Unravelling microalgal-bacterial interactions in aquatic ecosystems through 16S rRNA gene-based co-occurrence networks

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Abstract

Microalgae and bacteria are the most widespread and dominant planktonic organisms of aquatic ecosystems. Their interactions can directly influence the global carbon and nutrient cycling and therefore aquatic ecosystem productivity. A large number of microalgae inhabit the earth but most associations with bacteria are unknown. Compiling knowledge on such associations through conventional methods is labour intensive and impractical. Environmental sequencing data coupled with network analysis can generate microbial-association networks which can reveal taxon co-occurrence patterns. Thus, co-occurrence networks have potential to explore microalgal-bacterial associations in nature. The 16S rRNA marker gene can be used to assess bacteria and

microalgae, as it is present in algal chloroplasts. Here, we used 16S rRNA gene metabarcoding data from 10 Earth microbiome projects to investigate potential interactions between microalgae and bacteria. Co-occurrence patterns were readily revealed, including several previously known associations and a range of potentially new associations such as frequent co-occurrences of *Bacillariophyta* with uncultured *Planctomycetes OM190* and *Deltaproteobacteria order NB1-j*. In accordance with previous work, *Proteobacteria* and *Bacteroidetes* were the bacterial phyla most commonly associated with microalgae. We also detected *Planctomycetes* and *Verrucomicrobia* co-occurring with an array of microalgal groups implying successful associations with microalgae. Moreover, there was no clear taxonomic pattern visible among the co-occurring microalgae and bacteria. Our results also indicate that both intrinsic (metabolic functional potential) and extrinsic (geography) factors may influence microalgal-bacterial associations. This study reports a range of associations between microalgae and bacteria based on co-occurrences networks in aquatic ecosystems. Overall, we demonstrated the potential of co-occurrence networks to identify microalgal-bacterial associations and argue that this technique can serve as a hypothesis-generating framework to guide more focused research.

Keywords: microalgae, bacteria, microalgal-bacterial associations, co-occurrence networks, 16S rRNA gene

Background

Microalgae (photosynthetic micro-eukaryotes) and bacteria are the most widespread and dominant planktonic organisms in aquatic ecosystems. As primary producers, microalgae form the foundations of the food web and directly influence global carbon and nutrient cycling, as well as the energy flow in aquatic ecosystems. A wide spectrum of associations between microalgae and bacteria have been reported, predominantly related to nutrient exchange, with important bottom-up effects on primary production. Associations include increased bioavailability of vitamins (e.g.B12 [1, 2]), metals (e.g. iron [3, 4]) and growth promoting hormones [5] by bacteria in exchange for organic carbon from the algae. Apart from many beneficial interactions, some bacteria can have negative influences on algae by being algicidal and opportunistic pathogens [6, 7]. Thus, algal-bacterial interactions can range from mutualistic to parasitic, and a complex array of interactions can be hypothesised. For instance, previous work suggests that strong associations may exist between communities of microalgae and bacteria over a large geographical range in the open ocean [8]. However, the knowledge we have so far about specific microalgal-bacterial interactions represents only a small fraction of what potentially occurs in nature. Microalgae are highly diverse and innumerable, therefore gathering knowledge on their associations with equally ubiquitous and diverse bacteria is challenging.

High-throughput DNA sequencing such as 16S and 18S rRNA gene metabarcoding has been used to deliver insights into bacterial and eukaryotic community composition of diverse ecosystems. Microbial community abundance data can be used to identify associations between community members via microbial association networks [9]. A network consists of nodes representing taxa and edges representing the associations between taxa. Microbial association networks targeting positive correlations are termed co-occurrence networks. A positive relationship is presumed when taxonomically relevant units co-occur or exhibit similarity in their compositions over multiple samples [10] and biologically meaningful groups or communities of a network can be identified with network clustering [11]. Also, network metrics such as node degree, closeness centrality for example, can be used for quantitative description of communities and identify ecologically important taxa [12, 13]. Various network analyses have reported co-occurring microbial taxa in different environments, identified clusters of microbes representing metabolic consortia, defined keystone species, and documented recurrent microbial modules [[14–16]. Overall, networks provide insights into the structure of a community and taxon co-occurrence patterns, offering perspectives to use them to generate hypotheses about interactions that can be investigated with more focused studies. Thus, environmental sequencing data combined with network analysis can be a convenient addition to the toolkit for deriving interactions between organisms across myriads of environments.

Studies targeting 16S rRNA marker genes are generally focused on the bacterial communities and often disregard the chloroplast sequences that are also amplified. The shared origin of the chloroplasts of all oxygenic photosynthetic micro-eukaryotes and cyanobacteria [17] enable the use of 16S rRNA marker gene to concurrently estimate relative abundances of microalgae and bacteria across samples, facilitating the construction of correlation networks to identify co-occurring taxa and speculate on their potential interactions. Robust co-occurrences can be detected through analysis of a sufficient number of samples, ideally covering temporal and spatial gradients, as these provide adequate variability in taxon abundances [9]. This can be coupled with stringent network building steps such as filtration of low prevalence organisms to reveal significant co-occurrences [18]. The ever-expanding sequence databases can be a great starting point to investigate such correlations. Analysis of Tara Ocean dataset based on interaction networks has shown that environment and geography can only explain 18% of plankton community variation, while 95% of models based on Operational Taxonomic Units (OTU) composition alone were more accurate [19]. Similar observations have been shown in phytoplankton blooms where environmental parameters were insignificant in influencing the community structure of plankton [20]. These results indicate that biological interactions are more influential in determining the community structure than environmental factors. Thus, taxon-taxon co-occurrence networks built on taxon compositions

alone could capture potential interactions in nature. Our work is based on the premise that unknown associations between microalgae and bacteria may be discovered at large scales from existing 16S rRNA gene-based metabarcoding datasets using co-occurrence networks.

We investigated taxon-taxon co-occurrence networks to discover potential microalgal-bacterial interactions using 16S rRNA gene metabarcoding datasets from the Earth Microbiome Project (EMP) that have sampled aquatic environments (both marine and freshwaters including water column and sediment samples) and analysed them individually to recover co-occurring microalgae and bacteria using co-occurrence networks. Network modules, which represent ecological communities, were used to identify tight co-occurrences and in some instances were coupled with network metrics to evaluate the ecological relevance of taxa of interest. Using this approach, co-occurring taxa were recovered, representing both known and unknown associations. Discussion of some of these new discoveries are provided in detail to set the stage for future research.

Methods

Data Acquisition

Publicly available EMP datasets [21] were screened using the Qiita portal [22] and 10 studies (4 marine and 6 Freshwater environments) targeting aquatic environments were selected. Since the goal of this study was to individually

analyse samples representing a particular environment and reveal co-occurrences, studies targeting any aquatic samples (water and sediment samples) were selected. To our knowledge, based on study and sample information provided on qiita portal for the selected studies, no size fractionation was carried out on the samples (water samples) provided to EMP. The data analysed in this study have amplified the same 16S rRNA gene V4 hypervariable region using 515F- 'GTGCCAGCMGCCGCGGTAA' and 806R- 'GGACTACHVGGGTWTCTAAT' primer pair [23, 24] and sequenced on Illumina Hiseq2000. Detailed information on the selected EMP projects can be found in Supplementary material (Table S1) and can also be further explored using Qiita ids provided using the Qiita portal.

Sequencing Data Workflow

Raw demultiplexed reads were downloaded using the EBI accessions (provided in Qiita portal) from the European Nucleotide Archive and analysed individually employing a single bioinformatic pipeline built on Qiime2 version 2019.10 [25]. Primer sequences attached to all reads were trimmed using cutadapt [26]. Sequence denoising, chimera checking and dereplication was performed in DADA2 [27] to correct sequencing errors and remove low quality bases. Reads were truncated based on a median quality score of 30. The final outputs of DADA2, an abundance table of Amplicon Sequence Variants (ASVs) and fasta sequences of the ASVs were further processed as described hereafter. Taxonomy was assigned against Silva v132[30] 16S rRNA gene sequences trained with a

Naive Bayes classifier [28]. Chloroplast sequences were filtered using the Silva taxonomy file by identifying sequences assigned as “chloroplast”. These chloroplast sequences were then classified again using a Qiime2-compatible version of PhytoRef[29] database accessed at [30]. All the algal identities with PhytoRef had a confidence score of 0.7 or higher. Due to varying taxonomic confidence of each algal node, taxonomic rank Class will be used for their taxonomic identities. Where relevant, lower taxonomic affiliations will be provided.

The DADA2 abundance table was filtered to create a bacteria-only abundance table (by removing mitochondrial, Archaeal and chloroplast ASVs) and a chloroplast-only abundance table (by retaining only the ASV ids assigned as chloroplast). The bacteria-only table was then collapsed at the genus level to reduce weak links in downstream network building [31] and was merged with the chloroplast-only table to create the final abundance table. ASVs identified as microalgae were not collapsed since the 16S rRNA gene marker is highly conserved in algae and ASVs likely correspond to species or higher-level taxa [29]. This final abundance table was filtered to remove low prevalence organisms present in less than 10% of samples to prevent them from introducing artefacts in network inference.

Correlation analysis and network construction

We used a compositional data analysis tool, FastSpar [32], which is a rapid and parallelizable implementation of the SparCC algorithm [33] to compute correlations. FastSpar quantifies the correlation between all ASVs and assesses the statistical significance (p-values) of the inferred correlations using a bootstrap procedure. The correlation and p-value matrices created by FastSpar were used to create a network of significant correlations for each study separately. Co-occurrence networks were created using the igraph package [34] in R studio version 1.4.1106. Undirected weighted networks were created using statistically ($p<0.05$) significant correlations >0.5 or higher (0.5 for freshwater and 0.6 for marine datasets). Coefficient cut-off of 0.5 was selected for freshwater datasets as a value above that resulted in fewer algal nodes in networks compared to 0.5. The idea behind the coefficient cutoff selection was to preserve as many links as possible with microalgae in resulting networks while choosing a considerably higher coefficient cut off to report stronger links. Networks were visualised in Cytoscape version 3.8 [35].

Network Analysis and module detection

The Network Analyzer plugin [36] in Cytoscape was used to compute global network properties of each network to get an overview of node specific and edge-specific attributes. Networks were checked for the scale free nature by identifying the presence of highly connected nodes coexisting with nodes with fewer links

[37] using the node attributes. In order to identify communities, networks were clustered using the Cytoscape plugin clusterMaker [38] using the MCL clustering algorithm [39] with an inflation value of 2.0. Co-occurring microalgae and bacteria were identified using resulting modules (modules with nodes > or = 4). These co-occurring taxa (identified beyond the taxonomic rank Phylum) were recorded for each environment and summarised in heatmaps using Pheatmap v1.0.12 [40] in R.

Results and Discussion

16S rRNA gene co-occurrence networks can recover microalgal-bacterial associations

Our data show clear evidence for co-occurrences between microalgae and bacteria in aquatic habitats through network analysis of 16S rRNA metabarcoding data (Figure 1 and 2). From the 10 co-occurrence networks generated, we observed highly connected nodes coexisting with nodes with fewer links. This indicates the scale-free nature of the networks, a characteristic in real world networks [41, 42]. The clustered networks (modules/communities) comprised nodes representing microalgae or bacteria and the edges between them were instances of co-occurrence. Analysis of the modules identified 40 algal nodes associated with at least one of 76 bacterial nodes in marine environments (Figure 1, Table S2) and 112 algal nodes with at least one of 311 bacterial nodes in freshwater environments (Figure 2, Table S3).

These bacterial nodes were represented by different phyla such as *Proteobacteria*, *Bacteroidetes*, *Planctomycetes* and *Chloroflexi* (Figure S1). The summary of inferred associations showed that *Proteobacteria* and *Bacteroidetes* were the most common bacterial phyla associated with microalgae. Previous studies, using different techniques, have also found these two phyla to be the major bacterial groups affiliated with microalgae [43–45]. The microalgal nodes recovered too represented diverse phyla such as *Cryptophyta*, *Ochrophyta*, *Haptophyta*, *Chlorophyta*, *Streptophyta* and *Euglenophta* representing 17 different taxonomic classes.

We then investigated if this network approach can recover known associations. The inferred associations were investigated at a lower taxonomic level to identify known bacterial associates of microalgae proven using other techniques. We recognized known bacterial associates of microalgae such as *Flavobacteriales* [46, 47], *Rhizobiales* [48, 49],*Cytophagales* [50, 51] and *Rhodobacterales* [52] .Previously reported associations of microalgal genera with specific bacterial groups were also recovered in the analysis, including that between *Bacteroidetes* and the cosmopolitan *Prymnesiophyceae* genus *Phaeocystis* [53–55] (Table S2) and that of diatoms (*Bacillariophyta*) with the genus *Flavobacterium* (Table S3) [56–58]. The ability to identify previously known microalga-bacterial

associations suggest that the network approach used in this study can yield biologically meaningful results and can be further used to identify potential interactions which were previously unknown.

Emerging microalgal-bacterial associations that can guide functional studies

Our co-occurrence network analysis identified potential new interactions that have not been previously described. For instance, uncultured *Deltaproteobacteria* order *NB1-j* was identified as consistently co-occurring with *Bacillariophyta* in marine environments. In one environment where the *NB1-j-Bacillariophyta* link was observed (Surface water samples from Western English Channel, EBI accession-ERP016541), *Bacillariophyta* was the only microalgal node directly interacting with *NB1-j*. In another environment (Seawater metagenome samples from Catlin arctic survey (2010 expedition), EBI accession ERP020022), *NB1-j* was identified as the hub node with the highest node degree (43), in an algal-bacterial module consisting of 77 nodes and 817 edges. Node degree is the number of edges connected to a node. Hub nodes represent highly connected species and are usually considered as keystone species [59]. This *NB1-j* node also had the highest closeness centrality [0.69]. Closeness centrality measures how close a node is to another node and helps to identify centrally positioned taxa in the network [18]. Other than this *NB1-j* node, there were 3 more *NB1-j* nodes in this community. All together these 4 *NB1-j* nodes were directly interacting

(edges) with 57 nodes (out of 73 other nodes) of which 25 were representing microalgal nodes (Figure 3). Out of the 25 microalgal nodes, 13 represented the taxonomic class *Bacillariophyta*. Some of these *Bacillariophyta* were taxonomically identified at genus level as *Chaetoceros* and *Fragilariopsis*. Interestingly, except for one, all of these Bacillariophyta nodes represented top hub nodes of the community with node degrees > 26. Most connected taxa are believed to have ecological relevance to the community as their removal causes the highest impact on many associations [60].

Functional roles of *NB1-j* in marine ecosystems are largely unknown. It is believed to be involved in hydrocarbon degradation [61] and has been reported mostly from marine sediments [62, 63], mud volcanoes [61], sponges [64] and cyanobacterial mats [65]. To the best of our knowledge, this *Deltaproteobacteria* group is not reported in algal microbiomes. A predictive metagenomic approach based on sponge samples originating from reef sites in West Java (Indonesia) suggest that *NB1-j* may be involved in nitrogen metabolism [64]. It was found that *NB1-j* was responsible for the elevated predictive gene count corresponding to N-cycling genes such as those encoding nitric oxide reductase (*norB)*, nitrogenase (*nifD*) and hydroxylamine reductase. The available information indicates that the nitrogen cycling capacity of *NB1-j* may underly its association with algae, potentially facilitating the nitrogen needs of the algae while benefiting from algal organic carbon. However, a repertoire of interactions, as often

expected from a keystone species, can be hypothesised between *NB1-j* and microalgae in a community.

Bacillariophyta (*Fragilariopsis*, *Chaetoceros* and many other diatoms unidentified at lower taxonomic levels) also showed frequent co-occurrences with an uncultured clade of *Planctomycetes*, *OM190* (SILVA taxonomy) in both freshwater and marine environments. In the Catlin arctic survey samples (ERP02022), *OM190* demonstrated frequent associations with *Bacillariophyta*. Three *OM190* nodes were observed with high node degrees (29, 30 and 39) and these were directly connected to 59 nodes out of a total of 74 other nodes in the community. From the total of 35 microalgal nodes in this community, *OM190* were directly connected to 27 nodes out of which 15 nodes were represented by *Bacillariophyta* (Figure S2A). Similarly in a freshwater environment (Lake Superior, Michigan, EBI accession: ERP016492), *OM190* was identified as the 6th most connected node with a node degree of 89 and was directly connected to 32 microalgal nodes including *Bacillariophyta* (Figure S2B). As mentioned previously, highly connected nodes act as hub nodes in the community. Multiple *OM190* acting as top hub nodes within their habitats indicate that they have high co-occurrences with both microalgae and bacteria in their communities.

OM190 shows deep branching within the *Planctomycetes* group and is usually found in different environments such as soil and seawater. Members of this clade are usually considered to be associated with macroalgae [66], such as red [67] and brown algae [68]. Since *OM190* is yet uncultured, information on its metabolism is scarce. A metagenome-assembled-genome (MAG) for *OM190* (Likely *OM190*) with a rich diversity of secondary metabolite potential has been reported [69]. The production of secondary metabolites by *OM190*, including antimicrobial compounds may be one of the underlying reasons for their association with algae as they could protect the alga from undesired microbes. In a recent study [70], it was shown that diatoms produce fucose-containing sulfated polysaccharides (FCSP) which can be hypothesised as an energy source for *OM190*. Many *Planctomycetes* have abundant sulfatases, but these were not confirmed in the existing *OM190* MAG.

More generally speaking, *Planctomycetes* often associate with macroalgae and favour a biofilm lifestyle [68]. Protein clusters that may be involved in *Planctomycetes* symbiosis or biofilm maintenance have been reported [71], and production of sulfated polysaccharides by the alga that serve as the substrate for the abundant sulfatases produced by the *Planctomycetes* contributes to the reasons for successful associations between them [66, 71]. Although successful associations are known between macroalgae and *Planctomycetes*, interactions with microalgae are largely unknown. Apart from their associations with diatoms,

our network analysis identified taxa representing *Planctomycetes* (c_*Phycisphaerae*, c_*Planctomycetacia*) co-occurring with a range of microalgal groups. In a previous study, *Planctomycetes* closely related to *Pirellula* were identified as one of the dominant lineages associated with diatom blooms [72]. Results of our network analysis demonstrate that associations between *Planctomycetes* and microalgae may be as common as those they maintain with macroalgae. The role of *Planctomycetes* bacteria in global nitrogen, carbon and sulphur cycles is gaining attention [71, 73]. Thus, microalgal-*Planctomycetes* associations may be playing a crucial role in the global environmental cycles.

Members of the Gammaproteobacterial order *Cellvibrionales* were commonly associated with microalgal groups including *Prymnesiophyceae*, *Bacillariophyta*, *Cryptophyceae* and *Dictyochophyceae* in both marine and freshwater environments. The *Cellvibrionales* were taxonomically identified as *Halieaceae* and *Porticoccaceae*. They are considered oligotrophs and include strains capable of photoheterotrophic growth using light harvesting pigments such as proteorhodopsin [74]. As photoheterotrophs, they use light to generate energy and organic carbon compounds from the environment to satisfy their carbon needs [75]. *Cellvibrionales* benefit from associations with microalgae like *Mychonastes* [76]. They can assimilate organic carbon sources such as starch and glucose, suggesting they may benefit from the association by satisfying their carbon requirements to support the photoheterotrophic growth [77]. In return,

microalgae may be benefiting from the products of organic carbon remineralisation. The associations inferred from our network analysis showcases the ability of this bacterial group to potentially interact with a wide range of microalgae.

Verrucomicrobia were also consistently associated with an array of microalgae in fresh and marine environments indicating that they may be common associates of microalgae. Here in our study, all the Verrucomicrobial members co-occurring with microalgae in microalgal-bacterial communities were represented by the taxonomic class *Verrucomicrobiae*. Among the genus-specific associations revealed in our network analysis is that of the Verrucomicrobial genus *Lentimonas* and microalgal genera *Pyramimonas* (c_*Prasinophyceae*), *Phaeocystis*, *Tisochrysis*, *Haptolina*, and *Chrysochromulina* (c_*Prymnesiophyceae*). A recent study showed hundreds of *Lentimonas* enzymes able to digest brown algal fucoidan [78]. Although fucose-containing sulphated polysaccharides were regarded as a macroalgal polysaccharide, microalgae such as diatoms have the potential to produce them [70]. Our work suggests that other microalgae might produce these sulfated polysaccharides as well, or that members of *Lentimonas* may have a broader palate than just FCSP. Although widely distributed, functional roles of *Verrucomicrobia* in the aquatic ecosystem are not well understood. Primary reason for this is the lack of many cultured strains [79]. Some members of *Verrucomicrobia* have been shown to consume

algal extracellular polymeric substances [80–82] but little is known about other factors contributing to the associations between *Verrucomicrobia* and algae.

Both Intrinsic and Extrinsic factors influence microalgal-bacterial associations

There was no clear taxonomic pattern observed among the co-occurring microalgae and bacteria. In accordance with previous work on phytoplankton-bacteria co-occurrences [8], taxonomically diverse bacteria co-occurred with different microalgal groups. Since 16S rRNA gene is highly conserved in algae, and the sequenced fragment is short, most of the recovered algal nodes could not be identified at the species level. Therefore, we observed the co-occurring bacterial taxa of the same algal genus within and between environments and did not identify similar patterns. Moreover, except for a few, there was no recurrence of bacterial genera (the lowest taxonomic identity of bacterial nodes used in this study) across microalgal-bacterial communities of different environments. A plausible explanation for such observation could be the sample origin or geography. Interestingly, a recent study [83] has provided evidence for biogeographic differentiation of algal microbiomes, showing ecological boundaries driven by differences in environmental conditions altering the spatial scaling of the algal microbiomes.

To understand if there is any factor driving general patterns of interactions, some insights may be gleaned from known functions of the co-occurring bacteria. We noted that general patterns of interactions could be observed at a functional level. Our observation was that functional similarities are usually seen among the bacterial associates in different microalgal communities although they are taxonomically different. For instance, microalgae co-occur with bacterial groups equipped with specific metabolic functional potentials such as algal polysaccharide degradation and provision of vitamins. Co-occurrences with taxonomically diverse members of *Bacteroidetes* [55] and *Verrucomicrobia* [80] with polysaccharide degradation ability and *Rhizobiales* [84], *Rhodobacterales* [85] and *SAR116* [86] with Vitamin B12 synthesis ability can be cited as examples. As a summary, these results suggest that both intrinsic (functional) and extrinsic (geography) factors influence microalgal-bacterial associations.

Conclusion

Our study identified a range of interactions between microalgae and bacteria including both known and unknown associations. Network analysis indicated that there is no clear taxonomic pattern with regard to microalgal-bacterial associations. General patterns of interactions were observed at a functional level indicating the influence of intrinsic factors on these associations. The identification of previously known microalgal-bacterial associations suggests that the network approach used in this study yields biologically meaningful results and identifies a broad range of previously unknown algal-bacterial interactions.

Our study illustrates the promise of using 16S rRNA gene-based co-occurrence networks as a hypothesis-generating framework to guide focused research in future to clarify the functional nature of these potential interactions. The recovered associations will help enrich our understanding of the microalgal-bacterial interactions in aquatic ecosystems.

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Availability of data and material

No data was generated in this study and all the data analysed are publicly available. The EMP datasets analysed are available in European Nucleotide Archive and EMP Qiita portal under the Accession numbers and Qiita ids, respectively, provided in Supplementary material TableS1. FastSpar script used for the correlation analysis, R script used in generating networks and the networks files generated in Cytoscape can be found at https://melbourne.figshare.com/projects/Unravelling_microalgal-bacterial_interactions_in_aquatic_ecosystems_through_16S_rRNA_gene-based_co-occurrence_networks/140071

Competing interests

The authors declare that they have no competing interests

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Authors' contribution

UP, HV and AW formulated the project. UP analysed the data and wrote the manuscript with inputs from all the authors. HV, AW and KT contributed ideas and helped with analysis. All authors read and approved the final version of the manuscript.

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Figure legends

Figure 1: Summarised interactions in marine environments

Heatmap of co-occurring microalgae (columns) and bacteria (rows) in marine environments. “Taxonomy” represents the taxonomic affiliations of microalgal nodes at class level. “Taxonomy2” represents the taxonomic affiliations of bacteria (p_, c_, o_, f_ and g_ represent Phylum, Class, Order, Family and Genus, respectively). “Project” represents the accession numbers of EMP projects and indicate which project the microalgal and bacterial nodes were recovered from.

Figure 2: Summarised interactions in Freshwater environments

Heatmap of co-occurring microalgae (columns) and bacteria (rows) in freshwater environments**.** “Taxonomy” represents the taxonomic affiliations of microalgal nodes at class level. “Taxonomy2” represents the taxonomic affiliations of bacteria (p_, c_, o_, f_ and g_ represent Phylum, Class, Order, Family and Genus, respectively). “Project” represents the accessions of EMP projects and indicate which project the microalgal and bacterial nodes were recovered from.

Figure 3: Interactions of the Deltaproteobacterial order *NB1-j* with microalgae in a marine environment.

Figure shows the first neighbours (directly interacting taxa) including microalgal taxa co-occurring with Deltaproteobacterial order *NB1-j*. Nodes are labelled at the order level (If unclassified at the order level, higher taxonomic affiliations are provided). The edge width and node size are continuously mapped to edge weight (correlation strength) and node degree, respectively.

Supplementary Data

Figure S1: Major bacterial Phyla associated with microalgae in freshwater and marine environments

Bars represent the number of bacterial nodes affiliated with each phylum. The total number of bacterial nodes identified to be co-occurring with microalgae in marine environments were 76 and freshwater environments were 311.

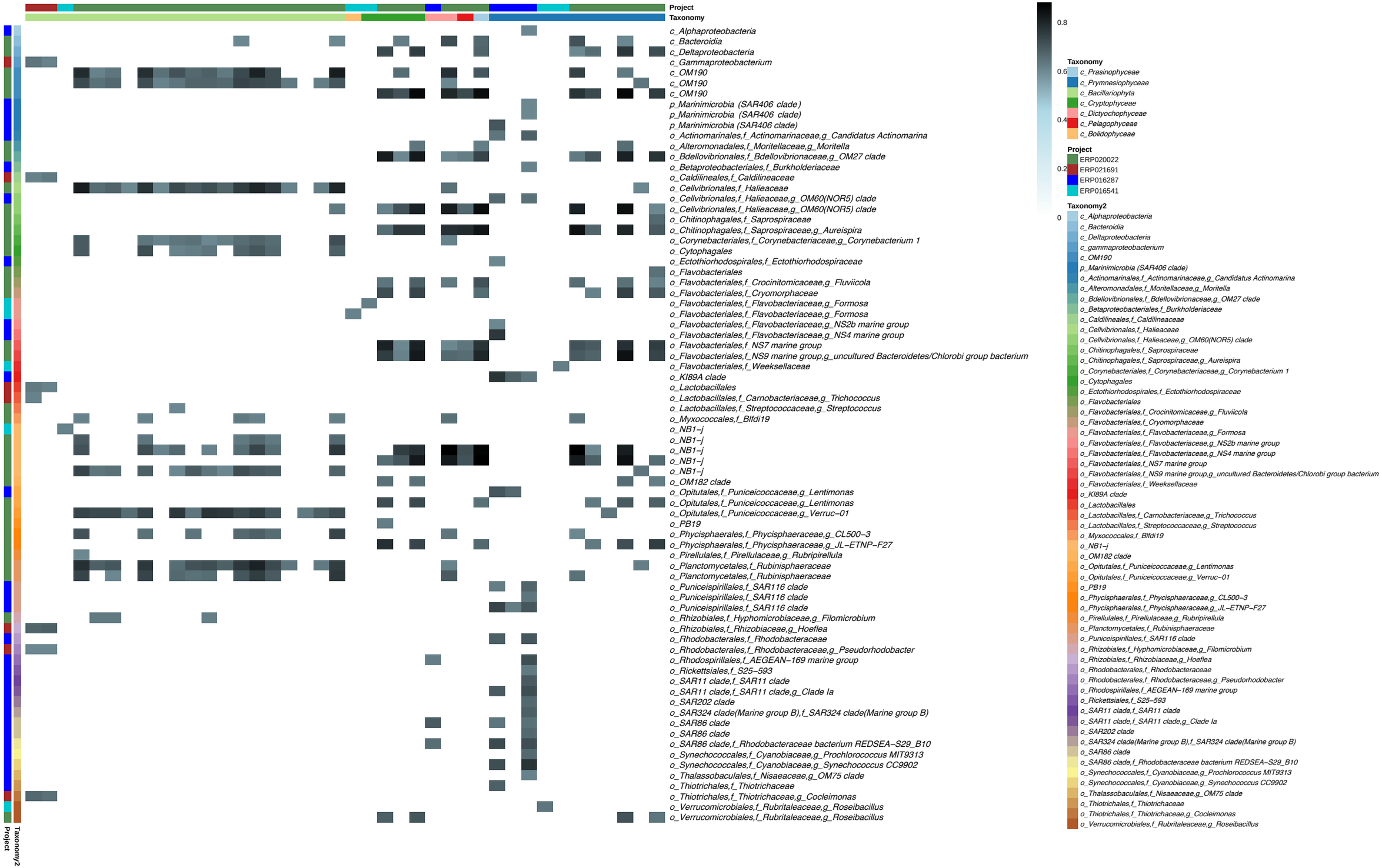
Figure S2: *Planctomycetes* class *OM190* interacting with microalgal taxa in a marine (A) and freshwater (B) environment.

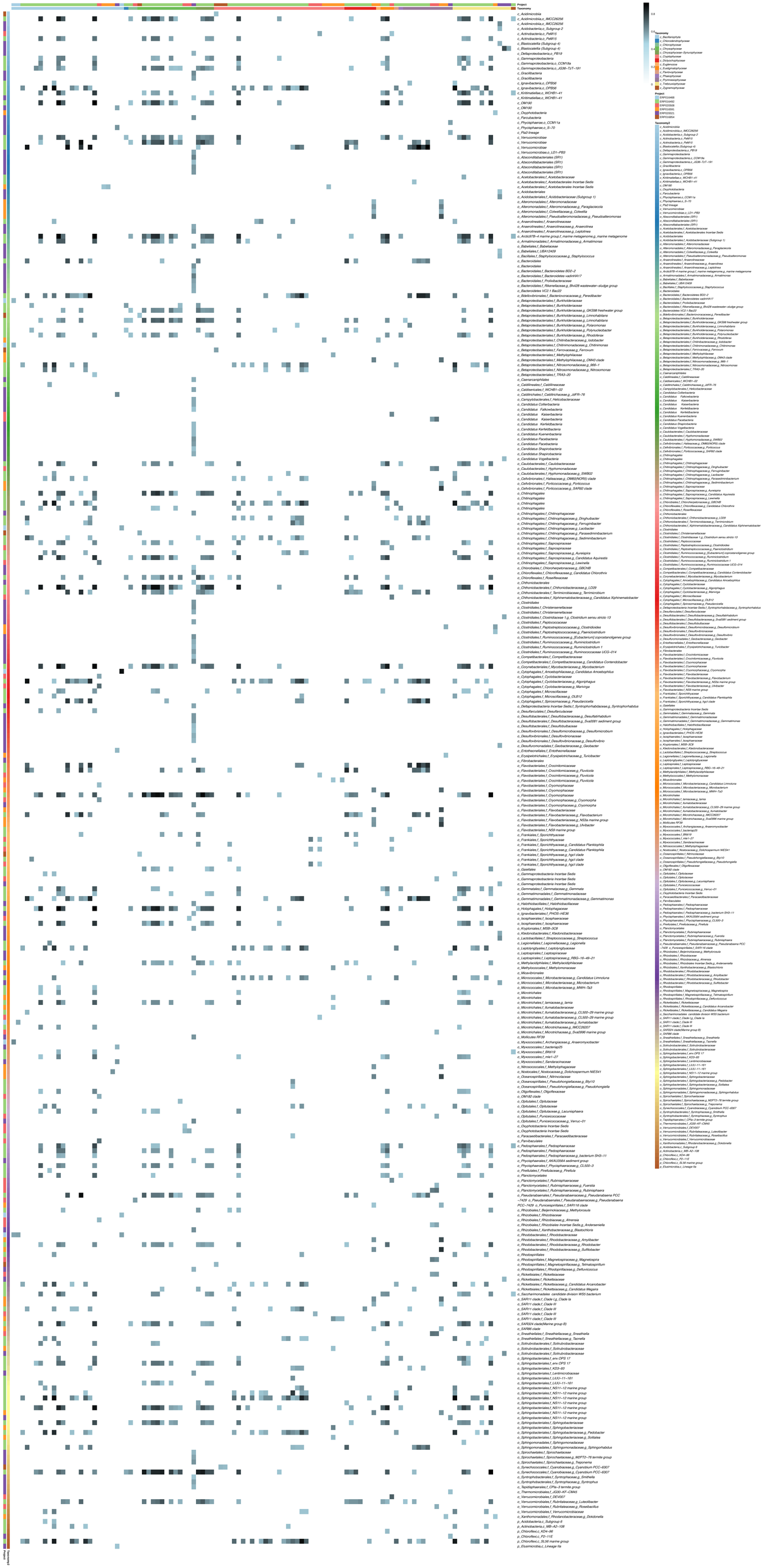
Networks (A, B) created from a microalgal-bacterial module by selecting the first neighbours of the *OM190* to showcase the complex interactions with the neighbouring microalgal taxa. The edge width and node size are continuously mapped to edge weight and node degree. Marine and Freshwater environments represent EMP project ERP020022 and ERP016492, respectively. Nodes labelled at order level (If unclassified at the order level, higher taxonomic affiliations are provided).

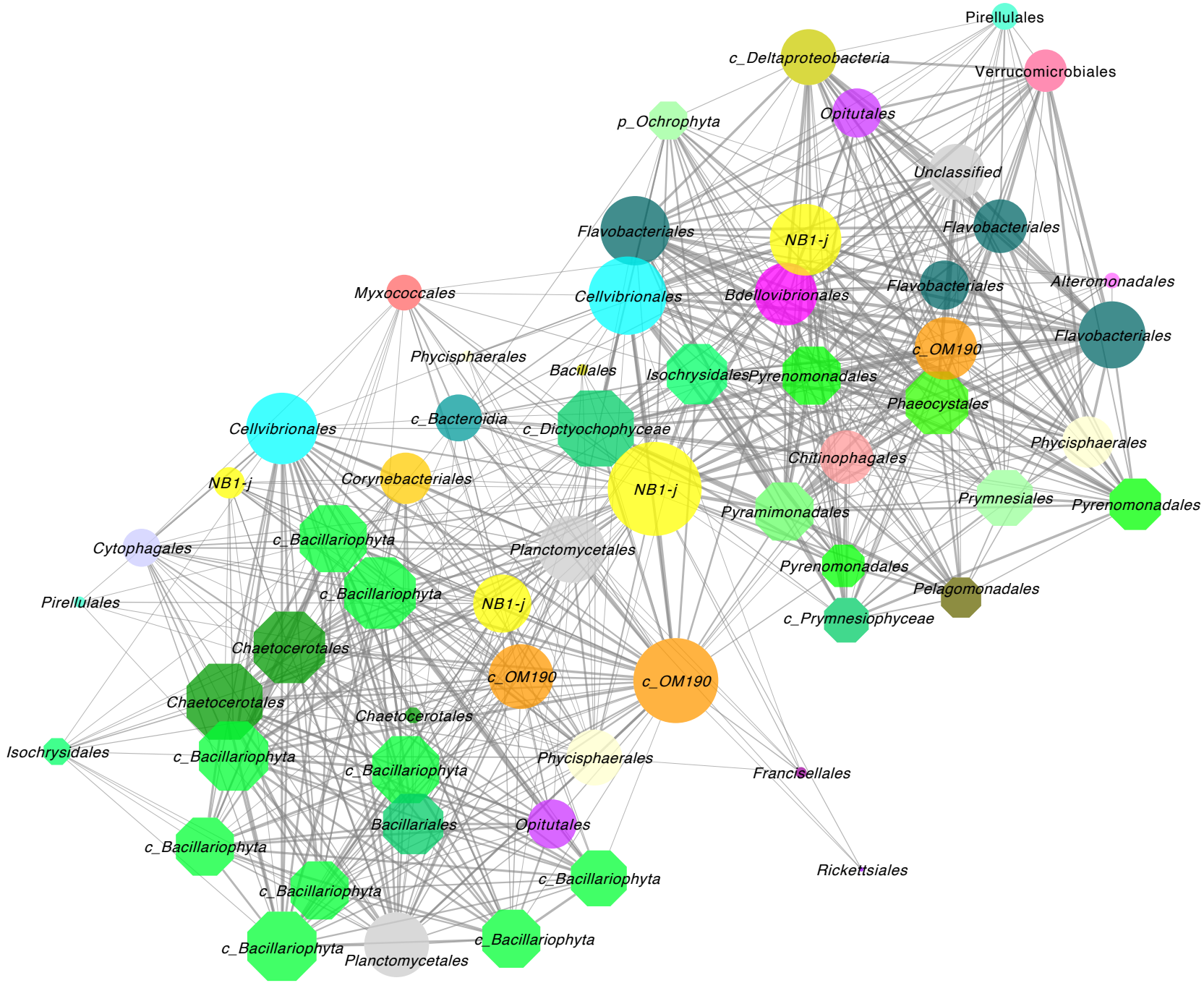
Table S1: Information on selected EMP studies

Table S2: Correlations recovered in marine environments between microalgae and bacteria

Table S3: Correlations recovered in freshwater environments between microalgae and bacteria


Project
Taxonomy
c_Alphaproteobacteria
c_Bacteroidia
c_Deltaproteobacteria
c_Gammaproteobacterium
c_OM190
c_OM190
c_OM190
p_Marinimicrobia (SAR406 clade)
p_Marinimicrobia (SAR406 clade)
p_Marinimicrobia (SAR406 clade)
o_Actinomarinales,f_Actinomarinaceae,g_Candidatus Actinomarina
o_Alteromonadales,f_Moritellaceae,g_Moritella
o_Bdellovibrionales,f_Bdellovibrionaceae,g_OM27 clade
o_Betaproteobacteriales,f_Burkholderiaceae
o_Caldilineales,f_Caldilineaceae
o_Cellvibrionales,f_Halieaceae
o_Cellvibrionales,f_Halieaceae,g_OM60(NOR5) clade
o_Cellvibrionales,f_Halieaceae,g_OM60(NOR5) clade
o_Chitinophagales,f_Saprospiraceae
o_Chitinophagales,f_Saprospiraceae,g_Aureispira
o_Corynebacteriales,f_Corynebacteriaceae,g_Corynebacterium 1
o_Cytophagales
o_Ectothiorhodospirales,f_Ectothiorhodospiraceae
o_Flavobacteriales
o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola
o_Flavobacteriales,f_Cryomorphaceae
o_Flavobacteriales,f_Flavobacteriaceae,g_Formosa
o_Flavobacteriales,f_Flavobacteriaceae,g_Formosa
o_Flavobacteriales,f_Flavobacteriaceae,g_NS2b marine group
o_Flavobacteriales,f_Flavobacteriaceae,g_NS4 marine group
o_Flavobacteriales,f_NS7 marine group
o_Flavobacteriales,f_NS9 marine group,g_uncultured Bacteroidetes/Chlorobi group bacterium
o_Flavobacteriales,f_Weeksellaceae
o_KI89A clade
o_Lactobacillales
o_Lactobacillales,f_Carnobacteriaceae,g_Trichococcus
o_Lactobacillales,f_Streptococcaceae,g_Streptococcus
o_Myxococcales,f_Blfdi19
o_NB1−j
o_NB1−j
o_NB1−j
o_NB1−j
o_NB1−j
o_OM182 clade
o_Opitutales,f_Puniceicoccaceae,g_Lentimonas
o_Opitutales,f_Puniceicoccaceae,g_Lentimonas
o_Opitutales,f_Puniceicoccaceae,g_Verruc−01
o_PB19
o_Phycisphaerales,f_Phycisphaeraceae,g_CL500−3
o_Phycisphaerales,f_Phycisphaeraceae,g_JL−ETNP−F27
o_Pirellulales,f_Pirellulaceae,g_Rubripirellula
o_Planctomycetales,f_Rubinisphaeraceae
o_Planctomycetales,f_Rubinisphaeraceae
o_Puniceispirillales,f_SAR116 clade
o_Puniceispirillales,f_SAR116 clade
o_Puniceispirillales,f_SAR116 clade
o_Rhizobiales,f_Hyphomicrobiaceae,g_Filomicrobium
o_Rhizobiales,f_Rhizobiaceae,g_Hoeflea
o_Rhodobacterales,f_Rhodobacteraceae
o_Rhodobacterales,f_Rhodobacteraceae,g_Pseudorhodobacter
o_Rhodospirillales,f_AEGEAN−169 marine group
o_Rickettsiales,f_S25−593
o_SAR11 clade,f_SAR11 clade
o_SAR11 clade,f_SAR11 clade,g_Clade Ia
o_SAR202 clade
o_SAR324 clade(Marine group B),f_SAR324 clade(Marine group B)
o_SAR86 clade
o_SAR86 clade
o_SAR86 clade,f_Rhodobacteraceae bacterium REDSEA−S29_B10
o_Synechococcales,f_Cyanobiaceae,g_Prochlorococcus MIT9313
o_Synechococcales,f_Cyanobiaceae,g_Synechococcus CC9902
o_Thalassobaculales,f_Nisaeaceae,g_OM75 clade
o_Thiotrichales,f_Thiotrichaceae
o_Thiotrichales,f_Thiotrichaceae,g_Cocleimonas
o_Verrucomicrobiales,f_Rubritaleaceae,g_Roseibacillus
o_Verrucomicrobiales,f_Rubritaleaceae,g_Roseibacillus
Project
Taxonomy2
0.8
0.6
0.4
0.2
0
Taxonomy
c_Prasinophyceae
c_Prymnesiophyceae
c_Bacillariophyta
c_Cryptophyceae
c_Dictyochophyceae
c_Pelagophyceae
c_Bolidophyceae
Project
ERP020022
ERP021691
ERP016287
ERP016541
Taxonomy2
c_Alphaproteobacteria
c_Bacteroidia
c_Deltaproteobacteria
c_gammaproteobacterium
c_OM190
p_Marinimicrobia (SAR406 clade)
o_Actinomarinales,f_Actinomarinaceae,g_Candidatus Actinomarina
o_Alteromonadales,f_Moritellaceae,g_Moritella
o_Bdellovibrionales,f_Bdellovibrionaceae,g_OM27 clade
o_Betaproteobacteriales,f_Burkholderiaceae
o_Caldilineales,f_Caldilineaceae
o_Cellvibrionales,f_Halieaceae
o_Cellvibrionales,f_Halieaceae,g_OM60(NOR5) clade
o_Chitinophagales,f_Saprospiraceae
o_Chitinophagales,f_Saprospiraceae,g_Aureispira
o_Corynebacteriales,f_Corynebacteriaceae,g_Corynebacterium 1
o_Cytophagales
o_Ectothiorhodospirales,f_Ectothiorhodospiraceae
o_Flavobacteriales
o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola
o_Flavobacteriales,f_Cryomorphaceae
o_Flavobacteriales,f_Flavobacteriaceae,g_Formosa
o_Flavobacteriales,f_Flavobacteriaceae,g_NS2b marine group
o_Flavobacteriales,f_Flavobacteriaceae,g_NS4 marine group
o_Flavobacteriales,f_NS7 marine group
o_Flavobacteriales,f_NS9 marine group,g_uncultured Bacteroidetes/Chlorobi group bacterium
o_Flavobacteriales,f_Weeksellaceae
o_KI89A clade
o_Lactobacillales
o_Lactobacillales,f_Carnobacteriaceae,g_Trichococcus
o_Lactobacillales,f_Streptococcaceae,g_Streptococcus
o_Myxococcales,f_Blfdi19
o_NB1−j
o_OM182 clade
o_Opitutales,f_Puniceicoccaceae,g_Lentimonas
o_Opitutales,f_Puniceicoccaceae,g_Verruc−01
o_PB19
o_Phycisphaerales,f_Phycisphaeraceae,g_CL500−3
o_Phycisphaerales,f_Phycisphaeraceae,g_JL−ETNP−F27
o_Pirellulales,f_Pirellulaceae,g_Rubripirellula
o_Planctomycetales,f_Rubinisphaeraceae
o_Puniceispirillales,f_SAR116 clade
o_Rhizobiales,f_Hyphomicrobiaceae,g_Filomicrobium
o_Rhizobiales,f_Rhizobiaceae,g_Hoeflea
o_Rhodobacterales,f_Rhodobacteraceae
o_Rhodobacterales,f_Rhodobacteraceae,g_Pseudorhodobacter
o_Rhodospirillales,f_AEGEAN−169 marine group
o_Rickettsiales,f_S25−593
o_SAR11 clade,f_SAR11 clade
o_SAR11 clade,f_SAR11 clade,g_Clade Ia
o_SAR202 clade
o_SAR324 clade(Marine group B),f_SAR324 clade(Marine group B)
o_SAR86 clade
o_SAR86 clade,f_Rhodobacteraceae bacterium REDSEA−S29_B10
o_Synechococcales,f_Cyanobiaceae,g_Prochlorococcus MIT9313
o_Synechococcales,f_Cyanobiaceae,g_Synechococcus CC9902
o_Thalassobaculales,f_Nisaeaceae,g_OM75 clade
o_Thiotrichales,f_Thiotrichaceae
o_Thiotrichales,f_Thiotrichaceae,g_Cocleimonas
o_Verrucomicrobiales,f_Rubritaleaceae,g_Roseibacillus


Project
Taxonomy
c_Acidimicrobiia
c_Acidimicrobiia,o_IMCC26256
c_Acidimicrobiia,o_IMCC26256
c_Acidobacteriia,o_Subgroup 2
c_Actinobacteria,o_Pdt15
c_Actinobacteria,o_Pdt15
c_Blastocatellia (Subgroup 4)
c_Blastocatellia (Subgroup 4)
c_Deltaproteobacteria,o_PB19
c_Gammaproteobacteria
c_Gammaproteobacteria,o_CCM19a
c_Gammaproteobacteria,o_JG36-Tz7-191
c_Gracilibacteria
c_Gracilibacteria
c_Ignavibacteria,o_OPB56
c_Ignavibacteria,o_OPB56
c_Kirtimatellae,o_WCHB1-41
c_Kirtimatellae,o_WCHB1-41
c_OM190
c_OM190
c_Oxyphotobacteria
c_Parcubacteria
c_Phycisphaerae,o_CCM11a
c_Phycisphaerae,o_S-70
c_Pla3 lineage
c_Verrucomicrobiae
c_Verrucomicrobiae
c_Verrucomicrobiae
c_Verrucomicrobiae,o_LD1-PB3
o_Absconditabacteriales (SR1)
o_Absconditabacteriales (SR1)
o_Absconditabacteriales (SR1)
o_Absconditabacteriales (SR1)
o_Absconditabacteriales (SR1)
o_Acetobacteriales,f_Acetobacteraceae
o_Acetobacterales,f_Acetobacteriales Incertae Sedis
o_Acetobacterales,f_Acetobacteriales Incertae Sedis
o_Acidobacteriales
o_Acidobacteriales,f_Acidobacteriaceae (Subgroup 1)
o_Alteromonadales,f_Alteromonadaceae
o_Alteromonadales,f_Alteromonadaceae,g_Paraglaciecola
o_Alteromonadales,f_Colwelliaceae,g_Colwellia
o_Alteromonadales,f_Pseudoalteromonadaceae,g_Pseudoalteromonas
o_Anaerolineales,f_Anaerolineaceae
o_Anaerolineales,f_Anaerolineaceae,g_Anaerolinea
o_Anaerolineales,f_Anaerolineaceae,g_Leptolinea
c_Arctic97B-4 marine group,f_marine metagenome,g_marine metagenome
o_Armatimonadales,f_Armatimonadaceae,g_Armatimonas
o_Babeliales,f_Babeliaceae
o_Babeliales,f_UBA12409
o_Bacillales,f_Staphylococcaceae,g_Staphylococcus
o_Bacteroidales
o_Bacteroidales
o_Bacteroidales,f_Bacteroidetes BD2-2
o_Bacteroidales,f_Bacteroidetes vadinHA17
o_Bacteroidales,f_Prolybacteraceae
o_Bacteroidales,f_Rikenellaceae,g_Bh428 wastewater-sludge group
o_Bacteroidetes VC2.1 Bac22
o_Bdellovibrionales,f_Bacteriovoracaceae,g_Peredibacter
o_Betaproteobacteriales,f_Burkholderiaceae
o_Betaproteobacteriales,f_Burkholderiaceae
o_Betaproteobacteriales,f_Burkholderiaceae,g_GK5B8 freshwater group
o_Betaproteobacteriales,f_Burkholderiaceae,g_Limnohabitans
o_Betaproteobacteriales,f_Burkholderiaceae,g_Limnohabitans
o_Betaproteobacteriales,f_Burkholderiaceae,g_Polaromonas
o_Betaproteobacteriales,f_Burkholderiaceae,g_Polyrubrobacter
o_Betaproteobacteriales,f_Burkholderiaceae,g_Rhodoferax
o_Betaproteobacteriales,f_Chitinibacteraceae,g_Iodobacter
o_Betaproteobacteriales,f_Chitinimonadaceae,g_Chitinimonas
o_Betaproteobacteriales,f_Ferrovaceae,g_Ferrovum
o_Betaproteobacteriales,f_Methylophilaceae
o_Betaproteobacteriales,f_Methylophilaceae,g_OM43 clade
o_Betaproteobacteriales,f_Nitrosomonadaceae,g_B65-1
o_Betaproteobacteriales,f_Nitrosomonadaceae,g_Nitrosomonas
o_Betaproteobacteriales,f_TRA3-20
o_Caenarcaniphilales
o_Caldilineales,f_Caldilineaceae
o_Caldilineales,f_WCHB1-32
o_Calditrichales,f_Calditrichaceae,g_JdFR-76
o_Campylobacterales,f_Helicobacteraceae
o_Candidatus Collierbacteria
o_Candidatus Falkowbacteria
o_Candidatus Kaiserbacteria
o_Candidatus Kaiserbacteria
o_Candidatus Kerfeldbacteria
o_Candidatus Kerfeldbacteria
o_Candidatus Kuenenbacteria
o_Candidatus Pacebacteria
o_Candidatus Pacebacteria
o_Candidatus Shapirobacteria
o_Candidatus Shapirobacteria
o_Candidatus Vogebacteria
o_Caulobacterales,f_Caulobacteraceae
o_Caulobacterales,f_Hyphomonadaceae
o_Caulobacterales,f_Hyphomonadaceae,g_SWB02
o_Cellvibrionales,f_Halieaceae,g_OM60(NOR5) clade
o_Cellvibrionales,f_Porticoccaceae,g_Porticoccus
o_Cellvibrionales,f_Porticoccaceae,g_SAR92 clade
o_Chitinophagales
o_Chitinophagales
o_Chitinophagales
o_Chitinophagales
o_Chitinophagales
o_Chitinophagales
o_Chitinophagales
o_Chitinophagales,f_Chitinophagaceae
o_Chitinophagales,f_Chitinophagaceae,g_Dinghubacter
o_Chitinophagales,f_Chitinophagaceae,g_Ferruginibacter
o_Chitinophagales,f_Chitinophagaceae,g_Lacibacter
o_Chitinophagales,f_Chitinophagaceae,g_Parasedimintbacterium
o_Chitinophagales,f_Chitinophagaceae,g_Sediminibacterium
o_Chitinophagales,f_Saprospiraceae
o_Chitinophagales,f_Saprospiraceae
o_Chitinophagales,f_Saprospiraceae,g_Aureispira
o_Chitinophagales,f_Saprospiraceae,g_Candidatus Aquirestis
o_Chitinophagales,f_Saprospiraceae,g_Lewinella
o_Chlorobiales,f_Chlorobiaceae[weak]g_GBC0B
o_Chloroflexales,f_Chlorroflexaceae,g_Candidatus Chlorothrix
o_Chlorofleales,f_Roseiflexaceae
o_Chlorroidobacteriales
o_Chlorroidobacteriales,f_Chlorroidobacteraceae,g_LD29
o_Chlorroidobacteriales,f_Terrimicrobiaceae,g_Terrimicrobium
o_Chlorroidobacteriales,f_Xiphinematobacteraceae,g_Candidatus Xiphinematobacter
o_Clostridiales
o_Clostridiales,f_Christensenellaceae
o_Clostridiales,f_Christensenellaceae
o_Clostridiales,f_Clostridiaceae 1,g_Clostridium sensu stricto 13
o_Clostridiales,f_Peptococcaceae
o_Clostridiales,f_Peptostreptococcaceae,g_Clostridioides
o_Clostridiales,f_Peptostreptococcaceae,g_Paeniclostridium
o_Clostridiales,f_Ruminococcaceae,g_[Eubacterium] coprostanoligenes group
o_Clostridiales,f_Ruminococcaceae,g_Ruminiclostridium
o_Clostridiales,f_Ruminococcaceae,g_Ruminiclostridium 1
o_Clostridiales,f_Ruminococcaceae,g_Ruminococcaceae UCG-014
o_Competibacterales,f_Competibacteraceae
o_Competibacterales,f_Competibacteraceae,g_Candidatus Contendobacter
o_Coynebacteriales,f_Mycobacteriaceae,g_Mycobacterium
o_Cytophagales,f_Amoebophilaceae,g_Candidatus Amoebophilus
o_Cytophagales,f_Cyclobacteriaceae
o_Cytophagales,f_Cyclobacteriaceae,g_Algoriphagus
o_Cytophagales,f_Cyclobacteriaceae,g_Marinigo
o_Cytophagales,f_Microscillaceae
o_Cytophagales,f_Microscillaceae,g_OLB12
o_Cytophagales,f_Spirosomaceae,g_Pseudarcicella
o_Deltaproteobacteria Incertae Sedis(f_Syntrophorhabdaceae,g_Syntrophorhabdus
o_Desulfarculales,f_Desulfarculaceae
o_Desulfobacterales,f_Desulfobacteraceae,g_Desulfatirhabdium
o_Desulfobacterales,f_Desulfobacteraceae,g_Sva0081 sediment group
o_Desulfobacterales,f_Desulfotomaculaceae
o_Desulfovibrionales,f_Desulfovibrionaceae,g_Desulfovibrio[corrected]
o_Desulfovibrionales,f_Desulfovibrionaceae
o_Desulfovibrionales,f_Desulfovibrionaceae,g_Desulfovibrio
o_Desulfuromonadales,f_Geobacteraceae,g_Geobacter
o_Entotheonellales,f_Entotheonellaceae
o_Erysipelotrichales,f_Erysipelotrichaceae,g_Turicibacter
o_Fibrobacterales
o_Flavobacteriales,f_Crocinitomicaceae
o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola
o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola
o_Flavobacteriales,f_Crocinitomicaceae,g_Fluviicola
o_Flavobacteriales,f_Cryomorphaceae
o_Flavobacteriales,f_Cryomorphaceae
o_Flavobacteriales,f_Cryomorphaceae
o_Flavobacteriales,f_Cryomorphaceae,g_Cryomorpha
o_Flavobacteriales,f_Cryomorphaceae,g_Cryomorpha
o_Flavobacteriales,f_Flavobacteriaceae
o_Flavobacteriales,f_Flavobacteriaceae,g_Flavobacterium
o_Flavobacteriales,f_Flavobacteriaceae,g_NS3a marine group
o_Flavobacteriales,f_Flavobacteriaceae,g_Ulvibacter
o_Flavobacteriales,f_NS9 marine group
o_Frankiales,f_Sporichthyaceae
o_Frankiales,f_Sporichthyaceae
o_Frankiales,f_Sporichthyaceae,g_Candidatus Planktophila
o_Frankiales,f_Sporichthyaceae,g_Candidatus Planktophila
o_Frankiales,f_Sporichthyaceae,g_hgcI clade
o_Frankiales,f_Sporichthyaceae,g_hgcI clade
o_Frankiales,f_Sporichthyaceae,g_hgcI clade
o_Gaiellales
o_Gammaproteobacteria Incertae Sedis
o_Gammaproteobacteria Incertae Sedis
o_Gammaproteobacteria Incertae Sedis
o_Gammatimonadales,f_Gemmatimonadaceae,g_Gemmata
o_Gammatimonadales,f_Gemmatimonadaceae
o_Gammatimonadales,f_Gemmatimonadaceae,g_Gemmatimonas
o_Haloblepharidales,f_Haloblepharidaceae
o_Holophagales,f_Holophagaceae
o_Ignavibacteriales,f_PHOS-HE36
o_Isosphaerales,f_Isosphaeraceae
o_Isosphaerales,f_Isosphaeraceae
o_Kryptoniales,f_MSB-3C8
o_Kiedxobacteriales,f_Kiedxobacteraceae
o_Lactobacillales,f_Streptococcaceae,g_Streptococcus
o_Legionellales,f_Legionellaceae,g_Legionella
o_Leptospirillales,f_Leptospirillaceae
o_Leptospiralles,f_Leptospiraceae
o_Leptospiralles,f_Leptospiraceae,g_RBG-16-49-21
o_Methylacidiphilales,f_Methylacidiphilaceae
o_Methylococcales,f_Methylomonadaceae
o_Micavibrionales
o_Micrococcales,f_Microbacteriaceae,g_Candidatus Limnoluna
o_Micrococcales,f_Microbacteriaceae,g_Microbacterium
o_Micrococcales,f_Microbacteriaceae,g_MWH-Ta3
o_Micrococcales
o_Micrococcales
o_Micrococcales,f_Jamaicaceae,g_Jamia
o_Micrococcales,f_Ilumatobacteraceae
o_Micrococcales,f_Ilumatobacteraceae,g_CL500-29 marine group
o_Micrococcales,f_Ilumatobacteraceae,g_CL500-29 marine group
o_Micrococcales,f_Ilumatobacteraceae,g_Ilumatobacter
o_Micrococcales,f_Micrococcaceae,g_IMCC26207
o_Micrococcales,f_Micrococcaceae,g_Sva0996 marine group
o_Moliscutes RF39
o_Myxococcales,f_Archangiacaceae,g_Anaeromyxobacter
o_Myxococcales,f_bacteriap25
o_Myxococcales,f_BIrii19
o_Myxococcales,f_mle1-27
o_Myxococcales,f_Sandaracinaceae
o_Nitrosococcales,f_Methylohagaceae
o_Nostocales,f_Nostocaceae,g_Dolichospermum NIES41
o_Oceanospirillales,f_Nitrincolaceae
o_Oceanospirillales,f_Pseudohongiellaceae,g_Bly10
o_Oceanospirillales,f_Pseudohongiellaceae,g_Pseudohongiella
o_Oligoflexales,f_Oligoflexaceae
o_OM182 clade
o_Opitutales,f_Opitutaceae
o_Opitutales,f_Opitutaceae
o_Opitutales,f_Opitutaceae,g_Lacunisphaera
o_Opitutales,f_Puniceicoccaceae
o_Opitutales,f_Puniceicoccaceae,g_Verruc-01
o_Oxyphotobacteria Incertae Sedis
o_Oxyphotobacteria Incertae Sedis
o_Paracaedibacteriales,f_Paracaedibacteraceae
o_Parcubacteria
o_Pedosphaerales,f_Pedosphaeraceae
o_Pedosphaerales,f_Pedosphaeraceae
o_Pedosphaerales,f_Pedosphaeraceae,g_bacterium SH3-11
o_Phycisphaerales,f_KAU0384 sediment group
o_Phycisphaerales,f_Phycisphaeraceae,g_CL500-3
o_Pirellulales,f_Pirellulaceae,g_Pirellula
o_Planctomycetales
o_Planctomycetales,f_Rubinisphaeraceae
o_Planctomycetales,f_Rubinisphaeraceae,g_Fuerstia
o_Planctomycetales,f_Rubinisphaeraceae,g_Rubinisphaera
o_Pseudanabaenales,f_Pseudanabaenaceae,g_Pseudanabaena PCC 7429
o_Pseudanabaenales,f_Pseudanabaenaceae,g_Pseudanabaena PCC-7429
o_Puniceispirillales,f_SAR116 clade
o_Rhizobiales,f_Beijerinckiaceae,g_Methylocella
o_Rhizobiales,f_Rhizobiaceae
o_Rhizobiales,f_Rhizobiaceae,g_Ahrensia
o_Rhizobiales,f_Rhizobiales Incertae Sedis,g_Andaseniella
o_Rhizobiales,f_Xanthobacteraceae,g_Blastochloris
o_Rhodobacterales,f_Rhodobacteraceae
o_Rhodobacterales,f_Rhodobacteraceae,g_Amylibacter
o_Rhodobacterales,f_Rhodobacteraceae,g_Rhodobacter
o_Rhodobacterales,f_Rhodobacteraceae,g_Sulfitobacter
o_Rhodospirillales
o_Rhodospirillales,f_Magnetospiraceae,g_Magnetospira
o_Rhodospirillales,f_Magnetospirillaceae,g_Telmatospirillum
o_Rhodospirillales,f_Rhodospirillaceae,g_Defluviicoccus
o_Rickettsiales,f_Rickettsiaceae
o_Rickettsiales,f_Rickettsiaceae
o_Rickettsiales,f_Rickettsiaceae,g_Candidatus Arcanobacter
o_Rickettsiales,f_Rickettsiaceae,g_Candidatus Megaira
o_Saccharimonadales candidate division W55 bacterium
o_SAR11 clade,f_Clade Ia
o_SAR11 clade,f_Clade Ia
o_SAR11 clade,f_Clade Ia,g_Clade Ia
o_SAR11 clade,f_Clade III
o_SAR11 clade,f_Clade III
o_SAR11 clade,f_Clade III
o_SAR11 clade,f_Clade III
o_SAR324 clade(Marine group B)
o_SAR86 clade
o_Sneathiales,f_Sneathiaceae,g_Sneathiella
o_Sneathiales,f_Sneathiaceae,g_Tazneia
o_Solirubrobacterales,f_Solirubrobacteraceae
o_Solirubrobacterales,f_Solirubrobacteraceae
o_Solirubrobacterales,f_Solirubrobacteraceae
o_Spirinbacteriales,f_env OPS 17
o_Spirinbacteriales,f_env OPS 17
o_Spirinbacteriales,f_KD3-93
o_Spirinbacteriales,f_Lentimicrobiaceae
o_Spirinbacteriales,f_LKJ1-11-161
o_Spirinbacteriales,f_LKJ1-11-161
o_Spirinbacteriales,f_NS11-12 marine group
o_Spirinbacteriales,f_NS11-12 marine group
o_Spirinbacteriales,f_NS11-12 marine group
o_Spirinbacteriales,f_NS11-12 marine group
o_Spirinbacteriales,f_NS11-12 marine group
o_Spirinbacteriales,f_NS11-12 marine group
o_Spirinbacteriales,f_Spirinbacteraceae
o_Spirinbacteriales,f_Spirinbacteraceae
o_Spirinbacteriales,f_Spirinbacteraceae,g_Pedobacter
o_Spirinbacteriales,f_Spirinbacteraceae,g_Solitalea
o_Spirinbacteriales,f_Spirinbacteraceae,g_Spirinbacteraceae
o_Spirinbacteriales,f_Spirinbacteraceae,g_Sphingorhabdus
o_Spirinbacteriales,f_Spirinbacteraceae
o_Spirochaetales,f_Spirochaetaceae
o_Spirochaetales,f_Spirochaetaceae,g_MDPT2-76 termite group
o_Spirochaetales,f_Spirochaetaceae,g_Treponema
o_Synechococcales,f_Cyanobiaceae,g_Cyanobium PCC-6307
o_Synechococcales,f_Cyanobiaceae,g_Cyanobium PCC-6307
o_Syntrophobacterales,f_Syntrophaceae,g_Smithella
o_Syntrophobacterales,f_Syntrophaceae,g_Syntrophus
o_Tepidiphilarales,f_CPla-3 termite group
o_Thermomicrobiales,f_JG30-KF-CM45
o_Verrucomicrobiales,f_DEV007
o_Verrucomicrobiales,f_Rubritaleaceae,g_Luteolibacter
o_Verrucomicrobiales,f_Rubritaleaceae,g_Roseibacillus
o_Verrucomicrobiales,f_Verrucomicrobiaceae
o_Xanthomonadales,f_Rhodanobacteraceae,g_Dokdonella
o_Acidobacteria,c_Subgroup 6
o_Actinobacteria,c_MB-A2-108
o_Chloroflexi,c_KD4-96
o_Chloroflexi,c_PL-11E
o_Chloroflexi,c_SL56 marine group
o_Elusimicrobia,c_Lineage IIa
Taxonomy3
Project


Pirellulales
c_Deltaproteobacteria
Verrucomicrobiales
p_Ochrophyta
Opitutales
Unclassified
Flavobacteriales
NB1-j
Flavobacteriales
Myxococcales
Cellvibrionales
Bdellovibrionales
Flavobacteriales
Alteromonadales
Flavobacteriales
c_OM190
Phycisphaerales
Bacillales
Isochrysidales
Pyrenomonadales
Phaeocystales
Cellvibrionales
c_Bacteroidia
c_Dictyochophyceae
Phycisphaerales
Chitinophagales
NB1-j
Corynebacteriales
NB1-j
Prymnesiales
Pyrenomonadales
Pyramimonadales
Cytophagales
c_Bacillariophyta
Planctomycetales
Pyrenomonadales
Pelagomonadales
Pirellulales
c_Bacillariophyta
NB1-j
c_Prymnesiophyceae
Chaetocerotales
c_OM190
c_OM190
Chaetocerotales
Chaetocerotales
Isochrysidales
c_Bacillariophyta
c_Bacillariophyta
Phycisphaerales
Francisellales
Bacillariales
Opitutales
c_Bacillariophyta
Rickettsiales
c_Bacillariophyta
c_Bacillariophyta
c_Bacillariophyta
c_Bacillariophyta
Planctomycetales