

Seasonal Dynamics of Epiphytic Microbial Communities on Marine Macrophyte Surfaces

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Running title: Seasonal dynamics of epiphytic communities

1 Summary

2 Surfaces of marine macrophytes (seagrasses and macroalgae) are inhabited by diverse
3 microbial communities. Most studies focusing on macrophyte epiphytic communities did not
4 take into account temporal changes or applied low sampling frequency approaches. Illumina
5 sequencing of the V4 16S rRNA region was performed to determine the seasonal dynamics
6 of epiphytic communities sampled from the surfaces of the seagrass *Cymodocea nodosa* and
7 invasive macroalga *Caulerpa cylindracea*. Leaves and thalli were sampled in a meadow of
8 *Cymodocea nodosa* invaded by the invasive *Caulerpa cylindracea* and in a monospecific
9 settlement of *Caulerpa cylindracea* located in the proximity of the meadow at monthly intervals.
10 For comparison the ambient prokaryotic plankton community was also characterized. Sequencing
11 results at the OTU level showed a clear differentiation between ambient water and epiphytic
12 communities and a host-specific community assemblage. In addition, successional changes were
13 observed that could be connected to the macrophyte growth cycle. Taxonomic analysis showed
14 similar high rank groups in the ambient water and epiphytic communities, with the exception of
15 *Desulfobacterota* that were found only on *Caulerpa cylindracea*. Only *Cyanobacteria* showed
16 seasonal change, while other high rank taxa were present throughout the year. In every analyzed
17 high rank taxa, phylogenetic groups present throughout the year comprised most of the sequences
18 and could be identified together with low proportion taxa showing seasonal patterns connected to
19 the macrophyte growth cycle. Taken together, epiphytic microbial communities of the seagrass
20 *Cymodocea nodosa* and the macroalgae *Caulerpa cylindracea* appear to be host-specific and
21 contain taxa that undergo successional changes.

22 **Introduction**

23 Marine macrophytes (seagrasses and macroalgae) are important ecosystem engineers that
24 form close associations with microorganism belonging to all three domains of life (Egan *et al.*,
25 2013; Tarquinio *et al.*, 2019). Microbes can live within macrophyte tissue as endophytes or can
26 form epiphytic communities on surfaces of leaves and thalli (Egan *et al.*, 2013; Hollants *et al.*,
27 2013; Tarquinio *et al.*, 2019). Epiphytic and endophytic microbial communities form a close
28 functional relationship with the macrophyte host. It was proposed that this close relationship
29 constitutes a holobiont, an integrated community where the macrophyte organism and its symbiotic
30 partners support each other (Margulis, 1991; Egan *et al.*, 2013; Tarquinio *et al.*, 2019).

31 Biofilms formed from microbial epiphytes can contain diverse taxonomic groups and harbor
32 cell densities from 10^2 to 10^7 cells cm^{-2} (Armstrong *et al.*, 2000; Bengtsson *et al.*, 2010; Burke
33 and Thomas *et al.*, 2011). In such an environment a number of positive and negative interactions
34 between the macrophyte and colonizing microorganisms have been described (Egan *et al.*, 2013;
35 Hollants *et al.*, 2013; Tarquinio *et al.*, 2019). Macrophytes can promote growth of associated
36 microbes by nutrient exudation, while in return microorganisms may support macrophyte
37 performance through improved nutrient availability, phytohormone production and protection
38 from toxic compounds, oxidative stress, biofouling organisms and pathogens (Egan *et al.*, 2013;
39 Hollants *et al.*, 2013; Tarquinio *et al.*, 2019). Beside this positive interactions, macrophytes can
40 negatively impact the associated microbes such as pathogenic bacteria by producing reactive
41 oxygen species and secondary metabolites (Egan *et al.*, 2013; Hollants *et al.*, 2013; Tarquinio *et*
42 *al.*, 2019).

43 All these ecological roles are carried out by a taxonomically diverse community of
44 microorganisms. At higher taxonomic ranks a core set of macrophyte epiphytic taxa was
45 described consisting mainly of *Alphaproteobacteria*, *Gammaproteobacteria*, *Desulfobacterota*,
46 *Bacteroidota*, *Cyanobacteria*, *Actinobacteriota*, *Firmicutes*, *Planctomycetota*, *Chloroflexi* and

47 *Verrucomicrobiota* (Crump and Koch, 2008; Tujula *et al.*, 2010; Lachnit *et al.*, 2011). In contrast,
48 at lower taxonomic ranks host specific microbial communities were described (Lachnit *et al.*,
49 2011; Roth-Schulze *et al.*, 2016). Recently, it was shown that even different morphological niches
50 within the same alga had a higher influence on bacterial community variation than biogeography
51 or environmental factors (Morrissey *et al.*, 2019). While there is high community variation
52 between host species it was observed that the majority of metagenome determined functions were
53 conserved both between host species and individuals (Burke and Peter Steinberg *et al.*, 2011;
54 Roth-Schulze *et al.*, 2016). This discrepancy between taxonomic and functional composition
55 could be explained by the lottery hypothesis. It postulates that an initial random colonization step
56 is performed from a set of functionally equivalent taxonomic groups resulting in taxonomically
57 different epiphytic communities sharing a core set of functional genes (Burke and Peter Steinberg
58 *et al.*, 2011; Roth-Schulze *et al.*, 2016). In addition, some of the variation in the observed data
59 could be attributed to different techniques used in various studies, such as different protocols
60 for epiphytic cell detachment and/or DNA isolation, as no standard protocol to study epiphytic
61 communities was established (Korlević *et al.*, unpublished; Ugarelli *et al.*, 2019).

62 The majority of studies describing macrophyte epiphytic communities did not encompass
63 seasonal changes (Crump and Koch, 2008; Lachnit *et al.*, 2009; Burke and Thomas *et al.*, 2011;
64 Roth-Schulze *et al.*, 2016; Ugarelli *et al.*, 2019). In addition, if seasonal changes were taken into
65 account low temporal frequency and/or methodologies that do not allow high taxonomic resolution
66 were used (Tujula *et al.*, 2010; Lachnit *et al.*, 2011; Miranda *et al.*, 2013; Michelou *et al.*, 2013).
67 In the present study we describe the seasonal dynamics of bacterial and archaeal communities on
68 the surfaces of the seagrass *Cymodocea nodosa* and siphonous macroalgae *Caulerpa cylindracea*
69 determined on a mostly monthly scale. Bacterial and archaeal epiphytes were sampled in a meadow
70 of *C. nodosa* invaded by the invasive *C. cylindracea* and in a locality of only *C. cylindracea*
71 located in the proximity of the meadow. In addition, for comparison, the community of the ambient
72 seawater was characterized.

73 **Results**

74 Sequencing of the 16S rRNA V4 region yielded a total of 1.8 million sequences after
75 quality curation and exclusion of eukaryotic, chloroplast, mitochondrial and no relative sequences
76 (Table S1). A total of 35 samples originating from epiphytic archaeal and bacterial communities
77 associated with surfaces of the seagrass *C. nodosa* and macroalga *C. cylindracea* were analyzed. In
78 addition, 18 samples (one of the samples was sequenced two times) originating from picoplankton
79 archaeal and bacterial communities in the ambient seawater were also processed for comparison.
80 The number of reads per sample ranged between 8,408 and 77,463 sequences (Table S1). Even
81 when the highest sequencing effort was applied the rarefaction curves did not level off that is a
82 common observation in high-throughput 16S rRNA amplicon sequencing approaches (Fig. S1).
83 Following quality curation and exclusion of sequences mentioned before reads were clustered
84 into 28,750 different OTUs at a similarity level of 97 %. Read numbers were normalized to the
85 minimum number of sequences, 8,408 (Table S1), through rarefaction resulting in 17,131 different
86 OTUs that ranged from 371 to 2,000 OTUs per sample (Fig. S2). To determine seasonal changes of
87 richness and diversity the Observed Number of OTUs, Chao1, ACE, Exponential Shannon (Jost,
88 2006) and Inverse Simpson were calculated after normalization through rarefaction. Generally,
89 richness estimators and diversity indices showed similar trends. On average, higher values were
90 found for *C. cylindracea* (mixed [Number of OTUs, $1,691.8 \pm 130.0$ OTUs] and monospecific
91 [Number of OTUs, $1,734.7 \pm 149.6$ OTUs]), middle values for *C. nodosa* (Number of OTUs,
92 $1,052.8 \pm 217.5$ OTUs) and lower values for picoplankton communities in the ambient seawater
93 (Number of OTUs, 528.1 ± 140.9 OTUs) (Fig. S2). Seasonal changes did not show such large
94 dissimilarities. *C. nodosa* communities showed a slow increase towards the end of the study,
95 while *C. cylindracea* (mixed and monospecific) communities were characterized by slightly larger
96 values in Spring and Summer in comparison to Autumn and Winter (Fig. S2).

97 To determine the proportion of shared archaeal and bacterial OTUs and communities
98 sampled in different environments the Jaccard's Similarity Coefficient on presence-absence

99 data and Bray-Curtis Similarity Coefficient were, respectively, calculated. Coefficients were
100 determined after normalization through rarefaction and binning of samples from a particular
101 environment. The highest proportion of shared OTUs and community was found between mixed
102 and monospecific *C. cylindracea* (Jaccard, 0.35; Bray-Curtis, 0.78), while lower shared values
103 were calculated between seawater and epiphytic communities (Fig. 1). Shared proportion between
104 *C. nodosa* and *C. cylindracea* were approximately in the middle between these two extremes. To
105 assess seasonal changes in the proportion of shared OTUs and communities the Jaccard's and
106 Bray-Curtis Similarity Coefficients were calculated between consecutive sampling points (Fig. 2).
107 Both coefficients showed similar trends. Temporal proportional changes were more pronounced
108 for seawater in comparison to *C. nodosa* and especially *C. cylindracea* associated communities
109 (Fig. 2). In addition, only 0.4 – 1.0 % of OTUs from each surface associated community were
110 found at every time point. These OTUs also made a high proportion of total sequences (41.1 – 53.3
111 %). To further disentangle the environmental and seasonal community dissimilarity a Principal
112 Coordinates Analysis (PCoA) based on Bray-Curtis distances and OTU abundances was applied.
113 It showed a clear separation between planktonic and surface associated communities (Fig. 3). In
114 addition, a separation of epiphytic bacterial and archaeal communities based on host species was
115 determined. This separation was further supported by ANOSIM ($R = 0.96, p < 0.001$). Seasonal
116 changes of *C. nodosa* associated communities indicated a separation between Spring, Summer
117 and Autumn/Winter samples (ANOSIM, $R = 0.52, p < 0.01$). For *C. cylindracea* associated
118 communities a separation between Summer and Autumn/Winter/Spring samples was observed
119 that was not so strongly supported (ANOSIM, $R = 0.31, p < 0.01$) (Fig. 3).

120 The taxonomic composition of both, macrophyte associated and seawater communities,
121 was dominated by bacterial (99.1 ± 2.1 %) over archaeal sequences (0.9 ± 2.1 %) (Fig. 4).
122 Higher relative abundances of chloroplast related sequences were only observed in surface
123 associated communities, with higher values in Autumn/Winter (37.2 ± 11.2 %) in comparison to
124 Spring/Summer (20.9 ± 9.7 %) (Fig. S3). Generally, at higher taxonomic ranks (phylum-class)
125 epiphytic and seawater microbial communities were composed of similar bacterial taxa.

126 Seawater communities were mainly comprised of *Actinobacteriota*, *Bacteroidota*, *Cyanobacteria*,
127 *Alphaproteobacteria*, *Gammaproteobacteria* and *Verrucomicrobiota*. Communities associated
128 with *C. nodosa* consisted of same groups with the addition of *Planctomycetota* whose contribution
129 was higher in summer 2018. In addition, communities from mixed and monospecific *C.*
130 *cylindracea* were similar and characterized by same groups as seawater and *C. nodosa*
131 communities with the addition of *Desulfobacterota* (Fig. 4). Larger differences between
132 environments and host species could be observed at lower taxonomic ranks (Fig. 5 – 9).

133 *Cyanobacteria* related sequences were comprising, on average, $5.5 \pm 4.4\%$ of total sequences
134 (Fig. 5). Higher proportions were found for *C. nodosa* ($16.4 \pm 5.3\%$) and *C. cylindracea* (mixed
135 [$(7.7 \pm 3.9\%)$] and monospecific [$(7.8 \pm 2.4\%)$]) associated communities in autumn and for
136 seawater communities in winter ($8.8 \pm 7.5\%$). Large taxonomic differences between surface
137 associated and seawater cyanobacterial communities were observed. Seawater communities
138 were mainly comprised of *Cyanobium* and *Synechococcus*, while surface associated communities
139 were consisted of *Pleurocapsa* and sequences without known relatives within *Cyanobacteriia*
140 (Fig. 5). In addition, seasonal changes in surface associated communities were observed with
141 *Pleurocapsa* and no relative *Cyanobacteriia* comprising larger proportions in autumn and winter
142 and *Acrophormium*, *Phormidesmis* and no relative *Nodosilineaceae* in spring and summer (Fig. 5).

143 Sequences classified as *Bacteroidota* were comprising, on average, $19.2 \pm 5.5\%$ of all
144 sequences (Fig. 6). Similarly to *Cyanobacteria*, large differences in the taxonomic composition
145 between seawater and surface associated communities were found (Fig. 6). The seawater
146 community was characterized by the NS4 and NS5 marine groups, uncultured *Cryomorphaceae*,
147 uncultured *Flavobacteriaceae*, NS11-12 marine group, *Balneola*, uncultured *Balneolaceae* and
148 *Formosa*. In contrast, in surface associated communities *Lewinella*, *Portibacter*, *Rubidimonas*, no
149 relative *Saprospiraceae*, uncultured *Saprospiraceae*, no relative *Flavobacteriaceae* and uncultured
150 *Rhodothermaceae* were found. Some groups showed slight seasonal changes such as no relative
151 *Flavobacteriaceae* that were more pronounced from November 2017 until June 2018. In contrast,

152 uncultured *Rhodothermaceae* showed higher proportions from June 2018 until the end of the study
153 period. Surface associated *Bacteroidota* communities were very diverse as could be observed in
154 the high proportion of taxa that grouped as other *Bacteroidota* (Fig. 6).

155 On average, *Alphaproteobacteria* were in comparison to other high rank taxa the largest
156 taxonomic group, comprising 29.2 ± 12.0 % of all sequences (Fig. 7). In accordance to previous
157 taxa, high differences between seawater and surface associated communities were observed.
158 Picoplankton communities were composed mainly of the SAR11 clade, AEGEAN-169 marine
159 group, SAR116 clade, no relative *Rhodobacteraceae*, HIMB11 and OCS116 clade, while surface
160 associated communities were composed in high proportion of no relative *Rhodobacteraceae* and to
161 a lesser degree of *Pseudoahrensia*, no relative *Alphaproteobacteria*, no relative *Hyphomonadaceae*
162 and *Amylibacter*. Representatives of no relative *Rhodobacteraceae* were comprising on average
163 40.6 ± 23.2 % of all alphaproteobacterial sequences from the epiphytic community (Fig. 7). In
164 addition, *Amylibacter* was detected mainly in *C. nodosa* from November 2017 until March 2018.

165 Sequences related to *Gammaproteobacteria* were comprising, on average, 18.6 ± 3.9 %
166 of all sequences (Fig. 8). Similarly to previous taxa, large taxonomic differences between
167 seawater and surface associated communities were found. Seawater communities were mainly
168 comprised of the OM60 (NOR5) clade, *Litoricola*, *Acinetobacter* and the SAR86 clade,
169 while epiphytic communities were mainly composed of no relative *Gammaproteobacteria* and
170 *Granulosicoccus*. Beside these two groups specific to all three epiphytic communities, *C. nodosa*
171 was characterized by *Arenicella*, no relative *Burkholderiales* and *Methylotenera*, while *Thioploca*,
172 no relative *Cellvibrionaceae* and *Reinekea* were more specific to both mixed and monospecific
173 *C. cylindracea*. In addition, *Arenicella* was more pronounced in November and December 2017,
174 while no relative *Burkholderiales* and *Methylotenera* were more characteristic for the period from
175 March until May 2018. For the *C. cylindracea* specific taxa no relative *Cellvibrionaceae* and
176 *Reinekea* showed some seasonality and were characteristic for samples originating from June to
177 October 2018. In addition, similarly to *Bacteroidota*, a large proportion of the surface associated

¹⁷⁸ community was grouped as other *Gammaproteobacteria* indicating high diversity within this
¹⁷⁹ group (Fig. 8).

¹⁸⁰ In contrast to previously described high rank taxa, *Desulfobacterota* were specific to *C.*
¹⁸¹ *cylindracea*. On average they comprised 11.2 ± 13.3 % of all sequences. Seawater and *C.*
¹⁸² *nodosa* communities consisted of only 0.1 ± 0.08 % and 1.0 ± 0.7 % *Desulfobacterota* sequences,
¹⁸³ respectively. In the mixed and monospecific *C. cylindracea* communities their proportion was 25.7
¹⁸⁴ ± 11.2 % and 24.0 ± 4.3 %, respectively (Fig. 9). The community consisted mainly of no relative
¹⁸⁵ *Desulfobacteraceae*, *Desulfatitalea*, no relative *Desulfobulbaceae*, *Desulfobulbus*, no relative
¹⁸⁶ *Desulfocapsaceae*, *Desulfopila*, *Desulforhopalus*, *Desulfotalea*, SEEP-SRB4 and uncultured
¹⁸⁷ *Desulfocapsaceae* (Fig. 9).

188 **Discussion**

189 Surfaces of marine macrophytes harbor biofilms consisting of diverse microbial taxa (Egan
190 *et al.*, 2013; Tarquinio *et al.*, 2019). No standard protocol has been developed to study these
191 macrophyte associated microbes (Ugarelli *et al.*, 2019). Different procedures for removal of
192 microbial cells from host surfaces were described, such as host tissue shaking (Nõges *et al.*, 2010),
193 scraping (Uku *et al.*, 2007) and ultrasonication (Cai *et al.*, 2014). All these methods showed
194 different removal efficiencies but none was enabling a complete removal of attached microbial
195 cells. In the present study, we applied an earlier developed removal protocol (Korlević *et al.*,
196 unpublished), based on a previous idea of direct cellular lysis (Burke *et al.*, 2009), to ensure an
197 almost complete cell detachment. The application of a direct lysis procedure coupled with a high
198 frequency sampling protocol and Illumina high resolution amplicon sequencing has enabled us to
199 make a detailed description of bacterial and archaeal communities associated with the surfaces of
200 two marine macrophytes, *C. nodosa* and *C. cylindracea*.

201 In the present study, highest richness values were observed for *C. cylindracea* (mixed and
202 monospecific), middle for *C. nodosa* and lowest for seawater derived communities. Higher values
203 for seagrass associated communities in comparison to seawater were described earlier and could
204 be attributed to a larger set of inhabitable microniches existing on macrophyte surfaces (Ugarelli
205 *et al.*, 2019). In addition, highest values observed for *C. cylindracea* are partly due to its contact
206 with the sediment. *C. cylindracea* stolon is attached to the sediment surface with rhizoids, so
207 the stolon and rhizoids are in a direct contact with the sediment. In addition, seasonal richness
208 differences observed for surface attached communities showed slightly higher values in spring
209 and summer. This pattern could be explained by a higher macrophyte growth in these seasons
210 (M. Najdek, personal communication; Zavodnik *et al.*, 1998; Ruitton *et al.*, 2005). During active
211 periods macrophytes exhibit a more dynamic chemical interaction with the surface community
212 probably causing an increase in the number of inhabitable microniches (Borges and Champenois,
213 2015; Rickert *et al.*, 2016).

214 Since the colonization of macrophyte surfaces is performed from a pool of prokaryotic cells
215 from the ambient seawater, it was interesting to see to which extent these two communities differ.
216 We observed a strong differentiation between the surface attached and seawater communities at
217 the level of OTUs that is in agreement with most published studies (Burke and Thomas *et al.*,
218 2011; Michelou *et al.*, 2013; Roth-Schulze *et al.*, 2016; Crump *et al.*, 2018; Ugarelli *et al.*, 2019).
219 These data indicate that marine macrophytes are selecting, from a pool of seawater microbial taxa,
220 the one that can colonize and proliferate on their surfaces (Salaün *et al.*, 2012; Michelou *et al.*,
221 2013). In contrast to these findings Fahimipour *et al.* (2017) found, in a global study of *Zostera*
222 *marina*, similarities between leaves and seawater samples. Discrepancies between our data and this
223 study could be explained by differences in studied seagrass species, methodological variations or
224 biogeographic trends as Fahimipour *et al.* (2017) were analyzing samples from different locations
225 throughout the northern hemisphere. It is possible that ambient seawater and leaves communities
226 from the same location are differing but are still more similar to each other when compared to
227 other sampling locations. Indeed, it was found that prokaryotic communities vary substantially
228 between different sampling sites (Bengtsson *et al.*, 2017). When the taxonomic composition at
229 high ranks was analyzed no such strong differentiation was noticed. Phyla and classes such as:
230 *Actinobacteriota*, *Bacteroidota*, *Cyanobacteria*, *Alphaproteobacteria*, *Gammaproteobacteria* and
231 *Verrucomicrobiota* were described that is in agreement with previously reported data (Burke and
232 Thomas *et al.*, 2011; Egan *et al.*, 2013; Michelou *et al.*, 2013). In contrast, when low taxonomic
233 ranks were analyzed (i.g. family and genus) a strong differentiation was observed. A similar
234 differentiation at lower taxonomic ranks was described for other species of macrophytes (Egan *et*
235 *al.*, 2013; Michelou *et al.*, 2013; Ugarelli *et al.*, 2019).

236 Beside differences between seawater and surface associated communities, there were
237 discussions if the prokaryotic epiphytic community is host-specific or there are generalists taxa
238 characteristic to all or many macrophytes (Egan *et al.*, 2013). Similarly to previously described
239 differences between seawater and surface attached communities, at high taxonomic ranks no
240 strong differentiation between communities associated with different host was observed. The only

241 high rank phylum that was differing between *C. nodosa* and *C. cylindracea* was *Desulfobacterota*,
242 whose sequences were more abundant in the *C. cylindracea* associated community. As already
243 mentioned, the rhizoids and part of the stolon are in contact with the sediment, so *Desulfobacterota*
244 are probably a part of the epiphytic community that was in contact with the sediment. Similar
245 high rank taxa found in this study were described to be specific for other species of macrophytes
246 (Burke and Thomas *et al.*, 2011; Lachnit *et al.*, 2011; Bengtsson *et al.*, 2017). In contrast to
247 high taxonomic ranks, a substantial differentiation between host specific communities was found,
248 which supports the host-specific hypothesis. Similar host-specificity was observed for different
249 species of macroalgae and seagrasses (Lachnit *et al.*, 2011; Roth-Schulze *et al.*, 2016; Ugarelli *et*
250 *al.*, 2019; Morrissey *et al.*, 2019). Taken together, at high taxonomic ranks a core set of taxa could
251 be described that is characteristic for all or many macrophytes, while at low taxonomic ranks a
252 community specific to host species could be identified (Egan *et al.*, 2013).

253 Seasonal richness changes in the epiphytic community were substantial as could be observed
254 in the proportion of OTUs that could be found at every sampling time ($\leq 1.0\%$). Interestingly,
255 these OTUs were accounting for a high proportion of sequences ($\leq 53.3\%$). A very similar
256 proportion of persistent OTUs and their sequence contribution was reported in high frequency
257 studies describing seasonal picoplankton changes (Gilbert *et al.*, 2009, 2012). In comparison to
258 the seawater community, a lower degree of seasonal shifts was observed for the surface associated
259 communities. It seems, microniches on the surfaces of macrophytes are providing more stable
260 conditions in comparison to the seawater. At the level of OTUs seasonal changes of *C. nodosa* and
261 *C. cylindracea* associated communities were identified that could be linked to the growth cycle of
262 the seagrass and macroalgae (M. Najdek, personal communication). *C. nodosa* was characterized
263 by a Spring community during maximum seagrass proliferation, a Summer community during a
264 biomass maximum and a Autumn/Winter community during a biomass senescence. In contrast,
265 *C. cylindracea* started to proliferate in late Spring and was characterized only by a Summer
266 community during maximal biomass increase and by a Autumn/Winter/Spring community when
267 the biomass was at the peak and the settlement started to subsequently decay. Similar seasonal

268 changes in the epiphytic community was also described for other macroalgae (Tujula *et al.*,
269 2010; Lachnit *et al.*, 2011). Higher temporal stability of *C. cylindracea* surface communities
270 in comparison to *C. nodosa* were also observed in the higher proportion of shared communities
271 between two consecutive sampling points.

272 Analysis of seasonal chloroplast sequence abundances showed higher values in Autumn/Winter
273 in comparison to Spring/Summer. This pattern is not surprising as seagrasses are known to harbor
274 more epiphytes during Autumn/Winter (Reyes and Sansón, 2001). Furthermore, we used an
275 adapted DNA isolation protocol that is known to partially coextract DNA from planktonic
276 eukaryotes (Korlević *et al.*, 2015). Strong seasonal fluctuations of high rank epiphytic taxa
277 were not observed, with the exception of *Cyanobacteria*. Cyanobacterial sequences were more
278 pronounced in November and December in comparison to Spring and Summer. Interestingly,
279 in these high proportion months the majority of cyanobacterial sequences were classified as
280 *Pleurocapsa*, a group known to colonized different living and nonliving surfaces (Burns *et al.*,
281 2004; Longford *et al.*, 2007; Mobberley *et al.*, 2012; Reisser *et al.*, 2014). It is possible that during
282 periods of low metabolic activity there is a reduced interaction and selection of the epiphytic
283 community by the seagrass, causing leaves to become a suitable surface for nonspecific colonizers
284 (Zavodnik *et al.*, 1998). *Pleurocapsa* was replaced in Spring and Summer by *Acrophormium*,
285 *Phormidesmis* and no relative *Nodosilineaceae*. A study of coastal microbial mats found also
286 higher proportion of *Nodosilineaceae* sequences in Summer, while *Phormidesmis* sequences
287 were at their peak in Autumn (Cardoso *et al.*, 2019). Other high rank taxa did not show strong
288 successional patterns. In every analyzed group, with the exception of *Desulfobacterota*, taxa
289 present throughout the year in similar proportions and season specific taxa could be identified.
290 Within *Bacteroidota* different groups withing the family *Saprospiraceae* (i.g. *Lewinella*,
291 *Portibacter* and *Rubidimonas*) were detected through the year. Members of this family are
292 often found in association with macrophytes and it is suggested that they are involved in the
293 hydrolysis and utilization of complex carbon sources (Burke and Thomas *et al.*, 2011; McIlroy
294 and Nielsen, 2014; Crump *et al.*, 2018). On the other hand, families *Flavobacteriaceae* and

295 *Rhodothermaceae* showed seasonal patterns, with *Flavobacteriaceae* being more pronounced
296 from November to June and *Rhodothermaceae* from June to October. Within *Alphaproteobacteria*
297 the family *Rhodobacteraceae* was comprising the majority of sequences throughout the year. This
298 metabolically versatile family is often associated with macrophyte surfaces and usually is one
299 of the most abundant groups (Burke and Thomas *et al.*, 2011; Michelou *et al.*, 2013; Pujalte *et*
300 *al.*, 2014). In addition, *Hyphomonadaceae* were found in all samples. Interestingly, some of the
301 species within this group contain stalks on their cells which can be used to attach to the macrophyte
302 surface (Weidner *et al.*, 2000; Abraham and Rohde, 2014). Within the *Gammaproteobacteria*,
303 sequences without known representatives were the most pronounced group present throughout the
304 year. In addition, *Granulosicoccus* was also found in almost all samples. *Gammaproteobacteria*
305 are often a major constituent of macrophyte epiphytic communities (Burke and Thomas *et al.*,
306 2011; Michelou *et al.*, 2013; Crump *et al.*, 2018). Beside these two groups other less pronounced
307 taxa showed seasonal and host-specific patterns. For example, *C. cylindracea* was characterized
308 by *Thioploca*, a known sulfur sediment bacteria and *Cellvibrionaceae*, a family whose cultured
309 members are known polysaccharide degraders (Jørgensen and Gallardo, 1999; Xie *et al.*, 2017).
310 *Desulfobacterota* were found only associated with *C. cylindracea* and no group within this phylum
311 showed seasonal patterns. The presence of this phylum only on *C. cylindracea* is to be expected
312 as part of the epiphytic community is directly in contact with the sediment. The *Desulfobacterota*
313 community was dominated by *Desulfatitalea* and no relative *Desulfocapsaceae*, known sulfate
314 sediment groups (Kuever, 2014; Higashioka *et al.*, 2015).

315 In temperate zones marine macrophytes are exhibiting growth cycles, so it is not surprising
316 that the associated epiphytic microbial community is undergoing partial seasonal changes. In
317 the present study, we could, in every analyzed high rank taxa, identify phylogenetic groups
318 that were present throughout the year and that were comprising most of the sequences and
319 lower proportion taxa showing seasonal patterns connected to the macrophyte growth cycle.
320 Studies focusing on functional comparisons between communities associated with different
321 hosts showed that the majority of functions could be found in every community, indicating

322 functional redundancy (Roth-Schulze *et al.*, 2016). This difference between taxonomic and
323 functional discrepancy was explained by the lottery hypothesis that hypothesizes an initial random
324 colonization step performed from a set of functionally equivalent taxonomic groups (Burke and
325 Peter Steinberg *et al.*, 2011; Roth-Schulze *et al.*, 2016). It is possible that functional redundancy is
326 a characteristic of high abundance taxa detected to be present throughout the year, while seasonal
327 and/or host-specific functions are an attribute of taxa displaying successional patterns. Further
328 studies connecting taxonomy with functional properties will be required to elucidate the degree of
329 functional redundancy or specificity in epiphytic microbial communities.

330 **Experimental procedures**

331 **Sampling**

332 Sampling was performed in the Bay of Funtana, northern Adriatic Sea (45°10'39" N,
333 13°35'42" E). Leaves and thalli were sampled in a meadow of *Cymodocea nodosa* invaded by the
334 invasive *Caulerpa cylindracea* (mixed settlement) and in a monospecific settlement of *Caulerpa*
335 *cylindracea* located in the proximity of the meadow at approximately monthly intervals from
336 December 2017 to October 2018 (Table S1). Leaves and thalli were collected by diving and
337 transported to the laboratory in containers placed on ice and filled with site seawater. Upon arrival
338 to the laboratory, *C. nodosa* leaves were cut into sections of 1 – 2 cm, while *C. cylindracea* thalli
339 were cut into 5 – 8 cm long sections. Leaves and thalli were washed three times with sterile
340 artificial seawater (ASW) to remove loosely attached microbial cells. Ambient seawater was
341 collected in 10 l containers by diving and transported to the laboratory where the whole container
342 volume was filtered through a 20 µm net. The filtrate was further sequentially filtered through 3
343 µm and 0.2 µm polycarbonate membrane filters (Whatman, United Kingdom) using a peristaltic
344 pump. Filters were briefly dried at room temperature and stored at –80 °C. Seawater samples
345 were also collected approximately monthly from July 2017 to October 2018.

346 **DNA isolation**

347 DNA from surfaces of *C. nodosa* and *C. cylindracea* was isolated using a previously
348 modified and adapted protocol that allows for a selective epiphytic DNA isolation (Korlević *et*
349 *al.*, unpublished; Massana *et al.*, 1997). Briefly, leaves and thalli are incubated in a lysis buffer
350 and treated with lysozyme and proteinase K. Following the incubations, the mixture containing
351 lysed epiphytic cells is separated from leaves and thalli and extracted using a phenol-chloroform
352 procedure. Finally, the extracted DNA is precipitated using isopropanol. DNA from seawater

353 picoplankton was isolated from 0.2 μ m polycarbonate filters according to Massana *et al.* (1997)
354 with a slight modification. Following the phenol-chloroform extraction steps 1/10 of chilled 3
355 M sodium acetate (pH 5.2) was added. DNA was precipitated by adding 1 volume of chilled
356 isopropanol, incubating the mixtures overnight at -20 °C and centrifuging at 20,000 \times g and 4 °C
357 for 21 min. The pellet was washed twice with 500 μ l of chilled 70 % ethanol and centrifuged after
358 each washing step at 20,000 \times g and 4 °C for 5 min. Dried pellets were resuspended in 50 – 100
359 μ l of deionized water.

360 **Illumina 16S rRNA sequencing**

361 Illumina MiSeq sequencing of the V4 16S rRNA region was performed as described
362 previously (Korlević *et al.*, unpublished). The V4 region of the 16S rRNA gene was amplified using
363 a two-step PCR procedure. In the first PCR the 515F (5'-GTGYCAGCMGCCGCGTAA-3')
364 and 806R (5'-GGACTACNVGGGTWTCTAAT-3') primers from the Earth Microbiome Project
365 (<http://press.igsb.anl.gov/earthmicrobiome/protocols-and-standards/16s/>) were used (Caporaso
366 *et al.*, 2012; Apprill *et al.*, 2015; Parada *et al.*, 2016). These primers contained on their 5' end
367 a tagged sequence. Purified PCR products were sent for Illumina MiSeq sequencing at IMGM
368 Laboratories, Martinsried, Germany. Before sequencing at IMGM, the second PCR amplification
369 of the two-step PCR procedure was performed using primers targeting the tagged region
370 incorporated in the first PCR. In addition, these primers contained adapter and sample-specific
371 index sequences. Beside samples, a positive and negative control for each sequencing batch was
372 sequenced. Negative control was comprised of PCR reactions without DNA template, while for
373 a positive control a mock community composed of evenly mixed DNA material originating from
374 20 bacterial strains (ATCC MSA-1002, ATCC, USA) was used. Sequences obtained in this study
375 have been deposited in the European Nucleotide Archive (ENA) at EMBL-EBI under accession
376 number PRJEB37267.

377 **Sequence analysis**

378 Obtained sequences were analyzed on the computer cluster Isabella (University Computing
379 Center, University of Zagreb) using mothur (version 1.43.0) (Schloss *et al.*, 2009) according
380 to the MiSeq Standard Operating Procedure (MiSeq SOP; https://mothur.org/wiki/MiSeq_SOP)
381 (Kozich *et al.*, 2013) and recommendations given from the Riffomonas project to enhance data
382 reproducibility (<http://www.riffomonas.org/>). For alignment and classification of sequences the
383 SILVA SSU Ref NR 99 database (release 138; <http://www.arb-silva.de>) was used (Quast *et al.*,
384 2013; Yilmaz *et al.*, 2014). Pipeline data processing and visualization was done using R (version
385 3.6.0) (R Core Team, 2019), packages vegan (version 2.5-6) (Oksanen *et al.*, 2019), and tidyverse
386 (version 1.3.0) (Wickham *et al.*, 2019) and multiple other packages (Xie, 2014, 2015, 2020;
387 Neuwirth, 2014; Xie *et al.*, 2018; Y. Xie, 2019b, 2019a; Allaire *et al.*, 2019; Zhu, 2019). The
388 detailed analysis procedure including the R Markdown file for this paper are available as a GitHub
389 repository (https://github.com/mkorlevic/Korlevic_EpiphyticDynamics_EnvironMicrobiol_2020).
390 Based on the ATCC MSA-1002 mock community included in the analysis an average sequencing
391 error rate of 0.01 % was determined, which is in line with previously reported values for
392 next-generation sequencing data (Kozich *et al.*, 2013; Schloss *et al.*, 2016). In addition, the
393 negative controls processed together with the samples yielded on average only 2 sequences after
394 sequence quality curation.

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399 for access to the cluster Isabella.

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575 **Figure legends**

576 **Fig. 1.** Proportion of shared bacterial and archaeal OTUs (Jaccard's Similarity Coefficient)
577 and shared bacterial and archaeal communities (Bray-Curtis Similarity Coefficient) between
578 assemblages associated with the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C.*
579 *cylindracea* [Mixed and Monospecific Settlement]) and communities in the ambient seawater.

580 **Fig. 2.** Proportion of shared bacterial and archaeal communities (Bray-Curtis Similarity
581 Coefficient) and shared bacterial and archaeal OTUs (Jaccard's Similarity Coefficient) between
582 consecutive sampling points and from the surfaces of macrophytes (*C. nodosa* [Mixed Settlement]
583 and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater.

584 **Fig. 3.** Principal Coordinates Analysis (PCoA) of Bray-Curtis distances based on OTU
585 abundances of bacterial and archaeal communities from the surfaces of macrophytes (*C. nodosa*
586 [Mixed Settlement] and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient
587 seawater. Samples from the same environment or same season are labeled in different colors. The
588 proportion of explained variation by each axis is shown on the corresponding axis in parentheses.

589 **Fig. 4.** Taxonomic classification and relative contribution of the most abundant (> 1 %) bacterial
590 and archaeal sequences on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C.*
591 *cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. NR – No Relative

592 **Fig. 5.** Taxonomic classification and relative contribution of the most abundant (> 1 %)
593 cyanobacterial sequences on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C.*
594 *cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. The proportion
595 of cyanobacterial sequences in the total bacterial and archaeal community is given above the
596 corresponding bar. NR – No Relative

597 **Fig. 6.** Taxonomic classification and relative contribution of the most abundant (> 2 %) sequences
598 within the *Bacteroidota* on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C.*

599 *cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. The proportion of
600 sequences classified as *Bacteroidota* in the total bacterial and archaeal community is given above
601 the corresponding bar. NR – No Relative

602 **Fig. 7.** Taxonomic classification and relative contribution of the most abundant (> 2 %)
603 alphaproteobacterial sequences on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement]
604 and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. The
605 proportion of alphaproteobacterial sequences in the total bacterial and archaeal community is
606 given above the corresponding bar. NR – No Relative

607 **Fig. 8.** Taxonomic classification and relative contribution of the most abundant (> 2 %)
608 gammaproteobacterial sequences on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement]
609 and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. The
610 proportion of gammaproteobacterial sequences in the total bacterial and archaeal community is
611 given above the corresponding bar. NR – No Relative

612 **Fig. 9.** Taxonomic classification and relative contribution of the most abundant (> 1 %) sequences
613 within the *Desulfobacterota* on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C.*
614 *cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. The proportion
615 of sequences classified as *Desulfobacterota* in the total bacterial and archaeal community is given
616 above the corresponding bar. NR – No Relative

617 **Figures**

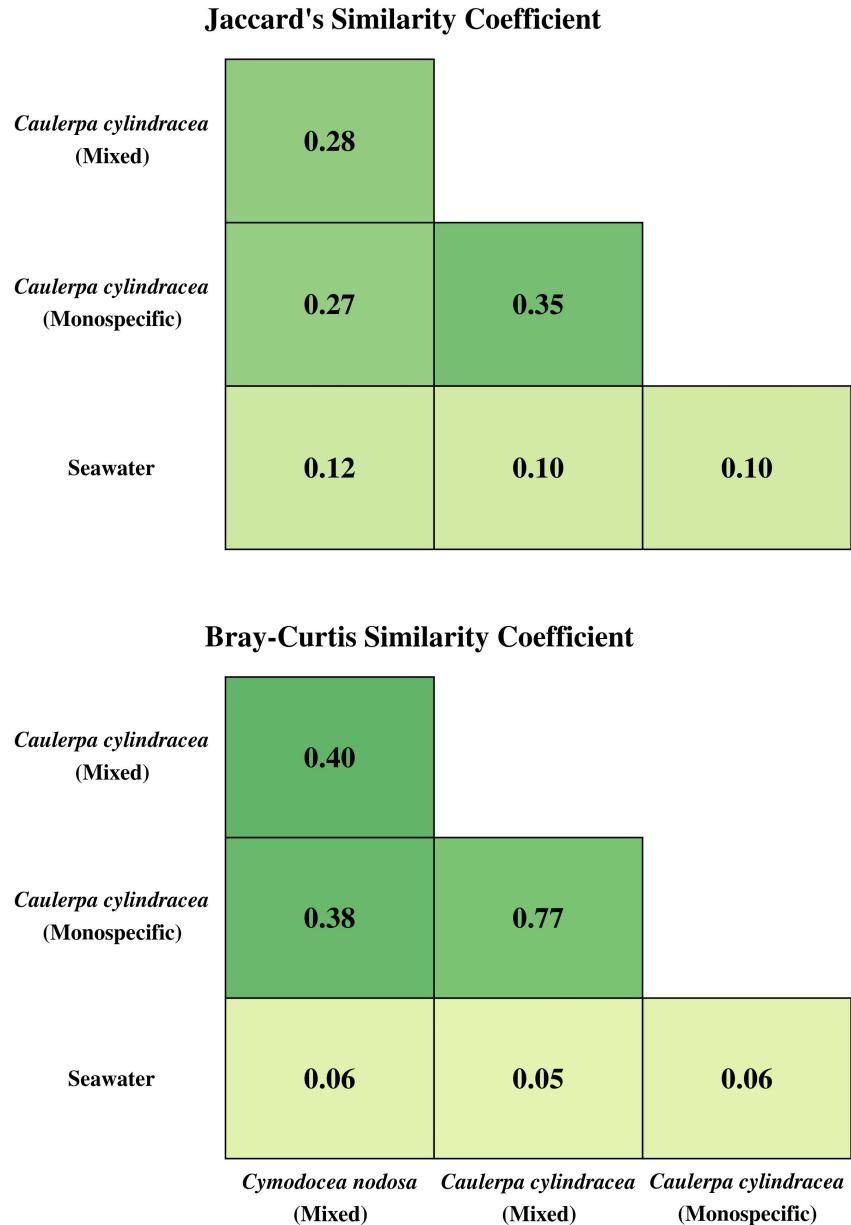


Fig. 1. Proportion of shared bacterial and archaeal OTUs (Jaccard's Similarity Coefficient) and shared bacterial and archaeal communities (Bray-Curtis Similarity Coefficient) between assemblages associated with the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C. cylindracea* [Mixed and Monospecific Settlement]) and communities in the ambient seawater.

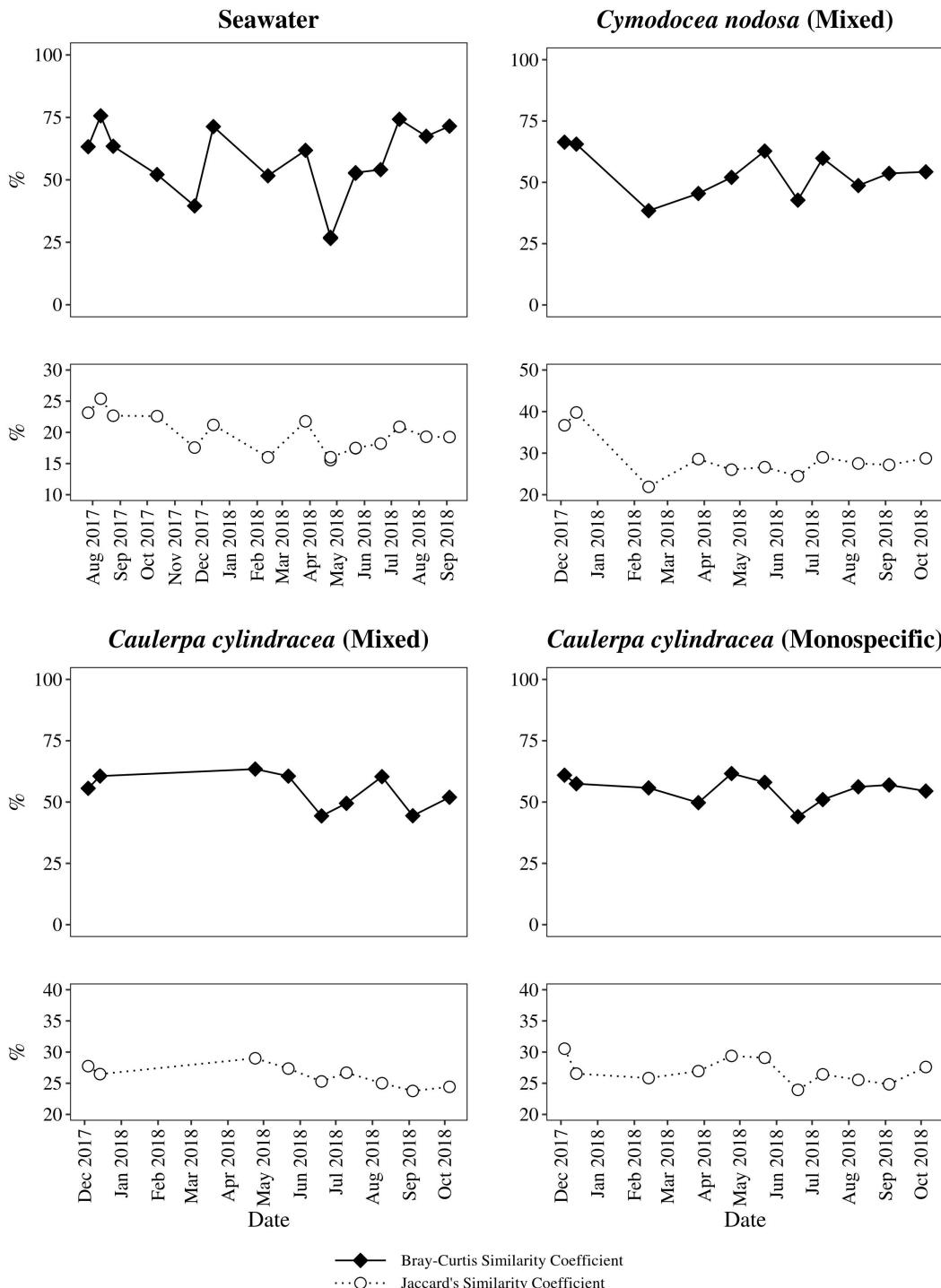


Fig. 2. Proportion of shared bacterial and archaeal communities (Bray-Curtis Similarity Coefficient) and shared bacterial and archaeal OTUs (Jaccard's Similarity Coefficient) between consecutive sampling points and from the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater.

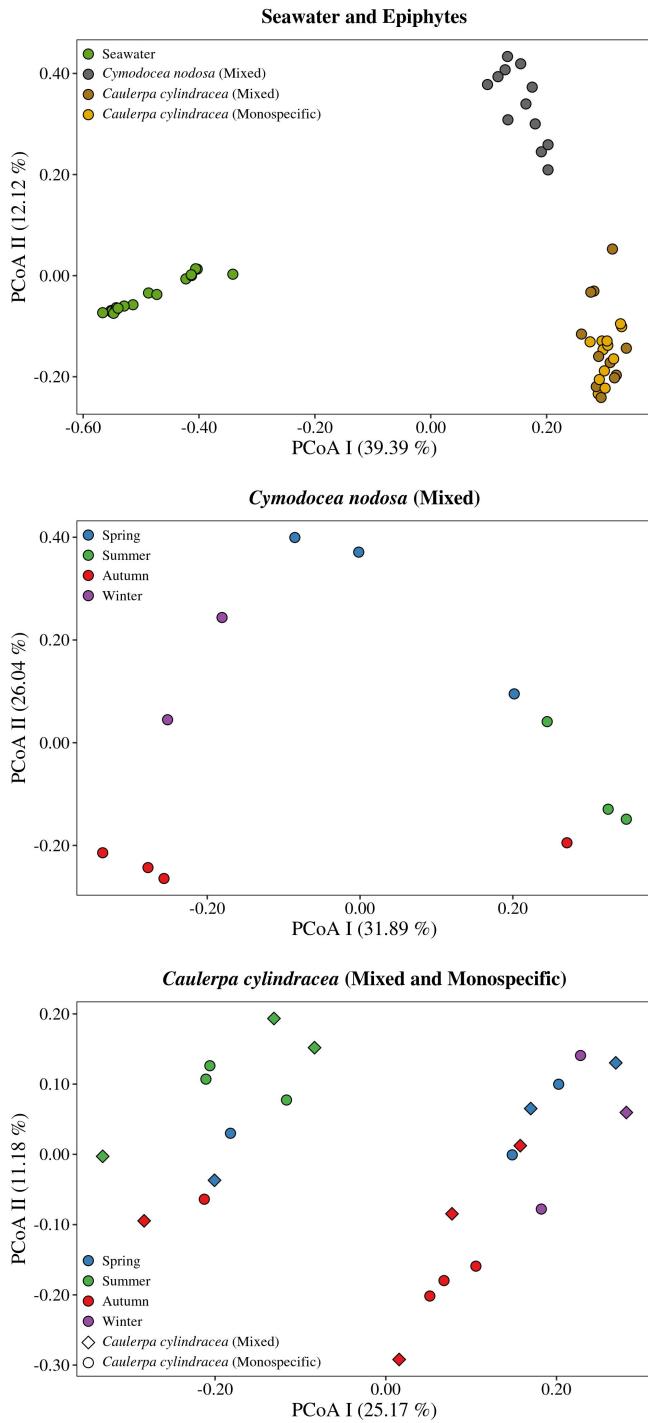


Fig. 3. Principal Coordinates Analysis (PCoA) of Bray-Curtis distances based on OTU abundances of bacterial and archaeal communities from the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. Samples from the same environment or same season are labeled in different colors. The proportion of explained variation by each axis is shown on the corresponding axis in parentheses.

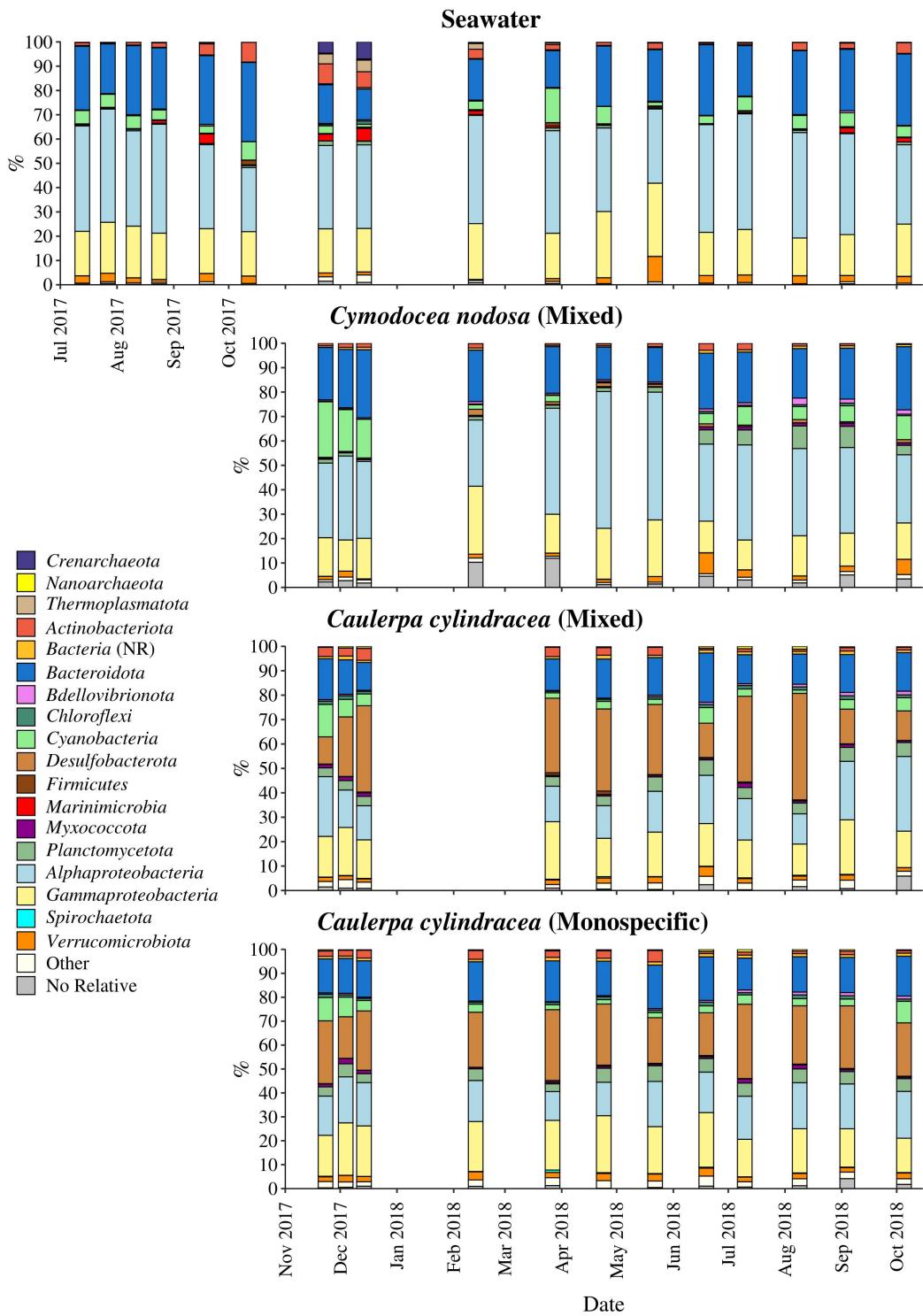


Fig. 4. Taxonomic classification and relative contribution of the most abundant (> 1 %) bacterial and archaeal sequences on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. NR – No Relative

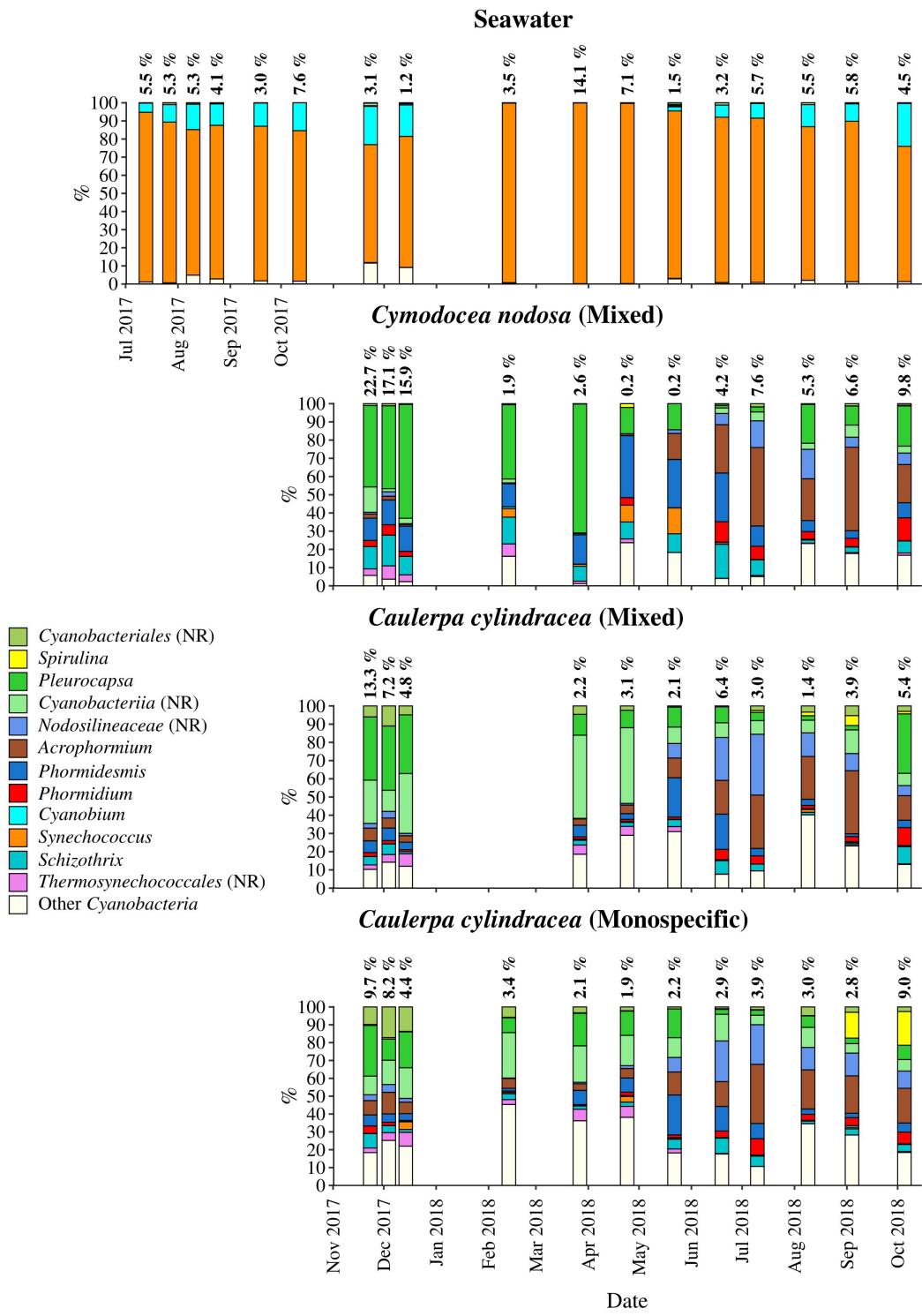


Fig. 5. Taxonomic classification and relative contribution of the most abundant (> 1 %) cyanobacterial sequences on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. The proportion of cyanobacterial sequences in the total bacterial and archaeal community is given above the corresponding bar. NR – No Relative

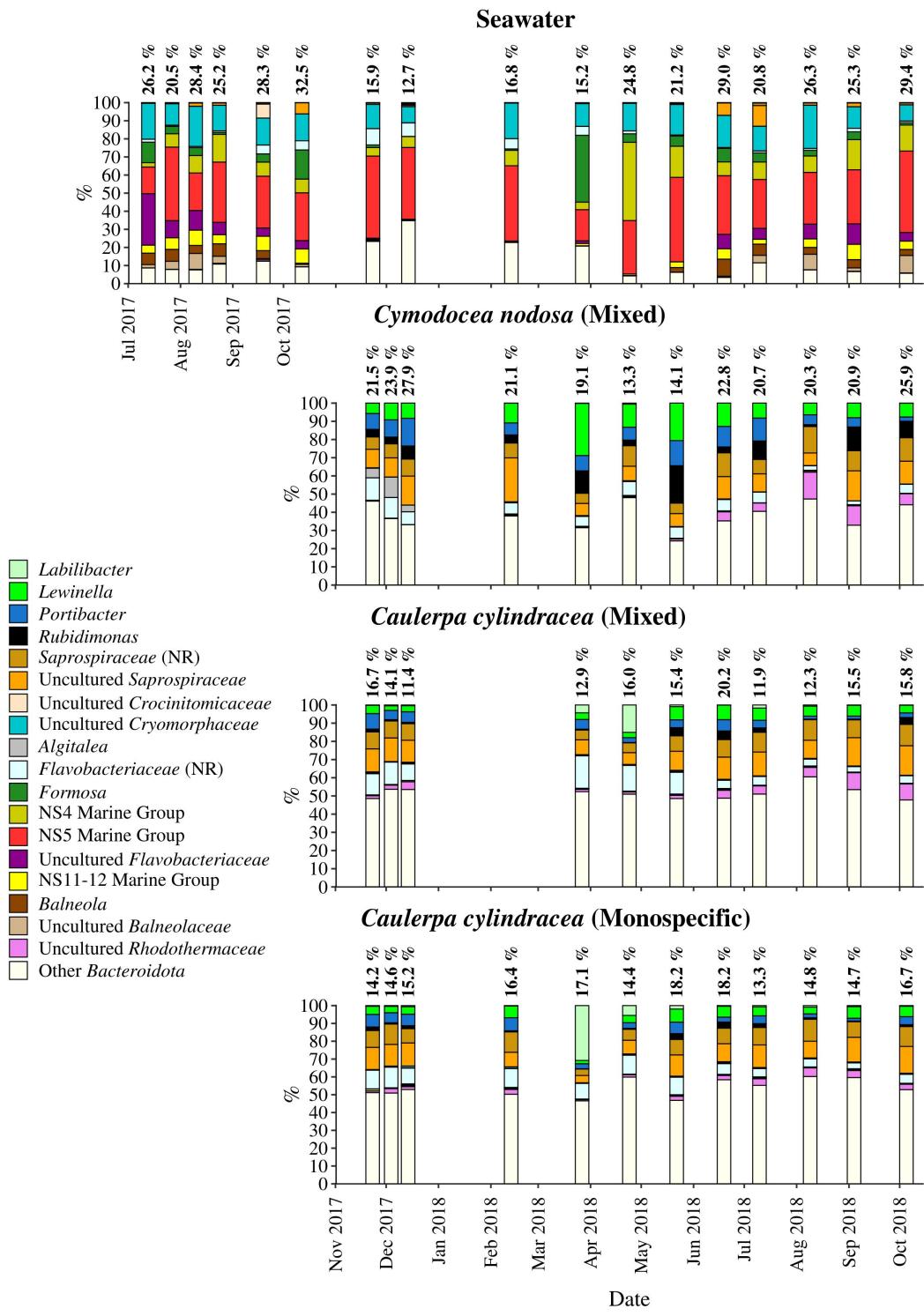


Fig. 6. Taxonomic classification and relative contribution of the most abundant (> 2 %) sequences within the *Bacteroidota* on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. The proportion of sequences classified as *Bacteroidota* in the total bacterial and archaeal community is given above the corresponding bar. NR – No Relative

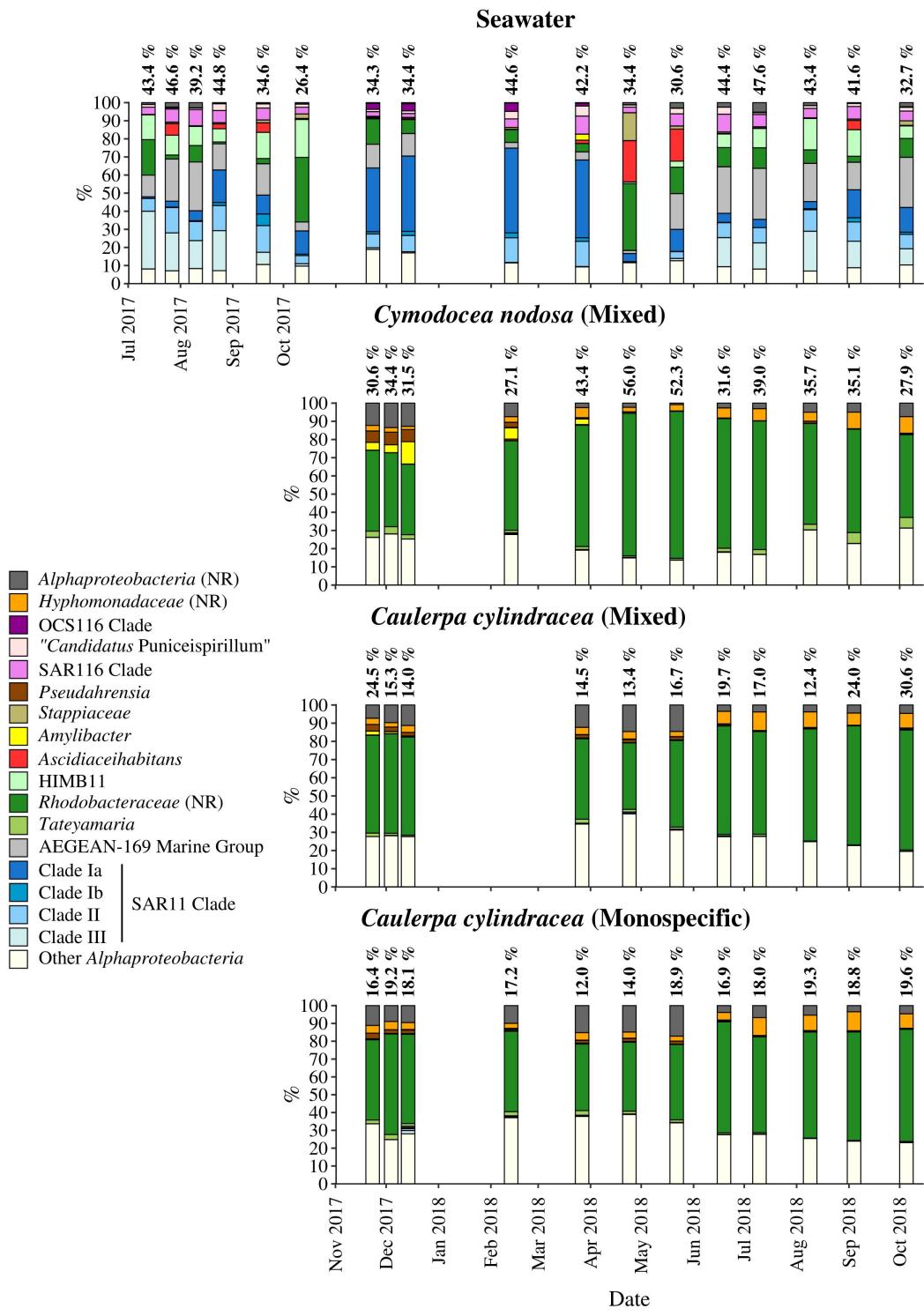


Fig. 7. Taxonomic classification and relative contribution of the most abundant (> 2 %) alphaproteobacterial sequences on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. The proportion of alphaproteobacterial sequences in the total bacterial and archaeal community is given above the corresponding bar. NR – No Relative

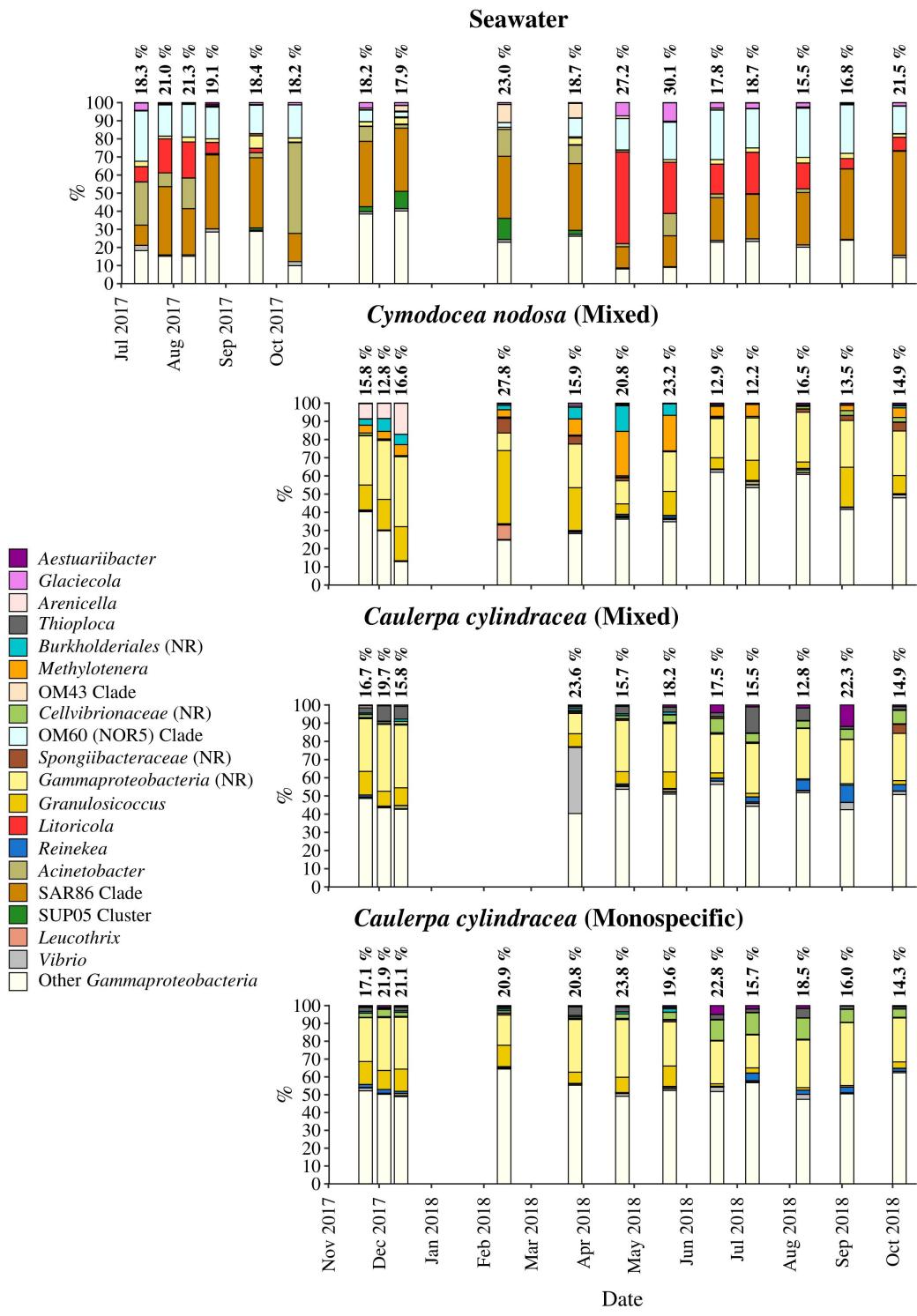


Fig. 8. Taxonomic classification and relative contribution of the most abundant (> 2 %) gammaproteobacterial sequences on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. The proportion of gammaproteobacterial sequences in the total bacterial and archaeal community is given above the corresponding bar. NR – No Relative

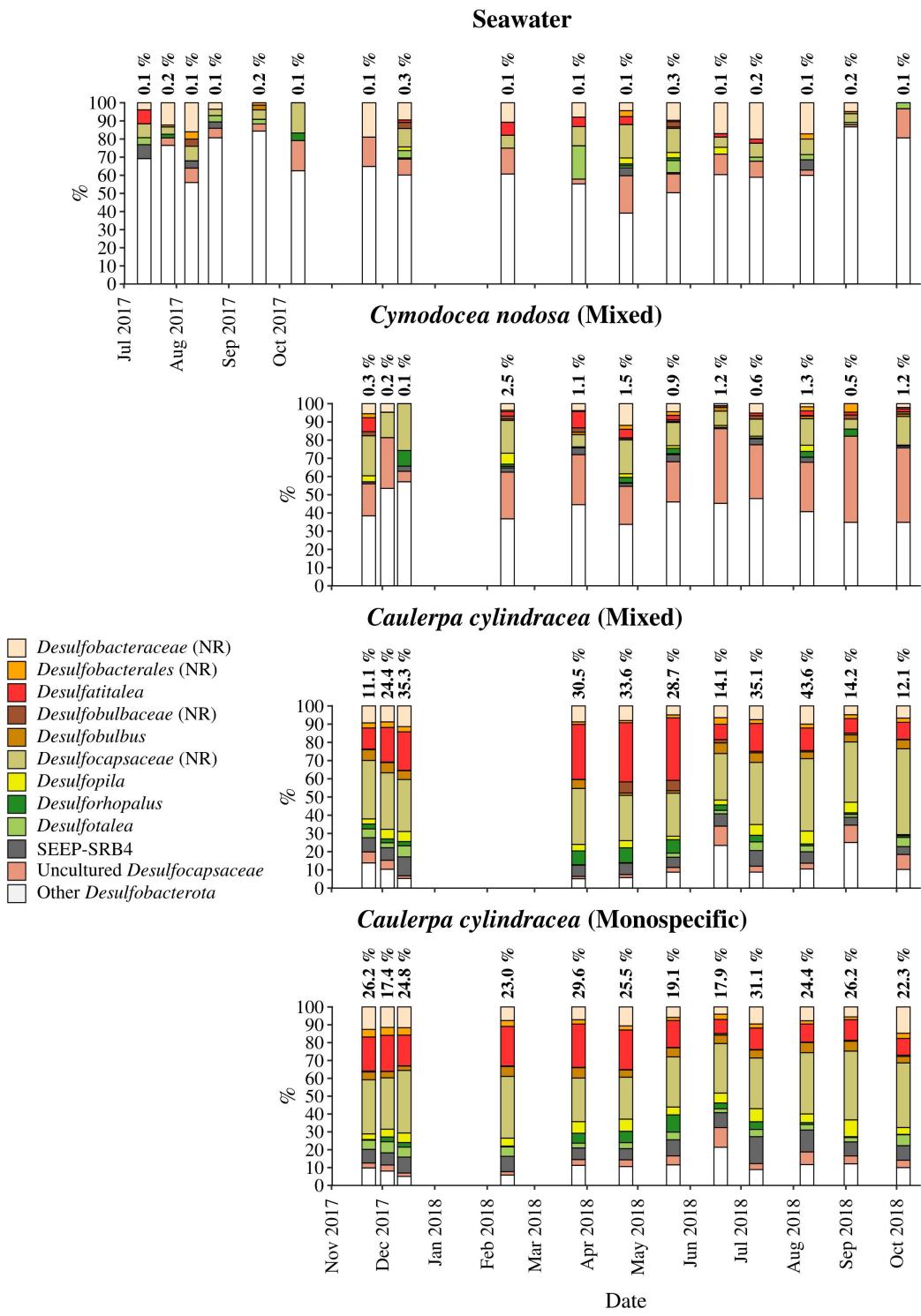


Fig. 9. Taxonomic classification and relative contribution of the most abundant (> 1 %) sequences within the *Desulfobacterota* on the surfaces of macrophytes (*C. nodosa* [Mixed Settlement] and *C. cylindracea* [Mixed and Monospecific Settlement]) and in the ambient seawater. The proportion of sequences classified as *Desulfobacterota* in the total bacterial and archaeal community is given above the corresponding bar. NR – No Relative