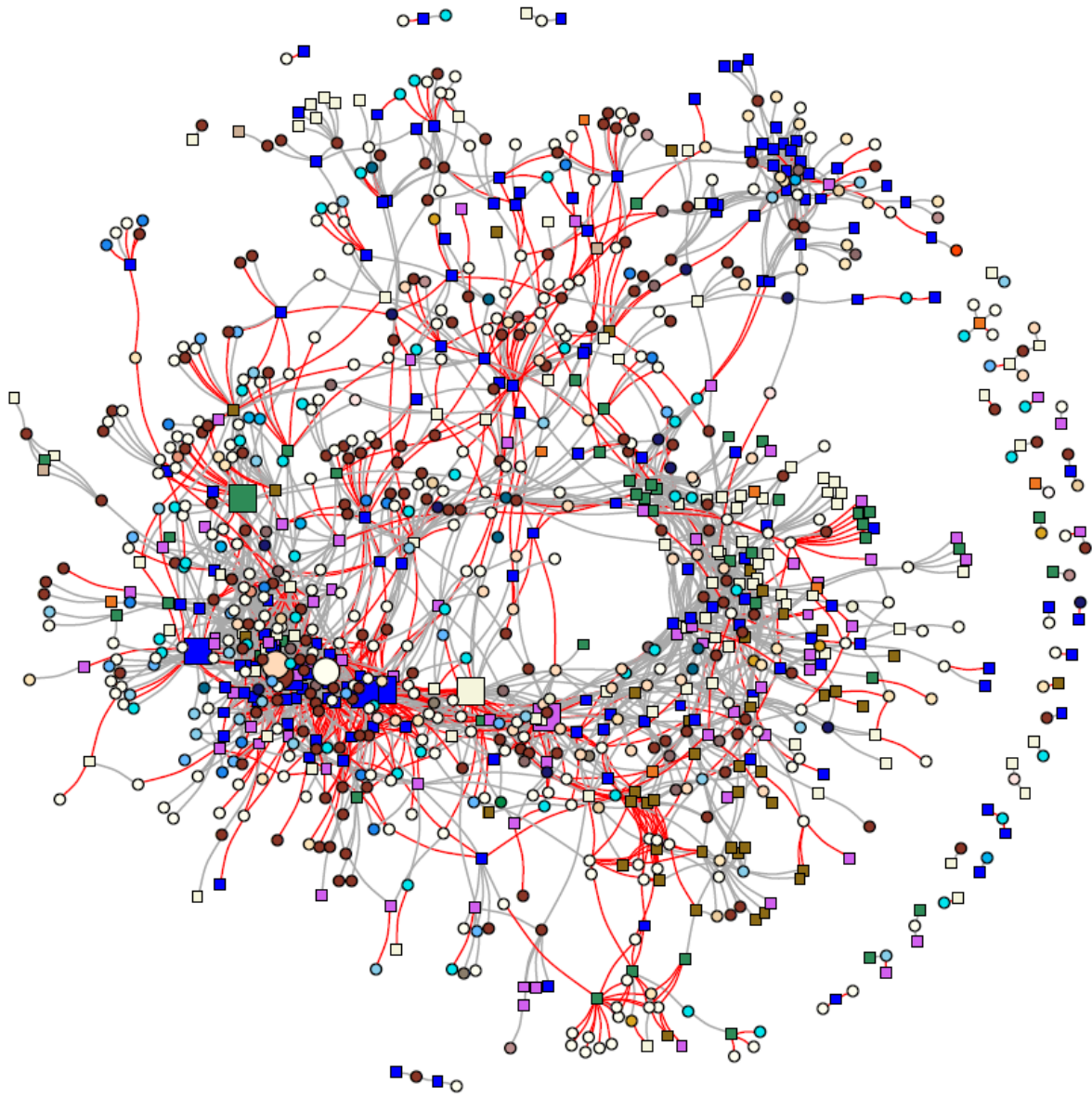


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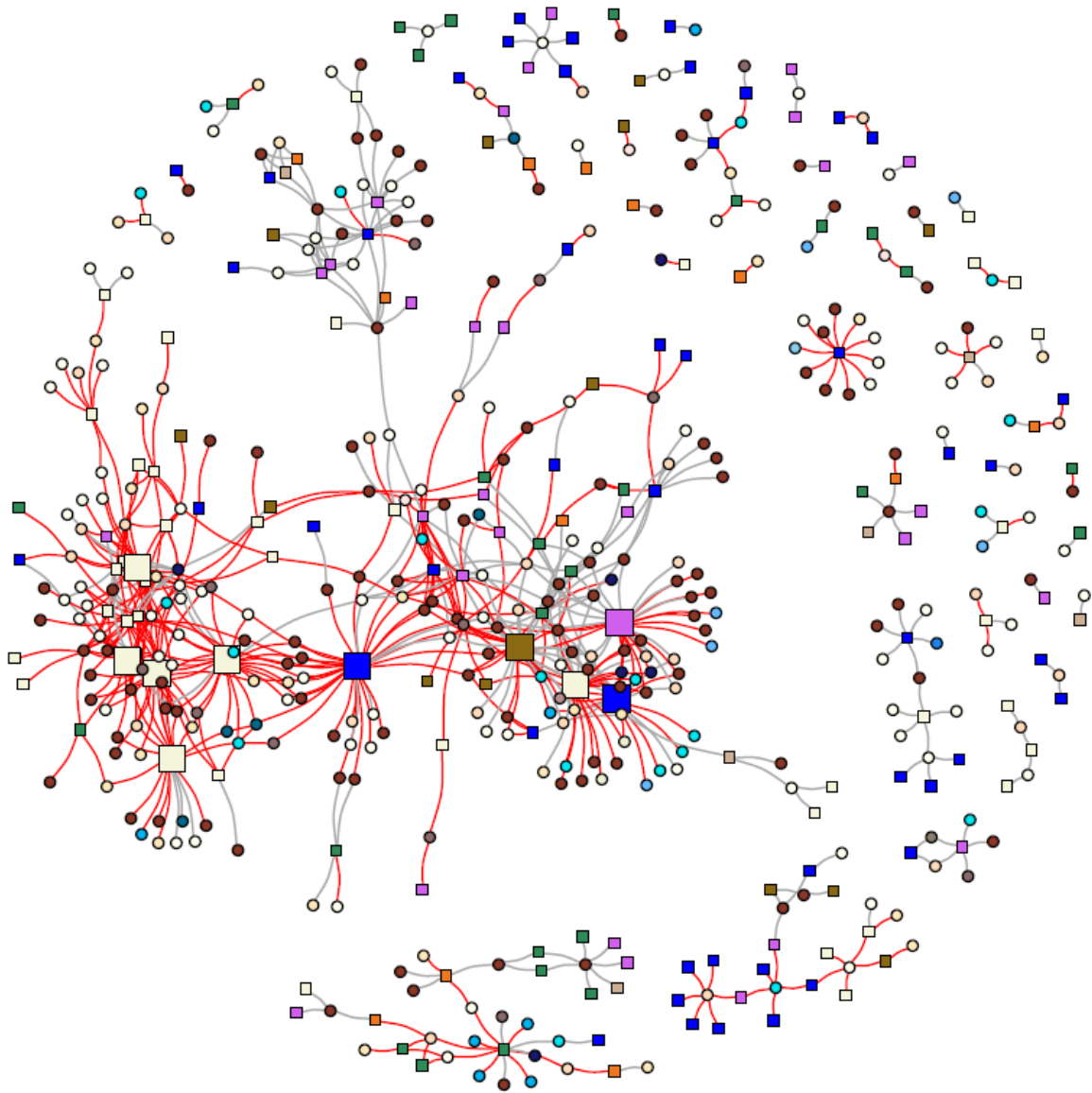
655

656 **Figure 5b.**



657

658 **Figure 5c.**



659

Benthic microbes along salinity gradient

Eukaryotes

- Eukaryota_unclassified(0)
- Alveolata
- Rhizaria
- Archaeplastida
- Stramenopiles
- Opisthokonta
- Hacrobia
- Amoebozoa

Bacteria

- Proteobacteria
- Bacteroidota
- Cyanobacteria
- Latescibacterota
- Patescibacteria
- Bdellovibrionota
- Actinobacteriota
- Spirochaetota
- ZUnclassified
- Fibrobacterota
- Desulfobacterota
- Gemmatimonadota
- Acidobacteriota
- Anck6
- Campylobacterota
- Chloroflexi
- Planctomycetota
- Myxococcota
- Sva0485
- Marinimicrobia_(SAR406_clade)

660

661

662 **Table 1.**

Factors	Bacteria spatial	Eukaryotes spatial	Bacteria temporal	Eukaryotes temporal
Salinity	0.22***	0.08*	0.29***	0.07***
Temperature	0.09***	ns	0.05**	0.06**
C/N ratio	0.07**	0.08*	0.09***	0.05**
Org. matter	0.12***	ns	0.07***	ns
Water content	0.09***	0.08**	0.05**	ns
Porosity	0.07**	ns	0.07**	ns
Mean grain size	0.10859**	ns	0.09814***	0.05437**
Sediment sorting	0.17089***	ns	0.19869***	0.06962**

663

664

665 **Figure legends**

666 **Figure 1.** Map of the Baltic Sea and the adjacent North Sea, including sampling sites: L (List), S
667 (Saltö), H (Herslev), G (Gollwitz), Ö (Öland), T (Tvärminne), P (Pori). Salinity gradient based on
668 Snoeijs-Leijonmalm and Andrén (2017).

669 **Figure 2.** Spatial patterns of microbial diversity of A, C) bacteria (16S), and B, D) microbial
670 eukaryotes (18S), per site in: L (List), S (Saltö), H (Herslev), G (Gollwitz), Ö (Öland), T (Tvärminne),
671 P (Pori). A) observed number of OTUs and alpha diversity index, Shannon Diversity, in bacteria
672 (16S) and B) observed number of OTUs and Shannon Diversity, in eukaryotes (18S), note y-axes are
673 not equal. C) average relative abundance of phyla/divisions in bacteria (16S) and D) eukaryotes (18S).

674 **Figure 3.** Distance based Redundancy Analysis (dbRDA) based on Bray-Curtis dissimilarity of
675 bacteria (16S) on spatial (A) and temporal scale (C) and microbial eukaryotes (18S) on spatial (B)
676 and temporal scale (D). A) Sediment characteristics represented by vectors sorting and porosity, B)
677 with sediment characteristics represented by vectors water content and sorting, C) and D) with all
678 sediment characteristics represented; note axes are not equal.

679 **Figure 4.** Temporal patterns of microbial diversity of A, C) bacteria (16S), and B, D) microbial
680 eukaryotes (18S), per site and collection time. Abbreviations of sample site and time: S1 (Saltö
681 August 2018), S2 (Saltö November 2018), S3 (Saltö April 2019), S4 (Saltö August 2019), H1
682 (Herslev August 2018), H2 (Herslev November 2018), H3 (Herslev April 2019), H4 (Herslev August
683 2019), Ö1 (Öland August 2018), Ö2 (Öland November 2018), Ö3 (Öland April 2019), Ö4 (Öland
684 August 2019). A) Observed number of OTUs and alpha diversity index, Shannon Diversity, in
685 bacteria (16S) and B) observed number of OTUs and Shannon Diversity, in eukaryotes (18S); note
686 y-axes are not equal. C) Average relative abundance of phyla/divisions in bacteria (16S) and D)
687 eukaryotes (18S).

688 **Figure 5.** Networks of microbial communities estimated from temporal samples; bacterial OTUs
689 represented by circles, microbial eukaryote OTUs represented by squares, assignment to specific
690 OTUs indicated in legends. Keystone species (OTUs with highest number of connections) indicated
691 by larger symbols (see supplementary Tables 8A-C). Negative correlations indicated by red
692 connections (lines) and positive correlations indicated by grey connections (lines). **Figure 5a**
693 Communities at the high salinity site Saltö. **Figure 5b** Communities at the medium salinity site
694 Herslev. **Figure 5c** Communities at the low salinity site Öland.

695 **Table 1.** Correlation of community diversity with measured environmental variables for the spatial
696 and temporal datasets calculated with Adonis on Bray-Curtis distance matrices for bacterial and
697 microbial eukaryote community dissimilarity assessment using 1000 permutations on environmental
698 parameters. Values indicate R², asterisks indicate significance level, *=p<0.001, **p=0.01,
699 ***p=0.001, ns=not significant.

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Benthic microbes along salinity gradient

705 **Supplementary table 1.** Table of primers.

Primer pair	Sequences	Amplicon size	Reference
16S 27F + 338R	F: 5'-AGA GTT TGA TCM TGG CTC AG-3'	311 bp	Ludwig et al. 1993, Suzuki and Giovannoni 1996
V1-V2	R: 5'-ATT ACC GCG GCT GCT GG-3'		
18S UNonMetF+ UNonMetR	F: 5'-GTG CCA GCA GCC GCG-3'	600 bp	Bower et al. 2004
V4	R: 5'-TTT AAG TTT CAG CCT TGC G-3'		
E572 + E1009R	F: 5'-CYG CGG TAA TTC CAG CTC-3'	400 bp	Comeau et al. 2011
	R: 5'-CRA AGA YGA TYA GAT ACC RT-3'		

706

707 **Supplementary table 2.** Thermocycling protocols for each target.

	UNonMetF/ UNonMetR	E572/E1009R
PCR conditions	1. 94°C, 2 min	1. 94°C, 2 min
	2. 94°C, 10 s	2. 94°C, 30 s
	3. 51,1 °C, 30 s	3. 55 °C, 30 s
	4. 72°C, 1 min	4. 72°C, 1 min
	5. 72°C, 5 min	5. 72°C, 5 min

708

709 **Supplementary table 3.** Target specific M13-linker primer and fusion primer sequences. Each
 710 sample was barcoded with 10-12 bp long unique barcode (marked with N) attached to IonA-forward
 711 fusion primer.

Primer	Sequence
M13_27F	TGTAACGACGGCCAGTAGAGTTTGATCMTGGCTCAG
M13_E572F	TGTAACGACGGCCAGTCYGCGGTAATTCCAGCTC
IonP1_338R	CCTCTCTATGGGCAGTCGGTGATTGCTGCCTCCCGTAGGAGT
IonP1_E1009R	CCTCTCTATGGGCAGTCGGTGATCRAAGAYGATYAGATACCRT
IonA_key_bc_M13	CCATCTCATCCCTGCGTGTCTCCGACTCAGNNNNNNNNNTGTAACGACGGCCAGT

712

Benthic microbes along salinity gradient

713 **Supplementary table 4.** Environmental variables measured at all samplings.

Site	Sample time	Salinity	Temp.	C/N ratio	Organic matter	Water-content	Porosity	M. grain size	Sorting
List	August 2018	33	22	9.48	0.940	17.59	0.34	1.41	1.27
Saltö	August 2018	26	18	10.46	1.16	24.03	0.43	2.24	1.76
	November 2018	25	3	8.86	1.24	27.22	0.50	2.82	0.82
	April 2019	23	11	8.57	1.07	21.20	0.40	2.35	1.53
	August 2019	22	18	7.77	1.34	25.17	0.47	2.16	1.90
Herslev	August 2018	15	23	6.31	1.06	21.56	0.40	1.37	0.70
	November 2018	16	5	4.40	1.16	23.35	0.48	2.15	0.85
	April 2019	15	15	1.94	1.02	22.46	0.40	2.35	0.85
	August 2019	15	17	8.30	1.23	20.37	0.37	2.06	1.05
Gollwitz	August 2018	13	23	9.83	1.42	27.63	0.49	2.78	0.89
Öland	August 2018	7	21	9.89	0.89	22.69	0.43	2.40	0.63
	November 2018	8	1	3.83	0.61	24.15	0.44	2.70	0.41
	April 2019	9	14	7.06	0.55	23.42	0.44	2.50	0.46
	August 2019	8	18	6.90	0.70	20.75	0.37	2.48	0.49
Tvärminne	August 2018	7	13	6.82	1.40	32.41	0.56	2.60	0.67

Benthic microbes along salinity gradient

Pori	August	6	18	8.64	0.24	22.42	0.40	2.49	0.63
	2018								

714

715 **Supplementary table 5a.** Differences in Shannon index between sites in spatial study by TukeyHSD
 716 test. Different letters indicate significantly different sites. No significant differences were found by
 717 Tukey HSD test for richness of bacteria and eukaryotes.

Spatial Dataset	Shannon Bacteria
Herslev	ab
List	ab
Pori	ab
Saltö	a
Tvärminne	ab
Öland	b
Gollwitz	ab

718

719 **Supplementary table 5b.** Differences in Shannon index and richness (observed diversity) between
 720 sites in temporal study tested by TukeyHSD test. Different letters for each site indicate significantly
 721 different sites.

Temporal Dataset	Bacteria		Eukaryote	
	Shannon	Observed	Shannon	Observed
Saltö	a	a	a	ab
Öland	b	a	ab	a
Herslev	a	a	b	b

722

723 **Supplementary table 6.** ANOVA test of alpha diversity measured by richness (observed) and
 724 Shannon against salinity. Note salinity is grouped to three categories as low (<10), medium (>10-20)
 725 and high (>20). Values indicate p value, asterisk indicate significance level, *=p<0.001, **p=0.01,
 726 ns=not significant.

Dataset	Observed	Shannon
Spatial Bacteria	ns	0.06
Temporal Bacteria	ns	0.00 **
Spatial Eukaryotes	ns	ns

Benthic microbes along salinity gradient

Temporal Eukaryotes	0.04 *	0.03 *
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727

728 **Supplementary table 7.** See attached excel-sheet. Correlation between OTUs and salinity.

729 **Supplementary table 8a.** Keystone species of high salinity site Saltö, temporal samples. OTU
730 identity listed as botu = bacterial OTU, eotu = eukaryote OTU.

OTU	Connections	Phylum	Order	Genus
botu515	60	Gammaproteobacteria	Haliaceae	Proteobacteria
botu607	55	Alphaproteobacteria	Rhodobacteraceae	Proteobacteria
botu331	53	Gammaproteobacteria	BD2-7	Proteobacteria
botu613	52	Gammaproteobacteria	BD7-8_fa	Proteobacteria
botu700	50	Gammaproteobacteria	Saccharospirillaceae	Proteobacteria
botu239	47	Alphaproteobacteria	uncultured	Proteobacteria
eotu228	45	Ochrophyta	Bacillariophyta	Stramenopiles
botu1484	44	Bacteroidia	Crocinitomicaceae	Bacteroidota
botu3889	43	Bacteroidia	Flavobacteriaceae	Bacteroidota
botu183	42	Gammaproteobacteria	Alteromonadaceae	Proteobacteria
eotu520	41	Unclassified	Unclassified Eukaryota	Unclassified Eukaryota
botu2817	41	Bacteroidia	Flavobacteriaceae	Bacteroidota
botu929	41	Alphaproteobacteria	Rhodobacteraceae	Proteobacteria
eotu1227	40	Unclassified	Unclassified Eukaryota	Unclassified Eukaryota
eotu356	40	Ochrophyta	Phaeophyceae	Stramenopiles

731

732 **Supplementary table 8b.** Keystone species of medium salinity site Herslev, temporal samples.
733 OTU identity listed as botu = bacterial OTU, eotu = eukaryote OTU.

OTU	Connections	Phylum	Order	Genus
botu1673	51	Bacteroidota	Flavobacteriales	Unclassified Flavobacteriaceae
eotu933	45	Alveolata	Dinophyceae	Dinophyceae
eotu3734	40	Alveolata	Dinophyceae	Unclassified Dinophyceae
eotu34	37	Stramenopiles	Bacillariophyta	Unclassified Raphid pennate
eotu1174	36	Opisthokonta	Ascomycota	Unclassified Pezizomycotina
botu607	35	Proteobacteria	Rhodobacterales	Unclassified Rhodobacteraceae
eotu113	30	Unclassified Eukaryota	Unclassified Eukaryota	Unclassified Eukaryota
eotu3124	28	Alveolata	Dinophyceae	Unclassified Dinophyceae
eotu4284	28	Alveolata	Dinophyceae	Unclassified Dinophyceae
botu370	28	Patescibacteria	Candidatus Campbellbacteria	Candidatus Campbellbacteria_ge
eotu363	27	Unclassified Eukaryota	Unclassified Eukaryota	Unclassified Eukaryota
eotu681	27	Stramenopiles	Unclassified Stramenopiles	Unclassified Stramenopiles
botu1222	27	Bacteroidota	Chitinophagales	uncultured
botu290	27	Bacteroidota	Flavobacteriales	Lutibacter

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botu4620	27	Bacteroidota	Flavobacteriales	Aquibacter
eotu852	26	Alveolata	Unclassified Alveolata	Unclassified Alveolata

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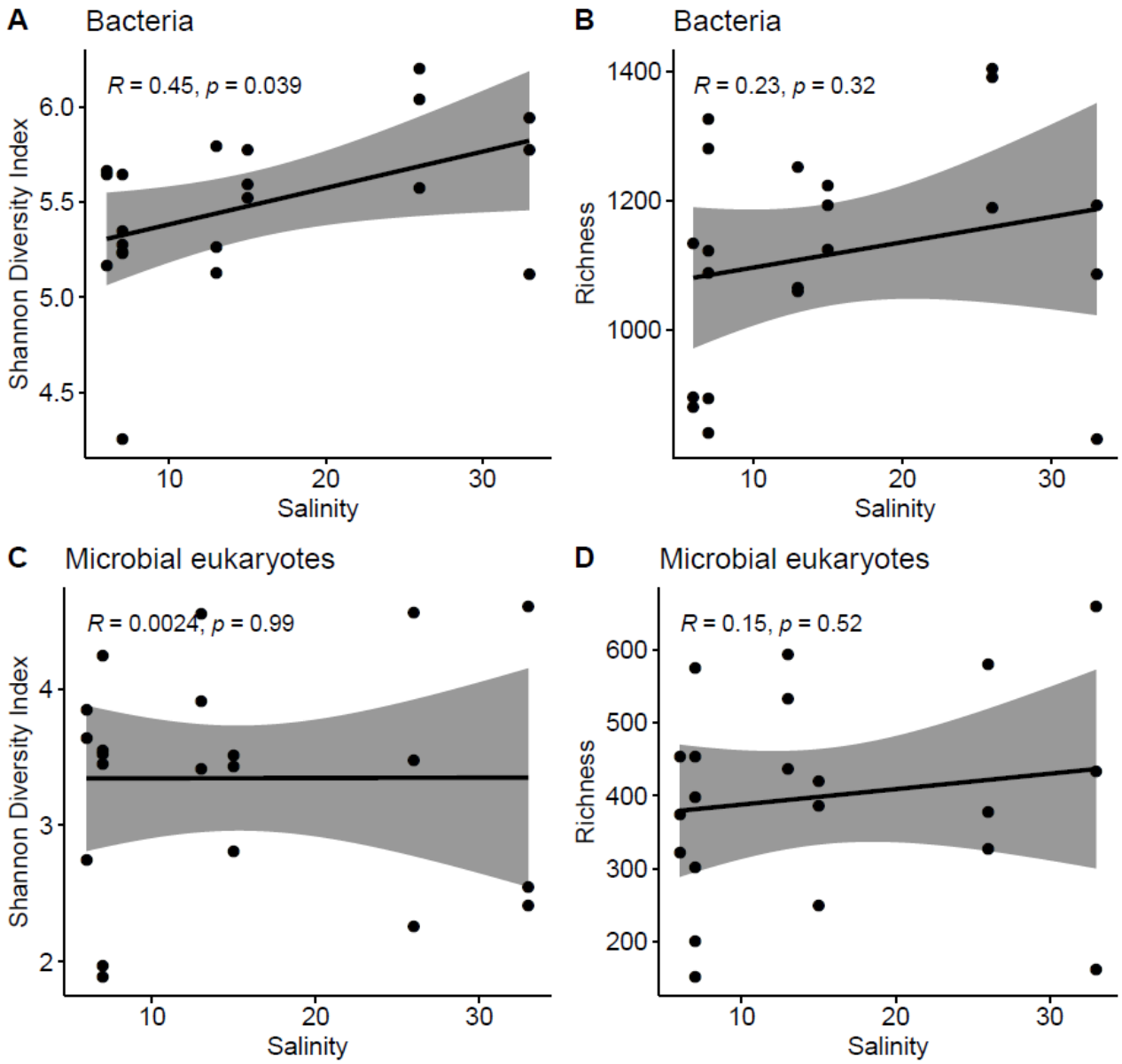
735 **Supplementary table 8c.** Keystone species of low salinity site Öland, temporal samples. OTU
736 identity listed as botu = bacterial OTU, eotu = eukaryote OTU.

OTU	Connections	Phylum	Order	Genus
eotu368	34	Alveolata	Dinophyceae	Unclassified Gymnodiniaceae
eotu338	32	Unclassified Eukaryota	Unclassified Eukaryota	Unclassified Eukaryota
eotu67	30	Archaeplastida	Chlorophyceae	Unclassified Chlamydomonadales
eotu3341	29	Stramenopiles	Phaeophyceae	Unclassified Phaeophyceae
eotu231	26	Stramenopiles	Bacillariophyta	Unclassified Raphid-pennate
eotu135	22	Alveolata	Unclassified Alveolata	Unclassified Alveolata
eotu176	22	Stramenopiles	Bacillariophyta	Unclassified Raphid-pennate
eotu497	21	Stramenopiles	Bacillariophyta	Unclassified Raphid-pennate
eotu393	20	Stramenopiles	Unclassified Ochrophyta	Unclassified Ochrophyta
eotu863	20	Stramenopiles	Bacillariophyta	Unclassified Raphid-pennate
eotu730	17	Stramenopiles	Unclassified Sagenista	Unclassified Sagenista

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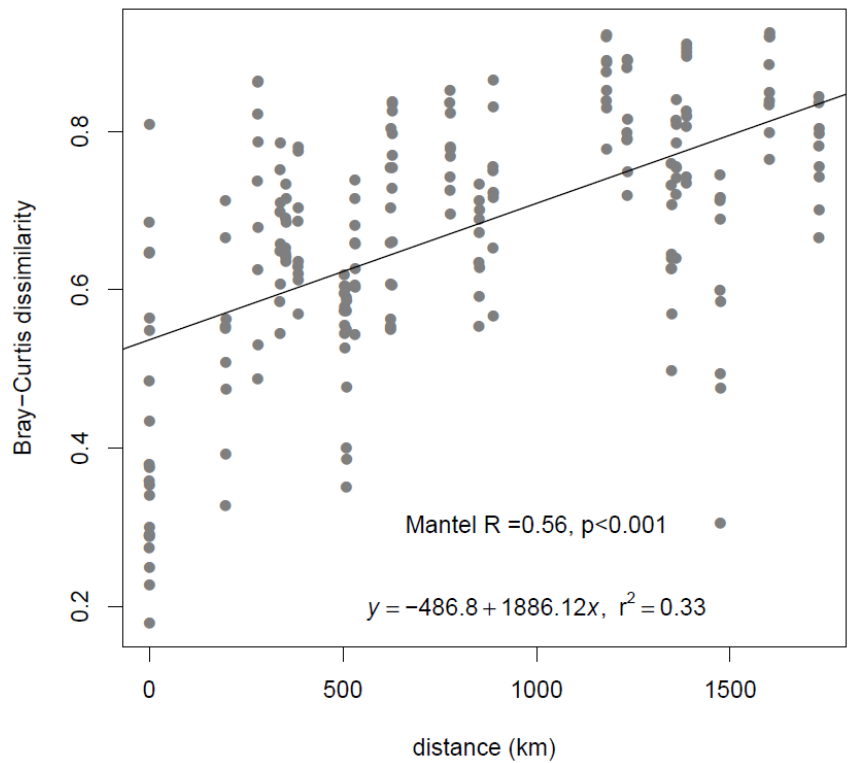
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739 **Supplementary figure 1.** Pearson correlation of alpha diversity and salinity for spatial samples.



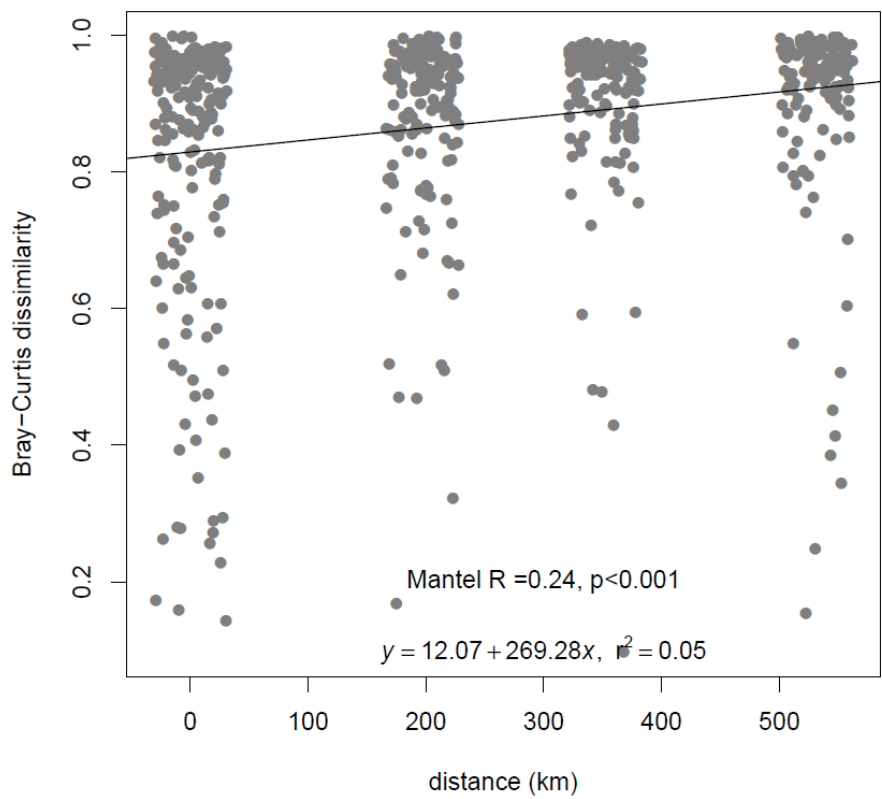
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741 **Supplementary figure 2a.** Analysis of distance-decay for spatial bacterial dataset.



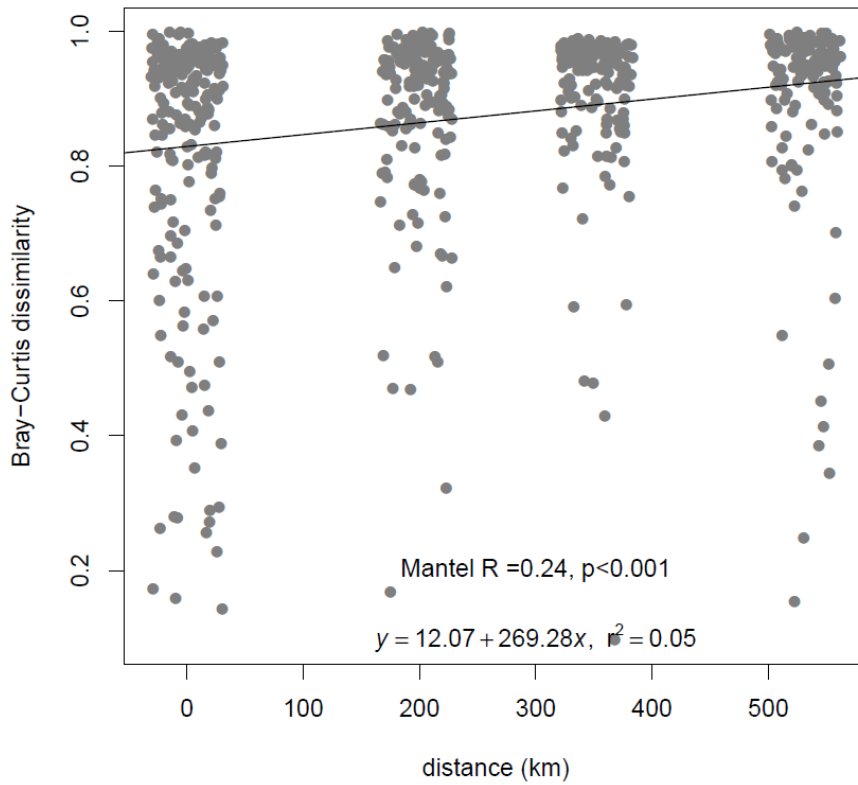
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743 **Supplementary figure 2b.** Analysis of distance-decay for temporal bacterial dataset.



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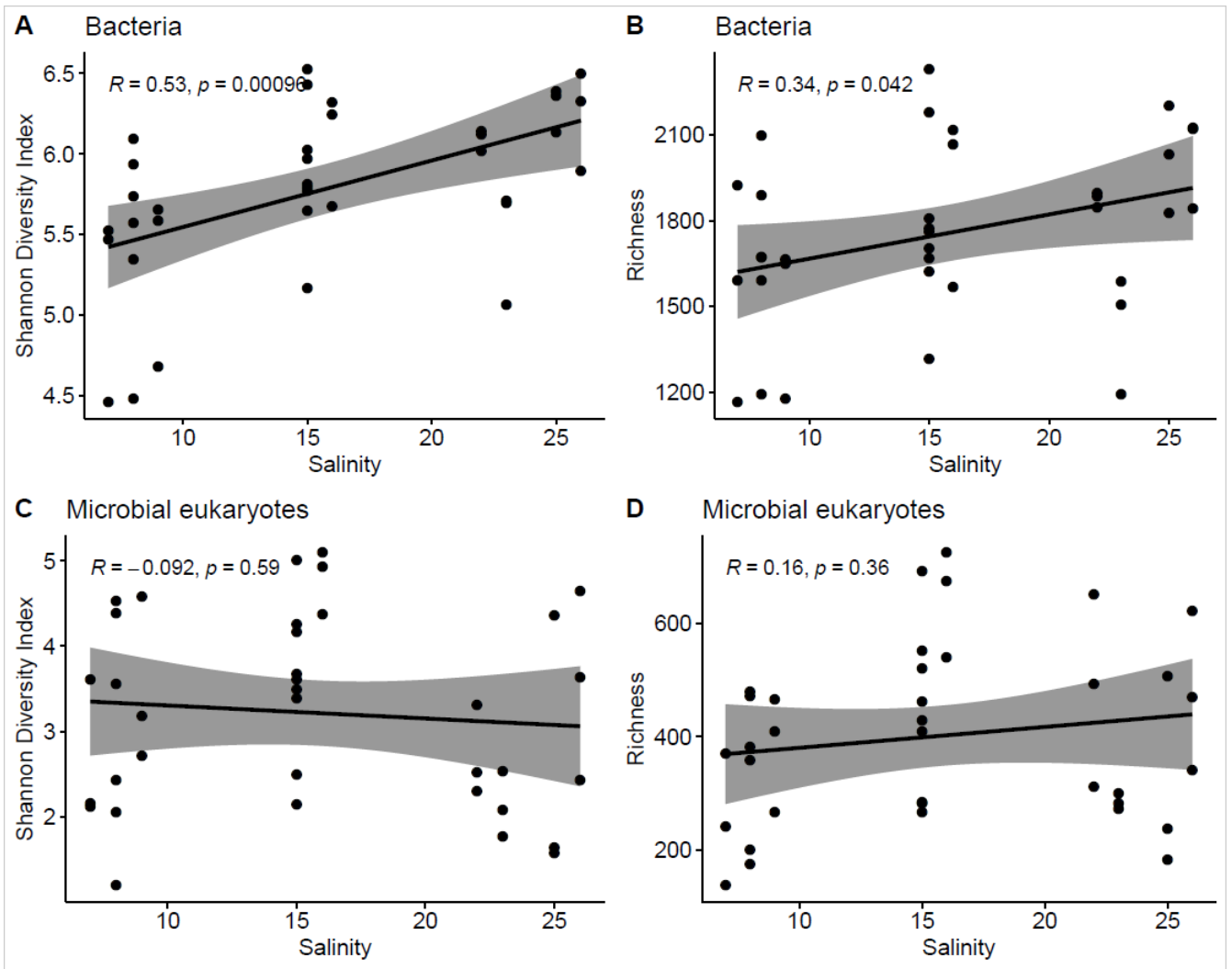
745 **Supplementary figure 1c.** Analysis of distance-decay for temporal microbial eukaryote dataset.



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747

748 **Supplementary figure 3.** Pearson correlation of alpha diversity and salinity for temporal samples.



749