



Analysis of microbial community biodiversity in activated sludge from a petrochemical plant

ARTICLES doi:10.4136/ambi-agua.2655

Received: 02 Oct. 2020; Accepted: 03 May 2021

Themis Collares Antunes¹; Leticia Marconatto²
Luiz Gustavo dos Anjos Borges²; Adriana Giongo²
Sueli Teresinha Van Der Sand^{3*}

¹Instituto de Ciências Básicas da Saúde. Programa de Pós-graduação em Microbiologia Agrícola e do Ambiente. Universidade Federal do Rio Grande do Sul (UFRGS), Rua Sarmento Leite, nº500, CEP: 90050-170, Porto Alegre, RS, Brazil. E-mail: themis.antunes@gmail.com

²Instituto do Petróleo e dos Recursos Naturais. Pontifícia Universidade Católica do Rio Grande do Sul (PUCRS), Avenida Ipiranga, nº 6681, CEP: 90619-900, Porto Alegre, RS, Brazil. E-mail: leticia.marconatto@pucrs.br, luizgaborges@gmail.com, adrianagiongo@gmail.com

³Departamento de Microbiologia, Imunologia e Parasitologia. Instituto de Ciências Básicas da Saúde. Universidade Federal do Rio Grande do Sul (UFRGS), Rua Sarmento Leite, nº500, CEP: 90050-170, Porto Alegre, RS, Brazil.

*Corresponding author. E-mail: svands@ufrgs.br

ABSTRACT

The active sludge process is one of the most-used techniques for the biodegradation of organic compounds present in effluents from an assortment of wastewaters. This study investigated the bacterial community structure of a petroleum industry's activated sludge and its physical and chemical parameters using high-throughput sequencing. Samples were collected over one year: autumn 2015 (C1), winter 2015 (C2), spring 2015 (C3), and summer 2016 (C4). Total DNA was extracted, and the primers targeting the V4 region of the 16S rRNA gene were used for amplicon sequencing. The majority of the detected microorganisms were considered rare microbiota, presenting a relative abundance below 1% of the total sequences. All of the sequences were classified at the phylum level, and up to 55% of the ASVs (Amplicon Sequence Variants) were associated with known bacterial genera. Proteobacteria was the most abundant phylum in three seasons, while the phylum *Armatimonadota* dominated in one season. The genus *Hyphomicrobium* was the most abundant in autumn, winter and summer, and an ASV belonging to the family *Fimbriimonadaceae* was the most abundant in the spring. Canonical Correspondence Analysis showed that physicochemical parameters of SS, SD and TSS are correlated, as well as ammoniacal nitrogen. Sample C3 presented the highest values of COD, AN and solids (SS, SD and TSS). The highest COD, AN, and solids values are correlated to the high frequency of the phylum *Armatimonadota* in C3.

Keywords: bacterial community, high throughput sequencing, wastewater sludge.



O lodo ativo da planta de uma indústria de petróleo é constituído por uma microbiota ainda a ser identificada

RESUMO

O processo de lodo ativo é uma das técnicas mais utilizadas para biodegradação de compostos orgânicos presentes nos efluentes de uma variedade de águas residuais. A estrutura da comunidade bacteriana do lodo ativado de uma indústria de petróleo e sua relação com parâmetros físicos e químicos foram investigadas por meio de sequenciamento de alto rendimento. As amostras foram coletadas durante um período de um ano: outono de 2015 (C1), inverno de 2015 (C2), primavera de 2015 (C3) e verão de 2016 (C4). O DNA total foi extraído e para amplificação foram utilizados primers específicos para região V4 do gene 16S rRNA. A maioria dos microrganismos detectados foi considerada microbiota rara, apresentando abundância relativa abaixo de 1% do total de sequências. Em geral, quase a totalidade das sequências (99,9%) foi classificada em nível de filo, mas apenas algumas ASVs (23,7%) foram associadas a gênero bacteriano conhecido. As proteobactérias foram o filo mais abundante em três das estações, enquanto o filo Armatimonadota dominou em uma estação. O gênero *Hyphomicrobium* foi o gênero mais abundante no outono, inverno e verão, e uma ASV pertencente à família *Fimbriimonadaceae* (filo Armatimonadetes) foi o microrganismo mais abundante na primavera. A Análise de Correspondência Canônica (CCA) indica uma diferença consistente da comunidade bacteriana da primavera quando comparada com amostras de outras estações. Os resultados mostram uma correlação entre o filo Armatimonadota e a alta concentração de DQO, NA e sólidos.

Palavras-chave: comunidade bacteriana, lodo ativado, sequenciamento de alto rendimento.

1. INTRODUCTION

Biological and industrial wastewater treatment plants (WWTP) are standout biotechnological processes in operation worldwide (Figuerola and Erijman, 2007), whose significance is increasing in a consistently developing human society. Most wastewater treatment processes use the natural self-depuration limit of aquatic conditions, which is the effect of microbial activity (Heidenwag *et al.*, 2001). It is crucial to recognize the relationship between microbial communities and their performance in the full-scale installations, since bacterial metabolism is essential for effective biological treatment of wastewater (Kwiatkowska and Zielinska, 2016).

Biological treatment by the active-sludge process is well known. This most-used technique for the biodegradation of organic compounds in effluents from a variety of wastewaters and their microbial community has been studied in urban, industrial, and petrochemical wastewaters (Zhang *et al.*, 2011; Sánchez *et al.*, 2013; Ye and Zhang, 2013). These studies have demonstrated that the most prevalent microorganisms in these samples are *Betaproteobacteria*, *Alphaproteobacteria*, *Nitrobacteria*, *Bacteroidetes*, *Firmicutes*, and *Actinobacteria*.

High-throughput sequencing technologies provide deep insights into the bacterial populations (Ibarbalz *et al.*, 2013) and have been used to reveal the bacterial range of some complex environments, including activated sludge samples (Claesson *et al.*, 2010; Zhang *et al.*, 2011; Yang *et al.*, 2014; Gwin *et al.*, 2018). Some microorganisms have not been completely identified (Krishnan *et al.*, 2016; Abe *et al.*, 2017), showing that there is much more to discover about the biodiversity of activated sludge. In this study, we accessed the microbial community diversity present in activated sludge from the petrochemical industry using amplicon sequencing based on the 16S rRNA gene.

2. MATERIAL AND METHODS

2.1. Active sludge samples collection

Activated sludge samples were collected from a wastewater treatment plant (WWTP) located in Triunfo, Rio Grande do Sul, Brazil (29°51'01.1" S 51°22'50.9" W) previously described by Antunes *et al.* (2018). The WWTP handles 450-m³ h⁻¹ of wastewater and is operated as a conventional activated-sludge treatment process, mechanically aerated by blades. One liter of sludge was collected directly from the input aeration tank (Figure 1) during four sampling collections over one year: Autumn 2015 (C1), Winter 2015 (C2), Spring 2015 (C3), and Summer 2016 (C4). Samples were collected using a collection bucket and transported on ice to the laboratory. The samples were thereafter kept at -80°C until further analysis. Active sludge chemical composition and physical parameters were summarized in Antunes *et al.* (2018).

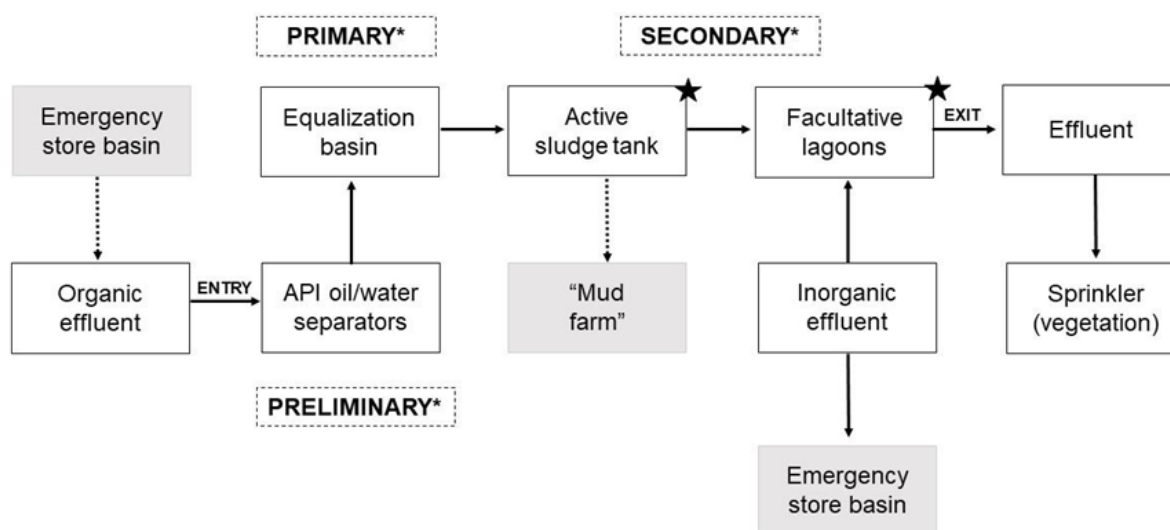


Figure 1. Schematic representation of the wastewater treatment plant. The black star indicates the sampling point. Arrows represent the effluent pathway.

The following parameters were determined by a certified laboratory, according to the American Public Health Association (APHA *et al.*, 2012): total organic carbon (TOC), chemical oxygen demand (COD), dissolved oxygen (DO), total suspended solids (TSS), solids suspended (SS), solids dissolved (SD); and total Kjeldahl nitrogen (TKN). The chemical results are listed in Table 1.

Table 1. Active sludge chemical parameters. Results are shown in mg L⁻¹. (Modified from Antunes *et al.*, 2018).

Parameter	Sampling time			
	C1	C2	C3	C4
Total organic carbon (TOC)	115	20	100	91
Chemical oxygen demand (COD)	399.5	13.33	637	83.6
Dissolved oxygen (DO)	2.1	2.02	0.7	0.5
Total suspended solids (TSS)	1286	788	1477	1625
Solids suspended (SS)	48	22	56	53
Solids dissolved (SD)	1241	678	1428	1508
Total Kjeldahl nitrogen (TKN)	67.67	13.08	25.54	27.53
Ammoniacal Nitrogen (AN)	8.74	4.32	11.49	8.44

2.2. DNA isolation and 16S rRNA gene fragment sequencing

Total DNA was extracted from 0.25 g of active sludge using the Dneasy PowerSoil Kit (Qiagen) following the manufacturer's standard protocol. The concentration and purity of the isolated DNA were determined using an ND-100Nanodrop spectrophotometer (Thermo Fisher). Partial 16S rRNA gene sequences were amplified using universal primers 515F and 806R, previously identified as suitable for bacteria and archaea (Bates *et al.*, 2011). Amplification was performed in a 25 μ L mixture, consisting of 1 μ L of genomic DNA, 2 mM MgCl₂, 0.2 μ M of each primer, 200 μ M of each dNTP, 1U Taq DNA polymerase and 1X reaction buffer. These primers amplify 291 bp from the V3-V4 hypervariable region of the prokaryotic 16S rRNA gene. Amplification was carried out in a Mastercycler Personal 5332 Thermocycler (EppendorfR) according to the following program: initial denaturation at 94°C for 2 min, followed by 25 cycles of 45 s at 94°C, 45 s at 55°C, 1 min at 72°C and a final cycle at 72°C for 6 min. For library construction, 100 ng of DNA was used as described in the Ion Plus Fragment Library manual kit. Barcode sequences were added to identify each sample from the total sequencing output, since all samples were sequenced in a multiplexed run. Amplicon sequencing was conducted on the Ion PGM System (Thermo Fisher) using an Ion 316 chip, following the manufacturer's instructions.

Sequences from 16S rRNA amplicon sequencing were processed using DADA2 (Divisive Amplicon Denoising Algorithm) (Callahan *et al.*, 2016) in R (R Core Team, 2019). Filtering, dereplication, sample inference, and chimera identification were performed, and the generated amplicon sequence variants (ASVs) were taxonomically assigned based on the SILVA database v. 138 (Quast *et al.*, 2013). The ASV data were imported into R using phyloseq (McMurdie and Holmes, 2013). Unassigned taxa and any residual ASVs identified as chloroplast, mitochondria, or eukaryote were excluded from the analysis. The remaining sequences were analyzed as described by Heinz *et al.* (2017). Sequencing results were deposited in the National Center for Biotechnology Information (NCBI) under BioProject ID PRJNA471748.

Canonical Correspondence Analysis (CCA) was used to evaluate linkages between microbial communities (ten most-abundant phyla) and chemical parameters (TOC, COD, DO, TSS, SS, SD, and TKN) using Past3 software (Hammer *et al.*, 2001).

3. RESULTS AND DISCUSSION

After removing the low-quality sequences, the amplicon sequencing from the four samples collected seasonally from the petrochemical industry active sludge yielded a total of 241,859 16S rRNA gene sequences samples, representing an average of 60,465 sequences per sample. The average sequence length was 273 bp.

The microbiota was classified within 31 phyla, 65 classes, 146 orders, 167 families and 185 genera or respective taxa. The domain *Bacteria* had the highest number of classified microorganisms (94.9% of the total sequences). The occurrence of four archaeal phyla was observed: *Crenarchaeota*, *Halobacterota*, *Nanoarchaeota*, *Aenigmarchaeota*. The phylum *Aenigmarchaeota* was present only in sequences from sample C3, comprising 0.10% of the total sequences in sample C3.

The classified bacterial community was composed of thirteen phyla with an abundance higher than 1% of the total sequences (Figure 2). *Proteobacteria* was the most abundant phylum in samples C1, C2, and C4, representing up to 37% of the total sequences in C2, followed by the phylum *Bacteroidota* present in samples C1, C2 and C4 (16.22%, 15.36% and 17.59% of the total sequences, respectively). In sample C3, the most abundant phylum was *Armatimonadota* and *Proteobacteria*; they represented 49.16% and 21.09% of the total sequences, respectively (Figure 2). *Armatimonadota* was the second-most abundant phylum in C1, after *Proteobacteria*, accounting for 11.74% of the total sequences. Unclassified sequences at the phylum level presented an average of 0.01% of the total sequences in the samples.

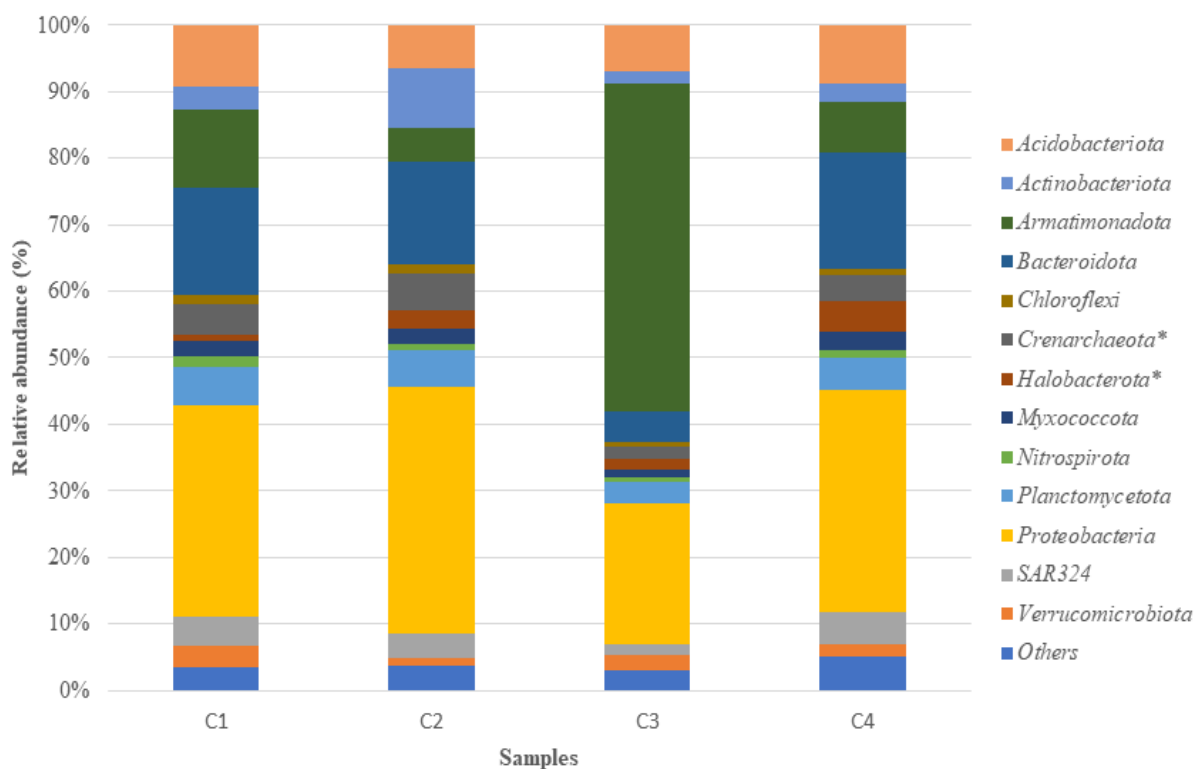


Figure 2. Classification of the most abundant phyla ($\geq 1\%$ of the total sequences in at least one sample) of microorganism present in activated sludge samples over a year (samples C1 to C4). “Others” represents the phyla whose abundances are lower than 1% of the total sequences. * *Archaea* phyla.

From the 336 detected taxa, 33 presented a relative abundance higher than 1% in at least one sample (Table 2) and were considered the predominant microbiota. From that, seventeen microorganisms were classified at the genus level. *Hyphomicrobium* was the most abundant genus in samples C1, C2 and, C4, accounting for 13.98%, 12.72% and 13.07% of the total sequences, respectively. The most abundant microorganism of sample C3 was a taxa belonging to the family *Fimbriimonadaceae* (phylum *Armatimonadota*), representing 48.96% of the total sequences in that sample. The majority of the 336 detected taxa were considered rare microbiota for presenting a relative abundance below 1% of the total sequences. From that, 185 microorganisms were classified at the genus level (Supplementary Table 1).

Canonical Correspondence Analysis (CCA) showed that the values of the physicochemical parameters of SS, SD and TSS are correlated, as well as ammoniacal nitrogen (Figure 3). According to the analyzed chemical parameters (Table 1), C3 presents the highest COD, AN and solids (SS, SD and TSS) compared to the other samples. These microbiological and chemical characteristics found in sample C3 make it different from C1, C2, and C4 (Figure 4). The highest COD, AN, and solids values are correlated to the high frequency of the phylum *Armatimonadota*.

Our study provided 16S rRNA gene sequence analyses of the microbial community present in activated sludge from the petrochemical industry. Our findings are in accordance with previous studies of activated sludge, with the predominance of *Proteobacteria* (Xia *et al.*, 2010). Sidhu *et al.* (2017) characterized and dissected the phylogenetic and functional structures from the sludge community at the phylum level and found the dominance of *Proteobacteria* in raw and dried sludge samples, representing 97.9% and 92.6%, respectively.

Table 2. Most abundant bacterial taxa present in the activated sludge samples.

Phylum	Class	Order	Family	Genus (or taxa)	Relative abundance (%)					
					C1	C2	C3	C4		
Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	Blastocatellaceae	3.59	1.46	2.15	2.03		
				OLB17	0.83	0.61	0.98	1.05		
				JGI_0001001-H03	1.38	0.64	1.41	2.09		
				<i>Stenotrophobacter</i>	1.64	1.41	0.95	1.35		
Actinobacteriota	Thermoleophilia	Gaiellales	67-14	Gaiellales	1.61	5.61	0.88	1.56		
		Solirubrobacterales		67-14	0.77	1.31	0.23	0.50		
Armatimonadota	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	Fimbriimonadaceae	11.07	4.92	48.96	7.49		
Bacteroidota	SJA-28	Sphingobacteriales	AKYH767	SJA-28	10.64	12.50	1.80	8.61		
	Bacteroidia			Chitinophagales	AKYH767	3.45	0.41	0.35	2.93	
				Saprosiraceae	Saprosiraceae	0.66	0.49	0.97	2.81	
Crenarchaeota*	Thermoprotei	Desulfurococcales	Desulfurococcaceae	<i>Sulfophobococcus</i>	2.51	4.18	1.25	3.03		
				<i>Thermogladius</i>	1.49	1.18	0.24	0.04		
Halobacterota*	Archaeoglobi	Archaeoglobales	Archaeoglobaceae	<i>Ferroglobus</i>	0.59	1.19	0.30	0.67		
				<i>Geoglobus</i>	0.39	1.70	0.97	3.11		
Myxococcota	Polyangia	Haliangiales	Haliangiaceae	<i>Haliangium</i>	1.42	1.05	0.75	1.15		
Nitrospirota	Nitrospiria	Nitrospirales	Nitrospiraceae	<i>Nitrospira</i>	1.44	0.98	0.65	1.13		
Planctomycetota	Phycisphaerae	S-70		S-70	0.87	0.80	0.58	1.31		
	OM190			OM190	0.30	1.09	0.32	0.74		
	Planctomycetes	Pirellulales	Pirellulaceae	Pirellulaceae	1.59	1.15	0.55	0.69		
		Gemmatales	Gemmataceae	Gemmataceae	1.10	0.86	0.35	0.22		
Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	<i>Hyphomicrobium</i>	13.98	12.72	4.79	13.07		
		Rhodobacterales	Rhodobacteraceae	<i>Rhodobacter</i>	1.27	0.79	0.78	0.33		
		Rickettsiales	AB1	AB1	0.00	2.09	0.35	0.00		
				Alphaproteobacteria	0.27	0.39	0.45	1.08		
	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae		Sulfuritalea	1.21	1.24	0.64	0.72	
			Nitrosomonadaceae		Ellin6067	0.98	2.19	0.84	1.60	
			Comamonadaceae		<i>Rubrivivax</i>	1.08	1.82	0.37	0.72	
			SC-I-84		SC-I-84	1.57	1.86	0.74	1.75	
			Coxiellales	Coxiellaceae		<i>Coxiella</i>	1.06	0.99	0.73	0.68
			Diplorickettsiales	Diplorickettsiaceae		Diplorickettsiaceae	0.66	2.74	0.92	0.13
	Gammaproteobacteria	Unknown_Family		<i>Candidatus Berkiella</i>	0.83	0.16	2.11	0.93		
SAR324				SAR324	4.33	3.59	1.68	4.77		
Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	<i>Candidatus Udaobacter</i>	1.24	0.36	0.41	0.95		

*Archaea phyla.

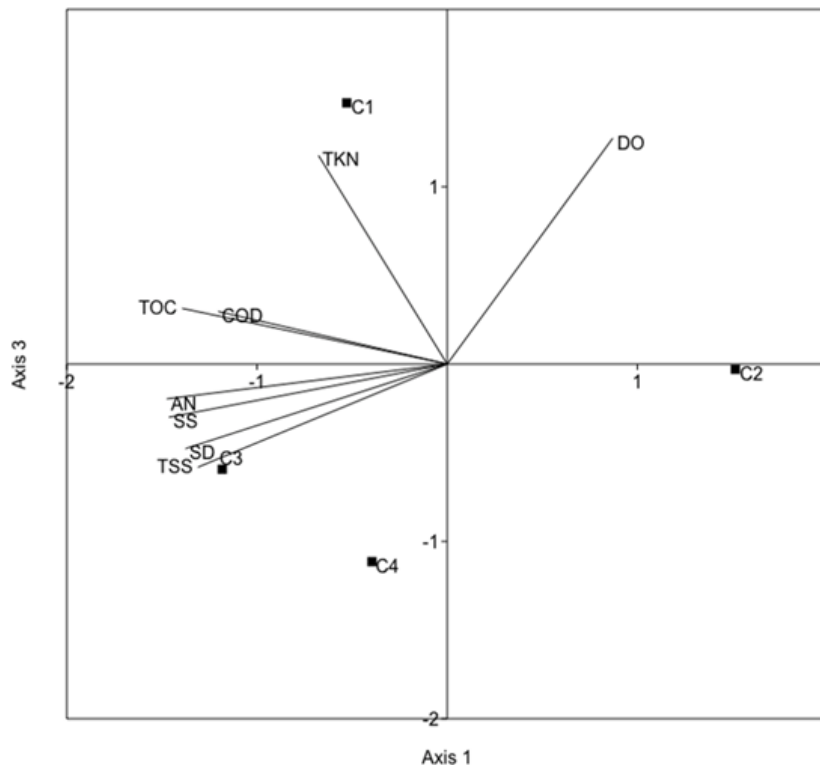


Figure 3. Canonical correlation analysis (CCA) associating the sample collection and chemical parameters to the activated sludge sampling point.

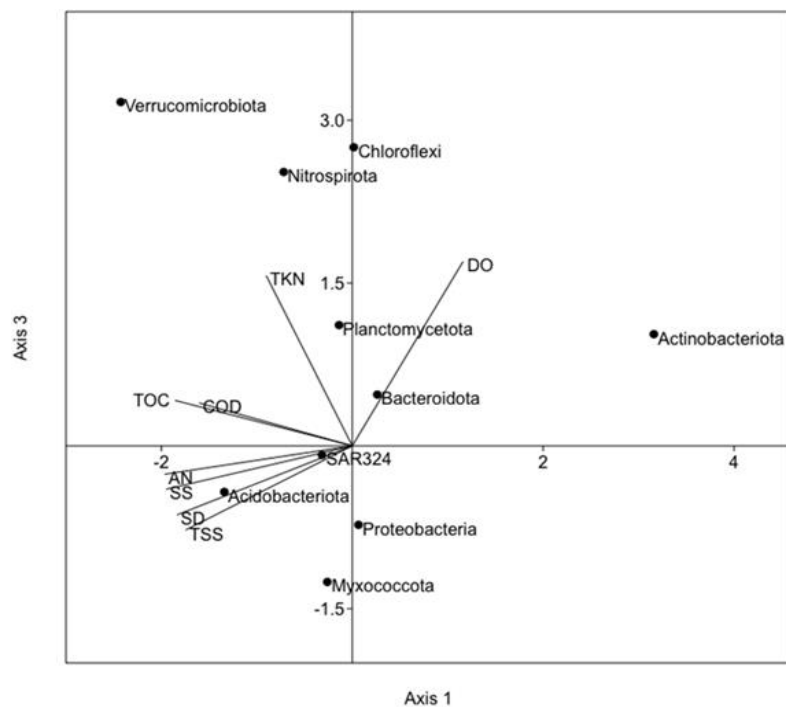


Figure 4. Canonical correlation analysis (CCA) associating the most abundant bacterial phyla and chemical parameters to the activated sludge sampling point.

Analysis of the microbial community revealed key groups for degradation of recalcitrant compounds present in the industrial effluent. *Proteobacteria* prevail in WWTPs treating pharmaceutical, oil refinery, and biological reactors (Xia *et al.*, 2010; Ibarbalz *et al.*, 2013;

Kwiatkowska and Zielinska, 2016). *Alphaproteobacteria* and *Gammaproteobacteria* were the most dominant class in *Proteobacteria*. The filamentous *Alphaproteobacteria* are versatile consumers of various organic substrates (Kragelund *et al.*, 2006). Most species are aerobic or facultatively anaerobic; many are oligotrophic, preferring to grow in environments with low nutrient concentration (Madigan *et al.*, 2016).

Activated sludge has a very diverse microbial community structure depending on both wastewater composition and operational conditions in the treatment plant. However, in several studies of microbial community structure, it has been found that the composition of activated sludge from different plants is quite similar in terms of overall dominating bacterial phylogenetic groups. In nutrient removal of activated sludge, the dominating group frequently found is *Alphaproteobacteria*, *Gammaproteobacteria* and *Betaproteobacteria* (Klausen *et al.*, 2004; Lee *et al.* 2002; Schmid *et al.*, 2003; Wagner and Loy, 2002). Studies in WWTPs suggested a higher diversity of active denitrifiers, including uncharacterized *Alphaproteobacteria*, *Gammaproteobacteria* and *Actinobacteria* (Osaka *et al.* 2006; Hagman *et al.*, 2008; Morgan-Sagastume *et al.*, 2008). Filamentous *Alphaproteobacteria* have been shown as essential microorganisms in industrial WWTPs, often related to bulking incidents or deteriorating settling sludge properties (Levantesi *et al.*, 2004).

At the order level, it was found that the dominant populations in the activated sludge samples were *Burkholderiales* and *Rhizobiales*, which represented 8.03% and 7.44% of those populations. This low percentage indicates a great diversity of the bacterial populations present in the activated sludge.

Sample C3 presented the most different microbial composition of the four samples, mainly because of the dominance of the individuals from the phylum *Armatimonadota* (Lee *et al.*, 2013). This phylum is found in a diverse array of environments, such as geothermal soils (Stott *et al.*, 2008), freshwater lakes and rivers (Crump and Hobbie, 2005), the water discharged from manures (Simpson *et al.*, 2004), and activated sludge (Dalevi *et al.*, 2001). Portillo *et al.* (2009) pointed out that this bacterial phylum could constitute an average of 5% among the total bacterial sequences recovered in hypersaline soils, geothermal springs, lake and river, bioreactors, and endolithic environments. Among the phylum *Armatimonadetes*, a more extensive geographical distribution was found in anaerobic niches (Harris *et al.*, 2004; Stott *et al.*, 2008). Chemical parameters influenced the bacterial community of C3. The canonical correlation analysis (CCA) shows that the phylum *Armatimonadota* presented a positive correlation with the increasing COD, TOC and total dissolved and suspended solids of the C3 sample. This sample showed the highest COD and the second-highest TOC and Solids (TSS, SS, and SD) quantification; these parameters contribute to the formation of an environment with low oxygen concentrations, which may have favored the occurrence of the phylum *Armatimonadota*. Also, sample C3 showed bacterial diversity differences between the other collections of activated sludge, such the phyla *Aenigmarchaeota*, *Caldisericota*, *Cloacimonadota*, MBNT15 and Sva0485, which were only detected in C3 (Supplementary Table 1).

CCA analysis also showed the correlation of *Actinobacteriota* with the presence of dissolved oxygen (DO). Most genera from this phylum are aerobic (Goodfellow and Williams, 1983) and this phylum presented significant quantification in sample C2 (2 mg per liter).

Nitrospirae shows a correlation with the presence of NTK. The ability to perform nitrite reduction was a physiological characteristic observed in *Nitrospirae* (Sidhu *et al.*, 2017). According to Ward *et al.* (2009), genomic evidence suggested that the role of acidobacteria in nitrogen cycling in soils and sediments is the reduction of nitrate, nitrite, and possibly nitric oxide due to assimilatory nitrate reductase gene sequences. The presence of *nif* genes related to conventional nitrogenase was found in a study by Inoue *et al.* (2015), suggesting nitrogen fixation ability in some *Bacteroidetes* species.

Acidobacteriota shows a correlation with the presence of AN, SS, SD and TSS. Bacteria belonging to the phylum *Acidobacteria* have also been observed in a wide variety of environments, including extreme (Hobel *et al.*, 2005), polluted (Bobbink *et al.*, 2010), and effluent wastewater environments (LaPara *et al.*, 2000). Ward *et al.* (2009) found that *Acidobacteria* were involved in nitrogen cycling, promoting the conversion of nitrate and nitrite.

All the sequences were classified at the phylum level, and up to 55% were associated with a bacterial genus. Among the most abundant microorganisms, *Hyphomicrobium* and *Fimbriimonadaceae* were described in the literature as potential denitrifiers and degradators. The genus *Hyphomicrobium* is a denitrifier and can degrade C-1 compounds such as methanol (Rissanen *et al.*, 2017). Sequences representing the phylum *Armatimonadetes* have been isolated by culture-independent methods from various environments, including aerobic and anaerobic wastewater treatment processes, the rhizosphere, hypersaline microbial mats and subsurface geothermal water streams (Portillo and Gonzalez, 2009; Lee *et al.*, 2013; Tamaki *et al.*, 2011). *Fimbriimonadaceae* belonging to *Armatimonadetes* was detected in an anammox consortia where ammonium was removed without nitrite and oxygen (Liang *et al.*, 2014).

4. CONCLUSION

Even with the advances brought about by the new generation sequencing, there are still challenges regarding the classification of the microorganisms in environmental samples. The classification of sequences at a lower taxonomic level, such as family or genus, is essential to understanding a WWTP as a whole and the real participation of each microorganism in the different stages of treatment. The present study contributed to the characterization of the microbial communities involved in the sewage treatment of the petrochemical industry. Identifying the microorganisms has the broader impact of contributing to the knowledge of biological wastewater treatment.

5. ACKNOWLEDGMENTS

We would like to thank Sistema Integrado de Tratamento de Efluentes Líquidos do Polo Petroquímico (SITEL-CORSAN) for authorizing the sample collection. We thank High Performance Computing Lab - LAD/PUCRS for allowing access to run the high-throughput sequences analyses. Luiz Gustavo A. Borges thanks PEGA/PUCRS. We also thank CNPq and CAPES for their financial support.

6. REFERENCES

- ABE, T.; USHIKI, N.; FUJITANI, H.; TSUNEDA, S. A rapid collection of yet unknown ammonia oxidizers in pure culture from activated sludge. **Water Research**, v. 108, p. 169-178, 2017. <https://doi.org/10.1016/j.watres.2016.10.070>
- ANTUNES, T. C.; BALLARINI, A. E.; VAN DER SAND, S. Temporal variation of bacterial population and response to physical and chemical parameters along a petrochemical industry wastewater treatment plant. **Annals of the Brazilian Academy of Sciences**, v. 91, n. 2, 2018. <https://doi.org/10.1590/0001-3765201920180394>
- APHA; AWWA; WEF. **Standard Methods for the examination of water and wastewater**. 22nd ed. Washington, 2012. 1496 p.
- BATES, S. T.; BERG-LYONS, D.; CAPORASO, W. W. A; KNIGHT, R.; FIERER, N. Examining the global distribution of dominant archaeal populations in soil. **The ISME Journal**, v. 5, p. 908-17, 2011. <https://doi.org/10.1038/ismej.2010.171>

- BOBBINK, R.; HICKS, K.; GALLOWAY, J.; SPRANGER, T.; ALKEMADE, R.; ASHMORE, M. *et al.* Global assessment of nitrogen deposition effects on terrestrial plant diversity: a synthesis. **Ecological Applications**, v. 20, p. 30–59, 2010. <http://dx.doi.org/10.1890/08-1140.1>
- CALLAHAN, B. J.; MCMURDIE, P. J.; ROSEN, M. J.; HAN, A. W.; JOHNSON, A. J.; HOLMES, S. P. DADA2: High-resolution sample inference from Illumina amplicon data. **Nature Methods**, v. 13, p. 581–583, 2016. <https://dx.doi.org/10.1038/nmeth.3869>
- CLAESSON, M. J.; WANG, Q.; O'SULLIVAN, O.; GREENE-DINIZ, R.; COLE J. R.; ROSS, R. P.; O'TOOLE, P. W. Comparison of two next-generation sequencing technologies for resolving highly complex microbiota composition using tandem variable 16S rRNA gene regions. **Nucleic Acids Research**, v. 38, p. e200, 2010. <https://doi.org/10.1093/nar/gkq873>
- CRUMP, B. C.; HOBBIE, J. E. Synchrony and seasonality in bacterioplankton communities of two temperate rivers. **Limnology Oceanography**, v. 50, p. 1718–1729, 2005. <https://doi.org/10.4319/lo.2005.50.6.1718>
- DALEVI, D.; HUGENHOLTZ, P.; BLACKALL, L. L. A multiple-outgroup approach to resolving division-level phylogenetic relationships using 16S rDNA data. **International Journal of Systematic Evolutionary Microbiology**, v. 51, p. 385–391, 2001. <https://doi.org/10.1099/00207713-51-2-385>
- FIGUEROLA, E. L.; ERIJMAN, L. Bacterial taxa abundance pattern in an industrial wastewater treatment system determined by the full rRNA cycle approach. **Environmental Microbiology**, v.9, p.1780-1789, 2007. <https://doi.org/10.1111/j.1462-2920.2007.01298.x>
- GOODFELLOW, M.; WILLIAMS, S. T. Ecology of Actinomycetes. **Annual Review of Microbiology**, v. 37, n. 1, p. 189-216, 1983. <https://doi.org/10.1146/annurev.mi.37.100183.001201>
- GWIN, C. A.; LEFEVRE, E.; ALITO, C. L.; GUNSCH, C. K. Microbial community response to silver nanoparticles and Ag⁺ in nitrifying activated sludge revealed by ion semiconductor sequencing. **The Science of the Total Environment**, v. 616–617, p. 1014–1021, 2018. <https://doi.org/10.1016/j.scitotenv.2017.10.217>
- HAGMAN, M.; NIELSEN, J. L.; NIELSEN, P. H.; JANSEN J. Mixed carbon sources for nitrate reduction in activated sludge-identification of bacteria and process activity studies. **Water Research**, v. 42, p. 1539-1546, 2008. <https://doi.org/10.1016/j.watres.2007.10.034>
- HAMMER, O.; HARPER, D. A. T.; RYAN, P. D. PAST: Paleontological Statistics Software Package for Education and Data Analysis. **Palaeontology Electronica**, v. 4, n. 1, p. 1-9, 2001.
- HARRIS, J. K.; KELLEY, S. T.; PACE, N. R. New perspective on uncultured bacterial phylogenetic division OP11. **Applied Environmental Microbiology**, v. 70, p. 845–849, 2004. <https://dx.doi.org/10.1128/AEM.70.2.845-849.2004>
- HEIDENWAG, I.; LANGHEINRICH, U.; LÜDERITZ, V. Self Purification in upland and lowland streams. **Acta Hydrochimica at Hydrobiologica**, v. 29, n. 1, p. 22-33, 2001.

- HEINZ, K. G. H.; ZANONI, P. R. S.; OLIVEIRA, R. R.; MEDINA-SILVA, R.; SIMÃO, T. L. L.; TRINDADE, F. J. *et al.* Recycled paper sludge microbial community as a potential source of cellulase and xylanase enzymes. **Waste Biomass Valorization**, v. 8, p. 1907-1917, 2017. <https://dx.doi.org/10.1007/s12649-016-9792-x>
- HOBEL, C. F. V.; MARTEINSSON, V. T.; HREGGVIDSSON, G. O.; KRISTJÁNSSON, J. K. Investigation of the microbial ecology of intertidal hot springs by using diversity analysis of 16 S rRNA and chitinase genes. **Applied Environmental Microbiology**, v. 71, p. 2771–2776, 2005. <https://dx.doi.org/10.1128/aem.71.5.2771-2776.2005>
- IBARBALZ, F. M.; FIGUEROLA, E. L. M.; ERIJMAN, L. Industrial activated sludge exhibit unique bacterial community composition at high taxonomic ranks. **Water research**, v. 47, p. 3854-3864, 2013. <https://doi.org/10.1016/j.watres.2013.04.010>
- INOUE, J.; OSHIMA, K.; SUDA, W.; SAKAMOTO, M.; IINO, T.; NODA, S.; OHKUMA, M. Distribution and Evolution of Nitrogen Fixation Genes in the Phylum Bacteroidetes. **Microbes Environmental**, v. 30, n. 1, p. 44–50, 2015. <http://doi.org/10.1264/jsme2.ME14142>
- KLAUSEN, M. M.; THOMSEN, T. R.; NIELSEN, J. L.; MIKKELSEN, L. H.; NIELSEN, P. H. Variations in microcolony strength of probe-defined bacteria in activated sludge flocs. **FEMS Microbiology Ecology**, v. 50, p.123–132, 2004. <https://doi.org/10.1016/j.femsec.2004.06.005>
- KRAGELUND, C.; KONG, Y.; VAN DER, W. J.; THELEN; K.; EIKELBOOM, D.; TANDOI, V. *et al.* Ecophysiology of different filamentous Alphaproteobacteria species from industrial wastewater treatment plants. **Microbiology**, v. 152, p.3003–3012, 2006. <https://doi.org/10.1099/mic.0.29249-0>
- KRISHNAN, M.; SUGANYA, T.; PANDIARAJAN, J. Bacterial community exploration through Ion Torrent sequencing from different treatment stages of CETP for tannery. **Expert Opinion Environmental Biology Journal**, v. 5, p. 3, 2016. <https://dx.doi.org/10.4172/2325-9655.1000136>
- KWIATKOWSKA, A. C.; ZIELINSKA, M. Bacterial communities in full-scale wastewater treatment systems. **World Journal Microbiology Biotechnology**, v. 32, p. 66, 2016. <https://dx.doi.org/10.1007/s11274-016-2012-9>
- LAPARA, T. M.; NAKATSU, C. H.; PANTEA, L.; ALLEMAN, J. E. Phylogenetic analysis of bacterial communities in mesophilic and thermophilic bioreactors treating pharmaceutical wastewater. **Applied Environmental Microbiology**, v. 66, p. 3951–3959, 2000. <https://dx.doi.org/10.1128/aem.66.9.3951-3959.2000>
- LEE, N.; LA COUR JANSSEN, J.; ASPEGREN, H.; HENZE, M. N. P. H.; WAGNER, M. Population dynamics in wastewater treatment plants with enhanced biological phosphorus removal operated without nitrogen removal. **Water Science Technology**, v. 46, p.163–170, 2002. <https://doi.org/10.2166/wst.2002.0472>
- LEE, K. C. Y.; HERBOLD, C. W.; DUNFIELD, P. F.; MORGAN, X. C.; MCDONALD, I. R.; STOTT, M. B. Phylogenetic delineation of the novel phylum Armatimonadetes (former candidate division OP10) and definition of two novel candidate divisions. **Applied Environmental Microbiology**, v. 79, p. 2484-2487, 2013. <https://doi.org/10.2166/wst.2002.0472>

- LEVANTESI, C.; BEIMFOHR, C.; GEURKINK, B.; ROSSETTI, S.; THELEN, K.; KROONEMAN, J. *et al.* Filamentous Alphaproteobacteria associated with bulking in industrial wastewater treatment plants. **System Applied Microbiology**, v. 27, p.716–727, 2004. <https://doi.org/10.1078/0723202042369974>
- LIANG, Y.; LI, D.; ZHANG, X.; ZENG, H.; YANG, Z.; ZHANG, J. Microbial characteristics and nitrogen removal of simultaneous partial nitrification, anammox and denitrification (SNAD) process treating low C/N ratio sewage. **Bioresource Technology**, v.169, p.103-109, 2014. <https://doi.org/10.1016/j.biortech.2014.06.064>
- MADIGAN, M. T.; MARTINKO, J. M.; BENDER, K. S.; BUCKLEY, D. H.; STAHL, D. A. **Microbiologia de Brock**. Porto Alegre: Artmed, 2016. 1032 p.
- MCMURDIE P. J.; HOLMES, S. Phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. **PLoS ONE**, v. 8, p. e61217, 2013. <https://dx.doi.org/10.1371/journal.pone.0061217>
- MORGAN-SAGASTUME, F.; NIELSEN, J. L.; NIELSEN, P. H. Substrate-dependent denitrification of abundant probe-defined denitrifying bacteria in activated sludge. **FEMS Microbiology Ecology**, v. 66, p. 447-461, 2008. <https://doi.org/10.1111/j.1574-6941.2008.00571.x>
- OSAKA, T.; YOSHIE, S.; TSUNEDA, S.; HIRATA, A.; IWAMI, N.; INAMORI, Y. Identification of acetate- or methanol-assimilating bacteria under nitrate-reducing conditions by stable-isotope probing. **Microbiology Ecology**, v. 52, p. 253-266, 2006. <https://doi.org/10.1007/s00248-006-9071-7>
- PORTILLO, M. C.; GONZALEZ, J. M. Members of the Candidate Division OP10 are spread in a variety of environments. **World Journal Microbiology Biotechnology**, v. 25, p. 347–353, 2009. <https://dx.doi.org/10.1007/s11274-008-9895-z>
- QUAST, C.; PRUESSE, E.; YILMAZ, P.; GERKEN, J.; SCHWEER, T.; YARZA, P. *et al.* The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. **Nucleic Acids Research**, v. 41, p. D590–D596, 2013. <https://dx.doi.org/10.1093/nar/gks1219>
- R CORE TEAM. **R**: A language and environment for statistical computing. Vienna: R Foundation for Statistical Computing, 2019.
- RISSANEN, A. J.; OJALA, A.; FRED, T.; TOIVONEN, J.; TIROLA, M. Methylophilaceae and Hyphomicrobium as target taxonomic groups in monitoring the function of methanol-fed denitrification biofilters in municipal wastewater treatment plants. **Journal of Industrial Microbiology Biotechnology**, v. 44, p. 35–47, 2017. <https://doi.org/10.1007/s10295-016-1860-5>
- SÁNCHEZ, O.; FERRERA, I.; GONZÁLEZ, J.M.; MAS, J. Assessing bacterial diversity in a seawater-processing wastewater treatment plant by 454-pyrosequencing of the 16S rRNA and amoA genes. **Microbial Biotechnology**, v. 6, n. 4, p. 435–442, 2013. <https://dx.doi.org/10.1111/1751-7915.12052>
- SCHMID, M.; THILL, A.; PURKHOLD, U.; WALCHER, M.; BOTTERO, J. Y.; GINESTET, P. *et al.* Characterization of activated sludge flocs by confocal laser scanning microscopy and image analysis. **Water Research**, v. 37, p. 2043–2052, 2003. [https://doi.org/10.1016/S0043-1354\(02\)00616-4](https://doi.org/10.1016/S0043-1354(02)00616-4)

- SIDHU, C.; VIKRAM, S.; PINNAKA, A. K. Unraveling the microbial interactions and metabolic potentials in pre- and post-treated sludge from a wastewater treatment plant using metagenomic studies. **Frontiers in Microbiology**, v. 8, p. 1382, 2017. <https://dx.doi.org/10.3389/fmicb.2017.01382>
- SIMPSON, J. M.; DOMINGO, J. W.; REASONER, D. J. Assessment of equine fecal contamination: the search for alternative bacterial source-tracking targets. **FEMS Microbiology Ecology**, v. 47, p. 65–75, 2004. [https://doi.org/10.1016/S0168-6496\(03\)00250-2](https://doi.org/10.1016/S0168-6496(03)00250-2)
- STOTT, M. B.; SAITO, J. A.; CROWE, M. A.; DUNFIELD, P. F.; HOU, S.; NAKASONE, E. *et al.* Culture-independent characterization of a novel microbial community at a hydrothermal vent at Brothers volcano, Kermadec arc, New Zealand. **Journal of Geophysical Research: Solid Earth**, v. 113, 2008. <https://dx.doi.org/10.1029/2007JB005477>
- TAMAKI, H.; TANAKA, Y.; MATSUZAWA, H.; MURAMATSU, M.; MENG, X.Y.; HANADA, S. *et al.* *Armatimonas rosea* gen. nov., sp nov., of a novel bacterial phylum, *Armatimonadetes* phyl. nov., formally called the candidate phylum OP10. **International Journal Systematic and Evolutionary Microbiology**. v.61, p.1442–1447, 2011. <https://doi.org/10.1099/ijs.0.025643-0>
- WAGNER, M.; LOY, A. Bacterial community composition and function in sewage treatment systems. **Current Opinion Biotechnology**. v. 13, p. 218-227, 2002. [https://doi.org/10.1016/S0958-1669\(02\)00315-4](https://doi.org/10.1016/S0958-1669(02)00315-4)
- WARD, N. L.; CHALLACOMBE, J. F.; JANSSEN, P. H.; HENRISSAT, B.; COUTINHO, P. M.; WU, M. *et al.* Three genomes from the phylum Acidobacteria provide insight into the lifestyles of these microorganisms in soils. **Applied Environmental Microbiology**, v. 75, p. 2046-56, 2009. <https://dx.doi.org/10.1128/AEM.02294-08>
- XIA, S.; DUAN, L.; SONG, Y.; LI, J.; PICENO, Y. M.; ANDERSEN, G. L.; COHEN, A. L. *et al.* Bacterial community structure in geographically distributed biological wastewater treatment reactors. **Environmental Science and Technology**, v. 44, p. 7391–7396, 2010. <https://doi.org/10.1021/es101554m>
- YANG, Y.; YU, K.; XIA, Y.; LAU, F. T.; TANG, D. T.; FUNG, W. C.; FANG, H. H. Metagenomic analysis of sludge from full-scale anaerobic digesters operated in municipal wastewater treatment plants. **Applied Microbiology Biotechnology**, v. 98, p. 5709, 2014. <https://doi.org/10.1007/s00253-014-5648-0>
- YE, L.; ZHANG, T. Bacterial communities in different sections of a municipal wastewater treatment plant revealed by 16S rDNA 454 pyrosequencing. **Applied Microbiology Biotechnology**, v. 97, p. 2681, 2013. <https://doi.org/10.1007/s00253-012-4082-4>
- ZHANG, T.; SHAO, M. F.; YE, L. 454 pyrosequencing reveals bacterial diversity of activated sludge from 14 sewage treatment plants. **The ISME Journal**, v. 6, p. 1137–1147, 2011. <https://doi.org/10.1038/ismej.2011.188>

Supplementary Table 1.

Kingdom	Phylum	Class	Order	Family	Genus (or taxa)	C1	C2	C3	C4
Bacteria	Armatimonadota	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae		11.07	4.92	48.96	7.49
Bacteria	Bacteroidota	SJA-28				10.64	12.50	1.80	8.61
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hypomicrobiaceae	Hypomicrobium	13.98	12.72	4.79	13.07
Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	OLB17	1.38	0.82	1.32	1.01
Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	OLB17	0.83	0.61	0.98	1.05
Bacteria	Actinobacteriota	Thermoleophilia	Gaiellales			1.61	5.61	0.88	1.56
Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	AKYH767		3.45	0.41	0.35	2.93
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Sulfuritalea	1.21	1.24	0.64	0.72
Archaea	Crenarchaeota	Thermoprotei	Desulfurococcales	Desulfurococcaceae	Sulfophobococcus	2.51	4.18	1.25	3.03
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	Ellin6067	0.98	2.19	0.84	1.60
Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	JGI_0001001-H03	1.38	0.64	1.41	2.09
Bacteria	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae		0.66	2.74	0.92	0.13
Bacteria	SAR324_clade (Marine_group_B)					4.33	3.59	1.68	4.77
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	1.27	0.79	0.78	0.33
Archaea	Halobacterota	Archaeoglobi	Archaeoglobales	Archaeoglobaceae	Ferroglobus	0.59	1.19	0.30	0.67
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	AB1		0.00	2.09	0.35	0.00
Bacteria	Myxococcota	Polyangia	Haliangiales	Haliangiaceae	Haliangium	1.42	1.05	0.75	1.15
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Rubrivivax	1.08	1.82	0.37	0.72
Bacteria	Actinobacteriota	Thermoleophilia	Solirubrobacterales	67-14		0.77	1.31	0.23	0.50
Bacteria	Nitrospirota	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira	1.44	0.98	0.65	1.13
Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Saprosiraceae		0.66	0.49	0.97	2.81
Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae		2.20	0.64	0.83	1.02
Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	Stenotrophobacter	1.64	1.41	0.95	1.35
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Candidatus_Udaeobacter	1.24	0.36	0.41	0.95
Bacteria	Proteobacteria	Alphaproteobacteria				0.27	0.39	0.45	1.08
Bacteria	Proteobacteria	Gammaproteobacteria	Coxiellales	Coxiellaceae	Coxiella	1.06	0.99	0.73	0.68
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	SC-I-84		1.57	1.86	0.74	1.75
Bacteria	Planctomycetota	Phycisphaerae	S-70			0.87	0.80	0.58	1.31
Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae		1.59	1.15	0.55	0.69
Bacteria	Planctomycetota	OM190				0.30	1.09	0.32	0.74
Bacteria	Planctomycetota	Planctomycetes	Gemmatales	Gemmataceae		1.10	0.86	0.35	0.22
Archaea	Halobacterota	Archaeoglobi	Archaeoglobales	Archaeoglobaceae	Geoglobus	0.39	1.70	0.97	3.11
Archaea	Crenarchaeota	Thermoprotei	Desulfurococcales	Desulfurococcaceae	Thermogladus	1.49	1.18	0.24	0.04
Bacteria	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Incertae_Sedis	Unknown_Family	Candidatus_Berkiella	0.83	0.16	2.11	0.93
Bacteria	Proteobacteria	Gammaproteobacteria	Ga0077536			0.53	0.57	0.41	0.79
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Waddliaceae	Waddlia	0.15	0.07	0.60	0.19
Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Ferruginibacter	0.50	0.73	0.51	0.91
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Rhizorhapis	0.57	0.15	0.24	0.75
Bacteria	Acidobacteriota	Blastocatellia	11_24			0.41	0.41	0.40	0.46
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Methylophilaceae	Methylotenera	0.07	0.24	0.51	0.26

Continue...

Continued...									
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Bradyrhizobium	0.40	0.48	0.51	0.61
Bacteria	Thermotogota	Thermotogae	Mesoaciditogales	Mesoaciditogaceae		0.17	0.82	0.30	0.39
Archaea	Halobacterota	Halobacteria	Halobacterales	Halobacteriaceae	Salarchaeum	0.00	0.00	0.29	0.71
Bacteria	Proteobacteria	Gammaproteobacteria	Nitrosococcales	Nitrosococcaceae	MSB-1D1	0.00	0.21	0.18	0.76
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	0.00	0.68	0.19	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae		0.46	0.44	0.16	0.33
Archaea	Nanoarchaeota	Nanoarchaeia	Nanoarchaeales	Nanopusillaceae	Candidatus_Nanopusillus	0.82	0.71	0.30	0.81
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Sutterellaceae		0.41	0.26	0.11	0.46
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	B1-7BS		0.46	0.30	0.15	0.47
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Simkaniaceae	Ga0074140	0.22	0.04	0.27	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Proteiniclasticum	0.00	0.20	0.24	0.09
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	0.59	0.92	0.24	0.43
Bacteria	Armatimonadota	Fimbriimonadia	Fimbriimonadales			0.68	0.15	0.21	0.13
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae		0.52	0.34	0.21	0.10
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae		0.54	0.00	0.27	0.00
Bacteria	Acidobacteriota	Vicinamibacteria	Subgroup_17			0.43	0.73	0.30	0.44
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales_Incertae_Sedis		0.56	0.18	0.31	0.24
Bacteria	Acidobacteriota	Thermoanaerobaculia	Thermoanaerobaculales	Thermoanaerobaculaceae	Subgroup_10	0.43	0.44	0.26	0.21
Bacteria	Proteobacteria	Gammaproteobacteria	AT-s16			0.04	0.00	0.26	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	EV818SWSAP88			0.36	0.13	0.28	0.10
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales_Incertae_Sedis	Nordella	0.33	0.23	0.27	0.32
Bacteria	Gemmatimonadota	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae		0.17	0.17	0.11	0.34
Bacteria	Myxococcota	Polyangia	Bifidi19			0.69	0.33	0.03	0.81
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Aminobacter	0.00	0.83	0.22	0.00
Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Leucobacter	0.00	0.26	0.15	0.10
Bacteria	Actinobacteriota	Acidimicrobiia	IMCC26256			0.31	0.42	0.14	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Pseudaminobacter	0.00	0.00	0.33	0.00
Bacteria	Planctomycetota	Phycisphaerae	mle1-8			0.31	0.41	0.28	0.62
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Defluviimonas	0.46	0.00	0.21	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	PLTA13			0.03	0.16	0.13	0.30
Bacteria	Proteobacteria	Alphaproteobacteria	Paracaedibacterales	Paracaedibacteraceae	Candidatus_Paracaedibacter	0.08	0.07	0.07	0.60
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudorhodoplanes	0.52	0.58	0.21	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hirschia	0.00	0.21	0.14	0.08
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae		0.04	0.19	0.35	0.29
Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Terrimonas	0.34	0.46	0.29	0.81
Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Microscillaceae		0.24	0.18	0.17	0.29
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	966-1	0.00	0.40	0.14	1.04
Bacteria	Planctomycetota	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	SM1A02	0.15	0.38	0.40	0.80
Bacteria	Planctomycetota	Phycisphaerae	CCM11a			0.12	0.04	0.19	0.02
Bacteria	Myxococcota	Polyangia	Polyangiales	Polyangiaceae	Pajaroellobacter	0.00	0.13	0.09	0.43
Bacteria	Dependentiae	Babeliae	Babeliales	Vermiphilaceae		0.00	0.45	0.45	0.09
Bacteria	Proteobacteria	Alphaproteobacteria	Micavibrionales			0.00	0.00	0.00	0.81

Continue...

Continued...

Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae		0.00	0.00	0.18	0.00
Bacteria	Desulfobacterota	Desulfobacteria	Desulfobacterales	Desulfolunaceae	Desulfoluna	0.03	0.06	0.13	0.46
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Uliginobacterium	0.00	0.17	0.07	0.21
Bacteria	Desulfobacterota					0.10	0.07	0.16	0.16
Bacteria	Planctomycetota	Planctomycetes				0.33	0.40	0.22	0.20
Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales			0.24	0.40	0.11	0.09
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	0.00	0.00	0.13	0.34
Archaea	Crenarchaeota	Thermoprotei	Geoarchaeales	SCGC_AAA261-C22		0.49	0.00	0.16	0.38
Bacteria	Chloroflexi	KD4-96				0.47	0.54	0.07	0.23
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Limnobacter	0.00	0.23	0.06	0.10
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Methylibium	0.00	0.00	0.14	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Beggiatoales	Beggiatoaceae	Candidatus_Allobeggiatoa	0.00	0.00	0.10	0.37
Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae	Galbitalea	0.33	0.11	0.07	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Denitratissoma	0.08	0.05	0.08	0.39
Bacteria	Proteobacteria	Alphaproteobacteria	Reyranelles	Reyranelleaceae		0.00	0.27	0.06	0.00
Bacteria	Dependentiae	Babeliae	Babeliales			0.44	0.13	0.13	0.62
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Parachlamydiaceae	Candidatus_Protochlamydia	0.27	0.00	0.17	0.00
Bacteria	Chloroflexi	Anaerolineae	RBG-13-54-9			0.32	0.24	0.15	0.16
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Amaricoccus	0.00	0.00	0.00	0.54
Bacteria	Bdellovibrionota	Oligoflexia	0319-6G20			0.25	0.06	0.14	0.28
Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales			0.00	0.08	0.09	0.24
Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Microbacteriaceae		0.00	0.32	0.00	0.12
Bacteria	Actinobacteriota	Coriobacteriia	Coriobacteriales	Atopobiaceae	Coriobacteriaceae_UCG-002	0.10	0.13	0.13	0.12
Bacteria	Actinobacteriota	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium	0.00	0.15	0.09	0.11
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	0.00	0.00	0.11	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Acidithiobacillales	Acidithiobacillaceae	KCM-B-112	0.16	0.00	0.06	0.09
Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	Vicinamibacteraceae		0.00	0.39	0.10	0.25
Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	Aridibacter	0.06	0.06	0.08	0.46
Bacteria	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	Hyalangium	0.02	0.38	0.04	0.00
Archaea	Aenigmarchaeota	Aenigmarchaeia	Aenigmarchaeales	Aenigmarchaeales_fa	Candidatus_Aenigmarchaeum	0.00	0.00	0.10	0.00
Archaea	Crenarchaeota	Thermoprotei				0.08	0.03	0.11	0.34
Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Arcticibacter	0.00	0.00	0.10	0.00
Bacteria	Cloacimonadota	Cloacimonadia	Cloacimonadales	SHA-41		0.00	0.00	0.15	0.00
Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae		0.38	0.19	0.14	0.24
Bacteria	NB1-j					0.26	0.27	0.06	0.21
Archaea	Crenarchaeota	Thermoprotei	Desulfurococcales	Desulfurococcaceae	Staphylothermus	0.00	0.09	0.12	0.00
Bacteria	Acidobacteriota	Holophagae	Subgroup_7			0.21	0.13	0.09	0.00
Bacteria	Bacteroidota	Kryptonia	Kryptoniales	BSV26		0.23	0.31	0.13	0.69
Bacteria	Myxococcota	Polyangia	MSB-4B10			0.02	0.00	0.09	0.00
Bacteria	Planctomycetota	Phycisphaerae	Tepidisphaerales	WD2101_soil_group		0.27	0.10	0.10	0.09
Bacteria	Chloroflexi	Dehalococcoidia	S085			0.15	0.07	0.06	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Ahniella	0.10	0.18	0.02	0.00

Continue...

Continued...

Bacteria	Acidobacteriota	Acidobacteriae	Bryobacterales	Bryobacteraceae	Bryobacter	0.00	0.07	0.11	0.15
Bacteria	Bacteroidota	Ignavibacteria	Ignavibacteriales	LD-RB-34		0.03	0.07	0.07	0.16
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Parachlamydiaceae	Neochlamydia	0.16	0.30	0.12	0.19
Bacteria	Latescibacterota					0.00	0.20	0.08	0.07
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	ADurb.Bin063-1	0.00	0.00	0.08	0.00
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Simkaniaceae	Candidatus_Fritschea	0.40	0.00	0.05	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales			0.12	0.00	0.08	0.21
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	SWB02	0.00	0.21	0.16	0.16
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales_Incertae_Sedis	Bauldia	0.29	0.26	0.10	0.15
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Methyloversatilis	0.00	0.00	0.07	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	CCM19a			0.08	0.11	0.05	0.10
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Fretibacter	0.08	0.00	0.01	0.28
Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	Thiocapsa	0.07	0.24	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Kordiimonadales	Temperatibacteraceae	Temperatibacter	0.00	0.00	0.07	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Magnetospiraceae		0.05	0.05	0.07	0.10
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Criblamydiaceae	Estrella	0.00	0.00	0.06	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	A0839		0.00	0.09	0.08	0.02
Bacteria	Dependentiae	Babeliae	Babeliales	UBA12409		0.00	0.00	0.04	0.10
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Parachlamydiaceae	Candidatus_Rubidus	0.31	0.09	0.03	0.07
Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Bacteroidetes_BD2-2		0.08	0.04	0.06	0.03
Bacteria	Firmicutes	Clostridia	Eubacteriales	Eubacteriaceae	Acetobacterium	0.12	0.04	0.02	0.17
Bacteria	Patescibacteria	Gracilibacteria	Candidatus_Peregrinibacteria			0.05	0.00	0.05	0.03
Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Thermonemataceae	Thermonema	0.00	0.15	0.06	0.00
Bacteria	Planctomycetota	Pla3_lineage				0.14	0.03	0.06	0.05
Bacteria	Myxococcota	Polyangia	Polyangiales	Birii41		0.00	0.00	0.02	0.25
Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	Pir4_lineage	0.08	0.18	0.04	0.08
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Pseudohoe flea	0.03	0.00	0.04	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Holosporales	Holosporaceae		0.20	0.00	0.05	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	Aquicella	0.16	0.00	0.00	0.25
Bacteria	Chloroflexi	Anaerolineae	SBR1031	A4b		0.05	0.09	0.09	0.14
Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	NS9_marine_group		0.00	0.03	0.01	0.14
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Martellella	0.00	0.18	0.00	0.00
Bacteria	Zixibacteria					0.00	0.04	0.05	0.06
Bacteria	Dadabacteria	Dadabacteriia	Dadabacteriales			0.03	0.02	0.03	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Kiloniellales	Fodinicurvataceae		0.00	0.14	0.05	0.00
Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacteriales	Vicinamibacteraceae	Luteitalea	0.20	0.05	0.04	0.00
Bacteria	Chloroflexi	Anaerolineae	SBR1031	A4b		0.00	0.04	0.07	0.00
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Criblamydiaceae		0.00	0.00	0.04	0.00
Archaea	Crenarchaeota	Thermoprotei	Thermoproteales	Thermoproteaceae	Caldivirga	0.00	0.04	0.04	0.00
Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	Rhodopirellula	0.18	0.04	0.04	0.03
Bacteria	Patescibacteria	Microgenomatia	Candidatus_Amesbacteria			0.27	0.00	8.45E-03	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocystis	0.00	0.15	0.02	0.00

Continue...

Continued...

Bacteria	MBNT15					0.00	0.00	0.04	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Legionella	0.12	0.03	0.02	0.00
Bacteria	Chloroflexi	Anaerolineae	01_20			0.00	0.03	0.03	0.03
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Lautropia	0.00	0.00	0.04	0.00
Bacteria	Aquificota	Desulfurobacteriia	Desulfurobacteriales	Desulfurobacteriaceae	Balnearium	0.00	0.00	0.04	0.00
Bacteria	Bdellovibrionota	Oligoflexia	Silvanigrellales	Silvanigrellaceae	Silvanigrella	0.00	0.02	0.02	0.26
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitales	Puniceicoccaceae	Cerasicoccus	0.13	0.05	0.00	0.00
Bacteria	Planctomycetota	Planctomycetes	Planctomycetales	Rubinisphaeraceae	Planctomicrobium	0.11	0.08	0.01	0.00
Bacteria	Firmicutes	Clostridia	Peptostreptococcales-Tissierellales	Peptostreptococcaceae	Romboutsia	0.07	0.05	0.02	0.03
Bacteria	Patescibacteria	Saccharimonadia	Saccharimonadales	Saccharimonadaceae	GTL1	0.19	0.00	0.03	0.00
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium_sensu_stricto_1	0.11	0.10	0.01	0.05
Bacteria	Dependentiae	Babeliae	Babeliales	Babeliaceae		0.00	0.02	0.04	0.14
Bacteria	Proteobacteria	Gammaproteobacteria	Steroidobacterales	Steroidobacteraceae		0.00	0.00	0.04	0.00
Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	SCGC_AAA286-E23		0.00	0.12	0.00	0.00
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Terrimicrobiaceae	FukuN18_freshwater_group	0.01	0.00	0.03	0.00
Bacteria	Proteobacteria	Saccharimonadia	Saccharimonadales			0.05	0.03	0.03	0.00
Bacteria	Acidobacteriota	Acidobacteriae	Acidobacteriales	Koribacteraceae	Candidatus_Koribacter	0.04	0.00	0.02	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Reyranellales	Reyranellaceae	Reyranella	0.00	0.04	0.08	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	T34		0.00	0.00	0.03	0.00
Bacteria	Dependentiae	Babeliae	Babeliales	UBA12411		0.09	8.83E-03	0.03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	MND1	0.00	0.05	0.03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Alcaligenaceae	Candidimonas	0.00	0.00	0.03	0.00
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Parachlamydiaceae		0.00	0.00	0.02	0.14
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitales	Puniceicoccaceae		0.11	0.03	0.01	0.00
Bacteria	Myxococcota	Polyangia	Polyangiales	Sandaracinaceae		0.13	0.13	0.04	0.00
Bacteria	Acidobacteriota	Acidobacteriae	Elev-16S-1166			0.00	0.00	0.03	0.00
Bacteria	Actinobacteriota	Thermoleophilia	Thermophilales	Thermoleophilaceae	Thermoleophilum	0.04	0.02	0.03	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Inquilinaceae	Inquilingus	0.05	0.00	0.03	0.00
Bacteria	Chloroflexi	Anaerolineae	SBR1031			0.00	0.00	0.05	0.06
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Alcaligenaceae	Derxia	0.00	0.00	0.03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae		0.00	0.00	0.03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Immundisolibacteriales	Immundisolibacteraceae	Immundisolibacter	0.00	0.00	0.03	0.13
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	cvE6		0.14	0.00	8.45E-03	0
Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillales_Incertae_Sedis	Stella	0.00	0.00	0.03	0
Bacteria	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.15	0.00	0.03	0.10
Bacteria	Proteobacteria	Gammaproteobacteria	Steroidobacteriales	Steroidobacteraceae	Steroidobacter	0.00	0.00	0.04	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	JG36-GS-52			0.05	0.00	0.02	0.06
Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae		0.00	0.02	0.03	0.03
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Pleomorphomonadaceae		0.00	0.00	0.02	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Holosporales	Holosporaceae	Candidatus_Paraholospira	0.00	0.02	0.02	0.00
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Methylacidiphilales	Methylacidiphilaceae		0.00	0.00	0.02	0.00

Continue...

Continued...									
Archaea	Crenarchaeota	Nitrososphaeria	Caldiarchaeales	Geothermarchaeaceae		0.00	8.83E-03	0.03	0.05
Bacteria	Chloroflexi	Dehalococcoidia	GIF9	AB-539-J10	Dsc1	0.00	0	0.02	0.00
Bacteria	Bacteroidota	Bacteroidia	Chitinophagales			0.00	0	0.00	0.10
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Qingshengfania	0.00	0	0.00	0.10
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Bosea	0.00	0.08	0.00	0.00
Bacteria	Patescibacteria	Parcubacteria	NA			0.00	0.00	0.02	0.05
Bacteria	Desulfobacterota	Desulfarculia	Desulfarculales	Desulfarculaceae	Dethiosulfatarculus	0.03	0.00	0.00	0.10
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methyloligellaceae	Rhodobium	0.00	0.03	0.02	0.00
Bacteria	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42	0.00	0.04	0.02	0.08
Bacteria	Proteobacteria	Bacteroidia	Bacteroidales	Prolixibacteraceae		0.00	0.00	0.02	0.00
Bacteria	Myxococcota	Polyangia	mle1-27			0.00	0.04	7.25E-03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiales_Incertae_Sedis	Candidatus_Branchiomonas	0.00	0.00	0.02	0.00
Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	env.OPS_17		0.02	0.00	0.03	0.03
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Neisseriaceae		0.04	0.00	0.02	0.00
Bacteria	Planctomycetota	Phycisphaerae	Tepidisphaerales	Tepidisphaeraceae		0.00	0.00	0.02	0.03
Bacteria	Aquificota	Aquificae	Aquificales	Aquificaceae	Hydrogenivirga	0.00	0.00	0.02	0.05
Bacteria	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	Pirellula	0.10	0.00	0.02	0.08
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Actinimicrobium	0.00	0.00	0.02	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Afipia	0.00	0.00	0.02	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Incertae_Sedis	Unknown_Family	Acidibacter	0.09	0.00	0.01	0.00
Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Iamiaceae	Iamia	0.00	0.06	0.00	0.04
Bacteria	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	Aggregicoccus	0.00	0.00	0.02	0.00
Bacteria	Cyanobacteria	Vampirivibrionia	Obscuribacterales	Obscuribacteraceae		0.08	0.00	7.25E-03	0.04
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Methyloterrigena	0.00	0.00	0.017	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Stappiaceae	Polymorphum	0.00	0.00	0.017	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	MN_122.2a	0.00	0.00	0.017	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	EC3			0.08	0.00	0.000	0.00
Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Nakamurellaceae	Nakamurella	0.00	0.06	0.000	0.00
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Roseimicrobium	0.00	0.00	0.016	0.00
Bacteria	Planctomycetota	Phycisphaerae	Phycisphaerales	Phycisphaeraceae		0.00	8.83E-03	0.016	0.00
Bacteria	Nitrospinota					0.00	0.00	0.016	0.00
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Chthoniobacter	0.00	0.00	0.016	0.04
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	T34		0.00	0.00	0.000	0.07
Bacteria	Cyanobacteria	Vampirivibrionia	Vampirivibrionales	Vampirivibrionaceae	Vampirivibrio	0.00	0.00	0.000	0.07
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methyloterricola	0.08	0.00	0.000	0.00
Bacteria	Chloroflexi	Anaerolineae	C10-SB1A			0.00	0.02	0.011	0.00
Bacteria	Desulfobacterota	Syntrophobacteria	Syntrophobacterales	Syntrophobacteraceae	Desulfacinum	0.00	0.00	0.014	0.07
Bacteria	Caldisericota	Caldisericia	Caldisericales	TTA-B15		0.00	0.00	0.014	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Neosaia	0.00	0.00	0.014	0.00
Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Cyclobacteriaceae	Anditalea	0.00	0.00	2.42E-03	0.07
Continue...									

Continued...

Archaea	Halobacterota	Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Methanomicrobium	0.00	0.00	0.00	0.07
Bacteria	Proteobacteria	Gammaproteobacteria	Thiomicrospirales	Thiomicrospiraceae	Hydrogenovibrio	0.07	0.00	0.00	0.00
Bacteria	Myxococcota	Polyangia	Polyangiales	Polyangiaceae	Labilithrix	0.00	0.05	0.00	0.00
Bacteria	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45		0.00	0.05	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Incertae_Sedis	Unknown_Family	Candidatus_Ovatusbacter	0.00	0.00	0.02	0.00
Bacteria	Planctomycetota	Phycisphaerae	Pla1_lineage			0.06	0.00	0.01	0.00
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraeae	Pedosphaera	0.01	0.00	0.01	0.00
Bacteria	Firmicutes	Bacilli	Acholeplasmatales	Acholeplasmataceae	DMI	0.00	0.00	0.00	0.06
Bacteria	Verrucomicrobiota	Kiritimatiellae	Kiritimatiellales	Kiritimatiellaceae		0.00	0.04	0.00	0.00
Bacteria	Patescibacteria	Microgenomatia	Candidatus_Gottesmanbacteria			0.00	0.04	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Tahibacter	0.00	0.00	0.01	0.00
Bacteria	Chloroflexi	Ktedonobacteria	C0119			0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Labraceae	Labrys	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	sediment-surface35			0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	SM2D12		0.00	0.00	0.00	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	Candidatus_Arcanobacter	0.00	0.00	0.00	0.05
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	Candidatus_Megaira	0.00	0.05	0.00	0.00
Bacteria	Actinobacteriota	Thermolephilia	Solirubrobacterales	Solirubrobacteraceae	Conexibacter	0.00	0.04	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	SM1B06		0.00	0.00	0.01	0.00
Bacteria	Firmicutes	Desulfotomaculia	Carboxydotherrmales	Carboxydotherrmaceae	Carboxydotherrmus	0.00	0.00	0.01	0.00
Bacteria	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae		0.00	0.00	0.01	0.02
Bacteria	Chloroflexi	OLB14				0.00	0.00	0.00	0.05
Bacteria	Planctomycetota	Planctomycetes	Planctomycetales	Schlesneriaceae	Schlesneria	0.05	0.00	7.25E-03	0.00
Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Ilumatobacteraceae		0.05	0.00	0.00	0.00
Bacteria	Actinobacteriota	Actinobacteria	Frankiales	Sporichthyaceae	Longivirga	0.00	0.04	0.00	0.00
Bacteria	Firmicutes	Bacilli	Erysipelotrichales	Erysipelotrichaceae	Bulleidia	0.00	0.00	9.66E-03	0.00
Bacteria	Bdellovibrionota	Oligoflexia	Silvanigrellales	Silvanigrellaceae		0.00	0.00	9.66E-03	0.00
Bacteria	Planctomycetota	Planctomycetes	Planctomycetales			0.01	8.83E-03	0.014491528	0.00
Bacteria	Planctomycetota	Phycisphaerae	Phycisphaerales	Phycisphaeraeae	CL500-3	0.00	0.00	9.66E-03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Thiomicrospirales	Thioglobaceae	Candidatus_Vesicomysocius	0.00	0.00	9.66E-03	0.00
Bacteria	Chloroflexi	Anaerolineae	KZNMV-5-B42			0.00	0.03	7.25E-03	0.00
Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Microtrichaceae		0.00	0.03	0.00	0.00
Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	Mangrovibacterium	0.00	0.00	8.45E-03	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Elsterales	Elsteraceae	Aliidongia	0.00	0.00	8.45E-03	0.00
Bacteria	Cyanobacteria	Cyanobacteriia	Phormidesmiales	Phormidesmiaceae	Phormidium_MBIC10002	0.00	0.00	8.45E-03	0.00
Bacteria	Chloroflexi	JG30-KF-CM66				0.00	0.00	0.011	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales_Incertae_Sedis	Phreatobacter	0.00	0.03	0.000	0.00
Bacteria	Planctomycetota	Planctomycetes	Planctomycetales	Rubinisphaeraeae	SH-PL14	0.00	0.03	8.45E-03	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	Rickettsia	0.00	0.03	0.00	0.00
Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales	Microtrichaceae	IMCC26207	0.00	0.03	0.00	0.00
Archaea	Halobacterota	Halobacteria	Halobacterales	Halobacteriaceae	Halocalculus	0.00	0.03	0.00	0.00

Continue...

Continued...									
Bacteria	Planctomycetota	Planctomycetes	Gemmatales	Gemmataceae	Gemmata	0.00	0.00	0.01	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Nereida	0.00	8.83E-03	0.00	0.03
Bacteria	Planctomycetota	Phycisphaerae	MSBL9			0.06	0.00	0.00	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	AB1		0.00	0.00	6.04E-03	0.00
Bacteria	Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	NK4A214_group	0.00	0.00	6.04E-03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Alcaligenaceae	Ampullimonas	0.00	0.00	6.04E-03	0.00
Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	FFCH9454		0.03	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Nitrocoales	Nitrococcaceae	Arhodomonas	0.03	0.00	0.00	0.00
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	SH3-11	0.00	0.018	0.00	0.02
Bacteria	Proteobacteria	Alphaproteobacteria	Holosporales	Holosporaceae	Candidatus_Bealeia	0.00	0.018	0.00	0.00
Bacteria	Patescibacteria	Microgenomatia	Candidatus_Pacebacteria			0.00	0.00	4.83E-03	0.00
Bacteria	Patescibacteria	MD2896-B216				0.00	0.00	4.83E-03	0.00
Bacteria	Planctomycetota	Planctomycetes	Isosphaerales	Isosphaeraceae		0.00	0.00	4.83E-03	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Anaplasmataceae	Candidatus_Xenolissoclinum	0.00	0.00	4.83E-03	0.00
Bacteria	Firmicutes	Clostridia	Eubacteriales	Eubacteriaceae		0.00	0.00	4.83E-03	0.00
Bacteria	Sva0485					0.00	0.00	4.83E-03	0.00
Bacteria	Myxococcota	Polyangia	Polyangiales	Amb-16S-1034		0.00	8.83E-03	0.00	0.02
Bacteria	Verrucomicrobiota	Chlamydiae	Chlamydiales	Simkaniaceae		0.00	0.00	0.00	0.02
Bacteria	Acidobacteriota	Acidobacteriae	Acidobacteriae_or	Acidobacteriae_fa	Paludibaculum	0.00	0.00	0.00	0.02
Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	Anaerolinea	0.02	0.00	2.42E-03	0.00
Bacteria	Actinobacteriota	Actinobacteria				0.02	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Ectothiorhodospirales	Ectothiorhodospiraceae	Thiohalospira	0.00	0.01	0.00	0.00
Bacteria	Firmicutes	Bacilli	Thermoactinomycetales	Thermoactinomycetaceae	Risungbinella	0.00	0.01	0.00	0.00
Bacteria	Firmicutes	Bacilli	Paenibacillales	Paenibacillaceae	Oxalophagus	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Niveibacterium	0.00	0.01	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae		0.00	0.01	0.00	0.00
Archaea	Crenarchaeota	Thermoprotei	Desulfurococcales	Desulfurococcaceae	Thermosphaera	0.00	0.00	3.62E-03	0.00
Bacteria	Planctomycetota	BD7-11				0.00	0.00	3.62E-03	0.00
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Opitutaceae	Ereboglobus	0.00	0.00	3.62E-03	0.00
Bacteria	Armatimonadota					0.00	0.00	3.62E-03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	HdN1	0.00	0.00	3.62E-03	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae		0.00	0.00	3.62E-03	0.00
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Variibacter	0.00	0.00	3.62E-03	0.00
Archaea	Crenarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Candidatus_Nitrocosmicus	0.00	0.00	0.00	0.02
Bacteria	Actinobacteriota	Acidimicrobiia	Acidimicrobiales	Acidimicrobiaceae	Ferrimicrobium	0.00	0.00	0.00	0.02
Bacteria	Firmicutes	Thermovenabuliales	Thermovenabulales	Thermovenabulales_fa	Fervidicola	0.00	0.00	0.00	0.02
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia/Shigella	0.01	0.00	0.00	0.00
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	Pseudofulvimonas	0.00	8.83E-03	0.00	0.00
Bacteria	Firmicutes	Clostridia	Clostridia_or	Hungateiclostridiaceae	Ruminiclostridium	0.00	8.83E-03	0.00	0.00

Continue...

Continued...

Bacteria	Proteobacteria	Alphaproteobacteria	Elsterales			0.00	0.00	2.42E-03	0.00
Bacteria	Actinobacteriota	Acidimicrobiia	Acidimicrobiales	Acidimicrobiaceae		0.00	0.00	2.42E-03	0.00
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Opitutaceae	Lacunisphaera	0.00	0.00	0.00	0.01
Bacteria	Acidobacteriota	Subgroup_11				0.00	0.00	0.00	0.01
Bacteria	Planctomycetota	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	I-8	0.00	0.00	0.00	0.01
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	Ellin517	0.00	0.00	0.00	0.01
Bacteria	Myxococcota	Polyangia	UASB-TL25			0.00	0.00	0.00	0.01
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	cr616	0.00	0.00	0.00	0.01
Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Croceibacter	0.00	0.00	0.00	0.01