

THESIS

PROCESSES GOVERNING THE PERFORMANCE OF OLEOPHILIC BIO-BARRIERS
(OBBS) – LABORATORY AND FIELD STUDIES

Submitted by

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ABSTRACT

PROCESSES GOVERNING THE PERFORMANCE OF OLEOPHILIC BIO-BARRIERS (OBBS) – LABORATORY AND FIELD STUDIES

Petroleum sheens, a potential Clean Water Act violation, can occur at petroleum refining, distribution, and storage facilities located near surface water. In general, sheen remedies can be prone to failure due to the complex processes controlling the flow of light non-aqueous phase liquid (LNAPL) at groundwater/surface water interfaces (GSIs). Even a small gap in a barrier designed to resist the movement of LNAPL can result in a sheen of large areal extent. The cost of sheen remedies, exacerbated by failure, has led to research into processes governing sheens and development of the oleophilic bio-barrier (OBB). OBBs involve 1) an oleophilic (oil-loving) plastic geocomposite which intercepts and retains LNAPL and 2) cyclic delivery of oxygen and nutrients via tidally driven water level fluctuations. The OBB retains LNAPL that escapes the natural attenuation system through oleophilic retention and enhances the natural biodegradation capacity such that LNAPL is retained or degraded instead of discharging to form a sheen.

Sand tank experiments were conducted to visualize the movement of LNAPL as a wetting and non-wetting fluid in a water-saturated tank. The goal was to demonstrate 1) the flow of LNAPL as a non-wetting fluid in sand, 2) the imbibition of LNAPL as a wetting fluid on the geocomposite, and 3) the breakthrough of LNAPL after saturating the geocomposite to the point of failure (sheens in the surface water). Dyed diesel was pumped through a tank with sand and geocomposite and photographed to document movement. Diesel was the non-wetting fluid in the sand and moved in

a dendritic pattern. Diesel was the wetting fluid on the geocomposite and uniformly imbibed horizontally across the geocomposite before breakthrough to the overlying sand layer.

A second set of laboratory experiments was designed to estimate the aerobic and anaerobic OBB degradation rates of LNAPL in field-inoculated sediment. Unfortunately, due to a flaw in the experimental design, the mass balance could not be completed, and degradation rates were not calculated. The setup was designed to emulate field conditions as best practically possible and to observe the effects of water table fluctuations, different loading rates, and iron. The effluent pumping system designed to remove water in the water fluctuation columns also inadvertently removed LNAPL, creating a mass balance discrepancy for the aerobic columns. Though degradation rates could not be calculated from this experiment, the experiment did visually document the changing redox conditions in the columns, such as formation of a black precipitant (likely iron sulfides) around LNAPL. Ideally, the limitations of this experimental design can be addressed for future research to eventually resolve degradation rates for OBBs.

The success of a 3.8 m by 9.3 m demonstration OBB at a field site on a tidal freshwater river resulted in replacing the demonstration OBB with a 3.8 m by 58 m full-scale OBB. The construction event provided a unique opportunity to sample the demonstration OBB after a four-year deployment. The sampling results advanced the mechanistic understanding of how OBBs work to reduce LNAPL releases at GSIs. Sampling revealed the material was suitable for field LNAPL loading rates and was not compromised by field conditions such as ice scour or sediment intrusion. LNAPL analysis showed no LNAPL on the geocomposite or in the underlying upper sediment (0-10 cm). Diesel range organic (DRO) concentrations in the low 1,000s of mg/kg were observed in the sediment 10-20 cm below the geocomposite. LNAPL composition analysis

suggests that the majority of the compounds are polar in the lower sediments (10-20 cm), providing a line of evidence that petroleum liquids have been oxygenated. Microbial data show the average number of bacterial 16s transcripts in the geocomposite is larger than in the sediment layers, confirming that the geocomposite is suitable substrate for microbe growth. The observation of ferric iron suggests that ferric/ferrous iron cycling may play a role in degradation processes, where the ferric iron acts as a “bank” of solid-phase electron acceptors. This sampling event suggests that LNAPL biodegradation rates in and below the OBB are comparable to the LNAPL loading rates.

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1. INTRODUCTION

Petroleum refining, distribution, and storage facilities are commonly located near surface water bodies. Due to historical releases of petroleum liquids, impacted subsurface media and groundwater extending to the surface water is a common condition. Spilled petroleum liquids, herein referred to as light non-aqueous phase liquids (LNAPLs), are a regulatory concern when there is a visible sheen on the surface water or adjoining shoreline (40 CFR §110, 2014). Sheens are thin films that spread out along the air-water interface and are commonly identified by an iridescent color as seen in Figure 1 (Sale et al., 2018; Chalfant, 2015). Historically, burning rivers caused by flammable LNAPL on surface water incited public support for the 1972 Clean Water Act (Sale et al., 2018). Today, sheens are still a driver for remedies at groundwater/surface water interfaces (GSIs). For example, the Gowanus Canal Superfund Site in Brooklyn, NY, will cost an estimated \$500 million to remediate a 2.9-km canal (US Environmental Protection Agency [EPA], 2013).



Figure 1. A photo of a hydrocarbon sheen (Chalfant, 2015)

Following Sale and Lyverse (2014), sheens form both periodically and sporadically at GSIs due to seeps, ebullition, and erosion. Because a small volume of LNAPL can produce a sheen of large areal extent, most sheen remediation technologies fail when any volume of LNAPL bypasses or overloads the absorptive barrier (Sale and Lyverse, 2014; Hawkins, 2013). Chevron has funded multiple students (Hawkins, 2013; Chalfant, 2015; Campbell, 2017) at Colorado State University (CSU) to study processes creating sheens and alternative sheen remedies that address the limitations and costs of current technologies. This thesis presents the results of laboratory and field studies conducted from 2016 to 2018, focusing on the processes governing oleophilic bio-barrier (OBB) performance.

The OBB technology was jointly developed by CSU, Chevron, and Arcadis. A patent for the OBB was issued by the US Patent Office in 2018 (Zimbron et al., 2018). The OBB uses an oleophilic (oil-loving) plastic geocomposite (geotextile and geonet) placed at a GSI where LNAPL is discharging to surface water. Geocomposites are a widely available, low-cost material commonly used in landfills. The nonwoven, felt-like geotextile has a high specific surface area that retains LNAPL. The open-latticed, rigid structure of the geonet provides a highly transmissive zone which floods and drains through natural water level fluctuations (e.g., tides). The water table fluctuations deliver oxygen via atmospheric air and/or oxygenated surface water to promote LNAPL degradation prior to discharge to surface water. The active removal of LNAPL via degradation can address problems associated with a finite retention capacity of a physical barrier and/or absorptive media remedy.

Additional OBB layers include clean sand fill, geotextile, and structural cover. The sand fill acts as a capillary barrier to preclude LNAPL movement upward out of the geocomposite as well as

acts as a filter pack to limit sediment intrusion into the geonet. The second geotextile layer protects the sand layer from the structural cover. The structural cover anchors the OBB in place and provides protection against bank erosion, wave action, and ice scour. Overall, the OBB is a promising sheen remedy that offers a simple installation, low capital and operation and maintenance (O&M) costs, and promising long-term performance.

1.1. Objectives

The theme of this thesis is to resolve processes governing the performance of OBBs in support of advancing OBBs as a sheen remedy. Laboratory and field studies investigated wetting and non-wetting fluid movement in the subsurface and LNAPL OBB degradation rates. Given resolution of critical processes, the OBB design can be improved with respect to cost and performance.

1.2. Organization

Chapter 2 is a review of work by others that is foundational to this thesis. Chapter 3 discusses the laboratory sand tank experiments which were designed to document the flow of LNAPL as the non-wetting fluid in sand and as the wetting fluid on a geocomposite. Objectives, methods, and results are presented. The second laboratory experiment was designed to estimate aerobic and anaerobic OBB degradation rates with sediment collected from a field site. Objectives, methods, and results including lessons learned are discussed in Chapter 4. Chapter 5 presents the results of destructive sampling of a field OBB and an updated OBB site conceptual model (SCM) in the format of a journal article. Last, Chapter 6 summarizes key results presented in this thesis and advances suggestions for future work.

2. PROBLEM STATEMENT

This chapter introduces critical knowledge needed to understand sheens and advance governing principles for OBBs. First, multiphase flow principles are addressed. LNAPL can occur as a wetting, intermediate wetting, and non-wetting phase. The occurrence of each of these phase behaviors is dependent on temporally varying water levels. Second, conditions at LNAPL-impacted tidal GSIs are advanced. Understanding the nutrient and electron-acceptor availability, especially oxygen, at GSIs creates novel opportunities to enhance the biologically-mediated degradation of LNAPLs. Next, current sheen remedy limitations are discussed. The limitations of current sheen remedies were the primary motivation for developing the OBB technology. Last, the governing principles for OBBs, as seen at the onset of this research effort, are presented.

2.1. Multiphase Flow and Wettability

This section discusses multiphase flow and wettability in the context of LNAPL at GSIs. At GSIs, LNAPLs can be the wetting, intermediate wetting, and non-wetting phase. The position of the LNAPL affects the distribution and movement of LNAPL in the subsurface and surface water. LNAPL typically infiltrates down through the unsaturated zone as an intermediate wetting phase between water, the wetting fluid on the soil, and non-wetting soil gasses. At the top of the water table, LNAPL spreads out laterally above the water table. Above the capillary fringe, LNAPL is present as an intermediate wetting fluid and spreads out along the air/water interface to form a sheen, even in the subsurface media. Below the capillary fringe, LNAPL can occur as either an intermediate wetting phase where gases are present or as a non-wetting phase. Though this thesis is focused on LNAPLs, many of the key principals also apply to NAPLs regardless of density.

In systems with two or more immiscible fluids, one fluid has a greater affinity for the porous media than the other(s). This concept is known as wettability. The wetting fluid is the fluid in direct contact with the solids and can spontaneously imbibe or enter pore throats, for example, a dry sponge wicking up water. This interaction generally leads to a more even or homogeneous distribution of the wetting fluid in the media. Imbibition is a function of specific surface area; therefore, material with a high specific surface acts as a sink for the wetting fluid (Figure 2a) (Pankow and Cherry, 1996). In contrast, movement of the non-wetting fluid is constrained by capillary pressure. Capillary pressure is a balancing force equal to the difference in interfacial tension between two immiscible fluids (Corey, 1994). A non-wetting fluid can only enter a pore throat when the capillary pressure is greater than the displacement pressure (Corey, 1994). Displacement pressure is inversely proportional to pore size; therefore, the non-wetting fluid preferentially flows into the larger pore throats in the system (Pankow and Cherry, 1996).

Capillary barriers utilize the principal of displacement pressure to impede the flow of a non-wetting fluid. As seen in Figure 2b, a wall of fine-grain material, with small pore sizes and therefore a higher displacement pressure, can limit the flow of non-wetting fluids so long as the capillary pressure is less than the displacement pressure (Pankow and Cherry, 1996). Non-wetting fluid flow tends to have a sparse, dendritic morphology. In contrast, wetting phases tend to form far more uniform NAPL distributions. The sand tank experiment in Chapter 3 demonstrates both the dendritic distribution of non-wetting phases and the more uniform distribution of wetting phases.

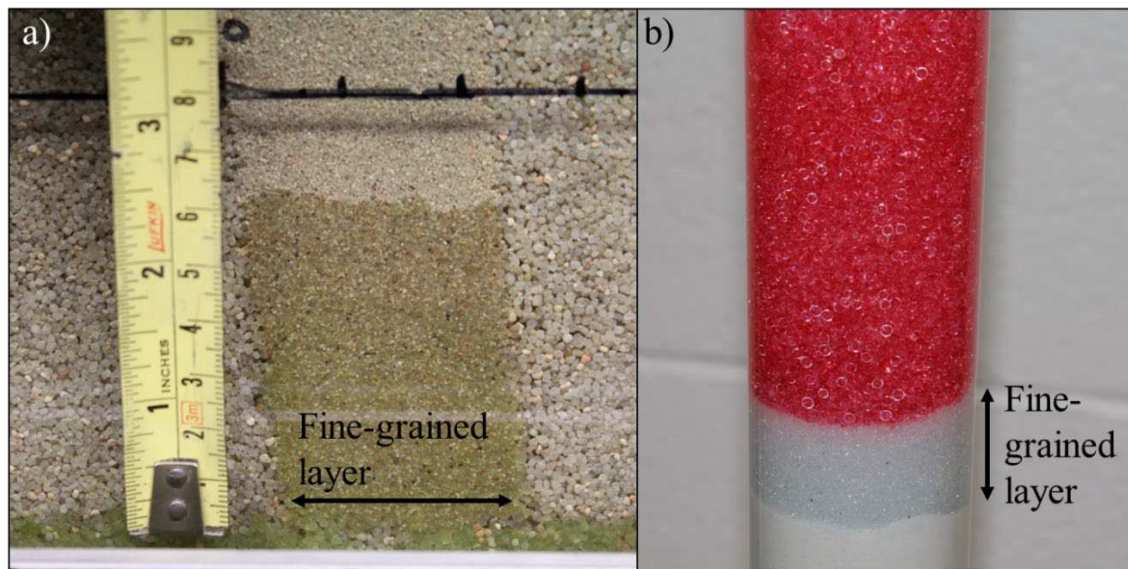


Figure 2. Examples of the different behavior between wetting and non-wetting fluids a) Water (light green) the wetting fluid imbibes into the fine-grained sand layer (Hawkins, 2013) b) TCE (red) the non-wetting fluid is precluded by the fine-grained glass beads in the water-wet system (Saller, 2014)

Generally, water is the wetting fluid in a NAPL/water system in porous media, though there are systems such as limestone where NAPL can be the preferential wetting fluid (Corey, 1994; Dwarakanath et al., 2002; Mercer and Cohen, 1990). In a typical three-phase system of NAPL/water/air, NAPL is the intermediate wetting fluid which follows wetting fluid behavior. An example of this system is shown in Figure 3 where LNAPL (diesel, dyed yellow) spreads out between the air/water interface.

Wettability is a function of surface chemistry and fluid composition and is not always easily predicted. The wetting fluid generally correlates to polarity, as the most polar fluid will wet polar soil particles (“like likes like”). However, Drake et al. (2013) and Dwarakanath et al. (2002) reported differences in the wetting properties of weathered field NAPLs compared to fresh NAPLs. Wettability can also be altered by the addition of surfactants and other chemicals that reduce the interfacial tension between fluids (Mercer and Cohen, 1990).

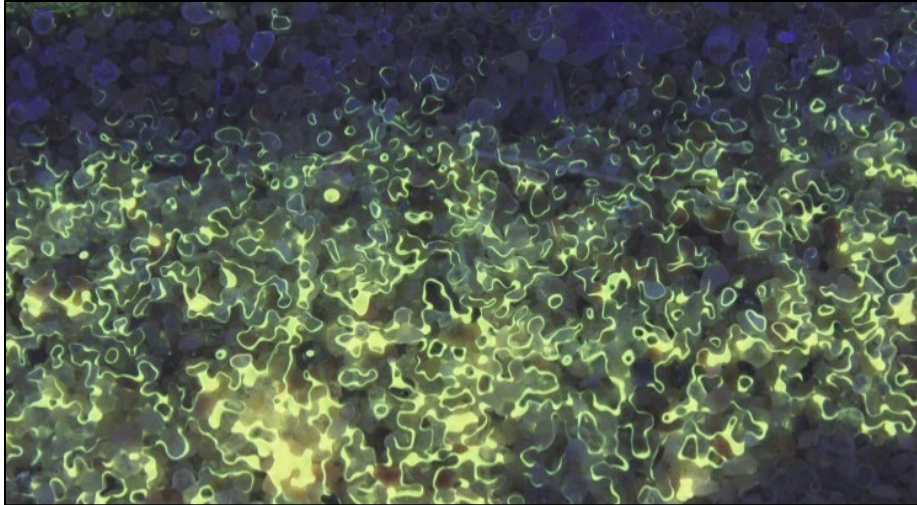


Figure 3. Dyed diesel (yellow) under ultraviolet light as the intermediate wetting fluid in air/water/NAPL system in sand forms sheens around pockets of air in the system

The difference in interfacial tensions in a three-phase system can result in the spreading of NAPL, as seen in Figure 3, or the formation of droplets and blobs in the pore space (Keller et al., 1997). NAPL will spread along the air/water interface as a sheen until the interfacial tensions between the three fluids are balanced. The spreading coefficient is defined as the interfacial tension of the air/water interface minus the interfacial tensions of the air/NAPL and NAPL/water interfaces (Blunt et al., 1995). If the spreading coefficient is positive, NAPL will spontaneously spread as a thin, molecular film (i.e., sheen) between the air and water (Blunt et al., 1995). The NAPL does not spread if the spreading coefficient is negative (Blunt et al., 1995). While sheens are typically associated with surface water (e.g., rivers, lakes, puddles in parking lots), sheens do form in porous media as the intermediate wetting fluid (Figure 3). At high water levels, such as during high tide, NAPL in the non-wetting phase can be trapped in porous media by capillary forces (Wilson et al., 1990). Effectively these “blobs” or “ganglia” of NAPL are immobile unless a high hydraulic gradient induces movement (Pankow and Cherry, 1996).

2.2. LNAPL at Groundwater/Surface Water Interfaces

Following Sale et al. (2018), LNAPL releases at GSIs can form sheens on surface water through three primary mechanisms: seeps, ebullition, and erosion. A seep is the discharge of NAPL from the groundwater to surface water, typically during low stage, particularly through a preferential flow path created by bioturbation or roots that expedite LNAPL movement through the sediment. Ebullition is described by Amos and Mayer (2006) as “the vertical transport of gas bubbles driven by buoyancy forces.” Natural processes generate gas, such as methane or CO₂, by degrading organic material and/or contamination. Once a sufficient volume of gas byproduct is generated, the gas bubble can carry NAPL (even DNAPL) as an intermediate wetting phase in a gas bubble through the overlying sediment and water column to the water surface where the NAPL spreads out and forms a sheen (McLinn and Stolzenburg, 2009). The final sheen forming process is erosion. Natural processes such as ice scour, wave action, and floods erode the sediment and can expose NAPL directly to the surface water. Overall, sheens can form at sites due to a combination of these mechanisms, and remediation strategies need to address all relevant sheen forming mechanisms.

The primary application of OBBs to date has been at tidal GSIs with twice daily fluctuations between a high and low stage. Limited literature is available that addresses the tidal influences on LNAPL movement at GSIs (Davit et al., 2012). The tidal effects on the groundwater are largely a function of the magnitude of the tidal fluctuations and the permeability of the aquifer (American Petroleum Institute [API], 2006). API (2006) suggests that frequent water cycling can create a large smear zone that traps LNAPL in immobile droplets and limits oil migration. However, LNAPL mobility governing equations are generally predicated on two-phase flow and do not incorporate transient three-phase flow and the occurrence of LNAPL as a wetting phase. Chronic

rising and falling water stages cycle LNAPL between occurrences as wetting and non-wetting phases. During the low stage, LNAPL is the wetting or intermediate wetting fluid and spreads along the air/water interfaces. The balance of buoyancy forces and gravity result in LNAPL “falling” with the water table to the low tide level. During the incoming tide, the LNAPL either rises with the air/water interface or is trapped as the less-mobile non-wetting phase depending on pore geometry supporting a hypothesis that LNAPL at GSIs tend to form homogeneous bodies due to LNAPL spreading as an intermediate wetting phase above the capillary fringe (as supported by field data shown in Chapter 5).

Chalfant (2015) introduces a conceptual mass balance model for LNAPL at GSIs that illustrates how sheens form based on the flux of LNAPL to a GSI and rates of degradation at a GSI. For a representative element of volume of porous media at a GSI, the LNAPL mass balance is between LNAPL entering the system from an upland LNAPL source and LNAPL lost through natural processes, primarily biodegradation. When the LNAPL retention/degradation rate is greater than the loading rate, there is no release of LNAPL to the surface water. However, when the LNAPL loading rate exceeds the retention/degradation rate, LNAPL discharges to the surface water (LNAPL seep).

Unfortunately, there is little data available about LNAPL fluxes or degradation rates at GSIs. To date, no practical method for resolving LNAPL loading or degradation rates at GSIs has been documented. The laboratory experiment in Chapter 4, designed to resolve natural degradation rates at GSIs, was largely unsuccessful. To provide an estimate of LNAPL loading and degradation rates, LNAPL fluxes documented by Mahler et al. (2012) were used to approximate LNAPL loading at GSIs. Mahler et al. (2012) measured LNAPL fluxes through 50 distal wells in LNAPL

bodies using single well tracer dilution techniques. These LNAPL fluxes can be applied to GSIs by imagining a GSI truncating the LNAPL body at the locations of the monitoring wells described by Mahler et al. (2012). This LNAPL flux represents a volume per unit area per time. Multiplying the LNAPL flux by the unit area and then dividing by a unit width and well convergence factor results in a volumetric discharge per unit width of shoreline. Assigning Q_{LNAPL} as the LNAPL loading rate per unit width of shoreline ($L^3/L/T$), then

$$Q_{LNAPL} = \frac{q_{LNAPL} b_{LNAPL} 2r}{2r\alpha} = \frac{q_{LNAPL} b_{LNAPL}}{\alpha} \quad (1)$$

where q_{LNAPL} is the LNAPL flux through a well (L/T), b_{LNAPL} is the LNAPL thickness in the well (L), r is the radius of the well (L), and α is the well convergence factor (unitless, assumed to be 1.5 for these calculations). Mahler et al. (2012) reported a mean q_{LNAPL} of 0.064 m/yr and 50% median range (25th and 75th quartile values) of 0.027 to 0.13 m/yr. Using Equation 1, this results in a median Q_{LNAPL} of 15 L/m/yr, with a 50% median range from 5.2 to 33 L/m/yr. Using a maximum sheen thickness of 5 μm (National Oceanic and Atmospheric Administration [NOAA], 2016) and an assumed shoreline length of 10 m, a discharge rate of 15 L/m/yr would create a sheen 8 m² every day. However, sheens of that size do not form on a daily basis, therefore the natural system assimilation rate is of comparable magnitude to these loading rates. There are no known published sheen flux rates in the literature. Estimated sheen fluxes range from 0.04 to 0.4 L/yr. This is equivalent to a sheen 0.1 to 1 m² area, 1 μm thick, along a 10 m shoreline forming every day. Assuming the largest loading rates correspond to the largest sheen rates, then the GSI assimilation rate is 5.2 to 33 L/yr/m. As seen in Figure 4, the apparent assimilation rate is 2 to 3 orders of magnitude greater than the typical sheen flux range. See Appendix A for supporting calculations. Equation 1 likely overestimates Q_{LNAPL} considering LNAPL thickness in the well does not

conveniently correlate to LNAPL thickness in the formation (Farr et al., 1990; Lenhard and Parker, 1990). However, these estimates suggest natural processes degrade the majority of the LNAPL arriving at GSIs. Seeps, ebullition, and erosion are local anomalies that allow LNAPL to episodically pass through the natural attenuation zones at GSIs.

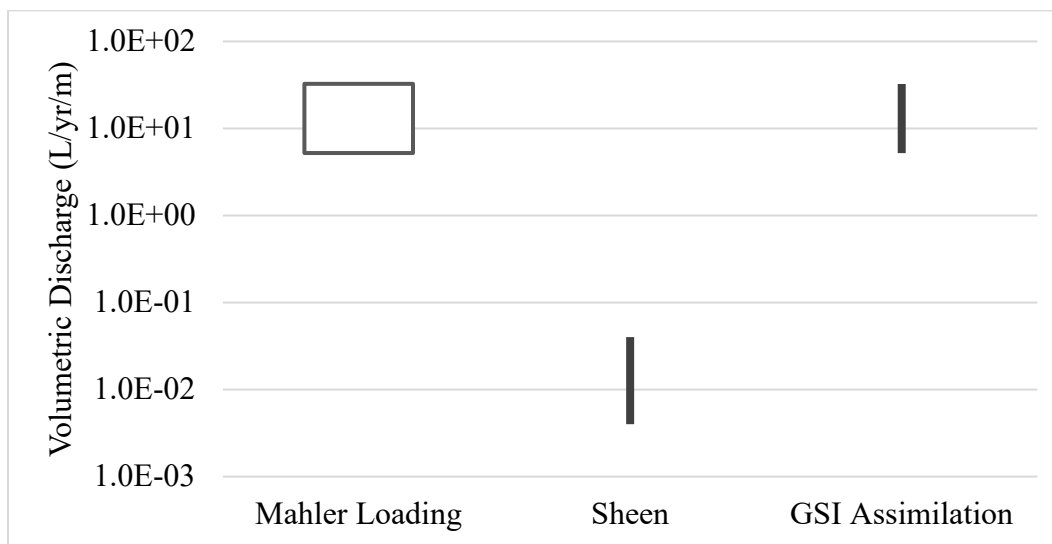


Figure 4. Comparison of the Mahler et al. (2012) LNAPL loading, sheen, and GSI assimilation volumetric discharge rates in L/yr/m. The Mahler loading represents the 50% median range.

A primary value of these estimated loading rates is a sense of scale of the natural system's degradation capacity. The bottom line is that the sediments at LNAPL-contaminated GSIs are powerful bioreactors that are capable of degrading the majority of LNAPL mass loading at GSIs. Field observations suggest that sheens form when local anomalies allow for LNAPL to bypass the bioreactor sediments. As previously discussed, this formation could be via bioturbation or other preferential flow paths carrying LNAPL to the surface water during low water stage (seeps), ebullition, or erosion physically removing the sediment to expose LNAPL to surface water. Careful consideration should be given before removing LNAPL-impacted sediments that can be actively depleting LNAPL at GSIs. Excavation could disrupt the microbial community which might lead

to increased loading to surface water. Excavation can also create a sheen similar to a sheen cause by erosion, as the excavation can expose LNAPL directly to surface water.

2.3. Limitations of Current Remedies

Current sheen remedies can be grouped into hydraulic controls, source removal, physical barriers, and absorptive barriers. Though remedies can be successful in preventing the formation of sheens, inappropriate applications and poor designs have resulted in numerous remedies falling short of performance expectations. This section highlights the limitations of current sheen remedies. Chalfant (2015) discusses the pros and cons of existing sheen management options in further detail.

In general, sheen remedies can be prone to failure due to the complicated, heterogeneous flow of NAPL which can bypass barriers or overload small areas of absorptive material. Hydraulic controls such as line drains can manipulate the flow of NAPL by altering the hydraulic gradient of the site. While systems have been successfully installed at sites, such as the Laramie Tie Plant to contain creosote (EPA, 1997), hydraulic controls could be difficult to implement at a tidal site with daily hydraulic fluctuations. Source removal such as NAPL recovery wells or in-situ remediation like soil vapor extraction can also be difficult to implement and costly to operate. Comprehensive site characterization is necessary to ensure the sufficient removal of the source NAPL. Physical barriers such as sheet pile walls and grout curtains are susceptible to failure when there are flaws in the integrity of the barrier. For example, corrosion in the sheet pile wall can provide an opening for NAPL to flow through. Furthermore, a physical barrier can preclude the flow of oxygen and nutrients to the system, reducing the system's degradation capacity. Organoclay, activated carbon, and other absorptive materials are limited by a finite sorption capacity and can be overloaded by

LNAPL preferentially flowing to a localized part of the barrier (Hawkins, 2013; Campbell, 2015). The limitations of current sheen remedies motivated CSU and Chevron to develop the OBB technology.

2.4. Initial Oleophilic Bio-Barrier Site Conceptual Model

The OBB was designed to mitigate the formation of sheens via seeps, ebullition, and erosion as well as overcome other remedy limitations such as a finite sorption capacity and high O&M costs. This section describes the design concepts for the OBB and the SCM prior to the work in Chapter 5, which elucidated how an acclimated OBB mitigates LNAPL. Details describing OBB proof-of-concept experiments can be found in Chalfant (2015).

To address the sheen processes of seeps and ebullition, an oleophilic (oil-loving) geocomposite was chosen to retain LNAPL. Material that did not irreversibly sorb LNAPL was selected so that LNAPL was bioavailable for microbial degradation. The OBB's treatment capacity is increased due to degradation losses as compared to the finite capacity of other absorptive caps. The geocomposite is comprised of a rigid high-density polyethylene (HDPE) geonet core (Figure 5a) thermally fused to a polypropylene (PP) nonwoven geotextile on both sides of the geonet core. The geonet has an open latticed structure that is hydraulically transmissive. Tidal pumping delivers oxygenated water and air through this highly transmissive layer and vertically through the different layers. As a carbon-based product, hydrocarbons preferentially wet onto the geotextile and geonet. The geotextile provides a high specific surface area sink for LNAPL to imbibe onto (Figure 5b). Therefore, as LNAPL moves with the groundwater towards surface water, the geocomposite can intercept and retain LNAPL to avoid sheens due to seeps. Likewise, the geocomposite can strip

LNAPL from ebullition gas bubbles, such that the gas either continues through to the surface or moves through the geonet and the LNAPL remains in the geocomposite, preventing sheens through ebullition. Geocomposites are widely used in landfill and other geotechnical applications. Therefore, commercially available configurations have been used for the OBB applications thus far. Customized geocomposites could also be used to best address specific site conditions. For example, a geocomposite with a thicker geotextile could be used to increase the LNAPL retention capacity of the geocomposite.

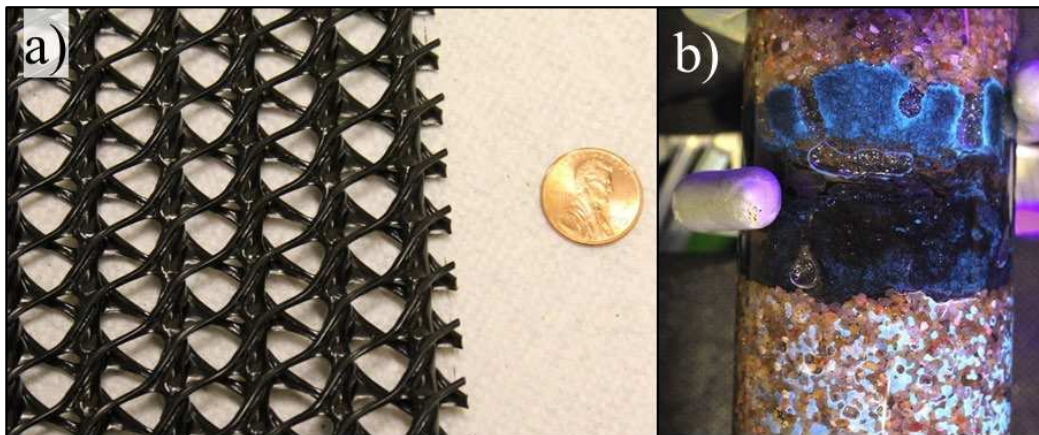


Figure 5. a) Sample of the geonet used, penny for scale; b) NAPL (blue) as the wetting fluid on the geocomposite and a non-wetting fluid in the sand

Sheen formation due to erosion can be mitigated by the OBB by installing an appropriate armoring layer. For sites with a high likelihood of erosion or ice scour, armoring such as Reno mattresses or marine mattresses can be installed to reinforce and stabilize the shoreline, thus reducing sheens releases associated with erosion. At sites where erosion is not a problem, a less robust anchoring system can be used to secure the OBB.

The “standard” OBB design is shown in Figure 6. The OBB is installed over LNAPL-impacted sediments. First, native sediments are leveled by spreading a thin layer of clean sand fill above the GSI. Next, a geocomposite is unrolled over the sand. Another layer of clean sand fill is placed above the geocomposite. A layer of geotextile covers this second sand layer. Finally, a structural cover is placed on top to anchor the entire OBB. Figure 7 shows an exploded view of the OBB layers with an explanation of each layer’s function.

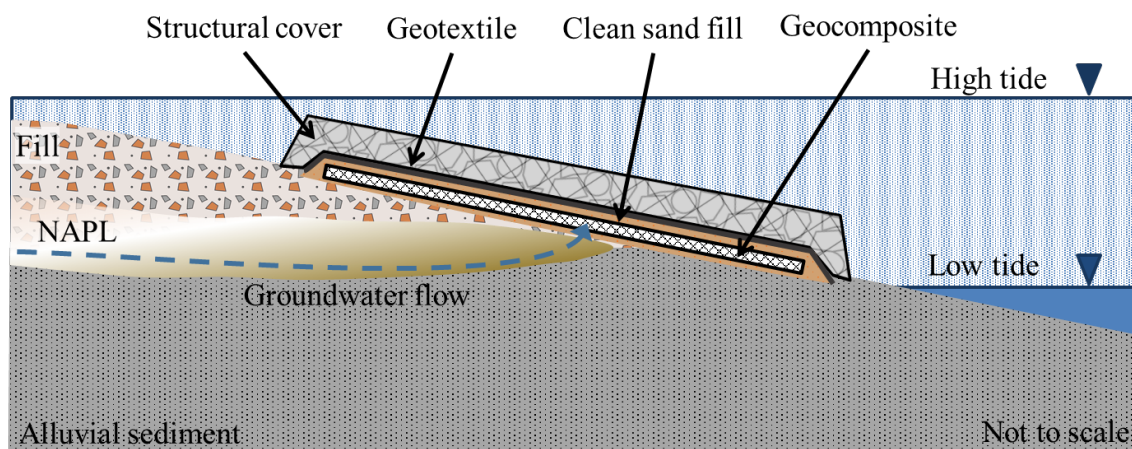


Figure 6. Typical construction of an OBB at a GSI

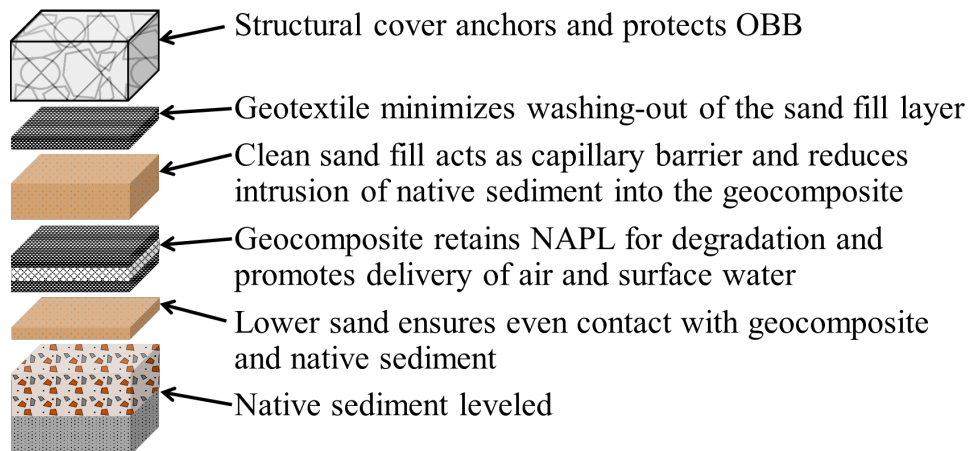


Figure 7. Schematic of the standard OBB layers, not to scale

LNAPL as the wetting fluid on the geocomposite is advantageous because spontaneous imbibition increases retention and surface area for microbial degradation. The bioavailability of NAPL, as discussed in Wilson et al. (1990), suggests that the size and shape distribution of trapped NAPL can increase the space in which reactions are occurring and overall LNAPL depletion rates. For example, if the entirety of a pore space is filled with NAPL save the thin water film around the media, then the microbes may not have adequate access to nutrients because flow is limited by diffusion through the water film. However, in pores occupied by flowing water, advection delivers nutrients to microbes. Therefore, the spreading of the NAPL on the geocomposite as the wetting fluid is beneficial for microbial accessibility, as the transmissive layer can deliver nutrients and oxygen to the microbes faster via advection rather than diffusion. This increased delivery of oxygen to the system is favorable because aerobic hydrocarbon degradation pathways are faster than anaerobic pathways (Lovley et al., 1994). The advantages of the geocomposite for LNAPL degradation are similar to the use of synthetic media for wastewater trickling filter plants. Trickling filters use rocks or other media as a substrate for microbial growth to biologically treat wastewater. The use of synthetic media such as corrugated plastic sheets has become popular because these media can provide larger surface area per volume for microbial growth and greater void ratios for increased air flow (Davis and Cornwell, 2013).

3. VISUALIZATION OF MULTIPHASE FLOW WITH AN OBB IN A SAND TANK

This chapter describes laboratory experiments designed to advance the understanding of OBB processes via a sand tank visualization study. First, the experimental objectives are introduced. Next, methods are presented. Finally, the results are advanced.

3.1. Experimental Objectives

Primary objectives were to demonstrate 1) the flow of an LNAPL as a non-wetting fluid in sand, 2) the imbibition of LNAPL as a wetting fluid on the geocomposite, and 3) the breakthrough of LNAPL after saturating the geocomposite to the point of failure (sheens in the surface water). The primary output is photos and videos illustrating critical processes. The value of this work is to show stakeholders the mechanisms of multiphase flow in support of evaluating OBBs as a remedy for sheens.

3.2. Methods

This section describes the methods used to conduct the sand tank experiment. Three iterations of this experiment were required to capture the dendritic movement of non-wetting LNAPL through the sand below the geocomposite. The final sand tank setup is discussed in this section, and the lessons learned from the first two iterations are discussed in the results.

A custom built sand tank was used for this experiment (Figure 8). A metal frame held two glass plates that were 1.2 m wide by 0.9 m high, spaced 3 cm apart with a plastic spacer with a rubber gasket that surrounded the sides and bottom of the tank. This tank was selected because it was thin

enough to represent two-dimensional flow but still wide enough to insert a representative strip of geocomposite.

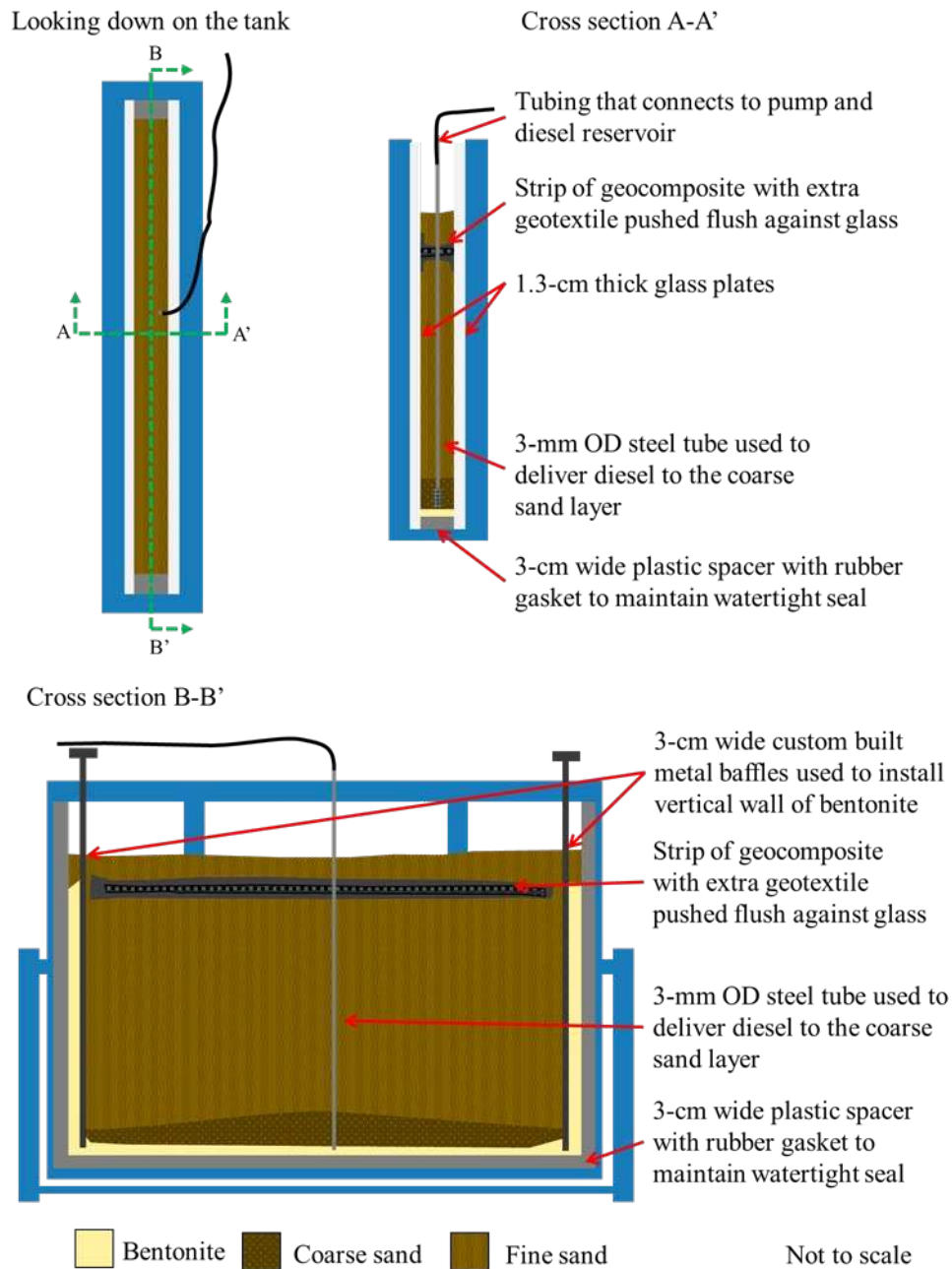


Figure 8. Sand tank diagram

Approximately 2.5 cm of dry bentonite (Wyo-Ben, Billings, MT) was rained evenly into the bottom of the tank. Custom built metal baffles 3 cm wide were inserted 2.5 cm from the vertical ends of the tank to create vertical walls of bentonite. The bentonite separated the sand layers from the plastic spacer to prevent preferential flow of LNAPL along the plastic spacer. A 3 mm OD, 0.9 m long steel tube with a mesh screen attached at the bottom was inserted into the center of the tank, resting on the bottom layer of bentonite. A 10 cm layer of 8/12 Colorado silica sand was rained into the tank, tapering to a depth of 5 cm at the edges the tank. Next, a 50 cm layer of 10/20 Colorado silica sand was rained into the tank. The lower coarse sand provided a low-displacement pressure zone for LNAPL to spread through below the overlying finer sand. The steel tube was connected to a peristaltic pump, and de-aired Fort Collins municipal tap water (1 hr at -85 kPa in a 20 L glass carboy) was pumped into the tank to saturate the sand and hydrate the bentonite. Pumping was stopped when the sand was fully wetted, and a strip of geocomposite was inserted above the sand layer. The geocomposite had been prepared by cutting a strip of geocomposite (GSE TenDrain 7.0 mm geocomposite with 400 g/m² weight geotextile, GSE Environmental, Houston, TX) about 7.6 cm wide and 100 cm long and trimming just the geonet to a width of 2 cm (the width of one complete channel), resulting in excess geotextile that could sit flush in the tank against the glass. Geotextile was wrapped and hot glued to the short ends to limit sand intrusion. A 5 cm layer of 10/20 Colorado silica sand was rained over the geocomposite. De-aired water was pumped into the tank until the water level was 5 cm above the top of the sand. Figure 9 is an annotated photo of the sand tank.

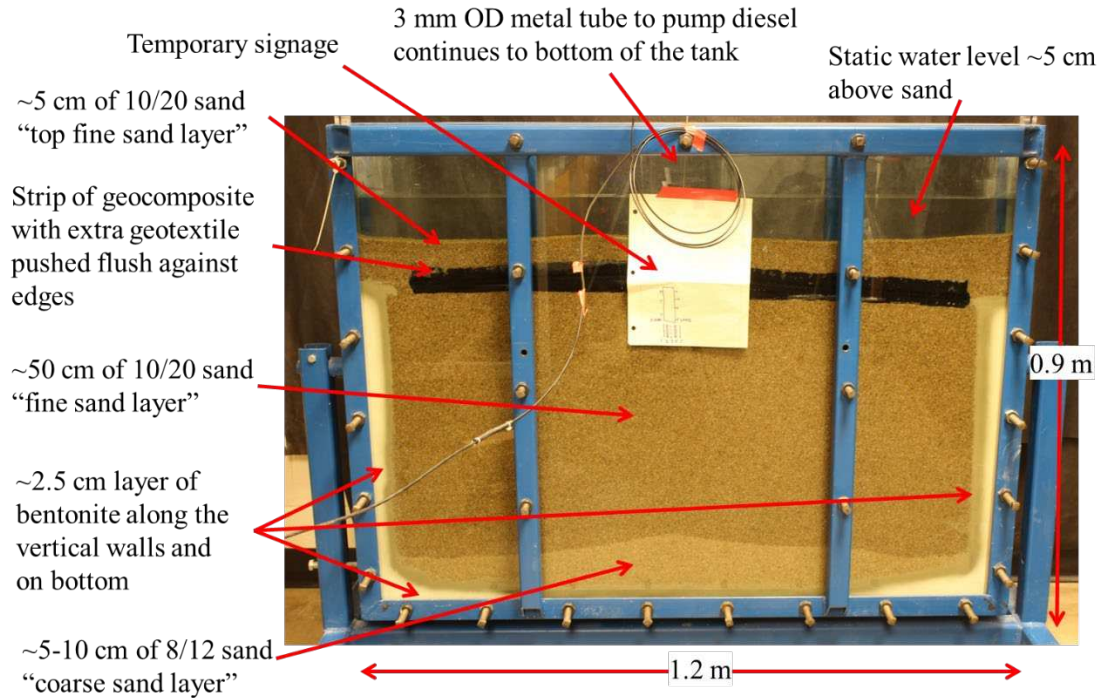


Figure 9. Annotated photo of the sand tank before any diesel injection

Retail diesel purchased from a gas station (Fort Collins, CO) was mixed with Stay-Brite® (Bright Solutions International, Troy, MI) 5% (m/m) Stay-Brite® to diesel. Stay-Brite® mixed with diesel fluoresces yellow under ultraviolet (UV) light. About 10 mL of the dyed diesel was pumped into the coarse sand layer every two hours, equivalent to 120 mL/day. Diesel was pumped into the tank over 76 hours. Photos were taken of the sand tank every two hours using a Canon Rebel T3i camera (Ōta, Tokyo, Japan) on constant settings and Canon EOS Utility remote capture program for Windows. An array of black lights (120 V AC, 60 Hz, 40 W, GE Home Electric Products, Inc., Fairfield, CT) were mounted around the tank to provide sufficient UV light for diesel fluorescence throughout the experiment. To preserve the longevity of the black light bulbs, lights were on a timer programmed to come on only during the photo capture period every two hours. Otherwise, the room was dark.

3.3. Results

This section discusses the results of the sand tank study. The main results of this experiment are: 1) as a non-wetting fluid in the sand, the diesel traveled along dendritic flow paths to the geocomposite and 2) as a wetting fluid on the geocomposite, the diesel spread across a greater width of the geocomposite and required a greater volume of diesel to move the same distance vertically as compared to the sand. Photos and a compiled video document the movement of the dyed diesel through the sand and geocomposite layers representing an OBB.

Initially, diesel advanced through the lower “coarse” low displacement pressure 8/12 sand where the sand layer was 10 cm thick (the center of the tank), shown in Figure 10a after ~60 mL of diesel was added to the tank. Once the capillary pressure exceeded the displacement pressure at the top of the coarse sand, diesel flowed into the overlying “fine” 10/12 sand. While the flow of LNAPL was generally in the vertical direction, the path was also dendritic in nature, as LNAPL flowed following the largest pore throats, as expected of a non-wetting fluid (Figure 10b). Between Figure 10a and Figure 10b, ~60 mL of diesel was added. Figure 10c shows the geocomposite in the photo before diesel moves into the top sand layer. Between Figure 10b and Figure 10c, ~250 mL of diesel was added. To estimate the retention capacity of the geocomposite in this experiment, the amount of diesel added between Figure 10b and Figure 10c (~250 mL) was divided by the area of the geotextile. This leads to an apparent retention capacity of 3 L NAPL/m² of geocomposite. Because some diesel added between Figure 10b and Figure 10c remained in the sand, 3 L NAPL/m² likely overestimates the amount of diesel on the geocomposite. The 3 L NAPL/m² retention capacity estimation is the same as what Chalfant (2015) reported. Figure 10d shows the sheen on air/water interface after a total of ~400 mL of diesel was added to the tank and what would be considered

failure of the OBB. Note that in Figure 10c, diesel has spread across the full width of the geocomposite due to spontaneous imbibition as a wetting fluid, while the diesel in the sand has spread only about 0.3 m laterally as a non-wetting fluid. This demonstration is an important observation for OBB sampling, explaining why a geocomposite sample may contain NAPL even if the underlying sediment does not.

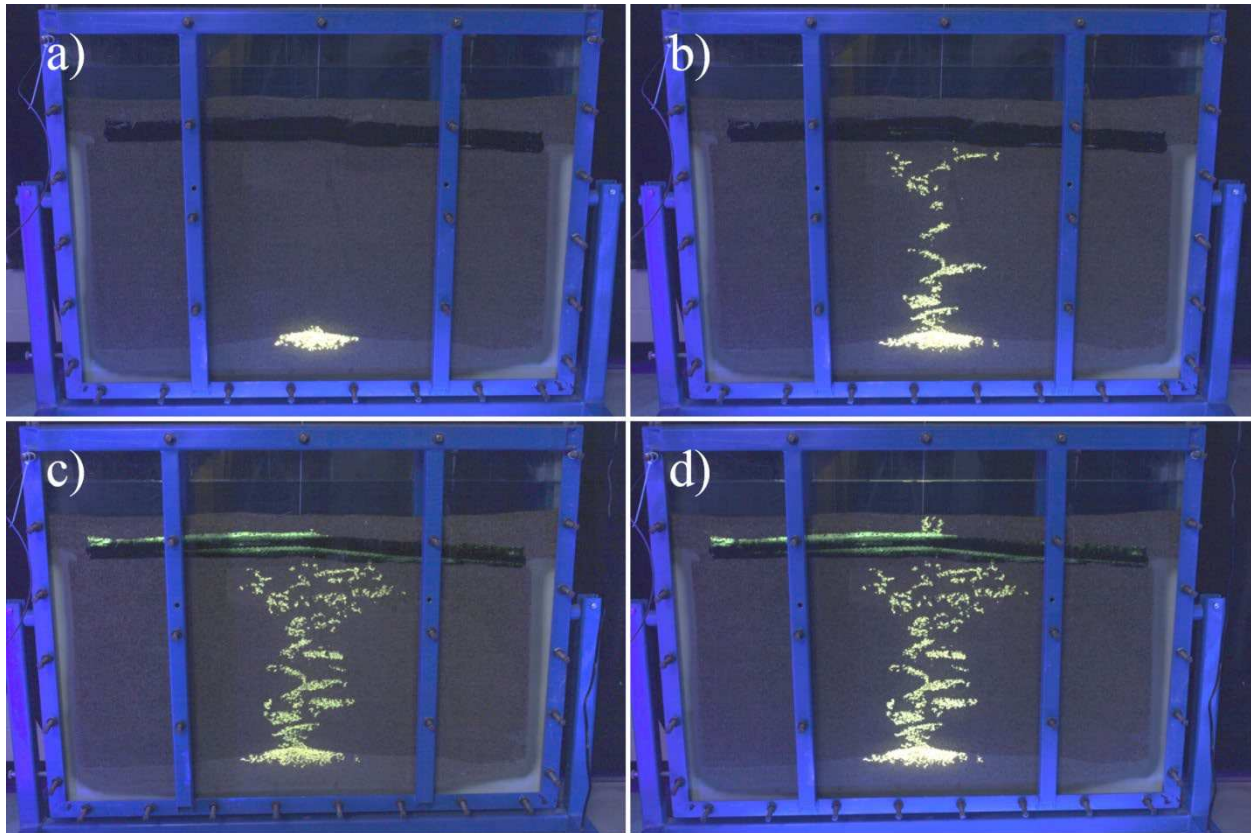


Figure 10. Photo of the sand tank after injecting a) ~60 mL, b) ~120 mL, c) ~370 mL, and d) ~400 mL of dyed diesel

As previously mentioned, the photos from Figure 10a-d are from the third iteration of this experiment, which successfully avoided diesel traveling through a preferential wetting flow path. The first tank was set up as described in Section 3.2 except without bentonite and a 20/40 Colorado silica sand instead of the 10/20. As seen in Figure 11a-b, the diesel saturated the coarse sand layer.

Then, instead of overcoming the displacement pressure to move into the fine sand, the diesel wicked up the plastic spacer, bypassing most of the sand and geocomposite. Diesel became a wetting fluid on the plastic spacer, and as such, was able to move through the tight pore spaces at the sand/spacer interface.

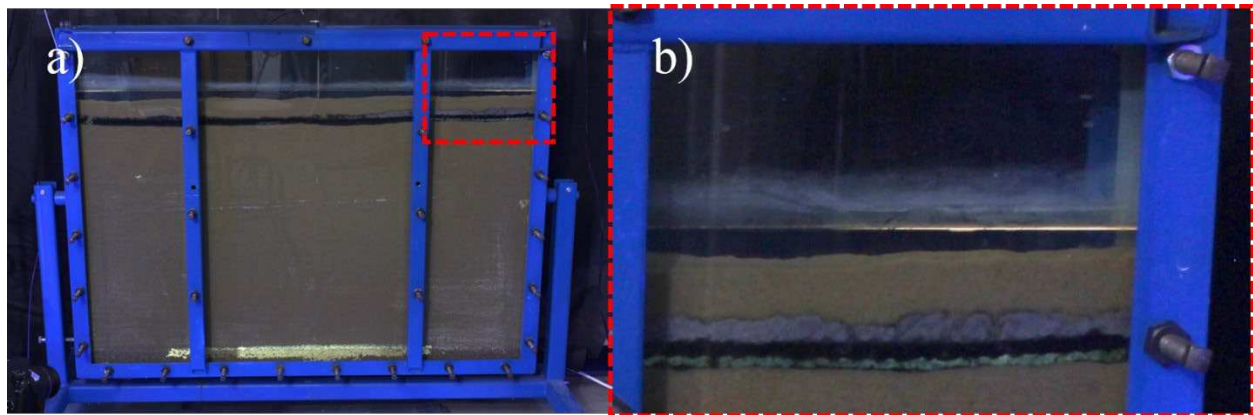


Figure 11. a) In this sand tank, diesel wicked up the plastic spacer to form a sheen without interacting with most of the sand and geocomposite b) Close up of the sheen

To mitigate LNAPL wetting on the plastic spacer, the second design introduced vertical walls of bentonite to prevent diesel contact with the plastic spacer. However, due to issues removing the metal baffle on the right side, the sand was not uniformly compacted. Also, a combination of 20/40 and 20/30 gradation Colorado silica sand was used as the fine sand layer (Figure 12a). First, the diesel saturated the coarse bottom layer. Then, diesel primarily traveled through the interface of the two sand gradations and the less compacted sand on the right side. After saturating the geocomposite, LNAPL discharged from the far left, and the diesel spread out to form a sheen (Figure 12b). This case is more reflective of a natural setting where the subsurface has been disturbed to create a preferential flow path (e.g., well construction, tree roots, animal burrows). This case also highlights dendritic LNAPL flow in the subsurface as a non-wetting phase, as compared to plug flow.

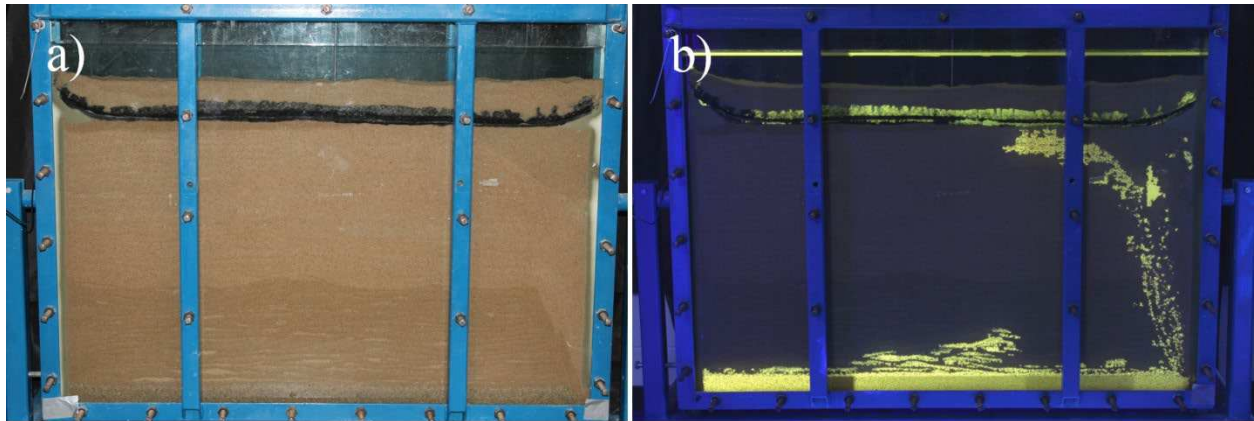


Figure 12. a) The second sand tank under white light and before any diesel had been added; the slight difference in color of the fine sand is indicative of the different sand gradations used. b) The second sand tank under UV light and after sufficient diesel had been pumped into the tank that a 10 mm layer of diesel has formed at the air/water interface.

The limitations of the results discussed thus far are that these tank studies were under static water conditions where the air/water interface was above the porous media. As seen in Figure 13a-d, when the third sand tank was drained, an LNAPL smear zone was created, and diesel was trapped in blobs and ganglia above the air/water interface. Therefore, while LNAPL may initially follow preferential flow paths, tidal influences and seasonal water tables may create a smear zone that redistributes the LNAPL making it difficult to identify the source zone. Also, notably absent in this study was active losses of LNAPL through biologically mediated degradation of LNAPL.

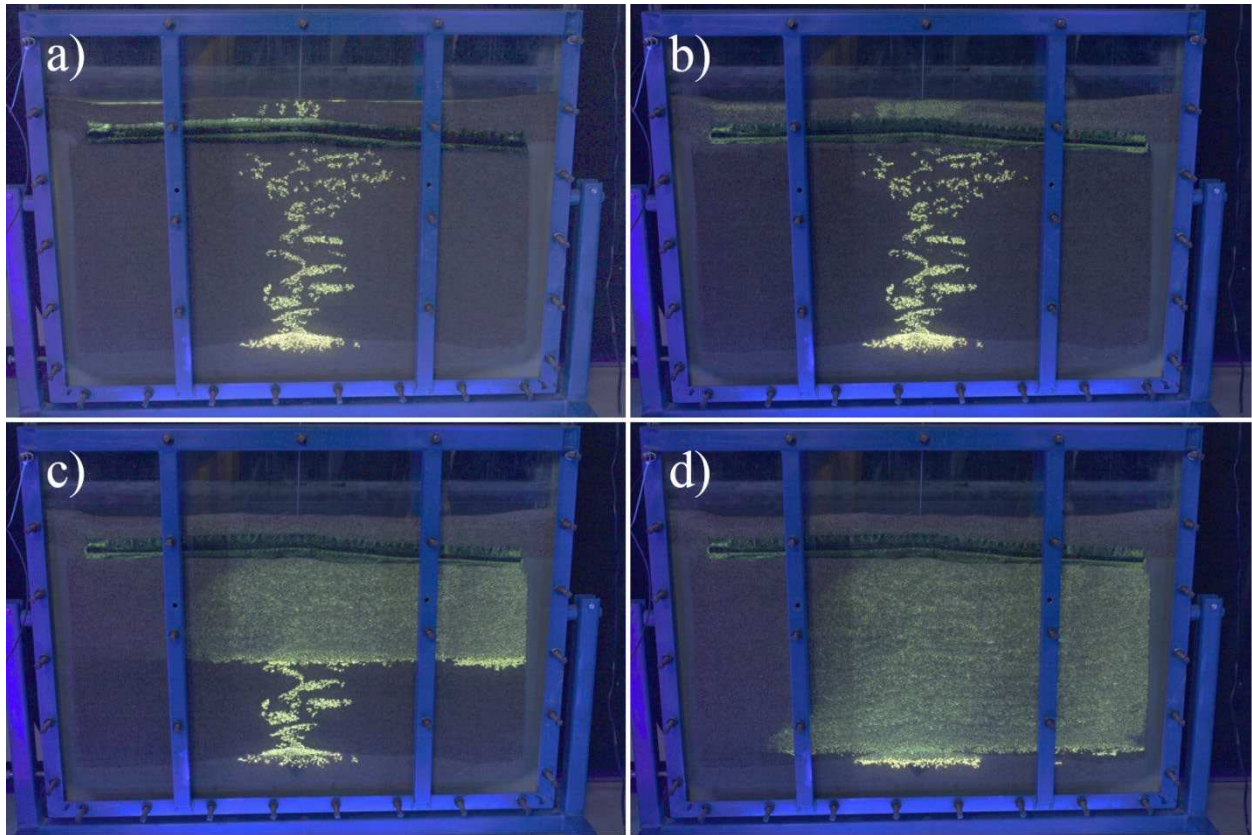


Figure 13. Photo of the sand tank at different times while pumping water out from the bottom

4. OBB AND FIELD SEDIMENT COLUMN MICROCOSM STUDY

This chapter describes a laboratory experiment designed to estimate the aerobic and anaerobic OBB degradation rates of LNAPL in field-inoculated sediment. Unfortunately, due to a flawed experimental design, the mass balance could not be completed, and degradation rates were not calculated. This experiment has been documented such that the faults can be accounted for in future experiments. The first section documents the experimental objectives. The next section presents methods. The last section discusses the results and lessons learned.

4.1. Experimental Objectives

This experiment was designed to estimate aerobic and anaerobic degradation rates as inputs for LNAPL GSI mass balance calculations. The goal was to emulate field conditions as best practically possible in the lab including using sediment from underneath an OBB system that had been active for four years. Field NAPL mixed with diesel was to be injected into the bottom of glass columns loaded with sediment and OBB layers until a sheen formed. The primary variable of interest was the time to breakthrough (sheen formation) under known loading rates between columns with water table fluctuations above and below the OBB designed to mimic tides (aerobic) compared against columns that were constantly submerged (anaerobic). Secondary experimental variables were different LNAPL loading rates and an iron amendment.

4.2. Methods

The experimental setup was sixteen glass columns with select duplicates for statistical comparison as detailed in Table 1. The primary experimental variable was columns with dynamic and static

water levels leading to aerobic and anaerobic conditions. The secondary experimental variable was the loading rates. There were also single variation columns including iron, uncapped (no geocomposite) with and without water fluctuation, upper sediment only, and OBB with heat-treated sediment. The iron-sand mix was to explore the effects of additional iron in the capping material. The uncapped columns were to estimate the system's natural degradation capacity. The anaerobic column with only upper sediment explored how coarser material would affect NAPL degradation. The heat-treated sediment column represented an attempted sterile control. Figure 14 shows a schematic of the different column configurations.

Table 1. Column Configurations and Loading Rates

Column #	Water fluctuations	Configuration	Loading Rate (Q) mL/day three times a week
1	Yes	OBB with heat-treated sediment	3
2	Yes	Uncapped	3
3	Yes	OBB with iron-sand mix	3
4	Yes	OBB	5
5	Yes	OBB	5
6	Yes	OBB	3
7	Yes	OBB	3
8	Yes	OBB	1
9	Yes	OBB	1
10	No	OBB	1
11	No	OBB	1
12	No	OBB	3
13	No	OBB	3
14	No	OBB	5
15	No	OBB with upper sediment only	5
16	No	Uncapped	3

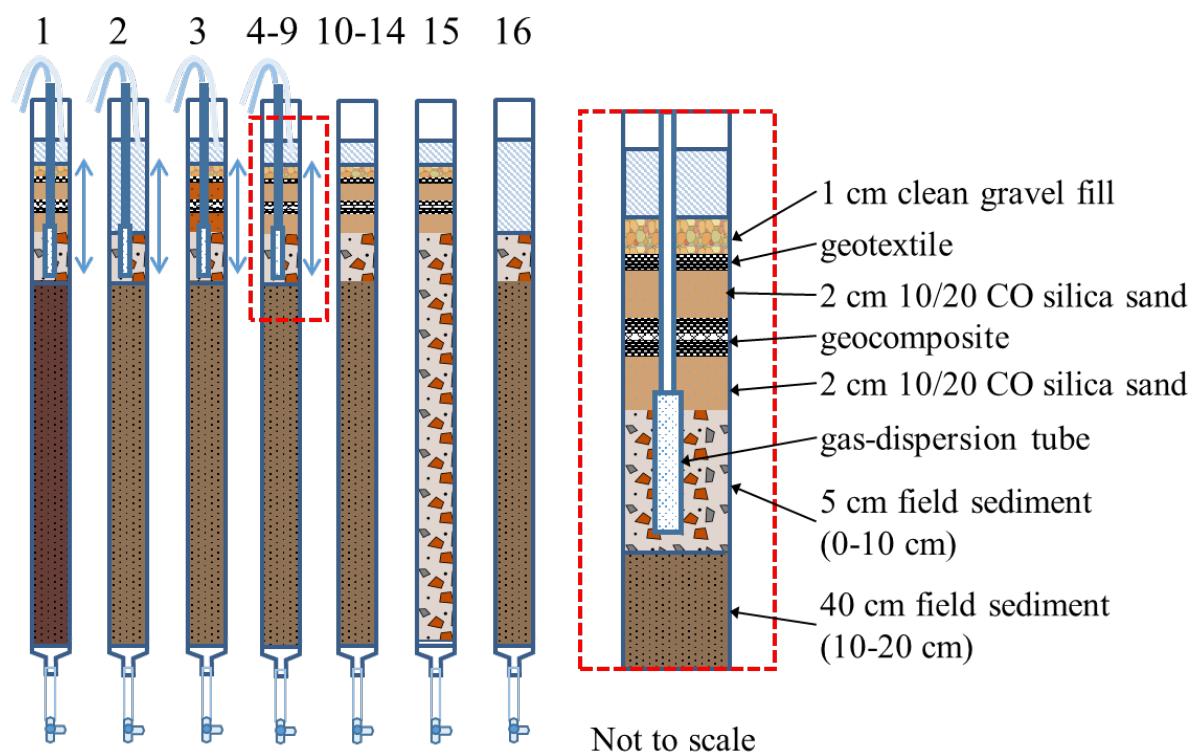


Figure 14. Schematic of the columns with a close up of the typical column. Water table fluctuations are indicated by the blue arrows.

4.2.1. Materials

LNAPL-impacted field sediment was collected from an OBB site during a sampling event discussed in Chapter 5. Approximately 20 kg of sediment from 0 to 10 cm (upper sediment) and 10 to 20 cm (lower sediment) below the geocomposite was collected using shovels and placed into separate black plastic trash bags. The bags were closed, placed in a cooler, shipped to CSU and stored at 4 °C. After 3 months, the separate sediment layers samples were mixed by hand using trowels. Gravel larger than 2.5 cm was removed based on visual inspection. Samples of each sediment were collected for density calculations and heat treatment. These samples were wrapped in aluminum foil, placed in resealable plastic bags, and returned to 4 °C. The homogenized sediment was wrapped up in large black garbage bags, secured with duct tape, and returned to 4

°C until the column loading event. A ferric iron-sand blend was prepared by mixing a 1:1 mass ratio 10/20 Colorado silica sand with the 500 mesh particle size hematite/iron (III) oxide (Alpha Chemicals) inside a resealable plastic bag.

Heat treatment was employed on sediment for one column in an attempt to create a sterilized experimental control. Sediments for the control were placed in glass baking pans in a layer about 2.5 cm deep. Sediments were baked in an Isotemp™ oven (Thermo Fisher Scientific, Waltham, MA) at 200 °C for 24 hours. Pans were removed from the oven and covered with aluminum foil until loaded into the column. Equipment, such as the glass column and tubing, was either autoclaved for 1 hour at 121 °C in a Steris Amsco® Lab 250 machine (Mentor, OH) or placed in boiling water for 20 minutes.

LNAPL from an onsite recovery well upgradient of the OBB was bailed and shipped to CSU. To ensure a sufficient volume of LNAPL for the entire duration of the experiment, the approximately 800 mL of field LNAPL was mixed at a 1:3 mass ratio with retail diesel (Fort Collins, CO). The LNAPL mixture was stored in a plastic fuel container.

4.2.2. Column Setup

Sixteen glass columns with fritted filter bases (41 mm ID x 61 cm length, Ace Glass, Inc., Vineland, NJ) were mounted onto a custom-made metal frame using clamps. Tygon® R-3606 tubing (6.35 mm ID x ~10 cm length) was attached to the bottom of the column. A barbed luer fitting and three-way tee (Cole-Parmer, Vernon Hills, IL) were attached to the end of the tubing to control the flow of liquids at the bottom of the column.

The following procedure describes how the columns were loaded with the exception of Columns 1, 2, 3, 15, and 16. About 200 mL of Fort Collins municipal tap water was placed into the columns. A 40 cm deep layer of the lower sediment was funneled into the column and allowed 24 hours for fines to settle. Upper sediment was funneled in 5 cm deep. Gas-dispersion tubes (12 C, 12 mm OD, 250 mm long x 8 mm diameter stem, Pyrex®, Corning, NY) were inserted into the aerobic columns after about 2 cm of upper sediment had been placed. Next, 2 cm of 10/20 Colorado silica sand was placed into the column. The geocomposite was installed in layers of a geonet disc (average diameter 38 mm, TenDrain 7.0 mm geonet, GSE Environmental, Houston, TX) between geotextiles discs (average diameter 62.5 mm, 400 g/m² nonwoven, needle-punched geotextile, GSE Environmental, Houston, TX). Geotextile discs had slits cut in the center to wrap around the stem of the gas diffuser (see Figure 15). The geotextile was cut with a larger diameter to ensure full contact with the sides of the glass columns. A second 2 cm layer of 10/20 Colorado silica sand was funneled in, and a geotextile disc was placed on top. Finally, about 1 cm of well-sorted gravel was funneled in as the final capping layer.

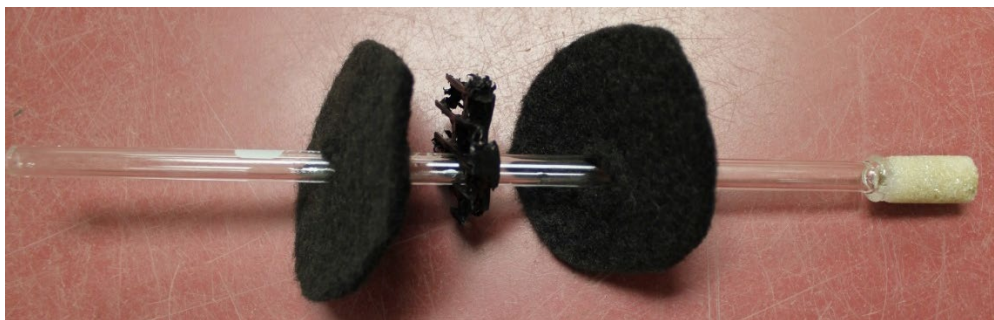


Figure 15. Example of the geotextile and geonet layers around the stem of the gas diffuser

Column 1 was loaded following the procedure described above except for the use of the heat-treated (sterilized) sediment. For Columns 2 and 16, only field sediment was placed with no

capping materials. Column 3 used the iron-sand mix for the sand capping layers. In Column 15, only upper sediment, no lower sediment, was used for the field sediment layers. Figure 16 is a photo of all the columns after loading.



Figure 16. Column experiment after setup was complete; Columns 1–16 (left to right)

Figure 17 shows a simplified diagram of the column setup with hydraulics. The hydraulics for the water-fluctuating columns consisted of fluorinated ethylene propylene (FEP) tubing (1.6 mm ID, Cole-Parmer, Vernon Hills, IL) controlled by a multi-channel peristaltic pump (REGLO Analog, ISMATEC®, Wertheim, Germany) on a digital plug-in timer (Intermatic DT620 Heavy Duty Indoor Digital Plug-In, Spring Grove, IL). Aerated Fort Collins municipal tap water was used for Columns 2–9. Autoclaved aerated Fort Collins municipal tap water was used for Column 1. Influent tubing was taped to the top of individual glass columns such that water freely dripped into the column. Effluent tubing was connected to the gas diffuser in the column. The idea was that the gas diffuser glass frit had small enough pore throats to allow water to be pulled through the diffuser but not LNAPL. Unfortunately, this was not the case, as once LNAPL levels reached the diffuser,

LNAPL was pulled into the effluent tubing. The pump flow rate and timers were adjusted for individual columns such that water table fluctuations were uniform across the columns. At first, the low water level was at the bottom of the diffuser, but in an attempt to mitigate LNAPL being pulled through the diffuser, the low water level was adjusted to the bottom of the geocomposite. A month after the columns had been set up, 7.6 cm by 7.6 cm pieces of Parafilm® M (Bemis Company, Neenah, WI) were placed on top of the anaerobic columns to mitigate evaporation water loss.

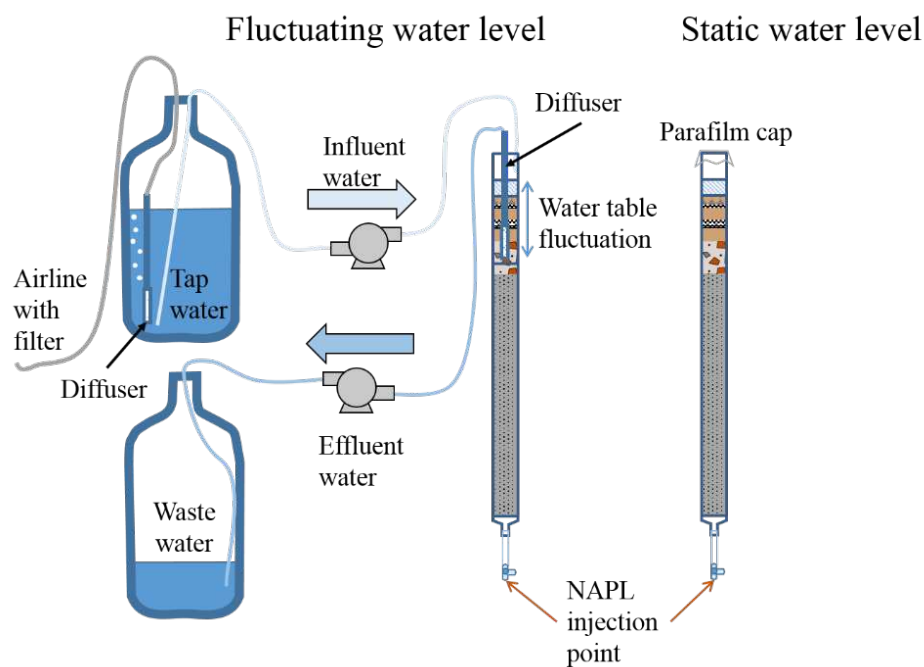


Figure 17. Simplified column configuration to show hydraulics

An array of white and UV lights were positioned around the columns such that NAPL in the columns evenly fluoresced, while providing enough white light to identify detail in the columns. Lights were plugged into a digital timer (Intermatic DT620 Heavy Duty Indoor Digital Plug-In, Spring Grove, IL) and programmed to turn on every two hours for five minutes. During this period,

a Canon Rebel T3i camera (Ōta, Tokyo, Japan) on manual settings was programmed to take a photo using Canon EOS Utility remote capture program for Windows. Otherwise, the columns were in a dark room.

4.2.3. Column Operation

After the columns were set up, the water table was raised and lowered twice daily for ten days before injecting NAPL to acclimatize the microbes to the new environment. NAPL injections were performed manually. Either 1 mL, 3 mL, or 5 mL was injected into a column three times a week on a consistent schedule. A 10 mL glass syringe was loaded with the respective volume of NAPL for a column and injected into the tee at the bottom of the column.

As the NAPL migrated upward in the column, eventually the water effluent gas diffuser began to pull NAPL from the column into the wastewater tubing. Individual wastewater was collected by column to attempt to account for the mass removed through the diffuser, but it became apparent that even with modifications, such as adjusting the range of water fluctuation, too much NAPL was removed by the diffuser to form a sheen. Therefore, NAPL injections and water fluctuations were stopped because there was no solution that did not significantly alter the premise of the experiment. Table 2 shows a summary timeline of the different setup events.

Table 2. Summary of Experiment Schedule

Date	Event
October 2017	Sediment collected from the field, shipped to CSU, and stored at 4 °C

January 2018	Sediment homogenized, heat treated, and mixed with iron
February 2018	Columns set up and loaded with sediment Columns exercised with water table fluctuations for 10 days LNAPL mixture prepared LNAPL injections begin
March 2018	LNAPL injected into columns three times a week LNAPL found in effluent wastewater
April 2018	LNAPL injected into columns three times a week LNAPL in effluent wastewater collected for mass balance
May 2018	LNAPL injections and water table fluctuations stop, columns remained in place to observe precipitation growth

4.3. Results

While this experiment failed to capture degradation rates, it did provide insight into future experimental designs and document changing redox conditions in the columns. For ten weeks, NAPL was injected into the columns. Afterwards, NAPL injections and water table fluctuations were discontinued, and the columns remained stagnant until disassembly. This stagnation period allowed for further microbial growth and changing redox conditions as electron acceptors were consumed.

Six columns formed sheens before NAPL injections were stopped. The static uncapped column (Column 16) formed a sheen first (Figure 18), followed by static 5 mL/day columns and the uncapped column with water table fluctuation (Figure 19), then the static 3 mL/day columns

(Figure 20). NAPL injections stopped before the static 1 mL/day columns formed sheens (Figure 21). The only column with water fluctuation that formed a sheen was Column 2, the uncapped column (Figure 19). Regardless of water table fluctuation, the increased retention capacity of OBBs delayed the formation of sheens as compared to the uncapped column for each hydraulic setting respectively.

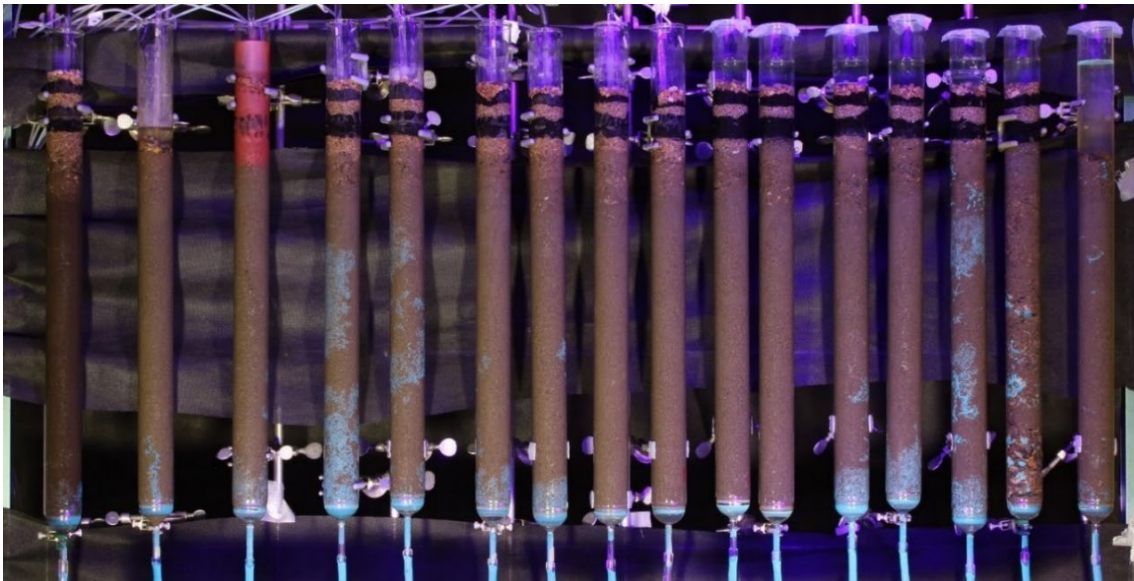


Figure 18. The columns after six injections; Column 16 has a sheen

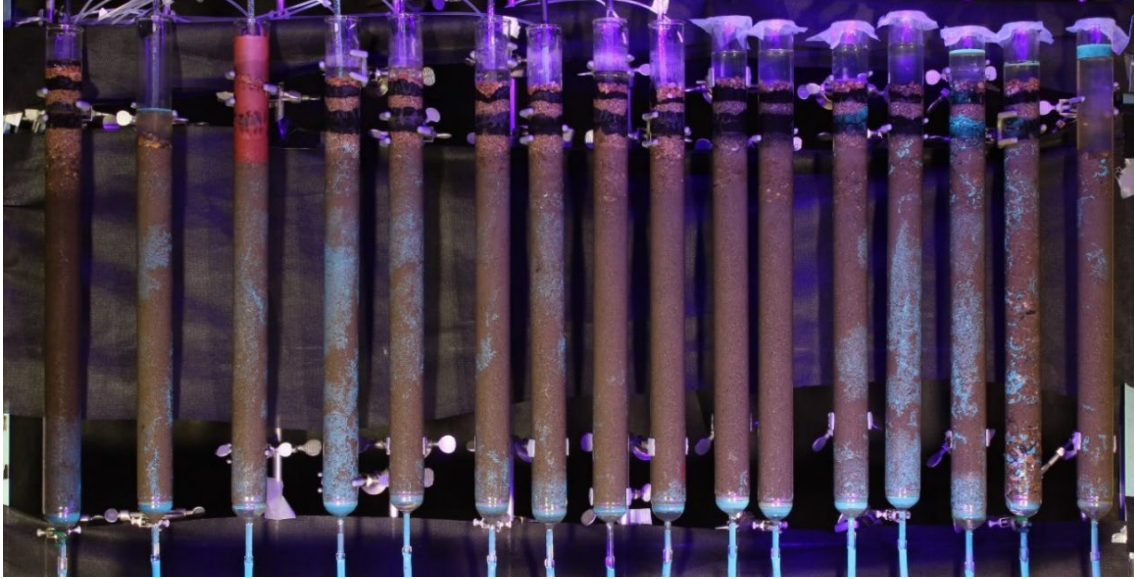


Figure 19. The columns after twelve injections; Columns 2, 14, and 15 now have sheens

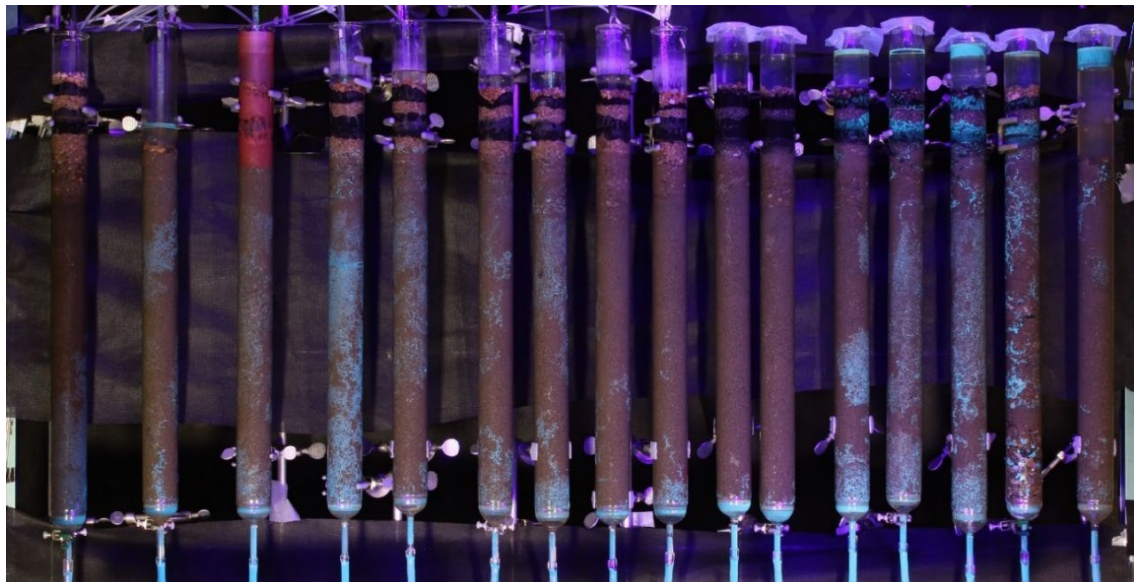


Figure 20. The columns after sixteen injections; Columns 12 and 13 now have sheens

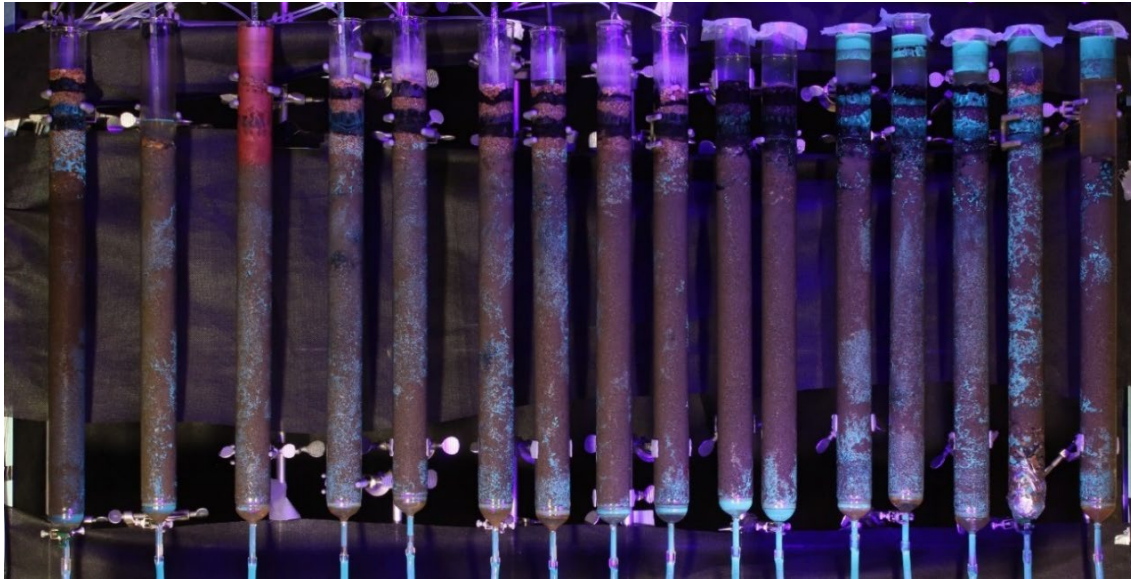


Figure 21. The columns after the last injection

For Columns 2–9, as NAPL migrated upward in the column, the gas diffuser began to pull both water and NAPL into the wastewater discharge tubing. As seen in Figure 22, in some columns, over 50% of the mass was removed through the effluent system (M removed). Because NAPL was removed through the diffuser, less NAPL moved upwards into the OBB capping system. The water fluctuation levels were adjusted such that the low water level became the bottom of the geocomposite, yet sufficient NAPL was still pumped out. Therefore, it was decided to stop NAPL injections and water table fluctuations. While this was an unsatisfactory conclusion to this experiment, no effective solution was identified that could solve the problem without significantly altering the experimental setup. No degradation rates were calculated because of the uncertainty of the mass removed for each column (Figure 22 only estimates the mass loss based on NAPL collected, but there were other NAPL losses not accounted for). The only conclusions from the NAPL loading that can be drawn from the data collected further support work by Campbell (2017) in that an OBB cap increases the retention capacity of a system to delay the formation of a sheen.

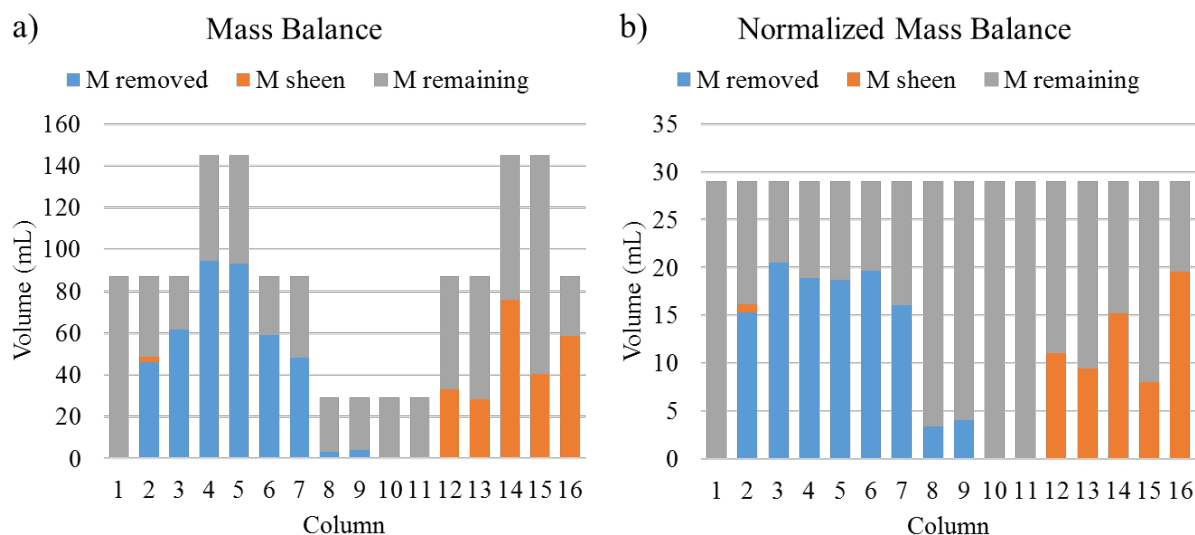


Figure 22. a) Mass balance of NAPL after 29 injections; b) Mass balance of NAPL after 29 injections normalized to the injection rate

NAPL pumping through the diffuser might have been avoided if a smaller frit size was used, increasing the entry pressure. Wrapping the frit in an oleophobic/hydrophilic material may also sufficiently increase the entry pressure. Placing the gas diffuser lower in the column would help ensure that NAPL is the non-wetting fluid around the diffuser frit such that NAPL behaves as a non-wetting fluid, instead of as an intermediate wetting fluid. With this adjustment, the small pore throats of the frit would reduce NAPL movement into the diffuser. There were discussions about pumping effluent water out through the bottom of the column, though likely NAPL would have been pulled through the bottom of this setup, especially since NAPL clung to the narrow neck at the bottom of the column after injection. Any similar experimental setups should resolve this flaw before conducting the experiment.

Secondary problems in this experiment were the potential capillary barriers inadvertently created by loading the dry sterile sediment into the column and the fine particle size of the iron used. The

baked sediment used for the sterile column had a negligible water content as compared to the sediment loaded into the other columns. Loading this column with dry sediment could have affected the settling and porosity, thus altering the NAPL flow up through the column. Baking the sediment could have also altered the sediment properties, such as organic carbon content; however, heating the sediment was determined to be the safest method of sterilizing the sediment (Sterilizing the sediment, regardless of the method used, changes some sediment properties.). The fine particle size of the iron also affected the porosity of the iron-sand cap in Column 3 and could have impeded NAPL flow into the OBB cap. While NAPL was pumped out of this column, suggesting that the NAPL was able to move up into the capping layer, future designs should use iron with a larger particle size to promote NAPL flow onto the OBB for degradation.

During this experiment precipitants formed in the columns (see Figure 23a-b for example). The most apparent was a black precipitant that formed in the clean sand fill of the columns without water fluctuations. Then, as more NAPL was added to the columns, the black precipitant formed around NAPL. After NAPL injections were stopped, the black precipitant formed in the columns with water table fluctuations as well, though not in Column 1. This precipitant was likely iron sulfide due to anaerobic sulfate reduction. Though not quantitative, the precipitant did act as a visual indicator of redox conditions, supporting the idea that columns with water table fluctuations were predominantly aerobic, and columns without water table fluctuations were predominantly anaerobic.

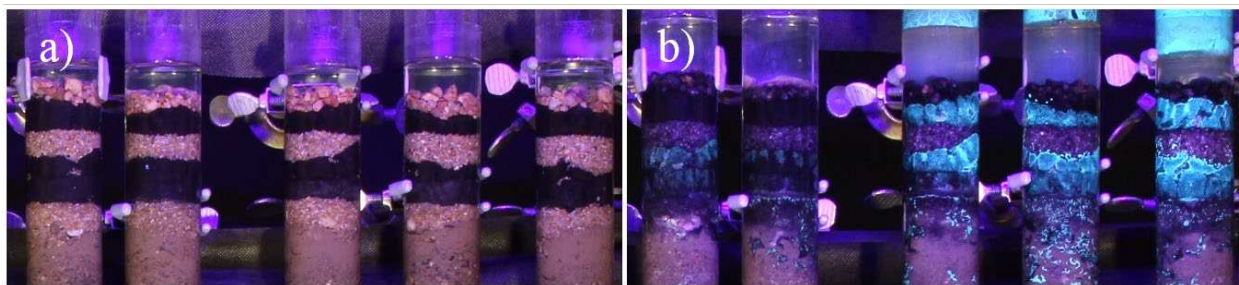


Figure 23. Close up of Columns 10–14 a) 2/26/2018 b) 5/7/2018 to show the formation of black precipitant in the columns

As the columns remained stagnant before disassembly, the water table fluctuation columns developed the black precipitant primarily around areas with NAPL. This precipitant was not observed in Column 1, suggesting significantly reduced microbial activity. Further precipitation was observed in Columns 10–14. A white precipitant appeared to form in Columns 10 and 11. In Columns 12–14, an orange precipitant formed on the top centimeter of the gravel layer (Figure 24a-b). This result suggests that oxygen or iron-oxidizing bacteria are converting the Fe(II) to Fe(III). Visual alteration can indicate changing redox conditions but not necessarily be used to quantify the iron transformed (Benner et al., 2002). However, the visual identification of precipitants could be used as a line of evidence for degradation processes, especially at non-tidal OBB sites.

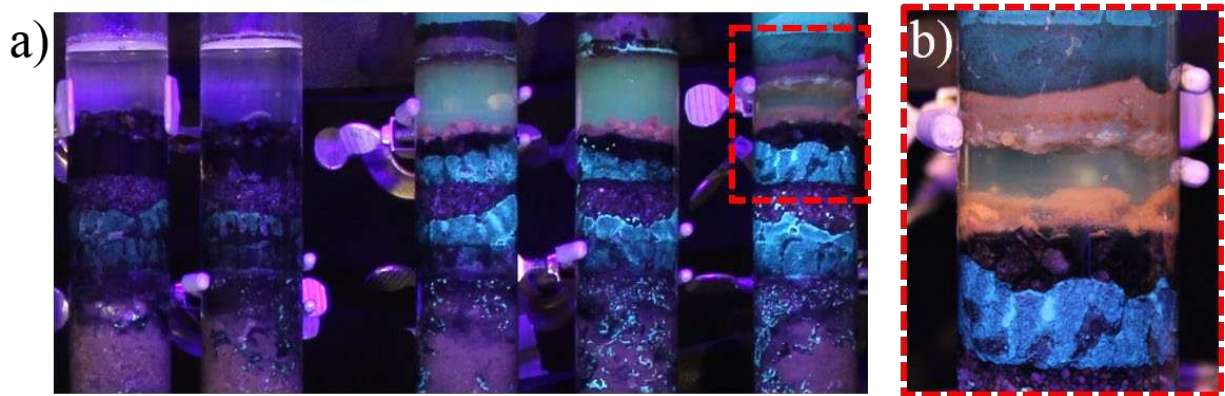


Figure 24. a) Close up of Columns 10–14 on 6/27/18 b) close up of column 14 and orange precipitant

5. FIELD PERFORMANCE OF AN OLEOPHILIC BIO-BARRIER FOR PETROLEUM AT A GROUNDWATER/SURFACE WATER INTERFACE

5.1. Summary

Sheens, a potential Clean Water Act violation, can occur in surface water adjacent to petroleum refining, distribution, and storage facilities. The oleophilic bio-barrier (OBB) was designed as a low-cost sheen management strategy that uses 1) an oleophilic (oil-loving) plastic geocomposite to intercept and retain petroleum liquid contamination from the groundwater and 2) the cyclic delivery of oxygen and nutrients via tidally-driven water level fluctuations. Destructive sampling of an OBB after a four-year field deployment has advanced the mechanistic understanding of how OBBs work. The OBB layers were systematically removed and sampled for petroleum compounds and microbial communities. Sampling revealed the OBB was addressing sheens and was not compromised by field conditions such as ice scour or sediment intrusion. Notably, sheens were observed adjacent to the barrier leading to the expanded 58 m final remedy. Petroleum composition analysis showed no petroleum liquid on the geocomposite or in the upper underlying sediment (0-10 cm). Diesel range organic (DRO) concentrations in the low 1,000s of mg/kg were observed in the sediment immediately below (10-20 cm) the upper sediment. Petroleum composition analysis suggests that the majority of the compounds are polar in the lower sediments, providing a line of evidence that petroleum compounds at the groundwater/surface water interface (GSI) have been oxygenated. Microbial data show that the number of bacterial 16s transcripts on the geocomposite are on average larger than in the sediment layers, confirming that the geocomposite is a suitable substrate for microbe growth. The sampling event suggests that petroleum biodegradation rates in and below the OBB are comparable to the petroleum loading rates. The advantage of the OBB is

that the geocomposite layer retains the petroleum liquids that exceed the natural assimilation capacity.

5.2. Introduction

Petroleum hydrocarbons are integral to modern society. Petroleum refining, distribution, and storage facilities are commonly located near surface water bodies. Due to historical releases of petroleum liquids, impacted subsurface media and groundwater extending to the surface water is a common condition. At groundwater/surface water interfaces (GSIs), sheens can form on the surface water, a potential Clean Water Act violation. Sheens are thin, iridescent films of non-aqueous phase liquids (NAPLs) that spread along the air-water interface (Figure 25). Sheens form via seeps, ebullition, and erosion. A small volume of petroleum liquid can form a sheen of large areal extent (Sale et al., 2018). Sheen remediation technologies can fail when NAPL bypasses the barrier or overloads the absorptive capacity (Hawkins, 2013). Other remediation strategies, such as hydraulic controls, have costly capital and operation and maintenance (O&M) expenses.



Figure 25. An iridescent sheen on the shoreline formed by a seep

The oleophilic bio-barrier (OBB) was developed to address the limitations and costs of current sheen management technologies. An oleophilic (oil-loving) plastic geocomposite intercepts and retains petroleum liquids from the groundwater in combination with the exchange of surface water and/or air to deliver oxygen and nutrients to support the biological degradation of the petroleum liquids. Additional layers of clean sand fill and geotextile increase the retention capacity of the OBB. A structural cover anchors the OBB in place, providing protection against erosion and ice scour (Figure 26). The OBB was designed to address seep, ebullition, and erosion formation mechanisms (Chalfant, 2015).

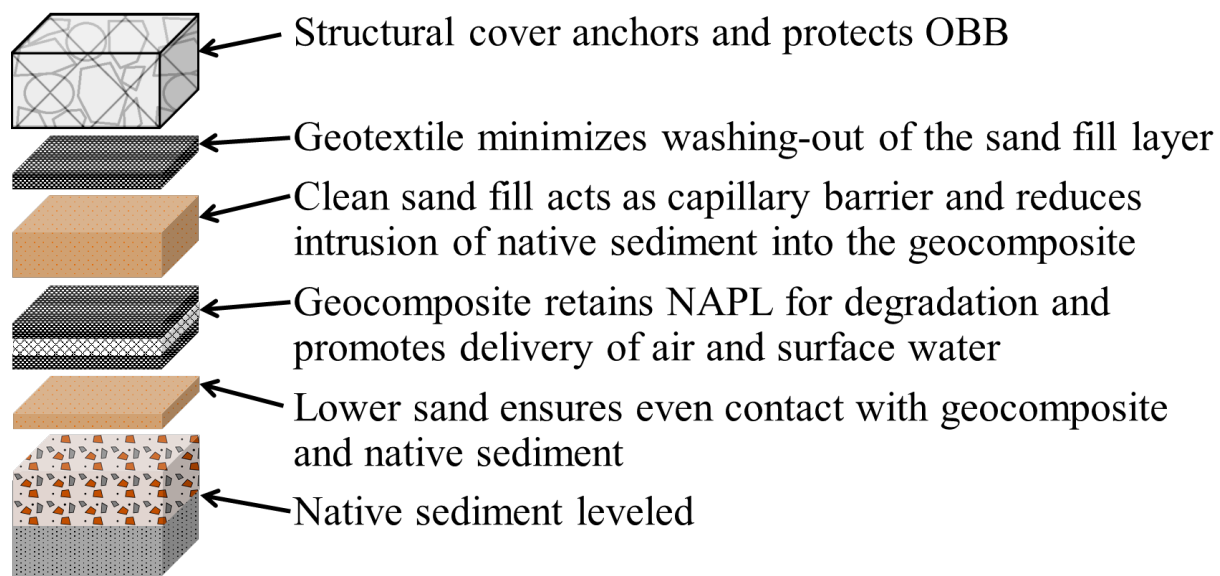


Figure 26. Schematic of the standard OBB layers, not to scale

The biodegradation of petroleum liquids has been used to mitigate petroleum releases. Enhancing degradation rates by supplementing oxygen and nutrients is challenging due to delivery constraints (Chapelle, 1999). Permeable reactive barriers (PRBs) overcome these delivery constraints by using the natural hydraulic gradient to bring contaminated water to degradation enhancing material such as zero-valent iron in a high permeability zone (Interstate Technology & Regulatory Council

[ITRC], 2011). Inspired by PRBs, the OBB couples petroleum liquid retention with the delivery of oxygen and nutrients through surface water exchange (e.g., tidal fluctuations). Native microbes from the sediment acclimate to the geocomposite and consume the petroleum liquids as a carbon source. So long as the treatment capacity (retention and degradation) is greater than the petroleum liquid loading, the OBB will mitigate the formation of sheens.

Chalfant (2015) discusses preliminary OBB research including proof-of-concept laboratory retention studies and the installation of test and demonstration OBBs at the field site sampled in this paper. To date, OBBs have been installed at three sites with studies supporting deployment at six more sites. The primary applications of OBBs are located at sites with twice daily tidal water level fluctuations.

This paper presents the current understanding of processes governing OBB performance based on the results of an OBB sampling event. The OBB had been deployed in the field for four years and was systematically disassembled for visual inspection of the structural cover, geocomposite, and underlying sediments. In addition, samples of the geocomposite and the sediment below the geocomposite were collected and analyzed for petroleum liquids and microbial communities. Results provide multiple lines of evidence supporting biological degradation in and below the OBB and suggest that the microbial degradation capacity is in excess of loading rates. Overall, results indicate that the optimization of biodegradation via construction of an aerobic petroleum-liquid retaining, water-permeable bioreactor is a viable technology for preventing sheens in surface water and, more generally, for managing degradable contaminants at GSIs.

5.3. Methods

The following section provides site information, insight from previous sampling events, methods used during sampling, and the procedure for petroleum and microbial analysis.

5.3.1. *Site Description*

The site is a petroleum liquids storage facility located on a large freshwater tidal river in northeastern US (Figure 27a). Sheens occur on the river bank due to historic petroleum spills. Observed sheen forming mechanisms include seeps, ebullition, and erosion. A durable armoring layer was needed at this site not only to anchor the OBB but also to offer sufficient protection from ice scour and river debris (Figure 27b). Groundwater flow is primarily perpendicular to the river. Tidal fluctuations are approximately 1.5 m with bank storage occurring at high tide and discharge of groundwater to surface water at low tide.

The shoreline is composed of a lower alluvial layer of sand and gravel. Above the sand and gravel, there is a fill layer of fine to coarse sand with fine to coarse gravel, likely sourced from river dredge spoils, which tapers out about halfway into the intertidal area. Episodic sheens have been observed discharging to the surface water along a “seep line” at the transition from the alluvium to the fill layer. About 6 m below ground surface is glaciolacustrine clay with minor amounts of silts. The clay layer acts as an aquitard (Arcadis, 2011).



Figure 27. a) The site shoreline looking north in August, pre-OBB installation, b) The site shoreline looking north in February; the OBB is covered in ice and snow

5.3.2. *Preliminary Field Studies*

A small-scale proof-of-concept OBB field study occurred from March to August 2013. Four 1 m by 1 m squares of Tendrain II 91010 geocomposite (Syntech, Baltimore, MD) anchored with cinderblocks and fitted with tubing and thermocouples were installed over the seep line. Biweekly inspections were performed to observe any petroleum liquid staining or sheens. Water samples collected during two sampling events were analyzed for ORP, pH, and major ion concentrations. Thermocouples collected continuous temperature data. During the pilot study deconstruction, the geocomposite pads were scanned under ultraviolet (UV) light and then subsampled for petroleum analysis. Underlying sediments and water samples were also collected for petroleum analysis. Results from this field study confirmed 1) petroleum liquid was discharging at the seep line, 2) the geocomposite retained petroleum liquid, and 3) petroleum liquid loading, less degradation, did not exceed the geocomposite retention capacity.

In November 2013, a 3.8 m by 9.3 m large-scale OBB demonstration was installed to cover a larger sheen area. The OBB consisted of geocomposite (Tendrain II 91010-2, Syntech, Baltimore, MD), 5–8 cm of clean sand fill (well-graded sand, coarse (#8) to fine (#100)), a geotextile (non-woven, 340 g/m²), and a Reno mattress (Diamond Wire Netting & Finished Product Company, Hebei, China). Six 15-cm PVC sample ports were included so that sample discs of geocomposite and underlying sediment could be sampled without disrupting the entire OBB system. Additional sample ports collected temperature and pressure data as well as allowed access for pore water samples. See Chalfant (2015) for further details of historical sampling and construction documents.

5.3.3. Destructive Sampling of the Demonstration OBB

The destructive sampling event took place October 2017, four years after the demonstration OBB was installed. First, the Reno mattresses, geotextile, and top sand layers were removed. Once cleared, the top of the geocomposite was scanned with UV lights in a blackout tent to determine if any petroleum liquids were present on the geocomposite. Two LED UV light bars (9 3-watt lights per bar, range 395 – 400 nm, OPPSK PRO Stage Lighting) were used inside a 0.9 m by 1.2 m by 1.5 m tent (5 cm PVC pipe frame and 0.15 mm solid black polyethylene sheeting cover) to visually identify and photograph any location where petroleum liquid fluorescence was visible.

Next, geocomposite and sediment samples were collected from fourteen locations (Figure 28). From the geocomposite, triangles with approximate 15 cm sides were cut out using a battery-powered angle grinder (Dewalt, Baltimore, MD) with an 11.4 cm metal cut-off disc (Diablo, High Point, NC). A hand trowel was used to scoop approximately 500 g of the sediment immediately below the geocomposite (0-10 cm) and 10 cm under the geocomposite (10-20 cm). All samples

were wrapped in aluminum foil and placed into individual resealable bags. Samples were then placed in a cooler with dry ice (-78 °C), shipped overnight to Colorado State University (CSU), and stored in a -80 °C freezer until analysis. Sediment samples were subdivided for analysis by unpacking and repacking quartered portions of sediment into aluminum foil packets. Geocomposite samples were subdivided using a Corona SL 4264 lopper (Corona, CA) to cut geocomposite into quarters and subsamples for microbial analysis.

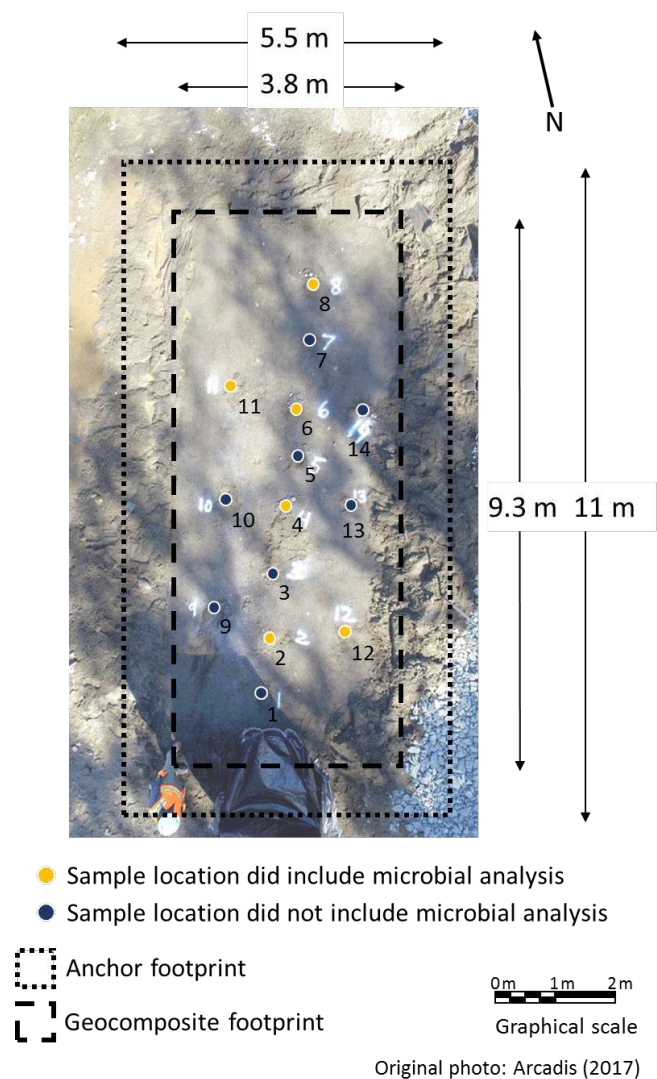


Figure 28. Location of the 14 sampling points overlaid on an overhead photo of the OBB with the structural cover, geotextile, and sand fill layer removed (Photo: Arcadis)

5.3.4. *Analysis*

Microbial analysis followed methods described in Irianni-Renno et al. (2016) and Irianni-Renno et al. (2018). The number of 16S ribosomal ribonucleic acid (rRNA) transcripts for bacteria and archaea was generated using high-throughput sequencing of the 16s transcripts. Quantitative polymerase chain reaction (qPCR) was performed using SYBR® Green (Life Technologies, Grand Island, NY) qPCR assays. Subsamples were pretreated to remove petroleum liquids and other potential contaminants that can affect RNA extraction and inhibit qPCR. Samples were submitted to Research and Testing Laboratory, LLC (Lubbock, TX) for analysis. Microbial community data at the genus level were then sorted based on putative electron acceptor and donor types into the following categories for archaea: methanogens, ammonia-oxidizing archaea, fermenters, methane-oxidizing nitrate reducers, and broadly classified. For bacteria, the data were sorted into the following categories: aerobic, iron oxidizers, methane oxidizers, nitrate reducers, iron reducers, sulfate reducers, fermenters, broadly classified, and other. Broadly classified represents organisms that were identified at a higher level than genus, such as the family level, and could not be assigned a putative electron acceptor/donor. Other includes organisms that were identified at the genus level, but could not be assigned a putative electron acceptor/donor. See Appendix C for details.

Petroleum samples were analyzed using methods described in Bojan (2018). Subsamples were extracted in toluene and analyzed using an Agilent Technologies 6890N Gas Chromatograph (Santa Clara, CA) equipped with a Flame Ionization Detector (GC/FID) and a Restek Rtx-5 column (30 m length x 0.32 mm inner diameter x 0.25 µm film thickness, Bellefonte, PA). Chromatographs were compared against a diesel range organics (DRO) (EPA/Wisconsin, Restek) calibration curve with concentrations from 50 mg/L to 300 mg/L. Samples were also analyzed on

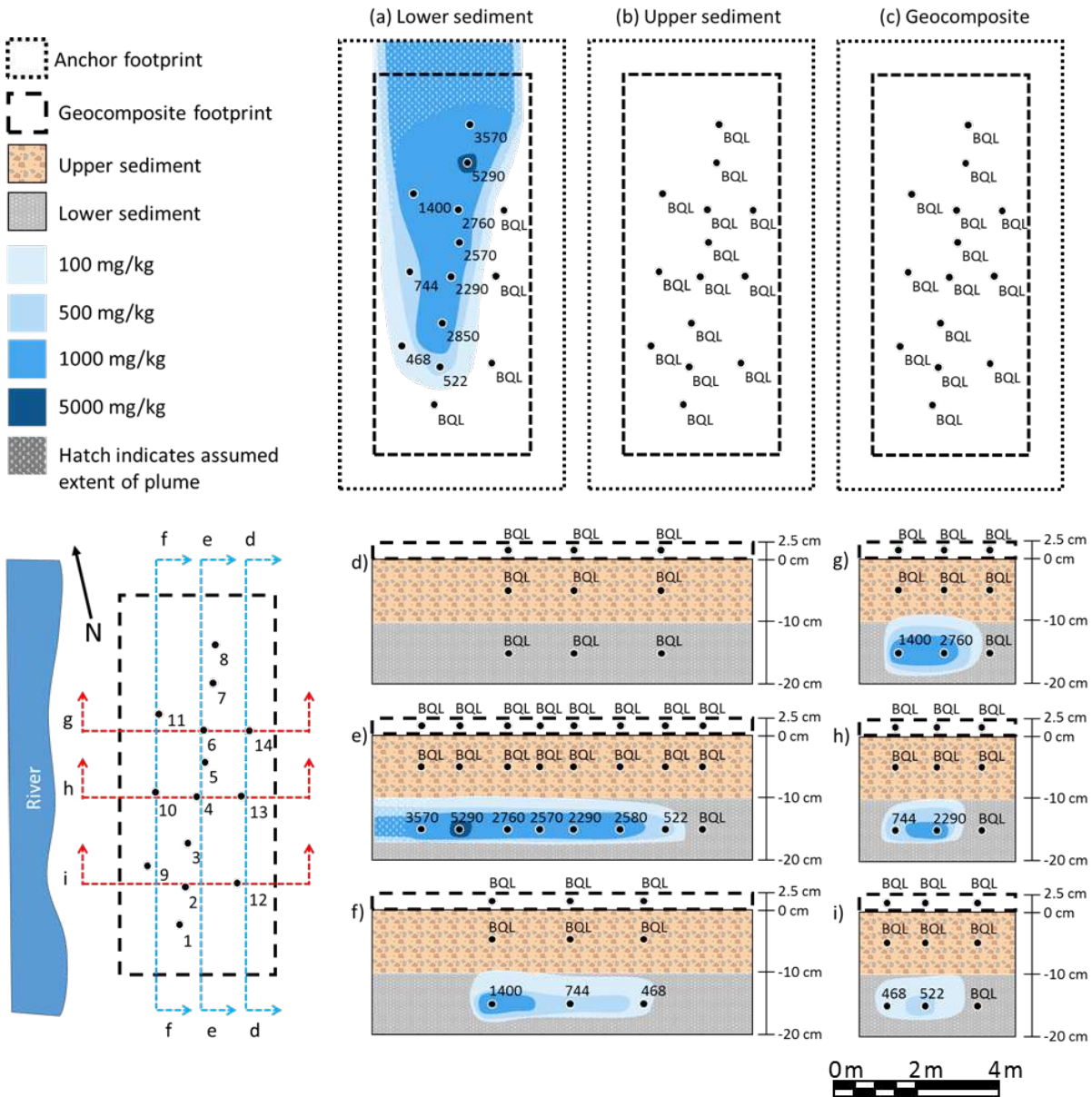
Agilent Technologies 6890N Network Gas Chromatograph with an Agilent 5973 Network Mass Selective Detector (GC/MS). Relative percent polar data were calculated by identifying peaks using the GC/MS library and comparing the relative integrated area for polar peaks against the integrated area for nonpolar compounds peaks. Compounds were classified as either polar, oxygenated hydrocarbons with at least one oxygen atom, or nonpolar, true hydrocarbons with no oxygen atoms. The relative percent polar data can be used to compare the polar/nonpolar ratio between samples but does not represent the overall polar/nonpolar ratio due to variations in the rate of ionization of the different compounds on the GC/MS. Recoveries for extraction of organic compounds from geocomposite were an average $108\% \pm 7\%$ for nonpolar compounds using DRO (EPA/Wisconsin, Restek) as the mixture compound and $104\% \pm 5\%$ for polar compounds using decanoic acid ($>98\%$, MilliporeSigma, Burlington, MA) as the mixture compound.

Due to the visual observation of iron hydroxides/oxides at the site, iron extractions were performed on the samples collected to evaluate total iron. Unfortunately, iron analysis was not anticipated, and samples were not properly preserved for iron analysis (i.e., immediately stored anaerobically in acid $\text{pH} < 2$). Subsamples of an average 3 g geocomposite or 12 g sediment were placed in 15 mL deionized, de-aired water in 50 mL conical centrifuge tubes (Falcon™, Fisher Scientific, Waltham, MA). Iron extraction was performed using an aliquot of the sample in DI water and after acidifying the water to $\text{pH} \approx 2.5$ by adding 25 μL of 70% nitric acid (MilliporeSigma, Burlington, MA). Samples were analyzed using FerroVer® reagent (Hach, Loveland, CO) which contains 1,10-phenanthroline, a colorimetric indicator for iron. Concentrations were determined using a spectrophotometer calibrated with a five-point calibration curve with values ranging from 0.090 mg/L to 2.5 mg/L. Samples with values outside the calibration curve were diluted with DI water until the value was within the calibration range.

5.4. Results

No petroleum liquids were observed while scanning the geocomposite with UV light. The interior of the geocomposite samples were open, free of sediment, precipitates, and biofouling. No petroleum liquids were observed in the geocomposite and underlying sediment (0-10 cm). No petroleum odors were detected until sampling of the lower sediment layer (10-20 cm). Sheens formed in the holes after samples of the lower sediment had been removed. Sheens were observed at the edges of the geocomposite footprint. An interval of orange precipitates (presumed to be ferric iron hydroxides) was observed above and below the geocomposite.

DRO compound concentrations were below GC/FID quantification limits (2 mg/kg) in the upper sediment and geocomposite (Figure 29). GC/MS was able to detect DRO compounds on the geocomposite, and these values were used to calculate the relative percentage of polar/nonpolar compounds. The polar/nonpolar ratio for compounds found on the geocomposite samples was 7% polar or less (Figure 30). GC/MS did not detect compounds in the upper sediment (quantification limit 6 mg/kg), so there is no polar ratio analysis for this layer. In the lower sediment, DRO concentrations ranged from below the GC/FID quantification limit (2 mg/kg) to 5,000 mg/kg. Based on the shape of the isoconcentration plume, the petroleum liquid contamination likely extends north beyond the sampling collection area. This area was subsequently addressed by a full-scale OBB installation. GC/MS analysis of the polar compounds showed that the contaminants in the lower sediment were a majority (>50%) polar compounds.



BQL = Below quantification limit (2 mg/kg)
Units: mg DRO/kg dry weight sample

Figure 29. Isoconcentration maps of the diesel range organics (DRO) analysis

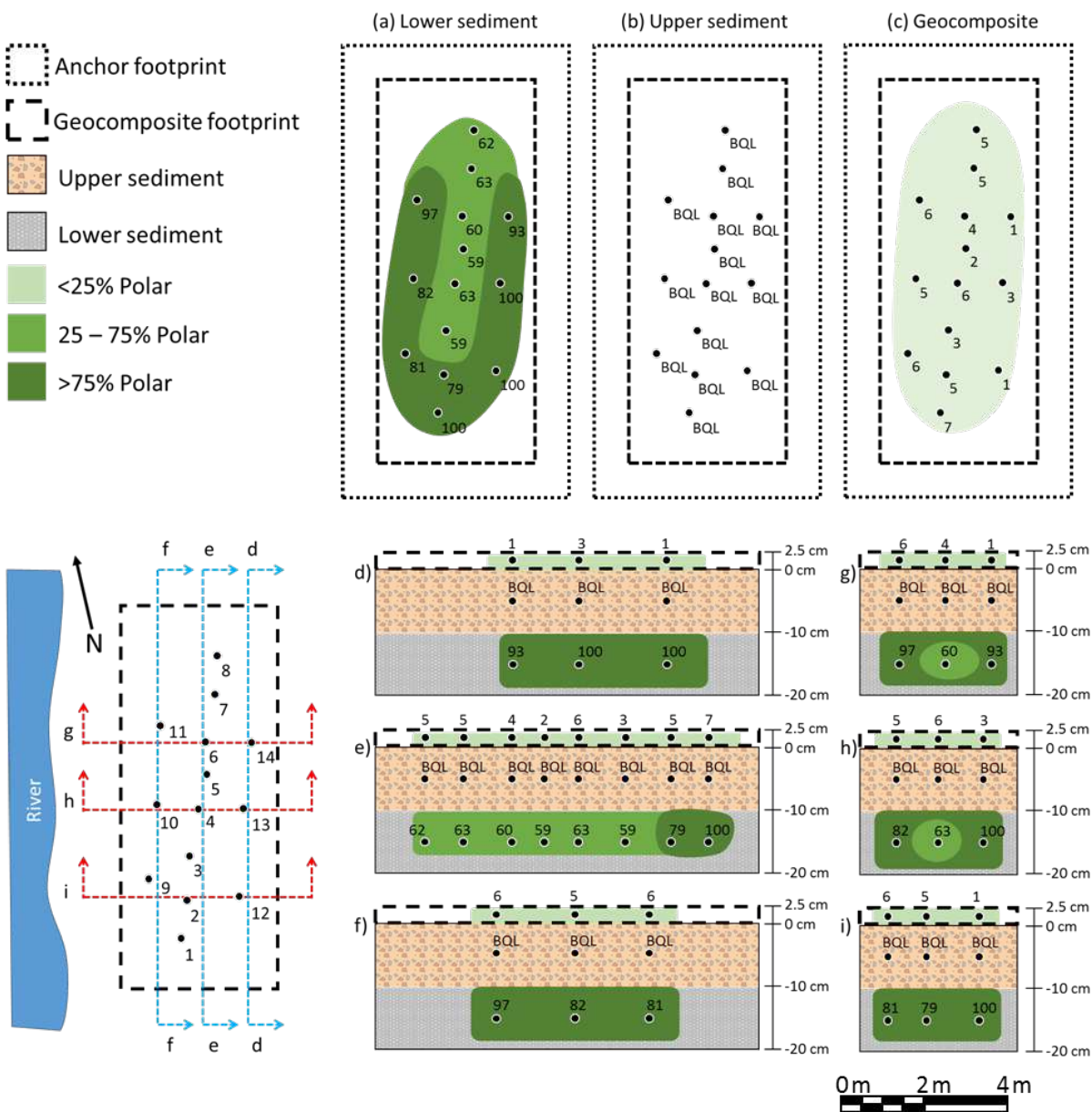


Figure 30. Isoconcentration maps of the petroleum liquid polar/nonpolar ratio analysis

Microbial analysis revealed that the number of bacterial 16S transcripts on the geocomposite were all on the order of 10^9 16S transcripts/g sample, while values ranged from 10^6 to 10^9 16S transcripts/g sample in the underlying sediment (Figure 31). The highest number of archaeal transcripts was found in the lower sediment (2.6×10^7 16S transcripts/g sample). Typical archaeal

levels were on the order of 10^5 to 10^6 16S transcripts/g sample. Further community analysis for the average relative abundance of putative electron acceptors and donors for bacteria and archaea per layer from the main seep line is shown in Figure 32 and Figure 33. Comparison of the sample points from the main seep line exclude outliers found in the upgradient and downgradient samples. The greatest difference in electron acceptors/donors for the average levels of archaea on the main seep line was between the percent methanogens and ammonia-oxidizing archaea (AOA). There was 28% and 24% greater average relative abundance of methanogens in the lower sediment than in the upper sediment and geocomposite, respectively. There was an average 31% and 8% relative abundance of AOA in the upper sediment and geocomposite, respectively, and no AOA in the lower sediment. For the relative abundance of bacteria between the three layers, the greatest difference in electron acceptors/donors was between the aerobes, the nitrate reducers/aerobes, and fermenters. There was an average 14% and 17% greater relative abundance of aerobic bacteria in the upper sediment and geocomposite than the lower sediment, respectively. The average number of nitrate reducers/aerobes was 4% higher in the upper sediment and geocomposite than the lower sediment. There were about 13% more fermenters and 2% more sulfate reducers/fermenters in the lower sediment than the other layers.

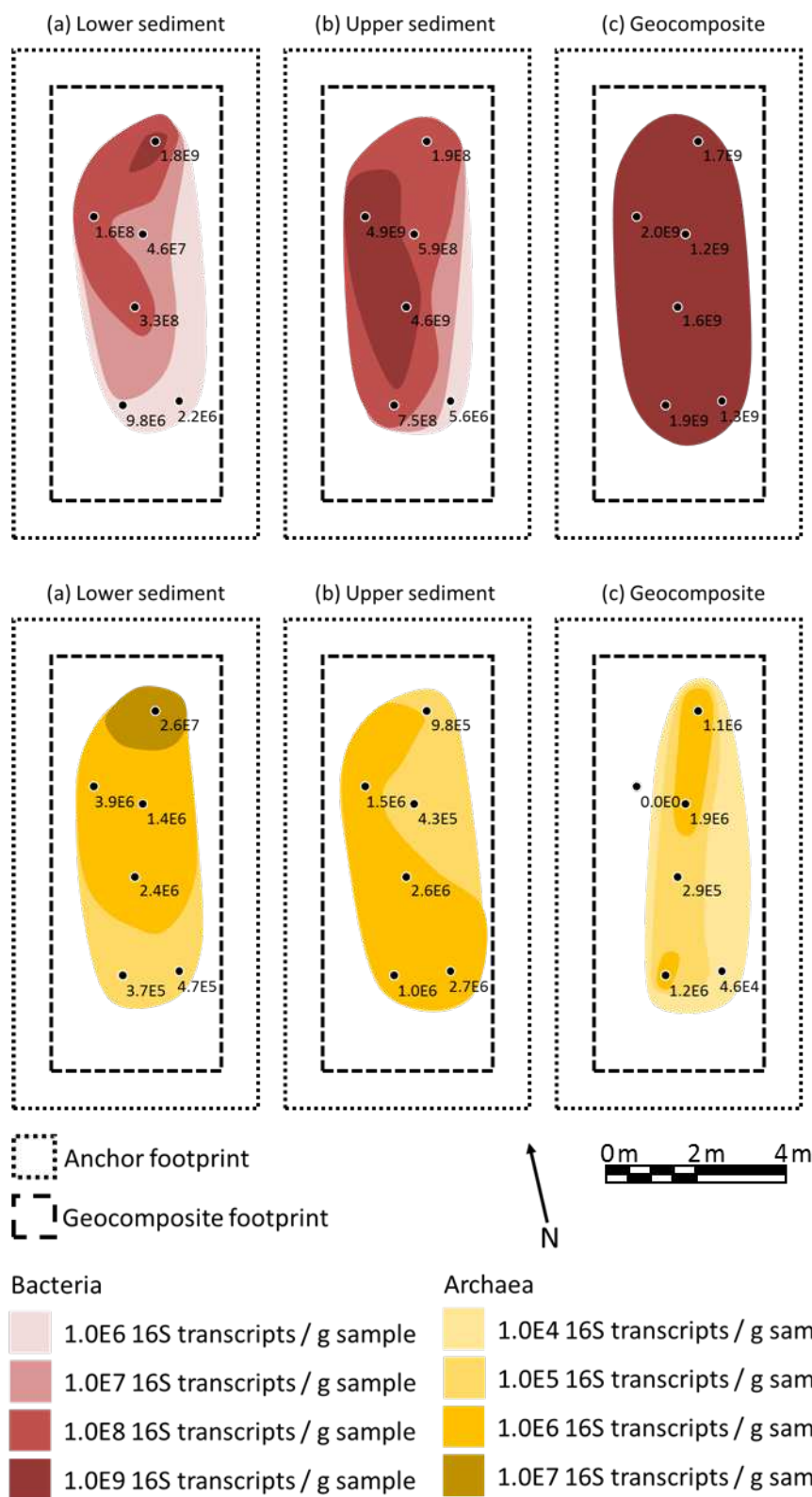


Figure 31. Isoconcentration maps of 16S transcripts analysis

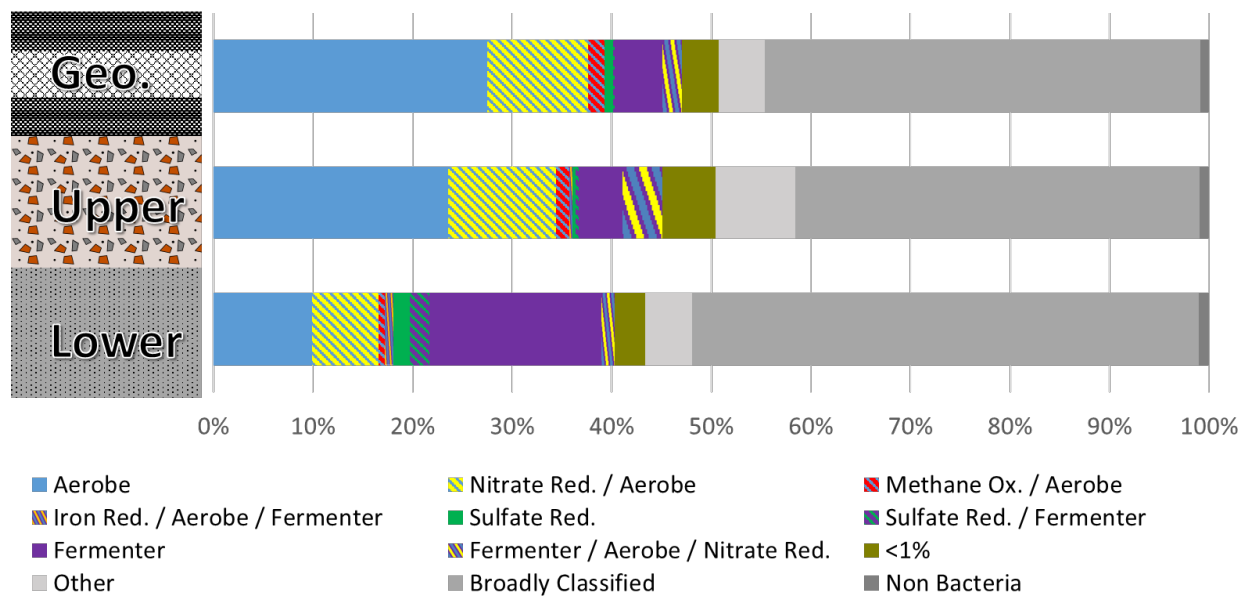


Figure 32. Average relative abundance of bacterial putative electron acceptors and donors of the main seep line samples by layer

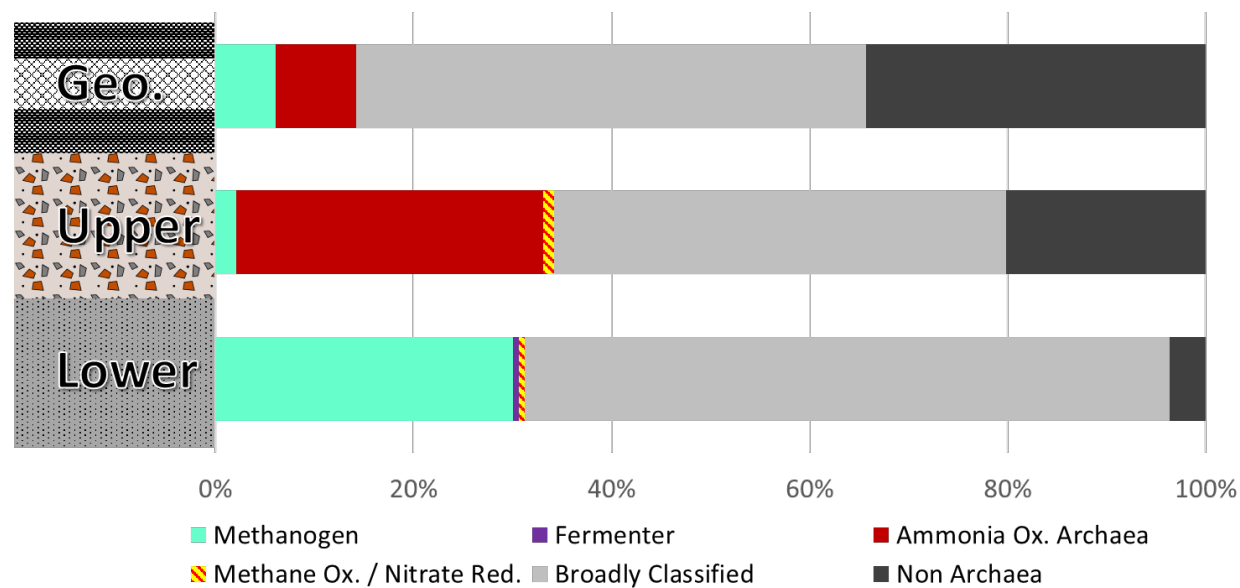


Figure 33. Average relative abundance of archaeal putative electron acceptors and donors of the main seep line samples by layer

Orange-colored water and sediments observed in the field suggest a high concentration of ferrous iron hydroxides in the system. Disturbing the sediment below the geocomposite revealed an

interface of orange colored sediment on top of gray/black sediment (Figure 34a-b). However, the laboratory iron analysis showed iron levels ranged from 0.2 mg/kg to 142 mg/kg with an average value of 12 mg/kg.

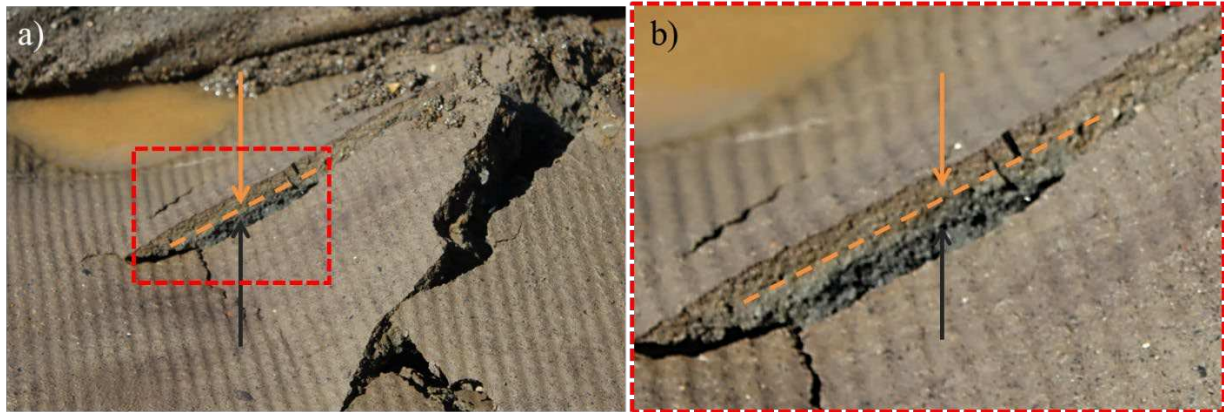


Figure 34. a) Photo of the iron interface in the upper sediment broken up with a shovel b) Close up of the interface, with the orange arrow indicating ferric iron and the black arrow indicating ferrous iron

5.5. Discussion

The results from the deconstruction event alleviated material compatibility concerns as the OBB was tested against four years of petroleum liquid loading and weather events such as ice scour. The Reno mattress layer effectively anchored the OBB in place and did not incur any significant damage over the four years. No noticeable signs of geocomposite deformation were observed during deconstruction and sampling. Geocomposite subsampling confirmed the geonet was intact and free of sediment and biofouling. The geotextile layer worked to keep native sediment out and the sand fill in. Material compatibility is important because excess clogging in the geonet would impede the flow of oxygen through this layer and reduce the OBB's degradation capacity.

No petroleum liquids were observed in the geocomposite and underlying sediment (0-10 cm). An interval of orange precipitates (presumed to be ferric iron hydroxides) was observed above and below the geocomposite. Ferric iron hydroxides/oxides are attributed to ferrous iron from the reduced petroleum-impacted plume reacting with oxygen delivered by the OBB. DRO compounds in these layers were below quantification limits for the GC/FID (2 mg/kg). Immediately below (10-20 cm), black sediment was encountered, containing visible petroleum liquids, and DRO concentrations in the low 1,000s mg/kg.

Analysis of the polar/nonpolar distribution of the petroleum constituents shows that in the lower sediments the ratio of the polar/nonpolar compounds is greater than 50%. This ratio provides a line of evidence that petroleum liquids have been oxygenated prior to arrival at the GSI. There are two hypotheses regarding the fate of the polar compounds in the upper sediment and geocomposite. One hypothesis is biodegradation. The high levels of microbial activity on the geocomposite suggest that there is a sufficient carbon source for microbes, which could be the polar compounds even though the oleophilic nature of the geocomposite may not be as effective retaining these polar compounds compared to nonpolar compounds. The second hypothesis is that these polar compounds have an increased water solubility and partition into the water. Then, tidal cycling flushes the polar compounds into the river. Pore water samples could be used to elucidate the fate of the polar metabolites.

Preliminary microbial data show that the average number of bacterial 16s transcripts in the geocomposite is larger than in the sediment layers, confirming that the geocomposite is a suitable substrate for microbes to inoculate. The relative abundance of electron acceptors/donors suggests aerobic conditions in the geocomposite and upper sediment. The greater abundance of anaerobic

microbes in the lower sediment suggests reducing conditions in this layer, visually identified by the gray/black sediment, which is to be expected of constantly saturated sediment.

A two order-of-magnitude reduction in DRO concentration occurs over a sharp orange-black interface, suggesting that the ferric iron can act as a “bank” of solid phase electron acceptors in the upper sediment. The abiotic oxidation of ferrous to ferric iron by oxygen in neutral pH water can occur in minutes (e.g., Singer and Stumm, 1970; Davison and Seed, 1983), suggesting that any ferrous iron in the groundwater would rapidly precipitate out as ferric iron upon exposure to oxygen in the geocomposite and upper sediment. Remaining oxygen in the system supports aerobic processes, including degradation. During times of low oxygen availability or in microniche anaerobic zones, ferric iron supports microbial iron-reducing petroleum liquid degradation processes. The reduced iron can then be recycled into ferric iron upon the reintroduction of oxygen.

Due to limited sample collection time, orange precipitants observed in the field were not explicitly collected for iron analysis. Local anomalies with high levels of orange precipitants, such as shown in Figure 35, are likely due to preferential flow paths delivering oxygen for the increased abiotic oxidation of iron. Iron analysis of the samples collected averaged 22 mg/kg. Low measured total iron could be due to incorrect preservation or analytical methods. Total iron reported at other contaminated sites is in the range of 100s to 1,000 mg/kg (Tuccillo et al., 1999; Vencelides et al., 2007; Heron et al., 1994). Whether the cause of high iron levels is the reduced petroleum liquid plume carrying ferrous iron to the surface where it can be oxidized, microbial iron cycling, or a combination of both is not resolved by this data.

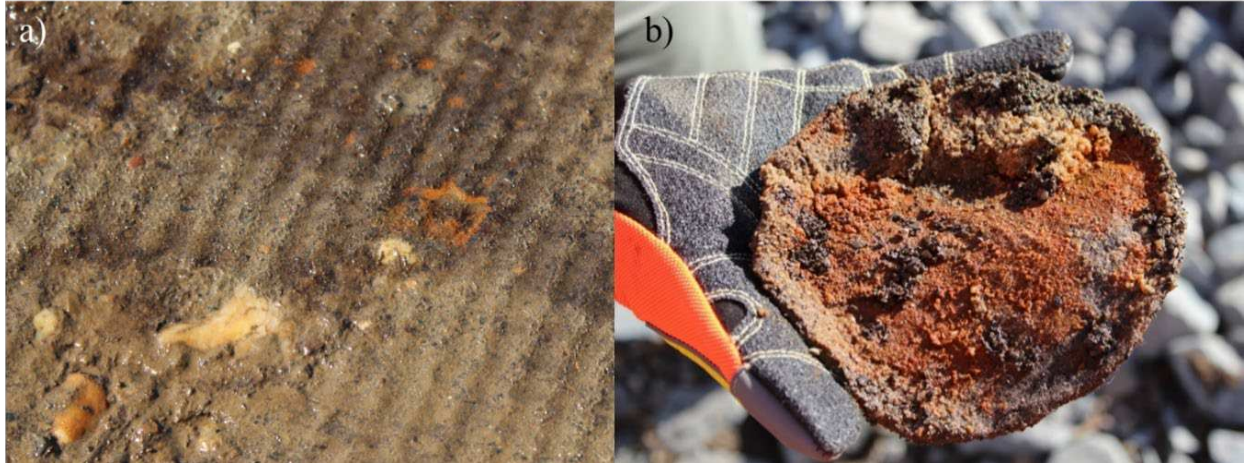


Figure 35. The orange is presumed to be iron hydroxides a) below the geocomposite b) on the geocomposite in a sample port

The original vision was that the OBB was designed to promote aerobic degradation of petroleum liquids retained by the geocomposite. Results of this sampling event suggest that at this site sufficient degradation occurs in the sediment such that petroleum liquids are degraded before reaching the OBB. In the top 20 cm of the system, the microbial community diversity includes microbes ranging from aerobes to methanogens. Iron can be cycled microbially between ferric iron as an electron acceptor and ferrous iron as an electron donor. Figure 36 graphically represents these processes. Ferrous iron and petroleum move with the groundwater towards the OBB at the surface. The geonet delivers oxygen, other electron acceptors, and nutrients to the system through tidal pumping. The oxygen converts ferrous iron into ferric iron precipitants that create an iron interface in the upper sediment. Remaining oxygen can be used for aerobic microbial processes including petroleum degradation.

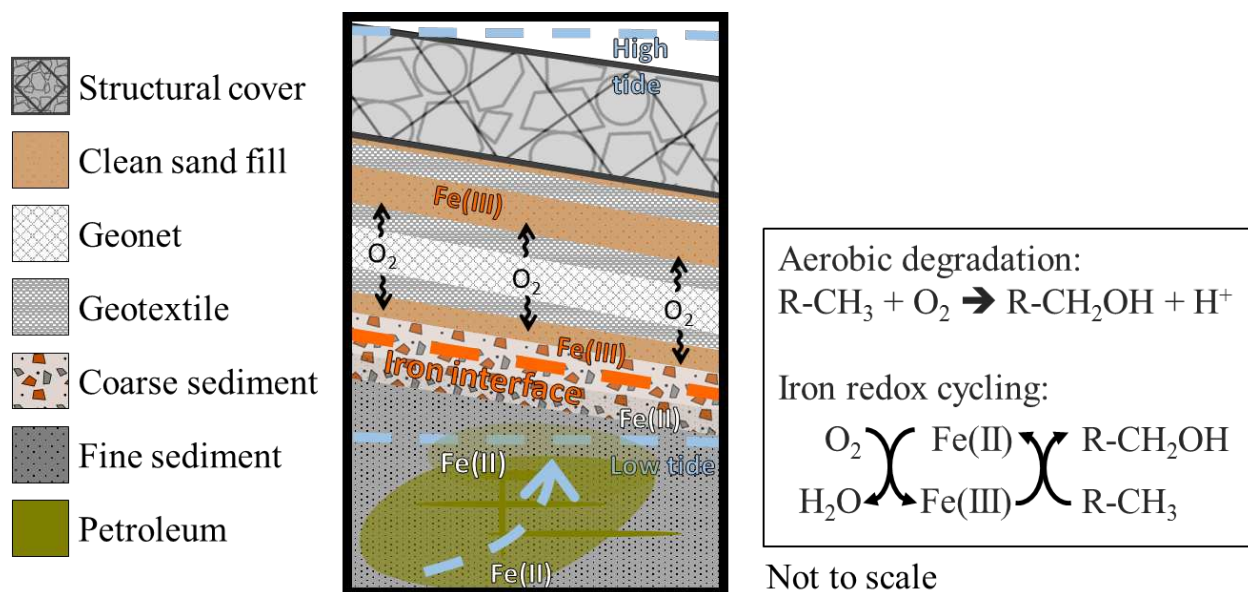


Figure 36. Revised site conceptual model for established OBBs at GSIs

The native system's ability to degrade petroleum liquids is supported by the OBB. While the geocomposite was essentially sterile upon installation, over time native microbes grew in the geocomposite as evidenced by the number 16S transcripts found on the geocomposite samples. In addition to being a substrate for microbial growth, the geocomposite also can retain petroleum liquid as an oleophilic material. The petroleum loading is analogous to an escalator carrying contamination up to the GSI, continuously depositing petroleum at the GSI (the top of the escalator). While the natural system has a degradation rate comparable to this petroleum loading rate, local anomalies can break through the system to form sheens via seeps and ebullition. However, the OBB can retain this excess petroleum to prevent sheens. Furthermore, the OBB delivers oxygen to the underlying microbial community which enhances the system's attenuation capacity.

The degradation capacity correlates to a thriving microbial population, ergo removing an established OBB might lead to increased loading to surface water due to the disruption to the microbial community. Therefore, while insight was gained from destructively sampling the demonstration OBB, removal of the old OBB likely disrupted the microbial community and reduced the degradation capacity until the new OBB acclimated. This hypothesis also demonstrates why excavating contaminated sediments can be negative. The established microbial community in the sediment is capable of petroleum degradation, but sheens can form when the system is overloaded (seeps, ebullition). Removal and replacement of the sediment would reduce the petroleum degrading microbial population, further overloading the system and creating more sheens.

5.6. Conclusions

OBBs are difficult to monitor. Challenges include collecting representative samples without compromising the integrity of the OBB and designing relevant real-time monitoring systems that are rugged enough to endure ice scour and river debris. Furthermore, visual inspections to identify sheens are problematic due to the spatial and temporal variability of sheen formation. Upstream contamination can also cause a false positive identification of a sheen unless samples are fingerprinted to identify the petroleum liquid source. Therefore, the upgrade of a demonstration OBB at a site to full-scale was a unique sampling opportunity. Valuable insight was gained through this process, and unfortunately to date, no apparent way to sample a full-scale OBB without resorting to destructive methods has been advanced. Overall, an improved understanding of the site conceptual model (SCM) for OBBs allows for better OBB designs and therefore more successful remedies.

The success of a demonstration OBB at mitigating sheens at a field site with low petroleum liquid loading lead to the installation of a full-scale remedy in the fall of 2017 and the opportunity to destructively sample the demonstration OBB after a four-year field deployment. Sample analysis revealed that a two order-of-magnitude reduction in DRO concentrations occurred over a sharp orange-black interface below the OBB, suggesting that in addition to the oxygen and nutrients delivered by the geonet, ferric iron can act as a bank of solid phase electrons to support anaerobic degradation processes. The presence of polar oxyhydrocarbons in the lower sediment provides another line of evidence of degradation. Furthermore, the number of bacterial 16s transcripts was on average higher on the geocomposite than in the native underlying sediment. These results have elucidated key insights into the conceptual model of the OBB.

Similar to how PRBs use the natural hydraulic gradient to bring contamination to the remediation treatment zone, OBBs also use natural hydraulic gradients to bring together the contamination, electron acceptors, and nutrients at GSIs. OBBs may work at non-tidal settings, but daily tidal fluctuations act as a passive pumping system and require none of the energy or capital for a hydraulic control system. Furthermore, the increased loading capacity of OBBs due to both retention and microbial degradation, as compared to finite sorption solutions, suggests a longer remediation lifetime, promoting a more sustainable use of materials for a similar installation cost (Chalfant, 2015).

OBB construction is less disruptive than other sheen remediation treatments, such as sheet pile walls. Due to a relatively simple construction procedure, OBBs can require less heavy machinery and a shorter construction window, which can be an important consideration for ecologically sensitive sites. The minimally invasive construction of OBBs also reduces the likelihood of

generating petroleum liquid discharge during construction. The low profile of the OBB can be integrated into the native environment or provide shoreline stabilization.

The OBB success at this site is likely due to the low petroleum loading rates. Though measuring petroleum fluxes at GSIs is difficult, speculative work discussed in Section 2.2 suggests that natural assimilation capacities at GSIs are two to three orders of magnitude greater than the sheen discharge rate. This rate is comparable to the two order of magnitude reduction in DRO concentrations at this site. Despite not knowing the specific petroleum loading rate, the OBB was successful. The uncertainty of petroleum loading rates can be addressed by installing additional retention layers in the OBB.

The OBB is a low-cost, sustainable sheen remedy that retains petroleum liquids and increases a site's natural degradation capacity through an increased exchange of surface water and air to deliver electron acceptors and nutrients to the contamination. Sampling of an OBB that was deployed for four years revealed that ferric iron may play a role in degradation processes by acting as a bank of solid phase electron acceptors. Future OBB work should use this revised SCM to optimize OBB systems for sites that are non-tidal, have higher loading rates, and/or have more recalcitrant petroleum liquids. Additional work should research the role of iron at these sites with sample collection focused on the ferric/ferrous iron interface. Real-time ORP monitoring with depth could be used to estimate where redox interface occurs as well as provide a line of evidence for petroleum degradation.

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6. CONCLUSIONS

This chapter reviews the sheen problem statement, laboratory visualization experiments, and a draft manuscript describing the field performance of an OBB. Lastly, suggestions for future work are presented.

6.1. Problem Statement

Sheens, a potential Clean Water Act violation, can occur at petroleum liquid facilities located near surface water. Petroleum liquids spilled into the environment spread along an air/water interface to form a sheen. The chemical and physical properties of petroleum are such that most hydrocarbons are immiscible with water. In systems with multiple immiscible fluids, the fluid with a greater affinity for the porous media is the wetting fluid which can spontaneously imbibe into small pore throats. In contrast, non-wetting fluid movement is limited by capillary pressure. In three-fluid systems, the intermediate wetting fluid spreads into a thin film or sheen to balance the interfacial tensions between fluids. LNAPL typically infiltrates down through the unsaturated zone as an intermediate wetting phase between water, the wetting fluid on the soil, and non-wetting soil gasses. At the top of the water table, LNAPL spreads out laterally (forms a sheen) about the water table (the air/water interface). Chronic rising and falling water stages (tides) cycle LNAPL between the wetting phase and the non-wetting phase, creating a largely uniform LNAPL body due to spreading during the (intermediate) wetting phase.

Sheens form at GSIs due to episodic seeps, ebullition, and erosion. In tidal settings, water table fluctuations likely create a petroleum smear zone between high and low stage. To date, no practical

method for resolving petroleum loading or degradation rates at GSIs has been documented. Loading rates were estimated using LNAPL fluxes as reported in Mahler et al. (2012). These calculations suggest a median loading rate of 15 L/m/yr. Considering typical sheen fluxes from 0.04 to 0.4 L/yr and a sheen thickness of 1 μm , the natural system's assimilation capacity is two to three orders of magnitude greater. The sediments at LNAPL-contaminated GSIs are powerful bioreactors that are capable of degrading the majority of LNAPL loading at GSIs.

Effective sheen remedies need to address all of the relevant mechanisms that create sheens. As sheens can be only molecules thick, a small volume of LNAPL can create a sheen of large areal extent. In general, sheen remedies can be prone to failure due to the complicated, heterogeneous flow of LNAPL that can bypass barriers or overload concentrated areas of absorptive material. Even a small gap in a barrier designed to preclude the movement of LNAPL can result in sheens. Organoclay, activated carbon, and other absorptive materials are limited by a finite sorption capacity and can be overloaded by LNAPL through preferential flow in a localized part of the barrier (Hawkins, 2013; Campbell, 2015).

The OBB was designed to overcome the limitations of current technologies for sheens. Using low-cost geocomposite, impacted shorelines can be covered by an OBB. The geocomposite is oleophilic, such that petroleum liquid acts as a wetting fluid that spreads out laterally on the geocomposite instead of overloading one area of a barrier and breaking through before the overall retention capacity is reached. Retained petroleum is still bioavailable for degradation, enhancing the treatment capacity of the OBB, as biodegradation reduces the petroleum mass on the OBB. Through the exchange of surface water and air due to tidal fluctuations, oxygen and nutrients are

delivered to the system to support biological treatment of the petroleum and reduce the formation of sheens.

6.2. Visualization of Multiphase Flow with an OBB in a Sand Tank

The goal of this experiment was to demonstrate 1) the flow of LNAPL as a non-wetting fluid in sand, 2) the imbibition of LNAPL as a wetting fluid on the geocomposite as the core of the OBB, and 3) the breakthrough of LNAPL after saturating the geocomposite to the point of failure (sheens on the surface water). Photographed under UV light, dyed diesel was pumped into a 1.2 m by 0.9 m water-saturated sand tank until a sheen formed. Three iterations of this experiment were required to capture the dendritic movement of non-wetting LNAPL through the sand below the geocomposite. However, as the wetting fluid, the LNAPL spreads out across almost the entirety of the geocomposite before enough LNAPL had built up and broke through into the top layer of sand and then formed a sheen on the water surface. LNAPL imbibing laterally across the geocomposite may explain why a geocomposite sample contains LNAPL even if the underlying sediment does not. Notably absent in this study was active losses of LNAPL through biologically mediated degradation of LNAPL. Also, the tank maintained a static water level. Draining the water from the bottom of the tank redistributed LNAPL throughout the sand, creating an LNAPL smear zone, thus showing the difficulty in identifying the LNAPL source in tidal settings.

6.3. OBB and Field Sediment Column Microcosm Study

This laboratory experiment was designed to estimate the aerobic and anaerobic OBB degradation rates of LNAPL in field-inoculated sediment. Unfortunately, due to a critical flaw in the experimental design, the mass balance could not be completed, and degradation rates were not

calculated. The setup was designed to emulate field conditions as best as practically possible and to observe the effects of water table fluctuations, different loading rates, and iron. Field LNAPL mixed with diesel was pumped into the bottom of glass columns loaded with field sediment and OBB layers. Columns were photographed under UV light, and the photographs were used to identify when columns formed sheens. Unfortunately, the same pumping system that pulled water out of the columns also removed LNAPL. Because a large volume of LNAPL was removed through the effluent system, insufficient LNAPL remained in the columns to flow onward onto the OBB and eventually form a sheen. Therefore, LNAPL injections were stopped when only six out of sixteen columns formed sheens. The column without any OBB layers and no water table fluctuation formed a sheen first. Next, the columns with the highest loading rates and no water table fluctuations and the uncapped column with water table fluctuations formed sheens. The final columns to form a sheen had no water table fluctuations and the middle LNAPL injection rate. These results are to be expected based on the LNAPL column study by Campbell (2017).

Though degradation rates could not be calculated from this experiment, the process did visually document the changing redox conditions in the columns. Especially apparent in columns without water table fluctuations, black precipitants, likely iron sulfides, formed in the OBB cap and in sediment surrounding LNAPL. After stopping LNAPL injections and water fluctuations, a similar precipitant was seen around the residual LNAPL in the columns with water fluctuations. Weeks later, this black precipitant in the columns without water table fluctuations began to shift to an orange precipitant. Further research into these precipitants could help design better OBB systems for sites without tidal fluctuations.

The other key lesson learned from this experiment is the role of capillary barriers. While consistently loading the columns is impossible, the sterile column was heat treated and had a negligible water content when loaded. As compared to the other columns which still had some residual moisture, this difference in water content could explain why NAPL movement was slower through the sterile column. The effects of capillary barriers may also have affected the iron-amended column. The fine particle size of the iron could have mitigated the flow of LNAPL into the OBB layers because the LNAPL never built up sufficient pressure to overcome the entry pressure of the iron-sand layer.

6.4. Field Performance of an Oleophilic Bio-Barrier for Petroleum at Groundwater/Surface Water Interfaces

The success of a 3.8 m by 9.3 m demonstration OBB resulted in replacing the demonstration OBB with a 3.8 m by 58 m full-scale OBB. The construction event was a unique opportunity to sample the different layers of an OBB after four years of field conditions. The sampling results advanced the mechanistic understanding of how OBBs work to reduce petroleum releases at GSIs.

The geocomposite layer was scanned under UV light to detect NAPL on the surface of the geocomposite, and none was observed. Geocomposite samples showed no signs of biofouling or sedimentation in the geonet and were structurally intact. Sediment samples collected from 0-10 cm (upper sediment) and 10-20 cm (lower sediment) showed no petroleum liquids in the upper sediment, but petroleum liquids were detected in the lower sediment as evident by sheens and petroleum odors after collecting lower sediment samples. Analysis using GC/FID and GC/MS compared toluene-extracted sample contamination levels against DRO standards. Results indicated that petroleum liquid levels were below quantification limits (2 mg/kg) for GC/FID for

the upper sediment and geocomposite. Concentrations in the lower sediment ranged from below quantification limits to 1,000s of mg/kg. This two order-of-magnitude change occurs over a sharp orange-black interface in the sediment below the geocomposite. The presence of orange precipitants, likely iron hydroxides, not present in the lower sediment suggests that ferrous iron from the reduced petroleum plume is oxidized and precipitates as orange ferric iron due to the increased oxygen at and below the OBB. This ferric iron is then available as an electron acceptor for microbial degradation of the hydrocarbon under anaerobic conditions. The reduced iron can then be cycled back to ferric iron upon the reintroduction of oxygen. Samples analyzed for total iron concentrations showed an average iron concentration of 12 mg/kg, one to two orders of magnitude lower than the total iron reported at other contaminated sites.

Lines of evidence supporting microbial degradation are the compositional shift of petroleum liquids into metabolites and the higher average number of bacterial 16S transcripts found on the geocomposite compared to underlying sediment. Using the GC/MS library to identify compound specific peaks, GC/MS analysis shows that the polar/nonpolar ratio of contaminants in the lower sediment is over 50%, as compared to the geocomposite layer where the relative composition was strongly nonpolar (<10% polar). The oxidation of hydrocarbons is likely the byproduct of microbial degradation. The number of bacterial 16S transcripts was higher on average in the geocomposite layer, likely due to the enhanced delivery of oxygen and nutrients from the geonet in the OBB. While the OBB was predicted to enhance biological treatment in the geocomposite layer, this evidence suggests that petroleum liquids are degraded underneath the OBB due to the low loading rate. The underlying sediment and OBB system is a bioreactor that mitigates the formation of sheens due to biodegradation processes. The OBB provides additional storage

through the oleophilic sorption capacity which retains any petroleum that escapes the native system, such as through a root or animal burrow tube.

6.5. Future Work

This section discusses recommendations for future work to advance OBBs. The unsatisfactory results of the experiment in Chapter 4 suggest further research into degradation rates. The OBB sampling in Chapter 5 suggests additional layers like activated carbon may support OBB application where dissolved-phase loading to surface water is a concern. Investigation at additional field sites will help resolve the efficiency of the OBB under a more broad set of conditions including sites without tidal water level fluctuations.

Creating a microcosm study with automated water table fluctuations is complicated. The work done in Chapter 4 provides a flawed experimental setup upon which future experiments could be based, but until an effective pumping system is designed, it is difficult to resolving aerobic/anaerobic degradation rates in the lab. For aerobic columns, air could be manually injected or pumped into the bottom of the column similar to the LNAPL for increased oxygen loading. Use of a well screen or hydrophilic filter could help mitigate LNAPL being drawn into the water effluent system but may create a preferential flow path for LNAPL in the system. Nanofiltration with filter pores so small that the LNAPL molecules cannot physically pass through the filter could be an option; however, smaller pore throats are more likely to plug. Further research into filtration used for water purification may elucidate a solution.

The success of the OBB to mitigate sheens at the site described in Chapter 5 is likely due to a low loading rate and tidal conditions. Additional layers could help adapt the OBB to a wider range of site conditions. Multiple layers of geocomposite or heavier weight geotextile would likely increase the retention capacity. A layer of activated carbon or other charged sorbent could reduce the levels of aqueous pollutants discharging into the surface water. Laboratory studies could test the best configuration for site-specific conditions.

Further research into the role of iron at GSIs with petroleum sheens may elucidate enhanced degradation processes through additional ferric iron at the GSI. Hematite or other iron oxide minerals could be placed below the geocomposite and increase the amount of iron available for degradation processes. Samples properly preserved for iron analysis collected above and below the iron interface may elucidate a pattern between ferrous and ferric iron.

Collecting representative samples from the OBB system without compromising the OBB system integrity is difficult. Ports built into the demonstration OBB design created preferential pathways for river sediment to accumulate into geocomposite sample discs. These sample discs accumulated layers of sediment up to 2 cm thick including organic material such as leaves and algae. These samples also had sediment inside the geonet which was not representative of geocomposite samples collected from the demonstration OBB. The sample ports were designed such that underlying sediment samples could be collected for analysis; however, removing too much sediment could create a cavity underneath the sample port and reduce the surface area contact between sediment and geocomposite, once again not representing normal conditions under the OBB. When pore water samples were collected during the pilot study, no aqueous petroleum compounds were detected in the water samples, suggesting that the water was primarily river water

instead of groundwater. Robust real-time monitoring systems could offer necessary lines of evidence to support OBB effectiveness. The evolution of real-time monitoring and the Internet of Things (IoT) may be the solution to OBB monitoring challenges. Coupling an internet-connected data logger with ORP, temperature, and pressure transducer sensors could provide continuous real-time data that can support SCMs with less bias than previous continuous monitoring systems.

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APPENDIX A

Table 3. Summary of Site Data and Measured LNAPL Flux Values

Site	Well	LNAPL thickness ^a (m)	LNAPL flux ^a (m/yr)	$\pm q_{LW}^a$ (m/yr)	Discharge (L/m/yr)
A	1	1.0	0.038	0.0033	25
A	2	0.63	0.092	0.018	39
A	3	1.28	0.031	0.0068	26
A	4	1.1	<0.0067	0.0067	4.9
A	5	0.38	0.047	0.019	12
B	1	0.06	0.025	0.0017	1.0
B	2	0.37	0.043	0.0029	11
B	3	0.08	0.047	0.0019	2.5
B	4	0.05	0.064	0.0041	2.1
B	5	0.57	0.032	0.0067	12
C	1	0.15	<0.0065	0.0065	0.65
C	2	0.13	<0.0065	0.0065	0.56
C	3	0.12	<0.0065	0.0065	0.52
C	4	0.40			
C	5	0.22	<0.013	0.013	1.9
C	6	0.27			
C	7	0.29			
C	8	0.30	<0.0064	0.0064	1.3
C	9	0.30	0.11	0.0064	22
C	10	0.29	0.066	0.0064	13
D	1	0.48	0.064	0.011	20
D	2	1.40	0.032	0.0064	30
D	3	0.70	0.16	0.0066	75
D	4	0.17	0.13	0.0063	15
D	5	0.15	0.23	0.014	23
D	6	0.19	0.088	0.019	11
D	7	0.55	<0.023	0.023	8.4
D	8	0.51	0.063	0.003	21
D	9	0.81	0.25	0.0082	135
D	10	0.74	0.029	0.0067	14

D	11	0.09	0.13	0.003	7.8
D	12	1.2			
D	13	1.1	2.6	2.6	1907
D	14	0.55	0.32	0.0066	117
D	15	0.47	0.18	0.006	56
D	16	0.37	0.081	0.0065	20
D	17	0.70	0.12	0.013	56
D	18	0.25	0.25	0.0055	42
D	19	0.52	0.23	0.003	80
D	20	0.50	0.33	0.013	110
D	21	0.92			
D	22	0.54	0.098	0.017	35
D	23	0.12			
E	1	1.5			
E	2	0.63	<0.071	0.071	30
E	3	0.61	<0.0090	0.009	3.7
E	4	1.5	<0.0064	0.0064	6.4
E	5	1.0	<0.016	0.016	11
E	6	1.2	<0.033	0.033	26
F	1	0.45	0.010		3.0
F	2	0.23	0.028		4.3
F	3	0.17	0.20		23
F	4	0.20	0.064		8.5
F	5	0.29	0.58		112
F	6	0.17	0.076		8.6
F	7	0.55	0.48		176
G		0.14	0.059		5.5
Mean		0.52	0.15	0.07	68
Median		0.45	0.064	0.007	15
25th Quartile			0.027		5.2
75th Quartile			0.13		33

^aData from Mahler et al. (2012)

The goal of these calculations is to provide ballpark loading estimation rates for LNAPL at GSIs
 From Mahler (2012), we have a table of LNAPL fluxes (m/yr) and LNAPL thickness in the well
 To calculate the volumetric flow rate per unit meter width shoreline per year:

$$\text{Discharge} = \frac{\text{LNAPL}_{\text{flux}} \cdot b_{\text{LNAPL}} \cdot 2\text{Radius}_{\text{well}}}{\alpha \cdot 2 \cdot \text{Radius}_{\text{well}}} = \frac{\text{LNAPL}_{\text{flux}} \cdot b_{\text{LNAPL}}}{\alpha}$$

Where LNAPL_flux is the unit volume flow per unit area per time; b_LNAPL is LNAPL thickness in monitoring well; and Radius_well is the well radius

Using Mahler(2012) data and an assumed α of 1.5, the median discharge rate is 15 L/m/yr
 Mahler LNAPL flux values (m/yr) were multiplied by the corresponding LNAPL thickness (m) then divided by 1.5 (α) and multiplied by 1000 to get an answer in L/m/yr
 The 25th and 75th median values provide a better range that does not include the extremely low and high "outliers" in the data set that skew the mean.

$$\text{Discharge} := 15 \cdot \frac{\text{L}}{\text{m} \cdot \text{yr}} = 41 \cdot \frac{\text{mL}}{\text{m} \cdot \text{day}} \quad \text{Discharge}_{25} := 5.2 \cdot \frac{\text{L}}{\text{m} \cdot \text{yr}} \quad \text{Discharge}_{75} := 33 \cdot \frac{\text{L}}{\text{m} \cdot \text{yr}}$$

NOAA(2016) describes a sheen as a thin layer of oil less than 0.005 mm (5 μm) thick

$$b := 0.005 \cdot \text{mm} \quad \frac{\text{Discharge}}{b} = 3000 \cdot \frac{\text{m}^2}{\text{m} \cdot \text{yr}} \quad \frac{\text{Discharge}}{b} = 8 \cdot \frac{\text{m}^2}{\text{m} \cdot \text{day}}$$

A thinner sheen would create a sheen of larger areal extent

$$b_2 := 0.001 \cdot \text{mm} \quad \frac{\text{Discharge}}{b_2} = 15000 \cdot \frac{\text{m}^2}{\text{m} \cdot \text{yr}} \quad \frac{\text{Discharge}}{b_2} = 41 \cdot \frac{\text{m}^2}{\text{m} \cdot \text{day}}$$

Seeing as sheens of such large areal extent do not form on a regular basis at GSIs, the natural systems degradation capacity must be on a similar order of magnitude as this 15 L/m/year loading rate.

For an assumed shoreline of 10 m, an average sheen thickness of 0.001 mm, and a sheen area of 0.1 m² to 1 m² seen daily, this equates to a loading rate of 0.014 to 0.14 L/yr

$$\text{Sheen}_{\text{low}} := \frac{b_2 \cdot 0.1 \cdot \text{m}^2}{\text{day}} = 0.04 \cdot \frac{\text{L}}{\text{yr}} \quad \text{Sheen}_{\text{high}} := \frac{b_2 \cdot 1 \cdot \text{m}^2}{\text{day}} = 0.4 \cdot \frac{\text{L}}{\text{yr}}$$

$$\text{Sheen}_{\text{low}} = 2.642 \times 10^{-5} \frac{\text{gal}}{\text{day}} \quad \text{Sheen}_{\text{high}} = 2.64 \times 10^{-4} \frac{\text{gal}}{\text{day}}$$

Assuming the high and low sheen rates correspond with the 25th and 75th discharge rates, a GSI assimilation rate can be calculated

$$\text{Discharge}_{75} - \frac{\text{Sheen}_{\text{high}}}{10 \cdot \text{m}} = 33 \frac{1}{\text{m}} \cdot \frac{\text{L}}{\text{yr}} \quad \text{Discharge}_{25} - \frac{\text{Sheen}_{\text{low}}}{10 \cdot \text{m}} = 5.2 \frac{1}{\text{m}} \cdot \frac{\text{L}}{\text{yr}}$$

Because the sheen discharge rate is 2-3 orders of magnitude lower than the NAPL discharge rate, this suggests that the GSI assimilation rate must be on a similar order of magnitude as the NAPL discharge rate

APPENDIX B

Table 4. Diesel Range Organic (DRO) Concentration (mg/kg sample dry weight)

Sample Location	Lower (0-10 cm)	Upper (10-20 cm)	Geocomposite
1	BQL	BQL	BQL
2	522	BQL	BQL
3	2,852	BQL	BQL
4	2,287	BQL	BQL
5	2,566	BQL	BQL
6	2,757	BQL	BQL
7	5,288	BQL	BQL
8	3,571	BQL	BQL
9	468	BQL	BQL
10	744	BQL	BQL
11	1,405	BQL	BQL
12	BQL	BQL	BQL
13	BQL	BQL	BQL
14	BQL	BQL	BQL

BQL – Below Quantification Limits – 2 mg/kg

Table 5. Relative Polar Peak Area (%)

Sample Location	Lower (0-10 cm)	Upper (10-20 cm)	Geocomposite
1	7	BQL	100
2	5	BQL	79
3	3	BQL	59
4	6	BQL	63
5	2	BQL	59
6	4	BQL	60
7	5	BQL	63
8	5	BQL	62
9	6	BQL	81
10	5	BQL	82
11	6	BQL	97
12	1	BQL	100
13	3	BQL	100
14	1	BQL	93

BQL – Below Quantification Limits – 6 mg/kg

Table 6. Iron Concentrations (mg/kg sample dry weight)

Sample Location	Deionized water			Acidified deionized water		
	Lower (0-10 cm)	Upper (10-20 cm)	Geo-composite	Lower (0-10 cm)	Upper (10-20 cm)	Geo-composite
1	9.0	2.2	102	4.3	4.4	52
2	10	11	37	2.5	6.3	46
3	14	14	85	6.8	6.5	47
4	8.8	0.2	142	7.4	5.1	63
5	5.9	1.6	99	6.2	6.9	50
6	12	1.9	60	5.7	5.7	26
7	16	1.4	71	8.2	5.2	41
8	6.8	5.3	26	3.6	5.3	17
9	17	17	45	6.4	8.1	20
10	29	16	53	11	13	26
11	11	2.0	46	7.9	6.5	13
12	16	5.3	34	4.8	1.3	25
13	14	2.8	93	5.6	4.0	30
14	14	6.8	40	6.8	5.1	34

Table 7. Bacterial and Archaeal Abundance (number of 16S transcripts per g sample)

	Bacteria			Archaea			Total		
Sample Location	Lower (0-10 cm)	Upper (10-20 cm)	Geo-composite	Lower (0-10 cm)	Upper (10-20 cm)	Geo-composite	Lower (0-10 cm)	Upper (10-20 cm)	Geo-composite
2	9.8E+06	7.5E+08	1.9E+09	3.7E+05	1.0E+06	1.2E+06	1.0E+07	7.5E+08	1.9E+09
4	3.3E+08	4.6E+09	1.6E+09	2.4E+06	2.6E+06	2.9E+05	3.3E+08	4.6E+09	1.6E+09
6	4.6E+07	5.9E+08	1.2E+09	1.4E+06	4.3E+05	1.9E+06	4.8E+07	5.9E+08	1.2E+09
8	1.8E+09	1.9E+08	1.7E+09	2.6E+07	9.8E+05	1.1E+06	1.8E+09	2.0E+08	1.7E+09
11	1.6E+08	4.9E+09	2.0E+09	3.9E+06	1.5E+06	0.0E+00	1.7E+08	4.9E+09	2.0E+09
12	2.2E+06	5.6E+06	1.3E+09	4.7E+05	2.7E+06	4.6E+04	2.7E+06	8.3E+06	1.3E+09

Table 8. Average Bacterial Putative Electron Acceptor/Donor per Layer for Main Seep Line (%)

	Lower (0-10 cm)	Upper (10-20 cm)	Geo- composite
Aerobe	9.79	23.51	27.13
Nitrate Red./Aerobe	6.53	10.83	9.98
Nitrate Red.	0.00	0.10	0.10
Methane Ox./Aerobe	0.66	1.34	1.61
Methane Ox./Nitrite Red.	0.06	0.00	0.10
Iron Ox./Aerobe	0.31	0.55	0.26
Iron Ox./Aerobe/Nitrate Red.	0.80	0.23	1.25
Iron Ox./Aerobe/Iron Red.	0.06	0.60	0.00
Iron Ox./Aerobe/Nitrate Red./Fermenter	0.00	0.23	0.00
Iron Red.	0.26	0.86	0.99
Iron Red./Aerobe	0.00	0.35	0.09
Iron Red./Aerobe/Nitrate Red.	0.06	0.22	0.00
Iron Red. / Nitrate Red.	0.00	0.00	0.00
Iron Red./Aerobe/Nitrate Red./Fermenter	0.21	0.65	0.69
Iron Red./Aerobe/Fermenter	0.86	0.31	0.00
Iron Red./Nitrate Red./Fermenter	0.00	0.11	0.00
Iron Red./Sulfate Red.	0.06	0.00	0.10
Iron Red./Fermenter	0.65	0.52	0.61
Iron Red./Sulfate Red./Fermenter	0.00	0.22	0.00
Sulfate Red.	1.61	0.35	0.90
Sulfate Red./Fermenter	1.94	0.27	0.14
Sulfate Red./Nitrate Red./Fermenter	1.17	0.00	0.00
Fermenter	17.00	4.41	4.71
Fermenter/Aerobe	0.19	0.30	0.33
Fermenter/Nitrate Red.	0.26	0.34	0.33
Fermenter/Aerobe/Nitrate Red.	1.32	3.96	1.97
Broadly Classified	50.17	40.49	43.11
Other	4.97	8.24	4.73
Non Bacteria	1.06	0.99	0.89
<1%	2.99	5.37	3.60
Total	100.00	100.00	100.00

Table 9. Average Archaeal Putative Electron Acceptor/Donor per Layer for Main Seep Line (%)

	Lower (0-10 cm)	Upper (10-20 cm)	Geocomposite
Methanogen	30.05	2.08	6.09
Ammonia Ox. Archaea	0.00	31.05	8.10
Methane Ox./Nitrate Red.	0.64	1.08	0.00
Fermenter	0.54	0.00	0.00
Broadly Classified	65.10	45.59	51.53
Non Archaea	3.66	20.20	34.29
Total	100.00	100.00	100.00

APPENDIX C

Aerobic Bacteria

Acetobacteraceae	Sievers, M. and Swings, J. (2015). Acetobacteraceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00174
Acidipila	Okamura, K., Kawai, A., Yamada, T., & Hiraishi, A. (2011). <i>Acidipila rosea</i> gen. nov., sp. nov., an acidophilic chemoorganotrophic bacterium belonging to the phylum Acidobacteria. <i>FEMS microbiology letters</i> , 317(2), 138-142. doi:10.1111/j.1574-6968.2011.02224.x Jiang, Y. W., Wang, J., Chen, M. H., Lv, Y. Y., & Qiu, L. H. (2016). <i>Acidipila dinghuensis</i> sp. nov., an acidobacterium isolated from forest soil. <i>International journal of systematic and evolutionary microbiology</i> , 66(1), 76-83. doi:10.1099/ijsem.0.000676
Acidisoma	Belova, S. E., Pankratov, T. A., Detkova, E. N., Kaparullina, E. N., & Dedysh, S. N. (2009). <i>Acidisoma tundrae</i> gen. nov., sp. nov. and <i>Acidisoma sibiricum</i> sp. nov., two acidophilic, psychrotolerant members of the Alphaproteobacteria from acidic northern wetlands. <i>International journal of systematic and evolutionary microbiology</i> , 59(9), 2283-2290. doi:10.1099/ijse.0.009209-0
Acidisphaera	Hiraishi, A. (2015). <i>Acidisphaera</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00878
Acidocella	Hiraishi, A. (2015). <i>Acidocella</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00879
Acidothermaceae	Normand, P., Berry, A. and Benson, D. R. (2015). Acidothermaceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00017
Acidothermus	Normand, P., Berry, A. and Benson, D. R. (2015). <i>Acidothermus</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00039
Acinetobacter	Juni, E. (2015). <i>Acinetobacter</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01203
Actinoallomurus	Tamura, T., Ishida, Y., Nozawa, Y., Otoguro, M., & Suzuki, K. I. (2009). Transfer of <i>Actinomadura spadix</i> Nonomura and Ohara 1971 to <i>Actinoallomurus spadix</i> gen. nov., comb. nov., and description of <i>Actinoallomurus amamiensis</i> sp. nov., <i>Actinoallomurus caesius</i> sp. nov., <i>Actinoallomurus coprocola</i> sp. nov., <i>Actinoallomurus fulvus</i> sp. nov., <i>Actinoallomurus iriomotensis</i> sp. nov., <i>Actinoallomurus luridus</i> sp. nov., <i>Actinoallomurus purpureus</i> sp. nov. and <i>Actinoallomurus yoronensis</i> sp. nov. <i>International journal of systematic and evolutionary microbiology</i> , 59(8), 1867-1874. doi:10.1099/ijse.0.006858-0 Tang, Y. L., Lin, H. P., Xie, Q. Y., Li, L., Peng, F., Deng, Z., & Hong, K. (2013). <i>Actinoallomurus acanthiterrae</i> sp. nov., an actinomycete isolated from rhizosphere soil of the mangrove plant <i>Acanthus ilicifolius</i> . <i>International journal of systematic and evolutionary microbiology</i> , 63(5), 1874-1879. doi:10.1099/ijse.0.043380-0

Actinoplanes	Vobis, G. , Schäfer, J. and Kämpfer, P. (2015). Actinoplanes. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00139
Adhaeribacter	Rickard, A. H., Stead, A. T., O'May, G. A., Lindsay, S., Banner, M., Handley, P. S., & Gilbert, P. (2005). Adhaeribacter aquaticus gen. nov., sp. nov., a Gram-negative isolate from a potable water biofilm. <i>International journal of systematic and evolutionary microbiology</i> , 55(2), 821-829. doi:10.1099/ijs.0.63337-0 Weon, H. Y., Kwon, S. W., Son, J. A., Kim, S. J., Kim, Y. S., Kim, B. Y., & Ka, J. O. (2010). Adhaeribacter aerophilus sp. nov., Adhaeribacter aerolatus sp. nov. and Segetibacter aerophilus sp. nov., isolated from air samples. <i>International journal of systematic and evolutionary microbiology</i> , 60(10), 2424-2429. doi:10.1099/ijs.0.018374-0
Agaricicola	Chu, J. N., Arun, A. B., Chen, W. M., Chou, J. H., Shen, F. T., Rekha, P. D., Kämpfer, P., Young, L. S., Lin, S. Y., & Young, C. C. (2010). Agaricicola taiwanensis gen. nov., sp. nov., an alphaproteobacterium isolated from the edible mushroom Agaricus blazei. <i>International journal of systematic and evolutionary microbiology</i> , 60(9), 2032-2035. doi:10.1099/ijs.0.016485-0
Aggregicoccus	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4 3
Agitococcus	Franzmann, P. D., & Skerman, V. B. D. (1981). Agitococcus lubricus gen. nov. sp. nov., a lipolytic, twitching coccus from freshwater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 31(2), 177-183. doi:10.1099/00207713-31-2-177
Algisphaera	Yoon, J., Jang, J. H., & Kasai, H. (2014). Algisphaera agarilytica gen. nov., sp. nov., a novel representative of the class Phycisphaerae within the phylum Planctomycetes isolated from a marine alga. <i>Antonie Van Leeuwenhoek</i> , 105(2), 317-324. doi:10.1007/s10482-013-0076-1
Alsobacter	Bao, Z., Sato, Y., Fujimura, R., & Ohta, H. (2014). Alsobacter metallidurans gen. nov., sp. nov., a thallium-tolerant soil bacterium in the order Rhizobiales. <i>International journal of systematic and evolutionary microbiology</i> , 64(3), 775-780. doi:10.1099/ijs.0.054783-0
Aminobacter	Urakami, T. (2015). Aminobacter. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00835
Angustibacter	Tamura, T., Ishida, Y., Otoguro, M., Yamamura, H., Hayakawa, M., & Suzuki, K. I. (2010). Angustibacter luteus gen. nov., sp. nov., isolated from subarctic forest soil. <i>International journal of systematic and evolutionary microbiology</i> , 60(10), 2441-2445. doi:10.1099/ijs.0.019448-0 Kim, S. J., Jang, Y. H., Hamada, M., Tamura, T., Ahn, J. H., Weon, H. Y., Suzuki, K. I., & Kwon, S. W. (2013). Angustibacter aerolatus sp. nov., isolated from air. <i>International journal of systematic and evolutionary microbiology</i> , 63(2), 610-615. doi: 10.1099/ijs.0.042218-0 Lee, S. D. (2013). Angustibacter peucedani sp. nov., isolated from rhizosphere soil. <i>International journal of systematic and evolutionary microbiology</i> , 63(2), 744-750. doi:10.1099/ijs.0.042275-0 Ko, D. H., & Lee, S. D. (2017). Angustibacter speluncae sp. nov., isolated from a lava cave stalactite. <i>International journal of systematic and evolutionary microbiology</i> , 67(9), 3283-3288. doi:10.1099/ijsem.0.002108
Aquicella	Albuquerque, L., Rainey, F. A. and Costa, M. S. (2018). Aquicella. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01465

Aquimonas	Saha, P., Krishnamurthi, S., Mayilraj, S., Prasad, G. S., Bora, T. C., & Chakrabarti, T. (2005). <i>Aquimonas voraii</i> gen. nov., sp. nov., a novel gammaproteobacterium isolated from a warm spring of Assam, India. <i>International journal of systematic and evolutionary microbiology</i> , 55(4), 1491-1495. doi:10.1099/ijs.0.63552-0
Aridibacter	Huber, K. J., Foesel, B. U., Pascual, J. and Overmann, J. (2017). <i>Aridibacter</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01427 Huber, K. J., Wüst, P. K., Rohde, M., Overmann, J., & Foesel, B. U. (2014). <i>Aridibacter famidurans</i> gen. nov., sp. nov. and <i>Aridibacter kavangonensis</i> sp. nov., two novel members of subdivision 4 of the Acidobacteria isolated from semiarid savannah soil. <i>International journal of systematic and evolutionary microbiology</i> , 64(6), 1866-1875. doi:10.1099/ijs.0.060236-0
Armatimonadetes	Tamaki, H., Tanaka, Y., Matsuzawa, H., Muramatsu, M., Meng, X. Y., Hanada, S., Mori, K. & Kamagata, Y. (2011). <i>Armatimonas rosea</i> gen. nov., sp. nov., of a novel bacterial phylum, Armatimonadetes phyl. nov., formally called the candidate phylum OP10. <i>International journal of systematic and evolutionary microbiology</i> , 61(6), 1442-1447. doi:10.1099/ijs.0.025643-0 Lee K.C.Y., Dunfield P.F., Stott M.B. (2014) The Phylum Armatimonadetes. In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E., Thompson F. (eds) <i>The Prokaryotes</i> . Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-38954-2_388
Armatimonas	Tamaki, H., Tanaka, Y., Matsuzawa, H., Muramatsu, M., Meng, X. Y., Hanada, S., Mori, K., & Kamagata, Y. (2011). <i>Armatimonas rosea</i> gen. nov., sp. nov., of a novel bacterial phylum, Armatimonadetes phyl. nov., formally called the candidate phylum OP10. <i>International journal of systematic and evolutionary microbiology</i> , 61(6), 1442-1447. doi:10.1099/ijs.0.025643-0
Aureibacter	Yoon, J., Adachi, K., Park, S., Kasai, H., & Yokota, A. (2011). <i>Aureibacter tunicatorum</i> gen. nov., sp. nov., a marine bacterium isolated from a coral reef sea squirt, and description of Flammeovirgaceae fam. nov. <i>International journal of systematic and evolutionary microbiology</i> , 61(10), 2342-2347. doi:10.1099/ijs.0.027573-0
Bacteriovorax	Baer, M. L., Ravel, J., Chun, J., Hill, R. T., & Williams, H. N. (2000). A proposal for the reclassification of <i>Bdellovibrio stolpii</i> and <i>Bdellovibrio starrii</i> into a new genus, <i>Bacteriovorax</i> gen. nov. as <i>Bacteriovorax stolpii</i> comb. nov. and <i>Bacteriovorax starrii</i> comb. nov., respectively. <i>International journal of systematic and evolutionary microbiology</i> , 50(1), 219-224. doi:10.1099/00207713-50-1-219 Williams, H. N. and Baer, M. L. (2015). <i>Bacteriovorax</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01006
Bauldia	Yee, B., Oertli, G. E., Fuerst, J. A., & Staley, J. T. (2010). Reclassification of the polyphyletic genus <i>Prosthecomicrobium</i> to form two novel genera, <i>Vasilyevaea</i> gen. nov. and <i>Bauldia</i> gen. nov. with four new combinations: <i>Vasilyevaea enhydra</i> comb. nov., <i>Vasilyevaea mishustinii</i> comb. nov., <i>Bauldia consociata</i> comb. nov. and <i>Bauldia litoralis</i> comb. nov. <i>International journal of systematic and evolutionary microbiology</i> , 60(12), 2960-2966. doi:10.1099/ijs.0.018234-0
Bdellovibrionales	McCauley, E. P., Haltli, B., & Kerr, R. G. (2015). Description of <i>Pseudobacteriovorax antillogorgiicola</i> gen. nov., sp. nov., a bacterium isolated from the gorgonian octocoral <i>Antillogorgia elisabethae</i> , belonging to the family <i>Pseudobacteriovoracaceae</i> fam. nov., within the order <i>Bdellovibrionales</i> . <i>International journal of systematic and evolutionary microbiology</i> , 65(2), 522-530. doi: 10.1099/ijs.0.066266-0
Beijerinckiaceae	Dedysh, S. N. and Dunfield, P. F. (2016). <i>Beijerinckiaceae</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00164.pub2

Bergeyella	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S. (2015). <i>Bergeyella</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00297 Hugo C.J., Bruun B., Jooste P.J. (2006) The Genera <i>Bergeyella</i> and <i>Weeksellia</i> . In: Dworkin M., Falkow S., Rosenberg E., Schleifer K.H., Stackebrandt E. (eds) <i>The Prokaryotes</i> . Springer, New York, NY. doi:10.1007/0-387-30747-8_18
Blastocatella	Foesel, B. U., Rohde, M., & Overmann, J. (2013). <i>Blastocatella fastidiosa</i> gen. nov., sp. nov., isolated from semiarid savanna soil–The first described species of <i>Acidobacteria</i> subdivision 4. <i>Systematic and applied microbiology</i> , 36(2), 82-89. doi:10.1016/j.syapm.2012.11.002 Foesel, B. U., Huber, K. J., Pascual, J. and Overmann, J. (2017). <i>Blastocatella</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01428
Blastochloris	Imhoff, J. F. (2015). <i>Blastochloris</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00815
Blastococcus	Stackebrandt, E. and Schumann, P. (2015). <i>Blastococcus</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00043
Brevundimonas	Vancanneyt, M. , Segers, P. , Abraham, W. and Vos, P. D. (2015). <i>Brevundimonas</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00791
Bryobacter	Kulichevskaya, I. S., Suzina, N. E., Liesack, W., & Dedysh, S. N. (2010). <i>Bryobacter aggregatus</i> gen. nov., sp. nov., a peat-inhabiting, aerobic chemo-organotroph from subdivision 3 of the <i>Acidobacteria</i> . <i>International journal of systematic and evolutionary microbiology</i> , 60(2), 301-306. doi:10.1099/ijs.0.013250-0
Burkholderiaceae	Garrity, G. M., Bell, J. A. and Lilburn, T. (2015). <i>Burkholderiaceae</i> fam. nov. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00181
Byssovorax	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. <i>Deltaproteobacteria</i> class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Caenispirillum	Huq, M. A. (2018). <i>Caenispirillum humi</i> sp. nov., a bacterium isolated from the soil of Korean pine garden. <i>Archives of microbiology</i> , 200(2), 343-348. doi:10.1007/s00203-017-1449-z Yoon, J. H., Kang, S. J., Park, S., & Oh, T. K. (2007). <i>Caenispirillum bisanense</i> gen. nov., sp. nov., isolated from sludge of a dye works. <i>International journal of systematic and evolutionary microbiology</i> , 57(6), 1217-1221. doi:10.1099/ijs.0.64910-0
Candidatus Berkiella	Mehari, Y. T., Hayes, B. J., Redding, K. S., Mariappan, P. V., Gunderson, J. H., Farone, A. L., & Farone, M. B. (2016). Description of ‘ <i>Candidatus Berkiella aquae</i> ’ and ‘ <i>Candidatus Berkiella cookevillensis</i> ’, two intranuclear bacteria of freshwater amoebae. <i>International journal of systematic and evolutionary microbiology</i> , 66(2), 536-541. doi:10.1099/ijsem.0.000750
Candidatus Koribacter	Campbell B.J. (2014) The Family <i>Acidobacteriaceae</i> . In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E., Thompson F. (eds) <i>The Prokaryotes</i> . Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-38954-2_160
Candidatus Magnetobacterium	Spring, S. and Schleifer, K. (2015). <i>Candidatus Magnetobacterium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P.

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Candidatus Nitrotoga	Alawi, M., Lipski, A., Sanders, T., & Spieck, E. (2007). Cultivation of a novel cold-adapted nitrite oxidizing betaproteobacterium from the Siberian Arctic. <i>The ISME journal</i> , 1(3), 256. doi:10.1038/ismej.2007.34
Candidatus Planktophilia	Jezbera, J., Sharma, A. K., Brandt, U., Doolittle, W. F., & Hahn, M. W. (2009). ‘Candidatus Planktophilia limnetica’, an actinobacterium representing one of the most numerically important taxa in freshwater bacterioplankton. <i>International journal of systematic and evolutionary microbiology</i> , 59(11), 2864-2869. doi:10.1099/ijs.0.010199-0
Candidatus Solibacter	Dedysh, S. N., Kulichevskaya, I. S., Huber, K. J., & Overmann, J. (2017). Defining the taxonomic status of described subdivision 3 Acidobacteria: proposal of Bryobacteraceae fam. nov. <i>International journal of systematic and evolutionary microbiology</i> , 67(2), 498-501. doi:10.1099/ijsem.0.001687
Caulobacteraceae	Garrity, G. M., Bell, J. A. and Lilburn, T. (2015). Caulobacteraceae. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00162
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Chelatococcus	Egli, T. W. and Auling, G. (2015). Chelatococcus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00796
Chondromyces	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Chryseolinea	Kim, J. J., Alkawally, M., Brady, A. L., Rijpstra, W. I. C., Damsté, J. S. S., & Dunfield, P. F. (2013). Chryseolinea serpens gen. nov., sp. nov., a member of the phylum Bacteroidetes isolated from soil. <i>International journal of systematic and evolutionary microbiology</i> , 63(2), 654-660. doi:10.1099/ijs.0.039404-0
Clavibacter	Saddler, G. S. and Kerr, E. M. (2015). Clavibacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00094
Cohnella	Kämpfer, P. , busse, H. and Tindall, B. J. (2015). Cohnella. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00551
Conexibacteraceae	Schumann, P. (2015). Conexibacteraceae. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00053 Albuquerque L., da Costa M.S. (2014) The Families Conexibacteraceae, Patulibacteraceae and Solirubrobacteraceae. In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E., Thompson F. (eds) <i>The Prokaryotes</i> . Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-30138-4_200

Conyzicola	Kim, S. B. (2017). Conyzicola. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01300
Corallococcus	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Coxiella	Drancourt, M. and Raoult, D. (2015). Coxiella. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01176 Price, C. T., Al-Quadani, T., Santic, M., Rosenshine, I., & Kwai, Y. A. (2011). Host proteasomal degradation generates amino acids essential for intracellular bacterial growth. <i>Science</i> , 334(6062), 1553-1557. doi:10.1126/science.1212868
Cystobacter	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Cystobacteraceae	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Daeguia	Yoon, J. H., Kang, S. J., Park, S., & Oh, T. K. (2008). Daeguia caeni gen. nov., sp. nov., isolated from sludge of a textile dye works. <i>International journal of systematic and evolutionary microbiology</i> , 58(1), 168-172. doi:10.1099/ijs.0.65483-0
Defluviicoccus	Burow, L. C., Kong, Y., Nielsen, J. L., Blackall, L. L., & Nielsen, P. H. (2007). Abundance and ecophysiology of Defluviicoccus spp., glycogen-accumulating organisms in full-scale wastewater treatment processes. <i>Microbiology</i> , 153(1), 178-185. doi:10.1099/mic.0.2006/001032-0 Maszenan, A. M., Seviour, R. J., Patel, B. K. C., Janssen, P. H., & Wanner, J. (2005). Defluvicoccus vanus gen. nov., sp. nov., a novel Gram-negative coccus/coccobacillus in the 'Alphaproteobacteria' from activated sludge. <i>International journal of systematic and evolutionary microbiology</i> , 55(5), 2105-2111. doi:10.1099/ijs.0.02332-0
Deinococcus	Battista, J. R. and Rainey, F. A. (2015). Deinococcaceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00092
Derxia	Kennedy, C. (2015). Derxia. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00929
Desemzia	Stackebrandt, E. (2015). Desemzia. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00594
Dichotomicrobium	Hirsch, P. (2015). Dichotomicrobium. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00817
Dokdonella	Yoon, J. H., Kang, S. J., & Oh, T. K. (2006). Dokdonella koreensis gen. nov., sp. nov., isolated from soil. <i>International journal of systematic and evolutionary microbiology</i> , 56(1), 145-150. doi:10.1099/ijs.0.63802-0 Ten, L. N., Jung, H. M., Im, W. T., Oh, H. W., Yang, D. C., Yoo, S. A., & Lee, S. T. (2009). Dokdonella ginsengisoli sp. nov., isolated from soil from a ginseng field, and emended description of the genus Dokdonella. <i>International journal of systematic and evolutionary microbiology</i> , 59(8), 1947-1952. doi:10.1099/ijs.0.004945-0 Li, Y., Zhang, J., Chen, Q., Yang, G., Cai, S., He, J., Zhou, S., & Li, S. P. (2013). Dokdonella kunshanensis sp. nov., isolated from activated sludge, and emended

	description of the genus <i>Dokdonella</i> . <i>International journal of systematic and evolutionary microbiology</i> , 63(4), 1519-1523. doi:10.1099/ijs.0.041798-0
Dongia	Liu, Y., Jin, J. H., Liu, Y. H., Zhou, Y. G., & Liu, Z. P. (2010). <i>Dongia mobilis</i> gen. nov., sp. nov., a new member of the family Rhodospirillaceae isolated from a sequencing batch reactor for treatment of malachite green effluent. <i>International journal of systematic and evolutionary microbiology</i>, 60(12), 2780-2785. doi:10.1099/ijs.0.020347-0 Baik, K. S., Hwang, Y. M., Choi, J. S., Kwon, J., & Seong, C. N. (2013). <i>Dongia rigui</i> sp. nov., isolated from freshwater of a large wetland in Korea. <i>Antonie van Leeuwenhoek</i>, 104(6), 1143-1150. doi:10.1007/s10482-013-0036-9 Kim, D. U., Lee, H., Kim, H., Kim, S. G., & Ka, J. O. (2016). <i>Dongia soli</i> sp. nov., isolated from soil from Dokdo, Korea. <i>Antonie van Leeuwenhoek</i>, 109(10), 1397-1402. doi:10.1007/s10482-016-0738-x
Endoecteinascidia	Schofield, M. M., Jain, S., Porat, D., Dick, G. J., and Sherman, D. H. (2015), Metagenomic analysis of the ET-743 producer. <i>Environ Microbiol</i> , 17: 3964-3975. doi:10.1111/1462-2920.12908
Enhygromyxa	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Ensifer	Balkwill, D. L. (2015). <i>Ensifer</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00846
Erythrobacteraceae	Tonon, L. A. C., Moreira, A. P. B., & Thompson, F. (2014). The family Erythrobacteraceae. In <i>The Prokaryotes</i> (pp. 213-235). Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-30197-1_376
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Ferruginibacter	Lim, J. H., Baek, S. H., & Lee, S. T. (2009). <i>Ferruginibacter alkalilentus</i> gen. nov., sp. nov. and <i>Ferruginibacter lapsinans</i> sp. nov., novel members of the family 'Chitinophagaceae' in the phylum Bacteroidetes, isolated from freshwater sediment. <i>International journal of systematic and evolutionary microbiology</i>, 59(10), 2394-2399. doi:10.1099/ijs.0.009480-0 Kang, H., Kim, H., Joung, Y., Jang, T. Y., & Joh, K. (2015). <i>Ferruginibacter paludis</i> sp. nov., isolated from wetland freshwater, and emended descriptions of <i>Ferruginibacter lapsinans</i> and <i>Ferruginibacter alkalilentus</i>. <i>International journal of systematic and evolutionary microbiology</i>, 65(8), 2635-2639. doi:10.1099/ijs.0.000311
Filomicrobium	Schlesner, H. (2015). <i>Filomicrobium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00818
Fimbriimonas	Im, W. T., Hu, Z. Y., Kim, K. H., Rhee, S. K., Meng, H., Lee, S. T., & Quan, Z. X. (2012). Description of <i>Fimbriimonas ginsengisoli</i> gen. nov., sp. nov. within the <i>Fimbriimonadia</i> class nov., of the phylum Armatimonadetes. <i>Antonie van Leeuwenhoek</i> , 102(2), 307-317. doi:10.1007/s10482-012-9739-6
Flaviumibacter	Han, Y., Zhang, F., Wang, Q., Zheng, S., Guo, W., Feng, L., & Wang, G. (2016). <i>Flaviumibacter stibioxidans</i> sp. nov., an antimony-oxidizing bacterium isolated from antimony mine soil. <i>International journal of systematic and evolutionary microbiology</i>, 66(11), 4676-4680. doi:10.1099/ijsem.0.001409 Zhang, L., Wang, Y., Wei, L., Wang, Y., Shen, X., & Li, S. (2013). <i>Taibaiella smilacinae</i> gen. nov., sp. nov., an endophytic member of the family Chitinophagaceae isolated from the stem of <i>Smilacina japonica</i>, and emended description of <i>Flaviumibacter petaseus</i>. <i>International journal of systematic and evolutionary microbiology</i>, 63(10), 3769-3776. doi:10.1099/ijs.0.051607-0

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Frankia	Normand, P. and Benson, D. R. (2015). Frankia. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00042
Gemmata	Fuerst, J. A., Lee, K. and Butler, M. K. (2015). Gemmata. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00783
Gemmatimonadales	Zhang, H., Sekiguchi, Y., Hanada, S., Hugenholtz, P., Kim, H., Kamagata, Y., & Nakamura, K. (2003). <i>Gemmatimonas aurantiaca</i> gen. nov., sp. nov., a Gram-negative, aerobic, polyphosphate-accumulating micro-organism, the first cultured representative of the new bacterial phylum Gemmatimonadetes phyl. nov. <i>International journal of systematic and evolutionary microbiology</i> , 53(4), 1155-1163. doi:10.1099/ijs.0.02520-0
Gemmatimonadetes	Zhang, H., Sekiguchi, Y., Hanada, S., Hugenholtz, P., Kim, H., Kamagata, Y., & Nakamura, K. (2003). <i>Gemmatimonas aurantiaca</i> gen. nov., sp. nov., a Gram-negative, aerobic, polyphosphate-accumulating micro-organism, the first cultured representative of the new bacterial phylum Gemmatimonadetes phyl. nov. <i>International journal of systematic and evolutionary microbiology</i> , 53(4), 1155-1163. doi:10.1099/ijs.0.02520-0
Gemmatimonas	Kamagata, Y. (2015). Gemmatimonas. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00775 Park, D., Kim, H., & Yoon, S. (2017). Nitrous oxide reduction by an obligate aerobic bacterium <i>Gemmatimonas aurantiaca</i> strain T-27. <i>Applied and environmental microbiology</i> , AEM-00502. doi:10.1128/AEM.00502-17
Gemmatirosa	DeBruyn, J. M., Fawaz, M. N., Peacock, A. D., Dunlap, J. R., Nixon, L. T., Cooper, K. E., & Radosevich, M. (2013). <i>Gemmatirosa kalamazoonensis</i> gen. nov., sp. nov., a member of the rarely-cultivated bacterial phylum Gemmatimonadetes. <i>The Journal of general and applied microbiology</i> , 59(4), 305-312. doi:jgam.59.305
Geodermatophilaceae	Normand, P. and Benson, D. R. (2015). Geodermatophilaceae. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00020
Gluconacetobacter	Sievers, M. and Swings, J. (2015). <i>Gluconacetobacter</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00883
Gluconobacter	Sievers, M. and Swings, J. (2015). Gluconobacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00884
Haematobacter	Helsel, L. O., Hollis, D., Steigerwalt, A. G., Morey, R. E., Jordan, J., Aye, T., Radosevic, J., Jannat-Khah, D., Thiry, D., Lonsway, D. R & Patel, J. B. (2007). Identification of "Haematobacter," a new genus of aerobic Gram-negative rods isolated from clinical specimens, and reclassification of <i>Rhodobacter massiliensis</i> as "Haematobacter massiliensis" comb. nov.". <i>Journal of clinical microbiology</i> , 45(4), 1238-1243. doi:10.1128/JCM.01188-06 Wang, D., Liu, H., Zheng, S., & Wang, G. (2014). <i>Paenirhodobacter ensiensis</i> gen. nov., sp. nov., a non-photosynthetic bacterium isolated from soil, and emended descriptions of the genera <i>Rhodobacter</i> and <i>Haematobacter</i> . <i>International journal</i>

	of systematic and evolutionary microbiology, 64(2), 551-558. doi: 10.1099/ijs.0.050351-0
Haliangium	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Haliscomenobacter	Kämpfer, P. (2015). Haliscomenobacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00357
Halobacillus	Spring, S. (2015). Halobacillus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00535
Hyalangium	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Hymenobacter	Hirsch, P., Ludwig, W., Hethke, C., Sittig, M., Hoffmann, B., & Gallikowski, C. A. (1998). Hymenobacter roseosalivarius gen. nov., sp. nov. from continental Antarctic soils and sandstone: bacteria of the Cytophaga/Flavobacterium/Bacteroides line of phylogenetic descent. <i>Systematic and applied microbiology</i> , 21(3), 374-383. doi:10.1016/S0723-2020(98)80047-7 Klassen, J. L., & Foght, J. M. (2011). Characterization of Hymenobacter isolates from Victoria Upper Glacier, Antarctica reveals five new species and substantial non-vertical evolution within this genus. <i>Extremophiles</i> , 15(1), 45-57. doi:10.1007/s00792-010-0336-1
Hyphomicrobiaceae	Oren, A., & Xu, X. W. (2014). The family Hyphomicrobiaceae. In <i>The Prokaryotes</i> (pp. 247-281). Springer Berlin Heidelberg. doi:10.1007/978-3-642-30197-1_257 Garrity, G. M., Bell, J. A. and Lilburn, T. (2015). Hyphomicrobiaceae. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00167
Ilumatobacter	Matsumoto, A., Kasai, H., Matsuo, Y., Ōmura, S., Shizuri, Y., & Takahashi, Y. (2009). Ilumatobacter fluminis gen. nov., sp. nov., a novel actinobacterium isolated from the sediment of an estuary. <i>The Journal of general and applied microbiology</i> , 55(3), 201-205.
Inhella	Chen, W. M., Sheu, F. S., Young, C. C., & Sheu, S. Y. (2012). Inhella fonticola sp. nov., isolated from spring water, and emended description of the genus Inhella. <i>International journal of systematic and evolutionary microbiology</i> , 62(5), 1048-1055. doi: 10.1099/ijs.0.034884-0 Song, J., Oh, H. M., Lee, J. S., Woo, S. B., & Cho, J. C. (2009). Inhella inkyongensis gen. nov., sp. nov., a new freshwater bacterium in the order Burkholderiales. <i>J. Microbiol. Biotechnol.</i> , 19(1), 5-10. doi:10.4014/jmb.0802.145
Jatrophihabitans	Madhaiyan, M., Hu, C. J., Kim, S. J., Weon, H. Y., Kwon, S. W., & Ji, L. (2013). Jatrophihabitans endophyticus gen. nov., sp. nov., an endophytic actinobacterium isolated from a surface-sterilized stem of Jatropha curcas L. <i>International journal of systematic and evolutionary microbiology</i> , 63(4), 1241-1248. doi:10.1099/ijs.0.039685-0 Lee, K. C., Suh, M. K., Eom, M. K., Kim, K. K., Kim, J. S., Kim, D. S., Ko, S. H., Shin, Y. K., & Lee, J. S. (2018). Jatrophihabitans telluris sp. nov., isolated from sediment soil of lava forest wetlands and the emended description of the genus Jatrophihabitans. <i>International journal of systematic and evolutionary microbiology</i> . doi:10.1099/ijsem.0.002639
Jeotgalicoccus	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S. (2015). Jeotgalicoccus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo,

	J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00566
Kineococcus	Normand, P. and Benson, D. R. (2015). Kineococcus . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00053
Kineosporia	Normand, P. and Benson, D. R. (2015). Kineosporia . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00054
Kineosporiaceae	Normand, P. and Benson, D. R. (2015). Kineosporiaceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00025
Kofleria	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Kofleriaceae	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Kribbella	Evtushenko, L. I. and Krausova, V. I. (2015). Kribbella. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00157
Labilithrix	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Labrys	Vasilyeva, L. V. (2015). <i>Labrys</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00821 Oren A. (2014) The Family <i>Xanthobacteraceae</i> . In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E., Thompson F. (eds) The Prokaryotes. Springer, Berlin, Heidelberg. doi: 10.1007/978-3-642-30197-1_258
Lautropia	Gerner-Smidt, P. (2015). Lautropia. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00937
Legionella	Winn, W. C. (2015). Legionella. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01178
Lentisphaerae	Choi, A., Yang, S. J., Rhee, K. H., & Cho, J. C. (2013). Lentisphaera marina sp. nov., and emended description of the genus Lentisphaera. <i>International journal of systematic and evolutionary microbiology</i> , 63(4), 1540-1544. doi:10.1099/ijs.0.046433-0 Choi, A., Song, J., Joung, Y., Kogure, K., & Cho, J. C. (2015). Lentisphaera profundus sp. nov., isolated from deep-sea water. <i>International journal of systematic and evolutionary microbiology</i> , 65(11), 4186-4190. doi:10.1099/ijs.0.000556 Cho, J. , Vergin, K. L., Morris, R. M. and Giovannoni, S. J. (2004), Lentisphaera araneosa gen. nov., sp. nov, a transparent exopolymer producing marine bacterium, and the description of a novel bacterial phylum, Lentisphaerae. <i>Environmental Microbiology</i> , 6: 611-621. doi:10.1111/j.1462-2920.2004.00614.x
Leptospira	Paster, B. J., & Dewhirst, F. E. (2000). Phylogenetic foundation of spirochetes. <i>Journal of molecular microbiology and biotechnology</i> , 2(4), 341-344.
Litorilinea	Kale, V., Björnsdóttir, S. H., Friðjónsson, Ó. H., Pétursdóttir, S. K., Ómarsdóttir, S., & Hreggviðsson, G. Ó. (2013). Litorilinea aerophila gen. nov., sp. nov., an aerobic member of the class Caldilineae, phylum Chloroflexi, isolated from an intertidal

	hot spring. <i>International journal of systematic and evolutionary microbiology</i> , 63(3), 1149-1154. doi:10.1099/ijs.0.044115-0
Lysobacter	Christensen, P. (2015). Lysobacter. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01232
Macrococcus	Schleifer, K. (2015). Macrococcus. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00567
Magnetococcus	Bazylinski, D. A., Williams, T. J., Lefevre, C. T., Berg, R. J., Zhang, C. L., Bowser, S. S., Dean, A. J., & Beveridge, T. J. (2013). <i>Magnetococcus marinus</i> gen. nov., sp. nov., a marine, magnetotactic bacterium that represents a novel lineage (<i>Magnetococcaceae</i> fam. nov., <i>Magnetococcales</i> ord. nov.) at the base of the Alphaproteobacteria. <i>International journal of systematic and evolutionary microbiology</i> , 63(3), 801-808. doi:10.1099/ijs.0.038927-0
Massilia	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S., (2015). Massilia. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00965
Mesorhizobium	Chen, W. X., Wang, E. T. and David Kuykendall, L. (2015). Mesorhizobium. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00839
Methylobacter	Doronina, N. V., Poroshina, M. N., Kaparullina, E. N., Ezhov, V. A., & Trotsenko, Y. A. (2013). Methylobacter halotolerans gen. nov., sp. nov. and Methylobacter solikamskensis sp. nov., two non-pigmented halotolerant obligately methylotrophic bacteria isolated from the Ural saline environments. <i>Systematic and applied microbiology</i> , 36(3), 148-154. doi:10.1016/j.syapm.2012.12.001
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Minicystis	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Moraxellaceae	Juni, E. and Bøvre, K. (2015). Moraxellaceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00231
Motilibacter	Lee, S. D. (2012). Motilibacter peucedani gen. nov., sp. nov., isolated from rhizosphere soil. <i>International journal of systematic and evolutionary microbiology</i> , 62(2), 315-321. doi:10.1099/ijs.0.030007-0
Mycobacterium	Magee, J. G. and Ward, A. C. (2015). Mycobacterium. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00029
Myxococcales	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Nakamurella	Chen, W. and Tao, T. (2015). Nakamurella. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00047 Sen, A., Daubin, V., Abrouk, D., Gifford, I., Berry, A. M., & Normand, P. (2014). Phylogeny of the class Actinobacteria revisited in the light of complete genomes. The orders 'Frankiales' and Micrococcales should be split into coherent entities: proposal of Frankiales ord. nov., Geodermatophilales ord. nov., Acidothermales

	ord. nov. and Nakamurellales ord. nov. <i>International journal of systematic and evolutionary microbiology</i> , 64(11), 3821-3832. doi:10.1099/ijs.0.063966-0
Nannocystaceae	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Nannocystis	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Nesterenkonia	Stackebrandt, E. (2015). Nesterenkonia. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00122
Nevskia	Leandro, T., França, L., Nobre, M. F., Schumann, P., Rosselló-Móra, R., & da Costa, M. S. (2012). Nevskia aquatilis sp. nov. and Nevskia persephonica sp. nov., isolated from a mineral water aquifer and the emended description of the genus Nevskia. <i>Systematic and applied microbiology</i> , 35(5), 297-301. doi:10.1016/j.syapm.2012.05.001 Cypionka, H., Babenzien, H. D., Glöckner, F. O., & Amann, R. (2006). The genus Nevskia. In <i>The Prokaryotes</i> (pp. 1152-1155). Springer, New York, NY. doi:10.1007/0-387-30746-x_46
Nitrosomonadaceae	Prosser J.I., Head I.M., Stein L.Y. (2014) The Family <i>Nitrosomonadaceae</i> . In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E., Thompson F. (eds) <i>The Prokaryotes</i> . Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-30197-1_372
Nitrosomonadales	Prosser J.I., Head I.M., Stein L.Y. (2014) The Family <i>Nitrosomonadaceae</i> . In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E., Thompson F. (eds) <i>The Prokaryotes</i> . Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-30197-1_372
Nitrosospira	Shaw, L. J., Nicol, G. W., Smith, Z. , Fear, J. , Prosser, J. I. and Baggs, E. M. (2006), <i>Nitrosospira</i> spp. can produce nitrous oxide via a nitrifier denitrification pathway. <i>Environmental Microbiology</i> , 8: 214-222. doi:10.1111/j.1462-2920.2005.00882.x
Nordella	La Scola, B., Barrassi, L., & Raoult, D. (2004). A novel alpha-Proteobacterium, Nordella oligomobilis gen. nov., sp. nov., isolated by using amoebal co-cultures. <i>Research in microbiology</i> , 155(1), 47-51. doi:10.1016/j.resmic.2003.09.012
Ohtaekwangia	Yoon, J. H., Kang, S. J., Lee, S. Y., Lee, J. S., & Park, S. (2011). Ohtaekwangia koreensis gen. nov., sp. nov. and Ohtaekwangia kribbensis sp. nov., isolated from marine sand, deep-branching members of the phylum Bacteroidetes. <i>International journal of systematic and evolutionary microbiology</i> , 61(5), 1066-1072. doi:10.1099/ijs.0.025874-0
Oligoflexus	Nakai, R., Nishijima, M., Tazato, N., Handa, Y., Karray, F., Sayadi, S., Isoda, H., & Naganuma, T. (2014). Oligoflexus tunisiensis gen. nov., sp. nov., a Gram-negative, aerobic, filamentous bacterium of a novel proteobacterial lineage, and description of Oligoflexaceae fam. nov., Oligoflexales ord. nov. and Oligoflexia classis nov. <i>International journal of systematic and evolutionary microbiology</i> , 64(10), 3353-3359. doi:10.1099/ijs.0.060798-0
Oscillochloris	Keppen, O. I., Gorlenko, V. M. and Pierson, B. K. (2015). Oscillochloris. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00383
Paludisphaera	Kulichevskaya, I. S., Ivanova, A. A., Suzina, N. E., Rijpstra, W. I. C., Damste, J. S. S., & Dedysh, S. N. (2016). Paludisphaera borealis gen. nov., sp. nov., a hydrolytic planctomycete from northern wetlands, and proposal of Isosphaeraceae fam. nov. <i>International journal of systematic and evolutionary microbiology</i> , 66(2), 837-844. doi: 10.1099/ijsem.0.000799
Panacagrimonas	Im, W. T., Liu, Q. M., Yang, J. E., Kim, M. S., Kim, S. Y., Lee, S. T., & Yi, T. H. (2010). Panacagrimonas perspica gen. nov., sp. nov., a novel member of

	Gammaproteobacteria isolated from soil of a ginseng field. <i>The Journal of Microbiology</i> , 48(2), 262-266. doi:10.1007/s12275-010-0067-0
Pedosphaera	Janssen, P. H. (2006). Identifying the dominant soil bacterial taxa in libraries of 16S rRNA and 16S rRNA genes. <i>Applied and environmental microbiology</i> , 72(3), 1719-1728. doi:AEM.72.3.1719-1728.2006 Kant, R., Van Passel, M. W., Sangwan, P., Palva, A., Lucas, S., Copeland, A., Lapidus, A., del Rio, T. G., Dalin, E., Tice, H., Bruce, D., Goodwin, L., Pitluck, S., Chertkov, O., Larimer, F. W., Land, M. L., Hauser, L., Brettin, T. S., Detter, J. C., Han S, de Vos, W. M., Janssen, P. H., & Smidt, H. (2011). Genome sequence of <i>Pedosphaera parvula</i> Ellin514, an aerobic verrucomicrobial isolate from pasture soil. <i>Journal of bacteriology</i> . doi:10.1128/JB.00299-11
Peredibacter	Koval, S. F., Williams, H. N., & Stine, O. C. (2015). Reclassification of <i>Bacteriovorax marinus</i> as <i>Halobacteriovorax marinus</i> gen. nov., comb. nov. and <i>Bacteriovorax litoralis</i> as <i>Halobacteriovorax litoralis</i> comb. nov. description of <i>Halobacteriovoraceae</i> fam. nov. in the class Deltaproteobacteria. <i>International journal of systematic and evolutionary microbiology</i> , 65(2), 593-597. doi:10.1099/ijs.0.070201-0 Piñeiro, S. A., Williams, H. N., & Stine, O. C. (2008). Phylogenetic relationships amongst the saltwater members of the genus <i>Bacteriovorax</i> using <i>rpoB</i> sequences and reclassification of <i>Bacteriovorax stolpii</i> as <i>Bacteriolyticum stolpii</i> gen. nov., comb. nov. <i>International journal of systematic and evolutionary microbiology</i> , 58(5), 1203-1209. doi:10.1099/ijs.0.65710-0
Permianibacter	Wang, H., Zheng, T., Hill, R. T., & Hu, X. (2014). <i>Permianibacter aggregans</i> gen. nov., sp. nov., a bacterium of the family Pseudomonadaceae capable of aggregating potential biofuel-producing microalgae. <i>International journal of systematic and evolutionary microbiology</i> , 64(10), 3503-3507. doi:10.1099/ijs.0.065003-0
Phaeospirillum	Imhoff, J. F. (2015). <i>Phaeospirillum</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00894
Phenylobacterium	Eberspächer, J. (2015). <i>Phenylobacterium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00793
Phyllobacteriaceae	Mergaert, J. and Swings, J. (2015). <i>Phyllobacteriaceae</i> fam. nov.. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00170
Pirellula	Fuerst, J. A. and Butler, M. K. (2015). <i>Pirellula</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00785
Polaromonas	Gosink, J. J. (2015). <i>Polaromonas</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00950
Polyangiaceae	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Polyangium	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Porphyrobacter	Hiraishi, A. and Imhoff, J. F. (2015). <i>Porphyrobacter</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00922

Pseudenhygromyxa	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Pseudobacteriovorax	McCauley, E. P., Haltli, B., & Kerr, R. G. (2015). Description of Pseudobacteriovorax antillogorgiicola gen. nov., sp. nov., a bacterium isolated from the gorgonian octocoral Antillogorgia elisabethae, belonging to the family Pseudobacteriovoracaceae fam. nov., within the order Bdellovibrionales. <i>International journal of systematic and evolutionary microbiology</i> , 65(2), 522-530. doi: 10.1099/ijs.0.066266-0
Pseudolabrys	Kämpfer, P., Young, C. C., Arun, A. B., Shen, F. T., Jäckel, U., Rossello-Mora, R., Lai, W. A., & Rekha, P. D. (2006). Pseudolabrys taiwanensis gen. nov., sp. nov., an alphaproteobacterium isolated from soil. <i>International journal of systematic and evolutionary microbiology</i> , 56(10), 2469-2472. doi:10.1099/ijs.0.64124-0
Pseudonocardia	Huang, Y. and Goodfellow, M. (2015). Pseudonocardia. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00184
Pseudoxanthobacter	Arun, A. B., Schumann, P., Chu, H. I., Tan, C. C., Chen, W. M., Lai, W. A., Kämpfer, P., Shen, F.T., Rekha, P.D., Hung, M.H., & Chou, J. H. (2008). <i>Pseudoxanthobacter soli</i> gen. nov., sp. nov., a nitrogen-fixing alphaproteobacterium isolated from soil. <i>International journal of systematic and evolutionary microbiology</i> , 58(7), 1571-1575. doi:10.1099/ijs.0.65206-0 Liu, X. M., Chen, K., Meng, C., Zhang, L., Zhu, J. C., Huang, X., Li, S. P. & Jiang, J. D. (2014). <i>Pseudoxanthobacter liyangensis</i> sp. nov., isolated from dichlorodiphenyltrichloroethane-contaminated soil. <i>International journal of systematic and evolutionary microbiology</i> , 64(10), 3390-3394. doi:10.1099/ijs.0.056507-0
Pseudoxanthomonas	Lipski, A. and Stackebrandt, E. S. (2015). Pseudoxanthomonas. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01234
Psychrobacter	Juni, E. (2015). Psychrobacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01205
Rhizobiaceae	Kuykendall, L. D. (2015). Rhizobiaceae. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00171
Rhizobium	Kuykendall, L. D., Young, J. M., Martínez-Romero, E., Kerr, A. and Sawada, H. (2015). Rhizobium. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00847
Rhodoligotrophos	Fukuda, W., Yamada, K., Miyoshi, Y., Okuno, H., Atomi, H., & Imanaka, T. (2012). Rhodoligotrophos appendicifer gen. nov., sp. nov., an appendaged bacterium isolated from a freshwater Antarctic lake. <i>International journal of systematic and evolutionary microbiology</i> , 62(8), 1945-1950. doi:10.1099/ijs.0.032953-0
Rhodopila	Madigan, M. T. and Imhoff, J. F. (2015). <i>Rhodopila</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00886
Rhodoplanes	Hiraishi, A. and Imhoff, J. F. (2015). <i>Rhodoplanes</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00826

Rhodopseudomonas	Imhoff, J. F. (2015). <i>Rhodopseudomonas</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00806
Rhodovastum	Okamura, K., Hisada, T., Kanbe, T., & Hiraishi, A. (2009). <i>Rhodovastum atsumiense</i> gen. nov., sp. nov., a phototrophic alphaproteobacterium isolated from paddy soil. <i>The Journal of general and applied microbiology</i> , 55(1), 43-50. doi:10.2323/jgam.55.43
Rhodovibrio	Imhoff, J. F. (2015). <i>Rhodovibrio</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00898
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Roseiflexus	van der Meer, M. T., Klatt, C. G., Wood, J., Bryant, D. A., Bateson, M. M., Lammerts, L., Schouten, S., Damsté, J. S. S., Madigan, M. T., & Ward, D. M. (2010). Cultivation and genomic, nutritional, and lipid biomarker characterization of <i>Roseiflexus</i> strains closely related to predominant <i>in situ</i> populations inhabiting Yellowstone hot spring microbial mats. <i>Journal of bacteriology</i> , 192(12), 3033-3042. doi:10.1128/JB.01610-09 Hanada, S., Takaichi, S., Matsuura, K., & Nakamura, K. (2002). <i>Roseiflexus castenholzii</i> gen. nov., sp. nov., a thermophilic, filamentous, photosynthetic bacterium that lacks chlorosomes. <i>International journal of systematic and evolutionary microbiology</i> , 52(1), 187-193. doi: 10.1099/00207713-52-1-187
Roseimicrobium	Otsuka, S., Ueda, H., Suenaga, T., Uchino, Y., Hamada, M., Yokota, A., & Senoo, K. (2013). <i>Roseimicrobium gellanilyticum</i> gen. nov., sp. nov., a new member of the class Verrucomicrobiae. <i>International journal of systematic and evolutionary microbiology</i> , 63(6), 1982-1986. doi:10.1099/ijs.0.041848-0
Rubrobacteraceae	Suzuki, K. (2015). Rubrobacteraceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00052 Albuquerque L., da Costa M.S. (2014) The Family Rubrobacteraceae. In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E., Thompson F. (eds) The Prokaryotes. Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-30138-4_202
Rubrobacterales	Suzuki, K. (2015). Rubrobacterales. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.obm00024 Suzuki, K. (2015). Rubrobacteraceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00052 Albuquerque L., da Costa M.S. (2014) The Family Rubrobacteraceae. In: Rosenberg E., DeLong E.F., Lory S., Stackebrandt E., Thompson F. (eds) The Prokaryotes. Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-30138-4_202
Saccharopolyspora	Kim, S. B. and Goodfellow, M. (2015). <i>Saccharopolyspora</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00186
Sandaracinus	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3

Saprospiraceae	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S. (2015). Saprospiraceae fam. nov.. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00071
Segetibacter	Weon, H. Y., Kwon, S. W., Son, J. A., Kim, S. J., Kim, Y. S., Kim, B. Y., & Ka, J. O. (2010). <i>Adhaeribacter aerophilus</i> sp. nov., <i>Adhaeribacter aerolatus</i> sp. nov. and <i>Segetibacter aerophilus</i> sp. nov., isolated from air samples. <i>International journal of systematic and evolutionary microbiology</i> , 60(10), 2424-2429. doi:10.1099/ijs.0.018374-0 An, D. S., Lee, H. G., Im, W. T., Liu, Q. M., & Lee, S. T. (2007). <i>Segetibacter koreensis</i> gen. nov., sp. nov., a novel member of the phylum Bacteroidetes, isolated from the soil of a ginseng field in South Korea. <i>International journal of systematic and evolutionary microbiology</i> , 57(8), 1828-1833. doi:10.1099/ijs.0.64803-0
Singulisphaera	Dedysh, S. N. and Kulichevskaya, I. S. (2015). Singulisphaera. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00789
Sinobacteraceae	Whitman, W. B., Lawson, P. A., & Losey, N. A. (2015). Response to Tindall (2014) on the legitimacy of the names Solimonadaceae Losey et al. 2013, Xanthomonadaceae Saddler and Bradbury 2005 and Xanthomonadales Saddler and Bradbury 2005. <i>International journal of systematic and evolutionary microbiology</i> , 65(3), 1086-1087. doi:10.1099/ijs.0.000061 Zhou, Y., Zhang, Y. Q., Zhi, X. Y., Wang, X., Dong, J., Chen, Y., Lai, R., & Li, W. J. (2008). Description of <i>Sinobacter flavus</i> gen. nov., sp. nov., and proposal of Sinobacteraceae fam. nov. <i>International journal of systematic and evolutionary microbiology</i> , 58(1), 184-189. doi:10.1099/ijs.0.65244-0 Losey, N. A., Stevenson, B. S., Verbarg, S., Rudd, S., Moore, E. R., & Lawson, P. A. (2013). <i>Fontimonas thermophila</i> gen. nov., sp. nov., a moderately thermophilic bacterium isolated from a freshwater hot spring, and proposal of Solimonadaceae fam. nov. to replace Sinobacteraceae Zhou et al. 2008. <i>International journal of systematic and evolutionary microbiology</i> , 63(1), 254-259. doi:10.1099/ijs.0.037127-0
Smaragdicoccus	Kasai, H. (2015). Smaragdicoccus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00035 Adachi, K., Katsuta, A., Matsuda, S., Peng, X., Misawa, N., Shizuri, Y., Kroppenstedt, R. M., Yokota, A., & Kasai, H. (2007). <i>Smaragdicoccus niigatensis</i> gen. nov., sp. nov., a novel member of the suborder Corynebacterineae. <i>International journal of systematic and evolutionary microbiology</i> , 57(2), 297-301. doi:10.1099/ijs.0.64254-0
Solimonas	Zhou, Y., Lai, R., & Li, W. J. (2014). The family solimonadaceae. In <i>The Prokaryotes</i> (pp. 627-638). Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-38922-1_373 Sheu, S. Y., Cho, N. T., Arun, A. B., & Chen, W. M. (2011). Proposal of <i>Solimonas aquatica</i> sp. nov., reclassification of <i>Sinobacter flavus</i> Zhou et al. 2008 as <i>Solimonas flava</i> comb. nov. and <i>Singularimonas varicoloris</i> Friedrich and Lipski 2008 as <i>Solimonas varicoloris</i> comb. nov. and emended descriptions of the genus <i>Solimonas</i> and its type species <i>Solimonas soli</i> . <i>International journal of systematic and evolutionary microbiology</i> , 61(9), 2284-2291. doi:10.1099/ijs.0.023010-0
Solirubrobacter	Zhang, L., Zhu, L., Si, M., Li, C., Zhao, L., Wei, Y., & Shen, X. (2014). <i>Solirubrobacter taibaiensis</i> sp. nov., isolated from a stem of <i>Phytolacca acinosa</i> Roxb. <i>Antonie van Leeuwenhoek</i> , 106(2), 279-285. doi:10.1007/s10482-014-0194-4 Whitman, W. B. (2015). Solirubrobacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00227

Solirubrobacterales	Whitman, W. B. and Suzuki, K. (2015). Solirubrobacteraceae. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00055
Sorangium	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
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Sphingomonadaceae	Glaeser, S. P., & Kämpfer, P. (2014). The family sphingomonadaceae. In <i>The Prokaryotes</i> (pp. 641-707). Springer Berlin Heidelberg. doi:10.1007/978-3-642-30197-1_302
Sphingomonas	Yabuuchi, E. and Kosako, Y. (2015). Sphingomonas. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00924
Spiribacter	López-Pérez, M., Ghai, R., Leon, M. J., Rodríguez-Olmos, Á., Copa-Patiño, J. L., Soliveri, J., Sanchez-Porro, C., Ventosa, A., & Rodriguez-Valera, F. (2013). Genomes of “Spiribacter”, a streamlined, successful halophilic bacterium. <i>BMC genomics</i> , 14(1), 787. doi:10.1186/1471-2164-14-787
Stella	Vasilyeva, L. V. (2015). Stella. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00889
Stenotrophobacter	Pascual, J., Huber, K. J., Foessel, B. U. and Overmann, J. (2017). Stenotrophobacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01429
Stigmatella	Kuever, J., Rainey, F. A., & Widdel, F. (2005). Class IV. Deltaproteobacteria class nov. In <i>Bergey's Manual® of Systematic Bacteriology</i> (pp. 922-1144). Springer, Boston, MA. doi:10.1007/978-0-387-29298-4_3
Tahibacter	Makk, J., Homonnay, Z. G., Kéki, Z., Lejtovicz, Z., Márialigeti, K., Spröer, C., Schumann, P., & Tóth, E. M. (2011). Tahibacter aquaticus gen. nov., sp. nov., a new gammaproteobacterium isolated from the drinking water supply system of Budapest (Hungary). <i>Systematic and applied microbiology</i> , 34(2), 110-115. doi:10.1016/j.syapm.2010.11.001 Wu, Y. D., Deng, S. K., Shi, C., Zhu, J. C., He, J., & Li, S. P. (2015). Tahibacter caeni sp. nov., isolated from activated sludge. <i>International journal of systematic and evolutionary microbiology</i> , 65(2), 633-638. doi:10.1099/ijs.0.068718-0
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Thermorudis	King, C. E., & King, G. M. (2014). Thermomicrobium carboxidum sp. nov., and Thermorudis peleae gen. nov., sp. nov., carbon monoxide-oxidizing bacteria isolated from geothermally heated biofilms. <i>International journal of systematic and evolutionary microbiology</i> , 64(8), 2586-2592. doi:10.1099/ijs.0.060327-0
Thermosporothrix	Yabe, S., Aiba, Y., Sakai, Y., Hazaka, M., & Yokota, A. (2010). Thermosporothrix hazakensis gen. nov., sp. nov., isolated from compost, description of Thermosporotrichaceae fam. nov. within the class Ktedonobacteria Cavaletti et al. 2007 and emended description of the class Ktedonobacteria. <i>International journal of systematic and evolutionary microbiology</i> , 60(8), 1794-1801. doi:10.1099/ijs.0.018069-0
Thiobacter	Hirayama, H., Takai, K., Inagaki, F., Nealson, K. H., & Horikoshi, K. (2005). Thiobacter subterraneus gen. nov., sp. nov., an obligately chemolithoautotrophic, thermophilic, sulfur-oxidizing bacterium from a subsurface hot aquifer. <i>International journal of systematic and evolutionary microbiology</i> , 55(1), 467-472. doi:10.1099/ijs.0.63389-0
Vampirovibrio	Soo, R. M., Woodcroft, B. J., Parks, D. H., Tyson, G. W., & Hugenholtz, P. (2015). Back from the dead; the curious tale of the predatory cyanobacterium Vampirovibrio chlorellavorus. <i>PeerJ</i> , 3, e968. doi:10.7717/peerj.968
Variibacter	Kim, K. K., Lee, K. C., Eom, M. K., Kim, J. S., Kim, D. S., Ko, S. H., Kim, B. H., & Lee, J. S. (2014). Variibacter gotjawalensis gen. nov., sp. nov., isolated from soil of a lava forest. <i>Antonie van Leeuwenhoek</i> , 105(5), 915-924. doi:10.1007/s10482-014-0146-z
Verrucomicrobia subdivision 3	Janssen, P. H. (2006). Identifying the dominant soil bacterial taxa in libraries of 16S rRNA and 16S rRNA genes. <i>Applied and environmental microbiology</i> , 72(3), 1719-1728. doi:AEM.72.3.1719-1728.2006
Verrucosispora	Stackebrandt, E. (2015). Verrucosispora. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00153
Williamsia	Kämpfer, P. (2015). Williamsia. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00036
Xanthobacteraceae	Oren, A. (2014). The family Xanthobacteraceae. In <i>The Prokaryotes</i> (pp. 709-726). Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-30197-1_258
Xanthomonadaceae	Saddler, G. S. and Bradbury, J. F. (2015). Xanthomonas. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01239
Zavarzinella	Kulichevskaya, I. S., Baulina, O. I., Bodelier, P. L., Rijpstra, W. I. C., Damste, J. S. S., & Dedysh, S. N. (2009). Zavarzinella formosa gen. nov., sp. nov., a novel stalked, Gemmata-like planctomycete from a Siberian peat bog. <i>International journal of systematic and evolutionary microbiology</i> , 59(2), 357-364. doi:10.1099/ijs.0.002378-0
Zhihengliuella	Busse, H. (2015). Zhihengliuella. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00126

Aerobic, Iron Oxidizing Bacteria

Acidithiomicrobium	Davis-Belmar, C. S., & Norris, P. R. (2009). Ferrous iron and pyrite oxidation by “Acidithiomicrobium” species. In <i>Advanced Materials Research</i> (Vol. 71, pp. 271-274). Trans Tech Publications. doi:10.4028/www.scientific.net/AMR.71-73.271
Arenimonas	Chen, F., Shi, Z., & Wang, G. (2012). <i>Arenimonas metalli</i> sp. nov., isolated from an iron mine. <i>International journal of systematic and evolutionary microbiology</i> , 62(8), 1744-1749. doi:10.1099/ijs.0.034132-0 Zhang, P., Peng, Y., Lu, J., Li, J., Chen, H., & Xiao, L. (2018). Microbial communities and functional genes of nitrogen cycling in an electrolysis augmented constructed wetland treating wastewater treatment plant effluent. <i>Chemosphere</i> , 211, 25-33. doi: 10.1016/j.chemosphere.2018.07.067 Shu, D., He, Y., Yue, H., & Wang, Q. (2016). Metagenomic and quantitative insights into microbial communities and functional genes of nitrogen and iron cycling in twelve wastewater treatment systems. <i>Chemical Engineering Journal</i> , 290, 21-30. doi:10.1016/j.cej.2016.01.024
Gallionella	Hallbeck, L. E. and Pedersen, K. (2015). <i>Gallionella</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00988
Thermomonas	Denner, E. B., Kämpfer, P. and Busse, H. (2015). <i>Thermomonas</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01238 Weber, K. A., Achenbach, L. A., & Coates, J. D. (2006). Microorganisms pumping iron: anaerobic microbial iron oxidation and reduction. <i>Nature Reviews Microbiology</i> , 4(10), 752. doi:10.1038/nrmicro1490
Leptothrix	Corstjens, P. L., De Vrind, J. P., Westbroek, P., & De Vrind-De Jong, E. W. (1992). Enzymatic iron oxidation by <i>Leptothrix discophora</i> : identification of an iron-oxidizing protein. <i>Applied and Environmental Microbiology</i> , 58(2), 450-454.
Ferritrophicum	Weiss, J. V., Rentz, J. A., Plaia, T., Neubauer, S. C., Merrill-Floyd, M., Lilburn, T., Bradburne, C., Megonigal, J. P., & Emerson, D. (2007). Characterization of neutrophilic Fe (II)-oxidizing bacteria isolated from the rhizosphere of wetland plants and description of <i>Ferritrophicum radiculicola</i> gen. nov. sp. nov., and <i>Sideroxydans paludicola</i> sp. nov. <i>Geomicrobiology Journal</i> , 24(7-8), 559-570. doi:10.1080/01490450701670152
Sideroxydans	Weiss, J. V., Rentz, J. A., Plaia, T., Neubauer, S. C., Merrill-Floyd, M., Lilburn, T., Bradburne, C., Megonigal, J. P., & Emerson, D. (2007). Characterization of neutrophilic Fe (II)-oxidizing bacteria isolated from the rhizosphere of wetland plants and description of <i>Ferritrophicum radiculicola</i> gen. nov. sp. nov., and <i>Sideroxydans paludicola</i> sp. nov. <i>Geomicrobiology Journal</i> , 24(7-8), 559-570. doi:10.1080/01490450701670152 Liu, J., Wang, Z., Belchik, S. M., Edwards, M. J., Liu, C., Kennedy, D. W., Merkle, E. D., Lipton, M. S., Butt, J. N., Richardson, D. J., Zachara, J. M., Fredrickson, J. K., Rosso, K. M., & Shi, L. (2012). Identification and characterization of MtoA: a decaheme c-type cytochrome of the neutrophilic Fe (II)-oxidizing bacterium <i>Sideroxydans lithotrophicus</i> ES-1. <i>Frontiers in microbiology</i> , 3, 37. doi:10.3389/fmicb.2012.00037
Rhodomicrobium	Imhoff, J. F. (2015). <i>Rhodomicrobium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00825
Chlorobium	Pfennig, N. and Overmann, J. (2015). <i>Chlorobium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J.

	Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00374 Heising, S., Richter, L., Ludwig, W., & Schink, B. (1999). <i>Chlorobium ferrooxidans</i> sp. nov., a phototrophic green sulfur bacterium that oxidizes ferrous iron in coculture with a “<i>Geospirillum</i>” sp. strain. <i>Archives of Microbiology</i>, 172(2), 116-124. doi:10.1007/s002030050748
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Aerobic, Iron Oxidizing, Nitrate Reducing Bacteria

Aquabacterium	Weber, K. A., Achenbach, L. A., & Coates, J. D. (2006). Microorganisms pumping iron: anaerobic microbial iron oxidation and reduction. <i>Nature Reviews Microbiology</i>, 4(10), 752. doi:10.1038/nrmicro1490 Manz, W., Kalmbach, S. and Szewzyk, U. (2015). Incertae Sedis I. <i>Aquabacterium</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00953 Chen, W. M., Cho, N. T., Yang, S. H., Arun, A. B., Young, C. C., & Sheu, S. Y. (2012). <i>Aquabacterium limnoticum</i> sp. nov., isolated from a freshwater spring. <i>International journal of systematic and evolutionary microbiology</i>, 62(3), 698-704. doi:10.1099/ijms.0.030635-0 Jeong, S. W., & Kim, J. (2015). <i>Aquabacterium olei</i> sp. nov., an oil-degrading bacterium isolated from oil-contaminated soil. <i>International journal of systematic and evolutionary microbiology</i>, 65(10), 3597-3602. doi:10.1099/ijsem.0.000458
Pedomicrobium	Hirsch, P. (2015). <i>Pedomicrobium</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00823
Pseudomonas	Weber, K. A., Achenbach, L. A., & Coates, J. D. (2006). Microorganisms pumping iron: anaerobic microbial iron oxidation and reduction. <i>Nature Reviews Microbiology</i>, 4(10), 752. doi:10.1038/nrmicro1490 Palleroni, N. J. (2015). <i>Pseudomonas</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01210
Thiobacillus	Kelly, D. P., Wood, A. P. and Stackebrandt, E. (2015). <i>Thiobacillus</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00969 Fortin, D., Davis, B. and Beveridge, T. (1996), Role of <i>Thiobacillus</i> and sulfate-reducing bacteria in iron biocycling in oxic and acidic mine tailings. <i>FEMS Microbiology Ecology</i>, 21: 11-24. doi:10.1111/j.1574-6941.1996.tb00329.x

Aerobic, Iron Oxidizing, Nitrate Reducing, Fermenting Bacteria

Rhodobacter	Imhoff, J. F. (2015). <i>Rhodobacter</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00862
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Aerobic, Iron Oxidizing, Iron Reducing Bacteria

Acidiferrobacter	Hallberg, K. B., Hedrich, S., & Johnson, D. B. (2011). Acidiferrobacter thiooxydans, gen. nov. sp. nov.; an acidophilic, thermo-tolerant, facultatively anaerobic iron-and sulfur-oxidizer of the family Ectothiorhodospiraceae. <i>Extremophiles</i> , 15(2), 271-279. doi:10.1007/s00792-011-0359-2
Ferrimicrobium	Weber, K. A., Achenbach, L. A., & Coates, J. D. (2006). Microorganisms pumping iron: anaerobic microbial iron oxidation and reduction. <i>Nature Reviews Microbiology</i> , 4(10), 752. doi:10.1038/nrmicro1490 Johnson, D. B., Bacelar-Nicolau, P., Okibe, N., Thomas, A., & Hallberg, K. B. (2009). Ferrimicrobium acidiphilum gen. nov., sp. nov. and Ferritrix thermotolerans gen. nov., sp. nov.: heterotrophic, iron-oxidizing, extremely acidophilic actinobacteria. <i>International journal of systematic and evolutionary microbiology</i> , 59(5), 1082-1089. doi:10.1099/ijs.0.65409-0 Norris, P. R. (2015). Ferrimicrobium . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00008

Aerobic, Methane Oxidizing Bacteria

Clonothrix	Murrell, J. C. (2010). The aerobic methane oxidizing bacteria (methanotrophs). In <i>Handbook of hydrocarbon and lipid microbiology</i> (pp. 1953-1966). Springer, Berlin, Heidelberg. doi:10.1007/978-3-540-77587-4_143
Crenothrix	Murrell, J. C. (2010). The aerobic methane oxidizing bacteria (methanotrophs). In <i>Handbook of hydrocarbon and lipid microbiology</i> (pp. 1953-1966). Springer, Berlin, Heidelberg. doi:10.1007/978-3-540-77587-4_143
Methylacidiphilum	Anvar, S. Y., Frank, J., Pol, A., Schmitz, A., Kraaijeveld, K., den Dunnen, J. T., & den Camp, H. J. O. (2014). The genomic landscape of the verrucomicrobial methanotroph Methylacidiphilum fumariolicum SolV. <i>BMC genomics</i> , 15(1), 914. doi:10.1186/1471-2164-15-914 Khadem, A. F., Pol, A., Wiczorek, A., Mohammadi, S. S., Francoijs, K. J., Stunnenberg, H. G., Jetten, M. S. M., & den Camp, H. J. O. (2011). Autotrophic methanotrophy in Verrucomicrobia: Methylacidiphilum fumariolicum SolV uses the Calvin Benson Bassham cycle for carbon dioxide fixation. <i>Journal of bacteriology</i> , JB-00407. doi:10.1128/JB.00407-11 Erikstad, H. A., & Birkeland, N. K. (2015). Draft genome sequence of “Candidatus Methylacidiphilum kamchatkense” strain Kam1, a thermoacidophilic methanotrophic Verrucomicrobium. <i>Genome announcements</i> , 3(2), e00065-15. doi:10.1128/genomeA.00065-15
Methylobacter	Murrell, J. C. (2010). The aerobic methane oxidizing bacteria (methanotrophs). In <i>Handbook of hydrocarbon and lipid microbiology</i> (pp. 1953-1966). Springer, Berlin, Heidelberg. doi:10.1007/978-3-540-77587-4_143
Methylobacterium	Green, P. N. (2015). Methylobacterium. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00830
Methylocaldum	Murrell, J. C. (2010). The aerobic methane oxidizing bacteria (methanotrophs). In <i>Handbook of hydrocarbon and lipid microbiology</i> (pp. 1953-1966). Springer, Berlin, Heidelberg. doi:10.1007/978-3-540-77587-4_143
Methylocapsa	Murrell, J. C. (2010). The aerobic methane oxidizing bacteria (methanotrophs). In <i>Handbook of hydrocarbon and lipid microbiology</i> (pp. 1953-1966). Springer, Berlin, Heidelberg. doi:10.1007/978-3-540-77587-4_143

Methyloceanibacter	Takeuchi, M., Katayama, T., Yamagishi, T., Hanada, S., Tamaki, H., Kamagata, Y., Oshima, K., Hattori, M., Marumo, K., Nedachi, M., Maeda, H., Suwa, Y., & Sakata, S. (2014). <i>Methyloceanibacter caenitepidi</i> gen. nov., sp. nov., a facultatively methylotrophic bacterium isolated from marine sediments near a hydrothermal vent. <i>International journal of systematic and evolutionary microbiology</i> , 64(2), 462-468. doi:10.1099/ijs.0.053397-0 Vekeman, B., Kerckhof, F. M., Cremers, G., De Vos, P., Vandamme, P., Boon, N., Op den Camp, H. J. M., & Heylen, K. (2016). New <i>Methyloceanibacter</i> diversity from North Sea sediments includes methanotroph containing solely the soluble methane monooxygenase. <i>Environmental microbiology</i> , 18(12), 4523-4536. doi:10.1111/1462-2920.13485
Methylocella	Murrell, J. C. (2010). The aerobic methane oxidizing bacteria (methanotrophs). In <i>Handbook of hydrocarbon and lipid microbiology</i> (pp. 1953-1966). Springer, Berlin, Heidelberg. doi:10.1007/978-3-540-77587-4_143
Methylococcales	Bowman, J. P. (2015). <i>Methylococcales</i> ord. nov. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.obm00099
Methylococcus	Murrell, J. C. (2010). The aerobic methane oxidizing bacteria (methanotrophs). In <i>Handbook of hydrocarbon and lipid microbiology</i> (pp. 1953-1966). Springer, Berlin, Heidelberg. doi:10.1007/978-3-540-77587-4_143
Methylocystaceae	Webb, H. K., Ng, H. J., & Ivanova, E. P. (2014). The family <i>Methylocystaceae</i> . In <i>The Prokaryotes</i> (pp. 341-347). Springer Berlin Heidelberg. doi:10.1007/978-3-642-30197-1_254
Methylocystis	Bowman, J. P. (2015). <i>Methylocystis</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00832
Methyloglobulus	Schink, B. and Deutzmann, J. S. (2016). <i>Methyloglobulus</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01412
Methylobacterium	Murrell, J. C. (2010). The aerobic methane oxidizing bacteria (methanotrophs). In <i>Handbook of hydrocarbon and lipid microbiology</i> (pp. 1953-1966). Springer, Berlin, Heidelberg. doi:10.1007/978-3-540-77587-4_143
Methyloparacoccus	Hoefman, S., van der Ha, D., Iguchi, H., Yurimoto, H., Sakai, Y., Boon, N., Vandamme, P., Heylen, K., & De Vos, P. (2014). <i>Methyloparacoccus murrellii</i> gen. nov., sp. nov., a methanotroph isolated from pond water. <i>International journal of systematic and evolutionary microbiology</i> , 64(6), 2100-2107. doi:10.1099/ijs.0.057760-0
Methylosinus	Bowman, J. P. (2015). <i>Methylosinus</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00833
Clonothrix	Murrell, J. C. (2010). The aerobic methane oxidizing bacteria (methanotrophs). In <i>Handbook of hydrocarbon and lipid microbiology</i> (pp. 1953-1966). Springer, Berlin, Heidelberg. doi:10.1007/978-3-540-77587-4_143
Crenothrix	Murrell, J. C. (2010). The aerobic methane oxidizing bacteria (methanotrophs). In <i>Handbook of hydrocarbon and lipid microbiology</i> (pp. 1953-1966). Springer, Berlin, Heidelberg. doi:10.1007/978-3-540-77587-4_143
Methylacidiphilum	Anvar, S. Y., Frank, J., Pol, A., Schmitz, A., Kraaijeveld, K., den Dunnen, J. T., & den Camp, H. J. O. (2014). The genomic landscape of the verrucomicrobial methanotroph <i>Methylacidiphilum fumariolicum</i> SolV. <i>BMC genomics</i> , 15(1), 914. doi:10.1186/1471-2164-15-914 Khadem, A. F., Pol, A., Wieczorek, A., Mohammadi, S. S., Francoijs, K. J., Stunnenberg, H. G., Jetten, M. S. M., & den Camp, H. J. O. (2011). Autotrophic methanotrophy in Verrucomicrobia: <i>Methylacidiphilum fumariolicum</i> SolV uses the Calvin

	Benson Bassham cycle for carbon dioxide fixation. <i>Journal of bacteriology</i>, JB-00407. doi:10.1128/JB.00407-11 Erikstad, H. A., & Birkeland, N. K. (2015). Draft genome sequence of “Candidatus <i>Methylacidiphilum kamchatkense</i>” strain Kam1, a thermoacidophilic methanotrophic Verrucomicrobium. <i>Genome announcements</i>, 3(2), e00065-15. doi:10.1128/genomeA.00065-15
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Aerobic, Nitrate Reducing Bacteria

Actinophytocola	Indananda, C., Matsumoto, A., Inahashi, Y., Takahashi, Y., Duangmal, K., & Thamchaipenet, A. (2010). <i>Actinophytocola oryzae</i> gen. nov., sp. nov., isolated from the roots of Thai glutinous rice plants, a new member of the family Pseudonocardiaceae. <i>International journal of systematic and evolutionary microbiology</i>, 60(5), 1141-1146. doi:10.1099/ijss.0.008417-0 Wang, W., Wang, B., Meng, H., Xing, Z., Lai, Q., & Yuan, L. (2017). <i>Actinophytocola xanthii</i> sp. nov., an actinomycete isolated from rhizosphere soil of the plant <i>Xanthium sibiricum</i>. <i>International journal of systematic and evolutionary microbiology</i>, 67(5), 1152-1157. doi:10.1099/ijsem.0.001781
Afipia	Weyant, R. S. and Whitney, A. M. (2015). <i>Afipia</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00798
Agrobacterium	Young, J. M., Kerr, A. and Sawada, H. (2015). <i>Agrobacterium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00842
Alcanivoracaceae	Golyshin, P. N., Harayama, S., Timmis, K. N. and Yakimov, M. M. (2015). <i>Alcanivoracaceae</i> fam. nov. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00226 Yakimov, M. M., Golyshin, P. N., Lang, S., Moore, E. R., Abraham, W. R., Lünsdorf, H., & Timmis, K. N. (1998). <i>Alcanivorax borkumensis</i> gen. nov., sp. nov., a new, hydrocarbon-degrading and surfactant-producing marine bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i>, 48(2), 339-348. doi:10.1099/00207713-48-2-339
Alkalilimnicola	Hoefl, S. E., Blum, J. S., Stolz, J. F., Tabita, F. R., Witte, B., King, G. M., Santini, J. M., & Oremland, R. S. (2007). <i>Alkalilimnicola ehrlichii</i> sp. nov., a novel, arsenite-oxidizing haloalkaliphilic gammaproteobacterium capable of chemoautotrophic or heterotrophic growth with nitrate or oxygen as the electron acceptor. <i>International journal of systematic and evolutionary microbiology</i> , 57(3), 504-512. doi:10.1099/ijss.0.64576-0
Amaricoccus	Maszenan, A. M., Seviour, R. J. and Patel, B. K. (2015). <i>Amaricoccus</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00851
Amphiplicatus	Zhen-Li, Z., Xin-Qi, Z., Nan, W., Wen-Wu, Z., Xu-Fen, Z., Yi, C., & Min, W. (2014). <i>Amphiplicatus metrioetherophilus</i> gen. nov., sp. nov., a thermotolerant alphaproteobacterium isolated from a hot spring. <i>International journal of systematic and evolutionary microbiology</i> , 64(8), 2805-2811. doi:10.1099/ijss.0.062471-0
Aquihabitans	Jin, L., Huy, H., Kim, K. K., Lee, H. G., Kim, H. S., Ahn, C. Y., & Oh, H. M. (2013). <i>Aquihabitans daechungensis</i> gen. nov., sp. nov., an actinobacterium isolated

	from reservoir water. <i>International journal of systematic and evolutionary microbiology</i> , 63(8), 2970-2974. doi:10.1099/ij.s.0.046060-0
Aquipuribacter	Tóth, E. M., Kéki, Z., Bohus, V., Borsodi, A. K., Márialigeti, K., & Schumann, P. (2012). Aquipuribacter hungaricus gen. nov., sp. nov., an actinobacterium isolated from the ultrapure water system of a power plant. <i>International journal of systematic and evolutionary microbiology</i> , 62(3), 556-562. doi:10.1099/ij.s.0.032672-0 Srinivas, T. N. R., Kumar, P. A., Tank, M., Sunil, B., Poorna, M., Zareena, B., & Shivaji, S. (2015). Aquipuribacter nitratreducens sp. nov., isolated from a soil sample of a mud volcano. <i>International journal of systematic and evolutionary microbiology</i> , 65(8), 2391-2396. doi:10.1099/ij.s.0.000269
Aquisalimonas	Márquez, M. C., Carrasco, I. J., Xue, Y., Ma, Y., Cowan, D. A., Jones, B. E., Grant, W. D., & Ventosa, A. (2007). Aquisalimonas asiatica gen. nov., sp. nov., a moderately halophilic bacterium isolated from an alkaline, saline lake in Inner Mongolia, China. <i>International journal of systematic and evolutionary microbiology</i> , 57(5), 1137-1142. doi:10.1099/ij.s.0.64916-0
Arthrobacter	Busse, H., Wieser, M. and Buczolits, S. (2015). Arthrobacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00118
Asticcacaulis	Poindexter, J. S. (2015). Asticcacaulis. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00790
Azoarcus	Reinhold-Hurek, B., Tan, Z. and Hurek, T. (2015). Azoarcus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00994
Beijerinckia	Arahal, D. R. (2016). Beijerinckia. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00795.pub2
Bradyrhizobium	Kuykendall, L. D. (2015). Bradyrhizobium. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00802
Caenimonas	Ryu, S. H., Lee, D. S., Park, M., Wang, Q., Jang, H. H., Park, W., & Jeon, C. O. (2008). Caenimonas koreensis gen. nov., sp. nov., isolated from activated sludge. <i>International journal of systematic and evolutionary microbiology</i> , 58(5), 1064-1068. doi:10.1099/ij.s.0.65416-0 Kim, S. J., Weon, H. Y., Kim, Y. S., Moon, J. Y., Seok, S. J., Hong, S. B., & Kwon, S. W. (2012). Caenimonas terrae sp. nov., isolated from a soil sample in Korea, and emended description of the genus Caenimonas Ryu et al. 2008. <i>Journal of Microbiology</i> , 50(5), 864-868. doi: 10.1007/s12275-012-1587-6
Candidatus Accumulibacter	Flowers, J. J., He, S., Yilmaz, S., Noguera, D. R. and McMahon, K. D. (2009), Denitrification capabilities of two biological phosphorus removal sludges dominated by different 'Candidatus Accumulibacter' clades. <i>Environmental Microbiology Reports</i> , 1: 583-588. doi:10.1111/j.1758-2229.2009.00090.x
Candidatus Alysiosphaera	Kragelund, C., Kong, Y., Van der Waarde, J., Thelen, K., Eikelboom, D., Tandoi, V., Thomsen, T. R., & Nielsen, P. H. (2006). Ecophysiology of different filamentous Alphaproteobacteria in industrial wastewater treatment plants. <i>Microbiology</i> , 152(10), 3003-3012. doi:10.1099/mic.0.29249-0
Candidatus Microthrix	McIlroy, S. J., Kristiansen, R., Albertsen, M., Karst, S. M., Rossetti, S., Nielsen, J. L., Tandoi, V., Seviour, R. J., & Nielsen, P. H. (2013). Metabolic model for the filamentous 'Candidatus Microthrix parvicella' based on genomic and metagenomic analyses. <i>The ISME journal</i> , 7(6), 1161. doi:10.1038/ismej.2013.6

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Catenulispora	Donadio, S. , Cavaletti, L. and Monciardini, P. (2015). Catenulispora. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00025
Caulobacter	Poindexter, J. S. (2015). Caulobacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00792
Chitinimonas	Chang, S. C., Wang, J. T., Vandamme, P., Hwang, J. H., Chang, P. S., & Chen, W. M. (2004). Chitinimonas taiwanensis gen. nov., sp. nov., a novel chitinolytic bacterium isolated from a freshwater pond for shrimp culture. <i>Systematic and applied microbiology</i> , 27(1), 43-49. Padakandla, S. R., & Chae, J. C. (2017). Chitinimonas naiadis sp. nov., isolated from a freshwater river. <i>J Microbiol Biotechnol</i> , 27, 1300-1305. doi:10.4014/jmb.1703.03075
Competibacter	Rubio-Rincón, F. J., Lopez-Vazquez, C. M., Welles, L., van Loosdrecht, M. C. M., & Brdjanovic, D. (2017). Cooperation between Candidatus Competibacter and Candidatus Accumulibacter clade I, in denitrification and phosphate removal processes. <i>Water research</i> , 120, 156-164. doi:10.1016/j.watres.2017.05.001 McIlroy, S. J., Albertsen, M., Andresen, E. K., Saunders, A. M., Kristiansen, R., Stokholm-Bjerregaard, M., Nielsen, K. L., & Nielsen, P. H. (2014). ‘Candidatus Competibacter’-lineage genomes retrieved from metagenomes reveal functional metabolic diversity. <i>The ISME journal</i> , 8(3), 613. doi:10.1038/ismej.2013.162
Conchiformibius	Xie, C. H., & Yokota, A. (2005). Phylogenetic analysis of Alysella and related genera of Neisseriaceae: Proposal of Alysella crassa comb. nov., Conchiformibium steedae gen. nov., comb. nov., Conchiformibium kuhniae sp. nov. and Bergeriella denitrificans gen. nov., comb. nov. <i>The Journal of general and applied microbiology</i> , 51(1), 1-10.
Conexibacter	Schumann, P. (2015). Conexibacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00225
Contendobacter	McIlroy, S. J., Albertsen, M., Andresen, E. K., Saunders, A. M., Kristiansen, R., Stokholm-Bjerregaard, M., Nielsen, K. L., & Nielsen, P. H. (2014). ‘Candidatus Competibacter’-lineage genomes retrieved from metagenomes reveal functional metabolic diversity. <i>The ISME journal</i> , 8(3), 613. doi:10.1038/ismej.2013.162
Craurococcus	Rathgeber, C. and Yurkov, V. V. (2015). Craurococcus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00882
Crenobacter	Dong, L., Ming, H., Zhou, E. M., Yin, Y. R., Liu, L., Feng, H. G., Xian, W. D., Nie, X., & Li, W. J. (2015). Crenobacter luteus gen. nov., sp. nov., isolated from a hot spring. <i>International journal of systematic and evolutionary microbiology</i> , 65(1), 214-219. doi:10.1099/ijs.0.060996-0
Cryobacterium	Liu, Q. , Zhou, Y. and Xin, Y. (2018). Cryobacterium. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00095.pub2
Defluviimonas	Foesel, B. U., Drake, H. L., & Schramm, A. (2011). Defluviimonas denitrificans gen. nov., sp. nov., and Pararhodobacter aggregans gen. nov., sp. nov., non-phototrophic Rhodobacteraceae from the biofilter of a marine aquaculture.

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Denitratisoma	Fahrbach, M., Kuever, J., Meinke, R., Kämpfer, P., & Hollender, J. (2006). <i>Denitratisoma oestradiolicum</i> gen. nov., sp. nov., a 17β-oestradiol-degrading, denitrifying betaproteobacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i>, 56(7), 1547-1552. doi:10.1099/ijs.0.63672-0
Emticicia	Liu, Q. M., Ten, L. N., Yu, H. S., Jin, F. X., Im, W. T., & Lee, S. T. (2008). <i>Emticicia ginsengisoli</i> sp. nov., a species of the family 'Flexibacteraceae' isolated from soil of a ginseng field. <i>International journal of systematic and evolutionary microbiology</i>, 58(5), 1100-1105. doi:10.1099/ijs.0.65386-0 Saha, P., & Chakrabarti, T. (2006). <i>Emticicia oligotrophica</i> gen. nov., sp. nov., a new member of the family 'Flexibacteraceae', phylum Bacteroidetes. <i>International journal of systematic and evolutionary microbiology</i>, 56(5), 991-995. doi: 10.1099/ijs.0.64086-0 Joung, Y., Seo, M. A., Kang, H., Kim, H., Ahn, T. S., Cho, J. C., & Joh, K. (2015). <i>Emticicia aquatica</i> sp. nov., a species of the family Cytophagaceae isolated from fresh water. <i>International journal of systematic and evolutionary microbiology</i>, 65(12), 4358-4362. doi:10.1099/ijsem.0.000577
Flavobacterium	Bernardet, J. and Bowman, J. P. (2015). <i>Flavobacterium</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00312
Gaiella	Albuquerque, L., Rainey, F. A. and Costa, M. S. (2018). <i>Gaiella</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01469
Geodermatophilus	Normand, P. and Benson, D. R. (2015). <i>Geodermatophilus</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00044
Haemophilus	Kilian, M. (2015). <i>Haemophilus</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01198
Haliea	Lucena, T., Pascual, J., Garay, E., Arahall, D. R., Macián, M. C., & Pujalte, M. J. (2010). <i>Haliea mediterranea</i> sp. nov., a marine gammaproteobacterium. <i>International journal of systematic and evolutionary microbiology</i>, 60(8), 1844-1848. doi:10.1099/ijs.0.017061-0 Urios, L., Intertaglia, L., Lesongeur, F., & Lebaron, P. (2009). <i>Haliea rubra</i> sp. nov., a member of the Gammaproteobacteria from the Mediterranean Sea. <i>International journal of systematic and evolutionary microbiology</i>, 59(5), 1188-1192. doi:10.1099/ijs.0.002220-0 Urios, L., Intertaglia, L., Lesongeur, F., & Lebaron, P. (2008). <i>Haliea salexigens</i> gen. nov., sp. nov., a member of the Gammaproteobacteria from the Mediterranean Sea. <i>International journal of systematic and evolutionary microbiology</i>, 58(5), 1233-1237. doi:10.1099/ijs.0.65470-0
Halothiobacillus	Kelly, D. P. and Wood, A. P. (2015). <i>Halothiobacillus</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M.

	Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01133
Herbaspirillum	Baldani, J. I., Baldani, V. L. and Döbereiner, J. (2015). Herbaspirillum. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00963
Hwangdonia	Jung, Y. T., Lee, J. S., & Yoon, J. H. (2013). Hwangdonia seohaensis gen. nov., sp. nov., a member of the family Flavobacteriaceae isolated from a tidal flat sediment. <i>International journal of systematic and evolutionary microbiology</i> , 63(9), 3186-3191. doi:10.1099/ijs.0.048744-0 Tang, M., Tan, L., Wu, H., Dai, S., Li, T., Chen, C., Li, J., Fan, J., Xiang, W., Li, X., & Wang, G. (2016). Gelatiniphilus marinus gen. nov., sp. nov., a bacterium from the culture broth of a microalga, Picochlorum sp. 122, and emended description of the genus Hwangdonia. <i>International journal of systematic and evolutionary microbiology</i> , 66(8), 2893-2898. doi:10.1099/ijsem.0.001074
Hydrogenophaga	Willems, A. and Gillis, M. (2015). Hydrogenophaga. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00947
Hydrogenophilales	Orlygsson, J., & Kristjansson, J. K. (2014). The Family Hydrogenophilaceae. In <i>The Prokaryotes</i> (pp. 859-868). Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-30197-1_244
Hyphomicrobium	Gliesche, C., Fesefeldt, A. and Hirsch, P. (2015). Hyphomicrobium. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00820
Iamia	Kurahashi, M., Fukunaga, Y., Sakiyama, Y., Harayama, S., & Yokota, A. (2009). Iamia majanohamensis gen. nov., sp. nov., an actinobacterium isolated from sea cucumber Holothuria edulis, and proposal of Iamiaceae fam. nov. <i>International journal of systematic and evolutionary microbiology</i> , 59(4), 869-873. doi:10.1099/ijs.0.005611-0
Ideonella	Malmqvist, Å., Moore, E. R. and Ternström, A. (2015). Incertae Sedis II. Ideonella. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00954
Janthinobacterium	Gillis, M. and Logan, N. A. (2015). Janthinobacterium. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00964 Gillis, M., & De Ley, J. (2006). The Genera Chromobacterium and Janthinobacterium. In <i>The Prokaryotes</i> (pp. 737-746). Springer, New York, NY. doi:10.1007/0-387-30745-1_32
Kaistia	Im, W. T., Yokota, A., Kim, M. K., & Lee, S. T. (2004). Kaistia adipata gen. nov., sp. nov., a novel α -proteobacterium. <i>The Journal of general and applied microbiology</i> , 50(5), 249-254. doi:10.2323/jgam.50.249 Lee, H. W., Yu, H. S., Liu, Q. M., Jung, H. M., An, D. S., Im, W. T., Jin, F. X., & Lee, S. T. (2007). Kaistia granuli sp. nov., isolated from anaerobic granules in an upflow anaerobic sludge blanket reactor. <i>International journal of systematic and evolutionary microbiology</i> , 57(10), 2280-2283. doi:10.1099/ijs.0.65023-0
Kingella	Henriksen, S. D., & Bøvre, K. (1976). Transfer of Moraxella kingae Henriksen and Bøvre to the genus Kingella gen. nov. in the family Neisseriaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 26(4), 447-450. doi:10.1099/00207713-26-4-447

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Knoellia	Groth, I. (2015). <i>Knoellia</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00079
Kocuria	Stackebrandt, E. and Schumann, P. (2015). <i>Kocuria</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00120
Magnetospirillum	Schüler, D. and Schleifer, K. (2015). <i>Magnetospirillum</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00893
Maricaulis	Poindexter, J. S. (2015). <i>Maricaulis</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00857
Marinicauda	Zhang, X. Y., Li, G. W., Wang, C. S., Zhang, Y. J., Xu, X. W., Li, H., Liu, A., Liu, C., Xie, B. B., Qin, Q. L., Xu, Z., Chen, X. L., Zhou, B. C., & Zhang, Y. Z. (2013). <i>Marinicauda pacifica</i> gen. nov., sp. nov., a prosthecate alphaproteobacterium of the family Hyphomonadaceae isolated from deep seawater. <i>International journal of systematic and evolutionary microbiology</i> , 63(6), 2248-2253. doi:10.1099/ijms.0.046656-0 Jeong, S. E., Jeon, S. H., Chun, B. H., Kim, D. W., & Jeon, C. O. (2017). <i>Marinicauda algicola</i> sp. nov., isolated from a marine red alga <i>Rhodorus marinus</i> . <i>International journal of systematic and evolutionary microbiology</i> , 67(9), 3423-3427. doi:10.1099/ijsem.0.002129
Marmoricola	Evtushenko, L. I. (2015). <i>Marmoricola</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00158
Meiothermus	Albuquerque, L., Rainey, F. A. and Costa, M. S. (2018). <i>Meiothermus</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00476.pub2
Methylibium	Nakatsu, C. H., Hristova, K., Hanada, S., Meng, X. Y., Hanson, J. R., Scow, K. M., & Kamagata, Y. (2006). <i>Methylibium petroleiphilum</i> gen. nov., sp. nov., a novel methyl tert-butyl ether-degrading methylotroph of the Betaproteobacteria. <i>International journal of systematic and evolutionary microbiology</i> , 56(5), 983-989. doi:10.1099/ijms.0.63524-0
Microbacterium	Suzuki, K. and Hamada, M. (2015). <i>Microbacterium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00104
Microlunatus	Hanada, S. and Nakamura, K. (2015). <i>Microlunatus</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00165
Micromonospora	Genilloud, O. (2015). <i>Micromonospora</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00148
Micropruina	Evtushenko, L. I. (2015). <i>Micropruina</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00166 Shintani, T., Liu, W. T., Hanada, S., Kamagata, Y., Miyaoka, S., Suzuki, T., & Nakamura, K. (2000). <i>Micropruina glycogenica</i> gen. nov., sp. nov., a new Gram-positive

	glycogen-accumulating bacterium isolated from activated sludge. <i>International journal of systematic and evolutionary microbiology</i> , 50(1), 201-207. doi:10.1099/00207713-50-1-201
Microvirga	Dahal, R. H., & Kim, J. (2017). <i>Microvirga soli</i> sp. nov., an alphaproteobacterium isolated from soil. <i>International journal of systematic and evolutionary microbiology</i> , 67(1), 127-132. doi:10.1099/ijsem.0.001582 Kanso, S., & Patel, B. K. (2003). <i>Microvirga subterranea</i> gen. nov., sp. nov., a moderate thermophile from a deep subsurface Australian thermal aquifer. <i>International journal of systematic and evolutionary microbiology</i> , 53(2), 401-406. doi:10.1099/ijms.0.02348-0
Moraxella	Juni, E. and Bøvre, K. (2015). <i>Moraxella</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01204
Nakamurellaceae	Sen, A., Daubin, V., Abrouk, D., Gifford, I., Berry, A. M., & Normand, P. (2014). Phylogeny of the class Actinobacteria revisited in the light of complete genomes. The orders 'Frankiales' and Micrococcales should be split into coherent entities: proposal of Frankiales ord. nov., Geodermatophilales ord. nov., Acidothermales ord. nov. and Nakamurellales ord. nov. <i>International journal of systematic and evolutionary microbiology</i> , 64(11), 3821-3832. doi:10.1099/ijms.0.063966-0 Yoon, J. H., Kang, S. J., Jung, S. Y., & Oh, T. K. (2007). <i>Humicoccus flavidus</i> gen. nov., sp. nov., isolated from soil. <i>International journal of systematic and evolutionary microbiology</i> , 57(1), 56-59. doi:10.1099/ijms.0.64246-0 Lee, S. D., Park, S. K., Yun, Y. W., & Lee, D. W. (2008). <i>Saxeibacter lacteus</i> gen. nov., sp. nov., an actinobacterium isolated from rock. <i>International journal of systematic and evolutionary microbiology</i> , 58(4), 906-909. doi:10.1099/ijms.0.65558-0
Neisseria	Tønjum, T. (2015). <i>Neisseria</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00981
Niastella	Weon, H. Y., Kim, B. Y., Yoo, S. H., Lee, S. Y., Kwon, S. W., Go, S. J., & Stackebrandt, E. (2006). <i>Niastella koreensis</i> gen. nov., sp. nov. and <i>Niastella yeongjuensis</i> sp. nov., novel members of the phylum Bacteroidetes, isolated from soil cultivated with Korean ginseng. <i>International journal of systematic and evolutionary microbiology</i> , 56(8), 1777-1782. doi:10.1099/ijms.0.64242-0 Kim, S. J., Ahn, J. H., Weon, H. Y., Hong, S. B., Seok, S. J., Kim, J. S., & Kwon, S. W. (2015). <i>Niastella gongjuensis</i> sp. nov., isolated from greenhouse soil. <i>International journal of systematic and evolutionary microbiology</i> , 65(9), 3115-3118. doi:10.1099/ijsem.0.000387
Nitrobacteria	Siddiqi, M. Z., Kim, S., Cho, J., Yoon, J., Joh, K., Seong, C., Bae, J., Jahng, K., Jeon, C., & Im, W. (2017). Description of 39 unrecorded bacterial species in Korea, belonging to the class Alphaproteobacteria. <i>Journal of Species Research</i> , 6(2), 141-153. Freitag, A. doi:10.12651/JSR.2017.6.2.141 Rudert, M. and Bock, E. (1987), Growth of <i>Nitrobacter</i> by dissimilatory nitrate reduction. <i>FEMS Microbiology Letters</i> , 48: 105-109. doi:10.1111/j.1574-6968.1987.tb02524.x
Nitrospina	Watson, S. W., & Waterbury, J. B. (1971). Characteristics of two marine nitrite oxidizing bacteria, <i>Nitrospina gracilis</i> nov. gen. nov. sp. and <i>Nitrococcus mobilis</i> nov. gen. nov. sp. <i>Archiv für Mikrobiologie</i> , 77(3), 203-230. doi:10.1007/BF00408114 Spieck, E., Keuter, S., Wenzel, T., Bock, E., & Ludwig, W. (2014). Characterization of a new marine nitrite oxidizing bacterium, <i>Nitrospina watsonii</i> sp. nov., a member of the newly proposed phylum "Nitrospinae". <i>Systematic and applied microbiology</i> , 37(3), 170-176. doi:10.1016/j.syapm.2013.12.005
Nitrospira	Spieck, E. and Bock, E. (2015). <i>Nitrospira</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00780

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Nitrospirillum	Chung, E. J., Park, T. S., Kim, K. H., Jeon, C. O., Lee, H. I., Chang, W. S., Aslam, Z., & Chung, Y. R. (2015). <i>Nitrospirillum irinus</i> sp. nov., a diazotrophic bacterium isolated from the rhizosphere soil of Iris and emended description of the genus <i>Nitrospirillum</i> . <i>Antonie van Leeuwenhoek</i> , 108(3), 721-729. doi:10.1007/s10482-015-0528-x Lin, S. Y., Hameed, A., Shen, F. T., Liu, Y. C., Hsu, Y. H., Shahina, M., Lai, W. A., & Young, C. C. (2014). Description of <i>Niveispirillum fermenti</i> gen. nov., sp. nov., isolated from a fermentor in Taiwan, transfer of <i>Azospirillum irakense</i> (1989) as <i>Niveispirillum irakense</i> comb. nov., and reclassification of <i>Azospirillum amazonense</i> (1983) as <i>Nitrospirillum amazonense</i> gen. nov. <i>Antonie van Leeuwenhoek</i> , 105(6), 1149-1162. doi:10.1007/s10482-014-0176-6
Nocardioides	Evtushenko, L. I., Krausova, V. I. and Yoon, J. (2015). <i>Nocardioides</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00159
Nocardiopsis	Hozzein, W. N. and Trujillo, M. E. (2015). <i>Nocardiopsis</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00195
Novosphingobium	Sohn, J. H., Kwon, K. K., Kang, J. H., Jung, H. B., & Kim, S. J. (2004). <i>Novosphingobium pentaromativorans</i> sp. nov., a high-molecular-mass polycyclic aromatic hydrocarbon-degrading bacterium isolated from estuarine sediment. <i>International journal of systematic and evolutionary microbiology</i> , 54(5), 1483-1487. doi:10.1099/ijs.0.02945-0
Oceanibaculum	Lai, Q., Yuan, J., Wu, C., & Shao, Z. (2009). <i>Oceanibaculum indicum</i> gen. nov., sp. nov., isolated from deep seawater of the Indian Ocean. <i>International journal of systematic and evolutionary microbiology</i> , 59(7), 1733-1737. doi:10.1099/ijs.0.004341-0 Dong, C., Lai, Q., Chen, L., Sun, F., Shao, Z., & Yu, Z. (2010). <i>Oceanibaculum pacificum</i> sp. nov., isolated from hydrothermal field sediment of the south-west Pacific Ocean. <i>International journal of systematic and evolutionary microbiology</i> , 60(1), 219-222. doi:10.1099/ijs.0.011932-0 Du, Y., Liu, X., Lai, Q., Li, W., Sun, F., & Shao, Z. (2017). <i>Oceanibaculum nanhaiense</i> sp. nov., isolated from surface seawater. <i>International journal of systematic and evolutionary microbiology</i> , 67(11), 4842-4845. doi:10.1099/ijsem.0.002388
Ornithinicoccus	Groth, I. (2015). <i>Ornithinicoccus</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00082
Paracoccus	Spanning, R. J., Stouthamer, A. H., Baker, S. C. and Verseveld, H. W. (2015). <i>Paracoccus</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00860
Paracraurococcus	Rathgeber, C. and Yurkov, V. V. (2015). <i>Paracraurococcus</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00885
Parasphingopyxis	Uchida, H., Hamana, K., Miyazaki, M., Yoshida, T., & Nogi, Y. (2012). <i>Parasphingopyxis lamellibrachiae</i> gen. nov., sp. nov., isolated from a marine annelid worm. <i>International journal of systematic and evolutionary microbiology</i> , 62(9), 2224-2228. doi:10.1099/ijs.0.034033-0

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Parvularcula	Cho, J. C., & Giovannoni, S. J. (2003). <i>Parvularcula bermudensis</i> gen. nov., sp. nov., a marine bacterium that forms a deep branch in the α-Proteobacteria. <i>International journal of systematic and evolutionary microbiology</i>, 53(4), 1031-1036. doi:10.1099/ijms.0.02566-0 Li, S., Tang, K., Liu, K., Yu, C. P., & Jiao, N. (2014). <i>Parvularcula oceanus</i> sp. nov., isolated from deep-sea water of the Southeastern Pacific Ocean. <i>Antonie van Leeuwenhoek</i>, 105(1), 245-251. doi:10.1007/s10482-013-0071-6 Zhang, X. Q., Wu, Y. H., Zhou, X., Zhang, X., Xu, X. W., & Wu, M. (2016). <i>Parvularcula flava</i> sp. nov., an alphaproteobacterium isolated from surface seawater of the South China Sea. <i>International journal of systematic and evolutionary microbiology</i>, 66(9), 3498-3502. doi:10.1099/ijsem.0.001225
Patulibacter	Takahashi, Y. (2015). <i>Patulibacter</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00226 Takahashi, Y., Matsumoto, A., Morisaki, K., & Ōmura, S. (2006). <i>Patulibacter minatonensis</i> gen. nov., sp. nov., a novel actinobacterium isolated using an agar medium supplemented with superoxide dismutase, and proposal of <i>Patulibacteraceae</i> fam. nov. <i>International journal of systematic and evolutionary microbiology</i>, 56(2), 401-406. doi:10.1099/ijms.0.63796-0 Reddy, G. S., & Garcia-Pichel, F. (2009). Description of <i>Patulibacter americanus</i> sp. nov., isolated from biological soil crusts, emended description of the genus <i>Patulibacter</i> Takahashi et al. 2006 and proposal of <i>Solirubrobacterales</i> ord. nov. and <i>Thermoleophilales</i> ord. nov. <i>International journal of systematic and evolutionary microbiology</i>, 59(1), 87-94. doi:10.1099/ijms.0.64185-0
Phreatobacter	Tóth, E. M., Vengring, A., Homonnay, Z. G., Kéki, Z., Spröer, C., Borsodi, A. K., Marialigeti, K., & Schumann, P. (2014). <i>Phreatobacter oligotrophus</i> gen. nov., sp. nov., an alphaproteobacterium isolated from ultrapure water of the water purification system of a power plant. <i>International journal of systematic and evolutionary microbiology</i>, 64(3), 839-845. doi:10.1099/ijms.0.053843-0 Lee, S. D., Joung, Y., & Cho, J. C. (2017). <i>Phreatobacter stygius</i> sp. nov., isolated from pieces of wood in a lava cave and emended description of the genus <i>Phreatobacter</i>. <i>International journal of systematic and evolutionary microbiology</i>, 67(9), 3296-3300. doi:10.1099/ijsem.0.002106 Kim, S. J., Ahn, J. H., Heo, J., Cho, H., Weon, H. Y., Hong, S. B., Kim, J. S., & Kwon, S. W. (2018). <i>Phreatobacter cathodiphilus</i> sp. nov., isolated from a cathode of a microbial fuel cell. <i>International journal of systematic and evolutionary microbiology</i>. doi:10.1099/ijsem.0.002904
Piscinibacter	Stackebrandt, E., Verbarg, S., Frühling, A., Busse, H. J., & Tindall, B. J. (2009). Dissection of the genus <i>Methylibium</i>: reclassification of <i>Methylibium fulvum</i> as <i>Rhizobacter fulvus</i> comb. nov., <i>Methylibium aquaticum</i> as <i>Piscinibacter aquaticus</i> gen. nov., comb. nov. and <i>Methylibium subsaxonicum</i> as <i>Rivibacter subsaxonicus</i> gen. nov., comb. nov. and emended descriptions of the genera <i>Rhizobacter</i> and <i>Methylibium</i>. <i>International journal of systematic and evolutionary microbiology</i>, 59(10), 2552-2560. doi:10.1099/ijms.0.008383-0 Chen, D. Z., Yu, N. N., Chu, Q. Y., Chen, J., Ye, J. X., Cheng, Z. W., Zhang, S. H. & Chen, J. M. (2018). <i>Piscinibacter caeni</i> sp. nov., isolated from activated sludge. <i>International journal of systematic and evolutionary microbiology</i>. doi:10.1099/ijsem.0.002891 Cho, S. H., Lee, H. J., & Jeon, C. O. (2016). <i>Piscinibacter defluvii</i> sp. nov., isolated from a sewage treatment plant, and emended description of the genus <i>Piscinibacter</i>

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Plantactinospora	Li, W. and Salam, N. (2016). Plantactinospora. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01318
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Povalibacter	Nogi, Y., Yoshizumi, M., Hamana, K., Miyazaki, M., & Horikoshi, K. (2014). Povalibacter uvarum gen. nov., sp. nov., a polyvinyl-alcohol-degrading bacterium isolated from grapes. <i>International journal of systematic and evolutionary microbiology</i> , 64(8), 2712-2717. doi:10.1099/ijse.0.062620-0
Promicromonospora	Schumann, P. and Stackebrandt, E. (2015). Promicromonospora. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00130
Prosthecomicrobium	Jenkins, C., Rainey, F. A., Ward, N. L. and Staley, J. T. (2015). Prosthecomicrobium. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00824
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Pseudorhodobacter	Uchino, Y., Hamada, T., & Yokota, A. (2002). Proposal of Pseudorhodobacter ferrugineus gen. nov., comb. nov., for a non-photosynthetic marine bacterium,

	<i>Agrobacterium ferrugineum</i>, related to the genus <i>Rhodobacter</i>. <i>The Journal of general and applied microbiology</i>, 48(6), 309-319. Li, A. H., Liu, H. C., Hou, W. G., & Zhou, Y. G. (2016). <i>Pseudorhodobacter sinensis</i> sp. nov. and <i>Pseudorhodobacter aquaticus</i> sp. nov., isolated from crater lakes. <i>International journal of systematic and evolutionary microbiology</i>, 66(8), 2819-2824. doi:10.1099/ijsem.0.001061 Zhang, Y., Jiang, F., Chang, X., Qiu, X., Ren, L., Qu, Z., Deng, S., Da, X., Kan, W., Kim, M., Fang, C., & Peng, F. (2016). <i>Pseudorhodobacter collinsensis</i> sp. nov., isolated from a till sample of an icecap front. <i>International journal of systematic and evolutionary microbiology</i>, 66(1), 178-183. doi:10.1099/ijsem.0.000693
Reyranella	Cui, Y., Chun, S. J., Ko, S. R., Lee, H. G., Srivastava, A., Oh, H. M., & Ahn, C. Y. (2017). <i>Reyranella aquatilis</i> sp. nov., an alphaproteobacterium isolated from a eutrophic lake. <i>International journal of systematic and evolutionary microbiology</i>, 67(9), 3496-3500. doi:10.1099/ijsem.0.002151 Pagnier, I., Raoult, D., & La Scola, B. (2011). Isolation and characterization of <i>Reyranella massiliensis</i> gen. nov., sp. nov. from freshwater samples by using an amoeba co-culture procedure. <i>International journal of systematic and evolutionary microbiology</i>, 61(9), 2151-2154. doi:10.1099/ijse.0.025775-0
Rhizobacter	Zhang, L. (2017). <i>Rhizobacter</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01211.pub2
Rhodanobacter	Kostka, J. E., Green, S. J., Rishishwar, L., Prakash, O., Katz, L. S., Mariño-Ramírez, L., Jordan, I. K., Munk, C., Ivanova, N., Mikhailova, N., Watson, D. B., Brown, S. D., Palumbo, A. V., & Brooks, S. C. (2012). Genome sequences for six <i>Rhodanobacter</i> strains, isolated from soils and the terrestrial subsurface, with variable denitrification capabilities. <i>Journal of bacteriology</i>, 194(16), 4461-4462. doi:10.1128/JB.00871-12
Rhodococcus	Jones, A. L. and Goodfellow, M. (2015). <i>Rhodococcus</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00033
Rivibacter	Stackebrandt, E., Verbarg, S., Frühling, A., Busse, H. J., & Tindall, B. J. (2009). Dissection of the genus <i>Methylibium</i>: reclassification of <i>Methylibium fulvum</i> as <i>Rhizobacter fulvus</i> comb. nov., <i>Methylibium aquaticum</i> as <i>Piscinibacter aquaticus</i> gen. nov., comb. nov. and <i>Methylibium subsaxonicum</i> as <i>Rivibacter subsaxonicus</i> gen. nov., comb. nov. and emended descriptions of the genera <i>Rhizobacter</i> and <i>Methylibium</i>. <i>International journal of systematic and evolutionary microbiology</i>, 59(10), 2552-2560. doi:10.1099/ijse.0.008383-0
Roseomonas	Weyant, R. S. and Whitney, A. M. (2015). <i>Roseomonas</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00888
Rubellimicrobium	Denner, E. B., Kolari, M., Hoornstra, D., Tsitko, I., Kämpfer, P., Busse, H. J., & Salkinoja-Salonen, M. (2006). <i>Rubellimicrobium thermophilum</i> gen. nov., sp. nov., a red-pigmented, moderately thermophilic bacterium isolated from coloured slime deposits in paper machines. <i>International journal of systematic and evolutionary microbiology</i>, 56(6), 1355-1362. doi:10.1099/ijse.0.063751-0 Cao, Y. R., Jiang, Y., Wang, Q., Tang, S. K., He, W. X., Xue, Q. H., Xu, L. H., & Jiang, C. L. (2010). <i>Rubellimicrobium roseum</i> sp. nov., a Gram-negative bacterium isolated from the forest soil sample. <i>Antonie van Leeuwenhoek</i>, 98(3), 389-394. doi:10.1007/s10482-010-9452-2
Ruegeria	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S., (2015). <i>Ruegeria</i>. In <i>Bergey's Manual of Systematics of Archaea</i>

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Saccharospirillum	Choi, A., Oh, H. M., & Cho, J. C. (2011). <i>Saccharospirillum aestuarii</i> sp. nov., isolated from tidal flat sediment, and an emended description of the genus <i>Saccharospirillum</i>. <i>International journal of systematic and evolutionary microbiology</i>, 61(3), 487-492. doi:10.1099/ijs.0.022996-0 Labrenz, M., Lawson, P. A., Tindall, B. J., Collins, M. D., & Hirsch, P. (2003). <i>Saccharospirillum impatiens</i> gen. nov., sp. nov., a novel γ-Proteobacterium isolated from hypersaline Ekho Lake (East Antarctica). <i>International journal of systematic and evolutionary microbiology</i>, 53(3), 653-660. doi:10.1099/ijs.0.02406-0 Chen, Y. G., Cui, X. L., Li, Q. Y., Wang, Y. X., Tang, S. K., Liu, Z. X., Wen, M. L., Peng, Q., & Xu, L. H. (2009). <i>Saccharospirillum salsuginis</i> sp. nov., a gammaproteobacterium from a subterranean brine. <i>International journal of systematic and evolutionary microbiology</i>, 59(6), 1382-1386. doi:10.1099/ijs.0.003616-0
Salinibacterium	Han, S. K., Nedashkovskaya, O. I., Mikhailov, V. V., Kim, S. B., & Bae, K. S. (2003). <i>Salinibacterium amurskyense</i> gen. nov., sp. nov., a novel genus of the family Microbacteriaceae from the marine environment. <i>International journal of systematic and evolutionary microbiology</i>, 53(6), 2061-2066. doi:10.1099/ijs.0.02627-0 Zhang, D. C., Liu, H. C., Xin, Y. H., Yu, Y., Zhou, P. J., & Zhou, Y. G. (2008). <i>Salinibacterium xinjiangense</i> sp. nov., a psychrophilic bacterium isolated from the China No. 1 glacier. <i>International journal of systematic and evolutionary microbiology</i>, 58(12), 2739-2742. doi:10.1099/ijs.0.65802-0
Schlegelella	Chou, Y. J., Sheu, S. Y., Sheu, D. S., Wang, J. T., & Chen, W. M. (2006). <i>Schlegelella aquatica</i> sp. nov., a novel thermophilic bacterium isolated from a hot spring. <i>International journal of systematic and evolutionary microbiology</i>, 56(12), 2793-2797. doi:10.1099/ijs.0.64446-0 Elbanna, K., Lütke-Eversloh, T., Van Trappen, S., Mergaert, J., Swings, J., & STEINBÜCHEL, A. (2003). <i>Schlegelella thermodepolymerans</i> gen. nov., sp. nov., a novel thermophilic bacterium that degrades poly (3-hydroxybutyrate-co-3-mercaptopropionate). <i>International journal of systematic and evolutionary microbiology</i>, 53(4), 1165-1168. doi:10.1099/ijs.0.02562-0
Schlesneria	Dedysh, S. N., Kulichevskaya, I. S. and Zavarzin, G. A. (2015). <i>Schlesneria</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00788
Sporichthya	Normand, P. and Benson, D. R. (2015). <i>Sporichthya</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00048 Tamura, T., Hayakawa, M., & Hatano, K. (1999). <i>Sporichthya brevicatena</i> sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i>, 49(4), 1779-1784. doi:10.1099/00207713-49-4-1779
Sporosarcina	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S., (2015). <i>Sporosarcina</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00563
Steroidobacter	Fahrbach, M., Kuever, J., Remesch, M., Huber, B. E., Kämpfer, P., Dott, W., & Hollender, J. (2008). <i>Steroidobacter denitrificans</i> gen. nov., sp. nov., a steroidal hormone-degrading gammaproteobacterium. <i>International journal of systematic and evolutionary microbiology</i> , 58(9), 2215-2223. doi:10.1099/ijs.0.65342-0

Sterolibacterium	Tarlera, S., & Denner, E. B. (2003). Sterolibacterium denitrificans gen. nov., sp. nov., a novel cholesterol-oxidizing, denitrifying member of the β -Proteobacteria. <i>International journal of systematic and evolutionary microbiology</i> , 53(4), 1085-1091. doi:10.1099/ijs.0.02039-0
Streptomyces	Kämpfer, P. (2015). Streptomyces. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00191
Subaequorebacter	del Rocío Bustillos-Cristales, M., Corona-Gutierrez, I., Castañeda-Lucio, M., Águila-Zempoaltécatl, C., Seynos-García, E., Hernández-Lucas, I., Muñoz-Rojas, J., Medina-Aparicio, L., & Fuentes-Ramírez, L. E. (2017). Culturable facultative methylotrophic bacteria from the cactus Neobuxbaumia macrocephala possess the locus xoxF and consume methanol in the presence of Ce ³⁺ and Ca ²⁺ . <i>Microbes and environments</i> , 32(3), 244-251. doi:10.1264/jsme2.ME17070 Foesel, B. U., Gößner, A. S., Drake, H. L., & Schramm, A. (2007). Geminicoccus roseus gen. nov., sp. nov., an aerobic phototrophic Alphaproteobacterium isolated from a marine aquaculture biofilter. <i>Systematic and applied microbiology</i> , 30(8), 581-586. doi:10.1016/j.syapm.2007.05.005
Sulfuricella	Kojima, H., & Fukui, M. (2010). Sulfuricella denitrificans gen. nov., sp. nov., a sulfur-oxidizing autotroph isolated from a freshwater lake. <i>International journal of systematic and evolutionary microbiology</i> , 60(12), 2862-2866. doi:10.1099/ijs.0.016980-0
Sulfurisoma	Kojima, H., & Fukui, M. (2014). Sulfurisoma sediminicola gen. nov., sp. nov., a facultative autotroph isolated from a freshwater lake. <i>International journal of systematic and evolutionary microbiology</i> , 64(5), 1587-1592. doi:10.1099/ijs.0.057281-0
Sulfuritalea	Watanabe, T., Miura, A., Iwata, T., Kojima, H. and Fukui, M. (2017), Dominance of Sulfuritalea species in nitrate-depleted water of a stratified freshwater lake and arsenate respiration ability within the genus. <i>Environmental Microbiology Reports</i> , 9: 522-527. doi:10.1111/1758-2229.12557
Tabrizicola	Tarhriz, V., Thiel, V., Nematzadeh, G., Hejazi, M. A., Imhoff, J. F., & Hejazi, M. S. (2013). Tabrizicola aquatica gen. nov. sp. nov., a novel alphaproteobacterium isolated from Qurugöl Lake nearby Tabriz city, Iran. <i>Antonie van Leeuwenhoek</i> , 104(6), 1205-1215. doi:10.1007/s10482-013-0042-y Ko, D. J., Kim, J. S., Park, D. S., Lee, D. H., Heo, S. Y., Seo, J. W., Kim, C. H., & Oh, B. R. (2018). Tabrizicola fusiformis sp. nov., isolated from an industrial wastewater treatment plant. <i>International journal of systematic and evolutionary microbiology</i> . doi:10.1099/ijsem.0.002760
Taonella	Xi, X. D., Dong, W. L., Zhang, J., Huang, Y., & Cui, Z. L. (2013). Taonella mepensis gen. nov., sp. nov., a member of the family Rhodospirillaceae isolated from activated sludge. <i>International journal of systematic and evolutionary microbiology</i> , 63(7), 2472-2476. doi:10.1099/ijs.0.047803-0
Tepidamorphus	Albuquerque, L., Rainey, F. A., Pena, A., Tiago, I., Veríssimo, A., Nobre, M. F., & da Costa, M. S. (2010). Tepidamorphus gemmatus gen. nov., sp. nov., a slightly thermophilic member of the Alphaproteobacteria. <i>Systematic and applied microbiology</i> , 33(2), 60-66. doi:10.1016/j.syapm.2010.01.002
Terasakiella	Satomi, M., Kimura, B., Hamada, T., Harayama, S., & Fujii, T. (2002). Phylogenetic study of the genus Oceanospirillum based on 16S rRNA and gyrB genes: emended description of the genus Oceanospirillum, description of Pseudospirillum gen. nov., Oceanobacter gen. nov. and Terasakiella gen. nov. and transfer of Oceanospirillum jannaschii and Pseudomonas stanieri to Marinobacterium as Marinobacterium jannaschii comb. nov. and Marinobacterium stanieri comb. no. <i>International journal of systematic and evolutionary microbiology</i> , 52(3), 739-747. doi:10.1099/00207713-52-3-739

	Yoon, J., & Kang, D. H. (2018). <i>Terasakiella salincola</i> sp. nov., a marine alphaproteobacterium isolated from seawater, and emended description of the genus <i>Terasakiella</i>. <i>International Journal of Systematic and Evolutionary Microbiology</i>. doi:10.1099/ijsem.0.002788 Han, S. B., Su, Y., Hu, J., Wang, R. J., Sun, C., Wu, D., Zhu, X. F., & Wu, M. (2016). <i>Terasakiella brassicae</i> sp. nov., isolated from the wastewater of a pickle-processing factory, and emended descriptions of <i>Terasakiella pusilla</i> and the genus <i>Terasakiella</i>. <i>International journal of systematic and evolutionary microbiology</i>, 66(4), 1807-1812. doi:10.1099/ijsem.0.000946
Terrabacter	Stackebrandt, E. (2015). <i>Terrabacter</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00087
Terrimonas	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S., (2015). <i>Terrimonas</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00355
Tetrasphaera	Seviour, R. J. and Maszenan, A. M. (2015). <i>Tetrasphaera</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00089
Thauera	Heider, J. and Fuchs, G. (2015). <i>Thauera</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01004
Thioalkalivibrio	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S., (2015). <i>Thioalkalivibrio</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01131
Thiohalomonas	Sorokin, D. Y., Tourova, T. P., Braker, G., & Muyzer, G. (2007). <i>Thiohalomonas denitrificans</i> gen. nov., sp. nov. and <i>Thiohalomonas nitratireducens</i> sp. nov., novel obligately chemolithoautotrophic, moderately halophilic, thiodenitrifying Gammaproteobacteria from hypersaline habitats. <i>International journal of systematic and evolutionary microbiology</i> , 57(7), 1582-1589. doi:10.1099/ijms.0.65112-0
Thiomonas	Kelly, D. P. and Wood, A. P. (2015). <i>Incertae Sedis VIII. Thiomonas</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00960
Zoogloea	Unz, R. F. (2015). <i>Zoogloea</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01005

Aerobic, Nitrate Reducing, Iron Reducing Bacteria

Anaeromyxobacter	Weber, K. A., Achenbach, L. A., & Coates, J. D. (2006). Microorganisms pumping iron: anaerobic microbial iron oxidation and reduction. <i>Nature Reviews Microbiology</i>, 4(10), 752. doi:10.1038/nrmicro1490 Wu, Q., Sanford, R. A., & Löffler, F. E. (2006). Uranium (VI) reduction by <i>Anaeromyxobacter dehalogenans</i> strain 2CP-C. <i>Applied and environmental microbiology</i>, 72(5), 3608-3614. doi:10.1128/AEM.72.5.3608-3614.2006
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	Kuever, J. , Rainey, F. A. and Widdel, F. W. (2015). Deltaproteobacteria class nov.. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.cbm00043
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Aerobic, Nitrate Reducing, Iron Reducing, Fermenting Bacteria

Bacillus	Weber, K. A., Achenbach, L. A., & Coates, J. D. (2006). Microorganisms pumping iron: anaerobic microbial iron oxidation and reduction. <i>Nature Reviews Microbiology</i> , 4(10), 752. doi:10.1038/nrmicro1490 Logan, N. A. and Vos, P. D. (2015). Bacillus. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00530
Paludibaculum	Kulichevskaya, I. S., Suzina, N. E., Rijpstra, W. I. C., Damste, J. S. S., & Dedysh, S. N. (2014). Paludibaculum fermentans gen. nov., sp. nov., a facultative anaerobe capable of dissimilatory iron reduction from subdivision 3 of the Acidobacteria. <i>International journal of systematic and evolutionary microbiology</i> , 64(8), 2857-2864. doi:10.1099/ijs.0.066175-0
Rhizomicrobium	Ueki, A., Kodama, Y., Kaku, N., Shiromura, T., Satoh, A., Watanabe, K., & Ueki, K. (2010). Rhizomicrobium palustre gen. nov., sp. nov., a facultatively anaerobic, fermentative stalked bacterium in the class Alphaproteobacteria isolated from rice plant roots. <i>The Journal of general and applied microbiology</i> , 56(3), 193-203. doi:10.2323/jgam.56.193 Kodama, Y., & Watanabe, K. (2011). Rhizomicrobium electricum sp. nov., a facultatively anaerobic, fermentative, prosthecate bacterium isolated from a cellulose-fed microbial fuel cell. <i>International journal of systematic and evolutionary microbiology</i> , 61(8), 1781-1785. doi:10.1099/ijs.0.023580-0
Shewanella	Bowman, J. P. (2015). Shewanella. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01100 Richter, H., Lanthier, M., Nevin, K. P., & Lovley, D. R. (2007). Lack of electricity production by Pelobacter carbinolicus indicates that the capacity for Fe (III) oxide reduction does not necessarily confer electron transfer ability to fuel cell anodes. <i>Applied and environmental microbiology</i> , 73(16), 5347-5353. doi:10.1128/AEM.00804-07

Aerobic, Nitrate Reducing, Fermenting Bacteria

Actinomyces	Schaal, K. P. and Yassin, A. A. (2015). Actinomyces. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00012
Actinotalea	Yi, H., Schumann, P., & Chun, J. (2007). Demequina aestuarii gen. nov., sp. nov., a novel actinomycete of the suborder Micrococccineae, and reclassification of Cellulomonas fermentans Bagnara et al. 1985 as Actinotalea fermentans gen. nov., comb. nov. <i>International journal of systematic and evolutionary microbiology</i> , 57(1), 151-156. doi:10.1099/ijs.0.64525-0 Bagnara, C., Toci, R., Gaudin, C., & Belaich, J. P. (1985). Isolation and characterization of a cellulolytic microorganism, Cellulomonas fermentans sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 35(4), 502-507. doi:10.1099/00207713-35-4-502

	Yan, Z. F., Lin, P., Li, C. T., Kook, M., & Yi, T. H. (2018). <i>Actinotalea solisilvae</i> sp. nov., isolated from forest soil and emended description of the genus <i>Actinotalea</i> . <i>International journal of systematic and evolutionary microbiology</i> . doi:10.1099/ijsem.0.002584
Cellulomonas	Stackebrandt, E. and Schumann, P. (2015). <i>Cellulomonas</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00063
Corynebacterium	Bernard, K. A. and Funke, G. (2015). <i>Corynebacterium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00026
Gemmobacter	Hirsch, P. and Schlesner, H. (2015). <i>Gemmobacter</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00853
Kouleothrix	Ward, L. M., Hemp, J., Shih, P. M., McGlynn, S. E., & Fischer, W. W. (2018). Evolution of phototrophy in the Chloroflexi phylum driven by horizontal gene transfer. <i>Frontiers in microbiology</i> , 9, 260. doi:10.3389/fmicb.2018.00260
Lentzea	Hansel, C. M., Lentini, C. J., Tang, Y., Johnston, D. T., Wankel, S. D., & Jardine, P. M. (2015). Dominance of sulfur-fueled iron oxide reduction in low-sulfate freshwater sediments. <i>The ISME journal</i> , 9(11), 2400. doi:10.1038/ismej.2015.50 Labeda, D. P. (2015). <i>Lentzea</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00182
Microbulbifer	Miyazaki, M., Nogi, Y., Ohta, Y., Hatada, Y., Fujiwara, Y., Ito, S., & Horikoshi, K. (2008). <i>Microbulbifer agarilyticus</i> sp. nov. and <i>Microbulbifer thermotolerans</i> sp. nov., agar-degrading bacteria isolated from deep-sea sediment. <i>International journal of systematic and evolutionary microbiology</i> , 58(5), 1128-1133. doi:10.1099/ijms.0.65507-0 González, J. M., Mayer, F., Moran, M. A., Hodson, R. E., & Whitman, W. B. (1997). <i>Microbulbifer hydrolyticus</i> gen. nov., sp. nov., and <i>Marinobacterium georgiense</i> gen. nov., sp. nov., two marine bacteria from a lignin-rich pulp mill waste enrichment community. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 47(2), 369-376. doi:10.1099/00207713-47-2-369 Ohta, Y. A., Hatada, Y., Nogi, Y., Miyazaki, M., Li, Z., Akita, M., Hidaka, Y., Goda, S., Ito, S., & Horikoshi, K. (2004). Enzymatic properties and nucleotide and amino acid sequences of a thermostable β -agarase from a novel species of deep-sea <i>Microbulbifer</i> . <i>Applied microbiology and biotechnology</i> , 64(4), 505-514. doi:10.1007/s00253-004-1573-y
Paenibacillus	Priest, F. G. (2015). <i>Paenibacillus</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00553
Photobacterium	Thyssen, A. and Ollevier, F. (2015). <i>Photobacterium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01076
Phycisphaera	Fukunaga, Y., Kurahashi, M., Sakiyama, Y., Ohuchi, M., Yokota, A., & Harayama, S. (2009). <i>Phycisphaera mikurensis</i> gen. nov., sp. nov., isolated from a marine alga, and proposal of <i>Phycisphaeraceae</i> fam. nov., <i>Phycisphaerales</i> ord. nov. and <i>Phycisphaerae</i> classis nov. in the phylum Planctomycetes. <i>The Journal of general and applied microbiology</i> , 55(4), 267-275. Yoon, J., Jang, J. H., & Kasai, H. (2014). <i>Algisphaera agarilytica</i> gen. nov., sp. nov., a novel representative of the class <i>Phycisphaerae</i> within the phylum Planctomycetes isolated

	from a marine alga. <i>Antonie Van Leeuwenhoek</i> , 105(2), 317-324. doi:10.1007/s10482-013-0076-1
Planctomyces	Ward, N. L., Staley, J. T. and Schmidt, J. M. (2015). Planctomyces. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00786
Propionibacterium	Patrick, S. and McDowell, A. (2015). Propionibacterium. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00167
Propioniferax	Yokota, A. (2015). Propioniferax. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00170
Rothia	Austin, B. (2015). Rothia. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00124
Saccharibacillus	Rivas, R., Garcia-Fraile, P., Zurdo-Pineiro, J. L., Mateos, P. F., Martinez-Molina, E., Bedmar, E. J., Sanchez-Raya, J., & Velazquez, E. (2008). <i>Saccharibacillus sacchari</i> gen. nov., sp. nov., isolated from sugar cane. <i>International journal of systematic and evolutionary microbiology</i> , 58(8), 1850-1854. doi:10.1099/ijs.0.65499-0 Kämpfer, P., Busse, H. J., Kleinhagauer, T., McInroy, J. A., & Glaeser, S. P. (2016). <i>Saccharibacillus endophyticus</i> sp. nov., an endophyte of cotton. <i>International journal of systematic and evolutionary microbiology</i> , 66(12), 5134-5139. doi:10.1099/ijsem.0.001484 Sun, J. Q., Wang, X. Y., Wang, L. J., Xu, L., Liu, M., & Wu, X. L. (2016). <i>Saccharibacillus deserti</i> sp. nov., isolated from desert soil. <i>International journal of systematic and evolutionary microbiology</i> , 66(2), 623-627. doi:10.1099/ijsem.0.000766
Sanguibacter	Ramos, C. P. and Fernández-Garayzábal, J. F. (2015). Sanguibacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00137 Ramos, C. P. and Fernández-Garayzábal, J. F. (2015). Sanguibacteraceae. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00040
Skermanella	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S., (2015). Skermanella. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00901
Staphylococcus	Schleifer, K. and Bell, J. A. (2015). Staphylococcus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00569
Streptococcus	Whiley, R. A. and Hardie, J. M. (2015). Streptococcus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00612
Thermogutta	Slobodkina, G. B., Kovaleva, O. L., Miroshnichenko, M. L., Slobodkin, A. I., Kolganova, T. V., Novikov, A. A., van Heerden, E., & Bonch-Osmolovskaya, E. A. (2015). <i>Thermogutta terrifontis</i> gen. nov., sp. nov. and <i>Thermogutta hypogea</i> sp. nov., thermophilic anaerobic representatives of the phylum Planctomycetes. <i>International journal of systematic and evolutionary microbiology</i> , 65(3), 760-765. doi:10.1099/ijs.0.000009
Vibrio	Farmer, J. , Michael Janda, J. , Brenner, F. W., Cameron, D. N. and Birkhead, K. M. (2015). Vibrio. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W.

	B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01078
Zhizhongheella	Dong, L., Ming, H., Liu, L., Zhou, E. M., Yin, Y. R., Duan, Y. Y., Nie, G. X., Feng, H. G., & Li, W. J. (2014). Zhizhongheella caldifontis gen. nov., sp. nov., a novel member of the family Comamonadaceae. <i>Antonie van Leeuwenhoek</i> , 105(4), 755-761. doi:10.1007/s10482-014-0131-6

Aerobic, Iron Reducing Bacteria

Aciditerrimonas	Itoh, T., Yamanoi, K., Kudo, T., Ohkuma, M., & Takashina, T. (2011). Aciditerrimonas ferrireducens gen. nov., sp. nov., an iron-reducing thermoacidophilic actinobacterium isolated from a solfataric field. <i>International journal of systematic and evolutionary microbiology</i> , 61(6), 1281-1285. doi:10.1099/ijs.0.023044-0
Sulfobacillus	Costa, M. S., Rainey, F. A. and Albuquerque, L. (2015). Sulfobacillus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00729

Aerobic, Iron Reducing, Fermenting Bacteria

Acidobacterium	Weber, K. A., Achenbach, L. A., & Coates, J. D. (2006). Microorganisms pumping iron: anaerobic microbial iron oxidation and reduction. <i>Nature Reviews Microbiology</i> , 4(10), 752. doi:10.1038/nrmicro1490 Thrash, J. C. and Coates, J. D. (2015). Acidobacterium. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00001 Pankratov, T. A., Kirsanova, L. A., Kaparullina, E. N., Kevbrin, V. V., & Dedysh, S. N. (2012). Telmatobacter bradus gen. nov., sp. nov., a cellulolytic facultative anaerobe from subdivision 1 of the Acidobacteria, and emended description of Acidobacterium capsulatum Kishimoto et al. 1991. <i>International journal of systematic and evolutionary microbiology</i> , 62(2), 430-437. doi:10.1099/ijs.0.029629-0
Rhodoferax	Richter, H., Lanthier, M., Nevin, K. P., & Lovley, D. R. (2007). Lack of electricity production by Pelobacter carbinolicus indicates that the capacity for Fe (III) oxide reduction does not necessarily confer electron transfer ability to fuel cell anodes. <i>Applied and environmental microbiology</i> , 73(16), 5347-5353. doi:10.1128/AEM.00804-07 Hiraishi, A. and Imhoff, J. F. (2015). Rhodoferax. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00951
Sulfurospirillum	Weber, K. A., Achenbach, L. A., & Coates, J. D. (2006). Microorganisms pumping iron: anaerobic microbial iron oxidation and reduction. <i>Nature Reviews Microbiology</i> , 4(10), 752. doi:10.1038/nrmicro1490 Stolz, J. F., Oremland, R. S., Paster', B. J., Dewhirst, F. E. and Vandamme, P. (2015). Sulfurospirillum. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01072

Aerobic, Fermenting Bacteria

Demequina	Yi, H., Schumann, P., & Chun, J. (2007). <i>Demequina aestuarii</i> gen. nov., sp. nov., a novel actinomycete of the suborder Micrococcineae, and reclassification of <i>Cellulomonas fermentans</i> Bagnara et al. 1985 as <i>Actinotalea fermentans</i> gen. nov., comb. nov. <i>International journal of systematic and evolutionary microbiology</i>, 57(1), 151-156. doi:10.1099/ijs.0.64525-0 Park, S., Jung, Y. T., Won, S. M., Lee, J. S., & Yoon, J. H. (2015). <i>Demequina activiva</i> sp. nov., isolated from a tidal flat. <i>International journal of systematic and evolutionary microbiology</i>, 65(7), 2042-2047. doi:10.1099/ijs.0.000217 Ue, H., Matsuo, Y., Kasai, H., & Yokota, A. (2011). <i>Demequina globuliformis</i> sp. nov., <i>Demequina oxidasica</i> sp. nov. and <i>Demequina aurantiaca</i> sp. nov., actinobacteria isolated from marine environments, and proposal of <i>Demequinaceae</i> fam. nov. <i>International journal of systematic and evolutionary microbiology</i>, 61(6), 1322-1329. doi:10.1099/ijs.0.024299-0
Abiotrophia	Ezaki, T. and Kawamura, Y. (2015). <i>Abiotrophia</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00580
Brochothrix	Sneath, P. H. (2015). <i>Brochothrix</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00546
Gemella	Collins, M. D. and Falsen, E. (2015). <i>Gemella</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00578
Granulicatella	Lawson, P. A. (2015). <i>Granulicatella</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00596
Ignavibacterium	Iino, T. (2018). <i>Ignavibacterium</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01505
Lacibacterium	Sheu, S. Y., Chen, Y. L., Young, C. C., & Chen, W. M. (2013). <i>Lacibacterium aquatile</i> gen. nov., sp. nov., a new member of the family Rhodospirillaceae isolated from a freshwater lake. <i>International journal of systematic and evolutionary microbiology</i>, 63(12), 4797-4804. doi:10.1099/ijs.0.055145-0
Leptotrichia	Eisenberg, T. , Glaeser, S. P., Blom, J. and Kämpfer, P. (2018). <i>Leptotrichia</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00771.pub2
Nostocoida type II	Seviour, E. M., Eales, K., Izzard, L., Beer, M., Carr, E. L., & Seviour, R. J. (2006). The in situ physiology of nostocoida limicola II, a filamentous bacterial morphotype in bulking activated sludge, using fluorescence in situ hybridization and microautoradiography. <i>Water Science and Technology</i>, 54(1), 47-53. doi:10.2166/wst.2006.370
Rubrivivax	Imhoff, J. F. (2015). <i>Incertae Sedis V. Rubrivivax</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00957
Telmatospirillum	Sizova, M. V., Panikov, N. S., Spiridonova, E. M., Slobodova, N. V., & Tourova, T. P. (2007). Novel facultative anaerobic acidotolerant <i>Telmatospirillum siberiense</i> gen. nov. sp. nov. isolated from mesotrophic fen. <i>Systematic and applied microbiology</i>, 30(3), 213-220. doi:10.1016/j.syapm.2006.06.003

Tepidisphaera	Kovaleva, O. L., Merkel, A. Y., Novikov, A. A., Baslerov, R. V., Toshchakov, S. V., & Bonch-Osmolovskaya, E. A. (2015). Tepidisphaera mucosa gen. nov., sp. nov., a moderately thermophilic member of the class Phycisphaerae in the phylum Planctomycetes, and proposal of a new family, Tepidisphaeraceae fam. nov., and a new order, Tepidisphaerales ord. nov. <i>International journal of systematic and evolutionary microbiology</i> , 65(2), 549-555. doi:10.1099/ijs.0.070151-0
Thermoflexus	Dodsworth, J. A. (2018). Thermoflexus. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01488

Nitrate Reducing

Hartmannibacter	Suarez, C., Ratering, S., Geissler-Plaum, R., & Schnell, S. (2014). Hartmannibacter diazotrophicus gen. nov., sp. nov., a phosphate-solubilizing and nitrogen-fixing alphaproteobacterium isolated from the rhizosphere of a natural salt-meadow plant. <i>International journal of systematic and evolutionary microbiology</i> , 64(9), 3160-3167. doi:10.1099/ijs.0.064154-0
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Nitrate Reducing, Iron Reducing Bacteria

Candidatus Brocadia	Oshiki, M., Shimokawa, M., Fujii, N., Satoh, H., & Okabe, S. (2011). Physiological characteristics of the anaerobic ammonium-oxidizing bacterium 'Candidatus Brocadia sinica'. <i>Microbiology</i> , 157(6), 1706-1713. doi:10.1099/mic.0.048595-0 Kartal, B., Van Niftrik, L., Rattray, J., Van De Vossenberg, J. L., Schmid, M. C., Sinnighe Damsté, J., Jetten, M. S. M., & Strous, M. (2008). Candidatus 'Brocadia fulgida': an autofluorescent anaerobic ammonium oxidizing bacterium. <i>FEMS microbiology ecology</i> , 63(1), 46-55. doi:10.1111/j.1574-6941.2007.00408.x
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Nitrate Reducing, Iron Reducing, Fermenting Bacteria

Geothrix	Weber, K. A., Achenbach, L. A., & Coates, J. D. (2006). Microorganisms pumping iron: anaerobic microbial iron oxidation and reduction. <i>Nature Reviews Microbiology</i> , 4(10), 752. doi:10.1038/nrmicro1490 Coates, J. D., Ellis, D. J., Gaw, C. V., & Lovley, D. R. (1999). Geothrix fermentans gen. nov., sp. nov., a novel Fe (III)-reducing bacterium from a hydrocarbon-contaminated aquifer. <i>International journal of systematic and evolutionary microbiology</i> , 49(4), 1615-1622. doi:10.1099/00207713-49-4-1615 Thrash, J. C. and Coates, J. D. (2015). Geothrix. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00005
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Nitrate Reducing, Fermenting Bacteria

Acetivibrio	Rainey, F. A. (2015). Acetivibrio. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00671
Caldithrix	Miroshnichenko, M. L., Kostrikina, N. A., Chernyh, N. A., Pimenov, N. V., Tourova, T. P., Antipov, A. N., Spring, S., Stackebrandt, E., & Bonch-Osmolovskaya, E. A. (2003). <i>Caldithrix abyssi</i> gen. nov., sp. nov., a nitrate-reducing, thermophilic, anaerobic bacterium isolated from a Mid-Atlantic Ridge hydrothermal vent, represents a novel bacterial lineage. <i>International journal of systematic and evolutionary microbiology</i> , 53(1), 323-329. doi:10.1099/ijs.0.02390-0 Miroshnichenko, M. L., Kolganova, T. V., Spring, S., Chernyh, N., & Bonch-Osmolovskaya, E. A. (2010). <i>Caldithrix palaeochoryensis</i> sp. nov., a thermophilic, anaerobic, chemo-organotrophic bacterium from a geothermally heated sediment, and emended description of the genus <i>Caldithrix</i> . <i>International journal of systematic and evolutionary microbiology</i> , 60(9), 2120-2123. doi:10.1099/ijs.0.016667-0
Moorella	Wiegel, J. (2015). Moorella. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00748
Opiritaceae	Rodrigues, J. L., & Isanapong, J. (2014). The family Opiritaceae. In <i>The Prokaryotes</i> (pp. 751-756). Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-38954-2_147 Wertz, J. T., Kim, E., Breznak, J. A., Schmidt, T. M., & Rodrigues, J. L. (2018). Second Correction for Wertz et al., "Genomic and Physiological Characterization of the Verrucomicrobia Isolate Geminisphaera colitermitum gen. nov., sp. nov., Reveals Microaerophily and Nitrogen Fixation Genes". <i>Applied and environmental microbiology</i> , 84(13), e00952-18. doi:10.1128/AEM.00952-18
Opiritatus	Janssen, P. H. (2015). Opiritatus. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01275 Chin, K. J., Liesack, W., & Janssen, P. H. (2001). <i>Opiritatus terrae</i> gen. nov., sp. nov., to accommodate novel strains of the division Verrucomicrobia isolated from rice paddy soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 51(6), 1965-1968. doi:10.1099/00207713-51-6-1965
Veillonella	Carlier, J. (2015). Veillonella. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00710

Nitrate Reducing, Sulfate Reducing, Fermenting Bacteria

Ammonifex	Huber, R. (2015). Ammonifex. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00744
Desulfomonile	Kuever, J., Rainey, F. A. and Widdel, F. (2015). Syntrophaceae fam. nov. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00208 DeWeerd, K. A., Todd Townsend, G. and Suflita, J. M. (2015). Desulfomonile. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01062

Nitrite Reducing, Methane Oxidizing Bacteria

Candidatus Methylomirabilis	Wu, M. L., Ettwig, K. F., Jetten, M. S., Strous, M., Keltjens, J. T., & van Niftrik, L. (2011). A new intra-aerobic metabolism in the nitrite-dependent anaerobic methane-oxidizing bacterium Candidatus 'Methylomirabilis oxyfera'. <i>Biochemical Society Transactions</i>, 39. 243-248. doi:10.1042/BST0390243 Luesken, F. A., Wu, M. L., Op den Camp, H. J., Keltjens, J. T., Stunnenberg, H. , Francoijs, K. , Strous, M. and Jetten, M. S. (2012), Effect of oxygen on the anaerobic methanotroph 'Candidatus Methylomirabilis oxyfera': kinetic and transcriptional analysis. <i>Environmental Microbiology</i>, 14: 1024-1034. doi:10.1111/j.1462-2920.2011.02682.x
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Iron Reducing Bacteria

Deferrisoma	Slobodkina, G. B., Reysenbach, A. L., Panteleeva, A. N., Kostrikina, N. A., Wagner, I. D., Bonch-Osmolovskaya, E. A., & Slobodkin, A. I. (2012). Deferrisoma camini gen. nov., sp. nov., a moderately thermophilic, dissimilatory iron (III)-reducing bacterium from a deep-sea hydrothermal vent that forms a distinct phylogenetic branch in the Deltaproteobacteria. <i>International journal of systematic and evolutionary microbiology</i>, 62(10), 2463-2468. doi:10.1099/ij.s.0.038372-0 Pérez-Rodríguez, I., Rawls, M., Coykendall, D. K., & Foustoukos, D. I. (2016). Deferrisoma palaeochoriense sp. nov., a thermophilic, iron (III)-reducing bacterium from a shallow-water hydrothermal vent in the Mediterranean Sea. <i>International journal of systematic and evolutionary microbiology</i>, 66(2), 830-836. doi:10.1099/ijsem.0.000798
Desulfuromonas	Roden, E. E., & Lovley, D. R. (1993). Dissimilatory Fe (III) reduction by the marine microorganism Desulfuromonas acetoxidans. <i>Applied and Environmental Microbiology</i>, 59(3), 734-742. Vandieken, V., Mußmann, M., Niemann, H., & Jørgensen, B. B. (2006). Desulfuromonas svalbardensis sp. nov. and Desulfuromusa ferrireducens sp. nov., psychrophilic, Fe (III)-reducing bacteria isolated from Arctic sediments, Svalbard. <i>International journal of systematic and evolutionary microbiology</i>, 56(5), 1133-1139. doi:10.1099/ij.s.0.63639-0
Fervidicola	Ogg, C. D., & Patel, B. K. (2009). Fervidicola ferrireducens gen. nov., sp. nov., a thermophilic anaerobic bacterium from geothermal waters of the Great Artesian Basin, Australia. <i>International journal of systematic and evolutionary microbiology</i>, 59(5), 1100-1107. doi:10.1099/ij.s.0.004200-0
Geoalkalibacter	Zavarzina, D. G., Kolganova, T. V., Boulygina, E. S., Kostrikina, N. A., Tourova, T. P., & Zavarzin, G. A. (2006). Geoalkalibacter ferrihydriticus gen. nov. sp. nov., the first alkaliphilic representative of the family Geobacteraceae, isolated from a soda lake. <i>Microbiology</i>, 75(6), 673-682. doi:10.1134/S0026261706060099
Geobacter	Coates, J. D. and Lovley, D. R. (2015). Geobacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedys). doi:10.1002/9781118960608.gbm01043

Iron Reducing, Sulfate Reducing Bacteria

Candidatus Desulforudis	Chivian, D., Brodie, E. L., Alm, E. J., Culley, D. E., Dehal, P. S., DeSantis, T. Z., Gihring, T. M., Lapidus, A., Lin, L. H., Lowry, S. R., & Moser, D. P. (2008). Environmental genomics reveals a single-species ecosystem deep within Earth. <i>Science</i>, 322(5899), 275-278. doi:10.1126/science.1155495 Junier, P., Junier, T., Podell, S., Sims, D. R., Detter, J. C., Lykidis, A., Han, C. S., Wigginton, N. S., Gaasterland, T., & Bernier-Latmani, R. (2010). The genome of the Gram-positive metal-and sulfate-reducing bacterium Desulfotomaculum reducens strain MI-1. <i>Environmental microbiology</i>, 12(10), 2738-2754. doi:10.1111/j.1462-2920.2010.02242.x
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Iron Reducing, Sulfate Reducing, Fermenting Bacteria

Desulfosporosinus	Hippe, H. and Stackebrandt, E. (2015). Desulfosporosinus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00660
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Iron Reducing, Fermenting Bacteria

Pelobacter	Schink, B., & Pfennig, N. (1982). Fermentation of trihydroxybenzenes by <i>Pelobacter acidigallici</i> gen. nov. sp. nov., a new strictly anaerobic, non-sporeforming bacterium. <i>Archives of Microbiology</i>, 133(3), 195-201. doi:10.1007/BF00415000 Richter, H., Lanthier, M., Nevin, K. P., & Lovley, D. R. (2007). Lack of electricity production by <i>Pelobacter carbinolicus</i> indicates that the capacity for Fe (III) oxide reduction does not necessarily confer electron transfer ability to fuel cell anodes. <i>Applied and environmental microbiology</i>, 73(16), 5347-5353. doi:10.1128/AEM.00804-07 Schink, B. (2015). <i>Pelobacter</i>. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01042
Thermoanaerobaculum	Losey, N. A., Stevenson, B. S., Busse, H. J., Damsté, J. S. S., Rijpstra, W. I. C., Rudd, S., & Lawson, P. A. (2013). <i>Thermoanaerobaculum aquaticum</i> gen. nov., sp. nov., the first cultivated member of Acidobacteria subdivision 23, isolated from a hot spring. <i>International journal of systematic and evolutionary microbiology</i> , 63(11), 4149-4157. doi:10.1099/ijs.0.051425-0

Sulfate Reducing Bacteria

Candidatus Blochmannia	Zientz, E., Feldhaar, H., Stoll, S., & Gross, R. (2005). Insights into the microbial world associated with ants. <i>Archives of microbiology</i> , 184(4), 199-206. doi:10.1007/s00203-005-0041-0
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Desulfatiglans	Suzuki, D., Li, Z., Cui, X., Zhang, C., & Katayama, A. (2014). Reclassification of <i>Desulfobacterium anilini</i> as <i>Desulfatiglans anilini</i> comb. nov. within <i>Desulfatiglans</i> gen. nov., and description of a 4-chlorophenol-degrading sulfate-reducing bacterium, <i>Desulfatiglans parachlorophenolica</i> sp. nov. <i>International journal of systematic and evolutionary microbiology</i> , 64(9), 3081-3086. doi:10.1099/ijs.0.064360-0
Desulfatimicrobium	Trabelsi, D., Chihaoui, S. A., & Mhamdi, R. (2017). Nodules and roots of <i>Vicia faba</i> are inhabited by quite different populations of associated bacteria. <i>Applied Soil Ecology</i> , 119, 72-79. doi:10.1016/j.apsoil.2017.06.002
Desulfobacca	Kuever, J. , Rainey, F. A. and Widdel, F. (2015). Syntrophaceae fam. nov. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00208 Stams, A. J. and Oude Elferink, S. J. (2015). <i>Desulfobacca</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01061
Desulfocaldus	Meyer, B., & Kuever, J. (2007). Phylogeny of the alpha and beta subunits of the dissimilatory adenosine-5'-phosphosulfate (APS) reductase from sulfate-reducing prokaryotes—origin and evolution of the dissimilatory sulfate-reduction pathway. <i>Microbiology</i> , 153(7), 2026-2044. doi:10.1099/mic.0.2006/003152-0 Deng, D., Weidhaas, J. L., & Lin, L. S. (2016). Kinetics and microbial ecology of batch sulfidogenic bioreactors for co-treatment of municipal wastewater and acid mine drainage. <i>Journal of Hazardous materials</i> , 305, 200-208. doi:10.1016/j.jhazmat.2015.11.041 Summer, E. J., Duggleby, S., Janes, C., & Liu, M. (2014, May). Microbial Populations in the O&G: Application of this Knowledge. In CORROSION 2014. NACE International.
Desulfocapsa	Kuever, J., Rainey, F. A. and Widdel, F. (2015). <i>Desulfocapsa</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01024
Desulfoglaeba	Davidova, I. A., Duncan, K. E., Choi, O. K., & Suflita, J. M. (2006). <i>Desulfoglaeba alkanexedens</i> gen. nov., sp. nov., an n-alkane-degrading, sulfate-reducing bacterium. <i>International journal of systematic and evolutionary microbiology</i> , 56(12), 2737-2742. doi:10.1099/ijs.0.64398-0
Desulfonatronum	Zhilina, T. N. (2015). <i>Desulfonatronum</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01033
Desulforhabdus	Kuever, J., Rainey, F. A. and Widdel, F. (2015). <i>Desulforhabdus</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01066
Desulfovirga	Kuever, J., Rainey, F. A. and Widdel, F. (2015). <i>Desulfovirga</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01067
Syntrophobacteraceae	Kuever, J. , Rainey, F. A. and Widdel, F. (2015). Syntrophobacteraceae fam. nov. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00209
Thermanaeromonas	Kaksonen, A. H., Plumb, J. J., Robertson, W. J., Spring, S., Schumann, P., Franzmann, P. D., & Puhakka, J. A. (2006). Novel thermophilic sulfate-reducing bacteria from a geothermally active underground mine in Japan. <i>Applied and environmental microbiology</i> , 72(5), 3759-3762. doi:10.1128/AEM.72.5.3759-3762.2006

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Desulfococcus	Kuever, J., Rainey, F. A. and Widdel, F. (2015). Desulfococcus. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01016
Desulfobacteraceae	Kuever, J., Rainey, F. A. and Widdel, F. (2015). Desulfobacteraceae fam. nov. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00193
Desulfocurvus	Hamdi, O., Hania, W. B., Postec, A., Bartoli, M., Hamdi, M., Bouallagui, H., Fauque, G., Ollivier, B., & Fardeau, M. L. (2013). Isolation and characterization of Desulfocurvus thunnarius sp. nov., a sulfate-reducing bacterium isolated from an anaerobic sequencing batch reactor treating cooking wastewater. <i>International journal of systematic and evolutionary microbiology</i> , 63(11), 4237-4242. doi:10.1099/ij.s.0.051664-0 Klouche, N., Basso, O., Lascourrèges, J. F., Cayol, J. L., Thomas, P., Fauque, G., Fardeau, M. L., & Magot, M. (2009). Desulfocurvus vexinensis gen. nov., sp. nov., a sulfate-reducing bacterium isolated from a deep subsurface aquifer. <i>International journal of systematic and evolutionary microbiology</i> , 59(12), 3100-3104. doi: 10.1099/ij.s.0.010363-0
Desulfosarcina	Kuever, J., Rainey, F. A. and Widdel, F. (2015). Desulfosarcina. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01020
Desulfotomaculum	Kuever, J. and Rainey, F. A. (2015). Desulfotomaculum. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00661
Desulfovibrio	Kuever, J., Rainey, F. A. and Widdel, F. (2015). Desulfovibrio. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01035
Desulfovibrionales	Kuever, J., Rainey, F. A. and Widdel, F. (2015). Desulfovibrionales ord. nov. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.obm00085
Syntrophobacter	McInerney, M. J., Stams, A. J. and Boone, D. R. (2015). Syntrophobacter. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01068

Fermenting Bacteria

Acetanaerobacterium	Dong, X. (2015). Acetanaerobacterium. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00670
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Acetonema	Rainey, F. A. (2015). Acetonema. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00686
Alkaliflexus	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S., (2015). Alkaliflexus . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00239
Allobaculum	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S., (2015). Allobaculum. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00759
Alloprevotella	Downes, J., Dewhirst, F. E., Tanner, A. C., & Wade, W. G. (2013). Description of Alloprevotella rava gen. nov., sp. nov., isolated from the human oral cavity, and reclassification of Prevotella tannerae Moore et al. 1994 as Alloprevotella tannerae gen. nov., comb. nov. International journal of systematic and evolutionary microbiology, 63(4), 1214-1218. doi:10.1099/ijs.0.041376-0
Alterococcus	Shieh, W. Y., & Jean, W. D. (1998). Alterococcus agarolyticus, gen. nov., sp. nov., a halophilic thermophilic bacterium capable of agar degradation. Canadian journal of microbiology, 44(7), 637-645. doi:10.1139/w98-051
Anaerococcus	Ezaki, T. and Ohkusu, K. (2015). Anaerococcus. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00712
Anaerofilum	Rainey, F. A. (2015). Anaerofilum. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00672
Anaerolinea	Yamada, T. and Sekiguchi, Y. (2018). Anaerolinea. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01478
Anaerolineaceae	Yamada, T. and Sekiguchi, Y. (2018). Anaerolineaceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00301
Anaerolineae	Yamada, T. and Sekiguchi, Y. (2018). Anaerolineae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.cbm00064
Bellilinea	Yamada, T. and Sekiguchi, Y. (2018). Bellilinea. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01479
Caldicoprobacter	Yokoyama, H. , Wagner, I. D. and Wiegel, J. (2017). Caldicoprobacter. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01380
Caldilinea	Grégoire, P., Bohli, M., Cayol, J. L., Joseph, M., Guasco, S., Dubourg, K., Cambar, J., Michotey, V., Bonin, P., Fardeau, M. L. & Ollivier, B. (2011). Caldilinea tarbellica sp. nov., a filamentous, thermophilic, anaerobic bacterium isolated from a deep hot aquifer in the Aquitaine Basin. International journal of systematic and evolutionary microbiology, 61(6), 1436-1441. doi:10.1099/ijs.0.025676-0

	Sekiguchi, Y., Yamada, T., Hanada, S., Ohashi, A., Harada, H., & Kamagata, Y. (2003). <i>Anaerolinea thermophila</i> gen. nov., sp. nov. and <i>Caldilinea aerophila</i> gen. nov., sp. nov., novel filamentous thermophiles that represent a previously uncultured lineage of the domain Bacteria at the subphylum level. <i>International journal of systematic and evolutionary microbiology</i> , 53(6), 1843-1851. doi:10.1099/ijs.0.02699-0
Capnocytophaga	Holt, S. C. (2015). <i>Capnocytophaga</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00299
Cellulosilyticum	Cai, S. , Shao, N. and Dong, X. (2016). <i>Cellulosilyticum</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01382
Chitinivibrionia	Sorokin, D. Y., Gumerov, V. M., Rakitin, A. L., Beletsky, A. V., Damsté, J. S., Muyzer, G. , Mardanov, A. V. and Ravin, N. V. (2014), Chitinolytic bacterium from the candidate phylum TG3. <i>Environ Microbiol</i> , 16: 1549-1565. doi:10.1111/1462-2920.12284
Clostridium	Rainey, F. A., Hollen, B. J. and Small, A. M. (2015). <i>Clostridium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00619
Coriobacteriaceae	Clavel, T., Lepage, P., & Charrier, C. (2014). The family coriobacteriaceae. In <i>The Prokaryotes</i> (pp. 201-238). Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-30138-4_343 König, H. (2015). <i>Coriobacteriaceae</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00049
Coriobacteriales	Gupta, R. S., Chen, W. J., Adeolu, M., & Chai, Y. (2013). Molecular signatures for the class Coriobacteriia and its different clades; proposal for division of the class Coriobacteriia into the emended order Coriobacteriales, containing the emended family Coriobacteriaceae and Atopobiaceae fam. nov., and Eggerthellales ord. nov., containing the family Eggerthellaceae fam. nov. <i>International journal of systematic and evolutionary microbiology</i> , 63(9), 3379-3397. doi:10.1099/ijs.0.048371-0
Coriobacteriia	Gupta, R. S., Chen, W. J., Adeolu, M., & Chai, Y. (2013). Molecular signatures for the class Coriobacteriia and its different clades; proposal for division of the class Coriobacteriia into the emended order Coriobacteriales, containing the emended family Coriobacteriaceae and Atopobiaceae fam. nov., and Eggerthellales ord. nov., containing the family Eggerthellaceae fam. nov. <i>International journal of systematic and evolutionary microbiology</i> , 63(9), 3379-3397. doi:10.1099/ijs.0.048371-0
Elusimicrobia	Brune, A. (2018). <i>Elusimicrobia</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.pbm00034
Elusimicrobium	Brune, A. (2018). <i>Elusimicrobium</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01490
Eubacteriaceae	Ludwig, W. , Schleifer, K. and Whitman, W. B. (2015). <i>Eubacteriaceae</i> fam. nov.. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00130
Exilispira	Imachi, H., Sakai, S., Hirayama, H., Nakagawa, S., Nunoura, T., Takai, K., & Horikoshi, K. (2008). <i>Exilispira thermophila</i> gen. nov., sp. nov., an anaerobic, thermophilic spirochaete isolated from a deep-sea hydrothermal vent

	chimney. International journal of systematic and evolutionary microbiology, 58(10), 2258-2265. doi:10.1099/ijs.0.65727-0
Faecalibacterium	Duncan, S. H. and Flint, H. J. (2015). Faecalibacterium. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00674
Faecalicoccus	De Maesschack, C. , Van Immerseel, F, Eeckhaut, V., De Baere, S., Cnockaert, M., Croubels, S., Haesebrouck, F., Ductelle, R., & Vandamme, P. (2014). Faecalicoccus acidiformans gen. nov., sp. nov., isolated from the chicken caecum, and reclassification of Streptococcus pleomorphus (Barnes et al. 1977), Eubacterium bifforme (Eggerth 1935) and Eubacterium cylindroides (Cato et al. 1974) as Faecalicoccus pleomorphus comb. nov., Holdemanella biformis gen. nov., comb. nov. and Faecalitalea cylindroides gen. nov., comb. nov., respectively, within the family Erysipelotrichaceae. International journal of systematic and evolutionary microbiology, 64(Pt 11), 3877-3884. doi: 10.1099/ijs.0.064626-0
Fibrobacteraceae	Spain, A. M., Forsberg, C. W. and Krumholz, L. R. (2015). Fibrobacteraceae fam. nov.. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00110
Formivibrio	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S., (2015). Formivibrio. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00977
Fusicatenibacter	Takada, T., Kurakawa, T., Tsuji, H., & Nomoto, K. (2013). Fusicatenibacter saccharivorans gen. nov., sp. nov., isolated from human faeces. International journal of systematic and evolutionary microbiology, 63(10), 3691-3696. doi:10.1099/ijs.0.045823-0 Hedberg, M. E., Moore, E. R., Svensson-Stadler, L., Hörstedt, P., Baranov, V., Hernell, O., Wai, S. N., Hammarström, S., & Hammarström, M. L. (2012). Lachnoanaerobaculum gen. nov., a new genus in the Lachnospiraceae: characterization of Lachnoanaerobaculum umeaense gen. nov., sp. nov., isolated from the human small intestine, and Lachnoanaerobaculum orale sp. nov., isolated from saliva, and reclassification of Eubacterium saburreum (Prévot 1966) Holdeman and Moore 1970 as Lachnoanaerobaculum saburreum comb. nov. International journal of systematic and evolutionary microbiology, 62(11), 2685-2690. doi:10.1099/ijs.0.033613-0
Fusobacterium	Gharbia, S. E., Shah, H. N. and Edwards, K. J. (2015). Fusobacterium. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00768
Gracilibacteraceae	Lee, Y. and Wiegel, J. (2017). Gracilibacteraceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00131.pub2
Hathewayia	Lawson, P. A., & Rainey, F. A. (2016). Proposal to restrict the genus Clostridium Prazmowski to Clostridium butyricum and related species. International journal of systematic and evolutionary microbiology, 66(2), 1009-1016. doi:10.1099/ijsem.0.000824 Lawson, P. A., & Rainey, F. A. (2016). Proposal to restrict the genus Clostridium Prazmowski to Clostridium butyricum and related species. International journal of systematic and evolutionary microbiology, 66(2), 1009-1016. doi:10.1099/ijsem.0.000824

Holophaga	Thrash, J. C. and Coates, J. D. (2015). Holophaga . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00006
Lachnoanaerobaculum	Hedberg, M. E., Moore, E. R., Svensson-Stadler, L., Hörstedt, P., Baranov, V., Hernell, O., Wai, S. N., Hammarstrom, S., & Hammarström, M. L. (2012). Lachnoanaerobaculum gen. nov., a new genus in the Lachnospiraceae: characterization of Lachnoanaerobaculum umeaense gen. nov., sp. nov., isolated from the human small intestine, and Lachnoanaerobaculum orale sp. nov., isolated from saliva, and reclassification of Eubacterium saburreum (Prévot 1966) Holdeman and Moore 1970 as Lachnoanaerobaculum saburreum comb. nov. International journal of systematic and evolutionary microbiology, 62(11), 2685-2690. doi:10.1099/ijs.0.033613-0
Lachnoclostridium	Yutin, N., & Galperin, M. Y. (2013). A genomic update on clostridial phylogeny: Gram-negative spore formers and other misplaced clostridia. Environmental microbiology, 15(10), 2631-2641. doi:10.1111/1462-2920.12173
Lactobacillus	Hammes, W. P. and Hertel, C. (2015). Lactobacillus. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00604
Latescibacteria	Farag, I. F. (2017). Exploring the Habitat Distribution, Metabolic Diversities and Potential Ecological Roles of Candidate Phyla “Aminicenantes”(OP8) and “Latescibacteria”(WS3)(Doctoral dissertation).
Leptolinea	Yamada, T. and Sekiguchi, Y. (2018). Leptolinea. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01480
Levilinea	Yamada, T. and Sekiguchi, Y. (2018). Levilinea. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01481
Longilinea	Yamada, T. and Sekiguchi, Y. (2018). Longilinea. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01482
Mobilitalea	Podosokorskaya, O. A., Bonch-Osmolovskaya, E. A., Beskorovaynyy, A. V., Toshchakov, S. V., Kolganova, T. V., & Kublanov, I. V. (2014). Mobilitalea sibirica gen. nov., sp. nov., a halotolerant polysaccharide-degrading bacterium. International journal of systematic and evolutionary microbiology, 64(8), 2657-2661. doi:10.1099/ijs.0.057109-0
Natronoanaerobium	Oren, A. (2014). The Family Natranaerobiaceae. In The Prokaryotes (pp. 261-266). Springer, Berlin, Heidelberg. doi: 10.1007/978-3-642-30120-9_360
Papillibacter	Patel, B. K. (2015). Papillibacter. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00677
Pelobacteraceae	Kuever, J. , Rainey, F. A. and Widdel, F. (2015). Desulfuromonales ord. nov. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.obm00087
Pelolinea	Imachi, H. , Takaki, Y. and Nakahara, N. (2018). Pelolinea. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01484
Peptoclostridium	Galperin, M. Y., Brover, V., Tolstoy, I., & Yutin, N. (2016). Phylogenomic analysis of the family Peptostreptococcaceae (Clostridium cluster XI) and proposal for

	reclassification of <i>Clostridium litorale</i> (Fendrich et al. 1991) and <i>Eubacterium acidaminophilum</i> (Zindel et al. 1989) as <i>Peptoclostridium litorale</i> gen. nov. comb. nov. and <i>Peptoclostridium acidaminophilum</i> comb. nov. International journal of systematic and evolutionary microbiology, 66(12), 5506-5513. doi:10.1099/ijsem.0.001548
Prevotella	Shah, H. N., & Collins, D. M. (1990). <i>Prevotella</i> , a new genus to include <i>Bacteroides melaninogenicus</i> and related species formerly classified in the genus <i>Bacteroides</i> . International Journal of Systematic and Evolutionary Microbiology, 40(2), 205-208. doi:10.1099/00207713-40-2-205
Romboutsia	Gerritsen, J., Fuentes, S., Grievink, W., van Niftrik, L., Tindall, B. J., Timmerman, H. M., Rijkers, G. T., & Smidt, H. (2014). Characterization of <i>Romboutsia ilealis</i> gen. nov., sp nov., isolated from the gastro-intestinal tract of a rat, and proposal for the reclassification of five closely related members of the genus <i>Clostridium</i> into the genera <i>Romboutsia</i> gen. nov., <i>Intestinibacter</i> gen. nov., <i>Terrisporobacter</i> gen. nov and <i>Asaccharospora</i> gen. nov. International Journal of Systematic and Evolutionary Microbiology, 64, 1600-1616. doi:10.1099/ijms.0.059543-0 Wang, Y., Song, J., Zhai, Y., Zhang, C., Gerritsen, J., Wang, H., Chen, X., Li, Y., Zhao, B., & Ruan, Z. (2015). <i>Romboutsia sedimentorum</i> sp. nov., isolated from an alkaline-saline lake sediment and emended description of the genus <i>Romboutsia</i> . International journal of systematic and evolutionary microbiology, 65(4), 1193-1198. doi:10.1099/ijms.0.000079
Smithella	Liu, Y., Balkwill, D. L., Aldrich, H. C., Drake, G. R., & Boone, D. R. (1999). Characterization of the anaerobic propionate-degrading syntrophs <i>Smithella propionica</i> gen. nov., sp. nov. and <i>Syntrophobacter wolinii</i> . International Journal of Systematic and Evolutionary Microbiology, 49(2), 545-556. doi:10.1099/00207713-49-2-545
Sporacetigenium	Chen, S., Song, L., & Dong, X. (2006). <i>Sporacetigenium mesophilum</i> gen. nov., sp. nov., isolated from an anaerobic digester treating municipal solid waste and sewage. International journal of systematic and evolutionary microbiology, 56(4), 721-725. doi:10.1099/ijms.0.63686-0
Sporobacter	Grech-Mora, I. , Fardeau, M. , Garcia, J. and Ollivier, B. (2015). <i>Sporobacter</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00679
Syntrophus	Kuever, J. and Schink, B. (2015). <i>Syntrophus</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01064
Tepidibacter	Slobodkin, A. (2015). <i>Tepidibacter</i> . In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00669
Terrimicrobium	Qiu, Y. L., Kuang, X. Z., Shi, X. S., Yuan, X. Z., & Guo, R. B. (2014). <i>Terrimicrobium sacchariphilum</i> gen. nov., sp. nov., an anaerobic bacterium of the class 'Spartobacteria' in the phylum Verrucomicrobia, isolated from a rice paddy field. International journal of systematic and evolutionary microbiology, 64(5), 1718-1723. doi:10.1099/ijms.0.060244-0
Terrisporobacter	Gerritsen, J., Fuentes, S., Grievink, W., van Niftrik, L., Tindall, B. J., Timmerman, H. M., Rijkers, G. T., & Smidt, H. (2014). Characterization of <i>Romboutsia ilealis</i> gen. nov., sp nov., isolated from the gastro-intestinal tract of a rat, and proposal for the reclassification of five closely related members of the genus <i>Clostridium</i> into the genera <i>Romboutsia</i> gen. nov., <i>Intestinibacter</i> gen. nov., <i>Terrisporobacter</i> gen. nov and <i>Asaccharospora</i> gen. nov. International Journal of Systematic and Evolutionary Microbiology, 64, 1600-1616. doi:10.1099/ijms.0.059543-0

	Deng, Y., Guo, X., Wang, Y., He, M., Ma, K., Wang, H., Chen, X., Kong, D., Yang, Z., & Ruan, Z. (2015). <i>Terrisporobacter petrolearius</i> sp. nov., isolated from an oilfield petroleum reservoir. <i>International journal of systematic and evolutionary microbiology</i> , 65(10), 3522-3526. doi:10.1099/ijsem.0.000450
Thermanaerotherrix	Grégoire, P., Fardeau, M. L., Joseph, M., Guasco, S., Hamaide, F., Biasutti, S., Michotey, V., Bonin, P., & Ollivier, B. (2011). Isolation and characterization of <i>Thermanaerotherrix daxensis</i> gen. nov., sp. nov., a thermophilic anaerobic bacterium pertaining to the phylum “Chloroflexi”, isolated from a deep hot aquifer in the Aquitaine Basin. <i>Systematic and applied microbiology</i> , 34(7), 494-497. doi:10.1016/j.syapm.2011.02.004
Thermomarinilinea	Nunoura, T., Hirai, M., Miyazaki, M., Kazama, H., Makita, H., Hirayama, H., Furushima, Y., Yamamoto, H., Imachi, H., & Takai, K. (2013). Isolation and characterization of a thermophilic, obligately anaerobic and heterotrophic marine Chloroflexi bacterium from a Chloroflexi-dominated microbial community associated with a Japanese shallow hydrothermal system, and proposal for <i>Thermomarinilinea lacunofontalis</i> gen. nov., sp. nov. <i>Microbes and environments</i> , 28(2), 228-235. doi:10.1264/jsme2.ME12193
Thermosediminibacter	Wiegel, J. (2015). <i>Thermosediminibacter</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00756
Treponema	Karami, A., Sarshar, M., Ranjbar, R., & Zanjani, R. S. (2014). The phylum spirochaetaceae. In <i>The Prokaryotes</i> (pp. 915-929). Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-38954-2_156 Smibert, R. M., Johnson, J. L., & Ranney, R. R. (1984). <i>Treponema socranskii</i> sp. nov., <i>Treponema socranskii</i> subsp. <i>socranskii</i> subsp. nov., <i>Treponema socranskii</i> subsp. <i>buccale</i> subsp. nov., and <i>Treponema socranskii</i> subsp. <i>paredis</i> subsp. nov. isolated from the human periodontia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 34(4), 457-462. doi:10.1099/00207713-34-4-457
Turicibacter	Bosshard, P. P. (2015). <i>Turicibacter</i> . In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00766
Youngiibacter	Lawson, P. A., Wawrik, B., Allen, T. D., Johnson, C. N., Marks, C. R., Tanner, R. S., Harriman, B. H., Strapoć, D., & Callaghan, A. V. (2014). <i>Youngiibacter fragilis</i> gen. nov., sp. nov., isolated from natural gas production-water and reclassification of <i>Acetivibrio multivorans</i> as <i>Youngiibacter multivorans</i> comb. nov. <i>International journal of systematic and evolutionary microbiology</i> , 64(1), 198-205. doi:10.1099/ijms.0.053728-0

Ammonia Oxidizing Archaea

Candidatus Nitrosoarchaeum	Blainey, P. C., Mosier, A. C., Potanina, A., Francis, C. A., & Quake, S. R. (2011). Genome of a low-salinity ammonia-oxidizing archaeon determined by single-cell and metagenomic analysis. <i>PLoS One</i> , 6(2), e16626. doi:10.1371/journal.pone.0016626
Candidatus Nitrosopelagicus	Stieglmeier, M., Alves, R. J., & Schleper, C. (2014). The phylum thaumarchaeota. In <i>The prokaryotes</i> (pp. 347-362). Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-38954-2_338
Candidatus Nitrosotalea	Stieglmeier, M., Alves, R. J., & Schleper, C. (2014). The phylum thaumarchaeota. In <i>The prokaryotes</i> (pp. 347-362). Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-38954-2_338

Nitrosopumilales	Mosier, A. C., Allen, E. E., Kim, M., Ferriera, S., & Francis, C. A. (2012). Genome sequence of “Candidatus Nitrosopumilus salaria” BD31, an ammonia-oxidizing archaeon from the San Francisco Bay estuary. <i>Journal of bacteriology</i> , 194(8), 2121-2122. doi:10.1128/JB.00013-12
Nitrososphaera	Kerou, M. and Schleper, C. (2016). Nitrososphaera. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01294
Thaumarchaeota	Stieglmeier, M., Alves, R. J., & Schleper, C. (2014). The phylum thaumarchaeota. In <i>The prokaryotes</i> (pp. 347-362). Springer, Berlin, Heidelberg. doi:10.1007/978-3-642-38954-2_338

Methane Oxidizing, Nitrate Reducing Archaea

Candidatus Methanoperedens	Vaksmas, A., Guerrero-Cruz, S., van Alen, T. A., Cremers, G., Ettwig, K. F., Lüke, C., & Jetten, M. S. (2017). Enrichment of anaerobic nitrate-dependent methanotrophic ‘Candidatus Methanoperedens nitroreducens’ archaea from an Italian paddy field soil. <i>Applied microbiology and biotechnology</i> , 101(18), 7075-7084. doi:10.1007/s00253-017-8416-0
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Methanogenic Archaea

Methanobacteriaceae	Boone, D. R., Whitman, W. B. and Koga, Y. (2015). Methanobacteriaceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00097
Methanobacterium	Boone, D. R. (2015). Methanobacterium. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00495
Methanocella	Sakai, S. and Imachi, H. (2016). Methanocella. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01366
Methanoculleus	Chong, S. C. and Boone, D. R. (2015). Methanoculleus. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00505
Methanofollis	Zellner, G. and Boone, D. R. (2015). Methanofollis. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00506
Methanolinea	Imachi, H. and Sakai, S. (2016). Methanolinea. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01367
Methanomassiliicoccus	Nkamga, V. D. and Drancourt, M. (2016). Methanomassiliicoccus. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P.

	Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01365
Methanomethylovorans	Cha, I. T., Min, U. G., Kim, S. J., Yim, K. J., Roh, S. W., & Rhee, S. K. (2013). Methanomethylovorans uponensis sp. nov., a methylotrophic methanogen isolated from wetland sediment. <i>Antonie Van Leeuwenhoek</i> , 104(6), 1005-1012. doi:10.1007/s10482-013-0020-4 Lomans, B. P., Maas, R., Luderer, R., den Camp, H. J. O., Pol, A., van der Drift, C., & Vogels, G. D. (1999). Isolation and characterization of Methanomethylovorans hollandica gen. nov., sp. nov., isolated from freshwater sediment, a methylotrophic methanogen able to grow on dimethyl sulfide and methanethiol. <i>Applied and environmental microbiology</i> , 65(8), 3641-3650.
Methanomicrobia	Mackelprang, R., Waldrop, M. P., DeAngelis, K. M., David, M. M., Chavarria, K. L., Blazewicz, S. J., Rubin, E. M., & Jansson, J. K. (2011). Metagenomic analysis of a permafrost microbial community reveals a rapid response to thaw. <i>Nature</i> , 480(7377), 368. doi:10.1038/nature10576
Methanomicrobiales	Boone, D. R., Whitman, W. B. and Koga, Y. (2015). Methanomicrobiales. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.obm00051
Methanoregula	Zinder, S. and Bräuer, S. (2016). Methanoregula. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01368
Methanosaeta	Patel, G. B. (2015). Methanosaeta. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00513
Methanosarcina	Boone, D. R. and Mah, R. A. (2015). Methanosarcina. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00519
Methanosphaerula	Zinder, S. and Cadillo-Quiroz, H. (2016). Methanosphaerula. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01369
Methanospirillum	Boone, D. R. (2015). Methanobacterium. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00495

Fermenting Archaea

Desulfurococcus	Zillig, W. (2015). Desulfurococcus. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00387
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Other

Caedibacter	Parasite	Görtz, H. and Schmidt, H. J. (2015). Incertae Sedis II Caedibacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i>
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Candidatus Babela	Parasite	Pagnier, I., Yutin, N., Croce, O., Makarova, K. S., Wolf, Y. I., Benamar, S., Raoult, D., Koonin, E. V., & La Scola, B. (2015). Babela massiliensis, a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae. <i>Biology direct</i> , 10(1), 13. doi:10.1186/s13062-015-0043-z
Candidatus Cyrtobacter	Parasite	Vannini, C., Ferrantini, F., Schleifer, K. H., Ludwig, W., Verni, F., & Petroni, G. (2010). "Candidatus Anadelfobacter veles" and "Candidatus Cyrtobacter comes," two new Rickettsiales species hosted by the protist ciliate Euplotes harpa (Ciliophora, Spirotrichea). <i>Applied and environmental microbiology</i> , 76(12), 4047-4054. doi:10.1128/AEM.03105-09 Boscaro, V., Petroni, G., Ristori, A., Verni, F., & Vannini, C. (2013). Candidatus Defluviella procrastinata" and "Candidatus Cyrtobacter zanobii", two novel ciliate endosymbionts belonging to the "Midichloria clade. <i>Microbial ecology</i> , 65(2), 302-310. doi:10.1007/s00248-012-0170-3
Candidatus Entotheonella	Parasite	Schmidt, E. W., Obratsova, A. Y., Davidson, S. K., Faulkner, D. J., & Haygood, M. G. (2000). Identification of the antifungal peptide-containing symbiont of the marine sponge Theonella swinhoei as a novel δ -proteobacterium, "Candidatus Entotheonella palauensis". <i>Marine Biology</i> , 136(6), 969-977. doi:10.1007/s002270000273 Newman, D. J., & Cragg, G. M. (2015). Endophytic and epiphytic microbes as "sources" of bioactive agents. <i>Frontiers in chemistry</i> , 3, 34. doi:10.3389/fchem.2015.00034 Brück, W. M., Sennett, S. H., Pomponi, S. A., Willenz, P., & McCarthy, P. J. (2008). Identification of the bacterial symbiont Entotheonella sp. in the mesohyl of the marine sponge Discodermia sp. <i>The ISME journal</i> , 2(3), 335. doi:10.1038/ismej.2007.91
Candidatus Paracaedibacter	Parasite	Görtz, H. and Schmidt, H. J. (2015). Incertae Sedis V. Candidatus Paracaedibacter. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01421
Candidatus Protochlamydia	Parasite	Horn, M. (2015). Protochlamydia. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00368
Micavibrio	Parasite	Baer, M. L. and Williams, H. N. (2015). Micavibrio. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01008
Pasteuria	Parasite	Sayre, R. M., Starr, M. P., Dickson, D. W., Preston, J. F., Giblin-Davis, R. M., Noel, G. R., Ebert, D. and Bird, G. W. (2015). Pasteuria. In <i>Bergey's Manual of Systematics of Archaea and Bacteria</i> (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00555

Rickettsia	Parasite	Yu, X. and Walker, D. H. (2015). Rickettsia. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm00916
Pasteuriaceae	Parasite	Whitman, W. B., Rainey, F., Kämpfer, P., Trujillo, M., Chun, J., DeVos, P., Hedlund, B. and Dedysh, S., (2015). Pasteuriaceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00115
Vermiphilus	Parasite	Delafont, V., Rodier, M. H., Maisonneuve, E., & Cateau, E. (2018). Vermamoeba vermiformis: a Free-Living Amoeba of Interest. <i>Microbial ecology</i> , 1-11. doi:10.1007/s00248-018-1199-8
Candidatus Chloroploca	Phototroph	Gorlenko, V. M., Bryantseva, I. A., Kalashnikov, A. M., Gaisin, V. A., Sukhacheva, M. V., Gruzdev, D. S., & Kuznetsov, B. B. (2014). Candidatus 'Chloroploca asiatica' gen. nov., sp. nov., a new mesophilic filamentous anoxygenic phototrophic bacterium. <i>Microbiology</i> , 83(6), 838-848. doi:10.1134/S0026261714060083
Chlorobi	Phototroph	Garrity, G. M. and Holt, J. G. (2015). Chlorobi phy. nov. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.pbm00006
Chlorobia	Phototroph	Garrity, G. M. and Holt, J. G. (2015). Chlorobi phy. nov. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.pbm00006
Chromatiaceae	Phototroph	Imhoff, J. F. (2015). Chromatiaceae. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.fbm00219
Ectothiorhodospiraceae	Phototroph	Tourova, T. P., Spiridonova, E. M., Berg, I. A., Slobodova, N. V., Boulygina, E. S., & Sorokin, D. Y. (2007). Phylogeny and evolution of the family Ectothiorhodospiraceae based on comparison of 16S rRNA, cbbL and nifH gene sequences. <i>International journal of systematic and evolutionary microbiology</i> , 57(10), 2387-2398. doi:10.1099/ijs.0.65041-0
Thiocystis	Phototroph	Imhoff, J. F. (2015). Thiocystis. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01118
Thiohalocapsa	Phototroph	Imhoff, J. F. and Caumette, P. (2015). Thiohalocapsa. In Bergey's Manual of Systematics of Archaea and Bacteria (eds W. B. Whitman, F. Rainey, P. Kämpfer, M. Trujillo, J. Chun, P. DeVos, B. Hedlund and S. Dedysh). doi:10.1002/9781118960608.gbm01121
Dehalococcoidia	Reductive dehalogenation	Löffler, F. E., Yan, J., Ritalahti, K. M., Adrian, L., Edwards, E. A., Konstantinidis, K. T., Müller, J. A., Fullerton, H., Zinder, S., & Spormann, A. M. (2013). Dehalococcoides mccartyi gen.

		nov., sp. nov., obligately organohalide-respiring anaerobic bacteria relevant to halogen cycling and bioremediation, belong to a novel bacterial class, Dehalococcoidia classis nov., order Dehalococcoidales ord. nov. and family Dehalococcoidaceae fam. nov., within the phylum Chloroflexi. <i>International journal of systematic and evolutionary microbiology</i> , 63(2), 625-635. doi:10.1099/ij.s.0.034926-0
Dehalogenimonas	Reductive dehalogenation	Moe, W. M., Yan, J., Nobre, M. F., da Costa, M. S., & Rainey, F. A. (2009). Dehalogenimonas lykanthroporepellens gen. nov., sp. nov., a reductively dehalogenating bacterium isolated from chlorinated solvent-contaminated groundwater. <i>International journal of systematic and evolutionary microbiology</i> , 59(11), 2692-2697. doi:10.1099/ij.s.0.011502-0 Brück, W. M., Sennett, S. H., Pomponi, S. A., Willenz, P., & McCarthy, P. J. (2008). Identification of the bacterial symbiont Entotheonella sp. in the mesohyl of the marine sponge Discodermia sp. The ISME journal, 2(3), 335. doi:10.1038/ismej.2007.91
Caldiserica	Non-sulfate sulfur compounds	Mori, K., Yamaguchi, K., Sakiyama, Y., Urabe, T., & Suzuki, K. I. (2009). Caldisericum exile gen. nov., sp. nov., an anaerobic, thermophilic, filamentous bacterium of a novel bacterial phylum, Caldiserica phyl. nov., originally called the candidate phylum OP5, and description of Caldiseriaceae fam. nov., Caldisericales ord. nov. and Caldisericia classis nov. <i>International journal of systematic and evolutionary microbiology</i> , 59(11), 2894-2898. doi:10.1099/ij.s.0.010033-0
Candidatus Omnitrophus	Non-sulfate sulfur compounds	Kolinko, S., Richter, M., Glöckner, F., Brachmann, A. and Schüler, D. (2016), Genomic analysis of an uncultivated multicellular magnetotactic prokaryote. <i>Environ Microbiol</i> , 18: 21-37. doi:10.1111/1462-2920.12907 Kolinko, S., Jogler, C., Katzmann, E., Wanner, G., Peplies, J. and Schüler, D. (2012), Single-cell analysis reveals a novel uncultivated magnetotactic bacterium within the candidate division OP3. <i>Environmental Microbiology</i> , 14: 1709-1721. doi:10.1111/j.1462-2920.2011.02609.x
Desulfurivibrio	Non-sulfate sulfur compounds	Sorokin, D. Y., Tourova, T. P., Mußmann, M., & Muyzer, G. (2008). Dethiobacter alkaliphilus gen. nov. sp. nov., and Desulfurivibrio alkaliphilus gen. nov. sp. nov.: two novel representatives of reductive sulfur cycle from soda lakes. <i>Extremophiles</i> , 12(3), 431-439. doi:10.1007/s00792-008-0148-8
Nautiliales	Non-sulfate sulfur compounds	Miroshnichenko, M. L., L'haridon, S., Schumann, P., Spring, S., Bonch-Osmolovskaya, E. A., Jeanthon, C., & Stackebrandt, E. (2004). Caminibacter profundus sp. nov., a novel thermophile of Nautiliales ord. nov. within the class 'Epsilonproteobacteria', isolated from a deep-sea hydrothermal vent. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 54(1), 41-45. doi:10.1099/ij.s.0.02753-0 Alain, K., Callac, N., Guégan, M., Lesongeur, F., Crassous, P., Cambon-Bonavita, M. A., Querellou, J., & Prieur, D. (2009). Nautilia abyssi sp. nov., a thermophilic, chemolithoautotrophic, sulfur-reducing bacterium isolated

		from an East Pacific Rise hydrothermal vent. International journal of systematic and evolutionary microbiology, 59(6), 1310-1315. doi:10.1099/ijs.0.005454-0 Miroshnichenko, M. L., Kostrikina, N. A., l'Haridon, S., Jeanthon, C., Hippe, H., Stackebrandt, E., & Bonch-Osmolovskaya, E. A. (2002). Nautilia lithotrophica gen. nov., sp. nov., a thermophilic sulfur-reducing epsilon-proteobacterium isolated from a deep-sea hydrothermal vent. International journal of systematic and evolutionary microbiology, 52(4), 1299-1304. doi:10.1099/00207713-52-4-1299
Pelagibacterales	Non-sulfate sulfur compounds	Qiu, Y. L., Hanada, S., Ohashi, A., Harada, H., Kamagata, Y., & Sekiguchi, Y. (2008). Syntrophorhabdus aromaticivorans gen. nov., sp. nov., the first cultured anaerobe capable of degrading phenol to acetate in obligate syntrophic associations with a hydrogenotrophic methanogen. <i>Applied and environmental microbiology</i> , 74(7), 2051-2058. doi:10.1128/AEM.02378-07
Syntrophorhabdaceae	Non-sulfate sulfur compounds	Qiu, Y. L., Hanada, S., Ohashi, A., Harada, H., Kamagata, Y., & Sekiguchi, Y. (2008). Syntrophorhabdus aromaticivorans gen. nov., sp. nov., the first cultured anaerobe capable of degrading phenol to acetate in obligate syntrophic associations with a hydrogenotrophic methanogen. <i>Applied and environmental microbiology</i> , 74(7), 2051-2058. doi:10.1128/AEM.02378-07
Syntrophorhabdus	Non-sulfate sulfur compounds	Qiu, Y. L., Hanada, S., Ohashi, A., Harada, H., Kamagata, Y., & Sekiguchi, Y. (2008). Syntrophorhabdus aromaticivorans gen. nov., sp. nov., the first cultured anaerobe capable of degrading phenol to acetate in obligate syntrophic associations with a hydrogenotrophic methanogen. <i>Applied and environmental microbiology</i> , 74(7), 2051-2058. doi:10.1128/AEM.02378-07
Candidatus Kuenenia	Anammox	Van Niftrik, L., Van Helden, M., Kirchen, S., Van Donselaar, E. G., Harhangi, H. R., Webb, R. I., Fuerst, J. A., Op den Camp, H. J., Jetten, M. S. and Strous, M. (2010), Intracellular localization of membrane-bound ATPases in the compartmentalized anammox bacterium 'Candidatus Kuenenia stuttgartiensis'. <i>Molecular Microbiology</i> , 77: 701-715. doi:10.1111/j.1365-2958.2010.07242.x

Cyanobacteria: Alkalinema, Anabaena, Aphanothece, Chamaesiphon, Chlorogloea, Chroococcidiopsis, Chroococcopsis, Cyanobacteria, Cylandrospermum, Gloeobacter, Jaaginema, Kamptonema, Leptolyngbya, Mastigocoleus, Microcystis, Microseira, Nostoc, Nostocales, Oscillatoriales, Phormidium, Pleurocapsa, Scytonema, Sphaerospermopsis, Stanieria, Stigonema, Symphyonema, Thermosynechococcus, Tolypothrix, Trichocoleus

Canidate Division – no information available – candidate division WPS-1, candidate division Zixibacteria

Broadly Classfied Bacteria: Acidimicrobiaceae, Acidimicrobiales, Acidimicrobiia, Acidobacteria, Acidobacteriaceae, Actinobacteria, Alphaproteobacteria, Bacteroidetes, Betaproteobacteria, Bradyrhizobiaceae, Burkholderiales, Caldilineaceae, Caldilineae, Caldilineales, Candidatus Aminicenantes, Candidatus Hydrogenedentes, Candidatus Microgenomates, Candidatus Parcubacteria, Candidatus Saccharibacteria, Chitinophagaceae, Chloroflexaceae, Chloroflexi, Clostridia, Deinococcus-Thermus, Deltaproteobacteria, Desulfuromonadales, Firmicutes, Frankiaceae, Frankiales, Gammaproteobacteria, Holophagae, Iamiaceae, Ignavibacteriales, Mycobacteriaceae, Nitrospiraceae, Nitrospirae, Nitrospirales, Omnitrophica, Oxalobacteraceae, Phycisphaeraceae, Planctomycetaceae, Planctomycetales, Planctomycetia, Proteobacteria, Rhizobiales, Rhodobacterales, Rhodobiaceae, Rhodocyclaceae, Rhodocyclales, Rhodospirillaceae, Rhodospirillales, Rubrobacteria, Ruminococcaceae, Solibacteraceae, Solibacteres, Sphaerobacteraceae, Sphingobacteriales, Spirochaetales, Spirochaetia, Sporichthyaceae, Syntrophaceae, Syntrophobacteriales, Thermomicrobia, Unclassified (Bacteria) , Verrucomicrobia

Broadly Classfied Archaea: Candidatus Aenigmarchaeota, Candidatus Aenigmarchaeum, Candidatus Bathyarchaeota, Candidatus Micrarchaeum, Crenarchaeota, Euryarchaeota, Thermoplasmata, Thermoplasmatales, Thermoprotei, Unclassified (Archaea)

Eukaryotes: Allapsa, Anneissia, Closteriopsis, Cyclotella, Delphineis, Euglenida, Fragilaria, Gonium, Hazardia, Neovahlkampfia, Oreochromis, Oryza, Pileolariaceae, Sedum,

Spermatozopsis, Stokesia, Synedra, Unclassified (Eukaryota), Unclassified (Unclassified Animal Kingdom)